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Evaluating Heuristics and Crowding on Center Selection in K-Means Genetic Algorithms

by

William McGarvey (wm305@nova.edu)

A dissertation report submitted in partial fulfillment of the requirements

for the degree of Doctor of Philosophy

in

Computer Information Systems

Graduate School of Computer and Information Sciences

Nova Southeastern University

2014

We hereby certify that this dissertation, submitted by William McGarvey, conforms to acceptable standards and is fully adequate in scope and quality to fulfill the dissertation requirements for the degree of Doctor of Philosophy.

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Graduate School of Computer and Information Sciences
Nova Southeastern University

2014

An Abstract of a Dissertation Report submitted to Nova Southeastern University in Partial Fulfillment of the Requirements for the Degree of Doctor Of Philosophy in Computer Information Systems

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Data clustering involves partitioning data points into clusters where data points within the same cluster have high similarity, but are dissimilar to the data points in other clusters. The k-means algorithm is among the most extensively used clustering techniques. Genetic algorithms (GA) have been successfully used to evolve successive generations of cluster centers. The primary goal of this research was to develop improved GA-based methods for center selection in k-means by using heuristic methods to improve the overall fitness of the initial population of chromosomes along with crowding techniques to avoid premature convergence. Prior to this research, no rigorous systematic examination of the use of heuristics and crowding methods in this domain had been performed.

The evaluation included computational experiments involving repeated runs of the genetic algorithm in which values that affect heuristics or crowding were systematically varied and the results analyzed. Genetic algorithm performance under the various configurations was analyzed based upon (1) the fitness of the partitions produced, and by (2) the overall time it took the GA to converge to good solutions. Two heuristic methods for initial center seeding were tested: Density and Separation. Two crowding techniques were evaluated on their ability to prevent premature convergence: Deterministic and Parent Favored Hybrid local tournament selection.

Based on the experiment results, the Density method provides no significant advantage over random seeding either in discovering quality partitions or in more quickly evolving better partitions. The Separation method appears to result in an increased probability of the genetic algorithm finding slightly better partitions in slightly fewer generations, and to more quickly converge to quality partitions. Both local tournament selection techniques consistently allowed the genetic algorithm to find better quality partitions than roulette-wheel sampling. Deterministic selection consistently found better quality partitions in fewer generations than Parent Favored Hybrid. The combination of Separation center seeding and Deterministic selection performed better than any other combination, achieving the lowest mean best SSE value more than twice as often as any other combination. On all 28 benchmark problem instances, the combination identified solutions that were at least as good as any identified by extant methods.

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Chapter 1

Introduction

Background

Data clustering involves partitioning data points into clusters where data points within the same cluster have high similarity, but are dissimilar to the data points in other clusters. Similarity is assessed using specific attribute value(s). Similarity is often measured with distance, where two or more objects are deemed to belong to the same cluster if they are close based upon the distance metric used. Clustering has wide applications in pattern recognition, statistics, data-mining, and machine learning.

Because of its computational efficiency the k-means algorithm is among the most extensively used clustering techniques. Given a set of data points $\{x_1,...,x_n\}$ in d-dimensional space and an integer *k*, the k-means algorithm attempts to partition the data points into *k* partitions (clusters) C_1,..., C_k such that the sum of the squared Euclidean distance (SSE) between each data point and the centroid of its cluster is minimized. SSE is defined as $\sum_{i=1}^{k}\sum_{j=1}^{n_i}\left\|x_{ji}-c_i\right\|^2$ where n_i is the number of data points in cluster C_i, x_{ji} is the jth data point in cluster C_i, and $c_i = \frac{1}{n_i}\sum_{j=1}^{n_i} x_{ji}$ is the centroid for cluster C_i. The algorithm starts with an initial set of *k* points, called centers. Partitions are formed by assigning data points to their closest center. Centers are then moved to the centroid of their partition, and data points are again assigned to their closest center. This process iterates until partitions are stable.

The k-means algorithm is an appropriate clustering technique under certain conditions:

1. The number of clusters is assumed to be known. This is because the algorithm does not determine the number of clusters, but instead assigns data points to a pre-defined number of clusters *k*.
2. K-means performs better when the data points in a cluster exhibit a Gaussian distribution in all directions about the cluster's centroid. In such a distribution, the density of data points is greater in areas near the centroid than in other areas of the data set space.
3. The *k* cluster centroids are well-separated from each other in the data set space, based upon the distance metric used.

Problem Statement

One drawback of k-means is that it is extremely sensitive to the initial choice of centers. While k-means will always terminate with a partition, different choices of initial cluster centers usually result in different partitions. Because of the algorithm's sensitivity, when random selection is used to choose initial centers, it is likely that k-means will produce partitions that are quite inferior to the global optimum. Finding a better method for initial center seeding is an active area of research.

To increase the likelihood of finding good k-partitions, genetic algorithms (GA), which are modeled after the process of natural evolution, have been successfully used to evolve successive generations of cluster centers. A classical problem of genetic algorithms is premature convergence. This occurs when there is not enough genetic diversity in the population of chromosomes. Through repeated selection pressure, the genes of a few closely related but less than optimal chromosomes can eventually dominate the gene pool, resulting in the GA becoming stuck on a local maximum and unable to explore better solutions.

Dissertation Goal

The goal of this research was to develop improved GA-based methods for center selection in k-means by investigating alternative initial center seeding strategies, and to empirically investigate factors that affect the rate of convergence to good quality partitions. Specifically, the research empirically investigated the merits of using:

1. alternative initialization strategies to introduce good centers and more quickly evolve better partitions,
2. techniques to prevent premature convergence, and
3. combinations of these strategies and techniques.

The alternative center seeding strategies were separately evaluated both with and without the use of techniques to prevent premature convergence. The evaluations employed synthetic data sets and also benchmark data sets previously used in other studies. The strategies and techniques were evaluated based upon (1) the fitness of the partitions produced as measured by their SSE, (2) the relative center seeding time cost as measured by percentage of overall execution time, and (3) the number of generations necessary to converge to good solutions. Evaluation factors included the fitness of partitions at convergence and the number of iterations necessary to converge.

Research Questions

Specific questions that this research addressed included:

1. Does the use of alternative strategies for selecting the initial population improve the rate of convergence to good quality partitions, thus providing an improved GA-based method for center selection in k-means, or does their use exacerbate premature convergence? Alternatively, does the additional execution time cost of implementing such strategies negate any benefit? Are the

benefits of alternative strategies affected by the degree of conformance to the k-means appropriateness conditions?

2. Are there effective techniques to reduce the risk of premature convergence? Is one technique better than others, in general, at mitigating premature convergence, or does effectiveness vary by configuration? Can inferences be made as to the circumstances under which a particular technique would be preferable?
3. What, if any, are the specific combinations of strategies and techniques that, on average, produce better partitions in fewer generations for each of the test configurations? Are there specific combinations that provide good quality solutions across all configurations? Does the analysis support general guidance regarding the specific combinations to employ based upon data characteristics or *k* values?

Relevance and Significance

Random selection is the method most often used by genetic algorithms for seeding the initial population of centers. As noted earlier, when random selection is used to choose initial centers, it is likely that k-means will produce partitions that are quite inferior to the global optimum. By evaluating the merits of alternative initialization strategies to more quickly evolve better partitions, the research provides new and useful information relevant to the development of improved GA-based methods for center seeding in k-means.

In traditional genetic algorithms, individuals are selected to pass to the next generation based upon their fitness without regard to their similarity to each other (Mengshoel & Goldberg, 2008). For example, roulette-wheel sampling with replacement will probabilistically select the most fit chromosomes regardless of genetic similarity. This method does nothing to prevent highly similar, highly fit chromosomes from dominating the population, leading to premature convergence. By evaluating the use of techniques to reduce the likelihood of premature convergence, new and useful information has been gained regarding the effectiveness of specific techniques, and the configurations and circumstances under which a particular technique might be employed.

Barriers and Issues

As an alternative to random selection, the approach to improve center selection was to use heuristic methods in genetic algorithms to seed the initial set of centers. Under the assumption that the data set space is appropriate for k-means as described above, the following heuristics were used:

1. A cluster center in an area of the data set space that is more densely populated with data points is preferred over one that is in a less densely populated area. This is based on the assumption that there is a higher probability that optimal centers will be located in regions of the data set space that are denser with data points. This heuristic will hereinafter be called the Density heuristic.
2. Cluster centers representing the genes of a chromosome are preferred to be as far as possible from each other. This is based on the given assumption that cluster centers are well separated. When a chromosome's cluster centers have greater separation and span more of the data set space, the probability of a center being in close proximity to an optimal cluster center is increased. This heuristic will hereinafter be called the Separation heuristic.

By using heuristics to improve the overall fitness of the initial population of chromosomes, it was hoped that genetic algorithms would more quickly converge to good quality solutions. This might not, however, have been the case for a couple of reasons. First, the time cost of using heuristic methods might negate any benefits of quicker convergence. Second, by limiting the diversity of selected genes, heuristics might increase the likelihood of premature convergence.

To reduce the effect of premature convergence, the local tournament algorithms deterministic crowding and probabilistic crowding were used as an alternative to roulette-wheel sampling which, as noted earlier, does nothing to prevent premature convergence. The deterministic crowding and probabilistic crowding algorithms are closely related. Both involve one-on-one tournaments where competition for survival is localized between a parent and a child. To minimize the distance measure between parent and child, both deterministic and probabilistic crowding use the genetic algorithm's selection and variance operators to implicitly create parent versus child match ups. The main difference between the algorithms are their replacement rules. With deterministic crowding, stronger, more fit individuals will always win out over weaker ones, whereas with probabilistic crowding, the probability that stronger chromosomes will win is proportional to their greater fitness. When deterministic and probabilistic crowding select chromosomes through local tournaments between genetically similar parents and offspring, the most fit of these individuals will probabilistically or deterministically be chosen for survival. This helps maintain a population of diverse solutions.

Genetic algorithms must carefully navigate the tradeoffs between search intensification and diversification. This research investigated the potential of using heuristics to improve the overall fitness of the population of chromosomes along with crowding techniques to avoid premature convergence to provide an improved GA-based method for center selection in k-means. Prior to this research, no rigorous systematic examination of the use of heuristics and crowding methods in this domain had been performed.

Chapter 2

Review of the Literature

Improved initial center selection in k-means, the use of genetic algorithms to improve k-means clustering, and crowding techniques to slow down convergence in genetic algorithms are the major areas of research that serve as the foundation and motivation for the proposed research. Each of these areas will be reviewed in this chapter, preceded by a general overview of clustering methods.

Data Clustering Methods

Data clustering attempts to organize data points into individual groups or a hierarchy of groups by abstracting an underlying structure. Data clustering makes no use of prior categorizations of data (the data is not pre-labeled), which distinguishes data clustering from discriminant analysis. Discriminant analysis employs supervised classification in which a collection of labeled, pre-classified data points are used to label newly encountered, unlabeled ones. In contrast, data clustering attempts to group given unlabeled data points into meaningful clusters where data points within the same cluster have high similarity, but are dissimilar to those in other clusters. Thus, in data clustering, defining similarity and specifying how to measure it are crucial tasks. The variety of techniques available to address these tasks has resulted in a wide assortment of clustering methods.

Attempts have been made to classify clustering methods, such as (Jain & Dubes, 1988), (Jain, Murty & Flynn, 1999), and (Xu & Wunsch, 2005). A common classification taxonomy makes a top level distinction between hierarchical and partitioned clustering methods. Hierarchical clustering methods produce a dendrogram in which multiple partitions are organized in a nested hierarchical series, while partitioned methods produce a single partition.

Hierarchical Clustering

Hierarchical clustering algorithms are further classified in Xu and Wunsch (2005) as either agglomerative or divisive. Agglomerative clustering starts with each cluster containing only one data point. A succession of merge operations follows until all data points are in one cluster or the stopping criteria are satisfied. In contrast, divisive clustering methods begin with all data points belonging to one cluster. Clusters are successively divided until all clusters contain only one data point or the stopping criteria is met.

There are many hierarchical agglomerative clustering algorithms and they typically differ in their definition of distance. According to (Jain, Murty & Flynn, 1999), the two most popular hierarchical agglomerative clustering methods are single-link and complete link algorithms. The two methods are similar in that both merge a pair clusters together to form a larger cluster based on a minimum distance similarity criteria. Also, both methods will determine the distance between a pair of clusters by measuring the distance between all pairs of data points drawn from the two clusters, drawing one data point from each cluster. They differ in the way the distance between a cluster pair is specified and measured. In single-link algorithms, this distance is based on the *minimum* of all pairwise distances between data points, while in complete-link algorithms the *maximum* distance is used. In contrast to single-link and complete link algorithms, which consider all data points in measuring inter-cluster distance, geometric clustering methods use the distance between cluster *centers* to represent inter-cluster distance (Xu & Wunsch, 2005).

The computational complexity in most hierarchical clustering algorithms is quite high and limits their applicability in large-scale data sets. To address this limitation, some hierarchical data clustering techniques have attempted to reduce computational complexity and improve performance. Examples cited in Xu and Wunsch include CURE (Guha, Rastogi, & Shim,1998), ROCK (Guha, Rastogi, & Shim, 2000) , Chameleon (Karypis, Han, & Kumar, 1999) and BIRCH (Zhang, Ramakrishnan, & Livny, 1996).

Partitioned Clustering

Partitioned clustering methods will typically determine similarity based upon an optimizing function that is applied locally over a subset of data points or globally over all of them. Examples of partitioned clustering methods include squared error algorithms, graph-theoretic algorithms, mixture-resolving algorithms, and nearest neighbor algorithms.

Squared error algorithms use SSE as the optimizing function where similarity is based on minimum SSE. The k-means algorithm is the most popular of these algorithms. Another example is the ISO-DATA (Ball & Hall, 1965) algorithm that permits splitting and merging of clusters. Clusters are merged when the distances between their centroids are less than a specified threshold and split when their variances exceed it.

Graph-theoretic algorithms construct a minimal spanning tree of the data points and then delete the edges having the greatest distance. Clusters are the subgraphs of the minimal spanning tree that are also connected components.

Mixture-resolving algorithms assume that clusters conform to one of several probability distributions, and finding clusters is equivalent to identifying the parameters of each distribution. A common approach for identifying these parameters is maximum likelihood (ML) estimation which considers the best estimate the one that has the highest probability of generating all of the data points. According to (Xu & Wunsch, 2005), the most popular ML method is the expectation-maximization (EM) algorithm which generates a series of parameter estimates.

Nearest neighbor algorithms assign unassigned data points to the cluster of its nearest assigned neighbor if the distance to this neighbor is within a threshold. This process continues until all data points are assigned to clusters or no additional data points can be assigned.

Fuzzy Clustering

A cross-cutting distinction can be made between firm and fuzzy clustering methods. A firm clustering method assigns a data point to no more than one cluster at any given time. A fuzzy clustering method can assign a data point to multiple clusters. Typically, a fuzzy clustering algorithm will use a membership function to determine the probability that any given point belongs to any given cluster. Thus, a data point would be assigned to all clusters except those where its probability of membership was zero.

An example of a fuzzy squared error algorithm is fuzzy c-means (Dunn, 1974 and Bezdek, 1981). Fuzzy c-means uses a membership function based upon the distance between a data point and a cluster center to determine the probability of cluster membership such that the summation of membership of each data point equals one. Let u_{ij} represent the probability of cluster membership of x_i, the *i*th data point, in the *j*th cluster. Then $u_{ij} = 1/\sum_{h=1}^{k}\left(d_{ij}/d_{ih}\right)^{\left(\frac{2}{m-1}\right)}$ where:

- k is the number of clusters,
- m is the fuzziness index, $m \in [1, \infty]$, and
- d_{ij} is the Euclidean distance between data point x_i and c_j, the center of the jth cluster.

The cluster membership probabilities of every data point/cluster pairing form a $n \times c$ matrix U where n is the number of data points.

After the initial cluster centers are selected and the initial matrix U^0 is formed, the c-means algorithm will iteratively perform the following steps:

1. For iteration q, reposition the cluster centers using matrix U^q and the formula $c_j = \left(\sum_{i=1}^{n}(u_{ij})^m x_i\right)/\left(\sum_{i=1}^{n}(u_{ij})^m\right), \forall j = 1,2,\dots k$ where n is the number of data points.
2. Update the cluster membership probability of each data point/cluster pair using the repositioned cluster centers and the membership function to form matrix U^{q+1}.
3. If the minimum value of the objective function $J(U,C) = \sum_{i=1}^{n}\sum_{j=1}^{k}(u_{ij})^m \|x_i - c_j\|^2$ is achieved or if $\|U^{q+1} - U^q\| < \varepsilon$ where ε is the termination value between 0 and 1, then the algorithm stops. Otherwise, it begins the next iteration.

According to (Jain, Murty & Flynn, 1999), fuzzy c-means does a better job of avoiding convergence to a local minimum than the firm k-means algorithm.

Initial Center Selection in K-Means

As noted by Bradley and Fayyad (1998, p.92), while random selection is the de facto standard method for choosing the initial cluster centers in k-means, it is not a good one. Finding a better method, however, has proven to be elusive, although several approaches have been proposed that utilize, at least to some extent, the Separation and Density heuristics. Examples of approaches that utilize the Separation heuristic include the Simple Cluster-Seeking (SCS) method (Tou &Gonzales,1974) which ensures that each center selected exceeds a user-defined distance from the other centers. Also, the KKZ algorithm (Katsavounidis, Kuo, & Zhang,1994) begins by choosing as the first cluster center a data point near the boundaries of the data set space. Subsequent centers are chosen by selecting the point that is furthest from its nearest center.

Methods for initial center selection that employ the Density heuristic include the Cluster Center Initialization Method (CCIA) of Khan and Ahmad (2004) which first sorts the data points based on an estimate of the data density around each point. The point at the top of the list is selected as the first cluster center and all points within a radius inversely proportional to the density of that point are pruned. The highest remaining point on the list is then selected as the next cluster center and the process is repeated until *k* centers are selected. Also, Daoud and Roberts (1996) proposed dividing the data set space into disjoint subspaces and assigning cluster centers to the subspaces based on the density of points within them.

The KD-Density Algorithm

Of special note is the *kd*-density algorithm (Redmond & Heneghan, 2005) which uses both Density and Separation heuristics to seed k-means with initial cluster centers. The algorithm begins by conceptually enclosing all the data points within a bounding box whose extrema are the minimum and maximum data point coordinates in each dimension. The box is then split at the median data point coordinate along the longest dimension, resulting in two sub-boxes. This splitting of boxes continues recursively until only leaf boxes remain. A leaf box is a box meeting a pre-determined criteria, such as containing no more than *n* data points. This collection of boxes is called a *kd*-tree. Note that although the number of data points in leaf boxes will be roughly the same, the coordinate-space volume of the boxes will vary significantly. In general, boxes whose data points are more densely packed will have smaller volumes.

Let L_j denote the jth leaf box, let N_j denote the number of data points in L_j, let m_j denote the mean value of the data points in L_j, and let V_j denote its volume. Let the density p_j of L_j be defined as $p_j = N_j/V_j$. Then the *kd*-density algorithm is as follows:

> *Create a kd-tree as described above for the given data points.*
> *Determine the rank density $\widehat{p_j}$ of each leaf box L_j (higher density → higher rank) and discard the 20% of leaf boxes with the lowest rank density.*
> *Calculate m_j for each L_j.*
> *Select m_z as the initial cluster center c_1 where L_z has the highest rank density.*
> *Do for $t = 2,....,k$ where k is the number of cluster centers {*
>
> > *For each m_j not selected as a cluster center, evaluate $g_j = d_j \times \widehat{p_j}$ where d_j denotes the shortest distance from m_j to the closest center already chosen.*
> > *Select the next center $c_t = m_x$ where x is the argument of $max_j(g_j)$.*

}
Proceed with the standard k-means algorithm.

Note that the first cluster center is chosen solely based on the Density heuristic, while the remaining centers are chosen based upon both Density and Separation heuristics.

Using synthetic data sets with each data set containing *k* Gaussian clusters, the authors compared the performance of the *kd*-density algorithm against the best results of 15 runs of the k-means algorithm where initial cluster centers were chosen uniformly at random. The *kd*-density algorithm returned a lower SSE value for 12 of the 36 data sets and in 495 of the 540 runs. The *kd*-density algorithm returned higher SSE values for 5 of the data sets and in only six runs.

The K-means++Algorithm

In motivating the proposed research, the k-means++ (Arthur & Vassilvitskii, 2007) algorithm, which employs the Separation heuristic, deserves mention. Under the assumption that it is preferable for the initial set of cluster centers to be well separated from each other, k-means++ selects these centers using the following algorithm:

Select a data point t_1 uniformly at random from T, the set of data points in the data set, as the initial cluster center c_1.
Do until the remaining $k-1$ cluster centers are chosen {
Without replacement choose a data point t_i uniformly at random from T.
Select the next center c_i, selecting $c_i = t_i$ as the next cluster center with probability $d(t_i)^2 \big/ \sum_{t \in T} d(t)^2$ where $d(t)$ denotes the shortest distance from data point t to the closest center already chosen.
}
Proceed with the standard k-means algorithm.

The authors use induction to show that k-means++ is $O(\log k)$ competitive with the optimal k-clustering on any given data set. More specifically, for a given data set with *k* clusters, let $\mathrm{SSE}_{\mathrm{OPT}}$ denote the SSE of the optimal partition, and let C denote the set of initial cluster centers. If C is selected with the k-means++ algorithm, then the corresponding SSE satisfies $(\mathrm{SSE} - \mathrm{SSE}_{\mathrm{OPT}}) \leq$

$8(\ln k + 2)SSE_{OPT}$. Further, using both synthetic and real-world data sets, the authors reported preliminary experiments where k-means++ consistently outperformed k-means in both accuracy (lower SSE) and speed (faster run time). Although the selection of initial centers with k-means++ is slower than with random selection, convergence occurs in fewer iterations resulting in a faster algorithm.

Because k-means++ chooses the first cluster center at random and probabilistically chooses the others based upon their distance from previously selected centers, k-means++ could be used by a genetic algorithm to select a diverse initial population of cluster centers. Using a deterministic algorithm such as *kd*-density for this task would result in a population of clones.

Genetic Algorithms for K-Means

Early efforts to employ GA methods to improve k-means clustering include (Babu & Murty, 1993) where encouraging results, in most cases, were reported on small data sets having well separated clusters. Later, Demiriz, Bennett, and Embrechts (1999) developed a genetic algorithm and a modified k-means objective function that also produced good clusters. The genetic k-means algorithm (GKA) reported in (Krishna & Murty, 1999) used a biased mutation operator and almost always converged to a globally optimal partition for small problem instances. GKA proved to be the inspiration for FGKA (a fast genetic k-means algorithm) which, as its name implies, was faster than GKA (Lu, Lu, Fotouhi, Deng, & Brown, 2004). Other attempts to use genetic algorithms to obtain good partitions under k-means were reported in (Pena, Lozano, & Larranaga, 1999), (Maulik & Bandyopadhyay, 2000), and (Bandyopadhyay & Maulik, 2002).

These early GA-based efforts typically employed crossover operations that swapped randomly selected subsets of centers between parents. This crossover method impeded the passing on of good subsets of centers between parents and offspring. Using a novel crossover operator that exchanges neighboring centers, (Laszlo & Mukherjee, 2006) presented a genetic algorithm for k-means clustering that identified superior partitions in low-dimensional data sets. However, because of a chromosomal representation that grows exponentially with increasing dimension, this method is limited to small data sets and low dimensional data.

The Laszlo and Mukherjee (2007) Genetic Algorithm

A significant motivator of the proposed research, the genetic algorithm presented in (Laszlo & Mukherjee, 2007) addressed the limitations of earlier genetic algorithms by employing a crossover operator that exchanges subsets of centers occupying the same area of data set space, under the premise that center selection is, to a significant extent, spatially decomposable. This crossover method is computationally inexpensive and scales well into higher-dimensional search spaces.

A chromosome containing k genes is represented as a set of k cluster centers. Upon initialization, an initial population of chromosomes is created by randomly selecting data points to serve as cluster centers. Because the crossover operation may produce offspring whose k values (number of genes) differ from their parents, the fitness of a chromosome is not determined by its partition's SSE value, but by a scaled fitness value.

To obtain scaled fitness values, chromosomes are segregated into subpopulations based upon their k value. A chromosome's partition is then determined by running k-means on its k centers until partition stability is achieved. Should this result in a useless center (it is not the closest center of any data point), the useless center is discarded and replaced by a random point. The raw SSE value of a chromosome's partition is subtracted from the SSE of the entire data set and linearly scaled such that the maximum scaled fitness in any subpopulation is f times the average scaled fitness of the subpopulation. An f value of 1.8 was used for the paper's reported results.

For a subpopulation with x number of chromosomes, roulette-wheel sampling with replacement is used to select x chromosomes from that subpopulation to go into the mating buffer. The probability of a chromosome being selected is proportional to its scaled fitness value. In the mating buffer, chromosomes are randomly paired. A chromosome pair will have a probability p of undergoing crossover.

For each crossover operation, a random point and a random vector are generated. A $(d-1)$-dimensional hyperplane is created that contains the random point and is normal to the random vector. The region of hyperspace bounded by this hyperplane and lying on its positive side becomes the crossover region. A crossover operation involves a chromosome pair swapping those centers which are contained in the crossover region. Because the number of centers contained in the crossover region of one member of a pair may be different than the number contained in the other member of the pair, new k-value subpopulations could result.

In addition to selection and crossover, mutation and replacement also occur with each generation. Regarding mutation, there is a low probability, called the mutation probability, that any given center within any chromosome could be replaced by a random data point. As for replacement, if a parent generation chromosome exists within a subpopulation that is more fit than every offspring in that subpopulation, this chromosome will replace a randomly chosen offspring chromosome.

Both benchmark and simulated data sets were used to evaluate the performance of the GA. Four data sets for which best known partitions had previously been published, German Town Data (GTD), British Town Data (BTD), TSP-LIB-1060, and TSP-LIB-3038, were employed for the benchmark experiments. The BTD data set has dimensionality of four, while the dimensionality of the other three data sets is two. The GA was also evaluated on four simulated data sets of higher, yet differing, dimensionality. The dimensions used were 10, 20, 50, and 100. The four data sets each contained 10,000 points and 50 randomly selected cluster centers. Each cluster center had 200 surrounding data points and was well separated from the others.

Computational experiment results indicate that the GA repeatedly found optimal partitions for the GTD and BTD data sets within a few generations. For the TSP-LIB-1060 and TSP-LIB-3838 data sets, the SSE of the best partitions found by the GA were compared to those reported in (Laszlo and Mukherjee, 2006) and (Hansen and Mladenovic, 2001). Results indicated that, in every instance, the GA identified solutions that were at least as good as the best partitions reported, and in many instances better. Reported results with the simulated data sets show the probably optimal partitions were identified by the GA within the first 20 generations in 10 consecutive runs.

With regard to motivating future research, it should be noted that the objective of genetic algorithms for k-means is to obtain good partitions containing *k* centers. In this light, it does not appear beneficial that the GA produces partitions with *k* values that differ from this number. Also, the GA chooses initial centers at random. Perhaps selection methods more biased toward Density and Separation heuristics would prove more advantageous to search intensification without sacrificing necessary diversification.

Crowding Techniques and Local Tournament Algorithms

As a means of slowing down convergence in genetic algorithms, crowding techniques strive to maintain diverse solutions by replacing population members with members that are similar to them. Crowding is inspired by the ecological phenomenon in which similar individuals in a natural population, such as a species, occupy the same environmental niche and therefore must compete against each other for resources. When a niche reaches its carrying capacity, weaker members of the niche are crowded out by the stronger ones.

An early crowding technique, preselection, was introduced by Cavicchio in 1970 (Mahfoud, 1995). Cavicchio contended that a replacement strategy that required comparing the fitness of an entire population was too computationally expensive. Instead, a preselection scheme was proposed whereby a child would replace its most inferior parent.

In 1975, the *crowding factor algorithm* was presented by De Jong (Mahfoud, 1995) in which members of the new generation replace similar members of the existing population. In this algorithm, a proportion of the existing population is selected using fitness criteria to undergo crossover and mutation, producing a new generation. For each offspring, a sample of *n* members of the existing population is taken (where *n* is the *crowding factor*) and the most similar member is replaced by the offspring.

Local tournament algorithms are a type of crowding technique in which similar members compete directly against each other for survival. One example is the *gene-invariant genetic algorithm* (GIGA), presented in (Culberson, 1992), where parents produce two pair of offspring. The offspring pairs compete against each other in a local tournament and the winning pair replaces their parents.

Another local tournament algorithm, *restricted tournament selection* (Harik, 1995), requires each new offspring to compete for survival against the most similar member of a sample of *w* members (where *w* is the *window size*) of the existing population. In (Mahfoud & Goldberg, 1995), two local tournament algorithms were introduced in which parent and child directly compete for survival. In *double acceptance and rejection*, both parents compete against both children in a single tournament and either the parents or the children survive. In *single acceptance and rejection*, each parent competes against a pre-determined child in two separate competitions.

The winners of local tournaments can be decided either deterministically or probabilistically, and both have been found to work well as crowding techniques (Mengshoel & Goldberg, 2008). Deterministic crowding (Mahfoud, 1995) implements the deterministic crowding replacement rule in which the parent p and child c compete in a deterministic tournament. With the deterministic crowding replacement rule, the probability $P(c)$ of an offspring winning the local tournament with fitness $f(c)$, where f is the SSE fitness function, over the parent with fitness $f(p)$ is:

$$P(c) = \begin{cases} 1 \; if \; f(c) > f(p) \\ \frac{1}{2} \; if \; f(c) = f(p) \\ 0 \; if \; f(c) < f(p) \end{cases}$$

Thus, with deterministic crowding, the most fit chromosome will always win out and go into the mating buffer.

Probabilistic crowding (Mengshoel and Goldberg, 1999) implements the probabilistic crowding replacement rule in which the parent p and child c compete in a probabilistic tournament. The probability $P(c)$ of c winning is:

$$P(c) = {f(c)}\Big/{f(c) + f(p)}$$

where f is the SSE fitness function. Thus, the probability that the most fit chromosomes will win and go into the mating buffer is proportional to their greater fitness.

Chapter 3

Methodology

Overview

The proposed research involved developing (1) a genetic algorithm that enabled the heuristic methods and crowding techniques to be evaluated, both independently and in combination; (2) algorithms to implement the heuristic methods of seeding initial centers; and (3) an implementation of the crowding techniques. Additional detail on each of these topics is provided in the subsections below, followed by descriptions of the test data sets and the experimental design.

The Genetic Algorithm

The genetic algorithm developed for the investigations was based on the genetic algorithm presented in (Laszlo & Mukherjee, 2007). There were several reasons for this. First, the Laszlo and Mukherjee GA has demonstrated an ability to find good partitions. Computational experiment results indicate that the GA repeatedly found known optimal partitions for small data sets and also for large data sets with well separated clusters. For high dimensionality data sets, reported results show the probably optimal partitions were identified by the GA within the first 20 generations in 10 consecutive runs. Also, with other benchmark data sets, the GA consistently identified the best known solutions. Second, the GA employs k-means as an operator to move centers, and implements region-based crossover. Prior studies by Laszlo and Mukherjee (2006, 2007) have shown these techniques to be advantageous. Region-based crossover also creates parent and child similarities that facilitate the use of local tournament algorithms. Third, random selection is employed for initial selection of cluster centers. As such, the Laszlo and Mukherjee GA provides a solid performance baseline with which heuristic methods can be compared.

The GA developed for these investigations, hereinafter referred to as the GA, accepts the following inputs:

T	the set of data points
k	number of cluster centers
z	number of chromosomes in initial population
p_1	proportion of chromosomes in initial population selected via Density algorithm
p_2	proportion of chromosomes in initial population selected via Separation algorithm
p_3	proportion of chromosomes in initial population selected at random
C	method for selecting chromosomes to go into the mating buffer
Pm	probability of mutation
Pc	probability of crossover
G	number of generations to execute before termination

Below is a high-level representation of the genetic algorithm program. Additional detail is provided in the subsections that follow.

begin
Do until z *chromosomes are selected {*
　　Select $z(p_1)$ *chromosomes using Density algorithm*
　　Select $z(p_2)$ *chromosomes using Separation algorithm*
　　Select $z(p_3)$ *chromosomes at random*
}
Move initial z *chromosomes to child buffer*
Do for G *generations {*
　　Do for each chromosome in child buffer {
　　　　Run k-means until partition stability is achieved
　　　　Determine fitness (SSE value)
　　}
　　If parent buffer not empty and if fittest parent chromosome is more fit than every chromosome in child buffer, Then {
　　　　Replace random chromosome in child buffer with fittest parent chromosome
　　}
　　Use method C *to select* z *chromosomes for mating buffer*
　　Randomly pair chromosomes in mating buffer

Do for each chromosome pair {
With probability Pc perform crossover
}
Do for each chromosome in mating buffer {
Do for each cluster center {
With probability Pm perform mutation
}
}
Move chromosomes in child buffer to parent buffer
Move chromosomes in mating buffer to child buffer
}
end

Initialization

The GA represents a chromosome containing k genes as a set of k cluster centers. An initial population of chromosomes is created by seeding each chromosome with k data points to serve as initial centers. The genetic algorithm has three methods available for seeding initial centers: the Density heuristic algorithm, the Separation heuristic algorithm, and random selection. Let p_1, p_2, and p_3 represent the proportion of chromosomes in the initial population created using the Density algorithm, the Separation algorithm, and random selection, respectively. Input parameters p_1, p_2, and p_3 specify the proportion of the initial population to be determined by each method such that $p_1 + p_2 + p_3 = 1$.

Selection

Each generation the genetic algorithm determines a chromosome's partition by running k-means on its k centers until partition stability is achieved. Useless centers are discarded and replaced by randomly chosen data points. The SSE of the resulting partition is used to measure a chromosome's fitness, with smaller SSEs representing greater fitness. A chromosome's fitness value is used in the selection of chromosomes to pass from one generation to the next. For a population with z number of chromosomes, z chromosomes are selected to go into the mating buffer. To select these chromosomes, either local tournaments or roulette-wheel sampling with replacement are used, as discussed below.

Crossover

In the mating buffer, chromosomes are randomly paired for crossover. A chromosome pair has a probability Pc of undergoing crossover, where Pc is the crossover probability. A crossover operation involves a chromosome pair swapping those centers which are contained in the crossover region. To determine the crossover region, a point and a vector are chosen uniformly at random. A $(d-1)$-dimensional hyperplane is created that contains the point and is normal to the vector. The region of hyperspace bounded by this hyperplane and lying on its positive side becomes the crossover region.

Members of a crossover pair could differ in the number of centers contained in the crossover region. In this event, should the centers be simply swapped, neither of the offspring chromosomes would have k centers, and new k-value subpopulations would result. To ensure offspring have exactly k centers, the genetic algorithm swaps x centers in a crossover operation, where x is the number of centers in the crossover region of the member of the crossover pair having the fewest centers in the crossover region. Thus, x centers residing in the crossover region of the member having the most centers in the crossover region are selected at random for crossover.

Mutation and replacement

In addition to selection and crossover, mutation could also occur with each generation. When mutation occurs, one of a chromosome's centers is replaced by a random data point. With a low probability of Pm, any given cluster center of any given chromosome could undergo mutation.

Density Algorithm

As noted earlier, the *kd*-density algorithm (Redmond & Heneghan, 2005) is a deterministic algorithm. For any given data set, the algorithm will always choose the same set of initial cluster centers. For this reason, it would be inappropriate to use the *kd*-algorithm to select an initial population of cluster centers since this would result in a population of clones. To implement the Density heuristic for initial center seeding, an algorithm that increases the probability that initial centers are chosen from denser regions of the data set space is required. This algorithm, called the Density algorithm, is as follows:

Do until k cluster centers are chosen {
Select a data point t uniformly at random from T, the set of data points in the data set.
Select a radius of length r such that r equals the n/k closest data point to t where n denotes the total number of data points.
Determine the density D_t of the area of space with radius r about t.
Select data point t as a cluster center with proportional probability $D_t/(D_t + D_T)$ where D_T denotes the density of the data set space.
}

Data point density for an area of data set space is defined as the number of data points within the data set space divided by the area of the space. The area of the data set space is defined as the area of a circle whose radius length is the distance between the centroid of the data set space and its furthest data point within the data set space. To select an initial center, the algorithm chooses a data point t at random. The probability of t being selected is proportional to the relative data point density of the area of space with radius r about t where r is the distance between t and its n/k closest data point.

Determining the density of the area of space around point t is the significant computational cost of the Density algorithm since, to determine the data points that lie within this space, the distance between t and each of the data points in the data set must be computed. The cost of finding the distance between two points is proportional to the dimensionality of the data. Note that the k-means operator must also determine the distance between a cluster center and each of the data points in the data set, and it does so iteratively until partition stability is achieved. Thus, the storage cost of the Density algorithm is no more than running k-means. Because the average probability of t being selected as a cluster center is 50%, and, on average, the number of iterations in k-means is greater than two, the computational cost of the Density algorithm is typically less than running k-means on the same population.

Separation Algorithm

To implement the Separation heuristic for initial center seeding, an algorithm is used that increases the probability that the initial centers chosen for a chromosome are well separated from each other. This algorithm, called the Separation algorithm, employs the k-means++ seeding algorithm (Arthur & Vassilvitskii, 2007) that is described by its authors as fast, simple, and O(log *k*)-competitive with the optimal clustering. The Separation algorithm is as follows:

> *Select a data point t_1 uniformly at random from T, the set of data points in the data set, as the initial cluster center c_1.*
> *Do until the remaining $k-1$ cluster centers are chosen {*
> *Without replacement choose a data point t_i uniformly at random from T.*
> *Select the next center c_i, selecting $c_i = t_i$ as the next cluster center with probability $d(t_i)^2 \big/ \sum_{t \in T} d(t)^2$ where $d(t)$ denotes the shortest distance from data point t to the closest center already chosen.*
> *}*

The significant computational cost of the Separation algorithm involves determining the distance between each point in T and a cluster center. This is performed $k-1$ times for each chromosome. Since the k-means operator must iteratively determine the distance between the k

cluster centers and each of the data points in the data set, the storage cost of the Separation algorithm is no more than running k-means on the same population, and the computational cost is less.

Selection Techniques

The genetic algorithm, based upon parameter C, uses either roulette-wheel sampling with replacement or local tournament algorithms as methods for selecting chromosomes to go into the mating buffer. Roulette-wheel sampling with replacement, also known as fitness proportionate selection, is a common selection method for genetic algorithms and was used in these evaluations as a baseline against which the local tournament algorithms were compared. With fitness proportionate selection, if f_i is the fitness of chromosome i, its selection probability is $p_i = \frac{f_i}{\sum_{j=1}^{N} f_j}$ where N is the number of chromosomes.

For this GA, roulette-wheel selection odds are determined by ranking chromosomes according to their fitness, from most fit to least. In the event there exists a chromosome *c* in the prior generation that is more fit than every chromosome in the new population, then *c* would replace a chromosome randomly chosen and would be ranked as the most fit. The number of chances for selection of the most fit chromosome equals the number of chromosomes. The number of selection chances for each successive chromosome in the ranking is incrementally decremented by one such that the least fit chromosome has one chance of selection. If R_i is the number of selection chances of chromosome i, then the fitness of chromosome i is $f_i = R_i$.

The other selection techniques are implemented in single acceptance and rejection local tournaments where each chromosome in the current generation competes with its most similar parent. Similarity between a parent and child is achieved implicitly through the crossover operator that exchanges subsets of centers. In this operation, parents produce offspring whose centers differ only within a subset of the data space. Similarity is determined by the number of common cluster centers.

For example, if a child chromosome contained seven centers, two of which were recently obtained through the crossover operation, then it would compete with the parent with whom it had five centers in common. In the case where no parent exists, the chromosome enters the mating buffer by default.

Preliminary testing was conducted to identify local tournament algorithms with good performance potential. Of the four algorithms tested, two algorithms, deterministic crowding and a hybrid deterministic/probabilistic crowding technique, found significantly better partitions than roulette-wheel sampling and were used in the evaluations. Deterministic crowding implements the deterministic crowding replacement rule as earlier described. The hybrid deterministic/probabilistic crowding technique, which has been named Parent Favored Hybrid (PFH), employs both replacement rules. First, a deterministic local tournament is conducted between each parent and child. If the parent wins, the parent goes into the mating buffer. Otherwise, the probabilistic crowding replacement rule is used to determine whether the parent or child enters the mating buffer. Additional information on the preliminary testing is provided in the Preliminary Tests section of this chapter.

Experiment Design

An experiment is a test of a specific combination of data set, *k* value, center seeding method, and selection technique. Experiments were designed to fully evaluate the alternative center seeding methods and local tournament algorithms. Important to this design was testing that included specific configuration elements:

1. Experiments using configurations that conformed to the three k-means appropriateness conditions were conducted to evaluate the advantages of using alternative center seeding methods in environments that conform to their underlying assumptions.

2. Testing with configurations that only partially conformed to the k-means appropriateness conditions was included to evaluate the extent that the use of alternative center seeding methods provided benefits in such environments.
3. Experiments using data that conforms to none of the k-means appropriateness assumptions and has no well defined clusters for any value of *k* were conducted to determine what benefit alternative center seeding methods would provide in this environment.
4. Testing with benchmark configurations was performed to compare experiment results with published information on current best-known partitions.
5. Testing with data of high dimensionality was performed since clustering applications typically involve high dimensional data.

Experiments were conducted with both synthetic and benchmark data sets. Three synthetic data sets were used. For each of the synthetic data sets, 200 data points were generated to exhibit a Gaussian distribution with a standard deviation of one about each of 50 generated cluster centers. The distance between generated cluster centers is consistent within each data set, but varies across them. The first data set, SYN1, has cluster centers separated by eight standard deviations, thus clusters are well separated and do not overlap. SYN1 conforms to all three k-means appropriateness conditions. The other two synthetic data sets were generated with overlapping centers. SYN2 has generated cluster centers separated by three standard deviations and some of a generated cluster's data points overlap with those of adjacent clusters. SYN3 has generated cluster centers separated by one standard deviation such that all of a generated cluster's data points overlap with those of other clusters.

Experiments were also conducted using two benchmark data sets for which best known partitions have previously been published for different values of *k*. TSP-LIB-1060 and TSP-LIB-

3038, originally generated to research the traveling salesman problem, do not have well defined clusters for any value of *k*.

The combination of data sets and k-values enabled an evaluation of the alternative center seeding methods and local tournament selection techniques over a variety of conditions. Table 3.1 details the key elements of each test data set. Table 3.2 contains a list of problem instances (a data set/*k*-value configuration) on which experiments were conducted in this evaluation.

Table 3.1: Key Elements of Test Data Sets

Data set	Number of data points	Meets k-means appropriateness conditions	Benchmark data	Dimensionality of data
TSP-LIB-1060	1,060	No	Yes	2
TSP-LIB-3038	3,038	No	Yes	2
SYN1	10,000	Yes	No	50
SYN2	10,000	Partially	No	50
SYN3	10,000	Partially	No	50

Table 3.2: List of Problem Instances

Data set	Values of *k* used	# of problem instances
TSP-LIB-1060	10, 20, 30, 50, 60, 70, 70, 90, 100, 110, 120, 130, 140, 150	14
TSP-LIB-3038	10, 20, 30, 40, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500	14
SYN1	50	1
SYN2	50	1
SYN3	50	1

Data Analysis

The data analysis involved correlating the genetic algorithm configuration (initial center seeding method(s), selection technique) and the data set configuration with evaluation results (partition fitness as measured by mean best SSE, relative center seeding time cost as measured by mean percentage of overall elapsed time, and the mean number of generations necessary for convergence). To determine the statistical significance of the results, *t* tests were used. Results that exceeded the alpha value of p = 0.02 (two tailed) are not considered significant.

To obtain mean values, an experiment involved at least 10 runs of the GA. In order to allow sufficient time for convergence, a run would not terminate until the last 100 generations resulted in no improvement on the best (least) SSE value. Values of parameters not under test remained constant throughout a problem instance. The problem instances utilized a population size μ of either 100 or 200 chromosomes, a crossover percentage P_c of either 80% or 100%, and a mutation rate P_m of 0.001.

Preliminary Tests

Preliminary tests were conducted with four local tournament algorithms to determine which ones demonstrated good potential in mitigating premature convergence and would be included in the evaluation. Results were considered good when, on average and in comparison with roulette-wheel sampling with replacement, significantly better partitions were found. The tests were conducted with the TSP-LIB-1060 data set and a *k* value of 100 because the genetic algorithm, using roulette-wheel sampling with replacement, exhibited evidence of premature convergence with this configuration. Specifically, after multiple runs of the GA, the same partition was not found as the best partition in every run. The four local tournament algorithms tested were deterministic crowding, probabilistic crowding, and two deterministic/probabilistic hybrid crowding techniques. The deterministic crowding and probabilistic crowding algorithms were described earlier. The first hybrid, named Child Favored Hybrid (CFH), conducts a deterministic local tournament between each parent and child. If the child wins, the child goes into the mating buffer. Otherwise, the probabilistic crowding replacement rule is used in a local tournament to determine whether the parent or child enters the mating buffer. The other hybrid deterministic/probabilistic crowding technique, named Parent Favored Hybrid (PFH), also employs both replacement rules. First, a deterministic local tournament is conducted between each parent and child. A probabilistic local tournament is then held only if the parent fails to win the deterministic local tournament. Otherwise, the parent goes into the mating buffer.

To obtain mean values and standard deviations, each test configuration involved 10 runs of the GA. In order to allow sufficient time for convergence, a run would not terminate until the last 100 generations resulted in no improvement on the best (least) SSE value. Values of parameters not under test remained constant throughout all experiments. The experiments utilized random center seeding, a population size μ of 200 chromosomes, a crossover percentage P_c of 80%, and a mutation rate P_m of 0.001. A 3.1 GHz AMD Athlon II X2 255 processor with 5 GB memory was used to run the experiments. Individual run results are shown in Appendix A, and a summary of the results is provided in Table 3.3.

Table 3.3: Summary of Preliminary Test Results

	Roulette-Wheel	**Probabilistic**	**Deterministic**	**CFH**	**PFH**
Best SSE (all runs)	9.6549E+07	1.0363E+08	9.6318E+07	1.0090E+08	9.6413E+07
Mean Best SSE	9.6584E+07	1.0484E+08	9.6371E+07	1.0261E+08	9.6393E+07
Standard Deviation	8.7649E+04	7.9433E+05	4.1121E+04	8.6743E+05	2.4020E+04
Variance	7.6823E+09	6.3095E+11	1.6909E+09	7.5243E+11	5.7696E+08
Value of *t*		-30.986[1]	6.593[1]	-20.853[1]	6.313[1]

1. *t* significant at p<0.001 (two tail)

The best SSE value represents the best SSE value found from all of the GA runs in that configuration. The mean best SSE value is the mean of the best SSE values found in each GA run of the configuration. The mean best SSE value of each local tournament algorithm was compared to the mean best SSE value of roulette-wheel sampling. To determine the statistical significance of the results, two-tailed *t* tests were used. The mean best SSE values of the deterministic crowding algorithm and the Parent Favored Hybrid algorithm were both significantly better than that of roulette-wheel sampling. Their *t*-test scores are statistically significant at $p<0.001$. The mean SSE values of the probabilistic crowding algorithm and the Child Favored Hybrid algorithm were both significantly worse than that of roulette-wheel sampling. Their *t*-test scores are statistically significant at $p<0.001$.

It is speculated that the deterministic crowding algorithm and the Parent Favored Hybrid algorithm perform better than the other two local tournament algorithms because in both of these algorithms parent chromosomes are never replaced with less fit child chromosomes. Thus, after n generations, a parent chromosome represents the most fit chromosome out of n deterministic local tournaments. In the other two algorithms, a chromosome, regardless of its fitness, will probably not remain in the gene pool very long since every generation it would have had to survive possible elimination in probabilistic local tournaments.

Chapter 4

Results

For each problem instance (data set/*k*-value configuration), nine experiments were conducted where each of the three center seeding methods were paired with each of the three selection techniques. For each such configuration, the results of the experiments are summarized in a table below. Individual run results are shown in Appendix A.

In the tables, the mean best SSE and mean generations until convergence values for each experiment are shown along with their percentage improvement over the Random/Roulette-Wheel experiment. The mean generations until convergence value is the mean generation the best SSE value was found. The chromosomes that resulted from initial seeding are considered generation zero.

Also, for each data set configuration, the mean best SSE and mean generations until convergence values are shown for each seeding method and selection technique along with their percentage improvement over the Random seeding method and Roulette-Wheel selection technique results, respectively. These values were obtained by averaging the respective values obtained from the three experiments conducted with each method and technique.

The genetic algorithm used in this research was not developed to achieve new best known k-means clustering solutions, but rather to evaluate center seeding methods and selection techniques. However, to investigate whether these methods and techniques improve upon extant methods, the best known result obtained from (Laszlo and Mukherjee, 2007) for different *k* values using data sets TSP-LIB-1060 and TSP-LIB-3038 is compared with the best result of each experiment in that configuration. In the tables, Proportion Improved expresses the proportion of the runs that improved upon the best known solution, and Error represents the difference between the best solution SSE and the best known SSE expressed as a percentage of the best known SSE.

Table 4.01: TSP-LIB-1060, k = 10, μ = 100, P_c = 100%, Runs = 10

Mean Best SSE and Mean Generations Until Convergence by Experiment

Experiment	Mean Best SSE	Improv. over Random/ RW	Generations until Convergence	Improv. over Random/ RW
Random, Roulette-Wheel	1.75484E+09	0.00%	2.9	0.00%
Separation, Roulette-Wheel	1.75484E+09	0.00%	4.1	-41.38%
Density, Roulette-Wheel	1.75484E+09	0.00%	4.3	-48.28%
Random, Deterministic	1.75484E+09	0.00%	6.1	-110.34%
Separation, Deterministic	1.75484E+09	0.00%	6.4	-120.69%
Density, Deterministic	1.75484E+09	0.00%	5	-72.41%
Random, Parent Favored Hybrid	1.75484E+09	0.00%	8.6	-196.55%
Separation, Parent Favored Hybrid	1.75484E+09	0.00%	9.3	-220.69%
Density, Parent Favored Hybrid	1.75484E+09	0.00%	8.8	-203.45%

Mean Best SSE by Center Seeding Method and Selection Technique

Seeding Method	Mean Best SSE	Improv. over Random	Selection Technique	Mean Best SSE	Improv. over RW
Random	1.75484E+09	0.00%	Roulette-Wheel	1.75484E+09	0.00%
Density	1.75484E+09	0.00%	Deterministic	1.75484E+09	0.00%
Separation	1.75484E+09	0.00%	Parent Favored Hybrid	1.75484E+09	0.00%

Mean Generations until Convergence by Center Seeding Method and Selection Technique

Seeding Method	Generations until Convergence	Improv. over Random	Selection Technique	Generations until Convergence	Improv. over RW
Random	5.87	0.00%	Roulette-Wheel	3.77	0.00%
Separation	6.60	-12.50%	Deterministic	5.83	-54.87%
Density	6.03	-2.84%	Parent Favored Hybrid	8.90	-136.28%

Best Known SSE (found in 200 generations): 1.7548E+09

Experiment	Best SSE	Gen. Found	Error	Proportion Improved
Random/Roulette-Wheel	1.75484E+09	1	0.00%	0%
Separation/Roulette-Wheel	1.75484E+09	2	0.00%	0%
Density/Roulette-Wheel	1.75484E+09	3	0.00%	0%
Random/Deterministic	1.75484E+09	3	0.00%	0%
Separation/Deterministic	1.75484E+09	0	0.00%	0%
Density/Deterministic	1.75484E+09	1	0.00%	0%
Random/Parent Favored Hybrid	1.75484E+09	4	0.00%	0%
Separation/Parent Favored Hybrid	1.75484E+09	4	0.00%	0%
Density/Parent Favored Hybrid	1.75484E+09	0	0.00%	0%

Table 4.02: TSP-LIB-1060, k = 20, μ = 100, P_c = 100%, Runs = 10

Mean Best SSE and Mean Generations Until Convergence by Experiment

Experiment	Mean Best SSE	Improv. over Random/ RW	Generations until Convergence	Improv. over Random/ RW
Random, Roulette-Wheel	7.91795E+08	0.00%	27.8	0.00%
Separation, Roulette-Wheel	7.91797E+08	0.00%	37.3	-34.17%
Density, Roulette-Wheel	7.91795E+08	0.00%	29.7	-6.83%
Random, Deterministic	7.91795E+08	0.00%	31.6	-13.67%
Separation, Deterministic	7.91795E+08	0.00%	28.6	-2.88%
Density, Deterministic	7.91795E+08	0.00%	29.5	-6.12%
Random, Parent Favored Hybrid	7.91795E+08	0.00%	56.7	-103.96%
Separation, Parent Favored Hybrid	7.91795E+08	0.00%	51.1	-83.81%
Density, Parent Favored Hybrid	7.91795E+08	0.00%	52	-87.05%

Mean Best SSE by Center Seeding Method and Selection Technique

Seeding Method	Mean Best SSE	Improv. over Random	Selection Technique	Mean Best SSE	Improv. over RW
Random	7.91795E+08	0.00%	Roulette-Wheel	7.91795E+08	0.00%
Density	7.91795E+08	0.00%	Deterministic	7.91795E+08	0.00%
Separation	7.91795E+08	0.00%	Parent Favored Hybrid	7.91795E+08	0.00%

Mean Generations until Convergence by Center Seeding Method and Selection Technique

Seeding Method	Generations until Convergence	Improv. over Random	Selection Technique	Generations until Convergence	Improv. over RW
Random	38.70	0.00%	Roulette-Wheel	31.60	0.00%
Separation	39.00	-0.78%	Deterministic	29.90	5.38%
Density	37.07	4.22%	Parent Favored Hybrid	53.27	-68.57%

Best Known SSE (found in 200 generations): 7.91794E+08

Experiment	Best SSE	Gen. Found	Error	Proportion Improved
Random/Roulette-Wheel	7.91795E+08	14	0.00%	0%
Separation/Roulette-Wheel	7.91795E+08	9	0.00%	0%
Density/Roulette-Wheel	7.91795E+08	11	0.00%	0%
Random/Deterministic	7.91795E+08	20	0.00%	0%
Separation/Deterministic	7.91795E+08	13	0.00%	0%
Density/Deterministic	7.91795E+08	23	0.00%	0%
Random/Parent Favored Hybrid	7.91795E+08	28	0.00%	0%
Separation/Parent Favored Hybrid	7.91795E+08	39	0.00%	0%
Density/Parent Favored Hybrid	7.91795E+08	33	0.00%	0%

Table 4.03: TSP-LIB-1060, k = 30, μ = 100, P_c = 100%, Runs = 10

Mean Best SSE and Mean Generations Until Convergence by Experiment

Experiment	Mean Best SSE	Improv. over Random/ RW	Generations until Convergence	Improv. over Random/ RW
Random, Roulette-Wheel	4.81394E+08	0.00%	79.4	0.00%
Separation, Roulette-Wheel	4.81343E+08	0.01%	88.9	-11.96%
Density, Roulette-Wheel	4.81410E+08	0.00%	93.1	-17.25%
Random, Deterministic	4.81252E+08	0.03%	116.8	-47.10%
Separation, Deterministic	4.81252E+08	0.03%	91.2	-14.86%
Density, Deterministic	4.81265E+08	0.03%	112.6	-41.81%
Random, Parent Favored Hybrid	4.81256E+08	0.03%	164.6	-107.30%
Separation, Parent Favored Hybrid	4.81266E+08	0.03%	149.7	-88.54%
Density, Parent Favored Hybrid	4.81266E+08	0.03%	187.8	-136.52%

Mean Best SSE by Center Seeding Method and Selection Technique

Seeding Method	Mean Best SSE	Improv. over Random	Selection Technique	Mean Best SSE	Improv. over RW
Random	4.81301E+08	0.00%	Roulette-Wheel	4.81382E+08	0.00%
Density	4.81314E+08	0.00%	Deterministic	4.81256E+08	0.03%
Separation	4.81287E+08	0.00%	Parent Favored Hybrid	4.81263E+08	0.02%

Mean Generations until Convergence by Center Seeding Method and Selection Technique

Seeding Method	Generations until Convergence	Improv. over Random	Selection Technique	Generations until Convergence	Improv. over RW
Random	120.27	0.00%	Roulette-Wheel	87.13	0.00%
Separation	109.93	8.59%	Deterministic	106.87	-22.65%
Density	131.17	-9.06%	Parent Favored Hybrid	167.37	-92.08%

Best Known SSE (found in 200 generations): 4.81251E+08

Experiment	Best SSE	Gen. Found	Error	Proportion Improved
Random/Roulette-Wheel	4.81252E+08	234	0.00%	0%
Separation/Roulette-Wheel	4.81257E+08	55	0.00%	0%
Density/Roulette-Wheel	4.81252E+08	125	0.00%	0%
Random/Deterministic	4.81252E+08	70	0.00%	0%
Separation/Deterministic	4.81252E+08	61	0.00%	0%
Density/Deterministic	4.81252E+08	72	0.00%	0%
Random/Parent Favored Hybrid	4.81252E+08	99	0.00%	0%
Separation/Parent Favored Hybrid	4.81252E+08	100	0.00%	0%
Density/Parent Favored Hybrid	4.81252E+08	130	0.00%	0%

Table 4.04: TSP-LIB-1060, k = 50, μ = 100, P_c = 100%, Runs = 10

Mean Best SSE and Mean Generations Until Convergence by Experiment				
Experiment	**Mean Best SSE**	**Improv. over Random/ RW**	**Generations until Convergence**	**Improv. over Random/ RW**
Random, Roulette-Wheel	2.56001E+08	0.00%	101.2	0.00%
Separation, Roulette-Wheel	2.55910E+08	0.04%	145	-43.28%
Density, Roulette-Wheel	2.55956E+08	0.02%	123	-21.54%
Random, Deterministic	2.55779E+08	0.09%	161.5	-59.58%
Separation, Deterministic	2.55705E+08	0.12%	197.8	-95.45%
Density, Deterministic	2.55744E+08	0.10%	179.1	-76.98%
Random, Parent Favored Hybrid	2.55776E+08	0.09%	250.7	-147.73%
Separation, Parent Favored Hybrid	2.55637E+08	0.14%	265.2	-162.06%
Density, Parent Favored Hybrid	2.55738E+08	0.10%	297.7	-194.17%

Mean Best SSE by Center Seeding Method and Selection Technique					
Seeding Method	**Mean Best SSE**	**Improv. over Random**	**Selection Technique**	**Mean Best SSE**	**Improv. over RW**
Random	2.55852E+08	0.00%	Roulette-Wheel	2.55956E+08	0.00%
Density	2.55813E+08	0.02%	Deterministic	2.55743E+08	0.08%
Separation	2.55751E+08	0.04%	Parent Favored Hybrid	2.55717E+08	0.09%

Mean Generations until Convergence by Center Seeding Method and Selection Technique					
Seeding Method	**Generations until Convergence**	**Improv. over Random**	**Selection Technique**	**Generations until Convergence**	**Improv. over RW**
Random	171.13	0.00%	Roulette-Wheel	123.07	0.00%
Separation	202.67	-18.43%	Deterministic	179.47	-45.83%
Density	199.93	-16.83%	Parent Favored Hybrid	271.20	-120.37%

Best Known SSE (found in 200 generations): 2.55509E+08				
Experiment	**Best SSE**	**Gen. Found**	**Error**	**Proportion Improved**
Random/Roulette-Wheel	2.55566E+08	36	0.02%	0%
Separation/Roulette-Wheel	2.55592E+08	51	0.03%	0%
Density/Roulette-Wheel	2.55545E+08	125	0.01%	0%
Random/Deterministic	2.55592E+08	221	0.03%	0%
Separation/Deterministic	2.55514E+08	213	0.00%	0%
Density/Deterministic	2.55510E+08	211	0.00%	0%
Random/Parent Favored Hybrid	2.55553E+08	317	0.02%	0%
Separation/Parent Favored Hybrid	2.55510E+08	228	0.00%	0%
Density/Parent Favored Hybrid	2.55534E+08	360	0.01%	0%

Table 4.05: TSP-LIB-1060, k = 60, μ = 100, P_c = 100%, Runs = 10

Mean Best SSE and Mean Generations Until Convergence by Experiment				
Experiment	**Mean Best SSE**	**Improv. over Random/ RW**	**Generations until Convergence**	**Improv. over Random/ RW**
Random, Roulette-Wheel	1.98254E+08	0.00%	213.7	0.00%
Separation, Roulette-Wheel	1.98087E+08	0.08%	178.9	16.28%
Density, Roulette-Wheel	1.98103E+08	0.08%	215.7	-0.94%
Random, Deterministic	1.97816E+08	0.22%	273.8	-28.12%
Separation, Deterministic	1.97465E+08	0.40%	241.9	-13.20%
Density, Deterministic	1.97761E+08	0.25%	260.4	-21.85%
Random, Parent Favored Hybrid	1.97969E+08	0.14%	429.7	-101.08%
Separation, Parent Favored Hybrid	1.97708E+08	0.28%	324.4	-51.80%
Density, Parent Favored Hybrid	1.97849E+08	0.20%	396.4	-85.49%

Mean Best SSE by Center Seeding Method and Selection Technique					
Seeding Method	**Mean Best SSE**	**Improv. over Random**	**Selection Technique**	**Mean Best SSE**	**Improv. over RW**
Random	1.98013E+08	0.00%	Roulette-Wheel	1.98148E+08	0.00%
Density	1.97904E+08	0.06%	Deterministic	1.97681E+08	0.24%
Separation	1.97753E+08	0.13%	Parent Favored Hybrid	1.97842E+08	0.15%

Mean Generations until Convergence by Center Seeding Method and Selection Technique					
Seeding Method	**Generations until Convergence**	**Improv. over Random**	**Selection Technique**	**Generations until Convergence**	**Improv. over RW**
Random	305.73	0.00%	Roulette-Wheel	202.77	0.00%
Separation	248.40	18.75%	Deterministic	258.70	-27.59%
Density	290.83	4.87%	Parent Favored Hybrid	383.50	-89.13%

Best Known SSE (found in 200 generations): 1.97273E+08				
Experiment	**Best SSE**	**Gen. Found**	**Error**	**Proportion Improved**
Random/Roulette-Wheel	1.97848E+08	318	0.29%	0%
Separation/Roulette-Wheel	1.97582E+08	244	0.16%	0%
Density/Roulette-Wheel	1.97768E+08	336	0.25%	0%
Random/Deterministic	1.97273E+08	320	0.00%	0%
Separation/Deterministic	1.97273E+08	246	0.00%	0%
Density/Deterministic	1.97273E+08	325	0.00%	0%
Random/Parent Favored Hybrid	1.97855E+08	482	0.30%	0%
Separation/Parent Favored Hybrid	1.97273E+08	409	0.00%	0%
Density/Parent Favored Hybrid	1.97273E+08	614	0.00%	0%

Table 4.06: TSP-LIB-1060, k = 70, μ = 100, P_c = 100%, Runs = 10

Mean Best SSE and Mean Generations Until Convergence by Experiment

Experiment	Mean Best SSE	Improv. over Random/ RW	Generations until Convergence	Improv. over Random/ RW
Random, Roulette-Wheel	1.58672E+08	0.00%	180	0.00%
Separation, Roulette-Wheel	1.58663E+08	0.01%	173.5	3.61%
Density, Roulette-Wheel	1.58583E+08	0.06%	186.2	-3.44%
Random, Deterministic	1.58524E+08	0.09%	224.7	-24.83%
Separation, Deterministic	1.58475E+08	0.12%	223.8	-24.33%
Density, Deterministic	1.58506E+08	0.10%	240.9	-33.83%
Random, Parent Favored Hybrid	1.58527E+08	0.09%	397	-120.56%
Separation, Parent Favored Hybrid	1.58503E+08	0.11%	384.2	-113.44%
Density, Parent Favored Hybrid	1.58551E+08	0.08%	359	-99.44%

Mean Best SSE by Center Seeding Method and Selection Technique

Seeding Method	Mean Best SSE	Improv. over Random	Selection Technique	Mean Best SSE	Improv. over RW
Random	1.58574E+08	0.00%	Roulette-Wheel	1.58639E+08	0.00%
Density	1.58547E+08	0.02%	Deterministic	1.58501E+08	0.09%
Separation	1.58547E+08	0.02%	Parent Favored Hybrid	1.58527E+08	0.07%

Mean Generations until Convergence by Center Seeding Method and Selection Technique

Seeding Method	Generations until Convergence	Improv. over Random	Selection Technique	Generations until Convergence	Improv. over RW
Random	267.23	0.00%	Roulette-Wheel	179.90	0.00%
Separation	260.50	2.52%	Deterministic	229.80	-27.74%
Density	262.03	1.95%	Parent Favored Hybrid	380.07	-111.27%

Best Known SSE (found in 200 generations): 1.58450E+08

Experiment	Best SSE	Gen. Found	Error	Proportion Improved
Random/Roulette-Wheel	1.58513E+08	96	0.04%	0%
Separation/Roulette-Wheel	1.58477E+08	296	0.02%	0%
Density/Roulette-Wheel	1.58458E+08	148	0.00%	0%
Random/Deterministic	1.58477E+08	253	0.02%	0%
Separation/Deterministic	1.58453E+08	259	0.00%	0%
Density/Deterministic	1.58477E+08	227	0.02%	0%
Random/Parent Favored Hybrid	1.58477E+08	473	0.02%	0%
Separation/Parent Favored Hybrid	1.58477E+08	315	0.02%	0%
Density/Parent Favored Hybrid	1.58477E+08	548	0.02%	0%

Table 4.07: TSP-LIB-1060, k = 80, μ = 100, P_c = 100%, Runs = 10

Mean Best SSE and Mean Generations Until Convergence by Experiment				
Experiment	**Mean Best SSE**	**Improv. over Random/ RW**	**Generations until Convergence**	**Improv. over Random/ RW**
Random, Roulette-Wheel	1.28971E+08	0.00%	290	0.00%
Separation, Roulette-Wheel	1.29025E+08	-0.04%	237.3	18.17%
Density, Roulette-Wheel	1.29072E+08	-0.08%	273.1	5.83%
Random, Deterministic	1.29021E+08	-0.04%	290.7	-0.24%
Separation, Deterministic	1.28914E+08	0.04%	238.4	17.79%
Density, Deterministic	1.28994E+08	-0.02%	318.8	-9.93%
Random, Parent Favored Hybrid	1.29014E+08	-0.03%	440.7	-51.97%
Separation, Parent Favored Hybrid	1.28998E+08	-0.02%	397.1	-36.93%
Density, Parent Favored Hybrid	1.29142E+08	-0.13%	377.6	-30.21%

Mean Best SSE by Center Seeding Method and Selection Technique					
Seeding Method	**Mean Best SSE**	**Improv. over Random**	**Selection Technique**	**Mean Best SSE**	**Improv. over RW**
Random	1.29002E+08	0.00%	Roulette-Wheel	1.29023E+08	0.00%
Density	1.29069E+08	-0.05%	Deterministic	1.28977E+08	0.04%
Separation	1.28979E+08	0.02%	Parent Favored Hybrid	1.29051E+08	-0.02%

Mean Generations until Convergence by Center Seeding Method and Selection Technique					
Seeding Method	**Generations until Convergence**	**Improv. over Random**	**Selection Technique**	**Generations until Convergence**	**Improv. over RW**
Random	340.47	0.00%	Roulette-Wheel	266.80	0.00%
Separation	290.93	14.55%	Deterministic	282.63	-5.93%
Density	323.17	5.08%	Parent Favored Hybrid	405.13	-51.85%

Best Known SSE (found in 200 generations): 1.28890E+08				
Experiment	**Best SSE**	**Gen. Found**	**Error**	**Proportion Improved**
Random/Roulette-Wheel	1.28891E+08	520	0.00%	0%
Separation/Roulette-Wheel	1.28892E+08	486	0.00%	0%
Density/Roulette-Wheel	1.28891E+08	320	0.00%	0%
Random/Deterministic	1.28890E+08	339	0.00%	0%
Separation/Deterministic	1.28890E+08	218	0.00%	0%
Density/Deterministic	1.28890E+08	339	0.00%	0%
Random/Parent Favored Hybrid	1.28906E+08	508	0.01%	0%
Separation/Parent Favored Hybrid	1.28890E+08	375	0.00%	0%
Density/Parent Favored Hybrid	1.29021E+08	470	0.10%	0%

Table 4.08: TSP-LIB-1060, k = 90, μ = 100, P_c = 100%, Runs = 10

Mean Best SSE and Mean Generations Until Convergence by Experiment

Experiment	Mean Best SSE	Improv. over Random/ RW	Generations until Convergence	Improv. over Random/ RW
Random, Roulette-Wheel	1.10711E+08	0.00%	383.5	0.00%
Separation, Roulette-Wheel	1.10757E+08	-0.04%	286.1	25.40%
Density, Roulette-Wheel	1.10828E+08	-0.11%	322.3	15.96%
Random, Deterministic	1.10531E+08	0.16%	419.7	-9.44%
Separation, Deterministic	1.10507E+08	0.18%	366.6	4.41%
Density, Deterministic	1.10538E+08	0.16%	449.1	-17.11%
Random, Parent Favored Hybrid	1.10573E+08	0.12%	672.4	-75.33%
Separation, Parent Favored Hybrid	1.10537E+08	0.16%	551.6	-43.83%
Density, Parent Favored Hybrid	1.10588E+08	0.11%	599.1	-56.22%

Mean Best SSE by Center Seeding Method and Selection Technique

Seeding Method	Mean Best SSE	Improv. over Random	Selection Technique	Mean Best SSE	Improv. over RW
Random	1.10605E+08	0.00%	Roulette-Wheel	1.10765E+08	0.00%
Density	1.10651E+08	-0.04%	Deterministic	1.10525E+08	0.22%
Separation	1.10600E+08	0.00%	Parent Favored Hybrid	1.10566E+08	0.18%

Mean Generations until Convergence by Center Seeding Method and Selection Technique

Seeding Method	Generations until Convergence	Improv. over Random	Selection Technique	Generations until Convergence	Improv. over RW
Random	491.87	0.00%	Roulette-Wheel	330.63	0.00%
Separation	401.43	18.39%	Deterministic	411.80	-24.55%
Density	456.83	7.12%	Parent Favored Hybrid	607.70	-83.80%

Best Known SSE (found in 200 generations): 1.10417E+08

Experiment	Best SSE	Gen. Found	Error	Proportion Improved
Random/Roulette-Wheel	1.10475E+08	602	0.05%	0%
Separation/Roulette-Wheel	1.10503E+08	237	0.08%	0%
Density/Roulette-Wheel	1.10520E+08	358	0.09%	0%
Random/Deterministic	1.10479E+08	403	0.06%	0%
Separation/Deterministic	1.10454E+08	332	0.03%	0%
Density/Deterministic	1.10479E+08	483	0.06%	0%
Random/Parent Favored Hybrid	1.10488E+08	751	0.06%	0%
Separation/Parent Favored Hybrid	1.10436E+08	1002	0.02%	0%
Density/Parent Favored Hybrid	1.10488E+08	576	0.06%	0%

Table 4.09: TSP-LIB-1060, $k = 100$, $\mu = 200$, $P_c = 80\%$, Runs = 20

Mean Best SSE and Mean Generations Until Convergence by Experiment

Experiment	Mean Best SSE	Improv. over Random/RW	Generations until Convergence	Improv. over Random/RW
Random, Roulette-Wheel	9.65327E+07	0.00%	307.7	0.00%
Separation, Roulette-Wheel	9.64952E+07	0.04%	326	-5.93%
Density, Roulette-Wheel	9.64986E+07	0.04%	323	-4.96%
Random, Deterministic	9.63755E+07	0.16%	427.9	-39.06%
Separation, Deterministic	9.63408E+07	0.20%	432.8	-40.64%
Density, Deterministic	9.63855E+07	0.15%	501.1	-62.85%
Random, Parent Favored Hybrid	9.63861E+07	0.15%	701.1	-127.85%
Separation, Parent Favored Hybrid	9.63833E+07	0.15%	604.2	-96.34%
Density, Parent Favored Hybrid	9.64362E+07	0.10%	718.3	-133.44%

Mean Best SSE by Center Seeding Method and Selection Technique

Seeding Method	Mean Best SSE	Improv. over Random	Selection Technique	Mean Best SSE	Improv. over RW
Random	9.64314E+07	0.00%	Roulette-Wheel	9.65088E+07	0.00%
Separation	9.64064E+07	0.03%	Deterministic	9.63673E+07	0.15%
Density	9.64401E+07	-0.01%	Parent Favored Hybrid	9.64019E+07	0.11%

Mean Generations until Convergence by Center Seeding Method and Selection Technique

Seeding Method	Generations until Convergence	Improv. over Random	Selection Technique	Generations until Convergence	Improv. over RW
Random	478.9	0.00%	Roulette-Wheel	318.9	0.00%
Separation	454.3	5.14%	Deterministic	453.9	-42.35%
Density	514.1	-7.35%	Parent Favored Hybrid	674.5	-111.54%

Best Known SSE (found in 200 generations): 9.63303E+07

Experiment	Best SSE	Gen. Found	Error	Proportion Improved
Random/Roulette-Wheel	9.63646E+07	313	0.04%	0%
Separation/Roulette-Wheel	9.63303E+07	458	0.00%	0%
Density/Roulette-Wheel	9.63477E+07	483	0.02%	0%
Random/Deterministic	9.63179E+07	505	-0.01%	10%
Separation/Deterministic	9.63179E+07	437	-0.01%	30%
Density/Deterministic	9.63303E+07	577	0.00%	0%
Random/Parent Favored Hybrid	9.63382E+07	855	0.01%	0%
Separation/Parent Favored Hybrid	9.63179E+07	773	-0.01%	10%
Density/Parent Favored Hybrid	9.63900E+07	895	0.06%	0%

Table 4.10: TSP-LIB-1060, k = 110, μ = 100, P_c = 100%, Runs = 10

Mean Best SSE and Mean Generations Until Convergence by Experiment

Experiment	Mean Best SSE	Improv. over Random/ RW	Generations until Convergence	Improv. over Random/ RW
Random, Roulette-Wheel	8.51712E+07	0.00%	448.8	0.00%
Separation, Roulette-Wheel	8.51099E+07	0.07%	441.6	1.60%
Density, Roulette-Wheel	8.51556E+07	0.02%	436.5	2.74%
Random, Deterministic	8.48959E+07	0.32%	505.9	-12.72%
Separation, Deterministic	8.49008E+07	0.32%	409.4	8.78%
Density, Deterministic	8.49209E+07	0.29%	476.9	-6.26%
Random, Parent Favored Hybrid	8.50391E+07	0.16%	667.6	-48.75%
Separation, Parent Favored Hybrid	8.49596E+07	0.25%	581.8	-29.63%
Density, Parent Favored Hybrid	8.49526E+07	0.26%	753.9	-67.98%

Mean Best SSE by Center Seeding Method and Selection Technique

Seeding Method	Mean Best SSE	Improv. over Random	Selection Technique	Mean Best SSE	Improv. over RW
Random	8.50354E+07	0.00%	Roulette-Wheel	8.51456E+07	0.00%
Density	8.50097E+07	0.03%	Deterministic	8.49058E+07	0.28%
Separation	8.49901E+07	0.05%	Parent Favored Hybrid	8.49838E+07	0.19%

Mean Generations until Convergence by Center Seeding Method and Selection Technique

Seeding Method	Generations until Convergence	Improv. over Random	Selection Technique	Generations until Convergence	Improv. over RW
Random	540.77	0.00%	Roulette-Wheel	442.30	0.00%
Separation	477.60	11.68%	Deterministic	464.07	-4.92%
Density	555.77	-2.77%	Parent Favored Hybrid	667.77	-50.98%

Best Known SSE (found in 200 generations): 8.48397E+07

Experiment	Best SSE	Gen. Found	Error	Proportion Improved
Random/Roulette-Wheel	8.48810E+07	864	0.05%	0%
Separation/Roulette-Wheel	8.48894E+07	499	0.06%	0%
Density/Roulette-Wheel	8.49759E+07	418	0.16%	0%
Random/Deterministic	8.48432E+07	688	0.00%	0%
Separation/Deterministic	8.48432E+07	579	0.00%	0%
Density/Deterministic	8.48494E+07	472	0.01%	0%
Random/Parent Favored Hybrid	8.48807E+07	891	0.05%	0%
Separation/Parent Favored Hybrid	8.48658E+07	573	0.03%	0%
Density/Parent Favored Hybrid	8.48728E+07	864	0.04%	0%

Table 4.11: TSP-LIB-1060, k = 120, μ = 100, P_c = 100%, Runs = 10

Mean Best SSE and Mean Generations Until Convergence by Experiment

Experiment	Mean Best SSE	Improv. over Random/ RW	Generations until Convergence	Improv. over Random/ RW
Random, Roulette-Wheel	7.58660E+07	0.00%	408.8	0.00%
Separation, Roulette-Wheel	7.59016E+07	-0.05%	449.7	-10.00%
Density, Roulette-Wheel	7.58217E+07	0.06%	482.4	-18.00%
Random, Deterministic	7.56909E+07	0.23%	519.9	-27.18%
Separation, Deterministic	7.56604E+07	0.27%	564.4	-38.06%
Density, Deterministic	7.56875E+07	0.24%	580.3	-41.95%
Random, Parent Favored Hybrid	7.57582E+07	0.14%	785.9	-92.25%
Separation, Parent Favored Hybrid	7.57579E+07	0.14%	674.7	-65.04%
Density, Parent Favored Hybrid	7.57243E+07	0.19%	876	-114.29%

Mean Best SSE by Center Seeding Method and Selection Technique

Seeding Method	Mean Best SSE	Improv. over Random	Selection Technique	Mean Best SSE	Improv. over RW
Random	7.57717E+07	0.00%	Roulette-Wheel	7.58631E+07	0.00%
Density	7.57445E+07	0.04%	Deterministic	7.56796E+07	0.24%
Separation	7.57733E+07	0.00%	Parent Favored Hybrid	7.57468E+07	0.15%

Mean Generations until Convergence by Center Seeding Method and Selection Technique

Seeding Method	Generations until Convergence	Improv. over Random	Selection Technique	Generations until Convergence	Improv. over RW
Random	571.53	0.00%	Roulette-Wheel	446.97	0.00%
Separation	562.93	1.50%	Deterministic	554.87	-24.14%
Density	646.23	-13.07%	Parent Favored Hybrid	778.87	-74.26%

Best Known SSE (found in 100 generations): 7.55451E+07

Experiment	Best SSE	Generation Found	Error	Proportion Improved
Random/Roulette-Wheel	7.56125E+07	455	0.09%	0%
Separation/Roulette-Wheel	7.56789E+07	298	0.18%	0%
Density/Roulette-Wheel	7.56524E+07	655	0.14%	0%
Random/Deterministic	7.56259E+07	434	0.11%	0%
Separation/Deterministic	7.56054E+07	785	0.08%	0%
Density/Deterministic	7.56176E+07	826	0.10%	0%
Random/Parent Favored Hybrid	7.56889E+07	903	0.19%	0%
Separation/Parent Favored Hybrid	7.56248E+07	713	0.11%	0%
Density/Parent Favored Hybrid	7.56145E+07	1034	0.09%	0%

Table 4.12: TSP-LIB-1060, k = 130, μ = 100, P_c = 100%, Runs = 10

Mean Best SSE and Mean Generations Until Convergence by Experiment				
Experiment	**Mean Best SSE**	**Improv. over Random/ RW**	**Generations until Convergence**	**Improv. over Random/ RW**
Random, Roulette-Wheel	6.78562E+07	0.00%	508.7	0.00%
Separation, Roulette-Wheel	6.78735E+07	-0.03%	463.1	8.96%
Density, Roulette-Wheel	6.78684E+07	-0.02%	568.3	-11.72%
Random, Deterministic	6.76683E+07	0.28%	510.3	-0.31%
Separation, Deterministic	6.76011E+07	0.38%	458	9.97%
Density, Deterministic	6.76495E+07	0.30%	528.6	-3.91%
Random, Parent Favored Hybrid	6.76631E+07	0.28%	821.2	-61.43%
Separation, Parent Favored Hybrid	6.76149E+07	0.36%	805.9	-58.42%
Density, Parent Favored Hybrid	6.77367E+07	0.18%	754.9	-48.40%

Mean Best SSE by Center Seeding Method and Selection Technique					
Seeding Method	**Mean Best SSE**	**Improv. over Random**	**Selection Technique**	**Mean Best SSE**	**Improv. over RW**
Random	6.77292E+07	0.00%	Roulette-Wheel	6.78660E+07	0.00%
Density	6.77515E+07	-0.03%	Deterministic	6.76396E+07	0.33%
Separation	6.76965E+07	0.05%	Parent Favored Hybrid	6.76716E+07	0.29%

Mean Generations until Convergence by Center Seeding Method and Selection Technique					
Seeding Method	**Generations until Convergence**	**Improv. over Random**	**Selection Technique**	**Generations until Convergence**	**Improv. over RW**
Random	613.40	0.00%	Roulette-Wheel	513.37	0.00%
Separation	575.67	6.15%	Deterministic	498.97	2.81%
Density	617.27	-0.63%	Parent Favored Hybrid	794.00	-54.67%

Best Known SSE (found in 100 generations): 6.75542E+07				
Experiment	**Best SSE**	**Generation Found**	**Error**	**Proportion Improved**
Random/Roulette-Wheel	6.76586E+07	686	0.15%	0%
Separation/Roulette-Wheel	6.76958E+07	599	0.21%	0%
Density/Roulette-Wheel	6.76638E+07	559	0.16%	0%
Random/Deterministic	6.75647E+07	506	0.02%	0%
Separation/Deterministic	6.75647E+07	529	0.02%	0%
Density/Deterministic	6.76015E+07	535	0.07%	0%
Random/Parent Favored Hybrid	6.75947E+07	827	0.06%	0%
Separation/Parent Favored Hybrid	6.75618E+07	1089	0.01%	0%
Density/Parent Favored Hybrid	6.75984E+07	835	0.07%	0%

Table 4.13: TSP-LIB-1060, k = 140, μ = 100, P_c = 100%, Runs = 10

Mean Best SSE and Mean Generations Until Convergence by Experiment

Experiment	Mean Best SSE	Improv. over Random/ RW	Generations until Convergence	Improv. over Random/ RW
Random, Roulette-Wheel	6.14595E+07	0.00%	524.6	0.00%
Separation, Roulette-Wheel	6.14120E+07	0.08%	509.1	2.95%
Density, Roulette-Wheel	6.16006E+07	-0.23%	401.2	23.52%
Random, Deterministic	6.11992E+07	0.42%	536	-2.17%
Separation, Deterministic	6.11742E+07	0.46%	558.6	-6.48%
Density, Deterministic	6.12030E+07	0.42%	560.6	-6.86%
Random, Parent Favored Hybrid	6.13066E+07	0.25%	789.2	-50.44%
Separation, Parent Favored Hybrid	6.12080E+07	0.41%	832.2	-58.64%
Density, Parent Favored Hybrid	6.12730E+07	0.30%	921.7	-75.70%

Mean Best SSE by Center Seeding Method and Selection Technique

Seeding Method	Mean Best SSE	Improv. over Random	Selection Technique	Mean Best SSE	Improv. over RW
Random	6.13218E+07	0.00%	Roulette-Wheel	6.14907E+07	0.00%
Density	6.13588E+07	-0.06%	Deterministic	6.11921E+07	0.49%
Separation	6.12647E+07	0.09%	Parent Favored Hybrid	6.12625E+07	0.37%

Mean Generations until Convergence by Center Seeding Method and Selection Technique

Seeding Method	Generations until Convergence	Improv. over Random	Selection Technique	Generations until Convergence	Improv. over RW
Random	616.60	0.00%	Roulette-Wheel	478.30	0.00%
Separation	633.30	-2.71%	Deterministic	551.73	-15.35%
Density	627.83	-1.82%	Parent Favored Hybrid	847.70	-77.23%

Best Known SSE (found in 100 generations): 6.11217E+07

Experiment	Best SSE	Generation Found	Error	Proportion Improved
Random/Roulette-Wheel	6.12183E+07	679	0.16%	0%
Separation/Roulette-Wheel	6.12603E+07	560	0.23%	0%
Density/Roulette-Wheel	6.12603E+07	560	0.23%	0%
Random/Deterministic	6.11299E+07	460	0.01%	0%
Separation/Deterministic	6.11513E+07	561	0.05%	0%
Density/Deterministic	6.11531E+07	516	0.05%	0%
Random/Parent Favored Hybrid	6.11600E+07	1149	0.06%	0%
Separation/Parent Favored Hybrid	6.11473E+07	930	0.04%	0%
Density/Parent Favored Hybrid	6.12084E+07	910	0.14%	0%

Table 4.14: TSP-LIB-1060, k = 150, μ = 100, P_c = 100%, Runs = 10

Mean Best SSE and Mean Generations Until Convergence by Experiment				
Experiment	**Mean Best SSE**	**Improv. over Random/ RW**	**Generations until Convergence**	**Improv. over Random/ RW**
Random, Roulette-Wheel	5.62225E+07	0.00%	540.2	0.00%
Separation, Roulette-Wheel	5.61869E+07	0.06%	539.4	0.15%
Density, Roulette-Wheel	5.61674E+07	0.10%	624.3	-15.57%
Random, Deterministic	5.60342E+07	0.33%	699.6	-29.51%
Separation, Deterministic	5.59868E+07	0.42%	673.8	-24.73%
Density, Deterministic	5.60097E+07	0.38%	808	-49.57%
Random, Parent Favored Hybrid	5.60930E+07	0.23%	953.5	-76.51%
Separation, Parent Favored Hybrid	5.60558E+07	0.30%	925	-71.23%
Density, Parent Favored Hybrid	5.61400E+07	0.15%	975	-80.49%

Mean Best SSE by Center Seeding Method and Selection Technique					
Seeding Method	**Mean Best SSE**	**Improv. over Random**	**Selection Technique**	**Mean Best SSE**	**Improv. over RW**
Random	5.61166E+07	0.00%	Roulette-Wheel	5.61923E+07	0.00%
Density	5.61057E+07	0.02%	Deterministic	5.60103E+07	0.32%
Separation	5.60765E+07	0.07%	Parent Favored Hybrid	5.60963E+07	0.17%

Mean Generations until Convergence by Center Seeding Method and Selection Technique					
Seeding Method	**Generations until Convergence**	**Improv. over Random**	**Selection Technique**	**Generations until Convergence**	**Improv. over RW**
Random	731.10	0.00%	Roulette-Wheel	567.97	0.00%
Separation	712.73	2.51%	Deterministic	727.13	-28.02%
Density	802.43	-9.76%	Parent Favored Hybrid	951.17	-67.47%

Best Known SSE (found in 100 generations): 5.59233E+07				
Experiment	**Best SSE**	**Generation Found**	**Error**	**Proportion Improved**
Random/Roulette-Wheel	5.60482E+07	751	0.22%	0%
Separation/Roulette-Wheel	5.60075E+07	737	0.15%	0%
Density/Roulette-Wheel	5.60184E+07	865	0.17%	0%
Random/Deterministic	5.59557E+07	744	0.06%	0%
Separation/Deterministic	5.59353E+07	662	0.02%	0%
Density/Deterministic	5.59170E+07	1204	-0.01%	10%
Random/Parent Favored Hybrid	5.60105E+07	840	0.16%	0%
Separation/Parent Favored Hybrid	5.59512E+07	1184	0.05%	0%
Density/Parent Favored Hybrid	5.59777E+07	1261	0.10%	0%

Table 4.15: TSP-LIB-3038, k = 10, μ = 100, P_c = 100%, Runs = 10

Mean Best SSE and Mean Generations Until Convergence by Experiment

Experiment	Mean Best SSE	Improv. over Random/ RW	Generations until Convergence	Improv. over Random/ RW
Random, Roulette-Wheel	5.60251E+08	0.00%	1.4	0.00%
Separation, Roulette-Wheel	5.60251E+08	0.00%	1.3	7.14%
Density, Roulette-Wheel	5.60251E+08	0.00%	2.2	-57.14%
Random, Deterministic	5.60251E+08	0.00%	2.8	-100.00%
Separation, Deterministic	5.60251E+08	0.00%	2.7	-92.86%
Density, Deterministic	5.60251E+08	0.00%	2.3	-64.29%
Random, Parent Favored Hybrid	5.60251E+08	0.00%	3.5	-150.00%
Separation, Parent Favored Hybrid	5.60251E+08	0.00%	1.5	-7.14%
Density, Parent Favored Hybrid	5.60251E+08	0.00%	3.2	-128.57%

Mean Best SSE by Center Seeding Method and Selection Technique

Seeding Method	Mean Best SSE	Improv. over Random	Selection Technique	Mean Best SSE	Improv. over RW
Random	5.60251E+08	0.00%	Roulette-Wheel	5.60251E+08	0.00%
Density	5.60251E+08	0.00%	Deterministic	5.60251E+08	0.00%
Separation	5.60251E+08	0.00%	Parent Favored Hybrid	5.60251E+08	0.00%

Mean Generations until Convergence by Center Seeding Method and Selection Technique

Seeding Method	Generations until Convergence	Improv. over Random	Selection Technique	Generations until Convergence	Improv. over RW
Random	2.57	0.00%	Roulette-Wheel	1.63	0.00%
Separation	1.83	28.57%	Deterministic	2.60	-59.18%
Density	2.57	0.00%	Parent Favored Hybrid	2.73	-67.35%

Best Known SSE (found in 200 generations): 5.60251E+08

Experiment	Best SSE	Gen. Found	Error	Proportion Improved
Random/Roulette-Wheel	5.60251E+08	0	0.00%	0%
Separation/Roulette-Wheel	5.60251E+08	0	0.00%	0%
Density/Roulette-Wheel	5.60251E+08	1	0.00%	0%
Random/Deterministic	5.60251E+08	1	0.00%	0%
Separation/Deterministic	5.60251E+08	1	0.00%	0%
Density/Deterministic	5.60251E+08	0	0.00%	0%
Random/Parent Favored Hybrid	5.60251E+08	2	0.00%	0%
Separation/Parent Favored Hybrid	5.60251E+08	0	0.00%	0%
Density/Parent Favored Hybrid	5.60251E+08	0	0.00%	0%

Table 4.16: TSP-LIB-3038, k = 20, μ = 100, P_c = 100%, Runs = 10

Mean Best SSE and Mean Generations Until Convergence by Experiment

Experiment	Mean Best SSE	Improv. over Random/ RW	Generations until Convergence	Improv. over Random/ RW
Random, Roulette-Wheel	2.66813E+08	0.00%	39.1	0.00%
Separation, Roulette-Wheel	2.66813E+08	0.00%	35.7	8.70%
Density, Roulette-Wheel	2.66813E+08	0.00%	23.3	40.41%
Random, Deterministic	2.66812E+08	0.00%	50.3	-28.64%
Separation, Deterministic	2.66812E+08	0.00%	50	-27.88%
Density, Deterministic	2.66812E+08	0.00%	53.3	-36.32%
Random, Parent Favored Hybrid	2.66812E+08	0.00%	92.9	-137.60%
Separation, Parent Favored Hybrid	2.66812E+08	0.00%	92.4	-136.32%
Density, Parent Favored Hybrid	2.66812E+08	0.00%	88.6	-126.60%

Mean Best SSE by Center Seeding Method and Selection Technique

Seeding Method	Mean Best SSE	Improv. over Random	Selection Technique	Mean Best SSE	Improv. over RW
Random	2.66813E+08	0.00%	Roulette-Wheel	2.66813E+08	0.00%
Density	2.66813E+08	0.00%	Deterministic	2.66812E+08	0.00%
Separation	2.66813E+08	0.00%	Parent Favored Hybrid	2.66812E+08	0.00%

Mean Generations until Convergence by Center Seeding Method and Selection Technique

Seeding Method	Generations until Convergence	Improv. over Random	Selection Technique	Generations until Convergence	Improv. over RW
Random	60.77	0.00%	Roulette-Wheel	32.70	0.00%
Separation	59.37	2.30%	Deterministic	51.20	-56.57%
Density	55.07	9.38%	Parent Favored Hybrid	91.30	-179.20%

Best Known SSE (found in 200 generations): 2.66812E+08

Experiment	Best SSE	Gen. Found	Error	Proportion Improved
Random/Roulette-Wheel	2.66812E+08	15	0.00%	0%
Separation/Roulette-Wheel	2.66812E+08	13	0.00%	0%
Density/Roulette-Wheel	2.66812E+08	15	0.00%	0%
Random/Deterministic	2.66812E+08	39	0.00%	0%
Separation/Deterministic	2.66812E+08	37	0.00%	0%
Density/Deterministic	2.66812E+08	37	0.00%	0%
Random/Parent Favored Hybrid	2.66812E+08	79	0.00%	0%
Separation/Parent Favored Hybrid	2.66812E+08	63	0.00%	0%
Density/Parent Favored Hybrid	2.66812E+08	52	0.00%	0%

Table 4.17: TSP-LIB-3038, k = 30, μ = 100, P_c = 100%, Runs = 10

Mean Best SSE and Mean Generations Until Convergence by Experiment

Experiment	**Mean Best SSE**	**Improv. over Random/ RW**	**Generations until Convergence**	**Improv. over Random/ RW**
Random, Roulette-Wheel	1.75545E+08	0.00%	42.9	0.00%
Separation, Roulette-Wheel	1.75539E+08	0.00%	39	9.09%
Density, Roulette-Wheel	1.75539E+08	0.00%	34.7	19.11%
Random, Deterministic	1.75539E+08	0.00%	48.6	-13.29%
Separation, Deterministic	1.75539E+08	0.00%	46	-7.23%
Density, Deterministic	1.75539E+08	0.00%	49.2	-14.69%
Random, Parent Favored Hybrid	1.75539E+08	0.00%	91.1	-112.35%
Separation, Parent Favored Hybrid	1.75539E+08	0.00%	90.7	-111.42%
Density, Parent Favored Hybrid	1.75539E+08	0.00%	90.2	-110.26%

Mean Best SSE by Center Seeding Method and Selection Technique

Seeding Method	**Mean Best SSE**	**Improv. over Random**	**Selection Technique**	**Mean Best SSE**	**Improv. over RW**
Random	1.75541E+08	0.00%	Roulette-Wheel	1.75541E+08	0.00%
Density	1.75539E+08	0.00%	Deterministic	1.75539E+08	0.00%
Separation	1.75539E+08	0.00%	Parent Favored Hybrid	1.75539E+08	0.00%

Mean Generations until Convergence by Center Seeding Method and Selection Technique

Seeding Method	**Generations until Convergence**	**Improv. over Random**	**Selection Technique**	**Generations until Convergence**	**Improv. over RW**
Random	60.87	0.00%	Roulette-Wheel	38.87	0.00%
Separation	58.57	3.78%	Deterministic	47.93	-23.33%
Density	58.03	4.65%	Parent Favored Hybrid	90.67	-133.28%

Best Known SSE (found in 200 generations): 1.75538E+08

Experiment	**Best SSE**	**Gen. Found**	**Error**	**Proportion Improved**
Random/Roulette-Wheel	1.75539E+08	18	0.00%	0%
Separation/Roulette-Wheel	1.75539E+08	21	0.00%	0%
Density/Roulette-Wheel	1.75539E+08	15	0.00%	0%
Random/Deterministic	1.75539E+08	30	0.00%	0%
Separation/Deterministic	1.75539E+08	31	0.00%	0%
Density/Deterministic	1.75539E+08	32	0.00%	0%
Random/Parent Favored Hybrid	1.75539E+08	79	0.00%	0%
Separation/Parent Favored Hybrid	1.75539E+08	66	0.00%	0%
Density/Parent Favored Hybrid	1.75539E+08	59	0.00%	0%

Table 4.18: TSP-LIB-3038, k = 40, μ = 100, P_c = 100%, Runs = 10

<table>
<tr><th colspan="5">Mean Best SSE and Mean Generations Until Convergence by Experiment</th></tr>
<tr><th>Experiment</th><th>Mean Best SSE</th><th>Improv. over Random/ RW</th><th>Generations until Convergence</th><th>Improv. over Random/ RW</th></tr>
<tr><td>Random, Roulette-Wheel</td><td>1.24963E+08</td><td>0.00%</td><td>100.7</td><td>0.00%</td></tr>
<tr><td>Separation, Roulette-Wheel</td><td>1.24962E+08</td><td>0.00%</td><td>98.7</td><td>1.99%</td></tr>
<tr><td>Density, Roulette-Wheel</td><td>1.24962E+08</td><td>0.00%</td><td>68.9</td><td>31.58%</td></tr>
<tr><td>Random, Deterministic</td><td>1.24961E+08</td><td>0.00%</td><td>69.5</td><td>30.98%</td></tr>
<tr><td>Separation, Deterministic</td><td>1.24961E+08</td><td>0.00%</td><td>65.1</td><td>35.35%</td></tr>
<tr><td>Density, Deterministic</td><td>1.24961E+08</td><td>0.00%</td><td>66.7</td><td>33.76%</td></tr>
<tr><td>Random, Parent Favored Hybrid</td><td>1.24961E+08</td><td>0.00%</td><td>136.4</td><td>-35.45%</td></tr>
<tr><td>Separation, Parent Favored Hybrid</td><td>1.24961E+08</td><td>0.00%</td><td>133.1</td><td>-32.17%</td></tr>
<tr><td>Density, Parent Favored Hybrid</td><td>1.24961E+08</td><td>0.00%</td><td>131.8</td><td>-30.88%</td></tr>
</table>

<table>
<tr><th colspan="6">Mean Best SSE by Center Seeding Method and Selection Technique</th></tr>
<tr><th>Seeding Method</th><th>Mean Best SSE</th><th>Improv. over Random</th><th>Selection Technique</th><th>Mean Best SSE</th><th>Improv. over RW</th></tr>
<tr><td>Random</td><td>1.24962E+08</td><td>0.00%</td><td>Roulette-Wheel</td><td>1.24962E+08</td><td>0.00%</td></tr>
<tr><td>Density</td><td>1.24961E+08</td><td>0.00%</td><td>Deterministic</td><td>1.24961E+08</td><td>0.00%</td></tr>
<tr><td>Separation</td><td>1.24961E+08</td><td>0.00%</td><td>Parent Favored Hybrid</td><td>1.24961E+08</td><td>0.00%</td></tr>
</table>

<table>
<tr><th colspan="6">Mean Generations until Convergence by Center Seeding Method and Selection Technique</th></tr>
<tr><th>Seeding Method</th><th>Generations until Convergence</th><th>Improv. over Random</th><th>Selection Technique</th><th>Generations until Convergence</th><th>Improv. over RW</th></tr>
<tr><td>Random</td><td>102.20</td><td>0.00%</td><td>Roulette-Wheel</td><td>89.43</td><td>0.00%</td></tr>
<tr><td>Separation</td><td>98.97</td><td>3.16%</td><td>Deterministic</td><td>67.10</td><td>24.97%</td></tr>
<tr><td>Density</td><td>89.13</td><td>12.79%</td><td>Parent Favored Hybrid</td><td>133.77</td><td>-49.57%</td></tr>
</table>

<table>
<tr><th colspan="5">Best Known SSE (found in 200 generations): 1.24961E+08</th></tr>
<tr><th>Experiment</th><th>Best SSE</th><th>Gen. Found</th><th>Error</th><th>Proportion Improved</th></tr>
<tr><td>Random/Roulette-Wheel</td><td>1.24961E+08</td><td>32</td><td>0.00%</td><td>0%</td></tr>
<tr><td>Separation/Roulette-Wheel</td><td>1.24961E+08</td><td>83</td><td>0.00%</td><td>0%</td></tr>
<tr><td>Density/Roulette-Wheel</td><td>1.24961E+08</td><td>35</td><td>0.00%</td><td>0%</td></tr>
<tr><td>Random/Deterministic</td><td>1.24961E+08</td><td>59</td><td>0.00%</td><td>0%</td></tr>
<tr><td>Separation/Deterministic</td><td>1.24961E+08</td><td>61</td><td>0.00%</td><td>0%</td></tr>
<tr><td>Density/Deterministic</td><td>1.24961E+08</td><td>50</td><td>0.00%</td><td>0%</td></tr>
<tr><td>Random/Parent Favored Hybrid</td><td>1.24961E+08</td><td>105</td><td>0.00%</td><td>0%</td></tr>
<tr><td>Separation/Parent Favored Hybrid</td><td>1.24961E+08</td><td>113</td><td>0.00%</td><td>0%</td></tr>
<tr><td>Density/Parent Favored Hybrid</td><td>1.24961E+08</td><td>103</td><td>0.00%</td><td>0%</td></tr>
</table>

Table 4.19: TSP-LIB-3038, $k = 50$, $\mu = 100$, $P_c = 100\%$, Runs = 10

Mean Best SSE and Mean Generations Until Convergence by Experiment

Experiment	Mean Best SSE	Improv. over Random/ RW	Generations until Convergence	Improv. over Random/ RW
Random, Roulette-Wheel	9.83175E+07	0.00%	274.7	0.00%
Separation, Roulette-Wheel	9.83246E+07	-0.01%	260.5	5.17%
Density, Roulette-Wheel	9.83456E+07	-0.03%	252.4	8.12%
Random, Deterministic	9.82568E+07	0.06%	235.8	14.16%
Separation, Deterministic	9.82563E+07	0.06%	263.6	4.04%
Density, Deterministic	9.82565E+07	0.06%	332.5	-21.04%
Random, Parent Favored Hybrid	9.82948E+07	0.02%	408.3	-48.63%
Separation, Parent Favored Hybrid	9.82517E+07	0.07%	439.7	-60.07%
Density, Parent Favored Hybrid	9.82685E+07	0.05%	406.3	-47.91%

Mean Best SSE by Center Seeding Method and Selection Technique

Seeding Method	Mean Best SSE	Improv. over Random	Selection Technique	Mean Best SSE	Improv. over RW
Random	9.82897E+07	0.00%	Roulette-Wheel	9.83292E+07	0.00%
Density	9.82902E+07	0.00%	Deterministic	9.82565E+07	0.07%
Separation	9.82775E+07	0.01%	Parent Favored Hybrid	9.82716E+07	0.06%

Mean Generations until Convergence by Center Seeding Method and Selection Technique

Seeding Method	Generations until Convergence	Improv. over Random	Selection Technique	Generations until Convergence	Improv. over RW
Random	306.27	0.00%	Roulette-Wheel	262.53	0.00%
Separation	321.27	-4.90%	Deterministic	277.30	-5.62%
Density	330.40	-7.88%	Parent Favored Hybrid	418.10	-59.26%

Best Known SSE (found in 200 generations): 9.82442E+07

Experiment	Best SSE	Gen. Found	Error	Proportion Improved
Random/Roulette-Wheel	9.82462E+07	155	0.00%	0%
Separation/Roulette-Wheel	9.82427E+07	244	0.00%	0%
Density/Roulette-Wheel	9.82426E+07	374	0.00%	0%
Random/Deterministic	9.82426E+07	203	0.00%	0%
Separation/Deterministic	9.82426E+07	215	0.00%	0%
Density/Deterministic	9.82426E+07	275	0.00%	0%
Random/Parent Favored Hybrid	9.82426E+07	440	0.00%	0%
Separation/Parent Favored Hybrid	9.82426E+07	396	0.00%	0%
Density/Parent Favored Hybrid	9.82426E+07	352	0.00%	0%

Table 4.20: TSP-LIB-3038, k = 100, μ = 100, P_c = 100%, Runs = 10

Mean Best SSE and Mean Generations Until Convergence by Experiment

Experiment	Mean Best SSE	Improv. over Random/ RW	Generations until Convergence	Improv. over Random/ RW
Random, Roulette-Wheel	4.77726E+07	0.00%	546.7	0.00%
Separation, Roulette-Wheel	4.77674E+07	0.01%	475.8	12.97%
Density, Roulette-Wheel	4.77373E+07	0.07%	546.2	0.09%
Random, Deterministic	4.76927E+07	0.17%	450.9	17.52%
Separation, Deterministic	4.76939E+07	0.16%	424.6	22.33%
Density, Deterministic	4.76830E+07	0.19%	582.2	-6.49%
Random, Parent Favored Hybrid	4.76949E+07	0.16%	863.3	-57.91%
Separation, Parent Favored Hybrid	4.76941E+07	0.16%	794.5	-45.33%
Density, Parent Favored Hybrid	4.77005E+07	0.15%	942.6	-72.42%

Mean Best SSE by Center Seeding Method and Selection Technique

Seeding Method	Mean Best SSE	Improv. over Random	Selection Technique	Mean Best SSE	Improv. over RW
Random	4.77200E+07	0.00%	Roulette-Wheel	4.77591E+07	0.00%
Density	4.77069E+07	0.03%	Deterministic	4.76898E+07	0.15%
Separation	4.77185E+07	0.00%	Parent Favored Hybrid	4.76965E+07	0.13%

Mean Generations until Convergence by Center Seeding Method and Selection Technique

Seeding Method	Generations until Convergence	Improv. over Random	Selection Technique	Generations until Convergence	Improv. over RW
Random	620.30	0.00%	Roulette-Wheel	522.90	0.00%
Separation	564.97	8.92%	Deterministic	485.90	7.08%
Density	690.33	-11.29%	Parent Favored Hybrid	866.80	-65.77%

Best Known SSE (found in 200 generations): 4.76642E+07

Experiment	Best SSE	Gen. Found	Error	Proportion Improved
Random/Roulette-Wheel	4.76788E+07	640	0.03%	0%
Separation/Roulette-Wheel	4.76947E+07	631	0.06%	0%
Density/Roulette-Wheel	4.77094E+07	600	0.09%	0%
Random/Deterministic	4.76780E+07	389	0.03%	0%
Separation/Deterministic	4.76700E+07	622	0.01%	0%
Density/Deterministic	4.76768E+07	539	0.03%	0%
Random/Parent Favored Hybrid	4.76777E+07	925	0.03%	0%
Separation/Parent Favored Hybrid	4.76800E+07	855	0.03%	0%
Density/Parent Favored Hybrid	4.76792E+07	977	0.03%	0%

Table 4.21: TSP-LIB-3038, $k =$ 150, $\mu = 200$, $P_c = 80\%$, Runs = 20

Mean Best SSE and Mean Generations Until Convergence by Experiment				
Experiment	**Mean Best SSE**	**Improv. over Random/ RW**	**Generations until Convergence**	**Improv. over Random/ RW**
Random, Roulette-Wheel	3.05908E+07	0.00%	708.3	0.00%
Separation, Roulette-Wheel	3.05689E+07	0.07%	678.6	4.19%
Density, Roulette-Wheel	3.05761E+07	0.05%	785.6	-10.91%
Random, Deterministic	3.05466E+07	0.14%	819.7	-15.74%
Separation, Deterministic	3.05407E+07	0.16%	741.2	-4.65%
Density, Deterministic	3.05482E+07	0.14%	862.4	-21.76%
Random, Parent Favored Hybrid	3.05509E+07	0.13%	1302.6	-83.92%
Separation, Parent Favored Hybrid	3.05460E+07	0.15%	1221.5	-72.46%
Density, Parent Favored Hybrid	3.05569E+07	0.11%	1329.9	-87.77%

Mean Best SSE by Center Seeding Method and Selection Technique					
Seeding Method	**Mean Best SSE**	**Improv. over Random**	**Selection Technique**	**Mean Best SSE**	**Improv. over RW**
Random	3.05628E+07	0.00%	Roulette-Wheel	3.05786E+07	0.00%
Density	3.05604E+07	0.01%	Deterministic	3.05452E+07	0.11%
Separation	3.05518E+07	0.04%	Parent Favored Hybrid	3.05512E+07	0.09%

Mean Generations until Convergence by Center Seeding Method and Selection Technique					
Seeding Method	**Generations until Convergence**	**Improv. over Random**	**Selection Technique**	**Generations until Convergence**	**Improv. over RW**
Random	943.5	0.00%	Roulette-Wheel	724.1	0.00%
Separation	880.4	6.69%	Deterministic	807.7	-11.55%
Density	992.6	-5.20%	Parent Favored Hybrid	1284.7	-77.41%

Best Known SSE (found in 100 generations): 3.0522E+07				
Experiment	**Best SSE**	**Generation Found**	**Error**	**Proportion Improved**
Random/Roulette-Wheel	3.05437E+07	927	0.07%	0%
Separation/Roulette-Wheel	3.05309E+07	686	0.03%	0%
Density/Roulette-Wheel	3.05469E+07	1038	0.08%	0%
Random/Deterministic	3.05356E+07	662	0.04%	0%
Separation/Deterministic	3.05277E+07	960	0.02%	0%
Density/Deterministic	3.05364E+07	1418	0.05%	0%
Random/Parent Favored Hybrid	3.05341E+07	1572	0.04%	0%
Separation/Parent Favored Hybrid	3.05322E+07	1233	0.03%	0%
Density/Parent Favored Hybrid	3.05394E+07	1215	0.06%	0%

Table 4.22: TSP-LIB-3038, k = 200, μ = 100, P_c = 100%, Runs = 10

Mean Best SSE and Mean Generations Until Convergence by Experiment

Experiment	Mean Best SSE	Improv. over Random/ RW	Generations until Convergence	Improv. over Random/ RW
Random, Roulette-Wheel	2.19519E+07	0.00%	963.6	0.00%
Separation, Roulette-Wheel	2.19340E+07	0.08%	1135.3	-17.82%
Density, Roulette-Wheel	2.19394E+07	0.06%	973.2	-1.00%
Random, Deterministic	2.19178E+07	0.16%	900.8	6.52%
Separation, Deterministic	2.18974E+07	0.25%	844	12.41%
Density, Deterministic	2.19137E+07	0.17%	844.4	12.37%
Random, Parent Favored Hybrid	2.19060E+07	0.21%	1559.9	-61.88%
Separation, Parent Favored Hybrid	2.19129E+07	0.18%	1247.3	-29.44%
Density, Parent Favored Hybrid	2.19302E+07	0.10%	1290.6	-33.94%

Mean Best SSE by Center Seeding Method and Selection Technique

Seeding Method	Mean Best SSE	Improv. over Random	Selection Technique	Mean Best SSE	Improv. over RW
Random	2.19252E+07	0.00%	Roulette-Wheel	2.19418E+07	0.00%
Density	2.19278E+07	-0.01%	Deterministic	2.19096E+07	0.15%
Separation	2.19148E+07	0.05%	Parent Favored Hybrid	2.19164E+07	0.12%

Mean Generations until Convergence by Center Seeding Method and Selection Technique

Seeding Method	Generations until Convergence	Improv. over Random	Selection Technique	Generations until Convergence	Improv. over RW
Random	1141.43	0.00%	Roulette-Wheel	1024.03	0.00%
Separation	1075.53	5.77%	Deterministic	863.07	15.72%
Density	1036.07	9.23%	Parent Favored Hybrid	1365.93	-33.39%

Best Known SSE (found in 200 generations): 2.18540E+07

Experiment	Best SSE	Gen. Found	Error	Proportion Improved
Random/Roulette-Wheel	2.19211E+07	1158	0.31%	0%
Separation/Roulette-Wheel	2.18863E+07	1083	0.15%	0%
Density/Roulette-Wheel	2.19138E+07	1166	0.27%	0%
Random/Deterministic	2.19020E+07	942	0.22%	0%
Separation/Deterministic	2.18868E+07	906	0.15%	0%
Density/Deterministic	2.18916E+07	934	0.17%	0%
Random/Parent Favored Hybrid	2.18776E+07	1836	0.11%	0%
Separation/Parent Favored Hybrid	2.18900E+07	1486	0.16%	0%
Density/Parent Favored Hybrid	2.18921E+07	1294	0.17%	0%

Table 4.23: TSP-LIB-3038, $k =$ 250, $\mu = 100$, $P_c = 100\%$, Runs = 10

Mean Best SSE and Mean Generations Until Convergence by Experiment

Experiment	Mean Best SSE	Improv. over Random/ RW	Generations until Convergence	Improv. over Random/ RW
Random, Roulette-Wheel	1.67022E+07	0.00%	1190.9	0.00%
Separation, Roulette-Wheel	1.66905E+07	0.07%	1208.7	-1.49%
Density, Roulette-Wheel	1.67240E+07	-0.13%	884.1	25.76%
Random, Deterministic	1.66293E+07	0.44%	1064	10.66%
Separation, Deterministic	1.66324E+07	0.42%	867.6	27.15%
Density, Deterministic	1.66293E+07	0.44%	985.1	17.28%
Random, Parent Favored Hybrid	1.66397E+07	0.37%	1574.2	-32.19%
Separation, Parent Favored Hybrid	1.66338E+07	0.41%	1512.9	-27.04%
Density, Parent Favored Hybrid	1.66393E+07	0.38%	1525	-28.05%

Mean Best SSE by Center Seeding Method and Selection Technique

Seeding Method	Mean Best SSE	Improv. over Random	Selection Technique	Mean Best SSE	Improv. over RW
Random	1.66571E+07	0.00%	Roulette-Wheel	1.67056E+07	0.00%
Density	1.66642E+07	-0.04%	Deterministic	1.66304E+07	0.45%
Separation	1.66522E+07	0.03%	Parent Favored Hybrid	1.66376E+07	0.41%

Mean Generations until Convergence by Center Seeding Method and Selection Technique

Seeding Method	Generations until Convergence	Improv. over Random	Selection Technique	Generations until Convergence	Improv. over RW
Random	1276.37	0.00%	Roulette-Wheel	1094.57	0.00%
Separation	1196.40	6.27%	Deterministic	972.23	11.18%
Density	1131.40	11.36%	Parent Favored Hybrid	1537.37	-40.45%

Best Known SSE (found in 200 generations): 1.65963E+07

Experiment	Best SSE	Gen. Found	Error	Proportion Improved
Random/Roulette-Wheel	1.66457E+07	1211	0.30%	0%
Separation/Roulette-Wheel	1.66568E+07	2199	0.36%	0%
Density/Roulette-Wheel	1.66715E+07	1134	0.45%	0%
Random/Deterministic	1.66165E+07	1418	0.12%	0%
Separation/Deterministic	1.66155E+07	801	0.12%	0%
Density/Deterministic	1.66065E+07	1114	0.06%	0%
Random/Parent Favored Hybrid	1.66208E+07	2056	0.15%	0%
Separation/Parent Favored Hybrid	1.66014E+07	1666	0.03%	0%
Density/Parent Favored Hybrid	1.66282E+07	1380	0.19%	0%

Table 4.24: TSP-LIB-3038, k = 300, μ = 100, P_c = 100%, Runs = 10

Mean Best SSE and Mean Generations Until Convergence by Experiment				
Experiment	**Mean Best SSE**	**Improv. over Random/ RW**	**Generations until Convergence**	**Improv. over Random/ RW**
Random, Roulette-Wheel	1.33880E+07	0.00%	1186	0.00%
Separation, Roulette-Wheel	1.33841E+07	0.03%	1165.4	1.74%
Density, Roulette-Wheel	1.33621E+07	0.19%	1431.6	-20.71%
Random, Deterministic	1.33013E+07	0.65%	954	19.56%
Separation, Deterministic	1.32868E+07	0.76%	1004.3	15.32%
Density, Deterministic	1.32985E+07	0.67%	1076.7	9.22%
Random, Parent Favored Hybrid	1.33060E+07	0.61%	1573.9	-32.71%
Separation, Parent Favored Hybrid	1.32995E+07	0.66%	1547.3	-30.46%
Density, Parent Favored Hybrid	1.33055E+07	0.62%	1709.7	-44.16%

Mean Best SSE by Center Seeding Method and Selection Technique					
Seeding Method	**Mean Best SSE**	**Improv. over Random**	**Selection Technique**	**Mean Best SSE**	**Improv. over RW**
Random	1.33317E+07	0.00%	Roulette-Wheel	1.33780E+07	0.00%
Density	1.33220E+07	0.07%	Deterministic	1.32955E+07	0.62%
Separation	1.33235E+07	0.06%	Parent Favored Hybrid	1.33037E+07	0.56%

Mean Generations until Convergence by Center Seeding Method and Selection Technique					
Seeding Method	**Generations until Convergence**	**Improv. over Random**	**Selection Technique**	**Generations until Convergence**	**Improv. over RW**
Random	1237.97	0.00%	Roulette-Wheel	1261.00	0.00%
Separation	1239.00	-0.08%	Deterministic	1011.67	19.77%
Density	1406.00	-13.57%	Parent Favored Hybrid	1610.30	-27.70%

Best Known SSE (found in 200 generations): 1.32770E+07				
Experiment	**Best SSE**	**Gen. Found**	**Error**	**Proportion Improved**
Random/Roulette-Wheel	1.33235E+07	2042	0.35%	0%
Separation/Roulette-Wheel	1.33292E+07	1639	0.39%	0%
Density/Roulette-Wheel	1.33152E+07	1877	0.29%	0%
Random/Deterministic	1.32873E+07	1021	0.08%	0%
Separation/Deterministic	1.32820E+07	1065	0.04%	0%
Density/Deterministic	1.32863E+07	1041	0.07%	0%
Random/Parent Favored Hybrid	1.32892E+07	1638	0.09%	0%
Separation/Parent Favored Hybrid	1.32862E+07	1556	0.07%	0%
Density/Parent Favored Hybrid	1.32879E+07	2217	0.08%	0%

Table 4.25: TSP-LIB-3038, k = 350, μ = 100, P_c = 100%, Runs = 10

Mean Best SSE and Mean Generations Until Convergence by Experiment

Experiment	Mean Best SSE	Improv. over Random/ RW	Generations until Convergence	Improv. over Random/ RW
Random, Roulette-Wheel	1.11474E+07	0.00%	1170.6	0.00%
Separation, Roulette-Wheel	1.11144E+07	0.30%	1737.5	-48.43%
Density, Roulette-Wheel	1.11328E+07	0.13%	1519.1	-29.77%
Random, Deterministic	1.10339E+07	1.02%	1455.2	-24.31%
Separation, Deterministic	1.10332E+07	1.02%	1254.3	-7.15%
Density, Deterministic	1.10366E+07	0.99%	1366	-16.69%
Random, Parent Favored Hybrid	1.10816E+07	0.59%	1664.8	-42.22%
Separation, Parent Favored Hybrid	1.10721E+07	0.68%	1613.1	-37.80%
Density, Parent Favored Hybrid	1.10657E+07	0.73%	1922.9	-64.27%

Mean Best SSE by Center Seeding Method and Selection Technique

Seeding Method	Mean Best SSE	Improv. over Random	Selection Technique	Mean Best SSE	Improv. over RW
Random	1.10876E+07	0.00%	Roulette-Wheel	1.11316E+07	0.00%
Density	1.10784E+07	0.08%	Deterministic	1.10346E+07	0.87%
Separation	1.10733E+07	0.13%	Parent Favored Hybrid	1.10732E+07	0.52%

Mean Generations until Convergence by Center Seeding Method and Selection Technique

Seeding Method	Generations until Convergence	Improv. over Random	Selection Technique	Generations until Convergence	Improv. over RW
Random	1430.20	0.00%	Roulette-Wheel	1475.73	0.00%
Separation	1534.97	-7.33%	Deterministic	1358.50	7.94%
Density	1602.67	-12.06%	Parent Favored Hybrid	1733.60	-17.47%

Best Known SSE (found in 200 generations): 1.10428E+07

Experiment	Best SSE	Gen. Found	Error	Proportion Improved
Random/Roulette-Wheel	1.11191E+07	1188	0.69%	0%
Separation/Roulette-Wheel	1.11089E+07	959	0.60%	0%
Density/Roulette-Wheel	1.10960E+07	2233	0.48%	0%
Random/Deterministic	1.10269E+07	1327	-0.14%	90%
Separation/Deterministic	1.10176E+07	1662	-0.23%	80%
Density/Deterministic	1.10268E+07	1265	-0.14%	90%
Random/Parent Favored Hybrid	1.10293E+07	2426	-0.12%	20%
Separation/Parent Favored Hybrid	1.10323E+07	2392	-0.10%	30%
Density/Parent Favored Hybrid	1.10366E+07	2103	-0.06%	10%

Table 4.26: TSP-LIB-3038, k = 400, μ = 100, P_c = 100%, Runs = 10

Mean Best SSE and Mean Generations Until Convergence by Experiment				
Experiment	**Mean Best SSE**	**Improv. over Random/ RW**	**Generations until Convergence**	**Improv. over Random/ RW**
Random, Roulette-Wheel	9.52099E+06	0.00%	1499	0.00%
Separation, Roulette-Wheel	9.52970E+06	-0.09%	1171.4	21.85%
Density, Roulette-Wheel	9.51800E+06	0.03%	1276.1	14.87%
Random, Deterministic	9.38820E+06	1.39%	1378.8	8.02%
Separation, Deterministic	9.37960E+06	1.49%	1403.1	6.40%
Density, Deterministic	9.38312E+06	1.45%	1544.5	-3.04%
Random, Parent Favored Hybrid	9.39335E+06	1.34%	2318.3	-54.66%
Separation, Parent Favored Hybrid	9.39815E+06	1.29%	1789.8	-19.40%
Density, Parent Favored Hybrid	9.42885E+06	0.97%	1797.2	-19.89%

Mean Best SSE by Center Seeding Method and Selection Technique					
Seeding Method	**Mean Best SSE**	**Improv. over Random**	**Selection Technique**	**Mean Best SSE**	**Improv. over RW**
Random	9.43418E+06	0.00%	Roulette-Wheel	9.52289E+06	0.00%
Separation	9.44332E+06	-0.10%	Deterministic	9.38364E+06	1.46%
Density	9.43582E+06	-0.02%	Parent Favored Hybrid	9.40679E+06	1.22%

Mean Generations until Convergence by Center Seeding Method and Selection Technique					
Seeding Method	**Generations until Convergence**	**Improv. over Random**	**Selection Technique**	**Generations until Convergence**	**Improv. over RW**
Random	1732.03	0.00%	Roulette-Wheel	1315.50	0.00%
Separation	1454.77	16.01%	Deterministic	1442.13	-9.63%
Density	1539.27	11.13%	Parent Favored Hybrid	1968.43	-49.63%

Best Known SSE (found in 200 generations): 9.38037E+06				
Experiment	**Best SSE**	**Gen. Found**	**Error**	**Proportion Improved**
Random/Roulette-Wheel	9.47304E+06	1772	0.99%	0%
Separation/Roulette-Wheel	9.46977E+06	1954	0.95%	0%
Density/Roulette-Wheel	9.46733E+06	1692	0.93%	0%
Random/Deterministic	9.37654E+06	1463	-0.04%	20%
Separation/Deterministic	9.36923E+06	1479	-0.12%	60%
Density/Deterministic	9.37559E+06	1391	-0.05%	40%
Random/Parent Favored Hybrid	9.37207E+06	3151	-0.09%	10%
Separation/Parent Favored Hybrid	9.37177E+06	2140	-0.09%	10%
Density/Parent Favored Hybrid	9.38096E+06	2541	0.01%	0%

Table 4.27: TSP-LIB-3038, k = 450, μ = 100, P_c = 100%, Runs = 10

Mean Best SSE and Mean Generations Until Convergence by Experiment				
Experiment	**Mean Best SSE**	**Improv. over Random/ RW**	**Generations until Convergence**	**Improv. over Random/ RW**
Random, Roulette-Wheel	8.33155E+06	0.00%	1028.3	0.00%
Separation, Roulette-Wheel	8.30412E+06	0.33%	1193.7	-16.08%
Density, Roulette-Wheel	8.28625E+06	0.54%	1294.2	-25.86%
Random, Deterministic	8.13425E+06	2.37%	1749	-70.09%
Separation, Deterministic	8.13383E+06	2.37%	1666.5	-62.06%
Density, Deterministic	8.13475E+06	2.36%	1923.8	-87.09%
Random, Parent Favored Hybrid	8.17201E+06	1.91%	2220	-115.89%
Separation, Parent Favored Hybrid	8.15796E+06	2.08%	2116.2	-105.80%
Density, Parent Favored Hybrid	8.14844E+06	2.20%	2589.6	-151.83%

Mean Best SSE by Center Seeding Method and Selection Technique					
Seeding Method	**Mean Best SSE**	**Improv. over Random**	**Selection Technique**	**Mean Best SSE**	**Improv. over RW**
Random	8.21260E+06	0.00%	Roulette-Wheel	8.30731E+06	0.00%
Density	8.18981E+06	0.28%	Deterministic	8.13428E+06	2.08%
Separation	8.19864E+06	0.17%	Parent Favored Hybrid	8.15947E+06	1.78%

Mean Generations until Convergence by Center Seeding Method and Selection Technique					
Seeding Method	**Generations until Convergence**	**Improv. over Random**	**Selection Technique**	**Generations until Convergence**	**Improv. over RW**
Random	1665.77	0.00%	Roulette-Wheel	1172.07	0.00%
Separation	1658.80	0.42%	Deterministic	1779.77	-51.85%
Density	1935.87	-16.21%	Parent Favored Hybrid	2308.60	-96.97%

Best Known SSE (found in 200 generations): 8.14437E+06				
Experiment	**Best SSE**	**Gen. Found**	**Error**	**Proportion Improved**
Random/Roulette-Wheel	8.26505E+06	2229	1.48%	0%
Separation/Roulette-Wheel	8.23930E+06	1991	1.17%	0%
Density/Roulette-Wheel	8.25417E+06	1290	1.35%	0%
Random/Deterministic	8.12506E+06	1792	-0.24%	80%
Separation/Deterministic	8.12844E+06	2033	-0.20%	90%
Density/Deterministic	8.12580E+06	1707	-0.23%	100%
Random/Parent Favored Hybrid	8.13241E+06	2565	-0.15%	20%
Separation/Parent Favored Hybrid	8.12902E+06	2931	-0.19%	50%
Density/Parent Favored Hybrid	8.13323E+06	2868	-0.14%	60%

Table 4.28: TSP-LIB-3038, k = 500, μ = 100, P_c = 100%, Runs = 10

Mean Best SSE and Mean Generations Until Convergence by Experiment				
Experiment	**Mean Best SSE**	**Improv. over Random/ RW**	**Generations until Convergence**	**Improv. over Random/ RW**
Random, Roulette-Wheel	7.34724E+06	0.00%	1174	0.00%
Separation, Roulette-Wheel	7.34748E+06	0.00%	1011.4	13.85%
Density, Roulette-Wheel	7.32146E+06	0.35%	1381.9	-17.71%
Random, Deterministic	7.13430E+06	2.90%	1884.3	-60.50%
Separation, Deterministic	7.13486E+06	2.89%	1682.3	-43.30%
Density, Deterministic	7.13971E+06	2.82%	1757.3	-49.68%
Random, Parent Favored Hybrid	7.16374E+06	2.50%	2388.5	-103.45%
Separation, Parent Favored Hybrid	7.15895E+06	2.56%	2235.2	-90.39%
Density, Parent Favored Hybrid	7.16711E+06	2.45%	2248.7	-91.54%

Mean Best SSE by Center Seeding Method and Selection Technique					
Seeding Method	**Mean Best SSE**	**Improv. over Random**	**Selection Technique**	**Mean Best SSE**	**Improv. over RW**
Random	7.21509E+06	0.00%	Roulette-Wheel	7.33873E+06	0.00%
Density	7.20943E+06	0.08%	Deterministic	7.13629E+06	2.76%
Separation	7.21376E+06	0.02%	Parent Favored Hybrid	7.16327E+06	2.39%

Mean Generations until Convergence by Center Seeding Method and Selection Technique					
Seeding Method	**Generations until Convergence**	**Improv. over Random**	**Selection Technique**	**Generations until Convergence**	**Improv. over RW**
Random	1815.60	0.00%	Roulette-Wheel	1189.10	0.00%
Separation	1642.97	9.51%	Deterministic	1774.63	-49.24%
Density	1795.97	1.08%	Parent Favored Hybrid	2290.80	-92.65%

Best Known SSE (found in 100 generations): 7.15643E+06				
Experiment	**Best SSE**	**Generation Found**	**Error**	**Proportion Improved**
Random/Roulette-Wheel	7.29540E+06	1894	1.94%	0%
Separation/Roulette-Wheel	7.31382E+06	1361	2.20%	0%
Density/Roulette-Wheel	7.29761E+06	1915	1.97%	0%
Random/Deterministic	7.12622E+06	1890	-0.42%	100%
Separation/Deterministic	7.12415E+06	1906	-0.45%	100%
Density/Deterministic	7.12304E+06	2122	-0.47%	100%
Random/Parent Favored Hybrid	7.12856E+06	4118	-0.39%	50%
Separation/Parent Favored Hybrid	7.12919E+06	2824	-0.38%	60%
Density/Parent Favored Hybrid	7.14146E+06	2195	-0.21%	50%

Table 4.29: SYN1, $k =$ 50, μ = 200, P_c = 80%, Runs = 20

Mean Best SSE and Mean Generations Until Convergence by Experiment				
Experiment	**Mean Best SSE**	**Improv. over Random/ RW**	**Generations until Convergence**	**Improv. over Random/ RW**
Random, Roulette-Wheel	1.08688E+05	0.00%	51.3	0.00%
Separation, Roulette-Wheel	9.92787E+04	8.66%	0	100.00%
Density, Roulette-Wheel	1.11824E+05	-2.89%	46	10.43%
Random, Deterministic	9.92787E+04	8.66%	42.7	16.86%
Separation, Deterministic	9.92787E+04	8.66%	0.1	99.81%
Density, Deterministic	9.92787E+04	8.66%	39.4	23.29%
Random, Parent Favored Hybrid	9.92787E+04	8.66%	57.9	-12.87%
Separation, Parent Favored Hybrid	9.92787E+04	8.66%	0	100.00%
Density, Parent Favored Hybrid	9.92787E+04	8.66%	51.1	0.39%

Mean Best SSE by Center Seeding Method and Selection Technique					
Seeding Method	**Mean Best SSE**	**Improv. over Random**	**Selection Technique**	**Mean Best SSE**	**Improv. over RW**
Random	1.02415E+05	0.00%	Roulette-Wheel	1.06597E+05	0.00%
Density	1.03461E+05	-1.02%	Deterministic	9.92787E+04	6.87%
Separation	9.92787E+04	3.06%	Parent Favored Hybrid	9.92787E+04	6.87%

Mean Generations until Convergence by Center Seeding Method and Selection Technique					
Seeding Method	**Generations until Convergence**	**Improv. over Random**	**Selection Technique**	**Generations until Convergence**	**Improv. over RW**
Random	50.6	0.00%	Roulette-Wheel	32.4	0.00%
Separation	0.0	99.93%	Deterministic	27.4	15.58%
Density	45.5	10.17%	Parent Favored Hybrid	36.3	-12.08%

Table 4.30: SYN2, k = 50, μ = 200, P_c = 80%, Runs = 20

Mean Best SSE and Mean Generations Until Convergence by Experiment				
Experiment	**Mean Best SSE**	**Improv. over Random/ RW**	**Generations until Convergence**	**Improv. over Random/ RW**
Random, Roulette-Wheel	9.93423E+04	0.00%	20.8	0.00%
Separation, Roulette-Wheel	9.93423E+04	0.00%	7.7	62.98%
Density, Roulette-Wheel	9.93423E+04	0.00%	23	-10.58%
Random, Deterministic	9.93423E+04	0.00%	26.2	-25.96%
Separation, Deterministic	9.93423E+04	0.00%	11.5	44.71%
Density, Deterministic	9.93423E+04	0.00%	29.8	-43.03%
Random, Parent Favored Hybrid	9.93423E+04	0.00%	48.9	-134.86%
Separation, Parent Favored Hybrid	9.93423E+04	0.00%	17.9	13.94%
Density, Parent Favored Hybrid	9.93423E+04	0.00%	53.1	-155.29%

Mean Best SSE by Center Seeding Method and Selection Technique					
Seeding Method	**Mean Best SSE**	**Improv. over Random**	**Selection Technique**	**Mean Best SSE**	**Improv. over RW**
Random	9.93423E+04	0.00%	Roulette-Wheel	9.93423E+04	0.00%
Density	9.93423E+04	0.00%	Deterministic	9.93423E+04	0.00%
Separation	9.93423E+04	0.00%	Parent Favored Hybrid	9.93423E+04	0.00%

Mean Generations until Convergence by Center Seeding Method and Selection Technique					
Seeding Method	**Generations until Convergence**	**Improv. over Random**	**Selection Technique**	**Generations until Convergence**	**Improv. over RW**
Random	32.0	0.00%	Roulette-Wheel	17.2	0.00%
Separation	12.4	61.29%	Deterministic	22.5	-30.97%
Density	35.3	-10.43%	Parent Favored Hybrid	40.0	-132.72%

Table 4.31: SYN3, $k =$ 50, μ = 200, P_c = 80%, Runs = 20

Mean Best SSE and Mean Generations Until Convergence by Experiment				
Experiment	**Mean Best SSE**	**Improv. over Random/ RW**	**Generations until Convergence**	**Improv. over Random/ RW**
Random, Roulette-Wheel	9.60466E+04	0.00%	274.4	0.00%
Separation, Roulette-Wheel	9.60466E+04	0.00%	245.3	10.61%
Density, Roulette-Wheel	9.60466E+04	0.00%	271.4	1.09%
Random, Deterministic	9.60465E+04	0.00%	315.4	-14.94%
Separation, Deterministic	9.60464E+04	0.00%	294.8	-7.45%
Density, Deterministic	9.60464E+04	0.00%	309.1	-12.67%
Random, Parent Favored Hybrid	9.60468E+04	0.00%	389.8	-42.08%
Separation, Parent Favored Hybrid	9.60466E+04	0.00%	396.7	-44.58%
Density, Parent Favored Hybrid	9.60467E+04	0.00%	450.8	-64.32%

Mean Best SSE by Center Seeding Method and Selection Technique					
Seeding Method	**Mean Best SSE**	**Improv. over Random**	**Selection Technique**	**Mean Best SSE**	**Improv. over RW**
Random	9.60466E+04	0.00%	Roulette-Wheel	9.60466E+04	0.00%
Density	9.60465E+04	0.00%	Deterministic	9.60464E+04	0.00%
Separation	9.60465E+04	0.00%	Parent Favored Hybrid	9.60467E+04	0.00%

Mean Generations until Convergence by Center Seeding Method and Selection Technique					
Seeding Method	**Generations until Convergence**	**Improv. over Random**	**Selection Technique**	**Generations until Convergence**	**Improv. over RW**
Random	326.5	0.00%	Roulette-Wheel	263.7	0.00%
Separation	312.2	4.37%	Deterministic	306.4	-16.22%
Density	343.8	-5.28%	Parent Favored Hybrid	412.4	-56.43%

Discussion of Center Seeding Method Results

To aid in the discussion of results, the table below shows comparisons between random center seeding and each of the heuristic center seeding methods, Density and Separation, based upon percentage improvement of mean best SSE and mean generations until convergence values. The average improvement of heuristic methods over random center seeding is shown for each problem instance. To help highlight the significance of such improvement, *t*-test scores are also shown. A discussion of the results of these comparisons follows.

Table 4:32: Percentage Improvement of Density and Separation Methods over Random

TSP-LIB-1060	Mean Best SSE Improvement				Mean Gen. Until Convergence Improvement			
	Density		Separation		Density		Separation	
	%	*t* score	%	*t* score	%	*t* score	%	*t* score
10	0.00000	0.0000	0.00000	0.0000	-2.84	-0.1864	-12.50	-0.7573
20	0.00000	0.0000	-0.00010	-0.9832	4.22	0.3366	-0.78	-0.0580
30	-0.00273	-0.4710	0.00290	0.5930	-9.06	-0.6229	8.59	0.6451
50	0.01545	0.5868	0.03960	1.6311	-16.83	-1.2113	-18.43	-1.2329
60	0.05519	1.2281	0.13124	2.8819[2]	4.87	0.4212	18.75	1.7387
70	0.01739	0.9458	0.01741	0.8778	1.95	0.1564	2.52	0.2128
80	-0.05217	-1.9503	0.01774	0.7593	5.08	0.6055	14.55	1.4946
90	-0.04214	-1.1420	0.00372	0.10279	7.12	0.7404	18.39	1.8856
100	-0.00897	-0.4951	0.02594	1.4662	-7.35	-0.9455	5.14	0.7360
110	0.03024	0.6084	0.05329	1.1558	-2.77	-0.3032	11.68	1.3801
120	0.03594	0.9591	-0.00208	-0.0411	-13.07	-1.2852	1.50	0.1653
130	-0.03298	-0.5606	0.04825	0.7660	-0.63	-0.0814	6.15	0.6810
140	-0.06049	-0.6789	0.09297	1.4732	-1.82	-0.1921	-2.71	-0.3173
150	0.01935	0.3511	0.07142	1.2196	-9.76	-1.0770	2.51	0.2836
TSP-LIB-3038								
10	0.00000	0.0000	0.00000	0.0000	0.00	0.0000	28.57	1.9452
20	-0.00001	-0.0705	0.00003	0.2044	9.38	0.6708	2.30	0.1500
30	0.00114	0.9848	0.00113	0.9790	4.65	0.3299	3.78	0.2729
40	0.00016	0.7988	0.00018	0.9744	12.79	1.0811	3.16	0.2581
50	-0.00046	-0.0268	0.01239	0.7830	-7.88	-0.6070	-4.90	-0.3584
100	0.02745	1.2011	0.00327	0.1179	-11.29	-1.0615	8.92	0.8870
150	0.00777	0.5279	0.03570	2.4992[1]	-5.20	-0.7942	6.69	1.1099
200	-0.01149	-0.3759	0.04777	0.7333	9.23	1.1218	5.77	0.7333
250	-0.04283	-0.6409	0.02913	0.4983	11.36	1.5460	6.27	0.7457
300	0.07285	0.8850	0.06192	0.6155	-13.57	-1.6378	-0.08	-0.0102
350	0.08355	0.6766	0.12954	1.1044	-12.06	-1.3324	-7.33	-0.8515
400	-0.09692	-0.5131	-0.01734	-0.0875	11.13	1.2363	16.01	1.8960
450	0.27748	1.0169	0.17002	0.5899	-16.21	-1.5764	0.42	0.0392
500	0.07852	0.2341	0.01843	0.0509	1.08	0.1137	9.51	0.9061
SYN1	-1.02082	-0.3833	3.06237	1.7474	10.17	0.8733	99.93	13.9049[3]
SYN2	0.00000	0.0000	0.00000	0.0000	-10.43	-0.9514	61.29	8.4536[3]
SYN3	0.00007	1.26537	0.00009	1.7657	-5.28	-0.7509	4.37	0.6257

1. *t* significant at $p<0.02$ (two tail)
2. *t* significant at $p<0.01$ (two tail)
3. *t* significant at $p<0.001$ (two tail)

Density Center Seeding Method

The Density center seeding method is based on the assumption that there is a higher probability that optimal centers will be located in regions of the data set space that are denser with data points. Because the two TSP-LIB data sets, originally generated to research the traveling salesman problem, do not conform to this assumption, it would not be unexpected if the Density method did no better than random selection on these data sets. This is indeed the case. Regarding the quality of partitions found, the Density method did not produce statistically significant improvement upon random center seeding in any of the 28 configurations tested. Nor did the Density method produce any improvement, however slight, consistently. Of the 25 configurations in which neither random center seeding nor the Density method runs always converged to the same best SSE value, the Density method has a lower mean best SSE value in 14 of them (56%) -- not a statistically significant improvement.

Also, evidence that the Density method would allow the genetic algorithm to more quickly converge was not observed in the experiments. None of the 28 configurations tested show statistically significant increase or reduction in mean generations until convergence by the Density method in comparisons with random center seeding. The Density method has higher mean generations until convergence values than random center seeding in 15 configurations, lower values in 12 of them, and the same value in one.

Unlike the TSP-LIB data sets, the three synthetic data sets contain data points that were generated in a Gaussian distribution about defined centers and therefore conform more closely to the k-means appropriateness assumptions. However, the Density method did not demonstrate statistically significant improvement over random center seeding in either the mean quality of partitions discovered or in mean generations until convergence with these data sets. The Density method produced mean best SSE values that, compared with random center seeding, were slightly higher with SYN1, the same with SYN2, and slightly lower with SYN3. In comparisons with random center seeding, mean generations until convergence values with the Density method were slightly less with SYN1, but slightly higher with the SYN2 and SYN3 data sets.

Based on these comparisons, the Density center seeding method provides no significant advantage over random seeding either in discovering quality partitions or in more quickly evolving better partitions. It should be noted that centers chosen at random will, like the Density method, also have a higher probability of lying in denser areas of data set space. This may account for their similar performance.

Separation Center Seeding Method

The Separation center seeding method employs the k-means++ algorithm which is $O(\log k)$ competitive with the optimal k-clustering on any given data set. Therefore, it might be expected that the Separation method would prove advantageous on all five test data sets. In two of the 31 problem instances tested (TSP-LIB-1060, k = 60 and TSP-LIB-3038, k = 150), the mean best SSE values obtained from experiments using the Separation method show statistically significant improvement over those obtained in experiments with random center seeding, and, in instances where they are worse, the differences are not statistically significant. Also, although the differences are slight, in the 28 problem instances where neither the random center seeding nor the Separation method runs always converged to the same best SSE value, the Separation method has lower mean best SSE values than random seeding in all but three of them (89.3%).

When compared with random center seeding, the Separation method did not produce statistically significant reductions in mean generations until convergence values in any TSP-LIB configuration tested. It did, however, consistently achieve lower values. In 21 of the 28 configurations tested (75%) the genetic algorithm using the Separation method has lower mean generations until convergence values than with random center seeding. Based on these TSP-LIB comparisons, the Separation center seeding method consistently, if only slightly, improves the genetic algorithm's performance with regard to mean best SSE and mean generations until convergence.

With the SYN1 data set, where generated cluster centers are well separated and clusters do not overlap, and SYN2, where about 30% of a generated cluster's data points overlap with those of adjacent clusters, the advantages of the Separation method are more apparent. With these data sets, the genetic algorithm would almost always converge to the apparently optimal partition. However, the Separation method has statistically significant lower mean time to convergence values. That is, the Separation method more quickly converged to the apparently optimal partition than random selection.

In the case of SYN1, in 58 out of the 60 runs using the Separation method the apparently optimal partition was found after running k-means on the initial centers. In the two experiments it did not, the partition was found in the next generation. This result, however, is more likely due to the benefits of the k++ algorithm than to its use in the genetic algorithm. With the SYN3 data set, where all of a generated cluster's data points overlap with those of other clusters, the advantages of the Separation method become less apparent. The Separation method has lower mean generations until convergence values, but the difference is not statistically significant.

The benefit of using the k++ algorithm in selecting centers to seed the genetic algorithm appears to result in an increased probability of the genetic algorithm finding slightly better partitions in slightly fewer generations with data sets that do not have well defined clusters for any value of k than it does using random center seeding. Furthermore, for data sets with well separated cluster centers, the Separation method appears to much more quickly converge to quality partitions than random center seeding.

Contribution of Center Seeding Time to Overall Elapsed Time

To determine the time cost of using heuristic methods for center seeding, the percentage contribution of center seeding time to overall elapsed time was calculated. The results of individual runs are provided in Appendix A, and a summary of the mean percentage contributions of the center seeding methods is shown in the table below. Although the mean percentage contribution for both the Density and Separation methods is consistently greater than random center seeding, the contribution to overall elapsed time is not considered significant. Only in the TSP-LIB-1060, k = 10 configuration, where convergence is quickly achieved, does this percentage contribution exceed one percent of overall elapsed time for either heuristic method.

Table 4.32: Percentage Contribution of Center Seeding Time to Overall Elapsed Time

Method	Minimum Configuration Mean	Maximum Configuration Mean	Average Configuration Mean
Random	0.000	0.078	0.002
Density	0.016	1.273[1]	0.160
Separation	0.032	1.110[1]	0.138

Note 1: Achieved in TSP-LIB-1060, k = 10 configuration

Discussion of Selection Technique Results

To aid in the discussion of results, the table below shows comparisons between Roulette-Wheel selection and the two local tournament techniques, Deterministic and Parent Favored Hybrid, based upon percentage improvement of mean best SSE and mean generations until convergence values. The average improvement of local tournament techniques over random center seeding is shown by problem instance. To help highlight the significance of such improvement, t-test scores are also shown. A discussion of the results of these comparisons follows.

Table 4:33: % Improvement of Deterministic and Parent Favored Hybrid over Roulette-Wheel

TSP-LIB-1060	**Mean Best SSE Improvement**				**Mean Gen. Until Convergence Improvement**			
	Deterministic		**PFH**		**Deterministic**		**PFH**	
	%	*t* score	%	*t* score	%	*t* score	%	*t* score
10	0.000000	0.0000	0.000000	0.0000	-54.87	-3.9052[5]	-136.28	-6.2241[5]
20	0.000099	0.9832	0.000099	0.9832	5.38	0.3539	-68.57	-4.1884[5]
30	0.026157	5.3818[5]	0.024753	5.0347[5]	-22.65	-1.3280	-92.08	-5.1226[5]
50	0.083288	3.2283[3]	0.093300	3.6213[5]	-45.83	-2.8711[2]	-120.37	-7.3574[5]
60	0.235838	5.3149[5]	0.154457	3.9261[5]	-27.59	-2.6570[1]	-89.13	-5.6571[5]
70	0.086943	4.9733[5]	0.070783	3.9489[5]	-27.74	-2.7787[2]	-111.27	-8.0163[5]
80	0.035652	1.2474	-0.022319	-0.7662	-5.93	-0.5681	-51.85	-4.4821[5]
90	0.216698	6.6628[5]	0.180255	5.3337[5]	-24.55	-2.5730[1]	-83.80	-6.8934[5]
100	0.146639	9.6738[5]	0.110792	7.0645[5]	-42.35	-5.4409[5]	-111.54	-14.3192[5]
110	0.281553	7.4160[5]	0.190048	4.6630[5]	-4.92	-0.5806	-50.98	-5.1044[5]
120	0.241855	6.0762[5]	0.153278	3.5058[5]	-24.14	-2.8501[2]	-74.26	-8.0310[5]
130	0.333569	6.8244[5]	0.286509	5.1585[5]	2.81	0.4386	-54.67	-6.7539[5]
140	0.485589	7.2043[5]	0.371100	5.1679[5]	-15.35	-2.1509	-77.23	-8.3418[5]
150	0.323882	7.8884[5]	0.170816	3.1920[3]	-28.02	-3.3829[4]	-67.47	-6.8831[5]
TSP-LIB-3038								
10	0.000000	0.0000	0.000000	0.0000	-59.18	-2.6954[2]	-67.35	-2.3592
20	0.000329	2.0112	0.000328	2.0073	-56.57	-3.0630[3]	-179.20	-7.9798[5]
30	0.001147	0.9908	0.001147	0.9908	-23.33	-1.3482	-133.28	-7.4344[5]
40	0.000945	5.3125[5]	0.000956	5.3845[5]	24.97	2.0242	-49.57	-3.8848[5]
50	0.073959	4.7223[5]	0.058572	3.5239[5]	-5.62	-0.4816	-59.26	-3.7963[5]
100	0.145047	7.2017[5]	0.131086	6.3910[5]	7.08	0.82503	-65.77	-6.9487[5]
150	0.109338	8.9198[5]	0.089449	6.9787[5]	-11.55	-2.3844	-77.41	-12.7022[5]
200	0.146462	6.5090[5]	0.115754	4.2657[5]	15.72	3.2385[4]	-33.39	-4.3407[5]
250	0.450314	12.6149[5]	0.406850	10.2513[5]	11.18	1.5360	-40.45	-4.7654[5]
300	0.617083	10.1289[5]	0.555915	8.8178[5]	19.77	3.0646[3]	-27.70	-3.7037[5]
350	0.870995	19.9424[5]	0.524637	6.5485[5]	7.94	1.3270	-17.47	-1.7872
400	1.462287	17.1459[5]	1.219251	10.7342[5]	-9.63	-1.1204	-49.63	-4.1502[5]
450	2.082851	23.7556[5]	1.779591	13.5559[5]	-51.85	-6.1233[5]	-96.97	-7.7419[5]
500	2.758479	35.5123[5]	2.390835	21.9666[5]	-49.24	-6.9496[5]	-92.65	-7.2122[5]
SYN1	6.865244	2.8487[2]	6.865244	2.8487[2]	15.58	0.8637	-12.08	-0.4167
SYN2	0.000000	0.0000	0.000000	0.0000	-30.97	-2.1475	-132.72	-6.5976[5]
SYN3	0.000176	4.2933[5]	-0.000117	-2.0673	-16.22	-1.9728	-56.43	-6.8959[5]

1. *t* significant at $p<0.02$ (two tail)
2. *t* significant at $p<0.01$ (two tail)
3. *t* significant at $p<0.005$ (two tail)
4. *t* significant at $p<0.002$ (two tail)
5. *t* significant at $p<0.001$ (two tail)

Local tournament selection techniques implement single acceptance and rejection local tournaments where each chromosome in the current generation competes with its most similar parent to participate in the next generation. The assumption is that this will produce a more diverse gene pool than Roulette-Wheel selection, thus avoiding premature convergence and allowing the genetic algorithm to find better quality partitions. Based on experiment results, this appears to be the case for both Deterministic and Parent Favored Hybrid selection techniques. With Deterministic selection, the most fit chromosome always wins the local tournament. With Parent Favored Hybrid, a most fit Parent will always win, and a most fit Child will probably win. Because Parent Favored Selection allows the possibility of Child chromosomes being removed from the gene pool in favor of less fit Parents, it might be expected that Deterministic selection would, on average, produce better partitions. Based on experiment results, this also appears to be the case.

Mean Best SSE Values

Excluding the instances where all runs of both Deterministic and Roulette-Wheel selection always produced the same best SSE value, mean best SSE values are lower with Deterministic selection than with Roulette-Wheel selection in every configuration tested (100%). In 24 of these 28 configurations (85.7%), the improvement in values produced with Deterministic selection is statistically significant.

The mean best SSE values obtained with Parent Favored Hybrid (PFH) selection do not show as much improvement over Roulette-Wheel as do those of Deterministic selection. Excluding the instances where all runs of both PFH and Roulette-Wheel selection always produced the same best SSE value, mean best SSE values are lower with PFH selection than with Roulette-Wheel selection in 26 of 28 configurations (92.9%). In 23 of these 28 configurations (82.1%), the improvement is statistically significant. In the two configurations where PFH produced higher mean best SSE values than Roulette-Wheel, the differences are not statistically significant. Comparing the mean best SSE values of the two local tournament selection techniques, Deterministic selection had lower values in 24 of the 31 configurations, higher values in two, and the same value as PFH in five configurations.

Because premature convergence is more likely to occur in larger search spaces, it might be expected that the improvement in mean best SSE with local tournament selection would tend to increase with the size of the search space. This appears to be the case. Starting with the TSP-LIB-3038, k = 150 configuration, the percentage improvement of Deterministic selection over Roulette-Wheel in mean best SSE increases with each increase in the value of k. The greatest percentage improvements with Deterministic selection in the TSP-LIB data sets are in the TSP-LIB-3038 configurations k = 300 through k = 500, culminating with the largest percentage increase (2.76%) at k = 500. With Parent Favored Hybrid selection, its largest percentage improvements in mean best SSE in the TSP-LIB data sets are in the TSP-LIB-3038 configurations k = 250 through k = 500, with the k =500 configuration having the largest percentage improvement (2.39%).

Mean Generations Until Convergence

Since the avoidance of premature convergence would seem to imply more generations until convergence, it might be expected that the mean generations until convergence values would be greater with local tournament selection than with Roulette-Wheel selection. This is clearly the case with Parent Favored Hybrid. The genetic algorithm experienced greater mean generations until convergence values with PFH selection than with Roulette-Wheel selection in all 31 configurations tested. In all but two of the configurations, the differences were statistically significant.

With Deterministic selection the results are less clear. In 22 of the 31 configurations tested (71%) the use of Deterministic selection resulted in resulted in higher mean times until convergence values than Roulette-Wheel selection. In 12 of these configurations the differences were statistically significant. However, of the nine configurations where Deterministic selection has lower mean generations until convergence values, in two of them, TSP-LIB-3038, k = 200 and TSP-LIB-3038, k = 300, the differences are statistically significant and Deterministic also has statistically significant lower mean best SSE values in these configurations.

Some insight can be gained from inspecting the standard deviations in mean generations until convergence values of the three selection methods. These values are shown in the table below for configurations with larger search spaces. The percentage column (%) indicates the standard deviation's percent of the mean.

Table 4:34: Generations Until Convergence Mean and Standard Deviation Values

TSP-LIB-3038	**Roulette-Wheel**			**Deterministic**			**Parent Favored Hybrid**		
	μ	**σ**	**%**	**μ**	**σ**	**%**	**μ**	**σ**	**%**
k = 500	1189.10	346.57	29.15	1774.63	244.49	13.78	2290.80	744.84	32.51
k = 450	1172.07	466.98	39.84	1779.77	223.04	12.53	2308.60	595.22	25.78
k = 400	1315.50	585.73	44.53	1442.13	163.49	11.34	1968.43	571.10	29.01
k = 350	1475.73	365.26	24.75	1358.50	177.37	13.06	1733.60	654.41	48.17
k = 300	1261.00	394.22	31.26	1011.67	170.94	16.90	1610.30	313.61	19.48
k = 250	1094.57	357.27	32.64	972.23	173.78	17.87	1537.37	312.19	20.31
k = 200	1024.03	226.55	22.12	863.07	127.27	14.75	1365.93	328.38	24.04

Use of Deterministic selection resulted in lower generations until convergence standard deviation values, and often lower mean values, than the other two selection techniques. With Parent Favored Hybrid, this is perhaps due to its probabilistic removal of Child chromosomes from the gene pool in favor of less fit Parents. Quality partitions must often be rediscovered, delaying convergence, and if quality partitions are not rediscovered, premature convergence may occur.

In the case of Roulette-Wheel, the greater variance could be a result of premature convergence in some of the runs, and also taking longer than Deterministic selection to achieve convergence in other runs. That is, Deterministic selection may converge to quality partitions more consistently and, sometimes, more quickly than Roulette-Wheel selection. This is illustrated in the following table which shows, for two of the configurations, the best SSE values and generation found from runs with Deterministic and Roulette-Wheel selection techniques paired with a center seeding method. In every comparison, fewer generations were required by Deterministic selection to find the partition, and in every case save one it found the better partition.

Table 4:35: Best SSE and Generation Found by Deterministic and Roulette-Wheel Selection

TSP-LIB-3038	**Roulette-Wheel**		**Deterministic**	
k = 300	**Best SSE**	**Gen. found**	**Best SSE**	**Gen. found**
Random	1.33235E+07	2042	1.32873E+07	1021
Separation	1.33292E+07	1639	1.32820E+07	1065
Density	1.33152E+07	1877	1.32863E+07	1041
k = 200				
Random	2.19211E+07	1158	2.19020E+07	942
Separation	2.18863E+07	1083	2.18868E+07	906
Density	2.19138E+07	1166	2.18916E+07	934

Both local tournament selection techniques have shown, based on experiment results, to consistently allow the genetic algorithm to find better quality partitions than with Roulette-Wheel selection. However, their performance is not equivalent. Deterministic selection consistently found better quality partitions in fewer generations than Parent Favored Hybrid. While both local tournament techniques consistently require more generations to reach convergence, Deterministic selection appears to better avoid premature convergence and to converge to quality partitions more consistently than either Parent Favored Hybrid or Roulette-Wheel selection.

Discussion of Combinations of Center Seeding Methods and Selection Techniques

A goal of this research was to investigate the performance of combinations of center seeding methods and selection techniques to better understand if there are specific combinations that, on average, produce better partitions, either in certain test configurations or across all of them. A discussion of the experiment results of these combinations follows. To facilitate this discussion, the table below shows, for each configuration, the mean best SSE rankings of the nine combinations of center seeding methods and selection techniques. A ranking of one indicates the combination has the lowest mean best SSE for the configuration. Combinations that have the same mean best SSE receive the same ranking. In the table, the specific center seeding method/selection technique combinations are noted as follows:

RRW	Random/Roulette Wheel
SRW	Separation/ Roulette-Wheel
DRW	Density/ Roulette-Wheel
RD	Random/Deterministic
SD	Separation/Deterministic
DD	Density/Deterministic
RPFH	Random/ Parent Favored Hybrid
SPFH	Separation/Parent Favored Hybrid
DPFH	Density/Parent Favored Hybrid

Table 4:36: Ranking of Center Seeding/Selection Combinations Based on Mean Best SSE

TSP-LIB-1060	RRW	SRW	DRW	RD	SD	DD	RPFH	SPFH	DPFH
k = 10	1	1	1	1	1	1	1	1	1
20	1	9	1	1	1	1	1	1	1
30	8	7	9	1	1	4	3	5	6
50	9	7	8	6	2	4	5	1	3
60	9	7	8	4	1	3	6	2	5
70	9	8	7	4	1	3	5	2	6
80	2	7	8	6	1	3	5	4	9
90	7	8	9	2	1	4	5	3	6
100	9	7	8	2	1	4	5	3	6
110	9	7	8	1	2	3	6	5	4
120	8	9	7	3	1	2	6	5	4
130	7	9	8	5	1	3	4	2	6
140	8	7	9	2	1	3	6	4	5
150	9	8	7	3	1	2	5	4	6
Mean	**6.86**	**7.21**	**7.00**	**2.93**	**1.14**	**2.86**	**4.50**	**3.00**	**4.86**
TSP-LIB-3038	RRW	SRW	DRW	RD	SD	DD	RPFH	SPFH	DPFH
k = 10	1	1	1	1	1	1	1	1	1
20	8	7	9	1	1	1	1	6	1
30	9	8	1	1	1	1	1	1	1
40	9	7	8	1	1	6	1	1	1
50	7	8	9	4	2	3	6	1	5
100	9	8	7	2	3	1	5	4	6
150	9	7	8	3	1	4	5	2	6
200	9	7	8	5	1	4	2	3	6
250	8	7	9	2	3	1	6	4	5
300	9	8	7	4	1	2	6	3	5
350	9	7	8	2	1	3	6	5	4
400	8	9	7	3	1	2	4	5	6
450	9	8	7	2	1	3	6	5	4
500	8	9	7	1	2	3	5	4	6
Mean	**8.00**	**7.21**	**6.86**	**2.29**	**1.43**	**2.50**	**3.93**	**3.21**	**4.07**
Synthetic Data Sets	RRW	SRW	DRW	RD	SD	DD	RPFH	SPFH	DPFH
SYN1	7	1	8	1	1	1	1	1	1
SYN2	1	1	1	1	1	1	1	1	1
SYN3	5	7	4	3	1	2	9	6	8
Mean	**7.13**	**3.00**	**4.33**	**1.67**	**1.00**	**1.33**	**3.67**	**2.67**	**3.33**
Mean All	**7.36**	**6.90**	**6.82**	**2.57**	**1.29**	**2.59**	**4.28**	**3.15**	**4.46**
Mean TSP	**7.43**	**7.21**	**6.93**	**2.61**	**1.29**	**2.68**	**4.21**	**3.11**	**4.46**
Total #1 Rankings	4	4	4	11	25	9	8	8	8

Because experiment results indicate the Separation center seeding method provides a consistent, if slight, improvement with regard to mean best SSE, and because Deterministic selection appears to consistently converge to better quality partitions than either Parent Favored Hybrid or Roulette-Wheel selection, it might be expected that the combination of the two would also perform well. This is clearly the case. The Separation/Deterministic combination performed better than any other combination.

In all three test data sets, Separation/Deterministic achieved the lowest mean best SSE value more times than any other combination, and has the best (lowest) ranking in all three as well. In 25 of the 32 configurations, Separation/Deterministic has the lowest mean best SSE value, more than twice the number of the next best combination, Random/Deterministic. Further, in no configuration does Separation/Deterministic have worse than the third lowest mean best SSE value.

Overall and in every data set, the Deterministic selection combinations were the three top-ranked configurations. Also overall and in the two TSP-LIB data sets, the Roulette-Wheel combinations were the lowest ranked. That the performance groupings of combinations are by selection technique is understandable since selection techniques affect every generation, whereas initial center seeding occurs just once. The exception to this grouping occurs in the synthetic data sets where, because of rapid convergence, the benefits of the k++ algorithm favor the Separation method combinations, and Separation/Roulette-Wheel is the fifth ranked combination.

Regarding the performance of Separation/Deterministic, perhaps the combination of Separation center seeding, region-based crossover, and Deterministic selection work well together in finding superior clusters under k-means. Separation center seeding selects initial centers with an objective of having them well separated spatially from each other. Region-based crossover preserves subsets of centers occupying the same region of space for use as building blocks for subsequent generations. Deterministic selection conducts local tournaments between chromosomes which share these building blocks. Thus, because of the way chromosomes are initially selected, maintained through crossover, and improved through local competitions, they evolve to represent good solutions to subsets of space that are spread throughout the data set space and eventually converge to good quality partitions.

Comparison with Best Known Results

The following table compares the lowest SSE values obtained in the experiments with prior best-known values for the 14 TSP-LIB-1060 and 14 TSP-LIB-3038 configurations. When multiple runs achieved the value, the run that converged in the fewest generations is shown. The Error column represents the difference between the best experiment SSE and the best known SSE expressed as a percentage of the best known SSE. As noted earlier, the genetic algorithm used in this research was not developed to achieve new best-known k-means clustering solutions. However, new best-known values were found in 8 of the 28 TSP-LIB configurations tested. Appendix B contains the output of the runs in which new best-known values were achieved.

Table 4:37: Comparison with Best Known SSE

TSP-LIB-1060					
k	**Best Known SSE[1]**	**SSE**	**Gens.**	**Error**	**Configuration[2]**
10	1.75484E+09	1.75484E+09	0	0.00	SD, μ = 100, P_c = 1.0
20	7.91794E+08	7.91795E+08	9	0.00	SRW, μ = 100, P_c = 1.0
30	4.81251E+08	4.81252E+08	61	0.00	SD, μ = 100, P_c = 1.0
50	2.55509E+08	2.55510E+08	211	0.00	DD, μ = 100, P_c = 1.0
60	1.97273E+08	1.97273E+08	246	0.00	SD, μ = 100, P_c = 1.0
70	1.58450E+08	1.58453E+08	259	0.00	SD, μ = 100, P_c = 1.0
80	1.28890E+08	1.28890E+08	218	0.00	SD, μ = 100, P_c = 1.0
90	1.10417E+08	1.10436E+08	1002	0.02	SPFH, μ = 100, P_c = 1.0
100	9.63303E+07	9.63179E+07	437	-0.01	SD, μ = 200, P_c = 0.8
110	8.48397E+07	8.48397E+07	530	0.00	SD, μ = 200, P_c = 1.0
120	7.55451E+07	7.56048E+07	619	0.08	SD, μ = 200, P_c = 1.0
130	6.75542E+07	6.75542E+07	411	0.00	SD, μ = 200, P_c = 1.0
140	6.11217E+07	6.11299E+07	450	0.01	SD, μ = 200, P_c = 1.0
150	5.59233E+07	5.59170E+07	1204	-0.01	DD, μ = 100, P_c = 1.0

TSP-LIB-3038					
k	**Best Known SSE[1]**	**SSE**	**Gens.**	**Error**	**Configuration[2]**
10	5.60251E+08	5.60251E+08	0	0.00	RRW, μ = 100, P_c = 1.0
20	2.66812E+08	2.66812E+08	13	0.00	SRW, μ = 100, P_c = 1.0
30	1.75538E+08	1.75539E+08	15	0.00	DRW, μ = 100, P_c = 1.0
40	1.24961E+08	1.24961E+08	32	0.00	RRW, μ = 100, P_c = 1.0
50	9.82442E+07	9.82426E+07	203	-0.002	RD, μ = 100, P_c = 1.0
100	4.76642E+07	4.76700E+07	622	0.01	SD, μ = 100, P_c = 1.0
150	3.05222E+07	3.05277E+07	960	0.02	SD, μ = 200, P_c = 0.8
200	2.18540E+07	2.18604E+07	1038	0.03	SD, μ = 200, P_c = 1.0
250	1.65963E+07	1.65970E+07	1202	0.00	SD, μ = 200, P_c = 1.0
300	1.32770E+07	1.32718E+07	906	-0.04	SD, μ = 200, P_c = 1.0
350	1.10428E+07	1.10137E+07	1295	-0.26	SD, μ = 200, P_c = 1.0
400	9.38037E+06	9.36129E+06	1562	-0.20	SD, μ = 200, P_c = 1.0
450	8.14437E+06	8.10160E+06	2073	-0.53	SD, μ = 200, P_c = 1.0
500	7.15643E+06	7.11014E+06	1702	-0.65	SD, μ = 200, P_c = 1.0

Note 1: Found in 200 generations

Note 2: DD = Density/Deterministic, RD = Random/Deterministic, SD = Separation/Deterministic, RRW = Random/Roulette-Wheel, DRW = Density/Roulette-Wheel, SRW = Separation/Roulette-Wheel, SPFH = Separation/Parent Favored Hybrid

Chapter 5

Conclusions, Implications, Recommendations, and Summary

Conclusions

The goal of this research was to develop improved GA-based methods for center selection in k-means by investigating alternative initial center seeding strategies, and to empirically investigate factors that affect the rate of convergence to good quality partitions. Specifically, the research empirically investigated the merits of using:

1. alternative initialization strategies to introduce good centers and more quickly evolve better partitions,
2. techniques to prevent premature convergence, and
3. combinations of these strategies and techniques.

The alternative center seeding strategies were separately evaluated both with and without the use of techniques to prevent premature convergence. The evaluations employed three synthetic data sets and also two benchmark data sets previously used in other studies. The strategies and techniques were evaluated based upon (1) the fitness of the partitions produced as measured by their SSE, (2) the relative center seeding time cost as measured by percentage of overall execution time, and (3) the number of generations necessary to converge to good solutions. Evaluation factors included the fitness of partitions at convergence and the number of iterations necessary to converge.

Based on these evaluations, specific research questions can be addressed:

Does the use of alternative strategies for selecting the initial population improve the rate of convergence to good quality partitions, thus providing an improved GA-based method for center selection in k-means, or does their use exacerbate premature convergence?

Two alternative strategies were evaluated, Density and Separation. The Density center seeding method is based on the assumption that there is a higher probability that optimal centers will be located in regions of the data set space that are denser with data points. The Separation center seeding method employs the k-means++ algorithm with an objective of having chromosome centers well separated spatially from each other. Based on the evaluations, the Density center seeding method provides no significant advantage over random seeding either in discovering quality partitions or in more quickly evolving better partitions. However, the Separation center seeding method appears to result in an increased probability of the genetic algorithm finding slightly better partitions in slightly fewer generations. Furthermore, for data sets with well separated cluster centers, the Separation method appears to much more quickly converge to quality partitions than random center seeding.

Does the additional execution time cost of implementing such strategies negate any benefit?

To determine the time cost of using heuristic methods for center seeding, the percentage contribution of center seeding time to overall elapsed time was calculated. Although the mean percentage contribution for both the Density and Separation methods is consistently greater than random center seeding, the contribution to overall elapsed time is not considered significant.

Are the benefits of alternative strategies affected by the degree of conformance to the k-means appropriateness conditions?

Yes. With the SYN1 data set, where generated cluster centers are well separated and clusters do not overlap, and SYN2, where about 30% of a generated cluster's data points overlap with those of adjacent clusters, the advantages of the Separation method is more apparent. The Separation method had statistically significant lower mean time to convergence values than random center seeding.

Are there effective techniques to reduce the risk of premature convergence? Is one technique better than others, in general, at mitigating premature convergence, or does effectiveness vary by configuration? Can inferences be made as to the circumstances under which a particular technique would be preferable?

Two local tournament selection techniques were evaluated, Deterministic and Parent Favored Hybrid. Local tournament selection techniques implement single acceptance and rejection local tournaments where each chromosome in the current generation competes with its most similar parent to participate in the next generation. With Deterministic selection, the most fit chromosome always wins the local tournament. With Parent Favored Hybrid, a most fit Parent will always win, and a most fit Child will probably win.

Across all data sets, both local tournament selection techniques have shown to consistently allow the genetic algorithm to find better quality partitions than with Roulette-Wheel selection. However, their performance is not equivalent. Deterministic selection consistently found better quality partitions in fewer generations than Parent Favored Hybrid. Deterministic selection appears to better avoid premature convergence and to converge to quality partitions more consistently than either Parent Favored Hybrid or Roulette-Wheel selection.

What, if any, are the specific combinations of strategies and techniques that, on average, produce better partitions in fewer generations for each of the test configurations? Are there specific combinations that provide good quality solutions across all configurations? Does the analysis support general guidance regarding the specific combinations to employ based upon data characteristics or k values?

In all five test data sets, the combination of Separation center seeding and Deterministic selection performed better than any other combination. The Separation/Deterministic combination achieved the lowest mean best SSE value more than twice as often as any other combination. Further, in no configuration does Separation/Deterministic have worse than the third lowest mean best SSE value. Regarding which combination to employ, while Deterministic selection often requires more generations to achieve convergence than Roulette-Wheel, and the mean percentage contribution to overall elapsed time of the Separation methods is consistently greater than random center seeding, these factors are not considered significant in comparison with their performance benefit across all tested configurations.

Implications

Prior to this research, no rigorous systematic examination of the use of heuristics and crowding methods on center selection in k-means genetic algorithms had been performed. This research has contributed to knowledge in the areas of clustering, crowding, and genetic algorithms. More specifically, this research has made the following contributions:

Clustering

The k-means++ algorithm has been shown to be $O(\log k)$ competitive with the optimal k-clustering on any given data set (Arthur & Vassilvitskii, 2007). Further, using both synthetic and real-world data sets, the authors reported preliminary experiments where k-means++ consistently outperformed k-means in both accuracy (lower SSE) and speed (faster run time). Because k-means++ chooses the first cluster center at random and probabilistically chooses the others based upon their distance from previously selected centers, k-means++ could be used by a genetic algorithm to select a diverse initial population of cluster centers. However, prior to this research, no rigorous evaluation of the use of k-means ++ with a genetic algorithm had been performed. As a result of this research, new insight has been gained regarding the applicability and effectiveness of this pairing.

Crowding

As a means of slowing down convergence in genetic algorithms, crowding techniques strive to maintain diverse solutions by replacing population members with members that are similar to them. Local tournament algorithms are a type of crowding technique in which similar members compete directly against each other for survival. The winners of local tournaments can be decided either deterministically or probabilistically, and both have been shown, analytically and experimentally, to provide stable and predictable convergence (Mengshoel & Goldberg, 2008). However, prior to this research, no rigorous evaluation had been done regarding their effectiveness and performance in genetic algorithms when compared with roulette-wheel sampling. The clear and consistent results of this research provide insight and guidance as to their usefulness and applicability, at least with regard to k-means genetic algorithms.

Genetic Algorithms

Random selection is the method most often used by genetic algorithms for seeding the initial population of chromosomes. By evaluating the merits of alternative initialization strategies to more quickly evolve better partitions under k-means, and providing results that indicate the extent of their effectiveness, this research provides new and useful information relevant to the development both of improved GA-based methods for center seeding in k-means, and genetic algorithms in general.

Likewise, in traditional genetic algorithms, individuals are typically selected to pass to the next generation by variants of roulette-wheel sampling which probabilistically select the most fit chromosomes regardless of genetic similarity. By evaluating the use of techniques to reduce the likelihood of premature convergence, this research provides new and useful information regarding the effectiveness of specific techniques, and the configurations and circumstances under which a particular technique might be employed.

Recommendations

The results of this research suggest future research in two areas. First, this research indicates that alternative approaches to choosing the initial population in genetic algorithms, other than random selection, have some benefit, at least with regard to k-means ++ and k-means genetic algorithms. Further investigation into the benefits of chromosome-seeding approaches that, similar to k-means ++, attempt to select initial chromosomes based on their probability of having close to optimal genes is suggested.

Second, this research indicates that local tournament selection implementing the Deterministic rule significantly improves the ability of k-means genetic algorithms to find quality partitions. Further investigation into the ability of Deterministic selection to improve genetic algorithm performance in other areas is suggested.

Summary

Data clustering involves partitioning data points into clusters where data points within the same cluster have high similarity, but are dissimilar to the data points in other clusters. Similarity is assessed using specific attribute value(s). Similarity is often measured with distance, where two or more objects are deemed to belong to the same cluster if they are close based upon the distance metric used. Clustering has wide applications in pattern recognition, statistics, data-mining, and machine learning.

Because of its computational efficiency the k-means algorithm is among the most extensively used clustering techniques. Given a set of data points $\{x_1,...,x_n\}$ in d-dimensional space and an integer k, the k-means algorithm attempts to partition the data points into k partitions (clusters) C_1,..., C_k such that the sum of the squared Euclidean distance (SSE) between each data point and the centroid of its cluster is minimized. SSE is defined as $\sum_{i=1}^{k}\sum_{j=1}^{n_i}\left\|x_{ji}-c_i\right\|^2$ where n_i is the number of data points in cluster C_i, x_{ji} is the jth data point in cluster C_i, and $c_i = \frac{1}{n_i}\sum_{j=1}^{n_i} x_{ji}$ is the centroid for cluster C_i. The algorithm starts with an initial set of k points, called centers. Partitions are formed by assigning data points to their closest center. Centers are then moved to the centroid of their partition, and data points are again assigned to their closest center. This process iterates until partitions are stable.

One drawback of k-means is that it is extremely sensitive to the initial choice of centers. While k-means will always terminate with a partition, different choices of initial cluster centers usually result in different partitions. Because of the algorithm's sensitivity, when random selection is used to choose initial centers, it is likely that k-means will produce partitions that are quite inferior to the global optimum. Finding a better method for initial center seeding is an active area of research.

To increase the likelihood of finding good k-partitions, genetic algorithms (GA), which are modeled after the process of natural evolution, have been successfully used to evolve successive generations of cluster centers. A classical problem of genetic algorithms is premature convergence. This occurs when there is not enough genetic diversity in the population of chromosomes. Through repeated selection pressure, the genes of a few closely related but less than optimal chromosomes can eventually dominate the gene pool, resulting in the GA becoming stuck on a local maxima and unable to explore better solutions.

The goal of this research was to develop improved GA-based methods for center selection in k-means by investigating alternative initial center seeding strategies, and to empirically investigate factors that affect the rate of convergence to good quality partitions. Specifically, the research empirically investigated the merits of using:

1. alternative initialization methods to introduce good centers and more quickly evolve better partitions,

2. techniques to prevent premature convergence, and
3. combinations of these strategies and techniques.

The research involved developing (1) a genetic algorithm that enabled the methods and techniques to be evaluated, both independently and in combination; (2) algorithms to implement alternative initialization methods for seeding initial centers; and (3) an implementation of techniques to prevent premature convergence.

The genetic algorithm developed for the investigations was based on the genetic algorithm presented in (Laszlo & Mukherjee, 2007). The Laszlo and Mukherjee GA has demonstrated an ability to find good partitions and provides a solid performance baseline with which methods and techniques can be compared.

Two alternative initialization methods for initial center seeding were tested, Density and Separation. The Density method increases the probability that initial centers are chosen from denser regions of the data set space. The Separation center seeding method employs the k-means++ algorithm with an objective of having chromosome centers well separated spatially from each other.

Two local tournament selection techniques were evaluated on their ability to prevent premature convergence, Deterministic and Parent Favored Hybrid. Local tournament selection techniques implement single acceptance and rejection local tournaments where each chromosome in the current generation competes with its most similar parent to participate in the next generation. With Deterministic selection, the most fit chromosome always wins the local tournament. With Parent Favored Hybrid, a most fit Parent will always win, and a most fit Child will probably win.

A combination of data sets and k-values enabled an evaluation of the alternative center seeding methods and local tournament selection techniques over a variety of conditions. Experiments were conducted with both synthetic and benchmark data sets. Three synthetic data sets were used.

The first data set, SYN1, has cluster centers separated by eight standard deviations, thus clusters are well separated and do not overlap. The other two synthetic data sets were generated with overlapping centers. SYN2 has generated cluster centers separated by three standard deviations and about 30% of a generated cluster's data points overlap with those of adjacent clusters. SYN3 has generated cluster centers separated by one standard deviation such that all of a generated cluster's data points overlap with those of other clusters.

Experiments were also conducted using two benchmark data sets for which best known partitions have previously been published for different values of k. TSP-LIB-1060 and TSP-LIB-3038, originally generated to research the traveling salesman problem, do not have well defined clusters for any value of *k*.

Based on the experiment results, the Density center seeding method provides no significant advantage over random seeding either in discovering quality partitions or in more quickly evolving better partitions. However, the Separation center seeding method appears to result in an increased probability of the genetic algorithm finding slightly better partitions in slightly fewer generations. Furthermore, for data sets with well separated cluster centers, the Separation method appears to much more quickly converge to quality partitions than random center seeding.

Regarding experiment results with selection techniques, across all data sets both local tournament selection techniques consistently allowed the genetic algorithm to find better quality partitions than Roulette-Wheel selection. However, their performance is not equivalent. Deterministic selection consistently found better quality partitions in fewer generations than Parent Favored Hybrid. Deterministic selection appears to better avoid premature convergence and to converge to quality partitions more consistently than either Parent Favored Hybrid or Roulette-Wheel selection.

The combination of Separation center seeding and Deterministic selection performed better than any other combination in all five test data sets. The Separation/Deterministic combination achieved the lowest mean best SSE value more than twice as often as any other combination. While Deterministic selection often requires more generations to achieve convergence than Roulette-Wheel, and the mean percentage contribution to overall elapsed time of the Separation methods is consistently greater than random center seeding, these factors are not considered significant in comparison with their performance benefit across all tested configurations.

The genetic algorithm used in this research was not developed to achieve new best-known k-means clustering solutions. However experiments often found partitions with lower SSE values than the prior best-known values. New best-known values were found in 8 of the 28 TSP-LIB configurations tested.

About Appendixes

Appendix A contains tables of experiment results. Appendix B contains the output of runs that produced new best-known solutions for some values of *k* with the TSP-LIB data sets. Appendix C contains a printout of the genetic algorithm source code.

In Appendix A, a run with a Best SSE value shown in bold indicates the lowest SSE value of the experiment. The % Seeding value indicates the percentage of elapsed time used for initial center seeding.

Appendix A: Experiment Results

Preliminary Tests

Random, Child Preferred Hybrid, TSP-LIB-1060, *k* = 100, u = 200, p = 0.8

Run	Best SSE	Gen. found
1	1.030686729491360E+08	89
2	1.019823346131080E+08	406
3	1.024802656525130E+08	94
4	1.008969170309110E+08	316
5	1.018306744016500E+08	199
6	1.029035243436180E+08	62
7	1.033635107388020E+08	207
8	1.026921341944900E+08	75
9	1.039756758673710E+08	110
10	1.028980750690680E+08	391
Mean	**1.026091784860670E+08**	**194.9**
Std. Dev.	**8.674297558065820E+05**	**132.7022147**
Var.	**7.524343812586670E+11**	**1.760987777777780E+04**

Random, Deterministic, TSP-LIB-1060, *k* = 100, u = 200, p = 0.8

Run	Best SSE	Gen. found
1	9.639479254094640E+07	384
2	9.641340104406090E+07	447
3	9.631786446113120E+07	505
4	9.633029639945040E+07	566
5	9.640722447926560E+07	403
6	9.640722447926560E+07	289
7	9.631786446113120E+07	607
8	9.633029639945040E+07	472
9	9.639752272068530E+07	349
10	9.639479254094640E+07	399
Mean	**9.637112795263340E+07**	**442.1**
Std. Dev.	**4.112051733353770E+04**	**97.91543971**
Var.	**1.690896945777780E+09**	**9.5874E+03**

Random, Parent Preferred Hybrid, TSP-LIB-1060, *k* = 100, u = 200, p = 0.8

Run	Best SSE	Gen. found
1	9.640369928548060E+07	683
2	9.635627301991570E+07	691
3	9.640653072414950E+07	449
4	9.639479254094640E+07	674
5	9.639479254094640E+07	762
6	9.640722447926560E+07	668
7	9.641340104406090E+07	847
8	9.640096910574170E+07	771
9	9.640722447926560E+07	534
10	**9.634145610248990E+07**	823
Mean	**9.639263633222620E+07**	**690.2**
Std. Dev.	**2.402009425460280E+04**	**123.5087041**
Var.	**5.769649280000000E+08**	**1.5254E+04**

Random, Probabilistic, TSP-LIB-1060, *k* = 100, u = 200, p = 0.8

	Random, Probabilistic	
Run	**Best SSE**	**Gen. found**
1	1.058160763601020E+08	36
2	1.060398959951100E+08	69
3	1.048667927651380E+08	121
4	1.042413189575560E+08	180
5	1.039045284535680E+08	233
6	1.055170608265700E+08	96
7	1.049954501933180E+08	206
8	**1.036313120404780E+08**	100
9	1.048573470982840E+08	104
10	1.045112060452350E+08	121
Mean	**1.048380988735360E+08**	**126.6**
Std. Dev.	**7.943265679890940E+05**	**61.66252238**
Var.	**6.309546966133330E+11**	**3.802266666666670E+03**

Random Roulette-Wheel, TSP-LIB-1060, *k* = 100, u = 200, p = 0.8

Run	Best SSE	Gen. found
1	9.654901317929910E+07	479
2	9.656236571547050E+07	594
3	9.659458839439540E+07	344
4	9.657436619539540E+07	495
5	9.661753350383720E+07	502
6	9.676431399333330E+07	118
7	9.645269207822220E+07	507
8	9.663563001201480E+07	394
9	9.647163493607370E+07	787
10	9.661675347289480E+07	508
Mean	**9.658388914809360E+07**	**472.8**
Std. Dev.	**8.764871768599930E+04**	**171.8803201**
Var.	**7.682297712000000E+09**	**2.9543E+04**

TSP-LIB-1060, *k* = 10 Results

Density, Deterministic, TSP-LIB-1060, *k* = 10, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.75484021406002E+09	6	0.68380%
2	1.75484021406002E+09	3	1.22640%
3	1.75484021406002E+09	6	1.21170%
4	1.75484021406002E+09	5	0.65530%
5	1.75484021406002E+09	5	1.31940%
6	1.75484021406002E+09	7	0.66860%
7	1.75484021406002E+09	4	0.90440%
8	**1.75484021406002E+09**	1	0.70820%
9	1.75484021406002E+09	7	0.77920%
10	1.75484021406002E+09	6	0.99470%
Mean	**1.75484021406002E+09**	**5**	**0.91517%**
Std. Dev.	**0.000000**	**1.885618083**	**0.0025773**
Var.	**0.000000**	**3.5556E+00**	**6.64247E-06**

Density, Parent Favored Hybrid, TSP-LIB-1060, *k* = 10, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.75484021406002E+09	16	0.56320%
2	1.75484021406002E+09	5	0.65820%
3	1.75484021406002E+09	8	0.65090%
4	1.75484021406002E+09	9	0.64780%
5	**1.75484021406002E+09**	0	0.69590%
6	1.75484021406002E+09	8	0.78170%
7	1.75484021406002E+09	10	0.75780%
8	1.75484021406002E+09	12	0.63830%
9	1.75484021406002E+09	12	0.66150%
10	1.75484021406002E+09	8	0.59580%
Mean	**1.75484021406002E+09**	**8.8**	**0.66511%**
Std. Dev.	**0.000000**	**4.315347289**	**0.000663353**
Var.	**0.000000**	**1.8622E+01**	**4.40037E-07**

Density, Roulette=Wheel, TSP-LIB-1060, *k* = 10, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	**1.75484021406002E+09**	3	1.85130%
2	1.75484021406002E+09	4	1.62090%
3	1.75484021406002E+09	5	1.73830%
4	1.75484021406002E+09	3	1.69160%
5	1.75484021406002E+09	4	1.89580%
6	1.75484021406002E+09	6	1.87700%
7	1.75484021406002E+09	6	1.68870%
8	1.75484021406002E+09	3	1.71380%
9	1.75484021406002E+09	4	1.73750%
10	1.75484021406002E+09	5	1.67150%
Mean	**1.75484021406002E+09**	**4.3**	**1.74864%**
Std. Dev.	**0.000000**	**1.159501809**	**0.000938265**
Var.	**0.000000**	**1.3444E+00**	**8.80341E-07**

Random, Deterministic, TSP-LIB-1060, *k* = 10, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.75484021406002E+09	5	0.08480%
2	1.75484021406002E+09	6	0.04420%
3	**1.75484021406002E+09**	3	0.19080%
4	1.75484021406002E+09	5	0.08560%
5	1.75484021406002E+09	10	0.08500%
6	1.75484021406002E+09	7	0.05240%
7	1.75484021406002E+09	5	0.00000%
8	1.75484021406002E+09	9	0.04510%
9	1.75484021406002E+09	4	0.00000%
10	1.75484021406002E+09	7	0.04500%
Mean	**1.75484021406002E+09**	**6.1**	**0.06329%**
Std. Dev.	**0.000000**	**2.183269719**	**0.000546201**
Var.	**0.000000**	**4.7667E+00**	**2.98336E-07**

Random, Parent Favored Hybrid, TSP-LIB-1060, *k* = 10, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.75484021406002E+09	12	0.08110%
2	1.75484021406002E+09	8	0.00000%
3	1.75484021406002E+09	8	0.03380%
4	1.75484021406002E+09	7	0.07820%
5	1.75484021406002E+09	16	0.06980%
6	1.75484021406002E+09	5	0.05220%
7	1.75484021406002E+09	11	0.03440%
8	**1.75484021406002E+09**	4	0.04140%
9	1.75484021406002E+09	8	0.00000%
10	1.75484021406002E+09	7	0.00000%
Mean	**1.75484021406002E+09**	**8.6**	**0.03909%**
Std. Dev.	**0.000000**	**3.533962208**	**0.000317084**
Var.	**0.000000**	**1.2489E+01**	**1.00542E-07**

Random, Roulette=Wheel, TSP-LIB-1060, *k* = 10, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.75484021406002E+09	2	0.11160%
2	1.75484021406002E+09	3	0.11320%
3	**1.75484021406002E+09**	1	0.00000%
4	1.75484021406002E+09	6	0.00000%
5	1.75484021406002E+09	5	0.23100%
6	1.75484021406002E+09	2	0.11570%
7	1.75484021406002E+09	4	0.19520%
8	1.75484021406002E+09	3	0.11090%
9	1.75484021406002E+09	2	0.11640%
10	1.75484021406002E+09	1	0.33500%
Mean	**1.75484021406002E+09**	**2.9**	**0.13290%**
Std. Dev.	**0.000000**	**1.663329993**	**0.001008673**
Var.	**0.000000**	**2.7667E+00**	**1.01742E-06**

Separation, Deterministic, TSP-LIB-1060, *k* = 10, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.75484021406002E+09	7	0.73180%
2	1.75484021406002E+09	7	1.37650%
3	1.75484021406002E+09	7	0.56580%
4	1.75484021406002E+09	4	1.13810%
5	1.75484021406002E+09	9	1.26190%
6	1.75484021406002E+09	7	0.83640%
7	1.75484021406002E+09	7	0.98230%
8	1.75484021406002E+09	6	1.14600%
9	1.75484021406002E+09	10	0.94790%
10	**1.75484021406002E+09**	0	0.96170%
Mean	**1.75484021406002E+09**	**6.4**	**0.99484%**
Std. Dev.	**0.000000**	**2.75680975**	**0.002454442**
Var.	**0.000000**	**7.6000E+00**	**6.02428E-06**

Separation, Parent Favored Hybrid, TSP-LIB-1060, *k* = 10, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.75484021406002E+09	7	0.73140%
2	1.75484021406002E+09	5	0.74920%
3	**1.75484021406002E+09**	4	1.04490%
4	1.75484021406002E+09	17	0.76350%
5	1.75484021406002E+09	17	0.82120%
6	1.75484021406002E+09	4	0.70350%
7	1.75484021406002E+09	9	1.08920%
8	1.75484021406002E+09	12	0.55440%
9	1.75484021406002E+09	8	0.80310%
10	1.75484021406002E+09	10	1.03240%
Mean	**1.75484021406002E+09**	**9.3**	**0.82928%**
Std. Dev.	**0.000000**	**4.80855719**	**0.001724847**
Var.	**0.000000**	**2.3122E+01**	**2.9751E-06**

Separation, Roulette=Wheel, TSP-LIB-1060, *k* = 10, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	**1.75484021406002E+09**	2	2.35470%
2	1.75484021406002E+09	5	2.10600%
3	1.75484021406002E+09	3	1.89110%
4	1.75484021406002E+09	5	1.78550%
5	1.75484021406002E+09	6	1.92080%
6	1.75484021406002E+09	2	2.42090%
7	1.75484021406002E+09	8	1.93610%
8	1.75484021406002E+09	4	1.97680%
9	1.75484021406002E+09	3	2.19440%
10	1.75484021406002E+09	3	2.35070%
Mean	**1.75484021406002E+09**	**4.1**	**2.09370%**
Std. Dev.	**0.000000**	**1.91195072**	**0.002250811**
Var.	**0.000000**	**3.6556E+00**	**5.06615E-06**

TSP-LIB-1060, *k* = 20 Results

Density, Deterministic, TSP-LIB-1060, *k* = 20, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	7.91794596229896E+08	33	0.50530%
2	7.91794596229896E+08	25	0.53300%
3	**7.91794596229896E+08**	23	0.45340%
4	7.91794596229896E+08	35	0.38950%
5	7.91794596229896E+08	24	0.59040%
6	7.91794596229896E+08	32	0.40610%
7	7.91794596229896E+08	25	0.77310%
8	7.91794596229896E+08	34	1.17000%
9	7.91794596229896E+08	30	0.95270%
10	7.91794596229896E+08	34	1.19960%
Mean	**7.91794596229896E+08**	**29.5**	**0.69731%**
Std. Dev.	**0.000000**	**4.74341649**	**0.003093069**
Var.	**0.000000**	**2.2500E+01**	**9.56708E-06**

Density, Parent Favored Hybrid, TSP-LIB-1060, *k* = 20, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	7.91794596229896E+08	50	0.37890%
2	7.91794596229896E+08	35	0.34600%
3	7.91794596229896E+08	56	0.23160%
4	**7.91794596229896E+08**	33	0.38580%
5	7.91794596229896E+08	49	0.45570%
6	7.91794596229896E+08	49	0.31470%
7	7.91794596229896E+08	76	0.31120%
8	7.91794596229896E+08	66	0.67750%
9	7.91794596229896E+08	59	0.43710%
10	7.91794596229896E+08	47	0.94300%
Mean	**7.91794596229896E+08**	**52**	**0.44815%**
Std. Dev.	**0.000000**	**13.05543735**	**0.002108799**
Var.	**0.000000**	**1.7044E+02**	**4.44703E-06**

Density, Roulette-Wheel, TSP-LIB-1060, *k* = 20, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	7.91794596229896E+08	52	0.85570%
2	7.91794596229896E+08	14	1.64580%
3	7.91794596229896E+08	14	1.94380%
4	7.91794596229896E+08	15	1.18040%
5	7.91794596229896E+08	13	1.98180%
6	7.91794596229896E+08	19	1.21800%
7	7.91794596229896E+08	88	0.76630%
8	**7.91794596229896E+08**	11	1.21010%
9	7.91794596229896E+08	54	1.75600%
10	7.91794596229896E+08	17	1.26810%
Mean	**7.91794596229896E+08**	**29.7**	**1.38260%**
Std. Dev.	**0.000000**	**26.03437898**	**0.004283018**
Var.	**0.000000**	**6.7779E+02**	**1.83442E-05**

Random, Deterministic, TSP-LIB-1060, *k* = 20, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	7.91794596229896E+08	37	0.03310%
2	7.91794596229896E+08	33	0.01580%
3	7.91794596229896E+08	31	0.01370%
4	7.91794596229896E+08	32	0.07860%
5	**7.91794596229896E+08**	20	0.02840%
6	7.91794596229896E+08	35	0.01090%
7	7.91794596229896E+08	37	0.04250%
8	7.91794596229896E+08	25	0.05440%
9	7.91794596229896E+08	35	0.08410%
10	7.91794596229896E+08	31	0.05390%
Mean	**7.91794596229896E+08**	**31.6**	**0.04154%**
Std. Dev.	**0.000000**	**5.399588462**	**0.000260857**
Var.	**0.000000**	**2.9156E+01**	**6.80465E-08**

Random, Parent Favored Hybrid, TSP-LIB-1060, *k* = 20, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	7.91794596229896E+08	73	0.04530%
2	7.91794596229896E+08	58	0.01010%
3	7.91794596229896E+08	64	0.00790%
4	7.91794596229896E+08	67	0.00400%
5	7.91794596229896E+08	65	0.01490%
6	7.91794596229896E+08	44	0.01410%
7	**7.91794596229896E+08**	28	0.01070%
8	7.91794596229896E+08	50	0.06410%
9	7.91794596229896E+08	67	0.06270%
10	7.91794596229896E+08	51	0.02840%
Mean	**7.91794596229896E+08**	**56.7**	**0.02622%**
Std. Dev.	**0.000000**	**13.59779394**	**0.000229482**
Var.	**0.000000**	**1.8490E+02**	**5.26622E-08**

Random, Roulette-Wheel, TSP-LIB-1060, *k* = 20, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	7.91794596229896E+08	17	0.04850%
2	7.91794596229896E+08	40	0.04170%
3	7.91794596229896E+08	21	0.04450%
4	**7.91794596229896E+08**	14	0.00000%
5	7.91794596229896E+08	18	0.00000%
6	7.91794596229896E+08	15	0.00000%
7	7.91794596229896E+08	46	0.00000%
8	7.91794596229896E+08	42	0.04250%
9	7.91794596229896E+08	47	0.03970%
10	7.91794596229896E+08	18	0.00000%
Mean	**7.91794596229896E+08**	**27.8**	**0.02169%**
Std. Dev.	**0.000000**	**13.98252878**	**0.000229714**
Var.	**0.000000**	**1.9551E+02**	**5.27685E-08**

Separation, Deterministic, TSP-LIB-1060, *k* = 20, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	7.91794596229896E+08	27	0.81700%
2	7.91794596229896E+08	31	0.68700%
3	7.91794596229896E+08	24	0.48730%
4	7.91794596229896E+08	22	0.58020%
5	7.91794596229896E+08	34	0.79210%
6	7.91794596229896E+08	41	0.41000%
7	**7.91794596229896E+08**	13	0.73800%
8	7.91794596229896E+08	34	0.82170%
9	7.91794596229896E+08	34	0.71120%
10	7.91794596229896E+08	26	1.39150%
Mean	**7.91794596229896E+08**	**28.6**	**0.74360%**
Std. Dev.	**0.000000**	**7.919034734**	**0.002669949**
Var.	**0.000000**	**6.2711E+01**	**7.12863E-06**

Separation, Parent Favored Hybrid, TSP-LIB-1060, *k* = 20, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	7.91794596229896E+08	43	0.21490%
2	7.91794596229896E+08	63	0.18330%
3	7.91794596229896E+08	53	0.37280%
4	7.91794596229896E+08	58	0.21800%
5	7.91794596229896E+08	46	0.29440%
6	7.91794596229896E+08	65	0.47470%
7	**7.91794596229896E+08**	39	0.39410%
8	7.91794596229896E+08	56	0.59060%
9	7.91794596229896E+08	39	0.66360%
10	7.91794596229896E+08	49	0.72940%
Mean	**7.91794596229896E+08**	**51.1**	**0.41358%**
Std. Dev.	**0.000000**	**9.421606374**	**0.001955972**
Var.	**0.000000**	**8.8767E+01**	**3.82583E-06**

Separation, Roulette-Wheel, TSP-LIB-1060, *k* = 20, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	7.91794596229896E+08	113	0.72000%
2	7.91794596229896E+08	15	1.08970%
3	7.91794596229896E+08	67	1.29730%
4	7.91794596229896E+08	45	1.10930%
5	7.91794596229896E+08	11	1.78900%
6	7.91794596229896E+08	46	1.18680%
7	**7.91794596229896E+08**	9	1.35460%
8	7.91794596229896E+08	40	1.59670%
9	7.91818101798586E+08	7	1.73370%
10	7.91794596229896E+08	20	1.42540%
Mean	**7.91796946786765E+08**	**37.3**	**1.33025%**
Std. Dev.	**7433.136141**	**33.2701067**	**0.003256817**
Var.	**55251512.888889**	**1.1069E+03**	**1.06069E-05**

TSP-LIB-1060, *k* = 30 Results

Density, Deterministic, TSP-LIB-1060, *k* = 30, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	4.81386552271715E+08	93	0.05310%
2	4.81251642935269E+08	154	0.04100%
3	4.81251642935269E+08	142	0.07990%
4	4.81251642935269E+08	82	0.10570%
5	**4.81251642935269E+08**	72	0.12540%
6	4.81251642935269E+08	104	0.12750%
7	4.81251642935269E+08	162	0.15120%
8	4.81251642935269E+08	109	0.16920%
9	4.81251642935269E+08	118	0.19320%
10	4.81251642935269E+08	90	0.23170%
Mean	**4.81265133868914E+08**	**112.6**	**0.12779%**
Std. Dev.	**42662.077753**	**30.93793069**	**0.0006077**
Var.	**1820052878.222220**	**9.5716E+02**	**3.69299E-07**

Density, Parent Favored Hybrid, TSP-LIB-1060, *k* = 30, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	4.81386552271715E+08	252	0.14970%
2	4.81251642935269E+08	154	0.21930%
3	4.81251642935269E+08	245	0.25630%
4	4.81258405627916E+08	137	0.16110%
5	4.81251642935269E+08	281	0.22350%
6	**4.81251642935269E+08**	130	0.11970%
7	4.81251642935269E+08	211	0.13780%
8	4.81251642935269E+08	160	0.07140%
9	4.81258405627916E+08	139	0.07400%
10	4.81251642935269E+08	169	0.03790%
Mean	**4.81266486407443E+08**	**187.8**	**0.14507%**
Std. Dev.	**42280.426446**	**54.96423079**	**0.000722434**
Var.	**1787634460.444440**	**3.0211E+03**	**5.21911E-07**

Density, Roulette-Wheel, TSP-LIB-1060, *k* = 30, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	4.81347797148871E+08	57	0.30630%
2	4.81505081673250E+08	146	0.20650%
3	4.81587978634841E+08	24	1.80980%
4	4.81605330852999E+08	22	0.77620%
5	4.81459678694229E+08	26	0.94970%
6	**4.81251642935269E+08**	125	0.36330%
7	4.81361607960363E+08	114	0.61940%
8	4.81258405627916E+08	62	1.02520%
9	4.81393314964362E+08	95	0.76850%
10	4.81326090118490E+08	260	0.99870%
Mean	**4.81409692861059E+08**	**93.1**	**0.78236%**
Std. Dev.	**126018.582221**	**73.57150717**	**0.004654812**
Var.	**15880683064.888900**	**5.4128E+03**	**2.16673E-05**

Random, Deterministic, TSP-LIB-1060, *k* = 30, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	4.81251642935269E+08	261	0.00400%
2	**4.81251642935269E+08**	70	0.00210%
3	4.81251642935269E+08	72	0.00290%
4	4.81251642935269E+08	91	0.00230%
5	4.81251642935269E+08	112	0.00500%
6	4.81251642935269E+08	161	0.00180%
7	4.81251642935269E+08	100	0.00210%
8	4.81251642935269E+08	118	0.00520%
9	4.81251642935269E+08	78	0.00220%
10	4.81251642935269E+08	105	0.00000%
Mean	**4.81251642935269E+08**	**116.8**	**0.00276%**
Std. Dev.	**0.000000**	**57.3116238**	**1.57987E-05**
Var.	**0.000000**	**3.2846E+03**	**2.496E-10**

Random, Parent Favored Hybrid, TSP-LIB-1060, *k* = 30, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	4.81251642935269E+08	217	0.00080%
2	4.81251642935269E+08	160	0.00090%
3	4.81291453705581E+08	205	0.00080%
4	4.81251642935269E+08	134	0.00110%
5	**4.81251642935269E+08**	99	0.00260%
6	4.81251642935269E+08	223	0.00150%
7	4.81251642935269E+08	193	0.00210%
8	4.81251642935269E+08	129	0.00210%
9	4.81258405627916E+08	104	0.00170%
10	4.81251642935269E+08	182	0.00280%
Mean	**4.81256300281565E+08**	**164.6**	**0.00164%**
Std. Dev.	**12533.167658**	**46.06565363**	**7.42668E-06**
Var.	**157080291.555556**	**2.1220E+03**	**5.51556E-11**

Random, Roulette-Wheel, TSP-LIB-1060, *k* = 30, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	4.81422244332091E+08	92	0.00110%
2	4.81422244332091E+08	27	0.00170%
3	4.81264884779231E+08	41	0.00380%
4	4.81354559841517E+08	26	0.00620%
5	**4.81251642935269E+08**	234	0.00260%
6	4.81482706485317E+08	130	0.00880%
7	4.81767278333054E+08	59	0.00970%
8	4.81258405627916E+08	64	0.00970%
9	4.81361135274129E+08	98	0.01160%
10	4.81354559841517E+08	23	0.01400%
Mean	**4.81393966178213E+08**	**79.4**	**0.00692%**
Std. Dev.	**152138.196826**	**64.86944153**	**4.48524E-05**
Var.	**23146030933.333300**	**4.2080E+03**	**2.01173E-09**

Separation, Deterministic, TSP-LIB-1060, *k* = 30, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	4.81251642935269E+08	86	0.11700%
2	4.81251642935269E+08	76	0.21120%
3	4.81251642935269E+08	113	0.24590%
4	4.81251642935269E+08	117	0.16450%
5	4.81251642935269E+08	79	0.32950%
6	4.81251642935269E+08	119	0.32270%
7	4.81251642935269E+08	105	0.32460%
8	4.81251642935269E+08	69	0.47650%
9	4.81251642935269E+08	87	0.47190%
10	**4.81251642935269E+08**	61	0.55570%
Mean	**4.81251642935269E+08**	**91.2**	**0.32195%**
Std. Dev.	**0.000000**	**20.90613945**	**0.001437276**
Var.	**0.000000**	**4.3707E+02**	**2.06576E-06**

Separation, Parent Favored Hybrid, TSP-LIB-1060, *k* = 30, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	4.81354559841517E+08	102	0.04540%
2	4.81251642935269E+08	168	0.06160%
3	**4.81251642935269E+08**	100	0.07760%
4	4.81291453705581E+08	133	0.11690%
5	4.81251642935269E+08	146	0.19860%
6	4.81251642935269E+08	229	0.18540%
7	4.81251642935269E+08	174	0.23910%
8	4.81251642935269E+08	151	0.36080%
9	4.81251642935269E+08	164	0.24440%
10	4.81251642935269E+08	130	0.27830%
Mean	**4.81265915702925E+08**	**149.7**	**0.18081%**
Std. Dev.	**33565.305262**	**37.78021234**	**0.001037965**
Var.	**1126629717.333330**	**1.4273E+03**	**1.07737E-06**

Separation, Roulette-Wheel, TSP-LIB-1060, *k* = 30, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	4.81258405627916E+08	20	0.13170%
2	4.81474830478084E+08	29	0.17190%
3	**4.81257028198441E+08**	55	0.28790%
4	4.81386552271715E+08	156	0.22550%
5	4.81482706485317E+08	266	0.28750%
6	4.81263790891087E+08	74	0.36690%
7	4.81347797148871E+08	51	0.47350%
8	4.81258405627916E+08	22	0.60330%
9	4.81347797148871E+08	105	0.63430%
10	4.81347797148871E+08	111	0.61280%
Mean	**4.81342511102709E+08**	**88.9**	**0.37953%**
Std. Dev.	**86176.997477**	**76.18172718**	**0.00189592**
Var.	**7426474894.222220**	**5.8037E+03**	**3.59451E-06**

TSP-LIB-1060, *k* = 50 Results

Density, Deterministic, TSP-LIB-1060, *k* = 50, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	2.55509536171518E+08	316	0.02140%
2	2.55867786723883E+08	111	0.04610%
3	**2.55509536171518E+08**	211	0.07150%
4	2.55618027345366E+08	232	0.07470%
5	2.55835453597895E+08	182	0.09450%
6	2.55867786723883E+08	94	0.14000%
7	2.55867786723883E+08	108	0.15900%
8	2.55693064462405E+08	156	0.15020%
9	2.55852089716958E+08	170	0.18470%
10	2.55815396530733E+08	211	0.18350%
Mean	**2.55743646416804E+08**	**179.1**	**0.11256%**
Std. Dev.	**148893.300164**	**67.60580185**	**0.000584386**
Var.	**22169214833.777800**	**4.5705E+03**	**3.41507E-07**

Density, Parent Favored Hybrid, TSP-LIB-1060, *k* = 50, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	2.55867786723883E+08	263	0.05400%
2	2.55712129672957E+08	297	0.05640%
3	2.55867786723883E+08	256	0.08520%
4	2.55802862267394E+08	273	0.08340%
5	2.55789559783863E+08	200	0.15030%
6	2.55543554641186E+08	326	0.11920%
7	**2.55534125025880E+08**	360	0.17920%
8	2.55603621938640E+08	341	0.12580%
9	2.55789559783863E+08	259	0.28330%
10	2.55866413088739E+08	402	0.20910%
Mean	**2.55737739965029E+08**	**297.7**	**0.13459%**
Std. Dev.	**132414.798072**	**59.65837931**	**0.000729426**
Var.	**17533678748.444400**	**3.5591E+03**	**5.32062E-07**

Density, Roulette-Wheel, TSP-LIB-1060, *k* = 50, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	2.56914666113471E+08	78	0.50200%
2	2.55791490379635E+08	165	0.84160%
3	2.55708701558668E+08	160	0.66640%
4	2.55947060665927E+08	81	0.73430%
5	2.55977103706443E+08	108	0.47750%
6	2.55809616404135E+08	114	0.50280%
7	2.55945170250721E+08	74	0.49480%
8	**2.55544941545704E+08**	125	0.45170%
9	2.55981701206325E+08	80	0.27100%
10	2.55944088528229E+08	245	0.11570%
Mean	**2.55956454035926E+08**	**123**	**0.50578%**
Std. Dev.	**365011.536641**	**54.12536887**	**0.002113311**
Var.	**133233421880.889000**	**2.9296E+03**	**4.46608E-06**

Random, Deterministic, TSP-LIB-1060, *k* = 50, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	2.55706922464038E+08	217	0.00290%
2	2.55867786723883E+08	113	0.00130%
3	2.55592782090750E+08	222	0.00000%
4	2.55867786723883E+08	113	0.00130%
5	2.55802862267394E+08	223	0.01080%
6	2.55814148638225E+08	115	0.01600%
7	2.55867786723883E+08	91	0.00190%
8	2.55814148638225E+08	168	0.01950%
9	2.55867786723883E+08	132	0.01010%
10	**2.55592001576452E+08**	221	0.00300%
Mean	**2.55779401257062E+08**	**161.5**	**0.00668%**
Std. Dev.	**110258.117395**	**54.58174298**	**6.93683E-05**
Var.	**12156852451.555600**	**2.9792E+03**	**4.81196E-09**

Random, Parent Favored Hybrid, TSP-LIB-1060, *k* = 50, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	2.55847123230937E+08	283	0.00000%
2	2.55791339245693E+08	158	0.00270%
3	2.55942898885143E+08	158	0.00160%
4	2.55787137284343E+08	345	0.00170%
5	**2.55552731277446E+08**	317	0.00120%
6	2.55867046479816E+08	187	0.00300%
7	2.55867786723883E+08	218	0.00160%
8	2.55705343945738E+08	253	0.00240%
9	2.55607055606472E+08	373	0.00140%
10	2.55794124049153E+08	215	0.00130%
Mean	**2.55776258672862E+08**	**250.7**	**0.00169%**
Std. Dev.	**121882.716026**	**76.65369455**	**8.55635E-06**
Var.	**14855396465.777800**	**5.8758E+03**	**7.32111E-11**

Random, Roulette-Wheel, TSP-LIB-1060, *k* = 50, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	**2.55566197825217E+08**	36	0.00150%
2	2.56239802092438E+08	117	0.00070%
3	2.55789559783863E+08	122	0.00260%
4	2.56039110634703E+08	48	0.00370%
5	2.55905082513275E+08	175	0.00420%
6	2.55699524922408E+08	135	0.00280%
7	2.56057990609972E+08	163	0.00420%
8	2.55869717319655E+08	65	0.00620%
9	2.55867786723883E+08	36	0.00830%
10	2.56972859554157E+08	115	0.00720%
Mean	**2.56000763197957E+08**	**101.2**	**0.00414%**
Std. Dev.	**390877.278801**	**51.55751912**	**2.45139E-05**
Var.	**152785047082.667000**	**2.6582E+03**	**6.00933E-10**

Separation, Deterministic, TSP-LIB-1060, *k* = 50, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	2.55867786723883E+08	115	0.05390%
2	2.55522838655049E+08	286	0.03760%
3	2.55697594326636E+08	304	0.07640%
4	2.55852089716958E+08	226	0.07810%
5	2.55867786723883E+08	92	0.11770%
6	2.55802862267394E+08	95	0.20610%
7	**2.55513697952302E+08**	213	0.15670%
8	2.55543554641186E+08	232	0.14930%
9	2.55513697952302E+08	322	0.15270%
10	2.55867786723883E+08	93	0.23510%
Mean	**2.55704969568348E+08**	**197.8**	**0.12636%**
Std. Dev.	**164386.435558**	**92.0625391**	**0.000652791**
Var.	**27022900195.555600**	**8.4755E+03**	**4.26136E-07**

Separation, Parent Favored Hybrid, TSP-LIB-1060, *k* = 50, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	2.55511466767290E+08	425	0.05350%
2	2.55789559783863E+08	338	0.15610%
3	2.55747024162730E+08	116	0.19580%
4	2.55509536171518E+08	257	0.15340%
5	2.55522838655049E+08	333	0.10500%
6	2.55511466767290E+08	204	0.13120%
7	**2.55509536171518E+08**	228	0.08240%
8	2.55674727507796E+08	267	0.08000%
9	2.55867786723883E+08	184	0.05170%
10	2.55727451015520E+08	300	0.03070%
Mean	**2.55637139372646E+08**	**265.2**	**0.10398%**
Std. Dev.	**139559.197093**	**88.6300676**	**0.00053773**
Var.	**19476769493.333300**	**7.8553E+03**	**2.89154E-07**

Separation, Roulette-Wheel, TSP-LIB-1060, *k* = 50, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	2.55942898885143E+08	69	0.15400%
2	2.55867786723883E+08	78	0.17440%
3	2.56487391708683E+08	100	0.24980%
4	2.55766452446627E+08	43	0.44460%
5	2.55869717319655E+08	88	0.27010%
6	2.55867786723883E+08	338	0.44970%
7	2.55819375933789E+08	344	0.30880%
8	2.55944088528229E+08	192	0.45380%
9	**2.55591578548239E+08**	51	0.71310%
10	2.55946359893807E+08	147	0.57800%
Mean	**2.55910343671194E+08**	**145**	**0.37963%**
Std. Dev.	**229090.925343**	**112.468267**	**0.001801489**
Var.	**52482652074.666700**	**1.2649E+04**	**3.24536E-06**

TSP-LIB-1060, *k* = 60 Results

Density, Deterministic, TSP-LIB-1060, *k* = 60, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.97462926601157E+08	218	0.06230%
2	1.97376472578189E+08	274	0.05100%
3	1.98044836300390E+08	232	0.10590%
4	1.97706121766965E+08	299	0.10120%
5	1.98098386195723E+08	130	0.21640%
6	**1.97273037639545E+08**	325	0.16020%
7	1.98044836300390E+08	161	0.29480%
8	1.97706121766965E+08	213	0.32660%
9	1.97848273866086E+08	570	0.14820%
10	1.98044836300390E+08	182	0.31680%
Mean	**1.97760584931580E+08**	**260.4**	**0.17834%**
Std. Dev.	**306226.710056**	**124.5357601**	**0.001044988**
Var.	**93774797952.000000**	**1.5509E+04**	**1.092E-06**

Density, Parent Favored Hybrid, TSP-LIB-1060, *k* = 60, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	**1.97273037639545E+08**	614	0.01830%
2	1.97349963888226E+08	555	0.01890%
3	1.98044836300390E+08	366	0.04270%
4	1.97913698079397E+08	585	0.03620%
5	1.98146867753599E+08	196	0.07310%
6	1.98031176739727E+08	371	0.06460%
7	1.97782831866829E+08	210	0.08980%
8	1.98069435436676E+08	343	0.09540%
9	1.97901823761419E+08	495	0.09000%
10	1.97971535902309E+08	229	0.11730%
Mean	**1.97848520736812E+08**	**396.4**	**0.06463%**
Std. Dev.	**301107.962648**	**158.1646119**	**0.000343135**
Var.	**90666005169.777800**	**2.5016E+04**	**1.17741E-07**

Density, Roulette-Wheel, TSP-LIB-1060, *k* = 60, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.98399954083742E+08	150	0.46460%
2	1.97841157448732E+08	149	0.55180%
3	1.98045061763329E+08	247	0.45110%
4	1.98093317858266E+08	357	0.28960%
5	**1.97768102340088E+08**	336	0.33620%
6	1.97855315920772E+08	276	0.25710%
7	1.97904889383199E+08	228	0.19620%
8	1.97913404261440E+08	164	0.23440%
9	1.98044836300390E+08	195	0.10090%
10	1.99162274515578E+08	55	0.19860%
Mean	**1.98102831387554E+08**	**215.7**	**0.30805%**
Std. Dev.	**412894.561452**	**92.43382017**	**0.001417898**
Var.	**170481918876.444000**	**8.5440E+03**	**2.01044E-06**

Random, Deterministic, TSP-LIB-1060, *k* = 60, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.97618449960142E+08	361	0.00220%
2	1.97995654112573E+08	208	0.00260%
3	1.98357751353882E+08	195	0.00290%
4	1.97855315920772E+08	284	0.00180%
5	1.97273037639545E+08	347	0.00180%
6	**1.97273037639545E+08**	320	0.00230%
7	1.98317752820661E+08	202	0.00240%
8	1.97908954045171E+08	228	0.00250%
9	1.97706121766965E+08	305	0.00170%
10	1.97855315920772E+08	288	0.00060%
Mean	**1.97816139118003E+08**	**273.8**	**0.00208%**
Std. Dev.	**369680.531900**	**61.61493325**	**6.47731E-06**
Var.	**136663695665.778000**	**3.7964E+03**	**4.19556E-11**

Random, Parent Favored Hybrid, TSP-LIB-1060, *k* = 60, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	**1.97855315920772E+08**	482	0.00010%
2	1.98049875437080E+08	281	0.00130%
3	1.98028566549703E+08	349	0.00080%
4	1.98044836300390E+08	395	0.00080%
5	1.98044836300390E+08	366	0.00080%
6	1.97939686954448E+08	414	0.00080%
7	1.97901911990485E+08	608	0.00070%
8	1.98044836300390E+08	315	0.00090%
9	1.97886141293255E+08	576	0.00090%
10	1.97898797202874E+08	511	0.00070%
Mean	**1.97969480424979E+08**	**429.7**	**0.00078%**
Std. Dev.	**79873.691221**	**110.4677429**	**2.93636E-06**
Var.	**6379806549.333330**	**1.2203E+04**	**8.62222E-12**

Random, Roulette-Wheel, TSP-LIB-1060, *k* = 60, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.97929488519485E+08	249	0.00050%
2	1.98228010454658E+08	123	0.00340%
3	1.98649747223235E+08	124	0.00480%
4	1.98162488490978E+08	187	0.00510%
5	1.98423865316050E+08	251	0.00240%
6	1.98350380621314E+08	291	0.00450%
7	1.98399954083742E+08	232	0.00290%
8	1.98451045859267E+08	148	0.00300%
9	1.98098386195723E+08	214	0.00430%
10	**1.97848273866086E+08**	318	0.00250%
Mean	**1.98254164063054E+08**	**213.7**	**0.00334%**
Std. Dev.	**249014.853640**	**67.60021367**	**1.393E-05**
Var.	**62008397333.333300**	**4.5698E+03**	**1.94044E-10**

Separation, Deterministic, TSP-LIB-1060, *k* = 60, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.97339813409374E+08	262	0.03400%
2	1.97273037639545E+08	375	0.03630%
3	1.97493905290987E+08	149	0.10000%
4	1.97706121766965E+08	230	0.09180%
5	1.97339725180308E+08	282	0.13130%
6	1.97326675763944E+08	238	0.17250%
7	1.97339725180308E+08	240	0.18580%
8	**1.97273037639545E+08**	246	0.19390%
9	1.97855315920772E+08	238	0.18100%
10	1.97706121766965E+08	159	0.28280%
Mean	**1.97465347955871E+08**	**241.9**	**0.14094%**
Std. Dev.	**213268.784351**	**62.73657448**	**0.000775398**
Var.	**45483574378.666700**	**3.9359E+03**	**6.01241E-07**

Separation, Parent Favored Hybrid, TSP-LIB-1060, *k* = 60, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.97649651942151E+08	322	0.04080%
2	1.97908865816105E+08	438	0.04510%
3	1.97536677569179E+08	346	0.07640%
4	1.98117973593294E+08	77	0.23030%
5	1.97848273866086E+08	702	0.10640%
6	1.97956079647013E+08	147	0.21170%
7	**1.97273037639545E+08**	409	0.16240%
8	1.97546423508341E+08	391	0.16910%
9	1.97490144516671E+08	303	0.24650%
10	1.97751243842397E+08	109	0.27800%
Mean	**1.97707837194078E+08**	**324.4**	**0.15667%**
Std. Dev.	**255393.282209**	**184.7173216**	**0.000858108**
Var.	**65225728597.333300**	**3.4120E+04**	**7.3635E-07**

Separation, Roulette-Wheel, TSP-LIB-1060, *k* = 60, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	**1.97582318841514E+08**	244	0.39610%
2	1.98164943154878E+08	99	0.51460%
3	1.98162263028039E+08	170	0.36050%
4	1.98044836300390E+08	198	0.42780%
5	1.98044836300390E+08	162	0.26600%
6	1.98409303550008E+08	195	0.25840%
7	1.97809556705609E+08	232	0.16760%
8	1.98337035835197E+08	125	0.24740%
9	1.97646945500625E+08	97	0.16310%
10	1.98667993627934E+08	267	0.08080%
Mean	**1.98087003284458E+08**	**178.9**	**0.28823%**
Std. Dev.	**340681.037286**	**59.4464278**	**0.00134936**
Var.	**116063569166.222000**	**3.5339E+03**	**1.82077E-06**

TSP-LIB-1060, *k* = 70 Results

Density, Deterministic, TSP-LIB-1060, *k* = 70, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.58476598196234E+08	310	0.05400%
2	**1.58476598196234E+08**	227	0.06350%
3	1.58476598196234E+08	343	0.07980%
4	1.58476598196234E+08	360	0.16480%
5	1.58498678339522E+08	170	0.20720%
6	1.58496957300865E+08	231	0.26180%
7	1.58585420583776E+08	175	0.26310%
8	1.58515181564254E+08	193	0.39590%
9	1.58577509343113E+08	118	0.36220%
10	1.58476598196234E+08	282	0.21240%
Mean	**1.58505673811270E+08**	**240.9**	**0.20647%**
Std. Dev.	**42113.813833**	**80.36921743**	**0.001192145**
Var.	**1773573315.555560**	**6.4592E+03**	**1.42121E-06**

Density, Parent Favored Hybrid, TSP-LIB-1060, *k* = 70, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.58587141622432E+08	350	0.01480%
2	1.58481904145271E+08	684	0.02150%
3	1.58544213899416E+08	235	0.05070%
4	**1.58476598196234E+08**	548	0.04030%
5	1.58640389045596E+08	201	0.07230%
6	1.58585420583776E+08	288	0.07360%
7	1.58496957300865E+08	319	0.07740%
8	1.58585420583776E+08	313	0.09090%
9	1.58529744092139E+08	308	0.10200%
10	1.58585420583776E+08	344	0.11140%
Mean	**1.58551321005328E+08**	**359**	**0.06549%**
Std. Dev.	**54342.802120**	**146.5719391**	**0.000328266**
Var.	**2953140142.222220**	**2.1483E+04**	**1.07758E-07**

Density, Roulette-Wheel, TSP-LIB-1060, *k* = 70, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.58826919841350E+08	171	0.44390%
2	1.58478319234890E+08	296	0.40540%
3	1.58550721906697E+08	147	0.56200%
4	**1.58476598196234E+08**	296	0.31130%
5	1.58545497855630E+08	165	0.22710%
6	1.58613692258759E+08	113	0.37290%
7	1.58637239894666E+08	111	0.28690%
8	1.58483625183928E+08	195	0.16030%
9	1.58481623202033E+08	286	0.10510%
10	1.58740347934167E+08	82	0.11910%
Mean	**1.58583458550835E+08**	**186.2**	**0.29940%**
Std. Dev.	**121571.854096**	**80.44155919**	**0.001496707**
Var.	**14779715708.444400**	**6.4708E+03**	**2.24013E-06**

Random, Deterministic, TSP-LIB-1060, *k* = 70, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.58585420583776E+08	180	0.00260%
2	1.58585420583776E+08	117	0.00260%
3	**1.58476598196234E+08**	253	0.00440%
4	1.58481904145271E+08	312	0.00510%
5	1.58504776384298E+08	300	0.00800%
6	1.58585420583776E+08	141	0.00590%
7	1.58481904145271E+08	336	0.00740%
8	1.58476598196234E+08	262	0.00120%
9	1.58529744092139E+08	171	0.01590%
10	1.58528023053483E+08	175	0.02490%
Mean	**1.58523580996426E+08**	**224.7**	**0.00780%**
Std. Dev.	**46871.478672**	**77.33627868**	**7.29018E-05**
Var.	**2196935512.888890**	**5.9809E+03**	**5.31467E-09**

Random, Parent Favored Hybrid, TSP-LIB-1060, *k* = 70, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.58476598196234E+08	525	0.00090%
2	1.58585420583776E+08	307	0.00270%
3	1.58585420583776E+08	413	0.00190%
4	1.58476598196234E+08	525	0.00270%
5	**1.58476598196234E+08**	473	0.00490%
6	1.58585420583776E+08	251	0.00350%
7	1.58532710013362E+08	329	0.00900%
8	1.58585420583776E+08	307	0.00650%
9	1.58453351527049E+08	521	0.00620%
10	1.58516902602910E+08	319	0.00610%
Mean	**1.58527444106713E+08**	**397**	**0.00444%**
Std. Dev.	**54599.115597**	**106.6666667**	**2.51714E-05**
Var.	**2981063424.000000**	**1.1378E+04**	**6.336E-10**

Random, Roulette-Wheel, TSP-LIB-1060, *k* = 70, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.58528023053483E+08	350	0.00450%
2	1.58683731230543E+08	174	0.00650%
3	1.58792131756985E+08	135	0.00560%
4	**1.58513148146798E+08**	96	0.00650%
5	1.58585420583776E+08	237	0.00510%
6	1.58625768439269E+08	162	0.00620%
7	1.58678104445615E+08	124	0.00380%
8	1.59153110975523E+08	186	0.00000%
9	1.58571212648425E+08	175	0.00620%
10	1.58590726532814E+08	161	0.00170%
Mean	**1.58672137781323E+08**	**180**	**0.00461%**
Std. Dev.	**188099.913620**	**70.82686245**	**2.20628E-05**
Var.	**35381577504.000000**	**5.0164E+03**	**4.86767E-10**

Separation, Deterministic, TSP-LIB-1060, *k* = 70, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.58473838588418E+08	231	0.08400%
2	1.58476598196234E+08	215	0.29730%
3	1.58476598196234E+08	144	0.26180%
4	1.58509896049630E+08	185	0.23570%
5	**1.58453351527049E+08**	259	0.16750%
6	1.58476598196234E+08	250	0.21360%
7	1.58476598196234E+08	205	0.16020%
8	1.58453351527049E+08	273	0.11950%
9	1.58476598196234E+08	183	0.08070%
10	1.58478319234890E+08	293	0.03970%
Mean	**1.58475174790821E+08**	**223.8**	**0.16600%**
Std. Dev.	**15563.057683**	**46.13458572**	**0.000854343**
Var.	**242208764.444444**	**2.1284E+03**	**7.29901E-07**

Separation, Parent Favored Hybrid, TSP-LIB-1060, *k* = 70, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.58585420583776E+08	222	0.03120%
2	1.58585420583776E+08	283	0.02790%
3	1.58496957300865E+08	376	0.04350%
4	1.58496957300865E+08	470	0.05360%
5	1.58479016580718E+08	335	0.06500%
6	1.58476598196234E+08	416	0.07060%
7	1.58476598196234E+08	538	0.07110%
8	1.58478319234890E+08	445	0.10290%
9	1.58473838588418E+08	442	0.10360%
10	**1.58476598196234E+08**	315	0.11440%
Mean	**1.58502572476201E+08**	**384.2**	**0.06838%**
Std. Dev.	**44451.476906**	**95.96967114**	**0.000306089**
Var.	**1975933799.111110**	**9.2102E+03**	**9.36902E-08**

Separation, Roulette-Wheel, TSP-LIB-1060, *k* = 70, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	**1.58457721811576E+08**	148	0.16110%
2	1.58837859339970E+08	199	0.16710%
3	1.58676711029155E+08	255	0.24910%
4	1.58625768439269E+08	82	0.31440%
5	1.58615010329251E+08	237	0.46280%
6	1.58699883259726E+08	152	0.67180%
7	1.58585420583776E+08	232	0.40060%
8	1.58705135690640E+08	204	0.51650%
9	1.58649282289305E+08	85	0.95880%
10	1.58773300637265E+08	141	0.91890%
Mean	**1.58662609340993E+08**	**173.5**	**0.48211%**
Std. Dev.	**104402.719437**	**61.50925856**	**0.002880778**
Var.	**10899927825.777800**	**3.7834E+03**	**8.29888E-06**

TSP-LIB-1060, *k* = 80 Results

Density, Deterministic, TSP-LIB-1060, *k* = 80, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.29101184124687E+08	265	0.05820%
2	1.29101249063777E+08	249	0.05380%
3	1.28894265839770E+08	263	0.11810%
4	**1.28890171414562E+08**	339	0.12760%
5	1.28890171414562E+08	439	0.18170%
6	1.28890171414562E+08	363	0.21540%
7	1.29024278394871E+08	248	0.22450%
8	1.29156126091095E+08	313	0.30170%
9	1.29105814320463E+08	264	0.15500%
10	1.28890171414562E+08	445	0.37150%
Mean	**1.28994360349291E+08**	**318.8**	**0.18075%**
Std. Dev.	**113412.715321**	**75.76689397**	**0.001014768**
Var.	**12862443996.444400**	**5.7406E+03**	**1.02975E-06**

Density, Roulette-Wheel, TSP-LIB-1060, *k* = 80, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.29030526859606E+08	343	0.18010%
2	1.29111026813289E+08	110	0.58060%
3	1.28895351771388E+08	343	0.49280%
4	1.29003485553340E+08	317	0.20860%
5	1.29367074518222E+08	109	0.53060%
6	1.29508489269923E+08	207	0.28230%
7	1.29069092543970E+08	208	0.24360%
8	**1.28891019280152E+08**	320	0.16430%
9	1.28894629489122E+08	474	0.10780%
10	1.28945598434635E+08	300	0.08650%
Mean	**1.29071629453365E+08**	**273.1**	**0.28772%**
Std. Dev.	**210008.610609**	**114.0764364**	**0.00180966**
Var.	**44103616529.777800**	**1.3013E+04**	**3.27487E-06**

Density, Parent Favored Hybrid, TSP-LIB-1060, *k* = 80, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.29105814320463E+08	351	0.03800%
2	1.29105814320463E+08	364	0.09330%
3	1.29348736550703E+08	171	0.21620%
4	1.29160782782283E+08	342	0.08120%
5	1.29253947629434E+08	254	0.11840%
6	1.29105814320463E+08	525	0.12510%
7	1.29105814320463E+08	442	0.14560%
8	**1.29021375862373E+08**	470	0.10570%
9	1.29105814320463E+08	422	0.20880%
10	1.29105814320463E+08	435	0.30930%
Mean	**1.29141972874757E+08**	**377.6**	**0.14416%**
Std. Dev.	**93113.826199**	**105.3029492**	**0.000795599**
Var.	**8670184629.333330**	**1.1089E+04**	**6.32978E-07**

Random, Deterministic, TSP-LIB-1060, *k* = 80, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.28890171414562E+08	383	0.00110%
2	1.29105814320463E+08	282	0.01030%
3	1.29105814320463E+08	224	0.00290%
4	1.29105814320463E+08	221	0.00510%
5	1.28918443089546E+08	323	0.00570%
6	**1.28890171414562E+08**	339	0.00230%
7	1.29105814320463E+08	250	0.00240%
8	1.29100336259097E+08	228	0.00380%
9	1.29100336259097E+08	276	0.00920%
10	1.28890171414562E+08	381	0.01120%
Mean	**1.29021288713328E+08**	**290.7**	**0.00540%**
Std. Dev.	**107096.945955**	**62.57093752**	**3.62369E-05**
Var.	**11469755832.888900**	**3.9151E+03**	**1.31311E-09**

Random, Parent Favored Hybrid, TSP-LIB-1060, *k* = 80, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.28919761160037E+08	590	0.00120%
2	**1.28905907173089E+08**	508	0.00150%
3	1.28941029688871E+08	426	0.00160%
4	1.28986761022672E+08	358	0.00130%
5	1.28996979891391E+08	395	0.00090%
6	1.29105814320463E+08	452	0.00040%
7	1.29105814320463E+08	328	0.00130%
8	1.29105814320463E+08	516	0.00090%
9	1.29086814296992E+08	370	0.00170%
10	1.28981572094948E+08	464	0.00030%
Mean	**1.29013626828939E+08**	**440.7**	**0.00111%**
Std. Dev.	**80666.003523**	**81.65244774**	**4.79467E-06**
Var.	**6507004124.444440**	**6.6671E+03**	**2.29889E-11**

Random, Roulette-Wheel, TSP-LIB-1060, *k* = 80, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.28920673964716E+08	158	0.00000%
2	1.28933760762413E+08	325	0.00440%
3	1.29032525664997E+08	177	0.00700%
4	1.28916121430576E+08	320	0.00760%
5	1.28891932084831E+08	217	0.01140%
6	1.29283741704050E+08	209	0.00710%
7	1.28934820824748E+08	402	0.01240%
8	1.28920203759815E+08	225	0.01620%
9	1.28986564878695E+08	347	0.00400%
10	**1.28891084219241E+08**	520	0.01040%
Mean	**1.28971142929408E+08**	**290**	**0.00805%**
Std. Dev.	**117989.372448**	**114.0789201**	**4.70018E-05**
Var.	**13921492010.666700**	**1.3014E+04**	**2.20917E-09**

Separation, Deterministic, TSP-LIB-1060, *k* = 80, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.28890171414562E+08	297	0.15140%
2	1.28904641221839E+08	203	0.24980%
3	1.28892397133379E+08	237	0.20620%
4	1.28890171414562E+08	233	0.20290%
5	1.28896403894194E+08	203	0.15660%
6	**1.28890171414562E+08**	218	0.13490%
7	1.28890171414562E+08	249	0.10550%
8	1.28890171414562E+08	333	0.08250%
9	1.28890171414562E+08	239	0.06010%
10	1.29105814320463E+08	172	0.04730%
Mean	**1.28914028505725E+08**	**238.4**	**0.13972%**
Std. Dev.	**67547.043531**	**46.97327846**	**0.000669157**
Var.	**4562603089.777780**	**2.2065E+03**	**4.47772E-07**

Separation, Parent Favored Hybrid, TSP-LIB-1060, *k* = 80, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.28890171414562E+08	535	0.26680%
2	1.29105814320463E+08	337	0.21770%
3	1.29105814320463E+08	304	0.26500%
4	1.29080801048364E+08	250	0.15690%
5	1.28892397133379E+08	549	0.14180%
6	1.29105814320463E+08	402	0.17280%
7	1.28917679371140E+08	354	0.20440%
8	1.28890171414562E+08	547	0.07120%
9	1.29105814320463E+08	318	0.04780%
10	**1.28890171414562E+08**	375	0.03850%
Mean	**1.28998464907842E+08**	**397.1**	**0.15829%**
Std. Dev.	**108440.430853**	**109.0896166**	**0.000839602**
Var.	**11759327043.555600**	**1.1901E+04**	**7.04932E-07**

Separation, Roulette-Wheel, TSP-LIB-1060, *k* = 80, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.28892693873476E+08	552	0.06450%
2	1.29113320983721E+08	104	0.46540%
3	1.28896390159391E+08	237	0.49810%
4	1.28931402493356E+08	181	0.31160%
5	1.29248270843166E+08	88	0.62040%
6	1.28946164025811E+08	277	0.24270%
7	1.29350848256046E+08	92	0.35080%
8	1.28900861968754E+08	302	0.14120%
9	**1.28892397133379E+08**	486	0.12180%
10	1.29076661756052E+08	54	0.16210%
Mean	**1.29024901149315E+08**	**237.3**	**0.29786%**
Std. Dev.	**166169.648337**	**171.4610743**	**0.001845893**
Var.	**27612352028.444400**	**2.9399E+04**	**3.40732E-06**

TSP-LIB-1060, *k* = 90 Results

Density, Deterministic, TSP-LIB-1060, *k* = 90, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.10534738043771E+08	299	0.05410%
2	1.10591966332331E+08	282	0.05830%
3	1.10524238545932E+08	480	0.08130%
4	1.10551447011634E+08	379	0.10720%
5	1.10530653838578E+08	425	0.15030%
6	1.10530653838578E+08	483	0.19560%
7	**1.10479083296657E+08**	483	0.15320%
8	1.10630572727071E+08	701	0.16620%
9	1.10507610193929E+08	520	0.25640%
10	1.10496303493863E+08	439	0.22030%
Mean	**1.10537726732234E+08**	**449.1**	**0.14429%**
Std. Dev.	**44849.646598**	**119.1557804**	**0.000686751**
Var.	**2011490800.000000**	**1.4198E+04**	**4.71626E-07**

Density, Parent Favored Hybrid, TSP-LIB-1060, *k* = 90, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.10560550023325E+08	654	0.03380%
2	1.10542152529740E+08	745	0.02720%
3	1.10600341054421E+08	445	0.08210%
4	1.10644237842045E+08	397	0.11320%
5	1.10606711117676E+08	647	0.08950%
6	1.10575569595813E+08	635	0.08710%
7	1.10525086411522E+08	613	0.16430%
8	1.10739447686921E+08	421	0.18110%
9	**1.10487678195451E+08**	576	0.20840%
10	1.10595212426514E+08	858	0.05140%
Mean	**1.10587698688343E+08**	**599.1**	**0.10381%**
Std. Dev.	**69670.020857**	**146.0406717**	**0.00062479**
Var.	**4853911806.222220**	**2.1328E+04**	**3.90363E-07**

Density, Roulette-Wheel, TSP-LIB-1060, *k* = 90, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.11087661675447E+08	427	0.21510%
2	1.10942435095637E+08	292	0.08530%
3	1.10845624023463E+08	363	0.15870%
4	1.10777340214018E+08	257	0.15850%
5	1.10741276231044E+08	499	0.25460%
6	1.10944515481207E+08	480	0.18600%
7	1.10780293806554E+08	294	0.52040%
8	1.11021941126121E+08	110	0.36770%
9	1.10618993830423E+08	143	0.75700%
10	**1.10520333848908E+08**	358	0.08860%
Mean	**1.10828041533282E+08**	**322.3**	**0.27919%**
Std. Dev.	**177239.489535**	**130.4641713**	**0.00213624**
Var.	**31413836650.666700**	**1.7021E+04**	**4.56352E-06**

Random, Deterministic, TSP-LIB-1060, *k* = 90, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.10545505598796E+08	585	0.00270%
2	1.10545505598796E+08	258	0.00140%
3	1.10512500362729E+08	490	0.00120%
4	1.10637127195792E+08	332	0.00130%
5	1.10479083296657E+08	483	0.00120%
6	1.10546502789193E+08	276	0.00150%
7	1.10545505598796E+08	400	0.00120%
8	1.10488621479469E+08	392	0.00130%
9	1.10525780703490E+08	578	0.00120%
10	**1.10479083296657E+08**	403	0.00020%
Mean	**1.10530521592038E+08**	**419.7**	**0.00132%**
Std. Dev.	**46771.752406**	**114.141287**	**6.0148E-06**
Var.	**2187596823.111110**	**1.3028E+04**	**3.61778E-11**

Random, Parent Favored Hybrid, TSP-LIB-1060, *k* = 90, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.10505245334979E+08	697	0.00080%
2	1.10619240693575E+08	581	0.00000%
3	**1.10488377778551E+08**	751	0.00170%
4	1.10548706998462E+08	557	0.00180%
5	1.10517079456243E+08	692	0.00310%
6	1.10527974355485E+08	957	0.00280%
7	1.10588657957793E+08	741	0.00000%
8	1.10749250837104E+08	299	0.00200%
9	1.10588657957793E+08	750	0.00630%
10	1.10592450069501E+08	699	0.00210%
Mean	**1.10572564143949E+08**	**672.4**	**0.00206%**
Std. Dev.	**75693.452575**	**170.195443**	**1.82221E-05**
Var.	**5729498762.666670**	**2.8966E+04**	**3.32044E-10**

Random, Roulette-Wheel, TSP-LIB-1060, *k* = 90, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.10796612887020E+08	397	0.00180%
2	1.10576978673445E+08	295	0.00180%
3	1.11049749739303E+08	418	0.00370%
4	1.10910699434266E+08	176	0.00430%
5	1.10555740485527E+08	483	0.00150%
6	1.10704521360559E+08	315	0.00690%
7	1.10663214745014E+08	454	0.00560%
8	1.10863470895080E+08	471	0.00910%
9	**1.10475122966247E+08**	602	0.00820%
10	1.10509434087495E+08	224	0.01410%
Mean	**1.10710554527396E+08**	**383.5**	**0.00570%**
Std. Dev.	**190282.139665**	**130.240163**	**3.99778E-05**
Var.	**36207292675.555600**	**1.6963E+04**	**1.59822E-09**

Separation, Deterministic, TSP-LIB-1060, *k* = 90, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.10479083296657E+08	517	0.18670%
2	1.10548706998462E+08	327	0.14040%
3	1.10557181005828E+08	386	0.10190%
4	1.10515440508351E+08	221	0.21870%
5	1.10479083296657E+08	436	0.14610%
6	1.10537087415871E+08	381	0.09780%
7	1.10479083296657E+08	427	0.06730%
8	1.10493754786388E+08	315	0.07280%
9	1.10531238531322E+08	324	0.04430%
10	**1.10454241201155E+08**	332	0.04980%
Mean	**1.10507490033735E+08**	**366.6**	**0.11258%**
Std. Dev.	**35144.401217**	**81.72474126**	**0.000588987**
Var.	**1235128936.888890**	**6.6789E+03**	**3.46906E-07**

Separation, Parent Favored Hybrid, TSP-LIB-1060, *k* = 90, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.10558772865627E+08	570	0.10940%
2	1.10657124966714E+08	248	0.17370%
3	1.10486754800998E+08	500	0.08410%
4	1.10498811757687E+08	452	0.09150%
5	1.10561972655046E+08	537	0.06970%
6	1.10524530006579E+08	671	0.06010%
7	1.10580233672141E+08	476	0.04390%
8	1.10537208307300E+08	585	0.04180%
9	1.10524238545932E+08	475	0.02410%
10	**1.10436107653530E+08**	1002	0.01950%
Mean	**1.10536575523155E+08**	**551.6**	**0.07178%**
Std. Dev.	**59512.495151**	**192.9658577**	**0.000461484**
Var.	**3541737079.111110**	**3.7236E+04**	**2.12967E-07**

Separation, Roulette-Wheel, TSP-LIB-1060, *k* = 90, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.10738550296695E+08	518	0.26460%
2	**1.10503165997636E+08**	237	0.45160%
3	1.10561549941257E+08	370	0.35100%
4	1.10547164528655E+08	235	0.46750%
5	1.11129488858296E+08	189	0.23290%
6	1.10638040000471E+08	423	0.12930%
7	1.10949715178883E+08	353	0.28240%
8	1.10875826840717E+08	243	0.15630%
9	1.10839093336591E+08	186	0.12650%
10	1.10789625280152E+08	107	0.16140%
Mean	**1.10757222025935E+08**	**286.1**	**0.26235%**
Std. Dev.	**199712.394310**	**125.8035947**	**0.001267676**
Var.	**39885040440.888900**	**1.5827E+04**	**1.607E-06**

TSP-LIB-1060, *k* = 100 Results

Density, Deterministic, TSP-LIB-1060, *k* = 100, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	9.64017925263360E+07	383	0.01810%
2	9.64134010440609E+07	446	0.01950%
3	9.64134010440609E+07	387	0.04630%
4	9.64072244792656E+07	428	0.04670%
5	9.64246395316506E+07	453	0.02970%
6	**9.63302963994504E+07**	577	0.05030%
7	9.63947925409464E+07	455	0.08310%
8	9.63477114518354E+07	535	0.06620%
9	9.63947925409464E+07	638	0.04590%
10	9.63372963848400E+07	685	0.06700%
11	9.63302963994504E+07	600	0.02730%
12	9.64204010294504E+07	329	0.05240%
13	9.64072244792656E+07	421	0.03110%
14	9.64072244792656E+07	611	0.04460%
15	9.63302963994504E+07	525	0.06100%
16	9.64175023055880E+07	391	0.08260%
17	9.63947925409464E+07	444	0.09330%
18	9.63975227206853E+07	516	0.06290%
19	9.63302963994504E+07	766	0.06980%
20	9.64099546590044E+07	432	0.10800%
Mean	**9.63855429677975E+07**	**501.1**	**0.05529%**
Std. Dev.	**3.55078052561020E+04**	**114.3107031**	**0.000245**
Var.	**1.26080423410526E+09**	**1.3067E+04**	**5.99E-08**

Density, Parent Favored Hybrid, TSP-LIB-1060, *k* = 100, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	9.63947925409464E+07	856	0.00890%
2	9.63902934663952E+07	760	0.00980%
3	9.64888442675150E+07	541	0.02310%
4	9.64099546590044E+07	590	0.02560%
5	9.64509370724127E+07	783	0.04150%
6	9.65530225372067E+07	418	0.04550%
7	**9.63899724275108E+07**	895	0.04680%
8	9.64121026679769E+07	897	0.05580%
9	9.66046000899635E+07	424	0.06660%
10	9.64166069604757E+07	673	0.06960%
11	9.64129454799444E+07	788	0.01170%
12	9.64072244792656E+07	1004	0.00980%
13	9.64036992854806E+07	883	0.02390%
14	9.64161312237997E+07	679	0.01970%
15	9.64134010440609E+07	828	0.03260%
16	9.64261220301293E+07	642	0.04150%
17	9.64513307174580E+07	658	0.04500%
18	9.64147167871796E+07	681	0.05580%
19	9.64072244792656E+07	619	0.06300%
20	9.64595972533150E+07	747	0.05660%
Mean	**9.64361759734653E+07**	**718.3**	**0.03764%**
Std. Dev.	**5.53197830950575E+04**	**156.1888533**	**0.000201**
Var.	**3.06027840168421E+09**	**2.4395E+04**	**4.05E-08**

Density, Roulette-Wheel Rank, TSP-LIB-1060, *k* = 100, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	9.64970776414205E+07	232	0.04710%
2	9.63598024578279E+07	208	0.08490%
3	9.64323528496337E+07	473	0.09490%
4	9.66466224959404E+07	189	0.08590%
5	9.66399642977610E+07	232	0.09210%
6	9.65504605628118E+07	305	0.11620%
7	9.64447520850693E+07	239	0.19910%
8	9.63689459445896E+07	606	0.12590%
9	9.66507973203333E+07	276	0.18110%
10	9.65517902648860E+07	228	0.03240%
11	9.68200988513021E+07	210	0.05560%
12	9.63585553225899E+07	551	0.04730%
13	9.64495370173954E+07	244	0.10140%
14	9.64311891517586E+07	385	0.07660%
15	9.64593774408926E+07	535	0.11390%
16	9.64470117964772E+07	193	0.09900%
17	9.64893186188699E+07	219	0.19710%
18	9.65745519396160E+07	326	0.13810%
19	9.64514993299520E+07	325	0.19720%
20	**9.63477114518354E+07**	483	0.14600%
Mean	**9.64985708420482E+07**	**322.95**	**0.11159%**
Std. Dev.	**1.21158579776563E+05**	**134.1752487**	**0.000515366**
Var.	**1.46794014534737E+10**	**1.8003E+04**	**2.65602E-07**

Random, Deterministic, TSP-LIB-1060, *k* = 100, u = 200, p = 0.8

Run	Best SSE	Gen. found
1	9.63947925409464E+07	384
2	9.64134010440609E+07	447
3	**9.63178644611312E+07**	505
4	9.63302963994504E+07	566
5	9.64072244792656E+07	403
6	9.64072244792656E+07	289
7	9.63178644611312E+07	607
8	9.63302963994504E+07	472
9	9.63975227206853E+07	349
10	9.63947925409464E+07	399
11	9.64072244792656E+07	438
12	9.63947925409464E+07	421
13	9.64134010440609E+07	299
14	9.64072244792656E+07	320
15	9.63429473873327E+07	485
16	9.63704284430683E+07	473
17	9.64072244792656E+07	391
18	9.63414560783116E+07	399
19	9.63781394136568E+07	402
20	9.63364729642457E+07	509
Mean	**9.63755295417877E+07**	**427.9**
Std. Dev.	**3.55495798598313E+04**	**83.17698315**
Var.	**1.26377262821053E+09**	**6.9184E+03**

Random, Parent Favored Hybrid, TSP-LIB-1060, *k* = 100, u = 200, p = 0.8

Run	Best SSE	Gen. found
1	9.64036992854806E+07	683
2	9.63562730199157E+07	691
3	9.64065307241495E+07	449
4	9.63947925409464E+07	674
5	9.63947925409464E+07	762
6	9.64072244792656E+07	668
7	9.64134010440609E+07	847
8	9.64009691057417E+07	771
9	9.64072244792656E+07	534
10	9.63414561024899E+07	823
11	9.64072244792656E+07	969
12	9.64161312237997E+07	683
13	9.63641914184384E+07	714
14	9.64246395316506E+07	611
15	**9.63382091895192E+07**	855
16	9.64099546590044E+07	588
17	9.63414299616856E+07	685
18	9.63947925409464E+07	695
19	9.63577074569999E+07	691
20	9.63421939649245E+07	629
Mean	**9.63861418874248E+07**	**701.1**
Std. Dev.	**2.95587804890527E+04**	**117.1894103**
Var.	**8.73721504000000E+08**	**1.3733E+04**

Random, Roulette-Wheel Rank, TSP-LIB-1060, *k* = 100, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	**9.63646045516827E+07**	313	0.00040%
2	9.66250617500743E+07	314	0.00010%
3	9.65161281042394E+07	343	0.00010%
4	9.64196536503081E+07	135	0.00010%
5	9.65084597093220E+07	291	0.00010%
6	9.64795255232971E+07	484	0.00010%
7	9.66647491537166E+07	349	0.00010%
8	9.67138369751818E+07	286	0.00010%
9	9.66853682175437E+07	146	0.00010%
10	9.65273515102566E+07	445	0.00010%
11	9.67558060625567E+07	270	0.00010%
12	9.64693345763531E+07	260	0.00010%
13	9.65988715124204E+07	231	0.00010%
14	9.64082113279837E+07	508	0.00010%
15	9.64633566650935E+07	224	0.00010%
16	9.64967470641176E+07	333	0.00010%
17	9.64115347612097E+07	356	0.00010%
18	9.65456766566720E+07	397	0.00010%
19	9.64999565328945E+07	262	0.00010%
20	9.64992217562893E+07	207	0.00010%
Mean	**9.65326728030606E+07**	**307.7**	**0.00012%**
Std. Dev.	**1.08494674042457E+05**	**99.88314225**	**6.7082E-07**
Var.	**1.17710942955789E+10**	**9.9766E+03**	**4.5E-13**

Separation, Deterministic, TSP-LIB-1060, *k* = 100, u = 200, p = 0.8

Run	Best SSE	Gen. found
1	9.63178644611312E+07	519
2	9.63302963994504E+07	401
3	9.63302963994504E+07	405
4	9.63302963994504E+07	556
5	9.63178644611312E+07	560
6	9.63178644611312E+07	506
7	9.63302963994504E+07	433
8	9.63975227206853E+07	307
9	9.63302963994504E+07	562
10	9.63310410113161E+07	346
11	9.63178644611312E+07	487
12	**9.63178644611312E+07**	437
13	9.64009691057417E+07	325
14	9.63372963848400E+07	496
15	9.63248644465208E+07	266
16	9.63302963994504E+07	520
17	9.64273697113895E+07	342
18	9.63477114518354E+07	408
19	9.63477114518354E+07	317
20	9.63302963994504E+07	462
Mean	**9.63407941692986E+07**	**432.75**
Std. Dev.	**3.09427043488615E+04**	**92.65151176**
Var.	**9.57450952421053E+08**	**8.5843E+03**

Separation, Parent Favored Hybrid, TSP-LIB-1060, *k* = 100, u = 200, p = 0.8

Run	Best SSE	Gen. found
1	9.63352795135163E+07	903
2	9.63947925409464E+07	705
3	9.63781394136568E+07	664
4	9.64036992854806E+07	500
5	9.64122075933314E+07	550
6	9.63420345826534E+07	689
7	9.64007874203939E+07	391
8	9.64308160964459E+07	526
9	9.64149377730703E+07	573
10	9.63650148390326E+07	477
11	9.63790168666630E+07	593
12	9.63178644611312E+07	774
13	9.64246395316506E+07	657
14	**9.63178644611312E+07**	773
15	9.63608068787943E+07	649
16	9.64246836631474E+07	410
17	9.63850562327212E+07	441
18	9.64303605323294E+07	467
19	9.64308160964459E+07	569
20	9.63178644611312E+07	772
Mean	**9.63833341121836E+07**	**604.15**
Std. Dev.	**4.01215197067477E+04**	**139.0835701**
Var.	**1.60973634357895E+09**	**1.9344E+04**

Separation, Roulette-Wheel Rank, TSP-LIB-1060, *k* = 100, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	9.64711860780717E+07	484	0.05360%
2	9.65446687735274E+07	349	0.11530%
3	9.65091726676457E+07	254	0.17640%
4	9.63302963994504E+07	546	0.13250%
5	9.64414177113401E+07	401	0.23170%
6	9.65968680624271E+07	122	0.26950%
7	9.65870250076891E+07	127	0.30420%
8	9.65049945420043E+07	495	0.29900%
9	9.67098274771028E+07	132	0.51910%
10	9.64923586128181E+07	278	0.25690%
11	9.64695343106904E+07	336	0.06390%
12	9.64814238420190E+07	460	0.04790%
13	9.65172966582782E+07	382	0.09240%
14	9.64694556032572E+07	190	0.16710%
15	9.64551059979717E+07	289	0.16610%
16	9.65092919200844E+07	120	0.28420%
17	9.64296636322014E+07	444	0.17230%
18	**9.63302963994504E+07**	458	0.24460%
19	9.64999151873456E+07	228	0.31770%
20	9.65538251047451E+07	424	0.22870%
Mean	**9.64951811994060E+07**	**325.95**	**0.20716%**
Std. Dev.	**8.49132629699891E+04**	**139.2591205**	**0.001133793**
Var.	**7.21026222821053E+09**	**1.9393E+04**	**1.28549E-06**

TSP-LIB-1060, *k* = 110 Results

Density, Deterministic, TSP-LIB-1060, *k* = 110, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	8.49427519367551E+07	598	0.14280%
2	8.49193972184895E+07	309	0.19690%
3	8.49693441941843E+07	524	0.12550%
4	8.49075603893072E+07	540	0.10470%
5	8.49419040711652E+07	587	0.11610%
6	**8.48494234899028E+07**	472	0.07720%
7	8.48610746271354E+07	533	0.08740%
8	8.50163067087083E+07	406	0.05250%
9	8.48532360706290E+07	435	0.05340%
10	8.49480806359605E+07	365	0.03690%
Mean	**8.49209079342237E+07**	**476.9**	**0.09934%**
Std. Dev.	**54317.300457**	**96.40937022**	**0.00048576**
Var.	**2950369128.888890**	**9.2948E+03**	**2.35963E-07**

Density, Parent Favored Hybrid, TSP-LIB-1060, *k* = 110, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	**8.48727947782081E+07**	864	0.06960%
2	8.49716867022548E+07	891	0.08570%
3	8.50360562136479E+07	566	0.12140%
4	8.49359218310986E+07	787	0.09350%
5	8.49154353188512E+07	845	0.06520%
6	8.49690863432902E+07	634	0.08300%
7	8.48892795315879E+07	1050	0.04440%
8	8.49655101374595E+07	751	0.05040%
9	8.50017663063357E+07	651	0.03510%
10	8.49680291900660E+07	500	0.02980%
Mean	**8.49525566352800E+07**	**753.9**	**0.06781%**
Std. Dev.	**49956.436275**	**167.5751573**	**0.000287876**
Var.	**2495645525.333330**	**2.8081E+04**	**8.28723E-08**

Density, Roulette-Wheel, TSP-LIB-1060, *k* = 110, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	8.50885014592879E+07	669	0.07360%
2	8.49943031323251E+07	273	0.31050%
3	8.50205157372625E+07	402	0.24840%
4	8.54281240984060E+07	357	0.21750%
5	8.52954279317713E+07	567	0.20690%
6	8.50435972185048E+07	411	0.17170%
7	8.50242780084907E+07	388	0.15500%
8	8.53205021909723E+07	399	0.12740%
9	8.53649003862138E+07	481	0.07960%
10	**8.49758598879693E+07**	418	0.04850%
Mean	**8.51556010051204E+07**	**436.5**	**0.16391%**
Std. Dev.	**175018.686967**	**111.5847959**	**0.000839337**
Var.	**30631540787.555600**	**1.2451E+04**	**7.04487E-07**

Random, Deterministic, TSP-LIB-1060, *k* = 110, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	**8.48432469251075E+07**	688	0.00070%
2	8.48894939875395E+07	435	0.00090%
3	8.49419040711652E+07	412	0.00070%
4	8.48705461976595E+07	489	0.00060%
5	8.49419040711652E+07	524	0.00080%
6	8.48610746271354E+07	572	0.00070%
7	8.49480806359605E+07	459	0.00070%
8	8.48610746271354E+07	509	0.00080%
9	8.48592863426535E+07	538	0.00070%
10	8.49419040711652E+07	433	0.00080%
Mean	**8.48958515556687E+07**	**505.9**	**0.00074%**
Std. Dev.	**42549.697291**	**82.01686818**	**8.43274E-07**
Var.	**1810476739.555560**	**6.7268E+03**	**7.11111E-13**

Random, Parent Favored Hybrid, TSP-LIB-1060, *k* = 110, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	8.49419040711652E+07	1039	0.00050%
2	8.50614269105693E+07	585	0.00050%
3	**8.48806940534866E+07**	891	0.00070%
4	8.51663072359550E+07	569	0.00050%
5	8.50808292227007E+07	597	0.00090%
6	8.51093743040285E+07	442	0.00090%
7	8.50332510336173E+07	672	0.00070%
8	8.49706804426791E+07	656	0.00050%
9	8.49480806359605E+07	778	0.00050%
10	8.51988245472809E+07	447	0.00050%
Mean	**8.50391372457443E+07**	**667.6**	**0.00062%**
Std. Dev.	**103500.594815**	**188.937497**	**1.68655E-06**
Var.	**10712373127.111100**	**3.5697E+04**	**2.84444E-12**

Random, Roulette-Wheel, TSP-LIB-1060, *k* = 110, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	8.51268537029549E+07	625	0.00110%
2	8.53058480788749E+07	389	0.00120%
3	8.51264089375269E+07	493	0.00150%
4	8.55241114911898E+07	196	0.00150%
5	8.49336143691073E+07	512	0.00110%
6	**8.48809528141075E+07**	864	0.00120%
7	8.52522374972667E+07	292	0.00100%
8	8.53887886000393E+07	538	0.00170%
9	8.50317167688547E+07	370	0.00130%
10	8.51417062417982E+07	209	0.00170%
Mean	**8.51712238501720E+07**	**448.8**	**0.00133%**
Std. Dev.	**200437.616434**	**203.6133591**	**2.54078E-06**
Var.	**40175238081.777800**	**4.1458E+04**	**6.45556E-12**

Separation, Deterministic, TSP-LIB-1060, *k* = 110, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	8.48432469251075E+07	579	0.06530%
2	8.49419040711652E+07	318	0.17930%
3	8.49419040711652E+07	418	0.17450%
4	8.49419040711652E+07	350	0.14610%
5	8.49419040711652E+07	473	0.11610%
6	8.48532360706290E+07	319	0.10380%
7	8.48594126354243E+07	675	0.09620%
8	8.48861769079452E+07	292	0.08620%
9	8.49308609012438E+07	339	0.04350%
10	8.48672511919307E+07	331	0.02200%
Mean	**8.49007800916941E+07**	**409.4**	**0.10330%**
Std. Dev.	**42542.511549**	**128.3945309**	**0.000525081**
Var.	**1809865288.888890**	**1.6485E+04**	**2.7571E-07**

Separation, Parent Favored Hybrid, TSP-LIB-1060, *k* = 110, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	**8.49768570074744E+07**	**559**	**0.18610%**
2	8.50873859503070E+07	402	0.21790%
3	8.49706804426791E+07	610	0.12080%
4	8.49445065439844E+07	786	0.08290%
5	8.49580120213565E+07	544	0.10990%
6	**8.48657703478228E+07**	573	0.09590%
7	8.49419040711652E+07	609	0.07130%
8	8.50044772787859E+07	555	0.10510%
9	8.49043327562662E+07	590	0.04480%
10	8.49419040711652E+07	590	0.02460%
Mean	**8.49595830491007E+07**	**581.8**	**0.10593%**
Std. Dev.	**59140.975305**	**93.35690179**	**0.000590515**
Var.	**3497654960.000000**	**8.7155E+03**	**3.48708E-07**

Separation, Roulette-Wheel, TSP-LIB-1060, *k* = 110, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	8.49838480525962E+07	698	0.18630%
2	8.53749721853873E+07	383	0.22870%
3	8.50042962408794E+07	815	0.20220%
4	**8.48894383731847E+07**	499	0.18510%
5	8.51387296627881E+07	512	0.15650%
6	8.52066107775059E+07	211	0.18270%
7	8.51348288304496E+07	470	0.13740%
8	8.50946535458306E+07	276	0.16490%
9	8.51232917074449E+07	301	0.10490%
10	8.51483787964011E+07	251	0.05480%
Mean	**8.51099048172468E+07**	**441.6**	**0.16035%**
Std. Dev.	**132751.154002**	**198.4261408**	**0.000505375**
Var.	**17622868888.888900**	**3.9373E+04**	**2.55404E-07**

TSP-LIB-1060, *k* = 120 Results

Density, Deterministic, TSP-LIB-1060, *k* = 120, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	7.56930159068322E+07	700	0.02080%
2	7.56600742570273E+07	612	0.13560%
3	7.56956995126245E+07	536	0.13980%
4	**7.56176311462740E+07**	826	0.10070%
5	7.56565636439236E+07	576	0.08160%
6	7.57688948986141E+07	633	0.11100%
7	7.56721229315141E+07	497	0.05770%
8	7.56920272536092E+07	590	0.09080%
9	7.56949998504509E+07	432	0.07930%
10	7.57239001625981E+07	401	0.06800%
Mean	**7.56874929563468E+07**	**580.3**	**0.08853%**
Std. Dev.	**40759.242093**	**125.4476872**	**0.000358932**
Var.	**1661315816.000000**	**1.5737E+04**	**1.28832E-07**

Density, Parent Favored Hybrid, TSP-LIB-1060, *k* = 120, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	7.56772046860694E+07	1054	0.05180%
2	7.57483049834376E+07	731	0.08170%
3	7.57312174551931E+07	880	0.08230%
4	**7.56145435789047E+07**	1034	0.06140%
5	7.57995135004316E+07	722	0.07040%
6	7.57194604426033E+07	857	0.04000%
7	7.57306232109472E+07	909	0.05200%
8	7.58295640211910E+07	850	0.03850%
9	7.56988536711532E+07	944	0.02490%
10	7.56936280187713E+07	779	0.01650%
Mean	**7.57242913568702E+07**	**876**	**0.05195%**
Std. Dev.	**60807.351003**	**114.2920236**	**0.000224797**
Var.	**3697533936.000000**	**1.3063E+04**	**5.05336E-08**

Density, Roulette-Wheel, TSP-LIB-1060, *k* = 120, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	7.57773696531290E+07	504	0.08620%
2	7.59158644458008E+07	346	0.31000%
3	7.59450026524802E+07	254	0.25980%
4	7.57728901956387E+07	438	0.20470%
5	**7.56523636379959E+07**	655	0.16260%
6	7.58294479735907E+07	422	0.09260%
7	7.58642107015230E+07	597	0.21770%
8	7.56632380094534E+07	773	0.12710%
9	7.59401644509074E+07	464	0.23920%
10	7.58562444828129E+07	371	0.18390%
Mean	**7.58216796203332E+07**	**482.4**	**0.18838%**
Std. Dev.	**105038.301835**	**155.269801**	**0.000727671**
Var.	**11033044852.444400**	**2.4109E+04**	**5.29504E-07**

Random, Deterministic, TSP-LIB-1060, *k* = 120, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	7.57150306618744E+07	587	0.00060%
2	**7.56258771436841E+07**	434	0.00070%
3	7.56889495784265E+07	347	0.00120%
4	7.57721860077113E+07	340	0.00120%
5	7.56781067763049E+07	735	0.00060%
6	7.56634209478965E+07	688	0.00100%
7	7.56691087411372E+07	808	0.00060%
8	7.56856615646379E+07	459	0.00070%
9	7.57163897014456E+07	376	0.00120%
10	7.56941541291604E+07	425	0.00070%
Mean	**7.56908885252279E+07**	**519.9**	**0.00085%**
Std. Dev.	**38733.932640**	**171.6226157**	**2.67706E-06**
Var.	**1500317537.777780**	**2.9454E+04**	**7.16667E-12**

Random, Parent Favored Hybrid, TSP-LIB-1060, *k* = 120, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	7.56941541291604E+07	1040	0.00040%
2	**7.56889495784265E+07**	903	0.00040%
3	7.57900453166526E+07	889	0.00040%
4	7.57423444921226E+07	684	0.00050%
5	7.57511424022585E+07	569	0.00050%
6	7.58947892057047E+07	498	0.00060%
7	7.58972959304529E+07	640	0.00050%
8	7.57150306618744E+07	812	0.00050%
9	7.57044823062958E+07	854	0.00050%
10	7.57042522397787E+07	970	0.00040%
Mean	**7.57582486262727E+07**	**785.9**	**0.00047%**
Std. Dev.	**78794.129810**	**179.4197128**	**6.74949E-07**
Var.	**6208514892.444440**	**3.2191E+04**	**4.55556E-13**

Random, Roulette-Wheel, TSP-LIB-1060, *k* = 120, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	7.57575357452081E+07	629	0.00130%
2	**7.56125032065160E+07**	455	0.00100%
3	7.57336155453505E+07	581	0.00110%
4	7.60694627231360E+07	175	0.00220%
5	7.60334761006904E+07	306	0.00160%
6	7.60235610708013E+07	327	0.00170%
7	7.58326315531801E+07	446	0.00150%
8	7.57510784991096E+07	587	0.00100%
9	7.59304349702201E+07	235	0.00140%
10	7.59159141807525E+07	347	0.00150%
Mean	**7.58660213594965E+07**	**408.8**	**0.00143%**
Std. Dev.	**152310.088896**	**156.1201816**	**3.653E-06**
Var.	**23198363179.555600**	**2.4374E+04**	**1.33444E-11**

Separation, Deterministic, TSP-LIB-1060, *k* = 120, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	7.56080532785178E+07	643	0.06970%
2	7.57102309964887E+07	484	0.12810%
3	**7.56054012825253E+07**	785	0.10690%
4	7.56828920311236E+07	606	0.10080%
5	7.57021835177939E+07	385	0.10900%
6	7.56449530188300E+07	667	0.07680%
7	7.57251671831686E+07	457	0.06450%
8	7.56519783318448E+07	602	0.05000%
9	7.56567983020901E+07	582	0.03460%
10	7.56167894184557E+07	433	0.03430%
Mean	**7.56604447360838E+07**	**564.4**	**0.07747%**
Std. Dev.	**43357.784107**	**123.0503059**	**0.0003275**
Var.	**1879897442.666670**	**1.5141E+04**	**1.07256E-07**

Separation, Parent Favored Hybrid, TSP-LIB-1060, *k* = 120, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	7.57373793204170E+07	741	0.06730%
2	7.57624850099613E+07	610	0.09130%
3	7.57011617156748E+07	725	0.08510%
4	7.60323982917604E+07	415	0.08980%
5	7.56772046860694E+07	888	0.06920%
6	7.57490490820642E+07	811	0.04370%
7	**7.56247985686709E+07**	713	0.03200%
8	7.58423978927392E+07	555	0.05310%
9	7.57209257786407E+07	751	0.03080%
10	7.57309850266256E+07	538	0.01680%
Mean	**7.57578785372624E+07**	**674.7**	**0.05791%**
Std. Dev.	**111827.310940**	**142.5693204**	**0.000266837**
Var.	**12505347472.000000**	**2.0326E+04**	**7.12019E-08**

Separation, Roulette-Wheel, TSP-LIB-1060, *k* = 120, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	7.57563913569222E+07	750	0.15540%
2	7.60610631302819E+07	397	0.25830%
3	7.58375179985939E+07	488	0.24840%
4	7.58300387471933E+07	576	0.13560%
5	7.58887300900875E+07	543	0.11230%
6	7.63795077184722E+07	360	0.15930%
7	7.57459699395640E+07	413	0.10400%
8	7.58263974219547E+07	367	0.09770%
9	7.60111329987493E+07	305	0.09670%
10	**7.56788656368046E+07**	298	0.05630%
Mean	**7.59015615038624E+07**	**449.7**	**0.14240%**
Std. Dev.	**204338.276373**	**141.1319713**	**0.000658703**
Var.	**41754131191.111100**	**1.9918E+04**	**4.33889E-07**

TSP-LIB-1060, *k* = 130 Results

Density, Deterministic, TSP-LIB-1060, *k* = 130, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	**6.76015449301936E+07**	535	0.12590%
2	6.76710408716268E+07	446	0.16580%
3	6.76266342112204E+07	467	0.15660%
4	6.77135886431908E+07	727	0.10770%
5	6.76950657287662E+07	534	0.09640%
6	6.76400391180447E+07	508	0.10450%
7	6.76266342112204E+07	444	0.09120%
8	6.76473122428072E+07	531	0.06840%
9	6.76406122389258E+07	594	0.03110%
10	6.76323801740784E+07	500	0.02400%
Mean	**6.76494852370074E+07**	**528.6**	**0.09716%**
Std. Dev.	**34090.320255**	**83.48812291**	**0.00046922**
Var.	**1162149935.111110**	**6.9703E+03**	**2.20167E-07**

Density, Parent Favored Hybrid, TSP-LIB-1060, *k* = 130, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	6.76272073321015E+07	1072	0.07480%
2	**6.75983988285860E+07**	835	0.09870%
3	6.77707618301286E+07	812	0.10960%
4	6.77301534698526E+07	644	0.07450%
5	6.81400702972761E+07	407	0.10780%
6	6.78951300855131E+07	758	0.06150%
7	6.76272073321015E+07	904	0.05170%
8	6.76266342112204E+07	662	0.03210%
9	6.76559313706940E+07	631	0.04550%
10	6.76952990805807E+07	824	0.02370%
Mean	**6.77366793838055E+07**	**754.9**	**0.06799%**
Std. Dev.	**167487.093340**	**180.9109357**	**0.000305706**
Var.	**28051926435.555600**	**3.2729E+04**	**9.34563E-08**

Density, Roulette-Wheel, TSP-LIB-1060, *k* = 130, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	6.79342836248302E+07	768	0.14950%
2	6.79900196628938E+07	616	0.18470%
3	6.77441514976531E+07	622	0.15660%
4	6.79780899613526E+07	514	0.13870%
5	6.79245091754348E+07	378	0.24880%
6	**6.76637577199083E+07**	559	0.10190%
7	6.79113397328041E+07	453	0.16650%
8	6.79113332715807E+07	550	0.08630%
9	6.76680619308415E+07	560	0.05560%
10	6.79583776663971E+07	663	0.02490%
Mean	**6.78683924243696E+07**	**568.3**	**0.13135%**
Std. Dev.	**126291.850283**	**109.0127923**	**0.000657129**
Var.	**15949631448.000000**	**1.1884E+04**	**4.31819E-07**

Random, Deterministic, TSP-LIB-1060, *k* = 130, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	6.78396199608857E+07	556	0.00070%
2	6.76034332214344E+07	657	0.00060%
3	6.76945675604407E+07	478	0.00070%
4	6.75701630130155E+07	574	0.00070%
5	6.76659943384018E+07	424	0.00060%
6	6.78110902829755E+07	433	0.00090%
7	6.76266342112204E+07	478	0.00050%
8	**6.75646644451026E+07**	506	0.00060%
9	6.76703689784497E+07	572	0.00070%
10	6.76362662066047E+07	425	0.00100%
Mean	**6.76682802218531E+07**	**510.3**	**0.00070%**
Std. Dev.	**92963.713805**	**77.65886942**	**1.49071E-06**
Var.	**8642252084.444440**	**6.0309E+03**	**2.22222E-12**

Random, Parent Favored Hybrid, TSP-LIB-1060, *k* = 130, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	6.76291245816162E+07	1140	0.00030%
2	6.76495636378668E+07	1008	0.00030%
3	6.76266342112204E+07	845	0.00040%
4	6.76704828111102E+07	851	0.00050%
5	6.76554893715404E+07	691	0.00050%
6	6.76615088694570E+07	705	0.00050%
7	6.76412619707827E+07	820	0.00040%
8	**6.75946897550449E+07**	827	0.00040%
9	6.78952086165957E+07	446	0.00060%
10	6.76069146648606E+07	879	0.00060%
Mean	**6.76630878490095E+07**	**821.2**	**0.00045%**
Std. Dev.	**84964.264776**	**186.3651136**	**1.08012E-06**
Var.	**7218926288.888890**	**3.4732E+04**	**1.16667E-12**

Random, Roulette-Wheel, TSP-LIB-1060, *k* = 130, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	6.76585849806489E+07	686	0.00110%
2	6.76881871389309E+07	589	0.00080%
3	6.79604113359207E+07	447	0.00120%
4	6.77774982798222E+07	563	0.00080%
5	6.76804235277725E+07	538	0.00080%
6	6.82779559166900E+07	280	0.00140%
7	6.78945300546372E+07	481	0.00090%
8	6.79218676815846E+07	396	0.00130%
9	6.78219250422354E+07	474	0.00120%
10	6.78804416584661E+07	633	0.00050%
Mean	**6.78561825616709E+07**	**508.7**	**0.00100%**
Std. Dev.	**182772.860645**	**119.2215957**	**2.82843E-06**
Var.	**33405918588.444400**	**1.4214E+04**	**8E-12**

Separation, Deterministic, TSP-LIB-1060, *k* = 130, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	**6.75646978154244E+07**	529	0.02940%
2	6.75713963486613E+07	424	0.15890%
3	6.76126328570947E+07	315	0.19690%
4	6.75681931662518E+07	638	0.08500%
5	6.77195621057093E+07	396	0.08320%
6	6.75943256931667E+07	328	0.10950%
7	6.75789728947752E+07	487	0.07410%
8	6.75920244297912E+07	630	0.06440%
9	6.76077404524464E+07	414	0.06670%
10	6.76016901804220E+07	419	0.07530%
Mean	**6.76011235943743E+07**	**458**	**0.09434%**
Std. Dev.	**44868.780654**	**112.3842615**	**0.000491906**
Var.	**2013207477.333330**	**1.2630E+04**	**2.41972E-07**

Separation, Parent Favored Hybrid, TSP-LIB-1060, *k* = 130, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	**6.75617643532770E+07**	1089	0.04760%
2	6.76342639424693E+07	756	0.07670%
3	6.76607320514270E+07	693	0.07340%
4	6.76235754999887E+07	845	0.07550%
5	6.75917538758712E+07	762	0.04570%
6	6.76460893900692E+07	940	0.07860%
7	6.76060151097132E+07	743	0.02780%
8	6.76059165353865E+07	636	0.04190%
9	6.76025408619156E+07	693	0.03770%
10	6.76166979066697E+07	902	0.01570%
Mean	**6.76149349526787E+07**	**805.9**	**0.05206%**
Std. Dev.	**28280.998772**	**138.092119**	**0.000225997**
Var.	**799814891.555556**	**1.9069E+04**	**5.10745E-08**

Separation, Roulette-Wheel, TSP-LIB-1060, *k* = 130, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	6.78E+07	890	0.001018
2	6.76E+07	521	0.000573
3	6.79E+07	365	0.002437
4	6.78E+07	402	0.001759
5	6.80E+07	248	0.002598
6	6.80E+07	239	0.002113
7	6.78E+07	529	0.000906
8	6.78E+07	554	0.001443
9	6.77E+07	599	0.000693
10	6.83E+07	284	0.000895
Mean	**6.78734530284077E+07**	**463.1**	**0.14435%**
Std. Dev.	**196998.817152**	**199.6087562**	**0.000742332**
Var.	**38808533959.111100**	**3.9844E+04**	**5.51057E-07**

TSP-LIB-1060, *k* = 140 Results

Density, Deterministic, TSP-LIB-1060, *k* = 140, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	6.11615907168324E+07	646	0.13170%
2	6.11838516289456E+07	668	0.13010%
3	6.11642784263411E+07	578	0.12730%
4	**6.11530780575792E+07**	516	0.11430%
5	6.12603635007045E+07	547	0.08940%
6	6.12284209784511E+07	619	0.06910%
7	6.12348853718677E+07	522	0.09400%
8	6.12019843153411E+07	412	0.08330%
9	6.12261056806503E+07	645	0.04300%
10	6.12153230157344E+07	453	0.03030%
Mean	**6.12029881692447E+07**	**560.6**	**0.09125%**
Std. Dev.	**36075.820083**	**86.2737246**	**0.000358766**
Var.	**1301464794.666670**	**7.4432E+03**	**1.28713E-07**

Density, Parent Favored Hybrid, TSP-LIB-1060, *k* = 140, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	6.12316571798618E+07	969	0.02910%
2	**6.12084406480830E+07**	910	0.07970%
3	6.13195997186503E+07	762	0.08850%
4	6.13654108094471E+07	770	0.06510%
5	6.13304637974469E+07	953	0.06520%
6	6.12307997400393E+07	836	0.05710%
7	6.12708459584835E+07	1149	0.04260%
8	6.12414134115362E+07	877	0.03120%
9	6.13173989455033E+07	871	0.04110%
10	6.12137185503267E+07	1120	0.01480%
Mean	**6.12729748759378E+07**	**921.7**	**0.05144%**
Std. Dev.	**55935.759693**	**131.1369513**	**0.000236087**
Var.	**3128809212.444440**	**1.7197E+04**	**5.57369E-08**

Density, Roulette-Wheel, TSP-LIB-1060, *k* = 140, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	6.12602577979848E+07	560	0.07060%
2	6.14742013116748E+07	544	0.25360%
3	6.20523203506961E+07	205	0.36060%
4	6.15497460399289E+07	531	0.19030%
5	6.17507534586185E+07	538	0.15940%
6	6.21594225053365E+07	149	0.31580%
7	6.13203262357597E+07	314	0.13720%
8	6.14828979810165E+07	380	0.17620%
9	6.13807355055333E+07	341	0.12560%
10	6.15750705443735E+07	450	0.04150%
Mean	**6.16005731730923E+07**	**401.2**	**0.18308%**
Std. Dev.	**300864.455823**	**148.0726548**	**0.001015802**
Var.	**90519420777.777800**	**2.1926E+04**	**1.03185E-06**

Random, Deterministic, TSP-LIB-1060, *k* = 140, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	6.11398911111977E+07	599	0.00050%
2	**6.11299176952483E+07**	460	0.00050%
3	6.11419290888495E+07	560	0.00040%
4	6.13061367716858E+07	492	0.00050%
5	6.11822376046066E+07	593	0.00080%
6	6.12687583285428E+07	499	0.00050%
7	6.12003596831146E+07	614	0.00050%
8	6.12337208772125E+07	518	0.00080%
9	6.12069658576806E+07	644	0.00040%
10	6.11816459110257E+07	381	0.00100%
Mean	**6.11991562929164E+07**	**536**	**0.00059%**
Std. Dev.	**57465.513987**	**80.9471707**	**2.02485E-06**
Var.	**3302285297.777780**	**6.5524E+03**	**4.1E-12**

Random, Parent Favored Hybrid, TSP-LIB-1060, *k* = 140, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	6.13185911721895E+07	736	0.00050%
2	6.12295140332185E+07	943	0.00050%
3	6.15081148654567E+07	589	0.00040%
4	**6.11599750435536E+07**	1149	0.00050%
5	6.14193122264300E+07	534	0.00040%
6	6.14801066927649E+07	640	0.00060%
7	6.12755864208783E+07	664	0.00040%
8	6.11990228804484E+07	1016	0.00040%
9	6.12135025934681E+07	786	0.00030%
10	6.12618678312377E+07	835	0.00030%
Mean	**6.13065593759646E+07**	**789.2**	**0.00043%**
Std. Dev.	**122113.120609**	**197.9420791**	**9.48683E-07**
Var.	**14911614224.888900**	**3.9181E+04**	**9E-13**

Random, Roulette-Wheel, TSP-LIB-1060, *k* = 140, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	**6.12182942386810E+07**	679	0.00080%
2	6.15546336110938E+07	608	0.00090%
3	6.13670889411598E+07	683	0.00120%
4	6.14076608576166E+07	660	0.00080%
5	6.14706659298339E+07	481	0.00130%
6	6.14302503342261E+07	561	0.00080%
7	6.15430902762825E+07	354	0.00170%
8	6.13099071632915E+07	517	0.00120%
9	6.18333996874826E+07	291	0.00110%
10	6.14604641125181E+07	412	0.00110%
Mean	**6.14595455152186E+07**	**524.6**	**0.00109%**
Std. Dev.	**166201.076627**	**138.9861704**	**2.84605E-06**
Var.	**27622797872.000000**	**1.9317E+04**	**8.1E-12**

Separation, Deterministic, TSP-LIB-1060, *k* = 140, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	6.11746125439906E+07	625	0.07940%
2	6.11756227888369E+07	753	0.13970%
3	**6.11512945962159E+07**	561	0.11940%
4	6.11660019367195E+07	504	0.10530%
5	6.11719432319548E+07	385	0.14210%
6	6.12003626678123E+07	426	0.08190%
7	6.11568017821062E+07	582	0.06540%
8	6.11773425282382E+07	522	0.05050%
9	6.11770417353400E+07	640	0.05010%
10	6.11910364702153E+07	588	0.02240%
Mean	**6.11742060281430E+07**	**558.6**	**0.08562%**
Std. Dev.	**14482.762781**	**106.6064413**	**0.000402717**
Var.	**209750417.777778**	**1.1365E+04**	**1.62181E-07**

Separation, Parent Favored Hybrid, TSP-LIB-1060, *k* = 140, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	6.11813898786692E+07	944	0.03540%
2	6.11803074736191E+07	926	0.01370%
3	6.12228537977795E+07	733	0.04160%
4	6.11882766651148E+07	612	0.07210%
5	6.12184389909880E+07	601	0.06040%
6	6.13615223304139E+07	649	0.08170%
7	6.11815068366896E+07	834	0.08770%
8	6.11848977487876E+07	916	0.07590%
9	**6.11472851799328E+07**	930	0.06290%
10	6.12136831503113E+07	1177	0.02710%
Mean	**6.12080162052306E+07**	**832.2**	**0.05585%**
Std. Dev.	**58420.777263**	**183.2180243**	**0.000250412**
Var.	**3412987216.000000**	**3.3569E+04**	**6.27063E-08**

Separation, Roulette-Wheel, TSP-LIB-1060, *k* = 140, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	6.13547023075432E+07	645	0.21560%
2	6.14376897899282E+07	290	0.26110%
3	6.14263000960242E+07	461	0.15970%
4	6.12785506560215E+07	528	0.17060%
5	6.15926968192235E+07	210	0.21470%
6	6.14016067821080E+07	523	0.12590%
7	6.16590622928255E+07	462	0.10610%
8	6.13255109860112E+07	541	0.07900%
9	6.12956296877207E+07	856	0.07110%
10	6.13483335843281E+07	575	: 0.000429
Mean	**6.14120083001734E+07**	**509.1**	**0.15598%**
Std. Dev.	**125091.592189**	**178.4865074**	**0.000659581**
Var.	**15647906436.444400**	**3.1857E+04**	**4.35047E-07**

TSP-LIB-1060, *k* = 150 Results

Density Deterministic, TSP-LIB-1060, *k* = 150, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	5.59170045745704E+07	1204	0.07740%
2	5.59964527861332E+07	1027	0.12350%
3	5.60204604635791E+07	699	0.11660%
4	5.60033018935913E+07	747	0.10630%
5	5.60333907836418E+07	915	0.10570%
6	5.60319248600407E+07	783	0.05740%
7	5.60306522702702E+07	834	0.06750%
8	5.60277394490128E+07	677	0.02280%
9	5.60274699175188E+07	553	0.10230%
10	5.60087048557374E+07	641	0.16640%
Mean	**5.60097101854096E+07**	**808**	**0.09459%**
Std. Dev.	**35057.144037**	**195.2787182**	**0.000399**
Var.	**1229003348.000000**	**3.8134E+04**	**1.6E-07**

Density, Parent Favored Hybrid, TSP-LIB-1060, *k* = 150, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	5.60506278433478E+07	1008	0.01430%
2	5.60477119881354E+07	1166	0.08280%
3	5.60569888688020E+07	1244	0.06950%
4	5.62667410014335E+07	689	0.09910%
5	5.62553508991345E+07	550	0.07820%
6	5.61254396249898E+07	1050	0.06260%
7	5.60618022523819E+07	1392	0.04430%
8	5.62369528522244E+07	696	0.05120%
9	5.63210102978737E+07	694	0.03910%
10	**5.59776615591642E+07**	1261	0.03180%
Mean	**5.61400287187487E+07**	**975**	**0.05729%**
Std. Dev.	**119074.979025**	**296.3601413**	**0.000259**
Var.	**14178850629.777800**	**8.7829E+04**	**6.72E-08**

Density, Roulette-Wheel, TSP-LIB-1060, *k* = 150, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	5.62962104229741E+07	619	0.06310%
2	5.60624799775502E+07	970	0.16430%
3	5.62731881555327E+07	300	0.29540%
4	5.62903694004397E+07	737	0.15190%
5	5.60879653749458E+07	535	0.16390%
6	5.60783951975670E+07	650	0.13350%
7	**5.60183735418316E+07**	865	0.11250%
8	5.63050132505171E+07	446	0.11870%
9	5.61258716812341E+07	538	0.11660%
10	5.61360845588937E+07	583	0.06210%
Mean	**5.61673951561486E+07**	**624.3**	**0.13820%**
Std. Dev.	**111552.781636**	**195.7674641**	**0.00066**
Var.	**12444023090.666700**	**3.8325E+04**	**4.36E-07**

Random, Deterministic, TSP-LIB-1060, *k* = 150, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	5.59782363926701E+07	893	0.00040%
2	5.60581809226826E+07	695	0.00050%
3	5.60172362078635E+07	667	0.00180%
4	5.60474892356542E+07	697	0.00070%
5	**5.59557431753088E+07**	744	0.00070%
6	5.59825543486065E+07	860	0.00040%
7	5.61606766700060E+07	392	0.00090%
8	5.60664441529003E+07	639	0.00050%
9	5.60191505832655E+07	668	0.00050%
10	5.60566870608063E+07	741	0.00070%
Mean	**5.60342398749764E+07**	**699.6**	**0.00071%**
Std. Dev.	**58463.950021**	**136.2988546**	**4.14863E-06**
Var.	**3418033452.000000**	**1.8577E+04**	**1.72111E-11**

Random, Roulette-Wheel, TSP-LIB-1060, *k* = 150, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	5.64445790200466E+07	423	0.00100%
2	5.61293482972548E+07	538	0.00090%
3	5.63559375062367E+07	324	0.00120%
4	5.62192304049725E+07	276	0.00110%
5	5.62600073338317E+07	551	0.00080%
6	5.63370721410507E+07	426	0.00100%
7	**5.60481546361869E+07**	751	0.00080%
8	5.62790733755561E+07	551	0.00330%
9	5.60966970464352E+07	716	0.00140%
10	5.60548210478327E+07	846	0.00070%
Mean	**5.62224920809404E+07**	**540.2**	**0.00122%**
Std. Dev.	**136579.496994**	**186.3138332**	**7.59825E-06**
Var.	**18653958999.111100**	**3.4713E+04**	**5.77333E-11**

Random, Parent Favored Hybrid, TSP-LIB-1060, *k* = 150, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	5.60325930726050E+07	1327	0.00030%
2	5.60104926959408E+07	840	0.00050%
3	5.60726715647733E+07	1128	0.00030%
4	5.61159846562335E+07	927	0.00030%
5	5.61552161717467E+07	850	0.00050%
6	5.60868998342291E+07	916	0.00030%
7	5.61826725793983E+07	795	0.00080%
8	5.60671410379966E+07	1037	0.00030%
9	5.60597355837564E+07	869	0.00050%
10	5.61464407221739E+07	846	0.00030%
Mean	**5.60929847918854E+07**	**953.5**	**0.00041%**
Std. Dev.	**55755.760169**	**165.4779274**	**1.66333E-06**
Var.	**3108704792.000000**	**2.7383E+04**	**2.76667E-12**

Separation, Deterministic, TSP-LIB-1060, *k* = 150, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	5.59579930446554E+07	808	0.08150%
2	5.59549469274251E+07	532	0.04050%
3	5.60222495404279E+07	666	0.05450%
4	5.59644751500136E+07	698	0.04840%
5	5.60447889108242E+07	483	0.09220%
6	5.60175547590645E+07	524	0.07450%
7	5.59752110972686E+07	1131	0.08020%
8	5.60471972431954E+07	598	0.11660%
9	5.59484577854002E+07	636	0.08600%
10	**5.59353140388703E+07**	662	0.11180%
Mean	**5.59868188497145E+07**	**673.8**	**0.07862%**
Std. Dev.	**41914.135049**	**186.7718751**	**0.000253**
Var.	**1756794716.888890**	**3.4884E+04**	**6.4E-08**

Separation, Parent Favored Hybrid, TSP-LIB-1060, *k* = 150, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	5.64572674467671E+07	307	0.07880%
2	5.60256035000803E+07	835	0.09210%
3	5.59827633466442E+07	964	0.05710%
4	5.60489698766895E+07	786	0.01630%
5	5.60234707700776E+07	837	0.02070%
6	5.60400450785021E+07	974	0.03850%
7	**5.59511944345735E+07**	1184	0.02780%
8	5.59580400807581E+07	1090	0.07480%
9	5.60483161703648E+07	1046	0.05620%
10	5.60222201047495E+07	1227	0.04320%
Mean	**5.60557890809207E+07**	**925**	**0.05055%**
Std. Dev.	**145466.789413**	**262.7127709**	**0.000258**
Var.	**21160586822.222200**	**6.9018E+04**	**6.63E-08**

Separation, Parent Favored Hybrid, TSP-LIB-1060, *k* = 150, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	5.64572674467671E+07	307	0.07880%
2	5.60256035000803E+07	835	0.09210%
3	5.59827633466442E+07	964	0.05710%
4	5.60489698766895E+07	786	0.01630%
5	5.60234707700776E+07	837	0.02070%
6	5.60400450785021E+07	974	0.03850%
7	**5.59511944345735E+07**	1184	0.02780%
8	5.59580400807581E+07	1090	0.07480%
9	5.60483161703648E+07	1046	0.05620%
10	5.60222201047495E+07	1227	0.04320%
Mean	**5.60557890809207E+07**	**925**	**0.05055%**
Std. Dev.	**145466.789413**	**262.7127709**	**0.000258**
Var.	**21160586822.222200**	**6.9018E+04**	**6.63E-08**

TSP-LIB-3038, *k* = 10 Results

Density, Deterministic, TSP-LIB-3038, *k* = 10, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	5.60251191254285E+08	1	0.13140%
2	5.60251191254285E+08	4	0.19520%
3	5.60251191254285E+08	1	0.33670%
4	5.60251191254285E+08	5	0.32600%
5	5.60251191254285E+08	3	0.42860%
6	5.60251191254285E+08	1	0.48510%
7	5.60251191254285E+08	0	0.56640%
8	5.60251191254285E+08	3	0.90400%
9	5.60251191254285E+08	5	0.69520%
10	5.60251191254285E+08	0	0.78300%
Mean	**5.60251191254285E+08**	**2.3**	**0.48516%**
Std. Dev.	**0.000000**	**1.946506843**	**0.002526848**
Var.	**0.000000**	**3.7889E+00**	**6.38496E-06**

Density, Parent Favored Hybrid, TSP-LIB-3038, *k* = 10, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	5.60251191254285E+08	1	0.13140%
2	5.60251191254285E+08	4	0.19520%
3	5.60251191254285E+08	1	0.33670%
4	5.60251191254285E+08	5	0.32600%
5	5.60251191254285E+08	3	0.42860%
6	5.60251191254285E+08	10	0.48510%
7	5.60251191254285E+08	0	0.56640%
8	5.60251191254285E+08	3	0.90400%
9	5.60251191254285E+08	5	0.69520%
10	5.60251191254285E+08	0	0.78300%
Mean	**5.60251191254285E+08**	**3.2**	**0.48516%**
Std. Dev.	**0.000000**	**3.047767854**	**0.002526848**
Var.	**0.000000**	**9.2889E+00**	**6.38496E-06**

Density, Roulette-Wheel, TSP-LIB-3038, *k* = 10, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	5.60251191254285E+08	1	1.76890%
2	5.60251191254285E+08	3	0.21870%
3	5.60251191254285E+08	5	0.32720%
4	5.60251191254285E+08	3	0.54130%
5	5.60251191254285E+08	1	0.61540%
6	5.60251191254285E+08	1	0.72620%
7	5.60251191254285E+08	4	0.86520%
8	5.60251191254285E+08	1	1.02050%
9	5.60251191254285E+08	1	1.24330%
10	5.60251191254285E+08	2	1.41780%
Mean	**5.60251191254285E+08**	**2.2**	**0.87445%**
Std. Dev.	**0.000000**	**1.475729575**	**0.004924204**
Var.	**0.000000**	**2.1778E+00**	**2.42478E-05**

Random, Deterministic, TSP-LIB-3038, *k* = 10, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	5.60251191254285E+08	3	0.00540%
2	**5.60251191254285E+08**	1	0.00340%
3	5.60251191254285E+08	3	0.00630%
4	5.60251191254285E+08	2	0.00460%
5	5.60251191254285E+08	3	0.00300%
6	5.60251191254285E+08	3	0.00540%
7	5.60251191254285E+08	4	0.01060%
8	5.60251191254285E+08	1	0.00690%
9	5.60251191254285E+08	5	0.00550%
10	5.60251191254285E+08	3	0.00240%
Mean	**5.60251191254285E+08**	**2.8**	**0.00535%**
Std. Dev.	**0.000000**	**1.229272594**	**2.34485E-05**
Var.	**0.000000**	**1.5111E+00**	**5.49833E-10**

Random, Parent Favored Hybrid, TSP-LIB-3038, *k* = 10, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	5.60251191254285E+08	4	0.000011
2	5.60251191254285E+08	3	0.000043
3	**5.60251191254285E+08**	2	0.000059
4	5.60251191254285E+08	7	0.000023
5	5.60251191254285E+08	4	0.000061
6	5.60251191254285E+08	6	0.000085
7	5.60251191254285E+08	2	0.00009
8	5.60251191254285E+08	3	0.000064
9	5.60251191254285E+08	2	0.000092
10	5.60251191254285E+08	2	0.000107
Mean	**5.60251191254285E+08**	**3.5**	**0.00635%**
Std. Dev.	**0.000000**	**1.779513042**	**3.11136E-05**
Var.	**0.000000**	**3.1667E+00**	**9.68056E-10**

Random, Roulette-Wheel, TSP-LIB-3038, *k* = 10, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	5.60251191254285E+08	1	0.01870%
2	5.60251191254285E+08	1	0.01520%
3	5.60251191254285E+08	3	0.01880%
4	5.60251191254285E+08	2	0.00630%
5	5.60251191254285E+08	2	0.00990%
6	5.60251191254285E+08	2	0.02000%
7	5.60251191254285E+08	0	0.01040%
8	5.60251191254285E+08	1	0.02580%
9	5.60251191254285E+08	0	0.02660%
10	5.60251191254285E+08	2	0.02310%
Mean	**5.60251191254285E+08**	**1.4**	**0.01748%**
Std. Dev.	**0.000000**	**0.966091783**	**6.92288E-05**
Var.	**0.000000**	**9.3333E-01**	**4.79262E-09**

Separation, Deterministic, TSP-LIB-3038, *k* = 10, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	5.60251191254285E+08	2	0.27710%
2	5.60251191254285E+08	3	0.22010%
3	**5.60251191254285E+08**	1	0.61710%
4	5.60251191254285E+08	3	0.37310%
5	5.60251191254285E+08	3	0.70930%
6	5.60251191254285E+08	2	0.39610%
7	5.60251191254285E+08	2	0.94360%
8	5.60251191254285E+08	6	0.55230%
9	5.60251191254285E+08	4	0.85130%
10	5.60251191254285E+08	1	1.19400%
Mean	**5.60251191254285E+08**	**2.7**	**0.61340%**
Std. Dev.	**0.000000**	**1.494434118**	**0.003141858**
Var.	**0.000000**	**2.2333E+00**	**9.87127E-06**

Separation, Parent Favored Hybrid, TSP-LIB-3038, *k* = 10, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	5.60251191254285E+08	1	0.001704
2	5.60251191254285E+08	1	0.005863
3	5.60251191254285E+08	2	0.002392
4	5.60251191254285E+08	3	0.003506
5	**5.60251191254285E+08**	0	0.004989
6	5.60251191254285E+08	3	0.006588
7	5.60251191254285E+08	2	0.007219
8	5.60251191254285E+08	1	0.008552
9	5.60251191254285E+08	1	0.004849
10	5.60251191254285E+08	1	0.007302
Mean	**5.60251191254285E+08**	**1.5**	**0.52964%**
Std. Dev.	**0.000000**	**0.971825316**	**0.002239744**
Var.	**0.000000**	**9.4444E-01**	**5.01645E-06**

Separation, Roulette-Wheel, TSP-LIB-3038, *k* = 10, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	5.60251191254285E+08	1	0.27130%
2	5.60251191254285E+08	1	0.29000%
3	5.60251191254285E+08	1	0.51030%
4	5.60251191254285E+08	1	0.46690%
5	5.60251191254285E+08	1	0.53180%
6	5.60251191254285E+08	2	0.57120%
7	5.60251191254285E+08	2	0.82800%
8	5.60251191254285E+08	3	0.86030%
9	**5.60251191254285E+08**	0	0.92780%
10	5.60251191254285E+08	1	1.01930%
Mean	**5.60251191254285E+08**	**1.3**	**0.62769%**
Std. Dev.	**0.000000**	**0.823272602**	**0.002647271**
Var.	**0.000000**	**6.7778E-01**	**7.00805E-06**

TSP-LIB-3038, *k* = 20 Results

Density, Deterministic, TSP-LIB-3038, *k* = 20, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	2.66812482108700E+08	102	0.02410%
2	**2.66812482108700E+08**	37	0.04520%
3	2.66812482108700E+08	50	0.07680%
4	2.66812482108700E+08	59	0.07990%
5	2.66812482108700E+08	39	0.10760%
6	2.66812482108700E+08	48	0.16180%
7	2.66812482108700E+08	53	0.16550%
8	2.66812482108700E+08	57	0.16010%
9	2.66812482108700E+08	47	0.18950%
10	2.66812482108700E+08	41	0.24910%
Mean	**2.66812482108700E+08**	**53.3**	**0.12596%**
Std. Dev.	**0.000000**	**18.61331662**	**0.000707006**
Var.	**0.000000**	**3.4646E+02**	**4.99858E-07**

Density, Parent Favored Hybrid, TSP-LIB-3038, *k* = 20, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	2.66812482108700E+08	70	0.01990%
2	2.66812482108700E+08	108	0.02830%
3	**2.66812482108700E+08**	52	0.000582
4	2.66812482108700E+08	77	0.000596
5	2.66812482108700E+08	98	0.000689
6	2.66812482108700E+08	78	0.000836
7	2.66812482108700E+08	126	0.000937
8	2.66812482108700E+08	99	0.001046
9	2.66812482108700E+08	90	0.001217
10	2.66812482108700E+08	88	0.001433
Mean	**2.66812482108700E+08**	**88.6**	**0.07818%**
Std. Dev.	**0.000000**	**20.83373333**	**0.000391833**
Var.	**0.000000**	**4.3404E+02**	**1.53533E-07**

Density, Roulette-Wheel, TSP-LIB3038, *k* = 20, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	**2.66812482108700E+08**	13	0.16170%
2	2.66813280878054E+08	19	0.15600%
3	2.66812482108700E+08	26	0.25110%
4	2.66812482108700E+08	18	0.28060%
5	2.66812532885819E+08	20	0.37340%
6	2.66821638513683E+08	18	0.41140%
7	2.66812482108700E+08	21	0.46350%
8	2.66812482108700E+08	70	0.54820%
9	2.66812482108700E+08	14	0.66480%
10	2.66812532885819E+08	14	0.72480%
Mean	**2.66813487781558E+08**	**23.3**	**0.40355%**
Std. Dev.	**2874.587507**	**16.85922102**	**0.001986263**
Var.	**8263253.333333**	**2.8423E+02**	**3.94524E-06**

Random, Deterministic, TSP-LIB-3038, *k* = 20, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	2.66812482108700E+08	54	0.00030%
2	**2.66812482108700E+08**	39	0.00050%
3	2.66812482108700E+08	63	0.00040%
4	2.66812482108700E+08	45	0.00080%
5	2.66812482108700E+08	52	0.00130%
6	2.66812482108700E+08	53	0.00080%
7	2.66812482108700E+08	56	0.00150%
8	2.66812482108700E+08	51	0.00140%
9	2.66812482108700E+08	51	0.00130%
10	2.66812482108700E+08	39	0.00120%
Mean	**2.66812482108700E+08**	**50.3**	**0.00095%**
Std. Dev.	**0.000000**	**7.469196**	**4.45346E-06**
Var.	**0.000000**	**5.5789E+01**	**1.98333E-11**

Random, Parent Favored Hybrid, TSP-LIB-3038, *k* = 20, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	2.66812482108700E+08	84	0.00040%
2	**2.66812482108700E+08**	79	0.00020%
3	2.66812482108700E+08	88	0.00050%
4	2.66812482108700E+08	80	0.00030%
5	2.66812482108700E+08	114	0.00030%
6	2.66812482108700E+08	98	0.00040%
7	2.66812482108700E+08	91	0.00040%
8	2.66812482108700E+08	117	0.00130%
9	2.66812482108700E+08	85	0.00070%
10	2.66812482108700E+08	93	0.00090%
Mean	**2.66812482108700E+08**	**92.9**	**0.00054%**
Std. Dev.	**0.000000**	**13.25351107**	**3.3731E-06**
Var.	**0.000000**	**1.7566E+02**	**1.13778E-11**

Random, Roulette-Wheel, TSP-LIB3038, *k* = 20, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	2.66820762532246E+08	19	0.00250%
2	2.66812482108700E+08	40	0.00240%
3	2.66813280878054E+08	16	0.00240%
4	2.66812482108700E+08	17	0.00370%
5	2.66812482108700E+08	21	0.00210%
6	2.66812574454947E+08	88	0.00290%
7	2.66812482108700E+08	120	0.00440%
8	2.66812482108700E+08	32	0.00610%
9	**2.66812482108700E+08**	15	0.00470%
10	2.66812482108700E+08	23	0.00380%
Mean	**2.66813399262615E+08**	**39.1**	**0.00350%**
Std. Dev.	**2599.153366**	**35.87153003**	**1.28582E-05**
Var.	**6755598.222222**	**1.2868E+03**	**1.65333E-10**

Separation, Deterministic, TSP-LIB-3038, *k* = 20, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	2.66812482108700E+08	45	0.03560%
2	2.66812482108700E+08	44	0.05090%
3	2.66812482108700E+08	44	0.07240%
4	2.66812482108700E+08	38	0.07060%
5	2.66812482108700E+08	52	0.07780%
6	2.66812482108700E+08	71	0.10050%
7	**2.66812482108700E+08**	37	0.13340%
8	2.66812482108700E+08	44	0.15160%
9	2.66812482108700E+08	80	0.14170%
10	2.66812482108700E+08	45	0.19180%
Mean	**2.66812482108700E+08**	**50**	**0.10263%**
Std. Dev.	**0.000000**	**14.2048505**	**0.000500583**
Var.	**0.000000**	**2.0178E+02**	**2.50583E-07**

Separation, Parent Favored Hybrid, TSP-LIB-3038, *k* = 20, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	2.66812482108700E+08	88	0.000288
2	2.66812482108700E+08	82	0.000261
3	2.66812532885819E+08	203	0.000419
4	2.66812482108700E+08	72	0.000503
5	**2.66812482108700E+08**	63	0.000668
6	2.66812482108700E+08	82	0.000935
7	2.66812482108700E+08	76	0.000844
8	2.66812482108700E+08	93	0.001078
9	2.66812482108700E+08	69	0.00104
10	2.66812482108700E+08	96	0.001111
Mean	**2.66812487186412E+08**	**92.4**	**0.07147%**
Std. Dev.	**16.057135**	**40.2470151**	**0.000330398**
Var.	**257.831581**	**1.6198E+03**	**1.09163E-07**

Separation, Roulette-Wheel, TSP-LIB-3038, *k* = 20, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	2.66812482108700E+08	83	0.12150%
2	2.66812482108700E+08	98	0.10870%
3	2.66813343319594E+08	64	0.19360%
4	2.66817750894854E+08	13	0.28830%
5	**2.66812482108700E+08**	15	0.26680%
6	2.66812532885819E+08	16	0.31290%
7	2.66812482108700E+08	16	0.35030%
8	2.66812482108700E+08	18	0.41140%
9	2.66812574454947E+08	18	0.58910%
10	2.66813280878054E+08	16	0.52950%
Mean	**2.66813189297677E+08**	**35.7**	**0.31721%**
Std. Dev.	**1638.084518**	**32.7517599**	**0.001596565**
Var.	**2683320.888889**	**1.0727E+03**	**2.54902E-06**

TSP-LIB-3038, *k* = 30 Results

Density, Deterministic, TSP-LIB-3038, *k* = 30, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.75538647150997E+08	44	0.07550%
2	1.75538647150997E+08	42	0.05610%
3	1.75538647150997E+08	58	0.11620%
4	1.75538647150997E+08	53	0.15140%
5	1.75538647150997E+08	32	0.21380%
6	1.75538647150997E+08	48	0.25360%
7	1.75538647150997E+08	64	0.17420%
8	1.75538647150997E+08	46	0.23650%
9	1.75538647150997E+08	56	0.28990%
10	1.75538647150997E+08	49	0.34680%
Mean	**1.75538647150997E+08**	**49.2**	**0.19140%**
Std. Dev.	**0.000000**	**9.089676684**	**0.000940129**
Var.	**0.000000**	**8.2622E+01**	**8.83842E-07**

Density, Parent Favored Hybrid, TSP-LIB-3038, *k* = 30, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.75538647150997E+08	83	0.04450%
2	**1.75538647150997E+08**	59	0.04050%
3	1.75538647150997E+08	97	0.06870%
4	1.75538647150997E+08	90	0.07350%
5	1.75538647150997E+08	104	0.10540%
6	1.75538647150997E+08	101	0.10030%
7	1.75538647150997E+08	83	0.14260%
8	1.75538647150997E+08	89	0.13630%
9	1.75538647150997E+08	94	0.16710%
10	1.75538647150997E+08	102	0.16920%
Mean	**1.75538647150997E+08**	**90.2**	**0.10481%**
Std. Dev.	**0.000000**	**13.27319772**	**0.000477538**
Var.	**0.000000**	**1.7618E+02**	**2.28043E-07**

Density, Roulette-Wheel, TSP-LIB-3038, *k* = 30, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.75538647150997E+08	20	0.24450%
2	1.75538647150997E+08	34	0.15620%
3	1.75538647150997E+08	16	0.34860%
4	1.75538647150997E+08	35	0.31110%
5	1.75538647150997E+08	24	0.44270%
6	1.75538647150997E+08	130	0.41840%
7	1.75538647150997E+08	27	0.58080%
8	1.75538647150997E+08	26	0.73240%
9	**1.75538647150997E+08**	15	0.69650%
10	1.75538647150997E+08	20	0.82950%
Mean	**1.75538647150997E+08**	**34.7**	**0.47607%**
Std. Dev.	**0.000000**	**34.15991803**	**0.002246034**
Var.	**0.000000**	**1.1669E+03**	**5.04467E-06**

Random, Deterministic, TSP-LIB3038, *k* = 30, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.75538647150997E+08	50	0.00020%
2	1.75538647150997E+08	46	0.00100%
3	1.75538647150997E+08	54	0.00140%
4	1.75538647150997E+08	43	0.00130%
5	1.75538647150997E+08	73	0.00090%
6	1.75538647150997E+08	45	0.00100%
7	1.75538647150997E+08	48	0.00100%
8	1.75538647150997E+08	49	0.00090%
9	1.75538647150997E+08	48	0.00110%
10	**1.75538647150997E+08**	30	0.00380%
Mean	**1.75538647150997E+08**	**48.6**	**0.00126%**
Std. Dev.	**0.000000**	**10.6687498**	**9.47746E-06**
Var.	**0.000000**	**1.1382E+02**	**8.98222E-11**

Random, Parent Favored Hybrid, TSP-LIB-3038, *k* = 30, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.75538647150997E+08	86	0.00010%
2	1.75538647150997E+08	120	0.00060%
3	1.75538647150997E+08	81	0.00060%
4	1.75538647150997E+08	93	0.00050%
5	1.75538647150997E+08	94	0.00050%
6	1.75538647150997E+08	83	0.00050%
7	1.75538647150997E+08	100	0.00050%
8	1.75538647150997E+08	86	0.00060%
9	**1.75538647150997E+08**	79	0.00060%
10	1.75538647150997E+08	89	0.00050%
Mean	**1.75538647150997E+08**	**91.1**	**0.00050%**
Std. Dev.	**0.000000**	**12.00416594**	**1.49071E-06**
Var.	**0.000000**	**1.4410E+02**	**2.22222E-12**

Random, Roulette-Wheel, TSP-LIB-3038, *k* = 30, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.75598605598479E+08	27	0.00220%
2	**1.75538647150997E+08**	18	0.00430%
3	1.75538647150997E+08	30	0.00190%
4	1.75538647150997E+08	155	0.00160%
5	1.75538647150997E+08	41	0.00180%
6	1.75538647150997E+08	73	0.00170%
7	1.75538647150997E+08	27	0.00180%
8	1.75538741971852E+08	18	0.00280%
9	1.75538647150997E+08	20	0.00840%
10	1.75538647150997E+08	20	0.00290%
Mean	**1.75544652477831E+08**	**42.9**	**0.00294%**
Std. Dev.	**18957.217799**	**42.73549137**	**2.08817E-05**
Var.	**359376106.666667**	**1.8263E+03**	**4.36044E-10**

Separation, Deterministic, TSP-LIB-3038, *k* = 30, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.75538647150997E+08	54	0.05670%
2	1.75538647150997E+08	42	0.05740%
3	**1.75538647150997E+08**	31	0.09130%
4	1.75538647150997E+08	31	0.10400%
5	1.75538647150997E+08	52	0.12610%
6	1.75538647150997E+08	56	0.12560%
7	1.75538647150997E+08	46	0.17120%
8	1.75538647150997E+08	49	0.17650%
9	1.75538647150997E+08	46	0.22170%
10	1.75538647150997E+08	53	0.23000%
Mean	**1.75538647150997E+08**	**46**	**0.13605%**
Std. Dev.	**0.000000**	**8.9690827**	**0.000621418**
Var.	**0.000000**	**8.0444E+01**	**3.86161E-07**

Separation, Parent Favored Hybrid, TSP-LIB-3038, *k* = 30, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.75538647150997E+08	81	0.02610%
2	1.75538647150997E+08	91	0.04220%
3	**1.75538647150997E+08**	66	0.05530%
4	1.75538647150997E+08	86	0.07680%
5	1.75538647150997E+08	101	0.07200%
6	1.75538647150997E+08	97	0.13570%
7	1.75538647150997E+08	103	0.09290%
8	1.75538647150997E+08	74	0.10270%
9	1.75538647150997E+08	124	0.11670%
10	1.75538647150997E+08	84	0.13770%
Mean	**1.75538647150997E+08**	**90.7**	**0.08581%**
Std. Dev.	**0.000000**	**16.5196852**	**0.000382117**
Var.	**0.000000**	**2.7290E+02**	**1.46013E-07**

Separation, Roulette-Wheel, TSP-LIB-3038, *k* = 30, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	**1.75538647150997E+08**	21	0.12280%
2	1.75538741971852E+08	20	0.16050%
3	1.75538904116529E+08	26	0.21410%
4	1.75538647150997E+08	26	0.28610%
5	1.75538647150997E+08	33	0.47150%
6	1.75538647150997E+08	35	0.38600%
7	1.75538647150997E+08	21	0.60810%
8	1.75538647150997E+08	34	0.42190%
9	1.75538647150997E+08	120	0.57290%
10	1.75538647150997E+08	54	0.56820%
Mean	**1.75538682329636E+08**	**39**	**0.38121%**
Std. Dev.	**83.431218**	**30.2030168**	**0.001781013**
Var.	**6960.768107**	**9.1222E+02**	**3.17201E-06**

TSP-LIB-3038, *k* = 40 Results

Density, Deterministic, TSP-LIB-3038, *k* = 40, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.24961056473113E+08	73	0.04690%
2	**1.24961056473113E+08**	50	0.05340%
3	1.24961056473113E+08	77	0.09370%
4	1.24961056473113E+08	63	0.09490%
5	1.24961056473113E+08	64	0.12170%
6	1.24961056473113E+08	59	0.15610%
7	1.24961466535255E+08	74	0.16710%
8	1.24961056473113E+08	59	0.20790%
9	1.24961056473113E+08	68	0.22660%
10	1.24961056473113E+08	80	0.23800%
Mean	**1.24961097479327E+08**	**66.7**	**0.14063%**
Std. Dev.	**129.673035**	**9.405081369**	**0.000694289**
Var.	**16815.096030**	**8.8456E+01**	**4.82038E-07**

Density, Parent Favored Hybrid, TSP-LIB-3038, *k* = 40, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	**1.24961056473113E+08**	**100**	**0.03090%**
2	**1.24961056473113E+08**	**174**	**0.02660%**
3	**1.24961056473113E+08**	**136**	**0.05050%**
4	1.24961056473113E+08	141	0.05100%
5	**1.24961056473113E+08**	103	0.07490%
6	1.24961056473113E+08	141	0.08020%
7	1.24961056473113E+08	135	0.10170%
8	1.24961056473113E+08	122	0.11550%
9	1.24961056473113E+08	126	0.12460%
10	1.24961056473113E+08	140	0.13370%
Mean	**1.24961056473113E+08**	**131.8**	**0.07896%**
Std. Dev.	**0.000000**	**21.12292067**	**0.000388628**
Var.	**0.000000**	**4.4618E+02**	**1.51032E-07**

Density, Roulette-Wheel, TSP-LIB-3038, *k* = 40, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.24962873820759E+08	47	0.17660%
2	1.24964087389381E+08	37	0.17600%
3	1.24964132696847E+08	29	0.37720%
4	1.24961056473113E+08	110	0.44070%
5	1.24961466535255E+08	35	0.39080%
6	1.24961056473113E+08	92	0.33610%
7	1.24961056473113E+08	72	0.89800%
8	1.24961056473113E+08	140	0.88730%
9	1.24962755895145E+08	92	0.95710%
10	**1.24961056473113E+08**	35	1.03220%
Mean	**1.24962059870295E+08**	**68.9**	**0.56720%**
Std. Dev.	**1288.430570**	**38.30999289**	**0.003370414**
Var.	**1660053.333333**	**1.4677E+03**	**1.13597E-05**

Random, Deterministic, TSP-LIB-3038, *k* = 40, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.24961056473113E+08	78	0.00020%
2	1.24961056473113E+08	78	0.00080%
3	1.24961056473113E+08	73	0.00130%
4	1.24961056473113E+08	70	0.00140%
5	1.24961056473113E+08	72	0.00080%
6	**1.24961056473113E+08**	59	0.00080%
7	1.24961056473113E+08	60	0.00080%
8	1.24961056473113E+08	69	0.00080%
9	1.24961056473113E+08	60	0.00080%
10	1.24961056473113E+08	76	0.00080%
Mean	**1.24961056473113E+08**	**69.5**	**0.00085%**
Std. Dev.	**0.000000**	**7.42742665**	**3.24037E-06**
Var.	**0.000000**	**5.5167E+01**	**1.05E-11**

Random, Parent Favored Hybrid, TSP-LIB-3038, *k* = 40, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.24961056473113E+08	147	0.00010%
2	1.24961056473113E+08	121	0.00060%
3	1.24961056473113E+08	129	0.00040%
4	1.24961056473113E+08	127	0.00050%
5	1.24961056473113E+08	133	0.00050%
6	1.24961056473113E+08	154	0.00040%
7	1.24961056473113E+08	143	0.00160%
8	**1.24961056473113E+08**	105	0.00050%
9	1.24961056473113E+08	130	0.00160%
10	1.24961056473113E+08	175	0.00550%
Mean	**1.24961056473113E+08**	**136.4**	**0.00117%**
Std. Dev.	**0.000000**	**19.3631953**	**1.60281E-05**
Var.	**0.000000**	**3.7493E+02**	**2.569E-10**

Random, Roulette-Wheel, TSP-LIB-3038, *k* = 40, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.24962873820759E+08	270	0.00080%
2	1.24962873820759E+08	63	0.00910%
3	1.24962315349202E+08	30	0.00130%
4	**1.24961056473113E+08**	32	0.00090%
5	1.24961056473113E+08	138	0.00110%
6	1.24964403670300E+08	91	0.00090%
7	1.24964529757275E+08	155	0.00110%
8	1.24962637736497E+08	66	0.00080%
9	1.24962315349202E+08	31	0.00160%
10	1.24962873820759E+08	131	0.00060%
Mean	**1.24962693627098E+08**	**100.7**	**0.00182%**
Std. Dev.	**1156.761764**	**75.4365812**	**2.57371E-05**
Var.	**1338097.777778**	**5.6907E+03**	**6.624E-10**

Separation, Deterministic, TSP-LIB-3038, *k* = 40, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	**1.24961056473113E+08**	61	0.03450%
2	1.24961056473113E+08	62	0.04920%
3	1.24961056473113E+08	67	0.10460%
4	1.24961056473113E+08	69	0.11580%
5	1.24961056473113E+08	69	0.13960%
6	1.24961056473113E+08	64	0.14500%
7	1.24961056473113E+08	63	0.18190%
8	1.24961056473113E+08	64	0.18610%
9	1.24961056473113E+08	67	0.22240%
10	1.24961056473113E+08	65	0.23080%
Mean	**1.24961056473113E+08**	**65.1**	**0.14099%**
Std. Dev.	**0.000000**	**2.806737925**	**0.000667868**
Var.	**0.000000**	**7.8778E+00**	**4.46047E-07**

Separation, Parent Favored Hybrid, TSP-LIB-3038, *k* = 40, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.24961056473113E+08	124	0.01610%
2	1.24961056473113E+08	138	0.02880%
3	1.24961056473113E+08	141	0.04870%
4	1.24961056473113E+08	135	0.06020%
5	1.24961056473113E+08	137	0.07480%
6	**1.24961056473113E+08**	113	0.09130%
7	1.24961056473113E+08	132	0.11600%
8	1.24961056473113E+08	133	0.10280%
9	1.24961056473113E+08	124	0.13410%
10	1.24961056473113E+08	154	0.13490%
Mean	**1.24961056473113E+08**	**133.1**	**0.08077%**
Std. Dev.	**0.000000**	**11.12005196**	**0.000421398**
Var.	**0.000000**	**1.2366E+02**	**1.77576E-07**

Separation, Roulette-Wheel, TSP-LIB-3038, *k* = 40, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.24961056473113E+08	210	0.13430%
2	1.24962315349202E+08	28	0.43020%
3	1.24961612854217E+08	28	0.47820%
4	1.24962873820759E+08	116	0.30550%
5	1.24961921142180E+08	78	0.43580%
6	1.24964736202394E+08	70	0.36130%
7	1.24961056473113E+08	174	0.18340%
8	**1.24961056473113E+08**	83	0.22020%
9	1.24961907081199E+08	88	0.12740%
10	1.24961466535255E+08	112	0.07640%
Mean	**1.24962000240455E+08**	**98.7**	**0.27527%**
Std. Dev.	**1128.904287**	**57.8735211**	**0.001460704**
Var.	**1274424.888889**	**3.3493E+03**	**2.13365E-06**

TSP-LIB-3038, *k* = 50 Results

Density, Deterministic, TSP-LIB-3038, *k* = 50, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	9.82443821446617E+07	504	0.02200%
2	9.82427437320353E+07	354	0.12680%
3	**9.82425550026207E+07**	275	0.14240%
4	9.82427437320353E+07	350	0.10390%
5	9.82487746311136E+07	281	0.12000%
6	9.82487746311136E+07	206	0.10260%
7	9.82514144749764E+07	332	0.06570%
8	9.83533167227466E+07	251	0.05280%
9	9.82459960774154E+07	270	0.06810%
10	9.82439216195344E+07	502	0.02270%
Mean	**9.82564622768253E+07**	**332.5**	**0.08270%**
Std. Dev.	**34167.905695**	**100.786077**	**0.000427217**
Var.	**1167445779.555560**	**1.0158E+04**	**1.82514E-07**

Density, Parent Favored Hybrid, TSP-LIB-3038, *k* = 50, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	9.83673266239927E+07	608	0.01830%
2	9.82685501883081E+07	202	0.02570%
3	9.82425550026207E+07	509	0.04050%
4	9.82734607419474E+07	258	0.06560%
5	9.82604517721203E+07	562	0.05130%
6	9.82425550026207E+07	483	0.03980%
7	**9.82425550026207E+07**	352	0.08640%
8	9.82427437320353E+07	443	0.06070%
9	9.83008575520925E+07	139	0.18840%
10	9.82434583602314E+07	507	0.09660%
Mean	**9.82684513978590E+07**	**406.3**	**0.06733%**

Density, Roulette-Wheel, TSP-LIB-3038, *k* = 50, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	9.83729502784477E+07	54	0.09280%
2	9.83246157416207E+07	339	0.38410%
3	9.83665026855355E+07	278	0.31890%
4	9.83703349325641E+07	295	0.28540%
5	9.83729690016457E+07	169	0.27200%
6	**9.82425550026207E+07**	374	0.22450%
7	9.82427437320353E+07	470	0.21710%
8	9.85483330377304E+07	99	0.24850%
9	9.82911033420798E+07	215	0.13940%
10	9.83235394350836E+07	231	0.08280%
Mean	**9.83455647189363E+07**	**252.4**	**0.22655%**
Std. Dev.	**87395.072325**	**126.408685**	**0.000975267**
Var.	**7637898666.666670**	**1.5979E+04**	**9.51146E-07**

Random, Deterministic, TSP-LIB-3038, *k* = 50, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	9.82425550026207E+07	349	0.00010%
2	9.82482872975687E+07	246	0.00010%
3	9.82441934152471E+07	193	0.00020%
4	9.83533167227466E+07	197	0.00030%
5	9.82524488204173E+07	187	0.00010%
6	**9.82425550026207E+07**	203	0.00030%
7	9.82437434100508E+07	233	0.00030%
8	9.82539458503620E+07	253	0.00030%
9	9.82430460849112E+07	235	0.00030%
10	9.82441934152471E+07	262	0.00020%
Mean	**9.82568285021792E+07**	**235.8**	**0.00022%**
Std. Dev.	**34153.820753**	**47.9624853**	**9.18937E-07**
Var.	**1166483472.000000**	**2.3004E+03**	**8.44444E-13**

Random, Parent Favored Hybrid, TSP-LIB-3038, *k* = 50, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	9.82425550026207E+07	703	0.00000%
2	9.82491210092271E+07	255	0.00010%
3	9.83646388708412E+07	555	0.00010%
4	9.83533167227466E+07	537	0.00070%
5	9.82427437320353E+07	517	0.00010%
6	9.82446844975375E+07	560	0.00010%
7	9.82884051136774E+07	89	0.00100%
8	**9.82425550026207E+07**	440	0.00010%
9	9.84017152471756E+07	93	0.00140%
10	9.83181791691143E+07	334	0.00140%
Mean	**9.82947914367596E+07**	**408.3**	**0.00050%**
Std. Dev.	**60632.859210**	**208.474379**	**5.73488E-06**
Var.	**3676343616.000000**	**4.3462E+04**	**3.28889E-11**

Random, Roulette-Wheel, TSP-LIB-3038, *k* = 50, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	9.83240128666784E+07	529	0.00020%
2	9.83873765187501E+07	394	0.00040%
3	9.83705214117391E+07	317	0.00030%
4	9.83735563783728E+07	193	0.00030%
5	9.83548594239697E+07	174	0.00020%
6	9.82503280353869E+07	328	0.00060%
7	**9.82461585273875E+07**	155	0.00060%
8	9.82489633605282E+07	67	0.00080%
9	9.82492982328254E+07	223	0.00020%
10	9.83700483952532E+07	367	0.00110%
Mean	**9.83175123150891E+07**	**274.7**	**0.00047%**
Std. Dev.	**61451.175199**	**137.034505**	**3.0203E-06**
Var.	**3776246933.333330**	**1.8778E+04**	**9.12222E-12**

Separation, Deterministic, TSP-LIB-3038, *k* = 50, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	9.83632025149654E+07	241	0.01540%
2	9.82487746311136E+07	218	0.02250%
3	9.82425550026207E+07	384	0.02640%
4	**9.82425550026207E+07**	215	0.03170%
5	9.82425550026207E+07	238	0.04570%
6	9.82425550026207E+07	259	0.05020%
7	9.82487746311136E+07	138	0.07250%
8	9.82425550026207E+07	248	0.06680%
9	9.82433661043734E+07	361	0.06990%
10	9.82456821800285E+07	334	0.04340%
Mean	**9.82562575074698E+07**	**263.6**	**0.04445%**
Std. Dev.	**37662.301434**	**74.97140196**	**0.000205043**
Var.	**1418448949.333330**	**5.6207E+03**	**4.20425E-08**

Separation, Parent Favored Hybrid, TSP-LIB-3038, *k* = 50, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	9.82441934152471E+07	493	0.01360%
2	9.82459960774154E+07	434	0.01380%
3	9.82586684489102E+07	513	0.02580%
4	**9.82425550026207E+07**	396	0.02750%
5	9.82430460849112E+07	693	0.03350%
6	9.82425550026207E+07	492	0.05150%
7	9.82487746311136E+07	217	0.07370%
8	9.82441934152471E+07	341	0.07050%
9	9.82939480997871E+07	227	0.08780%
10	9.82530289314825E+07	591	0.06420%
Mean	**9.82516959109356E+07**	**439.7**	**0.04619%**
Std. Dev.	**15745.085385**	**150.7470656**	**0.000268101**
Var.	**247907713.777778**	**2.2725E+04**	**7.18783E-08**

Separation, Roulette-Wheel, TSP-LIB-3038, *k* = 50, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	9.83554446263746E+07	193	0.02910%
2	9.83219523434057E+07	613	0.03640%
3	9.83712258988420E+07	409	0.07220%
4	9.82453512757793E+07	192	0.09060%
5	9.83547530786225E+07	154	0.12050%
6	9.82432560739862E+07	378	0.11080%
7	9.84911249744177E+07	54	0.21900%
8	9.82514702909222E+07	66	0.20240%
9	9.83690918053560E+07	302	0.18000%
10	**9.82427437320353E+07**	244	0.19330%
Mean	**9.83246414099741E+07**	**260.5**	**0.12543%**
Std. Dev.	**80758.385807**	**171.0011371**	**0.000697254**
Var.	**6521916878.222220**	**2.9241E+04**	**4.86163E-07**

TSP-LIB-3038, *k* = 100 Results

Density, Deterministic, TSP-LIB-3038, *k* = 100, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	4.76892879587104E+07	544	0.01870%
2	4.76789821192297E+07	586	0.09700%
3	4.76792432636601E+07	436	0.08690%
4	**4.76768169619401E+07**	539	0.09790%
5	4.76787606118794E+07	418	0.02380%
6	4.76794132043142E+07	661	0.03810%
7	4.76781971163115E+07	858	0.07240%
8	4.76789708704077E+07	723	0.05560%
9	4.76930857192971E+07	420	0.06690%
10	4.76968679313271E+07	637	0.04060%
Mean	**4.76829625757077E+07**	**582.2**	**0.05979%**
Std. Dev.	**7243.319957**	**142.629123**	**0.000291**
Var.	**52465684.000000**	**2.0343E+04**	**8.468E-08**

Density, Parent Favored Hybrid, TSP-LIB-3038, *k* = 100, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	4.77354979059946E+07	984	0.02000%
2	4.76858551457701E+07	995	0.05460%
3	4.77115946196231E+07	1087	0.05250%
4	4.76800395877807E+07	934	0.04580%
5	4.77129909757800E+07	963	0.04170%
6	4.76924694016899E+07	784	0.03900%
7	4.77248347109024E+07	651	0.03750%
8	4.76941584563716E+07	828	0.02260%
9	4.76886155312299E+07	1223	0.00990%
10	**4.76791808234150E+07**	977	0.01040%
Mean	**4.77005237158557E+07**	**942.6**	**0.03340%**
Std. Dev.	**19521.198768**	**159.487513**	**0.0001654**
Var.	**381077201.333333**	**2.5436E+04**	**2.736E-08**

Density, Roulette-Wheel, TSP-LIB-3038, *k* = 100, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	4.77368369309023E+07	698	0.01670%
2	4.77096370934225E+07	872	0.02070%
3	4.77398933389652E+07	411	0.05670%
4	4.77342901163692E+07	336	0.04630%
5	**4.77093601743438E+07**	600	0.06270%
6	4.77681446930854E+07	693	0.06180%
7	4.77552982973748E+07	694	0.08150%
8	4.77386764470817E+07	255	0.14650%
9	4.77707306834218E+07	316	0.14580%
10	4.77104232177475E+07	587	0.11630%
Mean	**4.77373290992714E+07**	**546.2**	**0.07550%**
Std. Dev.	**22801.221839**	**204.775107**	**0.0004679**
Var.	**519895717.333333**	**4.1933E+04**	**2.189E-07**

Random, Deterministic, TSP-LIB-3038, *k* = 100, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	4.76871140034120E+07	447	0.00010%
2	4.76811724419285E+07	489	0.00010%
3	4.76830809637399E+07	462	0.00020%
4	4.76921394959890E+07	658	0.00010%
5	4.77173365932240E+07	365	0.00010%
6	**4.76779585644368E+07**	389	0.00010%
7	4.76929426452194E+07	352	0.00010%
8	4.76928668629038E+07	619	0.00030%
9	4.77146462446551E+07	315	0.00010%
10	4.76874455788243E+07	413	0.00010%
Mean	**4.76926703394333E+07**	**450.9**	**0.00013%**
Std. Dev.	**13293.791985**	**112.3659201**	**6.74949E-07**
Var.	**176724905.333333**	**1.2626E+04**	**4.55556E-13**

Random, Parent Favored Hybrid, TSP-LIB-3038, *k* = 100, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	4.76874483296354E+07	772	0.00010%
2	4.76880179578561E+07	899	0.00040%
3	**4.76777017224184E+07**	925	0.00010%
4	4.77058983265520E+07	965	0.00010%
5	4.76897220236702E+07	1240	0.00030%
6	4.76913328446241E+07	859	0.00010%
7	4.76844227327697E+07	688	0.00010%
8	4.77139247749550E+07	998	0.00020%
9	4.77314272966063E+07	545	0.00000%
10	4.76786612691922E+07	742	0.00010%
Mean	**4.76948557278279E+07**	**863.3**	**0.00015%**
Std. Dev.	**17090.625240**	**191.6548112**	**1.17851E-06**
Var.	**292089471.111111**	**3.6732E+04**	**1.38889E-12**

Random, Roulette-Wheel, TSP-LIB-3038, *k* = 100, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	4.77251821263213E+07	952	0.00010%
2	4.78012142722874E+07	504	0.00020%
3	4.77839308451070E+07	367	0.00030%
4	4.77895263809727E+07	230	0.00020%
5	**4.76787825747318E+07**	640	0.00020%
6	4.78826093954763E+07	421	0.00020%
7	4.77197452296112E+07	970	0.00020%
8	4.77633541781582E+07	456	0.00020%
9	4.77557192143580E+07	392	0.00020%
10	4.78257838293730E+07	535	0.00020%
Mean	**4.77725848046397E+07**	**546.7**	**0.00020%**
Std. Dev.	**58098.086038**	**243.736219**	**4.71405E-07**
Var.	**3375387601.333330**	**5.9407E+04**	**2.22222E-13**

Separation, Deterministic, TSP-LIB-3038, *k* = 100, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	4.77171073029463E+07	368	0.01450%
2	4.77131828291366E+07	284	0.02010%
3	4.77193070721875E+07	416	0.02660%
4	**4.76699739372530E+07**	622	0.02350%
5	4.76910241185341E+07	303	0.04820%
6	4.76757398309529E+07	423	0.03880%
7	4.76799739936835E+07	580	0.04240%
8	4.76827316160471E+07	443	0.05840%
9	4.76913159952421E+07	480	0.06700%
10	4.76984502906555E+07	327	0.09270%
Mean	**4.76938806986639E+07**	**424.6**	**0.04322%**
Std. Dev.	**17677.636808**	**112.4892094**	**0.000242983**
Var.	**312498843.111111**	**1.2654E+04**	**5.90408E-08**

Separation, Parent Favored Hybrid, TSP-LIB-3038, *k* = 100, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	4.76805116258326E+07	1088	0.00880%
2	4.76869849915435E+07	954	0.01140%
3	4.77243937383506E+07	619	0.01760%
4	4.76937802578120E+07	572	0.02770%
5	**4.76799782394816E+07**	855	0.01680%
6	4.76803681813398E+07	652	0.03750%
7	4.76943671546488E+07	889	0.03390%
8	4.77021090934800E+07	659	0.04770%
9	4.77154723519671E+07	770	0.05030%
10	4.76834050449068E+07	887	0.05180%
Mean	**4.76941370679363E+07**	**794.5**	**0.03035%**
Std. Dev.	**15550.740404**	**167.4324076**	**0.000163284**
Var.	**241825527.111111**	**2.8034E+04**	**2.66616E-08**

Separation, Roulette-Wheel, TSP-LIB-3038, *k* = 100, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	4.77247828002750E+07	380	0.02930%
2	4.77847818677640E+07	493	0.02820%
3	4.77681908928660E+07	338	0.06470%
4	**4.76946521770426E+07**	631	0.05070%
5	4.77351180133196E+07	782	0.07490%
6	4.78894851413041E+07	303	0.08580%
7	4.78166888046105E+07	465	0.08260%
8	4.77123859179032E+07	547	0.13120%
9	4.77965517522487E+07	447	0.14040%
10	4.77515508542507E+07	372	0.13280%
Mean	**4.77674188221584E+07**	**475.8**	**0.08206%**
Std. Dev.	**57653.261178**	**146.4231311**	**0.000414028**
Var.	**3323898524.444440**	**2.1440E+04**	**1.71419E-07**

TSP-LIB-3038, *k* = 150 Results

Density, Deterministic, TSP-LIB-3038, *k* = 150, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	3.05435765218577E+07	755	0.03680%
2	3.05594711086178E+07	729	0.03460%
3	3.05504771285411E+07	734	0.02070%
4	3.05368120123501E+07	653	0.06150%
5	3.05507364152244E+07	1010	0.01090%
6	3.05516644847740E+07	638	0.02760%
7	3.05447432207513E+07	1152	0.02530%
8	3.05503246075848E+07	895	0.00790%
9	3.05486049051551E+07	848	0.00790%
10	3.05503575476581E+07	900	0.03200%
11	3.05484651308292E+07	834	0.04290%
12	3.05489990047783E+07	803	0.05270%
13	3.05508646461974E+07	1183	0.03850%
14	3.05413754442659E+07	710	0.03320%
15	3.05501760397641E+07	924	0.01240%
16	3.05548938760457E+07	615	0.01960%
17	3.05482608058692E+07	738	0.02540%
18	3.05568408324270E+07	909	0.00670%
19	**3.05363771239124E+07**	1418	0.02130%
20	3.05412485189830E+07	799	0.03010%
Mean	**3.05482134687793E+07**	**862.35**	**0.02740%**
Std. Dev.	**6021.313775**	**201.8418545**	**0.00014879**
Var.	**36256219.578947**	**4.0740E+04**	**2.21383E-08**

Density, Parent Favored Hybrid, TSP-LIB-3038, *k* = 150, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	3.05679246355054E+07	1494	0.02120%
2	3.05640334476617E+07	781	0.02630%
3	3.05659928661336E+07	1130	0.02240%
4	3.05594131326797E+07	1544	0.01040%
5	3.05520156045599E+07	1294	0.01800%
6	3.05525470480541E+07	1631	0.01790%
7	3.05486671559338E+07	1640	0.07490%
8	3.05598150218558E+07	1404	0.01870%
9	3.05578863636459E+07	983	0.02250%
10	3.05676337931276E+07	1146	0.02230%
11	3.05654618694117E+07	1416	0.02650%
12	3.05393619494133E+07	1215	0.00660%
13	3.05506382021147E+07	1411	0.03080%
14	3.05424805939739E+07	1501	0.01520%
15	3.05877572649888E+07	795	0.16360%
16	3.05579564004255E+07	982	0.15920%
17	3.05559731927708E+07	1334	0.13600%
18	3.05613794992338E+07	1324	0.15530%
19	3.05397887398806E+07	1738	0.02200%
20	3.05405923514555E+07	1835	0.02220%
Mean	**3.05568659566413E+07**	**1329.9**	**0.04960%**
Std. Dev.	**11826.900328**	**294.4328893**	**0.000551465**
Var.	**139875571.368421**	**8.6691E+04**	**3.04113E-07**

Density, Roulette-Wheel Rank, TSP-LIB-3038, *k* = 150, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	3.05601797422984E+07	612	0.02790%
2	3.05518030640887E+07	1386	0.04270%
3	3.05650082146318E+07	662	0.06080%
4	3.05514249806353E+07	897	0.02070%
5	3.05656887005146E+07	1008	0.03060%
6	3.05775394071699E+07	982	0.05380%
7	3.05854118067932E+07	670	0.10510%
8	3.05618798624941E+07	1070	0.06130%
9	**3.05469006879676E+07**	1038	0.04380%
10	3.06013615628768E+07	414	0.11230%
11	3.05787184052509E+07	368	0.04430%
12	3.05532291632499E+07	1071	0.01620%
13	3.05685397603241E+07	1084	0.04180%
14	3.06255660901195E+07	892	0.06690%
15	3.05825798734771E+07	484	0.11510%
16	3.06333615575635E+07	713	0.11220%
17	3.05518674085859E+07	730	0.03690%
18	3.06181094690389E+07	494	0.08960%
19	3.05527733902488E+07	625	0.09750%
20	3.05894179898503E+07	511	0.09000%
Mean	**3.05760680568590E+07**	**785.55**	**0.06348%**
Std. Dev.	**26050.725691**	**275.6940476**	**0.000329195**
Var.	**678640309.052632**	**7.6007E+04**	**1.08369E-07**

Random, Deterministic, TSP-LIB-3038, *k* = 150, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	3.05355581763761E+07	662	0.00000%
2	3.05552301262039E+07	637	0.00000%
3	3.05410262982690E+07	687	0.00000%
4	3.05483033743835E+07	924	0.00000%
5	3.05483911715471E+07	924	0.00000%
6	3.05576605414634E+07	712	0.00000%
7	3.05490835610671E+07	1079	0.00000%
8	3.05501448488278E+07	729	0.00000%
9	3.05503877266324E+07	826	0.00000%
10	3.05506301098644E+07	880	0.00000%
11	3.05535480819793E+07	637	0.00000%
12	3.05374711094008E+07	760	0.00000%
13	3.05563019958898E+07	802	0.00000%
14	3.05469312953456E+07	816	0.00000%
15	3.05355581763761E+07	864	0.00000%
16	3.05461223050339E+07	857	0.00000%
17	3.05434469798690E+07	952	0.00000%
18	3.05436640398535E+07	897	0.00000%
19	3.05443167777528E+07	827	0.00010%
20	3.05378660560605E+07	922	0.00000%
Mean	**3.05465821376098E+07**	**819.7**	**0.00001%**
Std. Dev.	**6701.476915**	**117.6467057**	**2.23607E-07**
Var.	**44909792.842105**	**1.3841E+04**	**5E-14**

Random, Parent Favored Hybrid, TSP-LIB-3038, *k* = 150, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	3.05732825665860E+07	761	0.00000%
2	3.05505328778658E+07	1688	0.00000%
3	**3.05340983326423E+07**	1572	0.00000%
4	3.05437810832520E+07	1368	0.00000%
5	3.05670673771022E+07	1210	0.00000%
6	3.05396454706894E+07	1439	0.00000%
7	3.05416290905721E+07	1070	0.00000%
8	3.05629305417634E+07	978	0.00000%
9	3.05503729933470E+07	1446	0.00000%
10	3.05528660350057E+07	1358	0.00000%
11	3.05738277212746E+07	847	0.00000%
12	3.05582664141159E+07	1230	0.00000%
13	3.05451337899123E+07	1422	0.00000%
14	3.05443726747828E+07	1111	0.00000%
15	3.05434469798690E+07	1585	0.00000%
16	3.05473636560241E+07	1552	0.00000%
17	3.05477323272482E+07	1738	0.00000%
18	3.05558510919849E+07	1307	0.00000%
19	3.05487520830553E+07	1251	0.00000%
20	3.05370015083369E+07	1119	0.00000%
Mean	**3.05508977307715E+07**	**1302.6**	**0.00000%**
Std. Dev.	**11269.768914**	**267.613311**	**0**
Var.	**127007691.368421**	**7.1617E+04**	**0**

Random, Roulette-Wheel by Rank, TSP-LIB-3038, *k* = 150, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	3.05773129067946E+07	719	0.00000%
2	3.06022147306921E+07	477	0.00010%
3	3.05889713367208E+07	523	0.00000%
4	3.05664548649769E+07	638	0.00000%
5	3.05738961027368E+07	695	0.00000%
6	3.05645385965680E+07	708	0.00010%
7	3.05587861856360E+07	889	0.00000%
8	3.05925805589655E+07	607	0.00010%
9	3.06557976068774E+07	822	0.00000%
10	3.05527697707006E+07	790	0.00000%
11	3.05867680052408E+07	588	0.00000%
12	3.05533502161915E+07	947	0.00010%
13	3.06372241498384E+07	748	0.00000%
14	3.05959827640711E+07	562	0.00000%
15	3.05767120696429E+07	882	0.00000%
16	**3.05436956092291E+07**	927	0.00000%
17	3.06133380920797E+07	712	0.00010%
18	3.06155323171567E+07	664	0.00010%
19	3.06188824301647E+07	599	0.00000%
20	3.06410138849197E+07	668	0.00000%
Mean	**3.05907911099602E+07**	**708.25**	**0.00003%**
Std. Dev.	**31648.131612**	**134.4704526**	**4.70162E-07**
Var.	**1001604234.526320**	**1.8082E+04**	**2.21053E-13**

Separation, Deterministic, TSP-LIB-3038, *k* = 150, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	3.05355581763761E+07	679	0.04150%
2	3.05401703068816E+07	710	0.04490%
3	**3.05276960813254E+07**	960	0.03590%
4	3.05530865170912E+07	896	0.03660%
5	3.05363786801207E+07	691	0.04450%
6	3.05358009760067E+07	781	0.07360%
7	3.05374904735432E+07	594	0.03000%
8	3.05380856735344E+07	553	0.05200%
9	3.05480951115160E+07	870	0.03240%
10	3.05527381354132E+07	655	0.02010%
11	3.05450235972192E+07	690	0.03670%
12	3.05376036766195E+07	906	0.02310%
13	3.05416298109983E+07	745	0.03470%
14	3.05365226154745E+07	710	0.03370%
15	3.05397282341251E+07	850	0.06750%
16	3.05434310753758E+07	677	0.06730%
17	3.05420615379575E+07	747	0.10110%
18	3.05471444138735E+07	679	0.10380%
19	3.05361575910732E+07	759	0.12850%
20	3.05391123721834E+07	671	0.12800%
Mean	**3.05406757528354E+07**	**741.15**	**0.05680%**
Std. Dev.	**6199.263386**	**107.0574243**	**0.000336436**
Var.	**38430866.526316**	**1.1461E+04**	**1.13189E-07**

Separation, Parent Favored Hybrid, TSP-LIB-3038, *k* = 150, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	3.05466994638803E+07	902	0.04930%
2	3.05728214789680E+07	868	0.01740%
3	3.05475341630880E+07	1424	0.03490%
4	3.05374045697391E+07	1489	0.01820%
5	3.05396652989969E+07	1077	0.01840%
6	3.05460195785260E+07	1113	0.02110%
7	3.05458763157271E+07	1089	0.02680%
8	3.05542096935313E+07	1350	0.04280%
9	3.05441675525104E+07	1390	0.01940%
10	3.05514361740594E+07	816	0.05320%
11	3.05369568302062E+07	1425	0.02870%
12	3.05365919834326E+07	1072	0.03050%
13	3.05631885485064E+07	1154	0.05070%
14	3.05370682382118E+07	1422	0.02910%
15	3.05415578177931E+07	1298	0.02870%
16	3.05481883223407E+07	1191	0.04710%
17	**3.05321577638635E+07**	1233	0.01860%
18	3.05446553594432E+07	1209	0.03100%
19	3.05513226162984E+07	1205	0.03520%
20	3.05415365782601E+07	1702	0.02070%
Mean	**3.05459529173691E+07**	**1221.45**	**0.03109%**
Std. Dev.	**9592.284992**	**223.1226887**	**0.000118744**
Var.	**92011931.368421**	**4.9784E+04**	**1.41001E-08**

Separation, Roulette-Wheel by Rank, TSP-LIB-3038, *k* = 150, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	3.05672299385899E+07	710	0.05770%
2	3.05685535205310E+07	700	0.11600%
3	3.05587150805270E+07	817	0.05460%
4	3.05940446908282E+07	529	0.07090%
5	3.05588254030750E+07	978	0.02590%
6	3.05664094994546E+07	767	0.13750%
7	3.05517630088722E+07	577	0.12420%
8	3.05744600948745E+07	587	0.11850%
9	3.05681694724596E+07	796	0.10990%
10	3.05454122155979E+07	737	0.10620%
11	3.05377120279269E+07	879	0.03450%
12	3.05817697536972E+07	753	0.03720%
13	3.05872418652648E+07	574	0.08220%
14	3.05610932685767E+07	438	0.10450%
15	3.05448459360104E+07	820	0.07090%
16	3.06020055305947E+07	459	0.07480%
17	3.05767416987998E+07	380	0.08640%
18	3.05901690930087E+07	407	0.05440%
19	3.06122676274123E+07	977	0.07440%
20	**3.05308521088899E+07**	686	0.09420%
Mean	**3.05689140917496E+07**	**678.55**	**0.08175%**
Std. Dev.	**21491.635102**	**179.3422118**	**0.000318352**
Var.	**461890379.368421**	**3.2164E+04**	**1.01348E-07**

TSP-LIB-3038, *k* = 200 Results

Density, Deterministic, TSP-LIB-3038, *k* = 200, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	2.19284947678499E+07	740	0.01650%
2	2.19400556005910E+07	812	0.01560%
3	2.19264026874544E+07	807	0.03630%
4	2.18950286288799E+07	701	0.04660%
5	2.19185324717908E+07	863	0.04890%
6	2.19294068879697E+07	1002	0.05430%
7	2.19111100612077E+07	791	0.06370%
8	2.18976939968533E+07	930	0.06340%
9	**2.18915781729143E+07**	934	0.10610%
10	2.18986122072663E+07	864	0.08300%
Mean	**2.19136915482777E+07**	**844.4**	**0.05344%**
Std. Dev.	**17235.158669**	**92.90760045**	**0.00027908**
Var.	**297050694.333333**	**8.6318E+03**	**7.78854E-08**

Density, Parent Favored Hybrid, TSP-LIB-3038, *k* = 200, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	2.19032183615273E+07	1715	0.00910%
2	**2.18921474294654E+07**	1294	0.00950%
3	2.19613949415108E+07	761	0.02550%
4	2.19439415818507E+07	1389	0.02190%
5	2.19320975415314E+07	1268	0.03360%
6	2.19052328491336E+07	1659	0.04490%
7	2.19782086402658E+07	660	0.06400%
8	2.19265585609377E+07	1008	0.06630%
9	2.19398486915613E+07	1601	0.04780%
10	2.19191802686749E+07	1551	0.05190%
Mean	**2.19301828866459E+07**	**1290.6**	**0.03745%**
Std. Dev.	**26869.106773**	**372.4081393**	**0.00020798**
Var.	**721948898.777778**	**1.3869E+05**	**4.32556E-08**

Density, Roulette-Wheel, TSP-LIB-3038, *k* = 200, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	2.19431896856229E+07	784	0.00990%
2	2.19480490234898E+07	910	0.01350%
3	2.19207611744004E+07	1025	0.02490%
4	2.19604354483834E+07	905	0.02890%
5	2.19340814900242E+07	929	0.04160%
6	2.19538282236058E+07	1136	0.04710%
7	**2.19138140211971E+07**	1166	0.04830%
8	2.19736762080391E+07	601	0.07030%
9	2.19219595663644E+07	1078	0.05730%
10	2.19242396998264E+07	1198	0.05760%
Mean	**2.19394034540954E+07**	**973.2**	**0.03994%**
Std. Dev.	**19661.093770**	**186.4300882**	**0.000200234**
Var.	**386558608.222222**	**3.4756E+04**	**4.00938E-08**

Random, Deterministic, TSP-LIB-3038, *k* = 200, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	2.19114543902327E+07	969	0.00010%
2	2.19340380732840E+07	1073	0.00020%
3	2.19035680535386E+07	858	0.00010%
4	**2.19019804502834E+07**	942	0.00010%
5	2.19339990168805E+07	810	0.00020%
6	2.19272478501993E+07	713	0.00010%
7	2.19217338613305E+07	930	0.00010%
8	2.19071000041297E+07	1055	0.00010%
9	2.19248149958103E+07	944	0.00010%
10	2.19121535676806E+07	714	0.00000%
Mean	**2.19178090263370E+07**	**900.8**	**0.00011%**
Std. Dev.	**12108.192764**	**125.9354332**	**5.67646E-07**
Var.	**146608332.000000**	**1.5860E+04**	**3.22222E-13**

Random, Parent Favored Hybrid, TSP-LIB-3038, *k* = 200, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	**2.18776193540754E+07**	1836	0.00010%
2	2.19064402913124E+07	1858	0.00010%
3	2.18940172747327E+07	1492	0.00010%
4	2.19090315479580E+07	2267	0.00010%
5	2.18921613196668E+07	1398	0.00010%
6	2.18934809255635E+07	1259	0.00010%
7	2.18992881892105E+07	1707	0.00010%
8	2.19484845405501E+07	894	0.00010%
9	2.19125715424693E+07	1603	0.00000%
10	2.19267564597243E+07	1285	0.00000%
Mean	**2.19059851445263E+07**	**1559.9**	**0.00008%**
Std. Dev.	**20085.000979**	**384.265085**	**4.21637E-07**
Var.	**403407264.333333**	**1.4766E+05**	**1.77778E-13**

Random, Roulette-Wheel, TSP-LIB-3038, *k* = 200, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	2.19339642091728E+07	1464	0.00020%
2	2.19357702698051E+07	991	0.00030%
3	2.19737854987674E+07	714	0.00030%
4	2.19228610530688E+07	1111	0.00030%
5	2.19919866680254E+07	528	0.00040%
6	**2.19210743697869E+07**	1158	0.00010%
7	2.19739025688385E+07	1055	0.00010%
8	2.19512931906337E+07	933	0.00010%
9	2.19426445247620E+07	785	0.00010%
10	2.19719459369471E+07	897	0.00000%
Mean	**2.19519228289808E+07**	**963.6**	**0.00019%**
Std. Dev.	**24570.162951**	**259.9872646**	**1.28668E-06**
Var.	**603692907.444444**	**6.7593E+04**	**1.65556E-12**

Separation, Deterministic, TSP-LIB-3038, *k* = 200, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	2.18924314885847E+07	910	0.02210%
2	2.18881656474546E+07	633	0.04130%
3	2.18955624733524E+07	640	0.05540%
4	2.19106751718882E+07	1174	0.06050%
5	2.18944544024938E+07	737	0.08150%
6	**2.18868004901833E+07**	906	0.01600%
7	2.19027531395111E+07	858	0.02140%
8	2.19050852958406E+07	783	0.03930%
9	2.18983694437503E+07	815	0.03970%
10	2.18995858633867E+07	984	0.03810%
Mean	**2.18973883416446E+07**	**844**	**0.04153%**
Std. Dev.	**7483.526761**	**162.9737539**	**0.000200125**
Var.	**56003172.777778**	**2.6560E+04**	**4.005E-08**

Separation, Parent Favored Hybrid, TSP-LIB-3038, *k* = 200, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	2.19192779624769E+07	1387	0.00690%
2	2.18989302994976E+07	1073	0.00800%
3	2.18954609048633E+07	1351	0.01490%
4	2.19514708684136E+07	750	0.02710%
5	2.19093257174316E+07	1448	0.02640%
6	2.19148177779863E+07	1210	0.02830%
7	2.19229991925226E+07	1448	0.02750%
8	2.19244622190519E+07	1222	0.04240%
9	2.19026439509339E+07	1098	0.04100%
10	**2.18899524634120E+07**	1486	0.03570%
Mean	**2.19129341356590E+07**	**1247.3**	**0.02582%**
Std. Dev.	**17986.294656**	**228.4775943**	**0.000125107**
Var.	**323506795.444444**	**5.2202E+04**	**1.56517E-08**

Separation, Roulette-Wheel, TSP-LIB-3038, *k* = 200, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	2.19462696353535E+07	1440	0.00970%
2	2.19375858987442E+07	816	0.01130%
3	2.19300950445700E+07	831	0.02100%
4	**2.18863236117962E+07**	1083	0.02610%
5	2.19453515381596E+07	1374	0.03410%
6	2.19532004978200E+07	1003	0.03820%
7	2.19380705972794E+07	1314	0.03560%
8	2.19265499824115E+07	1403	0.03860%
9	2.19361206357086E+07	995	0.05680%
10	2.19401479529577E+07	1094	0.04840%
Mean	**2.19339715394801E+07**	**1135.3**	**0.03198%**
Std. Dev.	**18449.825868**	**233.2371468**	**0.000151473**
Var.	**340396074.555556**	**5.4400E+04**	**2.2944E-08**

TSP-LIB-3038, *k* = 250 Results

Density, Deterministic, TSP-LIB-3038, *k* = 250, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.66318672984768E+07	1161	0.01520%
2	1.66484247010325E+07	951	0.01600%
3	1.66283458017620E+07	748	0.02290%
4	**1.66064844072521E+07**	1114	0.04660%
5	1.66336624456902E+07	891	0.03580%
6	1.66550057498725E+07	743	0.06250%
7	1.66134021803572E+07	1072	0.06020%
8	1.66356433308066E+07	928	0.06800%
9	1.66244755867031E+07	1320	0.07950%
10	1.66158255788963E+07	923	0.10600%
Mean	**1.66293137080849E+07**	**985.1**	**0.05127%**
Std. Dev.	**15171.007104**	**182.3393966**	**0.000296068**
Var.	**230159456.555556**	**3.3248E+04**	**8.76562E-08**

Density, Parent Favored Hybrid, TSP-LIB-3038, *k* = 250, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.66441534251730E+07	1480	0.00860%
2	1.66471990033111E+07	1585	0.00940%
3	1.66369963707663E+07	1638	0.01250%
4	1.66389530992512E+07	1577	0.02380%
5	1.66463124438743E+07	1668	0.01910%
6	1.66434985651428E+07	1701	0.03300%
7	1.66494104636739E+07	1131	0.03110%
8	**1.66281530254982E+07**	1380	0.04810%
9	1.66281745864399E+07	1478	0.04420%
10	1.66302812355636E+07	1612	0.05080%
Mean	**1.66393132218694E+07**	**1525**	**0.02806%**
Std. Dev.	**8095.040062**	**169.4966404**	**0.000159174**
Var.	**65529673.611111**	**2.8729E+04**	**2.53365E-08**

Density, Roulette-Wheel, TSP-LIB-3038, *k* = 250, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.67352584561880E+07	1019	0.01960%
2	1.67223424055776E+07	1273	0.02010%
3	1.67601288424529E+07	559	0.05390%
4	1.67457071001831E+07	478	0.09190%
5	1.67316527550665E+07	562	0.08780%
6	1.67227772788997E+07	977	0.06940%
7	1.67360634068119E+07	920	0.09440%
8	**1.66714736757471E+07**	1134	0.08540%
9	1.66960136841391E+07	1107	0.10430%
10	1.67190052182858E+07	812	0.09660%
Mean	**1.67240422823352E+07**	**884.1**	**0.07234%**
Std. Dev.	**25119.173694**	**273.0585814**	**0.000311769**
Var.	**630972887.055556**	**7.4561E+04**	**9.72E-08**

Random, Deterministic, TSP-LIB-3038, *k* = 250, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.66349969601667E+07	886	0.00000%
2	1.66247208833827E+07	1194	0.00000%
3	1.66192416637370E+07	1278	0.00010%
4	1.66325064141306E+07	1002	0.00010%
5	**1.66164689618835E+07**	1418	0.00010%
6	1.66264847231451E+07	1119	0.00010%
7	1.66301419003553E+07	784	0.00010%
8	1.66428399939687E+07	1124	0.00010%
9	1.66333522729370E+07	951	0.00010%
10	1.66323950533015E+07	884	0.00010%
Mean	**1.66293148827008E+07**	**1064**	**0.00008%**
Std. Dev.	**7799.390970**	**198.251804**	**4.21637E-07**
Var.	**60830499.500000**	**3.9304E+04**	**1.77778E-13**

Random, Parent Favored Hybrid, TSP-LIB-3038, *k* = 250, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.66391231492860E+07	1332	0.00000%
2	**1.66208244785688E+07**	2056	0.00000%
3	1.66464389181216E+07	2143	0.00010%
4	1.66560477667518E+07	1431	0.00010%
5	1.66394398385014E+07	1863	0.00010%
6	1.66410059816496E+07	1044	0.00010%
7	1.66351967940229E+07	1464	0.00030%
8	1.66437421151238E+07	1362	0.00010%
9	1.66433658580541E+07	1609	0.00010%
10	1.66320743600968E+07	1438	0.00020%
Mean	**1.66397259260177E+07**	**1574.2**	**0.00011%**
Std. Dev.	**9305.037880**	**345.81363**	**8.75595E-07**
Var.	**86583729.944444**	**1.1959E+05**	**7.66667E-13**

Random, Roulette-Wheel, TSP-LIB-3038, *k* = 250, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.67201259162500E+07	755	0.00010%
2	1.66722676335241E+07	1141	0.00010%
3	1.67262445013159E+07	1346	0.00010%
4	1.66889757410020E+07	1269	0.00010%
5	1.67336064636972E+07	1861	0.00010%
6	1.66928771724822E+07	1109	0.00000%
7	1.67527504504878E+07	741	0.00010%
8	1.66812664157454E+07	1059	0.00010%
9	**1.66456815922703E+07**	1211	0.00010%
10	1.67084492111755E+07	1417	0.00000%
Mean	**1.67022245097950E+07**	**1190.9**	**0.00008%**
Std. Dev.	**32094.522240**	**324.8467844**	**4.21637E-07**
Var.	**1030058357.833330**	**1.0553E+05**	**1.77778E-13**

Separation, Deterministic, TSP-LIB-3038, *k* = 250, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.66220673920687E+07	1039	0.03350%
2	1.66445790314818E+07	795	0.05020%
3	1.66340531843192E+07	968	0.04300%
4	1.66336647839555E+07	620	0.05110%
5	1.66290708578761E+07	1001	0.03340%
6	**1.66154613189283E+07**	801	0.02340%
7	1.66600144328746E+07	713	0.02990%
8	1.66238407995592E+07	985	0.01890%
9	1.66258762486280E+07	799	0.01230%
10	1.66356850067544E+07	955	0.00880%
Mean	**1.66324313056446E+07**	**867.6**	**0.03045%**
Std. Dev.	**12677.994980**	**140.7497385**	**0.000148082**
Var.	**160731556.722222**	**1.9810E+04**	**2.19283E-08**

Separation, Parent Favored Hybrid, TSP-LIB-3038, *k* = 250, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.66144138056197E+07	1436	0.00730%
2	1.66567879738884E+07	1276	0.01410%
3	1.67171522905292E+07	603	0.02020%
4	1.66228498318437E+07	1471	0.02010%
5	1.66174233331730E+07	2074	0.02230%
6	1.66315622105381E+07	1293	0.01100%
7	**1.66014077705173E+07**	1666	0.02410%
8	1.66302745575954E+07	1493	0.02770%
9	1.66288730812197E+07	1856	0.03030%
10	1.66172927765712E+07	1961	0.00460%
Mean	**1.66338037631496E+07**	**1512.9**	**0.01817%**
Std. Dev.	**32665.702367**	**421.2738486**	**8.61717E-05**
Var.	**1067048111.111110**	**1.7747E+05**	**7.42557E-09**

Separation, Roulette-Wheel, TSP-LIB-3038, *k* = 250, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.67219767205615E+07	498	0.02030%
2	1.66807508025061E+07	1475	0.01980%
3	1.66721649701524E+07	1264	0.03320%
4	1.66739525714135E+07	1291	0.04440%
5	1.66835587381209E+07	709	0.01130%
6	1.67036473498798E+07	1214	0.01770%
7	1.67294289831661E+07	920	0.04740%
8	1.67063664790812E+07	1017	0.05230%
9	1.66760787125967E+07	1500	0.02280%
10	**1.66568337092080E+07**	2199	0.03130%
Mean	**1.66904759036686E+07**	**1208.7**	**0.03005%**
Std. Dev.	**23630.143591**	**473.8982662**	**0.000140248**
Var.	**558383686.111111**	**2.2458E+05**	**1.96696E-08**

TSP-LIB-3038, *k* = 300 Results

Density, Deterministic, TSP-LIB-3038, *k* = 300, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.32897035125360E+07	1273	0.01630%
2	1.33068180287544E+07	1126	0.01590%
3	1.33075956634446E+07	968	0.01750%
4	1.33110107612207E+07	938	0.03710%
5	1.32959750469263E+07	1190	0.05440%
6	1.33035150605348E+07	907	0.04900%
7	1.32944573912337E+07	1001	0.07040%
8	1.32981021383365E+07	1153	0.07380%
9	**1.32863427158251E+07**	1041	0.10100%
10	1.32910482407785E+07	1170	0.12950%
Mean	**1.32984568559591E+07**	**1076.7**	**0.05649%**
Std. Dev.	**8413.975766**	**122.557968**	**0.0003804**
Var.	**70794988.194444**	**1.5020E+04**	**1.447E-07**

Density, Parent Favored Hybrid, TSP-LIB-3038, *k* = 300, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.32897035125360E+07	1273	0.01630%
2	1.33068180287544E+07	1126	0.01590%
3	1.33075956634446E+07	968	0.01750%
4	1.33110107612207E+07	938	0.03710%
5	1.32959750469263E+07	1190	0.05440%
6	1.33035150605348E+07	907	0.04900%
7	1.32944573912337E+07	1001	0.07040%
8	1.32981021383365E+07	1153	0.07380%
9	**1.32863427158251E+07**	1041	0.10100%
10	1.32910482407785E+07	1170	0.12950%
Mean	**1.32984568559591E+07**	**1076.7**	**0.05649%**
Std. Dev.	**8413.975766**	**122.557968**	**0.0003804**
Var.	**70794988.194444**	**1.5020E+04**	**1.447E-07**

Density, Roulette-Wheel, TSP-LIB-3038, *k* = 300, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.33551617855786E+07	1295	0.01380%
2	1.33576558558790E+07	1441	0.01430%
3	1.33652237188044E+07	1563	0.02440%
4	1.33399901424214E+07	2121	0.02370%
5	1.33605751679252E+07	761	0.05410%
6	1.33587730144287E+07	1662	0.04660%
7	1.33491511554635E+07	1488	0.07120%
8	1.33945627735881E+07	1313	0.06860%
9	1.34242279065378E+07	795	0.05860%
10	**1.33152328594017E+07**	1877	0.06060%
Mean	**1.33620554380028E+07**	**1431.6**	**0.04359%**
Std. Dev.	**29548.033640**	**426.218827**	**0.0002244**
Var.	**873086292.000000**	**1.8166E+05**	**5.035E-08**

Random, Deterministic, TSP-LIB-3038, *k* = 300, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.32897985608477E+07	1006	0.00000%
2	1.33134160010948E+07	857	0.00010%
3	1.33025979193149E+07	839	0.00000%
4	1.33148363204499E+07	689	0.00020%
5	1.32985559183109E+07	1003	0.00010%
6	**1.32872540049700E+07**	1021	0.00020%
7	1.33031579946646E+07	928	0.00000%
8	1.32997320167855E+07	922	0.00050%
9	1.32894154782879E+07	834	0.00000%
10	1.33138610462401E+07	1441	0.00040%
Mean	**1.33012625260966E+07**	**954**	**0.00015%**
Std. Dev.	**10401.578530**	**198.808115**	**1.78E-06**
Var.	**108192835.916667**	**3.9525E+04**	**3.167E-12**

Random, Parent Favored Hybrid, TSP-LIB-3038, *k* = 300, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.33517767086614E+07	842	0.00000%
2	**1.32891991348813E+07**	1638	0.00000%
3	1.32971730382631E+07	1787	0.00000%
4	1.32986341990213E+07	1297	0.00010%
5	1.33052879718795E+07	1609	0.00010%
6	1.32950615128603E+07	1691	0.00000%
7	1.32917738796491E+07	1542	0.00000%
8	1.33179408955720E+07	1742	0.00000%
9	1.33011882469724E+07	1675	0.00010%
10	1.33115533497946E+07	1916	0.00000%
Mean	**1.33059588937555E+07**	**1573.9**	**0.00003%**
Std. Dev.	**18345.593289**	**304.292421**	**4.83E-07**
Var.	**336560793.138889**	**9.2594E+04**	**2.333E-13**

Random, Roulette-Wheel, TSP-LIB-3038, *k* = 300, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.33840775711596E+07	1163	0.00000%
2	1.34792456687428E+07	1034	0.00010%
3	1.34011906020877E+07	941	0.00010%
4	1.33875324277625E+07	1266	0.00010%
5	**1.33234746251674E+07**	2042	0.00010%
6	1.33713255021224E+07	950	0.00000%
7	1.33966062289416E+07	1145	0.00010%
8	1.33802558316143E+07	861	0.00000%
9	1.33427472715836E+07	1421	0.00010%
10	1.34130578702214E+07	1037	0.00000%
Mean	**1.33879513599403E+07**	**1186**	**0.00006%**
Std. Dev.	**41855.111128**	**343.708856**	**5.164E-07**
Var.	**1751850327.500000**	**1.1814E+05**	**2.667E-13**

Separation, Deterministic, TSP-LIB-3038, *k* = 300, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.32848726115284E+07	1368	0.05430%
2	1.32906797898543E+07	1046	0.04660%
3	1.32895817647698E+07	799	0.04390%
4	1.32830947214600E+07	904	0.03610%
5	1.32945559998560E+07	1200	0.02700%
6	1.32835626241369E+07	1139	0.03450%
7	1.32868436105089E+07	846	0.02470%
8	1.32829350908702E+07	798	0.01880%
9	1.32893407696652E+07	878	0.01360%
10	**1.32820341892050E+07**	1065	0.00880%
Mean	**1.32867501171855E+07**	**1004.3**	**0.03083%**
Std. Dev.	**4149.351231**	**191.462819**	**0.0001487**
Var.	**17217115.638889**	**3.6658E+04**	**2.212E-08**

Separation, Parent Favored Hybrid, TSP-LIB-3038, *k* = 300, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.33398756661501E+07	924	0.01850%
2	1.32915103825045E+07	1378	0.00750%
3	1.32963555879217E+07	1763	0.02040%
4	1.32920233199423E+07	1960	0.02650%
5	**1.32861965848621E+07**	1556	0.01130%
6	1.33030304008241E+07	1641	0.03470%
7	1.32941677133392E+07	1373	0.02910%
8	1.33145559281995E+07	1200	0.01610%
9	1.32873878942016E+07	1894	0.00510%
10	1.32902500399986E+07	1784	0.02210%
Mean	**1.32995353517944E+07**	**1547.3**	**0.01913%**
Std. Dev.	**16454.069693**	**328.311184**	**9.484E-05**
Var.	**270736409.472222**	**1.0779E+05**	**8.995E-09**

Separation, Roulette-Wheel, TSP-LIB-3038, *k* = 300, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.34519254364565E+07	720	0.02110%
2	1.33506619172674E+07	1628	0.02610%
3	1.33383129049893E+07	1604	0.02160%
4	**1.33292188566263E+07**	1639	0.04350%
5	1.33302491624458E+07	1514	0.03520%
6	1.33601984791637E+07	1235	0.02010%
7	1.33566666230795E+07	1106	0.01500%
8	1.34229911217040E+07	653	0.03720%
9	1.34502760761952E+07	851	0.03560%
10	1.34507356056329E+07	704	0.04210%
Mean	**1.33841236183561E+07**	**1165.4**	**0.02975%**
Std. Dev.	**53106.464887**	**412.745873**	**0.0001014**
Var.	**2820296612.833330**	**1.7036E+05**	**1.029E-08**

TSP-LIB-3038, *k* = 350 Results

Density, Deterministic, TSP-LIB-3038, *k* = 350, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	**1.10268267319180E+07**	1265	0.01360%
2	1.10375283073814E+07	1347	0.01510%
3	1.10382097176018E+07	1478	0.03260%
4	1.10413904787323E+07	1321	0.03510%
5	1.10352393887640E+07	1288	0.04920%
6	1.10401003846681E+07	1201	0.03950%
7	1.10416173454462E+07	899	0.08570%
8	1.10281706343795E+07	1811	0.08760%
9	1.10466748530441E+07	1372	0.10260%
10	1.10303469857281E+07	1678	0.07000%
Mean	**1.10366104827663E+07**	**1366**	**0.05310%**
Std. Dev.	**6436.459251**	**252.087727**	**0.000315129**
Var.	**41428007.694444**	**6.3548E+04**	**9.9306E-08**

Density, Parent Favored Hybrid, TSP-LIB-3038, *k* = 350, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.11736956878454E+07	640	0.02370%
2	**1.10366437109779E+07**	2103	0.00920%
3	1.10482410140581E+07	2662	0.01880%
4	1.10531022149517E+07	1936	0.02320%
5	1.10499115101426E+07	2206	0.02870%
6	1.10639207528277E+07	1483	0.03840%
7	1.10433566573065E+07	2447	0.04190%
8	1.10462388824480E+07	2455	0.04680%
9	1.10938595772505E+07	1244	0.05480%
10	1.10482851477883E+07	2053	0.05660%
Mean	**1.10657255155597E+07**	**1922.9**	**0.03421%**
Std. Dev.	**41092.702046**	**626.631994**	**0.000159355**
Var.	**1688610161.472220**	**3.9267E+05**	**2.53941E-08**

Density, Roulette-Wheel, TSP-LIB-3038, *k* = 350, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	**1.11088963211344E+07**	959	0.01550%
2	1.11473659822621E+07	1600	0.01210%
3	1.11360135622488E+07	1829	0.01640%
4	1.11238698628066E+07	1468	0.04230%
5	1.11377593516067E+07	1449	0.04020%
6	1.11489917706904E+07	1285	0.04470%
7	1.11316065819763E+07	1268	0.06050%
8	1.11092094617771E+07	2640	0.06400%
9	1.11407013876540E+07	1130	0.07080%
10	1.11436136665972E+07	1563	0.07180%
Mean	**1.11328027948754E+07**	**1519.1**	**0.04383%**
Std. Dev.	**14520.872394**	**465.643748**	**0.000230277**
Var.	**210855735.083333**	**2.1682E+05**	**5.30276E-08**

Random, Deterministic, TSP-LIB-3038, *k* = 350, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.10506578995032E+07	1389	0.00000%
2	1.10314405993006E+07	1469	0.00000%
3	1.10371931735098E+07	1560	0.00010%
4	**1.10269243233904E+07**	1327	0.00000%
5	1.10330634495615E+07	1416	0.00000%
6	1.10280867399461E+07	1451	0.00010%
7	1.10326216132700E+07	1569	0.00010%
8	1.10364651521756E+07	1487	0.00010%
9	1.10307727095848E+07	1343	0.00000%
10	1.10321054435564E+07	1541	0.00020%
Mean	**1.10339331103798E+07**	**1455.2**	**0.00006%**
Std. Dev.	**6683.964276**	**86.57533649**	**6.99206E-07**
Var.	**44675378.444444**	**7.4953E+03**	**4.88889E-13**

Random, Parent Favored Hybrid, TSP-LIB-3038, *k* = 350, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.11520281866606E+07	869	0.00000%
2	1.11537142407176E+07	804	0.00010%
3	1.10535816089577E+07	1585	0.00000%
4	1.10855164770757E+07	1347	0.00010%
5	1.10868818986790E+07	1614	0.00000%
6	1.10874162021312E+07	1583	0.00010%
7	1.10763915857920E+07	1562	0.00000%
8	1.10561238969780E+07	1800	0.00000%
9	**1.10292984660478E+07**	2426	0.00000%
10	1.10349109501387E+07	3058	0.00000%
Mean	**1.10815863513178E+07**	**1664.8**	**0.00003%**
Std. Dev.	**42965.314502**	**670.0074295**	**4.83046E-07**
Var.	**1846018250.250000**	**4.4891E+05**	**2.33333E-13**

Random, Roulette-Wheel, TSP-LIB-3038, *k* = 350, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.11331449753651E+07	1329	0.00000%
2	1.11346283547952E+07	1725	0.00000%
3	1.11652191211399E+07	889	0.00000%
4	1.11223662369464E+07	1069	0.00000%
5	1.11447489889138E+07	1172	0.00000%
6	**1.11191344716811E+07**	1188	0.00000%
7	1.11364221483821E+07	1415	0.00000%
8	1.11259530631896E+07	1445	0.00010%
9	1.12286125875707E+07	506	0.00010%
10	1.11638755956155E+07	968	0.00010%
Mean	**1.11474105543599E+07**	**1170.6**	**0.00003%**
Std. Dev.	**32598.418182**	**339.9579059**	**4.83046E-07**
Var.	**1062656867.944440**	**1.1557E+05**	**2.33333E-13**

Separation, Deterministic, TSP-LIB-3038, *k* = 350, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.10521726527722E+07	1166	0.00810%
2	1.10277420948606E+07	1123	0.00940%
3	1.10274804456376E+07	1330	0.01510%
4	1.10393805243534E+07	1199	0.02030%
5	1.10296239095210E+07	1102	0.03180%
6	1.10296791177988E+07	1113	0.03690%
7	1.10436875202658E+07	1040	0.03980%
8	**1.10175595117077E+07**	1662	0.02720%
9	1.10301538574370E+07	1366	0.02420%
10	1.10350178862886E+07	1442	0.01580%
Mean	**1.10332497520643E+07**	**1254.3**	**0.02286%**
Std. Dev.	**9735.498603**	**193.4591832**	**0.000110568**
Var.	**94779933.055556**	**3.7426E+04**	**1.22254E-08**

Separation, Parent Favored Hybrid, TSP-LIB-3038, *k* = 350, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.10521726527722E+07	1166	0.00810%
2	1.10277420948606E+07	1123	0.00940%
3	1.10274804456376E+07	1330	0.01510%
4	1.10393805243534E+07	1199	0.02030%
5	1.10296239095210E+07	1102	0.03180%
6	1.10296791177988E+07	1113	0.03690%
7	1.10436875202658E+07	1040	0.03980%
8	**1.10175595117077E+07**	1662	0.02720%
9	1.10301538574370E+07	1366	0.02420%
10	1.10350178862886E+07	1442	0.01580%
Mean	**1.10332497520643E+07**	**1254.3**	**0.02286%**
Std. Dev.	**9735.498603**	**193.4591832**	**0.000110568**
Var.	**94779933.055556**	**3.7426E+04**	**1.22254E-08**

Separation, Roulette-Wheel, TSP-LIB-3038, *k* = 350, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	1.11207546863763E+07	1213	0.03430%
2	1.11257488864524E+07	1717	0.00650%
3	1.11073210192002E+07	1587	0.01050%
4	1.11108179459818E+07	1700	0.01680%
5	1.11102656504550E+07	1801	0.01110%
6	1.11171739619907E+07	1765	0.01630%
7	1.11049982787101E+07	1615	0.02150%
8	1.11385626741896E+07	1592	0.03050%
9	1.11127761829726E+07	2152	0.01540%
10	**1.10960374151265E+07**	2233	0.00500%
Mean	**1.11144456701455E+07**	**1737.5**	**0.01679%**
Std. Dev.	**11874.050554**	**290.1862429**	**9.63644E-05**
Var.	**140993076.555556**	**8.4208E+04**	**9.2861E-09**

TSP-LIB-3038, *k* = 400 Results

Density Deterministic, TSP-LIB-3038, *k* = 400, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	9.38925870678764E+06	1707	0.01470%
2	9.37931945624096E+06	1713	0.01290%
3	9.38583739700574E+06	1332	0.02110%
4	9.38987558997109E+06	1326	0.04080%
5	9.38462013892493E+06	1612	0.04480%
6	9.38112581010099E+06	1467	0.03960%
7	9.38816859202738E+06	1377	0.07550%
8	9.37708703629146E+06	1695	0.06430%
9	9.38034276085857E+06	1825	0.07090%
10	**9.37559400357139E+06**	1391	0.06270%
Mean	**9.38312294917801E+06**	**1544.5**	**0.04473%**
Std. Dev.	**5138.264205**	**185.9535486**	**0.000232203**
Var.	**26401759.041667**	**3.4579E+04**	**5.39185E-08**

Density, Parent Favored Hybrid, TSP-LIB-3038, *k* = 400, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	**9.38095672795812E+06**	2541	0.01440%
2	9.39120932031022E+06	2250	0.01510%
3	9.53971496449659E+06	731	0.05140%
4	9.40325020689030E+06	1819	0.05050%
5	9.38895270140689E+06	2532	0.02570%
6	9.45643713672438E+06	1180	0.02560%
7	9.42262007155622E+06	1450	0.01720%
8	9.39252624022641E+06	2453	0.03220%
9	9.51460994653957E+06	725	0.06110%
10	9.39822337842989E+06	2291	0.04230%
Mean	**9.42885006945386E+06**	**1797.2**	**0.03355%**
Std. Dev.	**56431.675989**	**727.2828886**	**0.00016808**
Var.	**3184534054.888890**	**5.2894E+05**	**2.82509E-08**

Density, Roulette-Wheel, TSP-LIB-3038, *k* = 400, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	9.54771328162252E+06	690	0.03080%
2	9.47520018520645E+06	1656	0.01750%
3	9.55774898668553E+06	641	0.05840%
4	**9.46732835321066E+06**	1692	0.03570%
5	9.57104408893883E+06	927	0.05050%
6	9.46775797774721E+06	2637	0.01990%
7	9.53202888125370E+06	1110	0.02860%
8	9.56718550602174E+06	812	0.04090%
9	9.50771678900819E+06	1207	0.04280%
10	9.48627107595344E+06	1389	0.04200%
Mean	**9.51799951256483E+06**	**1276.1**	**0.03671%**
Std. Dev.	**42069.690479**	**605.3998587**	**0.000128952**
Var.	**1769858856.958330**	**3.6651E+05**	**1.66285E-08**

Random, Deterministic, TSP-LIB-3038, *k* = 400, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	9.37759466139969E+06	1585	0.00000%
2	9.38483946608944E+06	1337	0.00010%
3	9.38597894848483E+06	1451	0.00010%
4	9.38865449347040E+06	1471	0.00010%
5	9.38414504902595E+06	1229	0.00010%
6	9.38398494473302E+06	1352	0.00010%
7	9.40602074383116E+06	1307	0.00010%
8	9.39521266746583E+06	1364	0.00010%
9	9.39907281089464E+06	1229	0.00010%
10	**9.37653614900929E+06**	1463	0.00000%
Mean	**9.38820399344043E+06**	**1378.8**	**0.00008%**
Std. Dev.	**9334.137110**	**113.5495976**	**4.21637E-07**
Var.	**87126115.597222**	**1.2894E+04**	**1.77778E-13**

Random, Parent Favored Hybrid, TSP-LIB-3038, *k* = 400, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	9.39928677355421E+06	1707	0.00000%
2	9.42459658178207E+06	1544	0.00000%
3	9.38354399985566E+06	2682	0.00000%
4	**9.37206790465364E+06**	3151	0.00000%
5	9.38970313246753E+06	2287	0.00010%
6	9.38885799577918E+06	2482	0.00010%
7	9.39115971558437E+06	2079	0.00010%
8	9.39467802853535E+06	2064	0.00000%
9	9.39115995422076E+06	3013	0.00010%
10	9.39847614455262E+06	2174	0.00010%
Mean	**9.39335302309854E+06**	**2318.3**	**0.00005%**
Std. Dev.	**13465.147160**	**521.9659525**	**5.27046E-07**
Var.	**181310188.027778**	**2.7245E+05**	**2.77778E-13**

Random, Roulette-Wheel, TSP-LIB-3038, *k* = 400, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	9.54503459008212E+06	1117	0.00010%
2	9.52172125353258E+06	877	0.00020%
3	9.53383123925519E+06	1030	0.00020%
4	9.51775107150349E+06	1845	0.00000%
5	9.51861615674602E+06	1976	0.00000%
6	9.49003597934843E+06	2491	0.00000%
7	9.47689541415528E+06	1839	0.00030%
8	9.53173123044451E+06	1331	0.00020%
9	**9.47304297014924E+06**	1772	0.00010%
10	9.60119564916471E+06	712	0.00090%
Mean	**9.52098555543816E+06**	**1499**	**0.00020%**
Std. Dev.	**37281.842196**	**569.7757844**	**2.66667E-06**
Var.	**1389935757.541670**	**3.2464E+05**	**7.11111E-12**

Separation, Deterministic, TSP-LIB-3038, *k* = 400, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	9.39522837680372E+06	1099	0.02390%
2	9.37835674404758E+06	1130	0.03500%
3	**9.36922963517314E+06**	1479	0.01010%
4	9.37254432348483E+06	1646	0.03930%
5	9.38989255183979E+06	1274	0.02440%
6	9.38081251904760E+06	1362	0.04310%
7	9.37897787460316E+06	1500	0.04020%
8	9.38084712067375E+06	1379	0.02860%
9	9.37547329227992E+06	1532	0.01620%
10	9.37462236753245E+06	1630	0.00700%
Mean	**9.37959848054859E+06**	**1403.1**	**0.02678%**
Std. Dev.	**7847.678916**	**190.976118**	**0.000127777**
Var.	**61586064.361111**	**3.6472E+04**	**1.63271E-08**

Separation, Parent Favored Hybrid, TSP-LIB-3038, *k* = 400, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	9.46966966020090E+06	822	0.04410%
2	9.38511268791484E+06	2169	0.01370%
3	**9.37177154574313E+06**	2140	0.02350%
4	9.38425513291983E+06	1892	0.02430%
5	9.38235478553389E+06	2146	0.02050%
6	9.41878542698412E+06	1169	0.01940%
7	9.38267425396823E+06	2094	0.01550%
8	9.40129977063491E+06	1595	0.01810%
9	9.39062889556831E+06	2076	0.00550%
10	9.39499323925238E+06	1795	0.00530%
Mean	**9.39815453987205E+06**	**1789.8**	**0.01899%**
Std. Dev.	**28215.804955**	**464.065082**	**0.000110144**
Var.	**796131649.236111**	**2.1536E+05**	**1.21317E-08**

Separation, Roulette-Wheel, TSP-LIB-3038, *k* = 400, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	9.61092205287766E+06	390	0.03170%
2	9.50000393925956E+06	1735	0.01130%
3	9.56853832515537E+06	591	0.07310%
4	9.52361148217891E+06	1458	0.03980%
5	9.49805685259739E+06	1083	0.05370%
6	9.47491550826117E+06	1682	0.05590%
7	9.48767727950103E+06	1591	0.06890%
8	9.56521413109666E+06	727	0.08540%
9	9.59825430739536E+06	503	0.12810%
10	**9.46977190480350E+06**	1954	0.07620%
Mean	**9.52969657831266E+06**	**1171.4**	**0.06241%**
Std. Dev.	**52009.854670**	**582.002138**	**0.00032275**
Var.	**2705024982.777780**	**3.3873E+05**	**1.04167E-07**

TSP-LIB-3038, *k* = 450 Results

Density, Deterministic, TSP-LIB-3038, *k* = 450, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	8.13412342727274E+06	1966	0.02080%
2	8.13424861843437E+06	2274	0.01660%
3	8.13011401594518E+06	1935	0.02770%
4	**8.12580043585858E+06**	1707	0.03060%
5	8.13174337301589E+06	2389	0.02910%
6	8.13389546161616E+06	1769	0.01550%
7	8.13738327121213E+06	1708	0.01300%
8	8.14156219361473E+06	1680	0.02950%
9	8.14157410331890E+06	2169	0.02910%
10	8.13702661735209E+06	1641	0.03070%
Mean	**8.13474715176408E+06**	**1923.8**	**0.02426%**
Std. Dev.	**4911.352562**	**270.396746**	**7.01E-05**
Var.	**24121383.986111**	**7.3114E+04**	**4.91E-09**

Density, Parent Favored Hybrid, TSP-LIB-3038, *k* = 450, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	**8.13323353041126E+06**	2868	0.02360%
2	8.18564266693860E+06	1948	0.03170%
3	8.15281158261185E+06	2381	0.01260%
4	8.14194957886003E+06	2893	0.03300%
5	8.14108842215008E+06	2939	0.03860%
6	8.14966232752525E+06	3067	0.06610%
7	8.15560795505052E+06	2274	0.05270%
8	8.14184401973304E+06	2648	0.00890%
9	8.14176824108947E+06	2601	0.02220%
10	8.14080436727995E+06	2277	0.01990%
Mean	**8.14844126916500E+06**	**2589.6**	**0.03093%**
Std. Dev.	**14642.984670**	**361.413337**	**0.000178**
Var.	**214417000.041667**	**1.3062E+05**	**3.16E-08**

Density, Roulette-Wheel, TSP-LIB-3038, *k* = 450, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	8.29811848621933E+06	855	0.07320%
2	8.31303062882672E+06	882	0.05070%
3	**8.25416998030303E+06**	1290	0.02450%
4	8.26640347309078E+06	1534	0.06020%
5	8.29139801724386E+06	1088	0.05380%
6	8.27581863528139E+06	1555	0.02080%
7	8.31678711194083E+06	978	0.02530%
8	8.29067863474026E+06	1603	0.02990%
9	8.27475595620769E+06	1825	0.03130%
10	8.28135748117157E+06	1332	0.03550%
Mean	**8.28625184050255E+06**	**1294.2**	**0.04052%**
Std. Dev.	**19789.358958**	**334.892951**	**0.000177**
Var.	**391618727.986111**	**1.1215E+05**	**3.15E-08**

Random, Deterministic, TSP-LIB-3038, *k* = 450, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	8.13370445227273E+06	1794	0.00000%
2	8.14552453652737E+06	1621	0.00000%
3	8.12760611136641E+06	1772	0.00000%
4	8.13328622222223E+06	1446	0.00010%
5	8.13640391154402E+06	1742	0.00010%
6	8.12915749058442E+06	1895	0.00000%
7	8.13895072673159E+06	1785	0.00000%
8	8.12675728062770E+06	1729	0.00000%
9	**8.12506254062050E+06**	1792	0.00010%
10	8.14606294015151E+06	1914	0.00010%
Mean	**8.13425162126485E+06**	**1749**	**0.00004%**
Std. Dev.	**7492.577966**	**134.5288073**	**5.16E-07**
Var.	**56138724.569444**	**1.8098E+04**	**2.67E-13**

Random, Parent Favored Hybrid, TSP-LIB-3038, *k* = 450, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	8.35923384844876E+06	628	0.00010%
2	**8.13241421172439E+06**	2565	0.00000%
3	8.14448786139971E+06	2183	0.00000%
4	8.15091610898271E+06	2618	0.00010%
5	8.14457775064937E+06	2679	0.00000%
6	8.15020900792261E+06	2452	0.00010%
7	8.14761887604620E+06	2283	0.00010%
8	8.16920698369409E+06	2042	0.00000%
9	8.17986487291044E+06	1863	0.00010%
10	8.14154239054834E+06	2887	0.00000%
Mean	**8.17200719123266E+06**	**2220**	**0.00005%**
Std. Dev.	**67200.848037**	**639.9442684**	**5.27E-07**
Var.	**4515953976.888890**	**4.0953E+05**	**2.78E-13**

Random, Roulette-Wheel, TSP-LIB-3038, *k* = 450, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	8.34914207943723E+06	870	0.00000%
2	8.28718043849484E+06	1457	0.00000%
3	8.30962633340270E+06	1076	0.00000%
4	8.40018627339604E+06	510	0.00010%
5	8.31445641096681E+06	951	0.00000%
6	8.37122596125819E+06	523	0.00000%
7	8.31033528106060E+06	1152	0.00000%
8	**8.26505323019761E+06**	2229	0.00000%
9	8.36983684927850E+06	592	0.00010%
10	8.33842080382393E+06	923	0.00000%
Mean	**8.33154636613165E+06**	**1028.3**	**0.00002%**
Std. Dev.	**41794.566968**	**516.3422745**	**4.22E-07**
Var.	**1746785828.027780**	**2.6661E+05**	**1.78E-13**

Separation Deterministic, TSP-LIB-3038, *k* = 450, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	8.12938547712843E+06	1761	0.01490%
2	8.14076805295815E+06	1481	0.02590%
3	8.12873103124099E+06	1675	0.03280%
4	8.14553115043290E+06	1756	0.01100%
5	**8.12844408023087E+06**	2033	0.03010%
6	8.13368988463203E+06	1218	0.05910%
7	8.13225723066378E+06	1768	0.06290%
8	8.13295395223666E+06	1271	0.08670%
9	8.13607317388168E+06	1794	0.04800%
10	8.13049681832613E+06	1908	0.03020%
Mean	**8.13383308517316E+06**	**1666.5**	**0.04016%**
Std. Dev.	**5569.933448**	**264.196581**	**0.000237**
Var.	**31024158.611111**	**6.9800E+04**	**5.61E-08**

Separation, Parent Favored Hybrid, TSP-LIB-3038, *k* = 450, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	8.14213221450217E+06	2138	0.01780%
2	8.23224997911257E+06	1017	0.04230%
3	8.13344424448053E+06	2457	0.02910%
4	8.13739695230882E+06	2687	0.03140%
5	**8.12901568769842E+06**	2931	0.01730%
6	8.15473138225108E+06	1674	0.01400%
7	8.14646634159452E+06	2002	0.02720%
8	8.14090730772007E+06	3430	0.02070%
9	8.21199027839106E+06	1027	0.05080%
10	8.15128214927849E+06	1799	0.02520%
Mean	**8.15796165373377E+06**	**2116.2**	**0.02758%**
Std. Dev.	**35005.303280**	**784.304193**	**0.000116**
Var.	**1225371257.750000**	**6.1513E+05**	**1.35E-08**

Separation, Roulette-Wheel, TSP-LIB-3038, *k* = 450, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	8.30628361803753E+06	938	0.03160%
2	8.35569766307302E+06	520	0.07890%
3	8.30108876796815E+06	1011	0.04790%
4	8.29384075700135E+06	1365	0.01420%
5	8.26011541641414E+06	2219	0.01970%
6	8.30917563911923E+06	1190	0.02880%
7	**8.23930416486291E+06**	1991	0.02010%
8	8.28685952175603E+06	1260	0.06260%
9	8.31733695074092E+06	711	0.07430%
10	8.37149833798702E+06	732	0.01720%
Mean	**8.30412008369603E+06**	**1193.7**	**0.03953%**
Std. Dev.	**39377.511136**	**549.694875**	**0.000246**
Var.	**1550588383.236110**	**3.0216E+05**	**6.06E-08**

TSP-LIB-3038, *k* = 500 Results

Density, Deterministic, TSP-LIB-3038, *k* = 500, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	7.14346574260461E+06	1676	0.02470%
2	7.13987668618326E+06	1361	0.02630%
3	7.14756667038239E+06	1241	0.05120%
4	7.13822626363636E+06	2325	0.04110%
5	7.13411693618327E+06	1780	0.05490%
6	7.13975600411255E+06	1908	0.03140%
7	7.13815113506495E+06	1733	0.02050%
8	**7.12303658095239E+06**	2122	0.03940%
9	7.14885957849928E+06	1434	0.05060%
10	7.14402906507936E+06	1993	0.05140%
Mean	**7.13970846626984E+06**	**1757.3**	**0.03915%**
Std. Dev.	**7394.807924**	**344.707944**	**0.000127371**
Var.	**54683184.229167**	**1.1882E+05**	**1.62234E-08**

Density, Parent Favored Hybrid, TSP-LIB-3038, *k* = 500, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	7.14978762683983E+06	2853	0.01000%
2	7.15663326677490E+06	2314	0.01510%
3	7.15619138253968E+06	2402	0.01830%
4	7.16105161309524E+06	2693	0.02040%
5	7.20793256295092E+06	1542	0.09440%
6	7.15078903914142E+06	2220	0.01800%
7	**7.14146442683983E+06**	2195	0.01590%
8	7.15203793246753E+06	3006	0.02960%
9	7.16462038059165E+06	2086	0.02600%
10	7.23059942882396E+06	1176	0.07510%
Mean	**7.16711076600650E+06**	**2248.7**	**0.03228%**
Std. Dev.	**28714.244690**	**562.152421**	**0.000285568**
Var.	**824507848.111111**	**3.1602E+05**	**8.15491E-08**

Density, Roulette-Wheel, TSP-LIB-3038, *k* = 500, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	7.36995595735931E+06	767	0.08460%
2	7.34817686771285E+06	1049	0.09960%
3	7.30261906684705E+06	1383	0.06840%
4	7.32507261957209E+06	1345	0.05030%
5	7.31982630378789E+06	1404	0.04190%
6	7.33467540252524E+06	1149	0.04210%
7	7.31214346991341E+06	1505	0.05140%
8	**7.29761078726551E+06**	1915	0.01540%
9	7.30005736291488E+06	1385	0.04120%
10	7.30447877456709E+06	1917	0.05900%
Mean	**7.32146166124653E+06**	**1381.9**	**0.05539%**
Std. Dev.	**23600.880527**	**354.4493225**	**0.000240163**
Var.	**557001561.631944**	**1.2563E+05**	**5.76781E-08**

Random, Deterministic, TSP-LIB-3038, *k* = 500, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	7.13251782420635E+06	1767	0.00000%
2	7.13123352150072E+06	1908	0.00000%
3	**7.12622269743867E+06**	1890	0.00000%
4	7.14671902467532E+06	1972	0.00010%
5	7.13611274855701E+06	2095	0.00010%
6	7.13460515862195E+06	1798	0.00010%
7	7.14162202734488E+06	1654	0.00010%
8	7.13530038809524E+06	1896	0.00000%
9	7.13209964022366E+06	1839	0.00000%
10	7.12652729538240E+06	2024	0.00000%
Mean	**7.13429603260462E+06**	**1884.3**	**0.00004%**
Std. Dev.	**6283.159451**	**128.5085816**	**5.16398E-07**
Var.	**39478092.680556**	**1.6514E+04**	**2.66667E-13**

Random, Parent Favored Hybrid, TSP-LIB-3038, *k* = 500, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	7.25122068369408E+06	943	0.00010%
2	7.17612759797980E+06	1855	0.00010%
3	7.15347921540404E+06	2625	0.00000%
4	7.14229834729437E+06	2942	0.00000%
5	7.13850784141414E+06	2921	0.00000%
6	7.16580877398989E+06	1794	0.00000%
7	7.19762206630592E+06	1397	0.00000%
8	7.14641948744588E+06	2845	0.00000%
9	7.13737957323232E+06	2445	0.00000%
10	**7.12855740046897E+06**	4118	0.00000%
Mean	**7.16374209872294E+06**	**2388.5**	**0.00002%**
Std. Dev.	**37107.912251**	**916.4666752**	**4.21637E-07**
Var.	**1376997151.638890**	**8.3991E+05**	**1.77778E-13**

Random, Roulette-Wheel, TSP-LIB-3038, *k* = 500, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	7.35217624148630E+06	955	0.00000%
2	7.37497832922078E+06	700	0.00000%
3	7.37678244708070E+06	738	0.00010%
4	7.36248903286435E+06	1160	0.00010%
5	7.30427453333333E+06	1310	0.00010%
6	7.33238510627707E+06	1453	0.00000%
7	7.34934692929294E+06	1151	0.00000%
8	7.38963809613997E+06	1166	0.00000%
9	**7.29540356883118E+06**	1894	0.00000%
10	7.33490241324231E+06	1213	0.00010%
Mean	**7.34723766977689E+06**	**1174**	**0.00004%**
Std. Dev.	**30924.709755**	**346.3748772**	**5.16398E-07**
Var.	**956337673.409722**	**1.1998E+05**	**2.66667E-13**

Separation, Deterministic, TSP-LIB-3038, *k* = 500, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	7.13860438769842E+06	1580	0.03060%
2	7.13022171024532E+06	1295	0.02190%
3	**7.12415178340550E+06**	1906	0.00660%
4	7.14658399047617E+06	1587	0.02100%
5	7.12738566601732E+06	1812	0.01490%
6	7.14289991803752E+06	1781	0.03250%
7	7.13967997467531E+06	1416	0.03520%
8	7.13684270331890E+06	1420	0.03930%
9	7.13775542918470E+06	1963	0.01220%
10	7.12446417871574E+06	2063	0.03490%
Mean	**7.13485897417749E+06**	**1682.3**	**0.02491%**
Std. Dev.	**7829.984001**	**260.2554514**	**0.000111758**
Var.	**61308649.451389**	**6.7733E+04**	**1.24899E-08**

Separation, Parent Favored Hybrid, TSP-LIB-3038, *k* = 500, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	7.18075817777779E+06	1421	0.02720%
2	7.22181243621934E+06	1057	0.04790%
3	7.14012660252526E+06	2731	0.02550%
4	7.18487925822511E+06	1603	0.01320%
5	7.16313022633478E+06	1636	0.03220%
6	7.13628635173160E+06	2688	0.02460%
7	**7.12919245411254E+06**	2824	0.02080%
8	7.15606207911254E+06	2187	0.03540%
9	7.14357710093795E+06	2983	0.03220%
10	7.13369348466812E+06	3222	0.03000%
Mean	**7.15895181716450E+06**	**2235.2**	**0.02890%**
Std. Dev.	**29350.588975**	**755.912076**	**9.25731E-05**
Var.	**861457073.208333**	**5.7140E+05**	**8.56978E-09**

Separation, Roulette-Wheel, TSP-LIB-3038, *k* = 500, u = 100, p = 1.0

Run	Best SSE	Gen. found	% Seeding
1	7.36087216075037E+06	656	0.05650%
2	7.39288803506494E+06	543	0.06320%
3	7.39802049556278E+06	781	0.02060%
4	7.32541047554111E+06	765	0.02510%
5	7.35543257518036E+06	950	0.03640%
6	7.33676400844156E+06	1128	0.02900%
7	7.33619287727272E+06	987	0.05250%
8	**7.31381689509656E+06**	1361	0.03130%
9	7.33652104422798E+06	1544	0.03560%
10	7.31883912150349E+06	1399	0.01020%
Mean	**7.34747576886419E+06**	**1011.4**	**0.03604%**
Std. Dev.	**29177.090273**	**338.8841821**	**0.000167509**
Var.	**851302596.826389**	**1.1484E+05**	**2.80594E-08**

SYN1, *k* = 50 Results

Density, Deterministic, SYN1, *k* = 50, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	**9.92787374569039E+04**	39	0.07940%
2	9.92787374569039E+04	28	0.07150%
3	9.92787374569039E+04	19	0.20980%
4	9.92787374569039E+04	55	0.20730%
5	9.92787374569039E+04	35	0.17750%
6	9.92787374569039E+04	50	0.19560%
7	9.92787374569039E+04	45	0.09580%
8	9.92787374569039E+04	41	0.06540%
9	9.92787374569039E+04	17	0.20600%
10	9.92787374569039E+04	45	0.19650%
11	9.92787374569039E+04	25	0.18640%
12	9.92787374569039E+04	71	0.18070%
13	9.92787374569039E+04	31	0.12410%
14	9.92787374569039E+04	49	0.10790%
15	9.92787374569039E+04	24	0.16000%
16	9.92787374569039E+04	31	0.15190%
17	9.92787374569039E+04	110	0.11040%
18	9.92787374569039E+04	23	0.13680%
19	9.92787374569039E+04	17	0.16090%
20	9.92787374569039E+04	32	0.14710%
Mean	**9.92787374569039E+04**	**39.35**	**0.14855%**
Std. Dev.	**0.000000**	**21.73349343**	**0.000475043**
Var.	**0.000000**	**4.7234E+02**	**2.25666E-07**

Density, Parent Favored Hybrid, SYN1, *k* = 50, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	**9.92787374569039E+04**	42	0.12600%
2	9.92787374569039E+04	42	0.18840%
3	9.92787374569039E+04	40	0.20200%
4	9.92787374569039E+04	58	0.22590%
5	9.92787374569039E+04	66	0.29210%
6	9.92787374569039E+04	71	0.08890%
7	9.92787374569039E+04	57	0.12090%
8	9.92787374569039E+04	57	0.08790%
9	9.92787374569039E+04	31	0.16120%
10	9.92787374569039E+04	42	0.15920%
11	9.92787374569039E+04	33	0.17040%
12	9.92787374569039E+04	40	0.16320%
13	9.92787374569039E+04	43	0.19470%
14	9.92787374569039E+04	61	0.05340%
15	9.92787374569039E+04	49	0.16470%
16	9.92787374569039E+04	55	0.17320%
17	9.92787374569039E+04	39	0.11240%
18	9.92787374569039E+04	69	0.10080%
19	9.92787374569039E+04	65	0.11800%
20	9.92787374569039E+04	62	0.12320%
Mean	**9.92787374569039E+04**	**51.1**	**0.15133%**
Std. Dev.	**0.000000**	**12.40500748**	**0.000550455**
Var.	**0.000000**	**1.5388E+02**	**3.03001E-07**

Density, Roulette Wheel Rank, SYN1, *k* = 50, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	**9.92787374569039E+04**	18	0.14600%
2	9.92787374569039E+04	12	0.15490%
3	1.62006708693650E+05	57	0.30460%
4	9.92787374569039E+04	19	0.31820%
5	9.92787374569039E+04	95	0.38150%
6	9.92787374569039E+04	19	0.31110%
7	9.92787374569039E+04	254	0.28930%
8	9.92787374569039E+04	15	0.36990%
9	9.92787374569039E+04	26	0.43790%
10	9.92787374569039E+04	17	0.12730%
11	9.92787374569039E+04	30	0.34770%
12	1.62005806424844E+05	21	0.46280%
13	9.92787374569039E+04	54	0.22400%
14	9.92787374569039E+04	22	0.45810%
15	9.92787374569039E+04	10	0.48230%
16	1.62005533081053E+05	63	0.51360%
17	1.62005308545881E+05	120	0.32540%
18	9.92787374569039E+04	17	0.27060%
19	9.92787374569039E+04	22	0.32820%
20	9.92787374569039E+04	28	0.30650%
Mean	**1.11824157802795E+05**	**45.95**	**0.32800%**
Std. Dev.	**25742.659387**	**56.98981904**	**0.001102179**
Var.	**662684512.291547**	**3.2478E+03**	**1.2148E-06**

Random, Deterministic, SYN1, *k* = 50, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	**9.92787374569039E+04**	53	0.00010%
2	9.92787374569039E+04	81	0.00010%
3	9.92787374569039E+04	37	0.00020%
4	9.92787374569039E+04	24	0.00040%
5	9.92787374569039E+04	46	0.00020%
6	9.92787374569039E+04	45	0.00030%
7	9.92787374569039E+04	26	0.00010%
8	9.92787374569039E+04	49	0.00010%
9	9.92787374569039E+04	28	0.00020%
10	9.92787374569039E+04	19	0.00030%
11	9.92787374569039E+04	43	0.00030%
12	9.92787374569039E+04	50	0.00030%
13	9.92787374569039E+04	36	0.00000%
14	9.92787374569039E+04	34	0.00010%
15	9.92787374569039E+04	21	0.00010%
16	9.92787374569039E+04	39	0.00000%
17	9.92787374569039E+04	99	0.00000%
18	9.92787374569039E+04	52	0.00000%
19	9.92787374569039E+04	32	0.00010%
20	9.92787374569039E+04	39	0.00010%
Mean	**9.92787374569039E+04**	**42.65**	**0.00015%**
Std. Dev.	**0.000000**	**19.34527006**	**1.19208E-06**
Var.	**0.000000**	**3.7424E+02**	**1.42105E-12**

Random, Parent Favored Hybrid, SYN1, *k* = 50, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	**9.92787374569039E+04**	73	0.00020%
2	9.92787374569039E+04	69	0.00020%
3	9.92787374569039E+04	19	0.00020%
4	9.92787374569039E+04	50	0.00020%
5	9.92787374569039E+04	33	0.00010%
6	9.92787374569039E+04	63	0.00040%
7	9.92787374569039E+04	78	0.00010%
8	9.92787374569039E+04	53	0.00020%
9	9.92787374569039E+04	54	0.00030%
10	9.92787374569039E+04	49	0.00000%
11	9.92787374569039E+04	59	0.00000%
12	9.92787374569039E+04	63	0.00000%
13	9.92787374569039E+04	57	0.00010%
14	9.92787374569039E+04	39	0.00010%
15	9.92787374569039E+04	94	0.00010%
16	9.92787374569039E+04	75	0.00030%
17	9.92787374569039E+04	90	0.00000%
18	9.92787374569039E+04	35	0.00000%
19	9.92787374569039E+04	57	0.00000%
20	9.92787374569039E+04	48	0.00000%
Mean	**9.92787374569039E+04**	**57.9**	**0.00013%**
Std. Dev.	**0.000000**	**18.82020191**	**1.20852E-06**
Var.	**0.000000**	**3.5420E+02**	**1.46053E-12**

Random, Roulette Wheel Rank, SYN1, *k* = 50, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	9.92787374569039E+04	26	0.00050%
2	**9.92787374569039E+04**	15	0.00020%
3	1.62005073875726E+05	136	0.00040%
4	9.92787374569039E+04	14	0.00050%
5	9.92787374569039E+04	35	0.00060%
6	9.92787374569039E+04	103	0.00040%
7	9.92787374569039E+04	104	0.00050%
8	9.92787374569039E+04	63	0.00100%
9	9.92787374569039E+04	34	0.00030%
10	1.62006134790546E+05	38	0.00030%
11	9.92787374569039E+04	19	0.00010%
12	1.62004702663475E+05	96	0.00020%
13	9.92787374569039E+04	21	0.00030%
14	9.92787374569039E+04	121	0.00030%
15	9.92787374569039E+04	34	0.00030%
16	9.92787374569039E+04	15	0.00000%
17	9.92787374569039E+04	19	0.00010%
18	9.92787374569039E+04	46	0.00010%
19	9.92787374569039E+04	70	0.00010%
20	9.92787374569039E+04	17	0.00010%
Mean	**1.08687722404856E+05**	**51.3**	**0.00032%**
Std. Dev.	**22979.723800**	**39.65920614**	**2.32322E-06**
Var.	**528067705.940022**	**1.5729E+03**	**5.39737E-12**

Separation, Deterministic, SYN1, *k* = 50, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	**9.92787374569039E+04**	0	0.37390%
2	9.92787374569039E+04	1	0.11260%
3	9.92787374569039E+04	0	0.34710%
4	9.92787374569039E+04	0	0.36050%
5	9.92787374569039E+04	0	0.27640%
6	9.92787374569039E+04	0	0.40320%
7	9.92787374569039E+04	1	0.09170%
8	9.92787374569039E+04	0	0.31180%
9	9.92787374569039E+04	0	0.16580%
10	9.92787374569039E+04	0	0.42680%
11	9.92787374569039E+04	0	0.33580%
12	9.92787374569039E+04	0	0.23300%
13	9.92787374569039E+04	0	0.17410%
14	9.92787374569039E+04	0	0.32420%
15	9.92787374569039E+04	0	0.30690%
16	9.92787374569039E+04	0	0.33750%
17	9.92787374569039E+04	0	0.24880%
18	9.92787374569039E+04	0	0.18740%
19	9.92787374569039E+04	0	0.26530%
20	9.92787374569039E+04	0	0.26060%
Mean	**9.92787374569039E+04**	**0.1**	**0.27717%**
Std. Dev.	**0.000000**	**0.307793506**	**0.000936329**
Var.	**0.000000**	**9.4737E-02**	**8.76712E-07**

Separation, Parent Favored Hybrid, SYN1, *k* = 50, u = 200, p = 0.8

Run	**Best SSE**	**Gen. found**	**% Seeding**
1	**9.92787374569039E+04**	0	0.39460%
2	9.92787374569039E+04	0	0.48840%
3	9.92787374569039E+04	0	0.49020%
4	9.92787374569039E+04	0	0.93910%
5	9.92787374569039E+04	0	0.87860%
6	9.92787374569039E+04	0	0.34740%
7	9.92787374569039E+04	0	0.14830%
8	9.92787374569039E+04	0	0.20090%
9	9.92787374569039E+04	0	0.37550%
10	9.92787374569039E+04	0	0.39360%
11	9.92787374569039E+04	0	0.37360%
12	9.92787374569039E+04	0	0.002051
13	9.92787374569039E+04	0	0.001706
14	9.92787374569039E+04	0	0.00241
15	9.92787374569039E+04	0	0.002339
16	9.92787374569039E+04	0	0.001976
17	9.92787374569039E+04	0	0.00189
18	9.92787374569039E+04	0	0.002223
19	9.92787374569039E+04	0	0.002458
20	9.92787374569039E+04	0	0.003504
Mean	**9.92787374569039E+04**	**0**	**0.35430%**
Std. Dev.	**0.000000**	**0**	**0.002161589**
Var.	**0.000000**	**0.0000E+00**	**4.67247E-06**

Separation, Roulette Wheel Rank, SYN1, *k* = 50, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	9.92787374569039E+04	0	0.33760%
2	9.92787374569039E+04	0	0.79270%
3	9.92787374569039E+04	0	0.61840%
4	9.92787374569039E+04	0	0.61470%
5	9.92787374569039E+04	0	0.20030%
6	9.92787374569039E+04	0	0.49060%
7	9.92787374569039E+04	0	0.65480%
8	9.92787374569039E+04	0	0.76760%
9	9.92787374569039E+04	0	0.40140%
10	9.92787374569039E+04	0	0.48630%
11	9.92787374569039E+04	0	0.51650%
12	9.92787374569039E+04	0	0.39590%
13	9.92787374569039E+04	0	0.42610%
14	9.92787374569039E+04	0	0.70480%
15	9.92787374569039E+04	0	0.65270%
16	9.92787374569039E+04	0	0.35970%
17	9.92787374569039E+04	0	0.78900%
18	9.92787374569039E+04	0	0.58430%
19	9.92787374569039E+04	0	0.75260%
20	9.92787374569039E+04	0	0.58240%
Mean	**9.92787374569039E+04**	**0**	**0.55642%**
Std. Dev.	**0.000000**	**0**	**0.001675971**
Var.	**0.000000**	**0.0000E+00**	**2.80888E-06**

SYN2, *k* = 50 Results

Density, Deterministic, SYN2, *k* = 50, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	9.93423397226885E+04	19	0.06940%
2	9.93423397226885E+04	22	0.17990%
3	9.93423397226885E+04	30	0.20520%
4	9.93423397226885E+04	33	0.12710%
5	9.93423397226885E+04	27	0.11130%
6	9.93423397226885E+04	35	0.14620%
7	9.93423397226885E+04	60	0.14460%
8	9.93423397226885E+04	21	0.03900%
9	9.93423397226885E+04	24	0.05320%
10	9.93423397226885E+04	26	0.09760%
11	9.93423397226885E+04	33	0.10870%
12	9.93423397226885E+04	34	0.13290%
13	9.93423397226885E+04	24	0.15450%
14	9.93423397226885E+04	19	0.19900%
15	9.93423397226885E+04	36	0.20270%
16	9.93423397226885E+04	29	0.19010%
17	9.93423397226885E+04	29	0.11620%
18	9.93423397226885E+04	36	0.10220%
19	9.93423397226885E+04	31	0.14050%
20	9.93423397226885E+04	27	0.13710%
Mean	**9.93423397226885E+04**	**29.75**	**0.13287%**
Std. Dev.	**0.000000**	**8.96117356**	**0.000478814**
Var.	**0.000000**	**8.0303E+01**	**2.29263E-07**

Density, Parent Favored Hybrid, SYN2, *k* = 50, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	9.93423397226885E+04	117	0.05210%
2	9.93423397226885E+04	72	0.07060%
3	9.93423397226885E+04	48	0.07420%
4	9.93423397226885E+04	44	0.19030%
5	9.93423397226885E+04	35	0.05900%
6	9.93423397226885E+04	39	0.05740%
7	9.93423397226885E+04	32	0.14840%
8	9.93423397226885E+04	31	0.17100%
9	9.93423397226885E+04	58	0.18130%
10	9.93423397226885E+04	37	0.19390%
11	9.93423397226885E+04	56	0.14920%
12	9.93423397226885E+04	42	0.07770%
13	9.93423397226885E+04	75	0.07840%
14	9.93423397226885E+04	63	0.07680%
15	9.93423397226885E+04	65	0.09830%
16	9.93423397226885E+04	55	0.10080%
17	9.93423397226885E+04	42	0.09270%
18	9.93423397226885E+04	53	0.08380%
19	9.93423397226885E+04	42	0.11000%
20	9.93423397226885E+04	56	0.10340%
Mean	**9.93423397226885E+04**	**53.1**	**0.10847%**
Std. Dev.	**0.000000**	**19.73748771**	**0.000465692**
Var.	**0.000000**	**3.8957E+02**	**2.16869E-07**

Density, Roulette-Wheel Rank, SYN2, *k* = 50, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	9.93423397226885E+04	23	0.19820%
2	9.93423397226885E+04	27	0.26010%
3	9.93423397226885E+04	10	0.45190%
4	9.93423397226885E+04	17	0.48480%
5	9.93423397226885E+04	12	0.59870%
6	9.93423397226885E+04	20	0.56230%
7	9.93423397226885E+04	11	0.29640%
8	9.93423397226885E+04	32	0.22300%
9	9.93423397226885E+04	13	0.34620%
10	9.93423397226885E+04	16	0.34590%
11	9.93423397226885E+04	11	0.13490%
12	9.93423397226885E+04	30	0.21310%
13	9.93423397226885E+04	105	0.30760%
14	9.93423397226885E+04	19	0.41640%
15	9.93423397226885E+04	23	0.47560%
16	9.93423397226885E+04	31	0.53000%
17	9.93423397226885E+04	12	0.002631
18	9.93423397226885E+04	21	0.002772
19	9.93423397226885E+04	14	0.003259
20	9.93423397226885E+04	13	0.003517
Mean	**9.93423397226885E+04**	**23**	**0.35315%**
Std. Dev.	**0.000000**	**20.55544492**	**0.001294247**
Var.	**0.000000**	**4.2253E+02**	**1.67508E-06**

Random, Deterministic, SYN2, *k* = 50, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	9.93423397226885E+04	37	0.00010%
2	9.93423397226885E+04	20	0.00010%
3	9.93423397226885E+04	22	0.00010%
4	9.93423397226885E+04	27	0.00010%
5	9.93423397226885E+04	37	0.00010%
6	9.93423397226885E+04	30	0.00010%
7	9.93423397226885E+04	21	0.00010%
8	9.93423397226885E+04	29	0.00000%
9	9.93423397226885E+04	21	0.00000%
10	9.93423397226885E+04	37	0.00000%
11	9.93423397226885E+04	18	0.00000%
12	9.93423397226885E+04	18	0.00000%
13	9.93423397226885E+04	22	0.00000%
14	9.93423397226885E+04	25	0.00000%
15	9.93423397226885E+04	23	0.00000%
16	9.93423397226885E+04	21	0.00010%
17	9.93423397226885E+04	41	0.00000%
18	9.93423397226885E+04	26	0.00000%
19	9.93423397226885E+04	29	0.00000%
20	9.93423397226885E+04	20	0.00000%
Mean	**9.93423397226885E+04**	**26.2**	**0.00004%**
Std. Dev.	**0.000000**	**7.030759486**	**5.02625E-07**
Var.	**0.000000**	**4.9432E+01**	**2.52632E-13**

Random, Parent Favored Hybrid, SYN2, *k* = 50, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	9.93423397226885E+04	84	0.00000%
2	9.93423397226885E+04	39	0.00010%
3	9.93423397226885E+04	39	0.00010%
4	9.93423397226885E+04	46	0.00010%
5	9.93423397226885E+04	43	0.00010%
6	9.93423397226885E+04	53	0.00010%
7	9.93423397226885E+04	40	0.00010%
8	9.93423397226885E+04	68	0.00010%
9	9.93423397226885E+04	46	0.00000%
10	9.93423397226885E+04	47	0.00000%
11	9.93423397226885E+04	52	0.00000%
12	9.93423397226885E+04	53	0.00000%
13	9.93423397226885E+04	34	0.00000%
14	9.93423397226885E+04	36	0.00020%
15	9.93423397226885E+04	53	0.00010%
16	9.93423397226885E+04	60	0.00010%
17	9.93423397226885E+04	47	0.00020%
18	9.93423397226885E+04	36	0.00010%
19	9.93423397226885E+04	70	0.00010%
20	9.93423397226885E+04	31	0.00010%
Mean	**9.93423397226885E+04**	**48.85**	**0.00008%**
Std. Dev.	**0.000000**	**13.44491686**	**6.15587E-07**
Var.	**0.000000**	**1.8077E+02**	**3.78947E-13**

Random, Roulette-Wheel Rank, SYN2, *k* = 50, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	9.93423397226885E+04	14	0.00020%
2	9.93423397226885E+04	17	0.00040%
3	9.93423397226885E+04	20	0.00030%
4	9.93423397226885E+04	59	0.00030%
5	9.93423397226885E+04	20	0.00030%
6	9.93423397226885E+04	15	0.00030%
7	9.93423397226885E+04	26	0.00020%
8	9.93423397226885E+04	16	0.00030%
9	9.93423397226885E+04	18	0.00030%
10	9.93423397226885E+04	13	0.00030%
11	9.93423397226885E+04	9	0.00030%
12	9.93423397226885E+04	37	0.00030%
13	9.93423397226885E+04	16	0.00010%
14	9.93423397226885E+04	27	0.00010%
15	9.93423397226885E+04	8	0.00010%
16	9.93423397226885E+04	21	0.00030%
17	9.93423397226885E+04	20	0.00000%
18	9.93423397226885E+04	33	0.00000%
19	9.93423397226885E+04	15	0.00010%
20	9.93423397226885E+04	12	0.00010%
Mean	**9.93423397226885E+04**	**20.8**	**0.00022%**
Std. Dev.	**0.000000**	**11.61034022**	**1.1821E-06**
Var.	**0.000000**	**1.3480E+02**	**1.39737E-12**

Separation, Deterministic, SYN2, *k* = 50, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	9.93423397226885E+04	8	0.19500%
2	9.93423397226885E+04	8	0.30750%
3	9.93423397226885E+04	12	0.13460%
4	9.93423397226885E+04	12	0.22950%
5	9.93423397226885E+04	9	0.05970%
6	9.93423397226885E+04	8	0.07080%
7	9.93423397226885E+04	13	0.13120%
8	9.93423397226885E+04	8	0.22050%
9	9.93423397226885E+04	12	0.21280%
10	9.93423397226885E+04	12	0.28890%
11	9.93423397226885E+04	10	0.31370%
12	9.93423397226885E+04	17	0.31940%
13	9.93423397226885E+04	15	0.15780%
14	9.93423397226885E+04	12	0.15260%
15	9.93423397226885E+04	10	0.18810%
16	9.93423397226885E+04	9	0.18700%
17	9.93423397226885E+04	16	0.17430%
18	9.93423397226885E+04	6	0.18980%
19	9.93423397226885E+04	13	0.18990%
20	9.93423397226885E+04	20	0.19530%
Mean	**9.93423397226885E+04**	**11.5**	**0.19592%**
Std. Dev.	**0.000000**	**3.53181033**	**0.000719664**
Var.	**0.000000**	**1.2474E+01**	**5.17916E-07**

Separation, Parent Favored Hybrid, SYN2, *k* = 50, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	9.93423397226885E+04	13	0.10840%
2	9.93423397226885E+04	22	0.17670%
3	9.93423397226885E+04	44	0.17640%
4	9.93423397226885E+04	24	0.21190%
5	9.93423397226885E+04	15	0.13280%
6	9.93423397226885E+04	16	0.30380%
7	9.93423397226885E+04	20	0.19460%
8	9.93423397226885E+04	16	0.20040%
9	9.93423397226885E+04	14	0.10690%
10	9.93423397226885E+04	23	0.05760%
11	9.93423397226885E+04	4	0.19780%
12	9.93423397226885E+04	15	0.26160%
13	9.93423397226885E+04	29	0.18760%
14	9.93423397226885E+04	6	0.27530%
15	9.93423397226885E+04	12	0.28190%
16	9.93423397226885E+04	26	0.13010%
17	9.93423397226885E+04	12	0.27290%
18	9.93423397226885E+04	15	0.15490%
19	9.93423397226885E+04	10	0.19730%
20	9.93423397226885E+04	22	0.23270%
Mean	**9.93423397226885E+04**	**17.9**	**0.19308%**
Std. Dev.	**0.000000**	**8.914211008**	**0.00065927**
Var.	**0.000000**	**7.9463E+01**	**4.34638E-07**

Separation, Roulette-Wheel by Rank, SYN2, *k* = 50, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	9.93423397226885E+04	8	0.33400%
2	9.93423397226885E+04	8	0.42390%
3	9.93423397226885E+04	4	0.48630%
4	9.93423397226885E+04	8	0.50460%
5	9.93423397226885E+04	8	0.47960%
6	9.93423397226885E+04	6	0.23070%
7	9.93423397226885E+04	5	0.46520%
8	9.93423397226885E+04	8	0.47960%
9	9.93423397226885E+04	6	0.58240%
10	9.93423397226885E+04	10	0.66510%
11	9.93423397226885E+04	8	0.33930%
12	9.93423397226885E+04	7	0.45760%
13	9.93423397226885E+04	10	0.46100%
14	9.93423397226885E+04	8	0.51520%
15	9.93423397226885E+04	6	0.26540%
16	9.93423397226885E+04	6	0.29050%
17	9.93423397226885E+04	9	0.45690%
18	9.93423397226885E+04	9	0.55300%
19	9.93423397226885E+04	13	0.64710%
20	9.93423397226885E+04	7	0.65710%
Mean	**9.93423397226885E+04**	**7.7**	**0.46473%**
Std. Dev.	**0.000000**	**2.00262985**	**0.001249358**
Var.	**0.000000**	**4.0105E+00**	**1.5609E-06**

SYN3, *k* = 50 Results

Density, Deterministic, SYN3, *k* = 50, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	9.60462353857666E+04	440	0.05650%
2	9.60465440956909E+04	279	0.04810%
3	9.60463386702524E+04	154	0.04880%
4	9.60462738905756E+04	176	0.06690%
5	9.60464592087165E+04	441	0.05990%
6	**9.60461612773171E+04**	234	0.06880%
7	9.60463478342367E+04	241	0.06190%
8	9.60465517737119E+04	293	0.02650%
9	9.60463011318114E+04	259	0.02850%
10	9.60466107138861E+04	233	0.05940%
11	9.60465260405101E+04	403	0.05010%
12	9.60465291976136E+04	264	0.05120%
13	9.60464980113236E+04	269	0.03570%
14	9.60463380253366E+04	355	0.02340%
15	9.60461711282681E+04	342	0.01760%
16	9.60463910278192E+04	197	0.05650%
17	9.60463310109472E+04	435	0.04770%
18	9.60464254279516E+04	511	0.05130%
19	9.60464119318801E+04	205	0.04460%
20	9.60461636840491E+04	451	0.03720%
Mean	**9.60463804733832E+04**	**309.1**	**0.04703%**
Std. Dev.	**0.137689**	**105.593511**	**0.000146142**
Var.	**0.018958**	**1.1150E+04**	**2.13574E-08**

Density, Parent Favored Hybrid, SYN3, *k* = 50, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	9.60468508207592E+04	245	0.02020%
2	9.60475964667513E+04	333	0.03890%
3	9.60463900645089E+04	453	0.04440%
4	9.60466478655082E+04	295	0.03490%
5	9.60467641695090E+04	476	0.04130%
6	9.60463427441872E+04	564	0.02510%
7	9.60468717129875E+04	496	0.04030%
8	9.60470889492407E+04	301	0.02080%
9	9.60471330828695E+04	403	0.03190%
10	9.60464178705351E+04	662	0.03460%
11	9.60468283181447E+04	373	0.04450%
12	9.60465529704313E+04	486	0.05230%
13	9.60463816599083E+04	468	0.02290%
14	9.60467209814711E+04	614	0.02380%
15	9.60467611372578E+04	291	0.03650%
16	9.60469204776327E+04	390	0.03000%
17	**9.60462339397047E+04**	519	0.03190%
18	9.60465359778999E+04	521	0.05250%
19	9.60466248952536E+04	546	0.03540%
20	9.60464815099465E+04	580	0.05850%
Mean	**9.60467072807253E+04**	**450.8**	**0.03604%**
Std. Dev.	**0.323915**	**117.902993**	**0.000108466**
Var.	**0.104921**	**1.3901E+04**	**1.17648E-08**

Density, Roulette Wheel by Rank, SYN3, *k* = 50, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	9.60462409282889E+04	300	0.11800%
2	9.60464051124276E+04	418	0.11300%
3	9.60464089417755E+04	277	0.18310%
4	9.60467551783897E+04	406	0.17460%
5	9.60469885880771E+04	225	0.08010%
6	9.60470355251929E+04	168	0.12850%
7	9.60468174869229E+04	233	0.10330%
8	9.60462101785456E+04	308	0.15360%
9	9.60464212836096E+04	223	0.19160%
10	9.60464512276041E+04	394	0.03980%
11	9.60466057822653E+04	285	0.18950%
12	**9.60461919530668E+04**	368	0.19600%
13	9.60464334019636E+04	146	0.17510%
14	9.60466037067005E+04	160	0.13600%
15	9.60467326207244E+04	223	0.14420%
16	9.60466694451424E+04	109	0.23040%
17	9.60468118848937E+04	101	0.39760%
18	9.60461988455615E+04	367	0.27020%
19	9.60466353533793E+04	331	0.23780%
20	9.60464457591642E+04	385	0.06280%
Mean	**9.60465531601848E+04**	**271.35**	**0.16626%**
Std. Dev.	**0.253938**	**101.174823**	**0.000802264**
Var.	**0.064485**	**1.0236E+04**	**6.43628E-07**

Random, Deterministic, SYN3, *k* = 50, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	9.60464136546331E+04	235	0.00010%
2	9.60467265108663E+04	280	0.00010%
3	9.60464855924895E+04	369	0.00000%
4	9.60468342483269E+04	196	0.00000%
5	9.60463260221319E+04	303	0.00000%
6	9.60464820756750E+04	308	0.00000%
7	9.60468401496766E+04	229	0.00000%
8	9.60466405594782E+04	144	0.00000%
9	9.60465341210170E+04	271	0.00000%
10	9.60461973425068E+04	342	0.00000%
11	9.60462671442038E+04	404	0.00000%
12	9.60466166470868E+04	336	0.00000%
13	9.60462393391090E+04	335	0.00000%
14	9.60465273153959E+04	230	0.00000%
15	9.60466666853746E+04	326	0.00000%
16	9.60462007404718E+04	441	0.00000%
17	9.60463766207765E+04	482	0.00000%
18	9.60465154768975E+04	221	0.00000%
19	9.60466352418601E+04	318	0.00000%
20	**9.60461192709430E+04**	537	0.00000%
Mean	**9.60464822379460E+04**	**315.35**	**0.00001%**
Std. Dev.	**0.212227**	**97.92493097**	**3.07794E-07**
Var.	**0.045040**	**9.5893E+03**	**9.47368E-14**

Random, Parent Favored Hybrid, SYN3, *k* = 50, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	9.60468952741548E+04	296	0.00000%
2	9.60467411019479E+04	355	0.00000%
3	9.60463547455767E+04	413	0.00000%
4	9.60469391878470E+04	284	0.00000%
5	9.60468396885171E+04	347	0.00000%
6	9.60472696028861E+04	230	0.00000%
7	9.60466945925307E+04	435	0.00000%
8	9.60463115150612E+04	388	0.00000%
9	9.60470081438207E+04	459	0.00000%
10	9.60466992602984E+04	406	0.00000%
11	9.60469642550299E+04	431	0.00000%
12	9.60463871322872E+04	483	0.00000%
13	9.60463760909207E+04	554	0.00000%
14	9.60466762830033E+04	553	0.00000%
15	9.60477356545377E+04	280	0.00000%
16	9.60467003706320E+04	302	0.00000%
17	9.60467593644353E+04	315	0.00000%
18	9.60468545090793E+04	508	0.00000%
19	9.60466518447105E+04	399	0.00000%
20	9.60468592697711E+04	358	0.00000%
Mean	**9.60467858943524E+04**	**389.8**	**0.00000%**
Std. Dev.	**0.329226**	**91.94197255**	**0**
Var.	**0.108389**	**8.4533E+03**	**0**

Random, Roulette Wheel by Rank, SYN3, *k* = 50, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	9.60465878541615E+04	82	0.00000%
2	9.60464834932185E+04	322	0.00000%
3	9.60465520035549E+04	107	0.00000%
4	9.60464777896326E+04	266	0.00000%
5	9.60470154206221E+04	220	0.00010%
6	9.60466945546507E+04	357	0.00010%
7	9.60465005103957E+04	111	0.00010%
8	9.60465212811017E+04	306	0.00010%
9	9.60465508483440E+04	238	0.00010%
10	9.60462701496885E+04	564	0.00010%
11	9.60463099248686E+04	432	0.00010%
12	9.60463109644385E+04	164	0.00010%
13	9.60470091762162E+04	255	0.00010%
14	9.60465071723962E+04	140	0.00010%
15	9.60468955943136E+04	196	0.00010%
16	9.60469064695866E+04	196	0.00010%
17	9.60466578494978E+04	408	0.00010%
18	**9.60462097184751E+04**	279	0.00010%
19	9.60463689056054E+04	491	0.00010%
20	9.60466119850195E+04	353	0.00010%
Mean	**9.60465720832894E+04**	**274.35**	**0.00008%**
Std. Dev.	**0.236024**	**131.543979**	**4.10391E-07**
Var.	**0.055707**	**1.7304E+04**	**1.68421E-13**

Separation, Deterministic, SYN3, *k* = 50, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	9.60460824091768E+04	392	0.03640%
2	9.60463978934679E+04	382	0.01780%
3	9.60463900858447E+04	272	0.04680%
4	9.60466979229688E+04	164	0.05870%
5	9.60464138210834E+04	434	0.05340%
6	9.60463708115053E+04	380	0.01650%
7	9.60463701133276E+04	347	0.11000%
8	9.60461482007029E+04	453	0.09370%
9	9.60466967053631E+04	204	0.06400%
10	9.60467019531118E+04	167	0.11140%
11	9.60463723938971E+04	171	0.08790%
12	9.60462452312846E+04	447	0.04730%
13	9.60463631969641E+04	237	0.05260%
14	9.60463961863051E+04	239	0.03580%
15	**9.60460714607540E+04**	267	0.06220%
16	9.60464316353051E+04	173	0.03420%
17	9.60463995285919E+04	147	0.10090%
18	9.60463874359348E+04	328	0.01750%
19	9.60462748369197E+04	423	0.05120%
20	9.60461805653731E+04	269	0.08390%
Mean	**9.60463696193941E+04**	**294.8**	**0.05911%**
Std. Dev.	**0.179885**	**106.1893046**	**0.000300049**
Var.	**0.032359**	**1.1276E+04**	**9.00297E-08**

Separation, Parent Favored Hybrid, SYN3, *k* = 50, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	9.60469155252123E+04	262	0.02960%
2	9.60464147531394E+04	558	0.03760%
3	9.60466598751215E+04	277	0.02210%
4	9.60468205583686E+04	383	0.02200%
5	9.60464226265601E+04	337	0.04460%
6	9.60466498901346E+04	353	0.03630%
7	9.60467662692505E+04	497	0.02650%
8	9.60462991138904E+04	526	0.03900%
9	9.60462812310484E+04	655	0.04890%
10	**9.60461001379658E+04**	523	0.04650%
11	9.60467672547144E+04	330	0.02780%
12	9.60465518492231E+04	448	0.03030%
13	9.60463140143456E+04	379	0.03730%
14	9.60466084663923E+04	217	0.04000%
15	9.60465073881123E+04	344	0.03730%
16	9.60465019459951E+04	551	0.02290%
17	9.60465191345637E+04	288	0.02350%
18	9.60473591781842E+04	294	0.05840%
19	9.60469205784490E+04	271	0.05850%
20	9.60463151943868E+04	440	0.05580%
Mean	**9.60465847492529E+04**	**396.65**	**0.03725%**
Std. Dev.	**0.288570**	**121.3760034**	**0.000119179**
Var.	**0.083272**	**1.4732E+04**	**1.42037E-08**

Separation, Roulette Wheel by Rank, SYN3, *k* = 50, u = 200, p = 0.8

Run	Best SSE	Gen. found	% Seeding
1	9.60467055722178E+04	243	0.10620%
2	9.60465152645271E+04	149	0.34360%
3	9.60467884381272E+04	214	0.18820%
4	9.60467691300889E+04	112	0.24610%
5	9.60462702239555E+04	324	0.05440%
6	9.60466761869670E+04	180	0.09710%
7	9.60467691281569E+04	177	0.17070%
8	9.60463886747332E+04	213	0.19350%
9	9.60463523884500E+04	240	0.16240%
10	9.60462962904199E+04	399	0.15510%
11	9.60464967626071E+04	240	0.12380%
12	9.60466459039976E+04	562	0.11680%
13	9.60468365062859E+04	186	0.18850%
14	9.60466740274825E+04	203	0.18270%
15	9.60470904697634E+04	139	0.11430%
16	9.60471610617264E+04	161	0.08880%
17	**9.60462507221704E+04**	107	0.20340%
18	9.60467782092484E+04	287	0.15040%
19	9.60463926884295E+04	292	0.15730%
20	9.60464331372996E+04	477	0.13700%
Mean	**9.60466145393327E+04**	**245.25**	**0.15902%**
Std. Dev.	**0.258914**	**118.9019388**	**0.000629707**
Var.	**0.067036**	**1.4138E+04**	**3.96531E-07**

Appendix B: Best Known Solutions

TSP-LIB-1060, *k* = 100: Separation, Deterministic

```
Random = 0
Density = 0
Separation = 200
Selection Method = 2
Number of centers = 100
After 0 generations new best SSE for g = 0 is 1.0637178211822496E8
After 2 generations new best SSE for g = 2 is 1.050430456941599E8
After 2 generations new best SSE for g = 4 is 1.0360189048759992E8
After 3 generations new best SSE for g = 7 is 1.0301113407687885E8
After 1 generations new best SSE for g = 8 is 1.0221164480078883E8
After 2 generations new best SSE for g = 10 is 1.011907661019302E8
After 3 generations new best SSE for g = 13 is 1.0113107903380544E8
After 2 generations new best SSE for g = 15 is 1.007451086815344E8
After 3 generations new best SSE for g = 18 is 1.0035394889387992E8
After 3 generations new best SSE for g = 21 is 1.0021060345415935E8
After 3 generations new best SSE for g = 24 is 9.98257570892657E7
After 4 generations new best SSE for g = 28 is 9.89214652742007E7
After 11 generations new best SSE for g = 39 is 9.8628194616164E7
After 7 generations new best SSE for g = 46 is 9.854750191423097E7
After 2 generations new best SSE for g = 48 is 9.850492751972923E7
After 4 generations new best SSE for g = 52 is 9.823906466941664E7
After 3 generations new best SSE for g = 55 is 9.822994526401116E7
After 2 generations new best SSE for g = 57 is 9.813316409370498E7
After 6 generations new best SSE for g = 63 is 9.809935969140026E7
After 10 generations new best SSE for g = 73 is 9.776787067881511E7
After 11 generations new best SSE for g = 84 is 9.768232380237891E7
After 1 generations new best SSE for g = 85 is 9.749015029796837E7
After 9 generations new best SSE for g = 94 is 9.727444996195781E7
After 5 generations new best SSE for g = 99 is 9.710253326716396E7
After 2 generations new best SSE for g = 101 is 9.687552310469568E7
After 9 generations new best SSE for g = 110 is 9.679547469718735E7
After 10 generations new best SSE for g = 120 is 9.667645883145547E7
After 17 generations new best SSE for g = 137 is 9.667331663602877E7
After 4 generations new best SSE for g = 141 is 9.666708442572509E7
After 2 generations new best SSE for g = 143 is 9.656277106931941E7
After 7 generations new best SSE for g = 150 is 9.655036202489193E7
After 23 generations new best SSE for g = 173 is 9.652770496754149E7
After 24 generations new best SSE for g = 197 is 9.651843774057616E7
After 5 generations new best SSE for g = 202 is 9.650644140931767E7
After 1 generations new best SSE for g = 203 is 9.647735634370887E7
After 2 generations new best SSE for g = 205 is 9.646755263751453E7
After 6 generations new best SSE for g = 211 is 9.646449457570513E7
After 11 generations new best SSE for g = 222 is 9.644854543818636E7
After 2 generations new best SSE for g = 224 is 9.644607861893895E7
After 4 generations new best SSE for g = 228 is 9.644523075334898E7
After 11 generations new best SSE for g = 239 is 9.641630887903695E7
After 37 generations new best SSE for g = 276 is 9.636806595251977E7
After 3 generations new best SSE for g = 279 is 9.636234495184094E7
After 72 generations new best SSE for g = 351 is 9.632196572265841E7
After 86 generations new best SSE for g = 437 is 9.631786446113127E7
Best SSE for g = 537 is 9.631786446113127E7
```

```
Best chromosome for g = 537 is center 0 is 1901.51 7894.46
Best chromosome for g = 537 is center 1 is 4197.10125 2779.3
Best chromosome for g = 537 is center 2 is 4213.366 3717.3920000000007
Best chromosome for g = 537 is center 3 is 4675.957777777778 4247.02
Best chromosome for g = 537 is center 4 is 5584.459 2957.924
Best chromosome for g = 537 is center 5 is 4261.094615384614 5138.703076923077
Best chromosome for g = 537 is center 6 is 4332.626666666667 5958.322500000001
Best chromosome for g = 537 is center 7 is 4203.35625 6932.639999999999
Best chromosome for g = 537 is center 8 is 6982.047058823529 1563.6058823529409
Best chromosome for g = 537 is center 9 is 6054.835 2598.175
Best chromosome for g = 537 is center 10 is 5059.038999999999 4821.616999999999
Best chromosome for g = 537 is center 11 is 5572.306428571429 3957.937142857144
Best chromosome for g = 537 is center 12 is 6433.71 3347.6500000000005
Best chromosome for g = 537 is center 13 is 5277.546666666666 5755.964000000001
Best chromosome for g = 537 is center 14 is 4482.149714285714 8501.181999999997
Best chromosome for g = 537 is center 15 is 5394.307 6675.317999999999
Best chromosome for g = 537 is center 16 is 5966.303846153846 4988.8107692307685
Best chromosome for g = 537 is center 17 is 6415.125 4227.033
Best chromosome for g = 537 is center 18 is 7035.62 2867.986
Best chromosome for g = 537 is center 19 is 7155.711666666666 3780.681666666667
Best chromosome for g = 537 is center 20 is 6488.513333333333 5795.935
Best chromosome for g = 537 is center 21 is 8106.476428571428 1548.91
Best chromosome for g = 537 is center 22 is 7894.766923076923 2871.06
Best chromosome for g = 537 is center 23 is 5337.595 8494.045
Best chromosome for g = 537 is center 24 is 9107.275 1548.91
Best chromosome for g = 537 is center 25 is 7495.986 4606.768000000001
Best chromosome for g = 537 is center 26 is 7121.071538461538 6195.655384615386
Best chromosome for g = 537 is center 27 is 8062.691250000001 4090.88
Best chromosome for g = 537 is center 28 is 9117.286000000002 2847.9980000000005
Best chromosome for g = 537 is center 29 is 6209.126666666667 8506.535
Best chromosome for g = 537 is center 30 is 8772.395384615385 3824.24
Best chromosome for g = 537 is center 31 is 8783.94076923077 4627.523076923077
Best chromosome for g = 537 is center 32 is 8192.910000000002 5954.914545454546
Best chromosome for g = 537 is center 33 is 10089.875454545456 1598.8763636363635
Best chromosome for g = 537 is center 34 is 9752.79 2962.9189999999994
Best chromosome for g = 537 is center 35 is 8101.927272727273 7090.47909090909
Best chromosome for g = 537 is center 36 is 10696.041666666668 2768.8891666666664
Best chromosome for g = 537 is center 37 is 9638.47076923077 4173.995384615385
Best chromosome for g = 537 is center 38 is 10189.958181818181 4378.748181818181
Best chromosome for g = 537 is center 39 is 9128.721428571427 6060.035714285715
Best chromosome for g = 537 is center 40 is 9850.17 5046.45923076923
Best chromosome for g = 537 is center 41 is 9841.195555555556 6850.7522222222215
Best chromosome for g = 537 is center 42 is 10216.489166666666 6070.742499999999
Best chromosome for g = 537 is center 43 is 12059.633333333333 2681.4516666666664
Best chromosome for g = 537 is center 44 is 13851.060000000001 2698.1040000000003
Best chromosome for g = 537 is center 45 is 10679.957142857142 3654.578571428571
Best chromosome for g = 537 is center 46 is 10638.490000000002 4916.551
Best chromosome for g = 537 is center 47 is 11394.814285714285 3540.3728571428574
Best chromosome for g = 537 is center 48 is 11197.407692307692 4377.697692307693
Best chromosome for g = 537 is center 49 is 12587.833333333336 3020.1011111111115
Best chromosome for g = 537 is center 50 is 12230.6 4192.891666666666
Best chromosome for g = 537 is center 51 is 11537.000000000002 5079.772222222222
Best chromosome for g = 537 is center 52 is 11316.185714285715 5745.970000000001
Best chromosome for g = 537 is center 53 is 11146.412499999999 6820.21875
Best chromosome for g = 537 is center 54 is 12437.227272727272 5041.917272727273
Best chromosome for g = 537 is center 55 is 13293.949999999999 4396.915
Best chromosome for g = 537 is center 56 is 13792.854545454546 3770.0809090909092
```

```
Best chromosome for g = 537 is center 57 is 14626.679999999998 3102.8200000000006
Best chromosome for g = 537 is center 58 is 12282.545454545454 5877.697272727273
Best chromosome for g = 537 is center 59 is 12376.56666666667 6868.517333333334
Best chromosome for g = 537 is center 60 is 14851.86 4077.139
Best chromosome for g = 537 is center 61 is 13560.844444444443 5301.835555555555
Best chromosome for g = 537 is center 62 is 14228.033333333333 4791.083333333332
Best chromosome for g = 537 is center 63 is 13224.842857142858 6766.684285714285
Best chromosome for g = 537 is center 64 is 13320.64 5885.872000000001
Best chromosome for g = 537 is center 65 is 14478.233333333335 5662.695000000001
Best chromosome for g = 537 is center 66 is 15352.26 2838.006
Best chromosome for g = 537 is center 67 is 15453.245454545455 3765.539090909091
Best chromosome for g = 537 is center 68 is 16179.600000000002 2875.7566666666667
Best chromosome for g = 537 is center 69 is 15673.221428571427 5692.435714285714
Best chromosome for g = 537 is center 70 is 14254.706666666669 6605.368666666667
Best chromosome for g = 537 is center 71 is 15201.435714285715 6791.665714285714
Best chromosome for g = 537 is center 72 is 13128.654545454547 8394.113636363634
Best chromosome for g = 537 is center 73 is 14111.271428571432 8444.079999999998
Best chromosome for g = 537 is center 74 is 17009.416666666664 1486.455
Best chromosome for g = 537 is center 75 is 17058.65 2783.0449999999996
Best chromosome for g = 537 is center 76 is 16667.872727272726 3515.7136363636364
Best chromosome for g = 537 is center 77 is 17880.966666666667 1498.9449999999997
Best chromosome for g = 537 is center 78 is 16807.1875 4215.795
Best chromosome for g = 537 is center 79 is 16313.05 4909.054999999999
Best chromosome for g = 537 is center 80 is 17614.072727272724 3933.603636363637
Best chromosome for g = 537 is center 81 is 17198.36923076923 5019.555384615384
Best chromosome for g = 537 is center 82 is 16047.446153846151 6330.176923076923
Best chromosome for g = 537 is center 83 is 16777.68571428571 6102.862857142857
Best chromosome for g = 537 is center 84 is 18736.40571428571 1491.8079999999998
Best chromosome for g = 537 is center 85 is 18380.076923076922 2947.929230769231
Best chromosome for g = 537 is center 86 is 17455.616666666665 6303.911666666666
Best chromosome for g = 537 is center 87 is 18217.68125 4899.686874999999
Best chromosome for g = 537 is center 88 is 18553.307692307695 4035.6292307692306
Best chromosome for g = 537 is center 89 is 18232.754545454543 5696.005454545455
Best chromosome for g = 537 is center 90 is 16827.742857142857 6909.441428571428
Best chromosome for g = 537 is center 91 is 19302.949999999997 2848.00125
Best chromosome for g = 537 is center 92 is 19326.566666666666 4052.711111111111
Best chromosome for g = 537 is center 93 is 19056.13636363636 4955.613636363636
Best chromosome for g = 537 is center 94 is 15112.085714285715 8444.079999999998
Best chromosome for g = 537 is center 95 is 16236.51176470588 8429.384117647058
Best chromosome for g = 537 is center 96 is 18873.416666666668 6187.328333333334
Best chromosome for g = 537 is center 97 is 18029.409999999996 7100.022999999999
Best chromosome for g = 537 is center 98 is 19715.8 7194.96
Best chromosome for g = 537 is center 99 is 21317.0 2098.53
Time Elapsed: 13309021
```

TSP-LIB-3038, *k* = 150: Density, Deterministic

```
Random = 0
Density = 100
Separation = 0
Selection Method = 2
Number of centers = 150
After 0 generations new best SSE for g = 0 is 7.086592961064674E7
After 2 generations new best SSE for g = 2 is 6.969649417892641E7
After 3 generations new best SSE for g = 5 is 6.952834080198032E7
After 1 generations new best SSE for g = 6 is 6.951140478417854E7
After 1 generations new best SSE for g = 7 is 6.869802932136667E7
After 2 generations new best SSE for g = 9 is 6.833412782801186E7
After 1 generations new best SSE for g = 10 is 6.792345584834458E7
After 1 generations new best SSE for g = 11 is 6.782881532126509E7
After 2 generations new best SSE for g = 13 is 6.690148648850903E7
After 1 generations new best SSE for g = 14 is 6.665982659429282E7
After 1 generations new best SSE for g = 15 is 6.603378087761697E7
After 3 generations new best SSE for g = 18 is 6.5195634664071426E7
After 2 generations new best SSE for g = 20 is 6.463252907356252E7
After 1 generations new best SSE for g = 21 is 6.445770740678319E7
After 2 generations new best SSE for g = 23 is 6.388455023192099E7
After 5 generations new best SSE for g = 28 is 6.35346931764368E7
After 2 generations new best SSE for g = 30 is 6.3177274310252964E7
After 1 generations new best SSE for g = 31 is 6.292026536809592E7
After 7 generations new best SSE for g = 38 is 6.2674784504863985E7
After 1 generations new best SSE for g = 39 is 6.189677269389003E7
After 4 generations new best SSE for g = 43 is 6.171471059911847E7
After 1 generations new best SSE for g = 44 is 6.165437794787972E7
After 3 generations new best SSE for g = 47 is 6.162744026075796E7
After 4 generations new best SSE for g = 51 is 6.1379568931256525E7
After 3 generations new best SSE for g = 54 is 6.137179204771559E7
After 1 generations new best SSE for g = 55 is 6.09885936941143E7
After 1 generations new best SSE for g = 56 is 6.0677898575336404E7
After 11 generations new best SSE for g = 67 is 6.057339534215426E7
After 4 generations new best SSE for g = 71 is 6.044014451103594E7
After 3 generations new best SSE for g = 74 is 5.976713953137573E7
After 7 generations new best SSE for g = 81 is 5.9646752714080885E7
After 2 generations new best SSE for g = 83 is 5.9478196832397915E7
After 3 generations new best SSE for g = 86 is 5.934102623914847E7
After 3 generations new best SSE for g = 89 is 5.9194066994886786E7
After 5 generations new best SSE for g = 94 is 5.912524669730147E7
After 2 generations new best SSE for g = 96 is 5.9063167193714306E7
After 1 generations new best SSE for g = 97 is 5.892707737462855E7
After 2 generations new best SSE for g = 99 is 5.8893221400165446E7
After 5 generations new best SSE for g = 104 is 5.857400036569347E7
After 5 generations new best SSE for g = 109 is 5.855635961517403E7
After 1 generations new best SSE for g = 110 is 5.8336929269597024E7
After 3 generations new best SSE for g = 113 is 5.822646366365979E7
After 3 generations new best SSE for g = 116 is 5.780661618146089E7
After 8 generations new best SSE for g = 124 is 5.7784141396364756E7
After 2 generations new best SSE for g = 126 is 5.7783415637533106E7
After 2 generations new best SSE for g = 128 is 5.776213421947085E7
After 12 generations new best SSE for g = 140 is 5.7762119922328E7
After 1 generations new best SSE for g = 141 is 5.7437030562823236E7
After 20 generations new best SSE for g = 161 is 5.740695574769298E7
```

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After 2 generations new best SSE for g = 163 is 5.737451085267783E7
After 5 generations new best SSE for g = 168 is 5.737449655553498E7
After 5 generations new best SSE for g = 173 is 5.7364475451891124E7
After 3 generations new best SSE for g = 176 is 5.735850523969224E7
After 4 generations new best SSE for g = 180 is 5.734593972170537E7
After 1 generations new best SSE for g = 181 is 5.730030027994045E7
After 5 generations new best SSE for g = 186 is 5.7210070863684475E7
After 4 generations new best SSE for g = 190 is 5.7105999865247004E7
After 4 generations new best SSE for g = 194 is 5.708239707325252E7
After 7 generations new best SSE for g = 201 is 5.7052747414151624E7
After 2 generations new best SSE for g = 203 is 5.699918368383444E7
After 1 generations new best SSE for g = 204 is 5.699466879300788E7
After 3 generations new best SSE for g = 207 is 5.677813402950072E7
After 4 generations new best SSE for g = 211 is 5.677659390321572E7
After 7 generations new best SSE for g = 218 is 5.6768669905015714E7
After 11 generations new best SSE for g = 229 is 5.6724926932831846E7
After 18 generations new best SSE for g = 247 is 5.671700293463184E7
After 2 generations new best SSE for g = 249 is 5.664441882221033E7
After 5 generations new best SSE for g = 254 is 5.664079006774635E7
After 7 generations new best SSE for g = 261 is 5.664009040557275E7
After 5 generations new best SSE for g = 266 is 5.659910220030841E7
After 1 generations new best SSE for g = 267 is 5.659448607750444E7
After 11 generations new best SSE for g = 278 is 5.659386921201002E7
After 4 generations new best SSE for g = 282 is 5.6446570877594076E7
After 39 generations new best SSE for g = 321 is 5.642846083402474E7
After 4 generations new best SSE for g = 325 is 5.642800760602161E7
After 1 generations new best SSE for g = 326 is 5.636890561943996E7
After 2 generations new best SSE for g = 328 is 5.63584563128838E7
After 9 generations new best SSE for g = 337 is 5.634519177058546E7
After 7 generations new best SSE for g = 344 is 5.63232814641766E7
After 6 generations new best SSE for g = 350 is 5.627955804363856E7
After 2 generations new best SSE for g = 352 is 5.6247812793720804E7
After 32 generations new best SSE for g = 384 is 5.622903775730672E7
After 22 generations new best SSE for g = 406 is 5.618130025114564E7
After 25 generations new best SSE for g = 431 is 5.61772235647119E7
After 11 generations new best SSE for g = 442 is 5.6157010603083566E7
After 21 generations new best SSE for g = 463 is 5.615170698678159E7
After 19 generations new best SSE for g = 482 is 5.615034121411021E7
After 5 generations new best SSE for g = 487 is 5.614782643676928E7
After 6 generations new best SSE for g = 493 is 5.6105861576738305E7
After 11 generations new best SSE for g = 504 is 5.6081854773284376E7
After 18 generations new best SSE for g = 522 is 5.606800200283572E7
After 33 generations new best SSE for g = 555 is 5.60532128507352E7
After 30 generations new best SSE for g = 585 is 5.604452705825914E7
After 1 generations new best SSE for g = 586 is 5.603407775170298E7
After 6 generations new best SSE for g = 592 is 5.603108566371948E7
After 19 generations new best SSE for g = 611 is 5.6025920779148184E7
After 4 generations new best SSE for g = 615 is 5.601719176925854E7
After 27 generations new best SSE for g = 642 is 5.601083576152318E7
After 58 generations new best SSE for g = 700 is 5.599109637103183E7
After 55 generations new best SSE for g = 755 is 5.597542921630057E7
After 39 generations new best SSE for g = 794 is 5.59572286932729E7
After 7 generations new best SSE for g = 801 is 5.595649827651147E7
After 21 generations new best SSE for g = 822 is 5.5956351814988144E7
After 14 generations new best SSE for g = 836 is 5.5952147476851285E7
After 27 generations new best SSE for g = 863 is 5.595183923875147E7
After 28 generations new best SSE for g = 891 is 5.594825461361314E7
```

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After 24 generations new best SSE for g = 915 is 5.59469749725386E7
After 31 generations new best SSE for g = 946 is 5.594406215128124E7
After 44 generations new best SSE for g = 990 is 5.593770614354588E7
After 67 generations new best SSE for g = 1057 is 5.5936840416324995E7
After 69 generations new best SSE for g = 1126 is 5.592336058230583E7
After 78 generations new best SSE for g = 1204 is 5.591700457457048E7
Best SSE for g = 1304 is 5.591700457457048E7
Best chromosome for g = 1304 is center 0 is 1901.51 7894.46
Best chromosome for g = 1304 is center 1 is 3973.172 2887.9739999999997
Best chromosome for g = 1304 is center 2 is 4570.316666666667 2598.1766666666667
Best chromosome for g = 1304 is center 3 is 4136.638333333333 3564.1650000000004
Best chromosome for g = 1304 is center 4 is 4370.158333333334 4013.851666666667
Best chromosome for g = 1304 is center 5 is 4247.13875 4890.31875
Best chromosome for g = 1304 is center 6 is 4795.498333333334 4222.038333333334
Best chromosome for g = 1304 is center 7 is 4353.478 5346.25
Best chromosome for g = 1304 is center 8 is 4184.59375 5802.181250000001
Best chromosome for g = 1304 is center 9 is 3602.88 7194.96
Best chromosome for g = 1304 is center 10 is 6405.113333333334 1632.1866666666667
Best chromosome for g = 1304 is center 11 is 5574.45 2648.1420000000003
Best chromosome for g = 1304 is center 12 is 5604.474999999999 3114.48
Best chromosome for g = 1304 is center 13 is 6112.024285714286 2633.8642857142863
Best chromosome for g = 1304 is center 14 is 5385.547500000001 4003.4425
Best chromosome for g = 1304 is center 15 is 5254.195 4621.7575
Best chromosome for g = 1304 is center 16 is 5885.9525 3953.4737499999997
Best chromosome for g = 1304 is center 17 is 4928.935 4954.856666666667
Best chromosome for g = 1304 is center 18 is 4586.995 6129.036666666667
Best chromosome for g = 1304 is center 19 is 5014.0019999999995 5586.082
Best chromosome for g = 1304 is center 20 is 4289.138571428572 6895.165714285714
Best chromosome for g = 1304 is center 21 is 5459.914444444444 5807.040000000001
Best chromosome for g = 1304 is center 22 is 6247.848571428571 3326.2357142857145
Best chromosome for g = 1304 is center 23 is 5782.396666666667 4985.394444444444
Best chromosome for g = 1304 is center 24 is 7105.675714285716 1548.91
Best chromosome for g = 1304 is center 25 is 4461.137272727272 8500.100606060605
Best chromosome for g = 1304 is center 26 is 5179.133333333333 6836.871666666666
Best chromosome for g = 1304 is center 27 is 7055.6375 2773.0525000000002
Best chromosome for g = 1304 is center 28 is 6699.793333333335 3369.857777777778
Best chromosome for g = 1304 is center 29 is 6505.197999999999 4077.138
Best chromosome for g = 1304 is center 30 is 6426.561428571428 4803.774285714286
Best chromosome for g = 1304 is center 31 is 7093.1625 3934.74
Best chromosome for g = 1304 is center 32 is 5717.0675 6432.9875
Best chromosome for g = 1304 is center 33 is 5081.835555555555 8516.25111111111
Best chromosome for g = 1304 is center 34 is 5737.915555555556 8471.837777777779
Best chromosome for g = 1304 is center 35 is 6488.513333333333 5795.935
Best chromosome for g = 1304 is center 36 is 8106.476428571428 1548.91
Best chromosome for g = 1304 is center 37 is 7722.835 2664.7933333333335
Best chromosome for g = 1304 is center 38 is 6980.573749999999 6158.182500000001
Best chromosome for g = 1304 is center 39 is 6905.51 6895.16
Best chromosome for g = 1304 is center 40 is 6355.07625 8519.02625
Best chromosome for g = 1304 is center 41 is 7722.833333333333 3314.34
Best chromosome for g = 1304 is center 42 is 8136.498000000001 2967.916
Best chromosome for g = 1304 is center 43 is 7495.986 4606.768000000001
Best chromosome for g = 1304 is center 44 is 8062.691250000001 4090.88
Best chromosome for g = 1304 is center 45 is 7556.035 6012.450000000001
Best chromosome for g = 1304 is center 46 is 9107.275 1548.91
Best chromosome for g = 1304 is center 47 is 10089.875454545456
1598.8763636363635
Best chromosome for g = 1304 is center 48 is 9117.286000000002 2847.9980000000005
```

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Best chromosome for g = 1304 is center 49 is 8606.876 3597.476
Best chromosome for g = 1304 is center 50 is 8590.196666666667 4796.636666666666
Best chromosome for g = 1304 is center 51 is 8837.064 4027.173999999999
Best chromosome for g = 1304 is center 52 is 9739.03125 2891.71875
Best chromosome for g = 1304 is center 53 is 9057.234 4566.796
Best chromosome for g = 1304 is center 54 is 8289.95888888889 5979.14
Best chromosome for g = 1304 is center 55 is 8031.4169999999995 7100.017999999999
Best chromosome for g = 1304 is center 56 is 9607.675000000001 3830.646666666667
Best chromosome for g = 1304 is center 57 is 9692.746000000001 4371.933
Best chromosome for g = 1304 is center 58 is 9582.658333333333 5038.131666666666
Best chromosome for g = 1304 is center 59 is 9148.974999999999 5987.468333333333
Best chromosome for g = 1304 is center 60 is 9169.8225 6807.724999999999
Best chromosome for g = 1304 is center 61 is 10433.325 2848.0
Best chromosome for g = 1304 is center 62 is 11008.8 2698.1059999999998
Best chromosome for g = 1304 is center 63 is 10679.957142857142 3654.578571428571
Best chromosome for g = 1304 is center 64 is 10278.21 4376.931
Best chromosome for g = 1304 is center 65 is 10212.696363636363 5064.62909090909
Best chromosome for g = 1304 is center 66 is 12059.633333333333
2681.4516666666664
Best chromosome for g = 1304 is center 67 is 11394.814285714285
3540.3728571428574
Best chromosome for g = 1304 is center 68 is 10850.316666666666 4821.616666666667
Best chromosome for g = 1304 is center 69 is 11081.077777777777 4313.639999999999
Best chromosome for g = 1304 is center 70 is 12667.257142857143
2912.2400000000002
Best chromosome for g = 1304 is center 71 is 12351.549999999997
3705.7316666666666
Best chromosome for g = 1304 is center 72 is 10183.125 5854.2283333333335
Best chromosome for g = 1304 is center 73 is 10091.401666666667 6345.55
Best chromosome for g = 1304 is center 74 is 9991.318333333335 6911.82
Best chromosome for g = 1304 is center 75 is 11481.400000000001 5090.875555555555
Best chromosome for g = 1304 is center 76 is 11048.820000000002 5895.864
Best chromosome for g = 1304 is center 77 is 11809.42857142857 4339.814285714286
Best chromosome for g = 1304 is center 78 is 13851.060000000001
2698.1040000000003
Best chromosome for g = 1304 is center 79 is 16863.4625 1473.96375
Best chromosome for g = 1304 is center 80 is 17480.644444444446
1521.1522222222222
Best chromosome for g = 1304 is center 81 is 18136.722222222223
1476.7388888888888
Best chromosome for g = 1304 is center 82 is 11839.460000000001 5586.082
Best chromosome for g = 1304 is center 83 is 11146.412499999999 6820.21875
Best chromosome for g = 1304 is center 84 is 12379.88 4526.8240000000005
Best chromosome for g = 1304 is center 85 is 12434.95 5071.442
Best chromosome for g = 1304 is center 86 is 13602.550000000003 3639.111666666667
Best chromosome for g = 1304 is center 87 is 13230.560000000001 4436.888
Best chromosome for g = 1304 is center 88 is 12218.1 6054.088333333333
Best chromosome for g = 1304 is center 89 is 12197.25 6995.094999999998
Best chromosome for g = 1304 is center 90 is 12740.16 5725.986
Best chromosome for g = 1304 is center 91 is 12530.02 6595.375999999999
Best chromosome for g = 1304 is center 92 is 13932.585714285713 4147.09
Best chromosome for g = 1304 is center 93 is 13496.5 5224.905714285714
Best chromosome for g = 1304 is center 94 is 14626.679999999998
3102.8200000000006
Best chromosome for g = 1304 is center 95 is 14486.55 3772.3525
Best chromosome for g = 1304 is center 96 is 14297.128571428571 4910.839999999999
Best chromosome for g = 1304 is center 97 is 13602.550000000001 5687.676666666667
```

Best chromosome for g = 1304 is center 98 is 14381.480000000001 5586.082
Best chromosome for g = 1304 is center 99 is 12922.85 7107.514999999999
Best chromosome for g = 1304 is center 100 is 13260.579999999998
6605.370000000001
Best chromosome for g = 1304 is center 101 is 15352.26 2838.006
Best chromosome for g = 1304 is center 102 is 15018.250000000002 4178.3175
Best chromosome for g = 1304 is center 103 is 15457.340000000002 3722.388
Best chromosome for g = 1304 is center 104 is 14042.462499999998 6589.13
Best chromosome for g = 1304 is center 105 is 14680.474999999999 6376.78
Best chromosome for g = 1304 is center 106 is 13310.650000000001
6095.724999999999
Best chromosome for g = 1304 is center 107 is 13128.654545454547
8394.113636363634
Best chromosome for g = 1304 is center 108 is 14461.5 7144.99
Best chromosome for g = 1304 is center 109 is 14111.271428571432
8444.079999999998
Best chromosome for g = 1304 is center 110 is 16179.600000000002
2875.7566666666667
Best chromosome for g = 1304 is center 111 is 15697.529999999999 5561.099
Best chromosome for g = 1304 is center 112 is 15241.349999999999 6849.3625
Best chromosome for g = 1304 is center 113 is 16029.5 4646.736666666667
Best chromosome for g = 1304 is center 114 is 15750.075000000003 6058.25125
Best chromosome for g = 1304 is center 115 is 15112.085714285715
8444.079999999998
Best chromosome for g = 1304 is center 116 is 16498.899999999998
3540.371428571428
Best chromosome for g = 1304 is center 117 is 16913.528571428567
2755.207142857143
Best chromosome for g = 1304 is center 118 is 16705.016666666666 4238.695
Best chromosome for g = 1304 is center 119 is 16483.18 5066.446
Best chromosome for g = 1304 is center 120 is 16112.8875 6383.025
Best chromosome for g = 1304 is center 121 is 16688.325 5920.8475
Best chromosome for g = 1304 is center 122 is 17085.1 3583.2000000000003
Best chromosome for g = 1304 is center 123 is 16379.766666666668
6961.783333333333
Best chromosome for g = 1304 is center 124 is 16112.885714285714
8444.079999999998
Best chromosome for g = 1304 is center 125 is 17630.783333333336 2848.0
Best chromosome for g = 1304 is center 126 is 17058.088888888888
5040.908888888889
Best chromosome for g = 1304 is center 127 is 17526.5125 4122.10875
Best chromosome for g = 1304 is center 128 is 17642.67142857143 4953.665714285714
Best chromosome for g = 1304 is center 129 is 18757.41818181818
1492.8893939393936
Best chromosome for g = 1304 is center 130 is 18577.337499999998 2798.035
Best chromosome for g = 1304 is center 131 is 18222.899999999998
3822.318333333333
Best chromosome for g = 1304 is center 132 is 18689.95 3347.6475
Best chromosome for g = 1304 is center 133 is 16946.866666666665
6495.446666666668
Best chromosome for g = 1304 is center 134 is 17401.4 6233.1275000000005
Best chromosome for g = 1304 is center 135 is 19398.866666666665
2798.036666666667
Best chromosome for g = 1304 is center 136 is 18314.6375 4521.82625
Best chromosome for g = 1304 is center 137 is 18829.34285714286
4025.7457142857143
Best chromosome for g = 1304 is center 138 is 17138.725 7095.025

```
Best chromosome for g = 1304 is center 139 is 16813.433333333334
8360.803333333335
Best chromosome for g = 1304 is center 140 is 18364.677777777775
5013.149999999999
Best chromosome for g = 1304 is center 141 is 18247.92222222222 5607.178888888889
Best chromosome for g = 1304 is center 142 is 19365.4875 4047.15875
Best chromosome for g = 1304 is center 143 is 18174.54 6315.572
Best chromosome for g = 1304 is center 144 is 19055.239999999998
4656.731999999999
Best chromosome for g = 1304 is center 145 is 18076.9375 7132.499999999999
Best chromosome for g = 1304 is center 146 is 19135.280000000002
5276.298000000001
Best chromosome for g = 1304 is center 147 is 18955.140000000003
6115.7119999999995
Best chromosome for g = 1304 is center 148 is 19715.8 7194.96
Best chromosome for g = 1304 is center 149 is 21317.0 2098.53
Time Elapsed: 1.3062412E7 Seeding Time: 10108.0
The seeding percentage time is : 0.000774
```

TSP-LIB-3038, *k* = 50: Random, Deterministic

```
Random = 100
Density = 0
Separation = 0
Selection Method = 2
Number of centers = 50
After 0 generations new best SSE for g = 0 is 1.0041490849878004E8
After 1 generations new best SSE for g = 1 is 1.0022846133652507E8
After 2 generations new best SSE for g = 3 is 9.997568222506225E7
After 1 generations new best SSE for g = 4 is 9.995272432935731E7
After 1 generations new best SSE for g = 5 is 9.899135722463347E7
After 9 generations new best SSE for g = 14 is 9.874230779491043E7
After 14 generations new best SSE for g = 28 is 9.872690523493984E7
After 8 generations new best SSE for g = 36 is 9.863349508546005E7
After 2 generations new best SSE for g = 38 is 9.861086330321509E7
After 2 generations new best SSE for g = 40 is 9.860714209071612E7
After 1 generations new best SSE for g = 41 is 9.857230631286824E7
After 1 generations new best SSE for g = 42 is 9.852763459070432E7
After 2 generations new best SSE for g = 44 is 9.849606596443124E7
After 12 generations new best SSE for g = 56 is 9.849078938639571E7
After 2 generations new best SSE for g = 58 is 9.848525450732623E7
After 1 generations new best SSE for g = 59 is 9.844715462900795E7
After 6 generations new best SSE for g = 65 is 9.844693180954982E7
After 1 generations new best SSE for g = 66 is 9.840730269555181E7
After 8 generations new best SSE for g = 74 is 9.840565898530759E7
After 2 generations new best SSE for g = 76 is 9.838352032084113E7
After 4 generations new best SSE for g = 80 is 9.829923604781541E7
After 2 generations new best SSE for g = 82 is 9.829424169292356E7
After 14 generations new best SSE for g = 96 is 9.82897570683796E7
After 5 generations new best SSE for g = 101 is 9.828724513154726E7
After 9 generations new best SSE for g = 110 is 9.827917043120179E7
After 10 generations new best SSE for g = 120 is 9.827268410581289E7
After 8 generations new best SSE for g = 128 is 9.826857567183582E7
After 1 generations new best SSE for g = 129 is 9.826849920845006E7
After 10 generations new best SSE for g = 139 is 9.826653508259809E7
After 2 generations new best SSE for g = 141 is 9.826408577293311E7
After 4 generations new best SSE for g = 145 is 9.826028423098476E7
After 3 generations new best SSE for g = 148 is 9.825897820278211E7
After 3 generations new best SSE for g = 151 is 9.82585760260485E7
After 1 generations new best SSE for g = 152 is 9.825721413701908E7
After 5 generations new best SSE for g = 157 is 9.825622575046171E7
After 3 generations new best SSE for g = 160 is 9.825226535739005E7
After 5 generations new best SSE for g = 165 is 9.825015176795831E7
After 6 generations new best SSE for g = 171 is 9.8249844910044E7
After 5 generations new best SSE for g = 176 is 9.824877463111366E7
After 24 generations new best SSE for g = 200 is 9.824809856815413E7
After 3 generations new best SSE for g = 203 is 9.824255500262077E7
Best SSE for g = 303 is 9.824255500262077E7
Best chromosome for g = 303 is center 0 is 182.67741935483872
268.56451612903226
Best chromosome for g = 303 is center 1 is 691.6818181818181
242.78787878787878
```

Best chromosome for g = 303 is center 2 is 1259.225806451613
215.70967741935485
Best chromosome for g = 303 is center 3 is 1751.267857142857
231.42857142857142
Best chromosome for g = 303 is center 4 is 2227.3846153846152
223.01923076923077
Best chromosome for g = 303 is center 5 is 2654.9661016949153
204.3728813559322
Best chromosome for g = 303 is center 6 is 329.27272727272725
716.9848484848485
Best chromosome for g = 303 is center 7 is 652.09375 1102.671875
Best chromosome for g = 303 is center 8 is 152.2469135802469
1208.5432098765432
Best chromosome for g = 303 is center 9 is 148.22972972972974
1630.2972972972973
Best chromosome for g = 303 is center 10 is 1018.0847457627119
737.3389830508474
Best chromosome for g = 303 is center 11 is 1386.5185185185185
659.2037037037037
Best chromosome for g = 303 is center 12 is 548.8703703703703
1478.9444444444443
Best chromosome for g = 303 is center 13 is 1092.2602739726028
1323.2876712328766
Best chromosome for g = 303 is center 14 is 513.1379310344828
1919.1206896551723
Best chromosome for g = 303 is center 15 is 197.89423076923077
2256.7403846153848
Best chromosome for g = 303 is center 16 is 788.3921568627451
2290.8627450980393
Best chromosome for g = 303 is center 17 is 1050.3818181818183
1907.9454545454546
Best chromosome for g = 303 is center 18 is 1820.5777777777778
697.4444444444445
Best chromosome for g = 303 is center 19 is 1512.173076923077
1190.6538461538462
Best chromosome for g = 303 is center 20 is 2225.0377358490564
691.7924528301887
Best chromosome for g = 303 is center 21 is 2065.1428571428573
1202.2142857142858
Best chromosome for g = 303 is center 22 is 1655.566037735849
1571.245283018868
Best chromosome for g = 303 is center 23 is 1595.7636363636364
2013.8363636363636
Best chromosome for g = 303 is center 24 is 2645.35 656.05
Best chromosome for g = 303 is center 25 is 2583.721518987342
1214.0759493670887
Best chromosome for g = 303 is center 26 is 2177.810810810811
1700.0675675675675
Best chromosome for g = 303 is center 27 is 2651.15873015873
1671.2063492063492
Best chromosome for g = 303 is center 28 is 165.67676767676767
2709.929292929293
Best chromosome for g = 303 is center 29 is 592.4848484848485
2767.0151515151515

```
Best chromosome for g = 303 is center 30 is 286.758064516129
3275.548387096774
Best chromosome for g = 303 is center 31 is 1297.6909090909091
2363.090909090909
Best chromosome for g = 303 is center 32 is 2187.223880597015
2185.776119402985
Best chromosome for g = 303 is center 33 is 1036.0714285714287
2781.0178571428573
Best chromosome for g = 303 is center 34 is 743.9833333333333
3253.5333333333333
Best chromosome for g = 303 is center 35 is 1580.4035087719299
2786.315789473684
Best chromosome for g = 303 is center 36 is 1815.1052631578948
2365.5263157894738
Best chromosome for g = 303 is center 37 is 2115.5862068965516
2785.103448275862
Best chromosome for g = 303 is center 38 is 2662.3636363636365
2189.4363636363637
Best chromosome for g = 303 is center 39 is 2503.6785714285716
2584.0714285714284
Best chromosome for g = 303 is center 40 is 177.84375 3701.84375
Best chromosome for g = 303 is center 41 is 584.5357142857143
3709.0535714285716
Best chromosome for g = 303 is center 42 is 1230.6923076923076
3184.019230769231
Best chromosome for g = 303 is center 43 is 1704.9666666666667
3231.983333333333
Best chromosome for g = 303 is center 44 is 1012.0 3715.6111111111113
Best chromosome for g = 303 is center 45 is 2189.346153846154
3232.3076923076924
Best chromosome for g = 303 is center 46 is 2593.7021276595747
3078.446808510638
Best chromosome for g = 303 is center 47 is 1484.4242424242425
3716.4545454545455
Best chromosome for g = 303 is center 48 is 1963.8541666666667
3738.4791666666665
Best chromosome for g = 303 is center 49 is 2661.7567567567567
3502.7297297297296
Time Elapsed: 6.6121391E7 Seeding Time: 219.0
The seeding percentage time is : 0.000003
```

TSP-LIB-3038, *k* = 300: Separation, Deterministic

```
Random = 0
Density = 0
Separation = 200
Selection Method = 2
Number of centers = 300
After 0 generations new best SSE for g = 0 is 1.5000705234960256E7
After 1 generations new best SSE for g = 1 is 1.4812444643720474E7
After 2 generations new best SSE for g = 3 is 1.47248183118761E7
After 1 generations new best SSE for g = 4 is 1.4647702684602786E7
After 3 generations new best SSE for g = 7 is 1.4644632664059114E7
After 1 generations new best SSE for g = 8 is 1.4612667780013153E7
After 1 generations new best SSE for g = 9 is 1.4509638413463697E7
After 1 generations new best SSE for g = 10 is 1.4490974901046677E7
After 2 generations new best SSE for g = 12 is 1.4476286182509439E7
After 3 generations new best SSE for g = 15 is 1.4461384415437462E7
After 1 generations new best SSE for g = 16 is 1.4454002327133171E7
After 1 generations new best SSE for g = 17 is 1.4325647400326181E7
After 4 generations new best SSE for g = 21 is 1.432084570678702E7
After 2 generations new best SSE for g = 23 is 1.4218291896666773E7
After 2 generations new best SSE for g = 25 is 1.4214988441868795E7
After 3 generations new best SSE for g = 28 is 1.416935683905656E7
After 2 generations new best SSE for g = 30 is 1.416129869763027E7
After 4 generations new best SSE for g = 34 is 1.4121035761030834E7
After 3 generations new best SSE for g = 37 is 1.4097296972236313E7
After 5 generations new best SSE for g = 42 is 1.4036441968075821E7
After 7 generations new best SSE for g = 49 is 1.3974697561469037E7
After 5 generations new best SSE for g = 54 is 1.3915867228760818E7
After 1 generations new best SSE for g = 55 is 1.3896185853430593E7
After 1 generations new best SSE for g = 56 is 1.3895384790000726E7
After 1 generations new best SSE for g = 57 is 1.3894359462800154E7
After 5 generations new best SSE for g = 62 is 1.3855811267972762E7
After 18 generations new best SSE for g = 80 is 1.3839701289371775E7
After 2 generations new best SSE for g = 82 is 1.381772620582772E7
After 2 generations new best SSE for g = 84 is 1.376877450535157E7
After 15 generations new best SSE for g = 99 is 1.3758889873079322E7
After 1 generations new best SSE for g = 100 is 1.3741112732111132E7
After 4 generations new best SSE for g = 104 is 1.372734741062012E7
After 1 generations new best SSE for g = 105 is 1.3706905462035054E7
After 7 generations new best SSE for g = 112 is 1.3688664041681789E7
After 7 generations new best SSE for g = 119 is 1.3633417312515128E7
After 3 generations new best SSE for g = 122 is 1.3631770428171694E7
After 19 generations new best SSE for g = 141 is 1.3617117753629565E7
After 8 generations new best SSE for g = 149 is 1.3616953578629563E7
After 3 generations new best SSE for g = 152 is 1.3612422933251977E7
After 1 generations new best SSE for g = 153 is 1.3608795975166352E7
After 2 generations new best SSE for g = 155 is 1.3591416487340944E7
After 7 generations new best SSE for g = 162 is 1.3588538062638763E7
After 1 generations new best SSE for g = 163 is 1.3587078079774404E7
After 2 generations new best SSE for g = 165 is 1.3577129809262978E7
After 6 generations new best SSE for g = 171 is 1.3567819619544359E7
After 1 generations new best SSE for g = 172 is 1.3567263457951352E7
After 2 generations new best SSE for g = 174 is 1.3566881893456545E7
After 4 generations new best SSE for g = 178 is 1.3566717718456542E7
After 1 generations new best SSE for g = 179 is 1.3556593950536499E7
```

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After 10 generations new best SSE for g = 189 is 1.35421712241148E7
After 5 generations new best SSE for g = 194 is 1.3537562464818548E7
After 8 generations new best SSE for g = 202 is 1.3524605811255446E7
After 5 generations new best SSE for g = 207 is 1.3520694867382644E7
After 9 generations new best SSE for g = 216 is 1.3505438605570145E7
After 3 generations new best SSE for g = 219 is 1.3491465296616847E7
After 19 generations new best SSE for g = 238 is 1.3484287664055414E7
After 3 generations new best SSE for g = 241 is 1.347806692111083E7
After 10 generations new best SSE for g = 251 is 1.3475757943242906E7
After 2 generations new best SSE for g = 253 is 1.3475593768242903E7
After 2 generations new best SSE for g = 255 is 1.3465719437813625E7
After 2 generations new best SSE for g = 257 is 1.3464214204502482E7
After 10 generations new best SSE for g = 267 is 1.3460600290241728E7
After 1 generations new best SSE for g = 268 is 1.3427512748770226E7
After 27 generations new best SSE for g = 295 is 1.3424879985547155E7
After 6 generations new best SSE for g = 301 is 1.3422648439442052E7
After 1 generations new best SSE for g = 302 is 1.3417807845274195E7
After 3 generations new best SSE for g = 305 is 1.34173751316961E7
After 4 generations new best SSE for g = 309 is 1.3411910882124528E7
After 8 generations new best SSE for g = 317 is 1.33794875786103E7
After 13 generations new best SSE for g = 330 is 1.3377947853638059E7
After 2 generations new best SSE for g = 332 is 1.337664462434513E7
After 25 generations new best SSE for g = 357 is 1.3376120842327159E7
After 10 generations new best SSE for g = 367 is 1.3373548773022862E7
After 15 generations new best SSE for g = 382 is 1.337041238903599E7
After 2 generations new best SSE for g = 384 is 1.3366047540155703E7
After 9 generations new best SSE for g = 393 is 1.336509307623074E7
After 1 generations new best SSE for g = 394 is 1.3363204737579096E7
After 3 generations new best SSE for g = 397 is 1.3346083993209563E7
After 11 generations new best SSE for g = 408 is 1.3345460296492392E7
After 9 generations new best SSE for g = 417 is 1.3332731919236314E7
After 6 generations new best SSE for g = 423 is 1.332846250983461E7
After 8 generations new best SSE for g = 431 is 1.332374622126762E7
After 12 generations new best SSE for g = 443 is 1.3318666791687071E7
After 46 generations new best SSE for g = 489 is 1.3317549909391588E7
After 3 generations new best SSE for g = 492 is 1.3314069263880575E7
After 4 generations new best SSE for g = 496 is 1.3308968511716073E7
After 10 generations new best SSE for g = 506 is 1.330828048021979E7
After 38 generations new best SSE for g = 544 is 1.3308158592082934E7
After 9 generations new best SSE for g = 553 is 1.33072310965931E7
After 4 generations new best SSE for g = 557 is 1.330575485762016E7
After 4 generations new best SSE for g = 561 is 1.3303924433707971E7
After 1 generations new best SSE for g = 562 is 1.330242707992564E7
After 1 generations new best SSE for g = 563 is 1.3301455651603961E7
After 10 generations new best SSE for g = 573 is 1.329908574876235E7
After 4 generations new best SSE for g = 577 is 1.3297526640429018E7
After 11 generations new best SSE for g = 588 is 1.3296695764418915E7
After 1 generations new best SSE for g = 589 is 1.329596847286324E7
After 29 generations new best SSE for g = 618 is 1.3295039567304768E7
After 10 generations new best SSE for g = 628 is 1.3294414661912596E7
After 6 generations new best SSE for g = 634 is 1.3292859278182434E7
After 2 generations new best SSE for g = 636 is 1.32923632213698E7
After 3 generations new best SSE for g = 639 is 1.3290976592154572E7
After 14 generations new best SSE for g = 653 is 1.3290329848379388E7
After 3 generations new best SSE for g = 656 is 1.3288544537956482E7
After 6 generations new best SSE for g = 662 is 1.3288476620834747E7
After 2 generations new best SSE for g = 664 is 1.328735191231546E7
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After 16 generations new best SSE for g = 680 is 1.328679179325118E7
After 4 generations new best SSE for g = 684 is 1.3285623536507932E7
After 7 generations new best SSE for g = 691 is 1.328294958489843E7
After 8 generations new best SSE for g = 699 is 1.3281835716636145E7
After 7 generations new best SSE for g = 706 is 1.3280436144483289E7
After 15 generations new best SSE for g = 721 is 1.3279931915201457E7
After 9 generations new best SSE for g = 730 is 1.327923468107447E7
After 13 generations new best SSE for g = 743 is 1.3279036947838265E7
After 5 generations new best SSE for g = 748 is 1.327719699364246E7
After 9 generations new best SSE for g = 757 is 1.3276436971420238E7
After 38 generations new best SSE for g = 795 is 1.3275986299342314E7
After 14 generations new best SSE for g = 809 is 1.3275313995518364E7
After 16 generations new best SSE for g = 825 is 1.3275289065215327E7
After 8 generations new best SSE for g = 833 is 1.3273834962850584E7
After 10 generations new best SSE for g = 843 is 1.3273810032547547E7
After 7 generations new best SSE for g = 850 is 1.3273320775981888E7
After 6 generations new best SSE for g = 856 is 1.3273084854048274E7
After 5 generations new best SSE for g = 861 is 1.3273059923745237E7
After 8 generations new best SSE for g = 869 is 1.3272034729481163E7
After 37 generations new best SSE for g = 906 is 1.3271846196472507E7
Best SSE for g = 1006 is 1.3271846196472507E7
Best chromosome for g = 1006 is center 0 is 31.5 90.33333333333333
Best chromosome for g = 1006 is center 1 is 173.0 136.6
Best chromosome for g = 1006 is center 2 is 326.0 135.125
Best chromosome for g = 1006 is center 3 is 482.625 151.5
Best chromosome for g = 1006 is center 4 is 674.2727272727273 128.72727272727272
Best chromosome for g = 1006 is center 5 is 45.0 353.4
Best chromosome for g = 1006 is center 6 is 173.77777777777777 300.77777777777777
Best chromosome for g = 1006 is center 7 is 313.8888888888889 311.6666666666667
Best chromosome for g = 1006 is center 8 is 497.45454545454544 310.54545454545456
Best chromosome for g = 1006 is center 9 is 270.57142857142856 493.42857142857144
Best chromosome for g = 1006 is center 10 is 46.6 577.8
Best chromosome for g = 1006 is center 11 is 447.7142857142857 485.2857142857143
Best chromosome for g = 1006 is center 12 is 693.3636363636364 322.54545454545456
Best chromosome for g = 1006 is center 13 is 480.6666666666667 656.5555555555555
Best chromosome for g = 1006 is center 14 is 93.28571428571429 787.5714285714286
Best chromosome for g = 1006 is center 15 is 255.4 706.3
Best chromosome for g = 1006 is center 16 is 76.16666666666667 1048.0833333333333
Best chromosome for g = 1006 is center 17 is 272.625 864.0
Best chromosome for g = 1006 is center 18 is 205.9 1037.3
Best chromosome for g = 1006 is center 19 is 439.09090909090907 797.0909090909091
Best chromosome for g = 1006 is center 20 is 80.21052631578948 1197.2105263157894
Best chromosome for g = 1006 is center 21 is 640.7142857142857 583.8571428571429
Best chromosome for g = 1006 is center 22 is 523.5714285714286 970.0
Best chromosome for g = 1006 is center 23 is 674.1 838.2
Best chromosome for g = 1006 is center 24 is 99.41176470588235 1326.235294117647
Best chromosome for g = 1006 is center 25 is 81.22222222222223 1462.1666666666667
Best chromosome for g = 1006 is center 26 is 53.333333333333336
1727.5833333333333
Best chromosome for g = 1006 is center 27 is 23.25 1979.5
Best chromosome for g = 1006 is center 28 is 96.22222222222223 1606.7777777777778
Best chromosome for g = 1006 is center 29 is 171.0 1800.625
Best chromosome for g = 1006 is center 30 is 310.92857142857144
1204.7142857142858
Best chromosome for g = 1006 is center 31 is 468.9166666666667 1112.3333333333333
Best chromosome for g = 1006 is center 32 is 690.0 1152.1818181818182
Best chromosome for g = 1006 is center 33 is 476.0 1268.076923076923
```

```
Best chromosome for g = 1006 is center 34 is 286.53846153846155
1401.3846153846155
Best chromosome for g = 1006 is center 35 is 471.5 1421.8333333333333
Best chromosome for g = 1006 is center 36 is 297.44444444444446 1570.111111111111
Best chromosome for g = 1006 is center 37 is 300.75 1724.0
Best chromosome for g = 1006 is center 38 is 455.7 1626.6
Best chromosome for g = 1006 is center 39 is 662.8888888888889 1332.7777777777778
Best chromosome for g = 1006 is center 40 is 639.8888888888889 1537.0
Best chromosome for g = 1006 is center 41 is 60.57142857142857 2193.0
Best chromosome for g = 1006 is center 42 is 318.0 1888.1818181818182
Best chromosome for g = 1006 is center 43 is 469.54545454545456 1821.0
Best chromosome for g = 1006 is center 44 is 177.41666666666666
2095.3333333333335
Best chromosome for g = 1006 is center 45 is 344.15384615384613
2068.3076923076924
Best chromosome for g = 1006 is center 46 is 168.0 2256.0
Best chromosome for g = 1006 is center 47 is 56.15384615384615 2352.923076923077
Best chromosome for g = 1006 is center 48 is 330.0 2215.3846153846152
Best chromosome for g = 1006 is center 49 is 52.333333333333336 2499.75
Best chromosome for g = 1006 is center 50 is 175.83333333333334
2414.1666666666665
Best chromosome for g = 1006 is center 51 is 146.08333333333334
2590.8333333333335
Best chromosome for g = 1006 is center 52 is 607.0 1712.0
Best chromosome for g = 1006 is center 53 is 675.0833333333334 1887.1666666666667
Best chromosome for g = 1006 is center 54 is 576.5833333333334 2063.4166666666665
Best chromosome for g = 1006 is center 55 is 621.3 2204.7
Best chromosome for g = 1006 is center 56 is 455.7142857142857 2369.714285714286
Best chromosome for g = 1006 is center 57 is 322.0 2371.5
Best chromosome for g = 1006 is center 58 is 630.0 2383.8888888888887
Best chromosome for g = 1006 is center 59 is 43.38461538461539 2679.6923076923076
Best chromosome for g = 1006 is center 60 is 56.083333333333336
2852.5833333333335
Best chromosome for g = 1006 is center 61 is 159.30769230769232 2742.769230769231
Best chromosome for g = 1006 is center 62 is 327.5 2573.75
Best chromosome for g = 1006 is center 63 is 497.625 2606.75
Best chromosome for g = 1006 is center 64 is 625.6 2599.7
Best chromosome for g = 1006 is center 65 is 310.77777777777777
2738.5555555555557
Best chromosome for g = 1006 is center 66 is 533.6666666666666 2766.1666666666665
Best chromosome for g = 1006 is center 67 is 708.3333333333334 2741.9166666666665
Best chromosome for g = 1006 is center 68 is 173.0 2893.8
Best chromosome for g = 1006 is center 69 is 300.25 2890.25
Best chromosome for g = 1006 is center 70 is 487.5 2941.6
Best chromosome for g = 1006 is center 71 is 664.2857142857143 2899.714285714286
Best chromosome for g = 1006 is center 72 is 116.45454545454545
3174.7272727272725
Best chromosome for g = 1006 is center 73 is 319.25 3136.625
Best chromosome for g = 1006 is center 74 is 516.2727272727273 3160.7272727272725
Best chromosome for g = 1006 is center 75 is 150.44444444444446 3344.777777777778
Best chromosome for g = 1006 is center 76 is 312.3333333333333 3290.5
Best chromosome for g = 1006 is center 77 is 708.5714285714286 3110.4285714285716
Best chromosome for g = 1006 is center 78 is 695.3636363636364 3262.5454545454545
Best chromosome for g = 1006 is center 79 is 517.5833333333334 3348.1666666666665
Best chromosome for g = 1006 is center 80 is 121.41666666666667
3520.9166666666665
```

```
Best chromosome for g = 1006 is center 81 is 334.61538461538464
3484.3076923076924
Best chromosome for g = 1006 is center 82 is 108.35714285714286 3666.214285714286
Best chromosome for g = 1006 is center 83 is 324.6363636363636 3647.6363636363635
Best chromosome for g = 1006 is center 84 is 87.4 3849.0666666666666
Best chromosome for g = 1006 is center 85 is 295.0 3814.7272727272725
Best chromosome for g = 1006 is center 86 is 702.25 3428.625
Best chromosome for g = 1006 is center 87 is 511.5 3552.0
Best chromosome for g = 1006 is center 88 is 494.3636363636364 3711.0
Best chromosome for g = 1006 is center 89 is 714.5 3601.4166666666665
Best chromosome for g = 1006 is center 90 is 504.25 3860.0
Best chromosome for g = 1006 is center 91 is 708.0 3794.4545454545455
Best chromosome for g = 1006 is center 92 is 871.25 129.83333333333334
Best chromosome for g = 1006 is center 93 is 1080.5 150.16666666666666
Best chromosome for g = 1006 is center 94 is 1275.2 108.8
Best chromosome for g = 1006 is center 95 is 882.7 313.7
Best chromosome for g = 1006 is center 96 is 1128.909090909091 345.09090909090907
Best chromosome for g = 1006 is center 97 is 984.8333333333334 511.3333333333333
Best chromosome for g = 1006 is center 98 is 888.9 671.7
Best chromosome for g = 1006 is center 99 is 889.4545454545455 873.0909090909091
Best chromosome for g = 1006 is center 100 is 1710.5555555555557 112.0
Best chromosome for g = 1006 is center 101 is 2114.375 113.625
Best chromosome for g = 1006 is center 102 is 2300.0 137.3846153846154
Best chromosome for g = 1006 is center 103 is 2478.1111111111113 100.0
Best chromosome for g = 1006 is center 104 is 2668.1428571428573
47.857142857142854
Best chromosome for g = 1006 is center 105 is 1455.3333333333333
133.91666666666666
Best chromosome for g = 1006 is center 106 is 1298.3076923076924
269.3076923076923
Best chromosome for g = 1006 is center 107 is 1492.923076923077
285.46153846153845
Best chromosome for g = 1006 is center 108 is 1108.8181818181818
596.6363636363636
Best chromosome for g = 1006 is center 109 is 1299.3333333333333
529.7777777777778
Best chromosome for g = 1006 is center 110 is 1462.2727272727273
533.5454545454545
Best chromosome for g = 1006 is center 111 is 1093.2727272727273
752.1818181818181
Best chromosome for g = 1006 is center 112 is 1289.6 661.7
Best chromosome for g = 1006 is center 113 is 1054.8333333333333 917.0
Best chromosome for g = 1006 is center 114 is 1514.2222222222222
690.8888888888889
Best chromosome for g = 1006 is center 115 is 1279.4444444444443
828.5555555555555
Best chromosome for g = 1006 is center 116 is 1467.142857142857 828.5714285714286
Best chromosome for g = 1006 is center 117 is 1199.5 1018.375
Best chromosome for g = 1006 is center 118 is 852.2 1109.4
Best chromosome for g = 1006 is center 119 is 835.0909090909091 1291.909090909091
Best chromosome for g = 1006 is center 120 is 1037.25 1142.4166666666667
Best chromosome for g = 1006 is center 121 is 1200.5454545454545
1194.8181818181818
Best chromosome for g = 1006 is center 122 is 1421.857142857143
1064.5714285714287
Best chromosome for g = 1006 is center 123 is 1892.2307692307693 148.0
```

Best chromosome for g = 1006 is center 124 is 1687.8181818181818
257.45454545454544
Best chromosome for g = 1006 is center 125 is 1903.111111111111
294.77777777777777
Best chromosome for g = 1006 is center 126 is 2109.9 259.8
Best chromosome for g = 1006 is center 127 is 1760.0 433.1666666666667
Best chromosome for g = 1006 is center 128 is 2293.7 287.5
Best chromosome for g = 1006 is center 129 is 2506.1666666666665 239.0
Best chromosome for g = 1006 is center 130 is 2668.0 206.16666666666666
Best chromosome for g = 1006 is center 131 is 2095.4285714285716 470.0
Best chromosome for g = 1006 is center 132 is 2431.6666666666665
391.1666666666667
Best chromosome for g = 1006 is center 133 is 1697.2222222222222
601.6666666666666
Best chromosome for g = 1006 is center 134 is 1908.4 585.1
Best chromosome for g = 1006 is center 135 is 1680.75 750.125
Best chromosome for g = 1006 is center 136 is 1895.8333333333333
748.0833333333334
Best chromosome for g = 1006 is center 137 is 2273.9 510.7
Best chromosome for g = 1006 is center 138 is 2116.75 647.5
Best chromosome for g = 1006 is center 139 is 1911.3333333333333
979.6666666666666
Best chromosome for g = 1006 is center 140 is 2136.6666666666665
843.6666666666666
Best chromosome for g = 1006 is center 141 is 1727.125 1076.5
Best chromosome for g = 1006 is center 142 is 2612.75 383.0
Best chromosome for g = 1006 is center 143 is 2302.5 697.0
Best chromosome for g = 1006 is center 144 is 2515.75 576.1666666666666
Best chromosome for g = 1006 is center 145 is 2371.3333333333335
884.1666666666666
Best chromosome for g = 1006 is center 146 is 2527.0 780.3333333333334
Best chromosome for g = 1006 is center 147 is 1039.5454545454545
1331.909090909091
Best chromosome for g = 1006 is center 148 is 817.5 1547.8
Best chromosome for g = 1006 is center 149 is 1049.4545454545455
1491.2727272727273
Best chromosome for g = 1006 is center 150 is 1214.3 1351.2
Best chromosome for g = 1006 is center 151 is 1386.8 1197.6
Best chromosome for g = 1006 is center 152 is 1578.111111111111 1161.888888888889
Best chromosome for g = 1006 is center 153 is 2067.6666666666665
1060.3333333333333
Best chromosome for g = 1006 is center 154 is 1910.0 1184.5833333333333
Best chromosome for g = 1006 is center 155 is 2160.6666666666665
1164.888888888889
Best chromosome for g = 1006 is center 156 is 1403.125 1346.625
Best chromosome for g = 1006 is center 157 is 844.0909090909091 1868.0
Best chromosome for g = 1006 is center 158 is 996.2 1664.0
Best chromosome for g = 1006 is center 159 is 994.875 1896.625
Best chromosome for g = 1006 is center 160 is 1254.0 1517.0
Best chromosome for g = 1006 is center 161 is 1560.1666666666667 1321.5
Best chromosome for g = 1006 is center 162 is 780.8333333333334 2120.0
Best chromosome for g = 1006 is center 163 is 920.4166666666666
2079.0833333333335
Best chromosome for g = 1006 is center 164 is 1418.1 1599.7
Best chromosome for g = 1006 is center 165 is 1176.3636363636363
1876.090909090909

Best chromosome for g = 1006 is center 166 is 1548.4444444444443 1537.7777777777778
Best chromosome for g = 1006 is center 167 is 1738.875 1318.25
Best chromosome for g = 1006 is center 168 is 1704.909090909091 1517.7272727272727
Best chromosome for g = 1006 is center 169 is 1917.7 1374.7
Best chromosome for g = 1006 is center 170 is 2301.8333333333335 1103.9166666666667
Best chromosome for g = 1006 is center 171 is 2096.4615384615386 1304.923076923077
Best chromosome for g = 1006 is center 172 is 1712.1666666666667 1700.8333333333333
Best chromosome for g = 1006 is center 173 is 2002.1818181818182 1611.2727272727273
Best chromosome for g = 1006 is center 174 is 1877.25 1605.625
Best chromosome for g = 1006 is center 175 is 2313.1666666666665 1272.9166666666667
Best chromosome for g = 1006 is center 176 is 2196.6 1535.3
Best chromosome for g = 1006 is center 177 is 913.8181818181819 2277.5454545454545
Best chromosome for g = 1006 is center 178 is 1153.111111111111 2051.0
Best chromosome for g = 1006 is center 179 is 1371.888888888889 1844.5555555555557
Best chromosome for g = 1006 is center 180 is 894.7 2458.6
Best chromosome for g = 1006 is center 181 is 1193.4545454545455 2190.7272727272725
Best chromosome for g = 1006 is center 182 is 1191.4 2329.1
Best chromosome for g = 1006 is center 183 is 1586.3636363636363 1858.1818181818182
Best chromosome for g = 1006 is center 184 is 1776.125 1962.0
Best chromosome for g = 1006 is center 185 is 1905.125 1769.25
Best chromosome for g = 1006 is center 186 is 1440.2222222222222 2060.6666666666665
Best chromosome for g = 1006 is center 187 is 1637.4545454545455 2076.181818181818
Best chromosome for g = 1006 is center 188 is 1456.4 2217.2
Best chromosome for g = 1006 is center 189 is 2174.875 1694.5
Best chromosome for g = 1006 is center 190 is 2035.7777777777778 1852.4444444444443
Best chromosome for g = 1006 is center 191 is 2189.2 1858.8
Best chromosome for g = 1006 is center 192 is 1182.25 2503.0
Best chromosome for g = 1006 is center 193 is 1428.0 2368.25
Best chromosome for g = 1006 is center 194 is 1629.1818181818182 2270.7272727272725
Best chromosome for g = 1006 is center 195 is 1820.9 2160.6
Best chromosome for g = 1006 is center 196 is 2008.8 2094.7
Best chromosome for g = 1006 is center 197 is 1808.5 2334.8
Best chromosome for g = 1006 is center 198 is 2178.6 2095.4
Best chromosome for g = 1006 is center 199 is 1980.5454545454545 2263.181818181818
Best chromosome for g = 1006 is center 200 is 915.7692307692307 2668.3846153846152
Best chromosome for g = 1006 is center 201 is 1640.0 2461.222222222222
Best chromosome for g = 1006 is center 202 is 1979.5555555555557 2404.5555555555557
Best chromosome for g = 1006 is center 203 is 1439.3333333333333 2549.6666666666665

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Best chromosome for g = 1006 is center 204 is 896.9 2853.6
Best chromosome for g = 1006 is center 205 is 1116.0 2724.6
Best chromosome for g = 1006 is center 206 is 1324.0 2729.5833333333335
Best chromosome for g = 1006 is center 207 is 1109.9 2871.0
Best chromosome for g = 1006 is center 208 is 917.3636363636364 3049.090909090909
Best chromosome for g = 1006 is center 209 is 883.5 3243.75
Best chromosome for g = 1006 is center 210 is 1530.8333333333333
2722.1666666666665
Best chromosome for g = 1006 is center 211 is 1527.2222222222222
2875.222222222222
Best chromosome for g = 1006 is center 212 is 1316.5454545454545
2925.5454545454545
Best chromosome for g = 1006 is center 213 is 1129.1818181818182
3118.818181818182
Best chromosome for g = 1006 is center 214 is 1315.8181818181818
3144.5454545454545
Best chromosome for g = 1006 is center 215 is 1510.888888888889 3096.0
Best chromosome for g = 1006 is center 216 is 1827.75 2491.875
Best chromosome for g = 1006 is center 217 is 1746.0 2742.0
Best chromosome for g = 1006 is center 218 is 2508.6 1042.1
Best chromosome for g = 1006 is center 219 is 2506.1 1212.9
Best chromosome for g = 1006 is center 220 is 2485.0 1377.5833333333333
Best chromosome for g = 1006 is center 221 is 2361.714285714286 1504.0
Best chromosome for g = 1006 is center 222 is 2348.5 1656.625
Best chromosome for g = 1006 is center 223 is 2345.6 1825.2
Best chromosome for g = 1006 is center 224 is 1103.4 3280.7
Best chromosome for g = 1006 is center 225 is 939.1428571428571 3449.0
Best chromosome for g = 1006 is center 226 is 1312.9166666666667
3314.3333333333335
Best chromosome for g = 1006 is center 227 is 905.0 3667.5454545454545
Best chromosome for g = 1006 is center 228 is 1110.090909090909
3597.7272727272725
Best chromosome for g = 1006 is center 229 is 2521.6 1637.9
Best chromosome for g = 1006 is center 230 is 2527.8 1827.5
Best chromosome for g = 1006 is center 231 is 2337.8888888888887
2059.4444444444443
Best chromosome for g = 1006 is center 232 is 2169.75 2260.8333333333335
Best chromosome for g = 1006 is center 233 is 2327.090909090909 2231.181818181818
Best chromosome for g = 1006 is center 234 is 2181.3333333333335
2408.6666666666665
Best chromosome for g = 1006 is center 235 is 1958.2727272727273
2661.7272727272725
Best chromosome for g = 1006 is center 236 is 1752.5 2909.5
Best chromosome for g = 1006 is center 237 is 1723.7272727272727
3112.3636363636365
Best chromosome for g = 1006 is center 238 is 1949.8 2856.0
Best chromosome for g = 1006 is center 239 is 1537.8 3256.5
Best chromosome for g = 1006 is center 240 is 1444.6666666666667
3551.4444444444443
Best chromosome for g = 1006 is center 241 is 1291.0 3631.0833333333335
Best chromosome for g = 1006 is center 242 is 2510.222222222222
2039.5555555555557
Best chromosome for g = 1006 is center 243 is 2158.3636363636365
2635.090909090909
Best chromosome for g = 1006 is center 244 is 2357.8888888888887
2420.777777777778
Best chromosome for g = 1006 is center 245 is 2347.0 2618.5
```

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Best chromosome for g = 1006 is center 246 is 1946.1 3125.5
Best chromosome for g = 1006 is center 247 is 1760.1666666666667
3286.8333333333335
Best chromosome for g = 1006 is center 248 is 1633.6666666666667
3413.222222222222
Best chromosome for g = 1006 is center 249 is 1964.75 3327.75
Best chromosome for g = 1006 is center 250 is 1625.7777777777778
3611.777777777778
Best chromosome for g = 1006 is center 251 is 1762.7777777777778
3673.3333333333335
Best chromosome for g = 1006 is center 252 is 2152.1111111111113
2798.3333333333335
Best chromosome for g = 1006 is center 253 is 2126.3333333333335
2960.777777777778
Best chromosome for g = 1006 is center 254 is 2323.6666666666665
2759.1111111111113
Best chromosome for g = 1006 is center 255 is 2334.0 2925.5555555555557
Best chromosome for g = 1006 is center 256 is 2145.6 3146.9
Best chromosome for g = 1006 is center 257 is 2334.6363636363635
3137.7272727272725
Best chromosome for g = 1006 is center 258 is 2332.625 3290.625
Best chromosome for g = 1006 is center 259 is 2140.3333333333335
3311.777777777778
Best chromosome for g = 1006 is center 260 is 1941.0 3641.0
Best chromosome for g = 1006 is center 261 is 2108.3333333333335
3646.3333333333335
Best chromosome for g = 1006 is center 262 is 2391.5 3435.3333333333335
Best chromosome for g = 1006 is center 263 is 2810.8 114.9
Best chromosome for g = 1006 is center 264 is 2810.8 307.7
Best chromosome for g = 1006 is center 265 is 2744.125 546.875
Best chromosome for g = 1006 is center 266 is 2746.3571428571427
727.3571428571429
Best chromosome for g = 1006 is center 267 is 2710.875 999.375
Best chromosome for g = 1006 is center 268 is 2639.5 1221.8
Best chromosome for g = 1006 is center 269 is 2789.0 1180.0
Best chromosome for g = 1006 is center 270 is 2635.0 1517.375
Best chromosome for g = 1006 is center 271 is 2773.909090909091
1376.1818181818182
Best chromosome for g = 1006 is center 272 is 2661.0 1745.6
Best chromosome for g = 1006 is center 273 is 2773.7272727272725
1582.6363636363637
Best chromosome for g = 1006 is center 274 is 2780.7 1777.7
Best chromosome for g = 1006 is center 275 is 2525.1 2220.5
Best chromosome for g = 1006 is center 276 is 2709.6 2059.8
Best chromosome for g = 1006 is center 277 is 2748.0 2204.4615384615386
Best chromosome for g = 1006 is center 278 is 2511.8888888888887
2456.4444444444443
Best chromosome for g = 1006 is center 279 is 2751.3076923076924 2354.0
Best chromosome for g = 1006 is center 280 is 2508.75 2601.25
Best chromosome for g = 1006 is center 281 is 2709.714285714286
2493.4285714285716
Best chromosome for g = 1006 is center 282 is 2493.777777777778
2782.8888888888887
Best chromosome for g = 1006 is center 283 is 2693.1666666666665 2655.5
Best chromosome for g = 1006 is center 284 is 2511.8571428571427
2987.714285714286
```

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Best chromosome for g = 1006 is center 285 is 2677.8571428571427
2916.4285714285716
Best chromosome for g = 1006 is center 286 is 2550.230769230769
3159.5384615384614
Best chromosome for g = 1006 is center 287 is 2557.0714285714284 3357.0
Best chromosome for g = 1006 is center 288 is 2762.0 3144.5454545454545
Best chromosome for g = 1006 is center 289 is 2781.777777777778
3350.4444444444443
Best chromosome for g = 1006 is center 290 is 2793.3333333333335
3517.3333333333335
Best chromosome for g = 1006 is center 291 is 886.0769230769231
3825.4615384615386
Best chromosome for g = 1006 is center 292 is 1122.357142857143 3801.714285714286
Best chromosome for g = 1006 is center 293 is 1346.142857142857
3820.1428571428573
Best chromosome for g = 1006 is center 294 is 1533.2307692307693
3780.076923076923
Best chromosome for g = 1006 is center 295 is 1708.6363636363637
3852.6363636363635
Best chromosome for g = 1006 is center 296 is 1954.2666666666667
3826.5333333333333
Best chromosome for g = 1006 is center 297 is 2142.3333333333335 3825.5
Best chromosome for g = 1006 is center 298 is 2444.5 3754.0
Best chromosome for g = 1006 is center 299 is 2733.1666666666665
3877.8333333333335
Time Elapsed: 2.5010369E8 Seeding Time: 24181.0
The seeding percentage time is : 0.000097
```

TSP-LIB-3038, *k* = 350: Separation, Deterministic

```
Random = 0
Density = 0
Separation = 200
Selection Method = 2
Number of centers = 350
After 0 generations new best SSE for g = 0 is 1.251340513795089E7
After 1 generations new best SSE for g = 1 is 1.2455660880846795E7
After 1 generations new best SSE for g = 2 is 1.236948390644204E7
After 1 generations new best SSE for g = 3 is 1.224641706970945E7
After 5 generations new best SSE for g = 8 is 1.2237674952628763E7
After 1 generations new best SSE for g = 9 is 1.2160810744895378E7
After 2 generations new best SSE for g = 11 is 1.2128120050603032E7
After 4 generations new best SSE for g = 15 is 1.212638003653376E7
After 1 generations new best SSE for g = 16 is 1.2103522358998666E7
After 1 generations new best SSE for g = 17 is 1.2052985474089777E7
After 2 generations new best SSE for g = 19 is 1.2004063354736941E7
After 4 generations new best SSE for g = 23 is 1.1994926944777425E7
After 1 generations new best SSE for g = 24 is 1.195571869151127E7
After 1 generations new best SSE for g = 25 is 1.1855669237185027E7
After 2 generations new best SSE for g = 27 is 1.182953070309412E7
After 8 generations new best SSE for g = 35 is 1.1807231953768453E7
After 4 generations new best SSE for g = 39 is 1.1749421785642147E7
After 2 generations new best SSE for g = 41 is 1.173233745630759E7
After 7 generations new best SSE for g = 48 is 1.1726158282561854E7
After 1 generations new best SSE for g = 49 is 1.172571201573984E7
After 2 generations new best SSE for g = 51 is 1.1710644358262602E7
After 2 generations new best SSE for g = 53 is 1.1699298501584563E7
After 1 generations new best SSE for g = 54 is 1.1685288697990887E7
After 1 generations new best SSE for g = 55 is 1.1639360607228898E7
After 1 generations new best SSE for g = 56 is 1.1638181317257736E7
After 5 generations new best SSE for g = 61 is 1.1627470123862246E7
After 4 generations new best SSE for g = 65 is 1.1611134240001675E7
After 1 generations new best SSE for g = 66 is 1.1582791717324352E7
After 3 generations new best SSE for g = 69 is 1.1542269634651482E7
After 8 generations new best SSE for g = 77 is 1.1538097035295283E7
After 8 generations new best SSE for g = 85 is 1.1532197084687551E7
After 3 generations new best SSE for g = 88 is 1.152888870612446E7
After 7 generations new best SSE for g = 95 is 1.1508213985941833E7
After 5 generations new best SSE for g = 100 is 1.14932859809178E7
After 1 generations new best SSE for g = 101 is 1.1491268746393519E7
After 1 generations new best SSE for g = 102 is 1.1479103647949284E7
After 1 generations new best SSE for g = 103 is 1.1470216702589078E7
After 1 generations new best SSE for g = 104 is 1.146328964300422E7
After 13 generations new best SSE for g = 117 is 1.1463156129548233E7
After 3 generations new best SSE for g = 120 is 1.1446715316985795E7
After 1 generations new best SSE for g = 121 is 1.1389136273451526E7
After 7 generations new best SSE for g = 128 is 1.1382337008585868E7
After 1 generations new best SSE for g = 129 is 1.1380948853030307E7
After 9 generations new best SSE for g = 138 is 1.135642518385502E7
After 6 generations new best SSE for g = 144 is 1.1349985094966136E7
After 10 generations new best SSE for g = 154 is 1.1348322850591103E7
After 5 generations new best SSE for g = 159 is 1.1337877817723962E7
```

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After 4 generations new best SSE for g = 163 is 1.1321981215409592E7
After 14 generations new best SSE for g = 177 is 1.1314492744866244E7
After 5 generations new best SSE for g = 182 is 1.1314294969344553E7
After 2 generations new best SSE for g = 184 is 1.1313714278055277E7
After 1 generations new best SSE for g = 185 is 1.131202751875902E7
After 4 generations new best SSE for g = 189 is 1.1272844904251318E7
After 8 generations new best SSE for g = 197 is 1.1267937877705658E7
After 13 generations new best SSE for g = 210 is 1.1258575901443036E7
After 13 generations new best SSE for g = 223 is 1.1236133858319448E7
After 7 generations new best SSE for g = 230 is 1.1230669762090694E7
After 5 generations new best SSE for g = 235 is 1.1229373105921857E7
After 2 generations new best SSE for g = 237 is 1.1213034509343445E7
After 22 generations new best SSE for g = 259 is 1.1211646673681896E7
After 2 generations new best SSE for g = 261 is 1.120518747428403E7
After 9 generations new best SSE for g = 270 is 1.120231999511599E7
After 16 generations new best SSE for g = 286 is 1.1201092851426356E7
After 1 generations new best SSE for g = 287 is 1.1192056368306698E7
After 5 generations new best SSE for g = 292 is 1.1183248182378734E7
After 3 generations new best SSE for g = 295 is 1.1166796681135524E7
After 11 generations new best SSE for g = 306 is 1.1164917872097338E7
After 6 generations new best SSE for g = 312 is 1.1153761359698633E7
After 3 generations new best SSE for g = 315 is 1.1152898118481515E7
After 12 generations new best SSE for g = 327 is 1.1152019381576752E7
After 13 generations new best SSE for g = 340 is 1.1147393949222991E7
After 18 generations new best SSE for g = 358 is 1.1130265159057608E7
After 5 generations new best SSE for g = 363 is 1.1126587943334438E7
After 21 generations new best SSE for g = 384 is 1.1122800517399255E7
After 17 generations new best SSE for g = 401 is 1.1122027146270381E7
After 4 generations new best SSE for g = 405 is 1.1122027034015985E7
After 1 generations new best SSE for g = 406 is 1.1120910045007765E7
After 5 generations new best SSE for g = 411 is 1.1113587153160717E7
After 7 generations new best SSE for g = 418 is 1.111321523286991E7
After 5 generations new best SSE for g = 423 is 1.1108612552788861E7
After 11 generations new best SSE for g = 434 is 1.1107603739738028E7
After 9 generations new best SSE for g = 443 is 1.1106368963492068E7
After 4 generations new best SSE for g = 447 is 1.110157338524808E7
After 3 generations new best SSE for g = 450 is 1.110013086392216E7
After 1 generations new best SSE for g = 451 is 1.1100076316844236E7
After 18 generations new best SSE for g = 469 is 1.1099571961288681E7
After 9 generations new best SSE for g = 478 is 1.1098479722286044E7
After 2 generations new best SSE for g = 480 is 1.1094022109293506E7
After 1 generations new best SSE for g = 481 is 1.1088178567374317E7
After 11 generations new best SSE for g = 492 is 1.1084593132949023E7
After 2 generations new best SSE for g = 494 is 1.1083753678259263E7
After 4 generations new best SSE for g = 498 is 1.1079424845465649E7
After 6 generations new best SSE for g = 504 is 1.1077869061444107E7
After 6 generations new best SSE for g = 510 is 1.1074773820571093E7
After 12 generations new best SSE for g = 522 is 1.1074197251703847E7
After 6 generations new best SSE for g = 528 is 1.1073274354481623E7
After 8 generations new best SSE for g = 536 is 1.1068939727056284E7
After 3 generations new best SSE for g = 539 is 1.1068768858513718E7
After 8 generations new best SSE for g = 547 is 1.1067845961291494E7
After 23 generations new best SSE for g = 570 is 1.106407379628984E7
After 11 generations new best SSE for g = 581 is 1.106283649628984E7
```

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After 6 generations new best SSE for g = 587 is 1.1056099622416502E7
After 5 generations new best SSE for g = 592 is 1.1052582435661588E7
After 23 generations new best SSE for g = 615 is 1.1052369033280635E7
After 6 generations new best SSE for g = 621 is 1.1052150138675222E7
After 2 generations new best SSE for g = 623 is 1.1050313209634814E7
After 10 generations new best SSE for g = 633 is 1.1049714707478646E7
After 2 generations new best SSE for g = 635 is 1.1045866712423718E7
After 20 generations new best SSE for g = 655 is 1.1042983432803337E7
After 16 generations new best SSE for g = 671 is 1.1042003609282412E7
After 14 generations new best SSE for g = 685 is 1.1040995298470981E7
After 15 generations new best SSE for g = 700 is 1.1039924264466086E7
After 3 generations new best SSE for g = 703 is 1.1039412044264086E7
After 12 generations new best SSE for g = 715 is 1.103801570418472E7
After 15 generations new best SSE for g = 730 is 1.1037393526798215E7
After 17 generations new best SSE for g = 747 is 1.10360345909646E7
After 4 generations new best SSE for g = 751 is 1.1035054767443677E7
After 9 generations new best SSE for g = 760 is 1.1033235258635836E7
After 22 generations new best SSE for g = 782 is 1.1031574901695536E7
After 2 generations new best SSE for g = 784 is 1.1031438521139983E7
After 4 generations new best SSE for g = 788 is 1.1030927045901334E7
After 17 generations new best SSE for g = 805 is 1.1028075270687653E7
After 8 generations new best SSE for g = 813 is 1.1027800529020982E7
After 5 generations new best SSE for g = 818 is 1.1026470351831498E7
After 17 generations new best SSE for g = 835 is 1.1026174903169068E7
After 23 generations new best SSE for g = 858 is 1.1024975654487187E7
After 22 generations new best SSE for g = 880 is 1.1024584354337325E7
After 14 generations new best SSE for g = 894 is 1.102064335043568E7
After 38 generations new best SSE for g = 932 is 1.1020446822297156E7
After 13 generations new best SSE for g = 945 is 1.1019548417848825E7
After 5 generations new best SSE for g = 950 is 1.1019435119594283E7
After 1 generations new best SSE for g = 951 is 1.1019268423801208E7
After 2 generations new best SSE for g = 953 is 1.101920865137363E7
After 5 generations new best SSE for g = 958 is 1.1019176716009004E7
After 5 generations new best SSE for g = 963 is 1.1018230701739928E7
After 14 generations new best SSE for g = 977 is 1.101820850454824E7
After 11 generations new best SSE for g = 988 is 1.1018198699131446E7
After 4 generations new best SSE for g = 992 is 1.1017678310664337E7
After 3 generations new best SSE for g = 995 is 1.1017000018478757E7
After 5 generations new best SSE for g = 1000 is 1.101697508817572E7
After 7 generations new best SSE for g = 1007 is 1.1016946019613717E7
After 23 generations new best SSE for g = 1030 is 1.1016677618820066E7
After 8 generations new best SSE for g = 1038 is 1.1016390899822406E7
After 9 generations new best SSE for g = 1047 is 1.1016043270637698E7
After 12 generations new best SSE for g = 1059 is 1.1015659911907539E7
After 49 generations new best SSE for g = 1108 is 1.1015099201809302E7
After 1 generations new best SSE for g = 1109 is 1.1015074271506265E7
After 5 generations new best SSE for g = 1114 is 1.1014999750727044E7
After 32 generations new best SSE for g = 1146 is 1.1014797619369518E7
After 42 generations new best SSE for g = 1188 is 1.1014488765334662E7
After 3 generations new best SSE for g = 1191 is 1.1014434078574207E7
After 1 generations new best SSE for g = 1192 is 1.101436773668553E7
After 21 generations new best SSE for g = 1213 is 1.101429430674881E7
After 9 generations new best SSE for g = 1222 is 1.101412334700855E7
After 9 generations new best SSE for g = 1231 is 1.1014059565334665E7
```

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After 15 generations new best SSE for g = 1246 is 1.1013813392066268E7
After 49 generations new best SSE for g = 1295 is 1.1013677456426902E7
Best SSE for g = 1395 is 1.1013677456426902E7
Best chromosome for g = 1395 is center 0 is 31.5 90.33333333333333
Best chromosome for g = 1395 is center 1 is 173.0 136.6
Best chromosome for g = 1395 is center 2 is 173.77777777777777
300.77777777777777
Best chromosome for g = 1395 is center 3 is 45.0 353.4
Best chromosome for g = 1395 is center 4 is 38.77777777777778
570.2222222222222
Best chromosome for g = 1395 is center 5 is 326.0 135.125
Best chromosome for g = 1395 is center 6 is 313.8888888888889
311.6666666666667
Best chromosome for g = 1395 is center 7 is 270.57142857142856
493.42857142857144
Best chromosome for g = 1395 is center 8 is 493.55555555555554
143.44444444444446
Best chromosome for g = 1395 is center 9 is 497.45454545454544
310.54545454545456
Best chromosome for g = 1395 is center 10 is 692.7272727272727
124.27272727272727
Best chromosome for g = 1395 is center 11 is 691.7 311.1
Best chromosome for g = 1395 is center 12 is 447.7142857142857
485.2857142857143
Best chromosome for g = 1395 is center 13 is 178.25 692.0
Best chromosome for g = 1395 is center 14 is 83.2 819.4
Best chromosome for g = 1395 is center 15 is 273.125 823.0
Best chromosome for g = 1395 is center 16 is 378.77777777777777
672.3333333333334
Best chromosome for g = 1395 is center 17 is 637.2 512.0
Best chromosome for g = 1395 is center 18 is 571.25 679.125
Best chromosome for g = 1395 is center 19 is 448.1111111111111
812.7777777777778
Best chromosome for g = 1395 is center 20 is 62.77777777777778
1036.7777777777778
Best chromosome for g = 1395 is center 21 is 233.11111111111111
990.7777777777778
Best chromosome for g = 1395 is center 22 is 132.44444444444446
1110.6666666666667
Best chromosome for g = 1395 is center 23 is 42.5 1192.0
Best chromosome for g = 1395 is center 24 is 544.8333333333334 969.0
Best chromosome for g = 1395 is center 25 is 299.875 1167.25
Best chromosome for g = 1395 is center 26 is 135.16666666666666
1263.0833333333333
Best chromosome for g = 1395 is center 27 is 43.0 1347.3
Best chromosome for g = 1395 is center 28 is 451.44444444444446
1075.111111111111
Best chromosome for g = 1395 is center 29 is 482.7 1200.7
Best chromosome for g = 1395 is center 30 is 319.44444444444446
1279.5555555555557
Best chromosome for g = 1395 is center 31 is 51.07692307692308
1514.5384615384614
Best chromosome for g = 1395 is center 32 is 135.5 1420.9
Best chromosome for g = 1395 is center 33 is 280.4 1423.0
```

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Best chromosome for g = 1395 is center 34 is 120.15384615384616
1616.4615384615386
Best chromosome for g = 1395 is center 35 is 297.44444444444446
1570.111111111111
Best chromosome for g = 1395 is center 36 is 50.0 1720.6153846153845
Best chromosome for g = 1395 is center 37 is 171.0 1800.625
Best chromosome for g = 1395 is center 38 is 300.75 1724.0
Best chromosome for g = 1395 is center 39 is 23.25 1979.5
Best chromosome for g = 1395 is center 40 is 182.0 2091.2727272727275
Best chromosome for g = 1395 is center 41 is 879.1818181818181
138.9090909090909
Best chromosome for g = 1395 is center 42 is 1083.6363636363637
141.45454545454547
Best chromosome for g = 1395 is center 43 is 1275.2 108.8
Best chromosome for g = 1395 is center 44 is 1455.3333333333333
133.91666666666666
Best chromosome for g = 1395 is center 45 is 882.7 313.7
Best chromosome for g = 1395 is center 46 is 1092.142857142857
290.14285714285717
Best chromosome for g = 1395 is center 47 is 789.0 626.5
Best chromosome for g = 1395 is center 48 is 984.8333333333334
511.3333333333333
Best chromosome for g = 1395 is center 49 is 1163.8 402.2
Best chromosome for g = 1395 is center 50 is 1298.3076923076924
269.3076923076923
Best chromosome for g = 1395 is center 51 is 1689.2857142857142
115.28571428571429
Best chromosome for g = 1395 is center 52 is 1492.923076923077
285.46153846153845
Best chromosome for g = 1395 is center 53 is 669.625 837.0
Best chromosome for g = 1395 is center 54 is 922.8571428571429
691.2857142857143
Best chromosome for g = 1395 is center 55 is 1823.25 149.875
Best chromosome for g = 1395 is center 56 is 1940.4285714285713
132.28571428571428
Best chromosome for g = 1395 is center 57 is 1687.8181818181818
257.45454545454544
Best chromosome for g = 1395 is center 58 is 2103.4285714285716
120.42857142857143
Best chromosome for g = 1395 is center 59 is 1903.111111111111
294.77777777777777
Best chromosome for g = 1395 is center 60 is 1108.8181818181818
596.6363636363636
Best chromosome for g = 1395 is center 61 is 1299.3333333333333
529.7777777777778
Best chromosome for g = 1395 is center 62 is 1462.2727272727273
533.5454545454545
Best chromosome for g = 1395 is center 63 is 1760.0 433.1666666666667
Best chromosome for g = 1395 is center 64 is 2109.9 259.8
Best chromosome for g = 1395 is center 65 is 1697.2222222222222
601.6666666666666
Best chromosome for g = 1395 is center 66 is 1908.4 585.1
Best chromosome for g = 1395 is center 67 is 897.7777777777778
852.4444444444445
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Best chromosome for g = 1395 is center 68 is 1289.6 661.7
Best chromosome for g = 1395 is center 69 is 1093.2727272727273
752.1818181818181
Best chromosome for g = 1395 is center 70 is 836.5714285714286
1018.8571428571429
Best chromosome for g = 1395 is center 71 is 1054.8333333333333 917.0
Best chromosome for g = 1395 is center 72 is 1279.4444444444443
828.5555555555555
Best chromosome for g = 1395 is center 73 is 1514.2222222222222
690.8888888888889
Best chromosome for g = 1395 is center 74 is 1467.142857142857
828.5714285714286
Best chromosome for g = 1395 is center 75 is 1199.5 1018.375
Best chromosome for g = 1395 is center 76 is 686.625 1126.625
Best chromosome for g = 1395 is center 77 is 852.375 1161.125
Best chromosome for g = 1395 is center 78 is 1037.25 1142.4166666666667
Best chromosome for g = 1395 is center 79 is 1680.75 750.125
Best chromosome for g = 1395 is center 80 is 1887.3636363636363
749.4545454545455
Best chromosome for g = 1395 is center 81 is 1421.857142857143
1064.5714285714287
Best chromosome for g = 1395 is center 82 is 475.7 1321.5
Best chromosome for g = 1395 is center 83 is 693.375 1254.375
Best chromosome for g = 1395 is center 84 is 830.6666666666666
1319.3333333333333
Best chromosome for g = 1395 is center 85 is 632.2 1395.2
Best chromosome for g = 1395 is center 86 is 1200.5454545454545
1194.8181818181818
Best chromosome for g = 1395 is center 87 is 1039.5454545454545
1331.909090909091
Best chromosome for g = 1395 is center 88 is 1386.8 1197.6
Best chromosome for g = 1395 is center 89 is 469.1111111111111
1441.4444444444443
Best chromosome for g = 1395 is center 90 is 455.625 1607.125
Best chromosome for g = 1395 is center 91 is 615.8333333333334 1548.0
Best chromosome for g = 1395 is center 92 is 465.57142857142856
1748.857142857143
Best chromosome for g = 1395 is center 93 is 607.0 1712.0
Best chromosome for g = 1395 is center 94 is 759.0 1573.7142857142858
Best chromosome for g = 1395 is center 95 is 872.5 1512.3333333333333
Best chromosome for g = 1395 is center 96 is 1214.3 1351.2
Best chromosome for g = 1395 is center 97 is 316.55555555555554
1870.4444444444443
Best chromosome for g = 1395 is center 98 is 469.6666666666667
1866.3333333333333
Best chromosome for g = 1395 is center 99 is 1059.7 1488.2
Best chromosome for g = 1395 is center 100 is 333.1 2027.4
Best chromosome for g = 1395 is center 101 is 682.3076923076923
1888.6153846153845
Best chromosome for g = 1395 is center 102 is 996.2 1664.0
Best chromosome for g = 1395 is center 103 is 1578.111111111111
1161.888888888889
Best chromosome for g = 1395 is center 104 is 1403.125 1346.625
Best chromosome for g = 1395 is center 105 is 1560.1666666666667 1321.5
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Best chromosome for g = 1395 is center 106 is 1254.0 1517.0
Best chromosome for g = 1395 is center 107 is 1724.142857142857
1062.4285714285713
Best chromosome for g = 1395 is center 108 is 2249.285714285714
100.42857142857143
Best chromosome for g = 1395 is center 109 is 2366.777777777778
150.33333333333334
Best chromosome for g = 1395 is center 110 is 2504.0 108.75
Best chromosome for g = 1395 is center 111 is 2512.5 249.1
Best chromosome for g = 1395 is center 112 is 2291.090909090909
279.8181818181818
Best chromosome for g = 1395 is center 113 is 2066.2 466.0
Best chromosome for g = 1395 is center 114 is 2245.125 481.75
Best chromosome for g = 1395 is center 115 is 2431.6666666666665
391.1666666666667
Best chromosome for g = 1395 is center 116 is 2128.4 615.3
Best chromosome for g = 1395 is center 117 is 2060.8333333333335
744.6666666666666
Best chromosome for g = 1395 is center 118 is 1913.2 929.2
Best chromosome for g = 1395 is center 119 is 2313.75 607.625
Best chromosome for g = 1395 is center 120 is 2298.8888888888887
730.6666666666666
Best chromosome for g = 1395 is center 121 is 2160.1428571428573
858.4285714285714
Best chromosome for g = 1395 is center 122 is 1915.4444444444443
1083.4444444444443
Best chromosome for g = 1395 is center 123 is 2079.75 1057.0
Best chromosome for g = 1395 is center 124 is 1818.5 1223.0
Best chromosome for g = 1395 is center 125 is 1735.5 1347.1666666666667
Best chromosome for g = 1395 is center 126 is 2014.3 1237.4
Best chromosome for g = 1395 is center 127 is 2172.25 1162.75
Best chromosome for g = 1395 is center 128 is 69.0 2172.5833333333335
Best chromosome for g = 1395 is center 129 is 499.3333333333333 2073.5
Best chromosome for g = 1395 is center 130 is 851.125 1842.375
Best chromosome for g = 1395 is center 131 is 1000.7142857142857
1885.2857142857142
Best chromosome for g = 1395 is center 132 is 626.875 2063.125
Best chromosome for g = 1395 is center 133 is 905.875 2000.5
Best chromosome for g = 1395 is center 134 is 1139.857142857143
1865.2857142857142
Best chromosome for g = 1395 is center 135 is 1425.5 1567.2
Best chromosome for g = 1395 is center 136 is 1387.4 1744.2
Best chromosome for g = 1395 is center 137 is 1433.8 1883.0
Best chromosome for g = 1395 is center 138 is 1264.6666666666667
1887.3333333333333
Best chromosome for g = 1395 is center 139 is 1581.5555555555557
1528.3333333333333
Best chromosome for g = 1395 is center 140 is 1720.3333333333333
1521.888888888889
Best chromosome for g = 1395 is center 141 is 1712.1666666666667
1700.8333333333333
Best chromosome for g = 1395 is center 142 is 1571.2857142857142
1846.5714285714287
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Best chromosome for g = 1395 is center 143 is 1923.4444444444443
1383.888888888889
Best chromosome for g = 1395 is center 144 is 2128.875 1330.0
Best chromosome for g = 1395 is center 145 is 1877.25 1605.625
Best chromosome for g = 1395 is center 146 is 168.0 2256.0
Best chromosome for g = 1395 is center 147 is 323.9166666666667 2168.75
Best chromosome for g = 1395 is center 148 is 401.25 2272.5
Best chromosome for g = 1395 is center 149 is 55.92307692307692
2316.923076923077
Best chromosome for g = 1395 is center 150 is 55.23076923076923
2469.923076923077
Best chromosome for g = 1395 is center 151 is 175.83333333333334
2414.1666666666665
Best chromosome for g = 1395 is center 152 is 49.666666666666664
2602.8888888888887
Best chromosome for g = 1395 is center 153 is 314.75 2368.5833333333335
Best chromosome for g = 1395 is center 154 is 49.333333333333336
2718.1111111111113
Best chromosome for g = 1395 is center 155 is 157.5 2592.1
Best chromosome for g = 1395 is center 156 is 165.16666666666666
2741.5833333333335
Best chromosome for g = 1395 is center 157 is 56.083333333333336
2852.5833333333335
Best chromosome for g = 1395 is center 158 is 780.8333333333334 2120.0
Best chromosome for g = 1395 is center 159 is 617.2222222222222
2213.777777777778
Best chromosome for g = 1395 is center 160 is 919.3333333333334
2136.1111111111113
Best chromosome for g = 1395 is center 161 is 462.4 2444.4
Best chromosome for g = 1395 is center 162 is 630.0 2383.8888888888887
Best chromosome for g = 1395 is center 163 is 1153.111111111111 2051.0
Best chromosome for g = 1395 is center 164 is 915.2222222222222
2294.6666666666665
Best chromosome for g = 1395 is center 165 is 1193.4545454545455
2190.7272727272725
Best chromosome for g = 1395 is center 166 is 894.7 2458.6
Best chromosome for g = 1395 is center 167 is 327.5 2573.75
Best chromosome for g = 1395 is center 168 is 310.77777777777777
2738.5555555555557
Best chromosome for g = 1395 is center 169 is 627.625 2581.625
Best chromosome for g = 1395 is center 170 is 500.0 2639.3333333333335
Best chromosome for g = 1395 is center 171 is 173.0 2893.8
Best chromosome for g = 1395 is center 172 is 300.25 2890.25
Best chromosome for g = 1395 is center 173 is 502.625 2804.5
Best chromosome for g = 1395 is center 174 is 630.1 2729.3
Best chromosome for g = 1395 is center 175 is 113.33333333333333
3158.3333333333335
Best chromosome for g = 1395 is center 176 is 483.5 2961.375
Best chromosome for g = 1395 is center 177 is 651.2142857142857
2889.5714285714284
Best chromosome for g = 1395 is center 178 is 323.0 3115.8333333333335
Best chromosome for g = 1395 is center 179 is 160.25 3295.625
Best chromosome for g = 1395 is center 180 is 307.55555555555554
3247.3333333333335
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Best chromosome for g = 1395 is center 181 is 94.83333333333333
3422.6666666666665
Best chromosome for g = 1395 is center 182 is 259.0 3516.0
Best chromosome for g = 1395 is center 183 is 335.8888888888889
3378.5555555555557
Best chromosome for g = 1395 is center 184 is 107.15384615384616
3583.3846153846152
Best chromosome for g = 1395 is center 185 is 103.36363636363636
3723.3636363636365
Best chromosome for g = 1395 is center 186 is 0.5 3893.75
Best chromosome for g = 1395 is center 187 is 1440.2222222222222
2060.6666666666665
Best chromosome for g = 1395 is center 188 is 1191.4 2329.1
Best chromosome for g = 1395 is center 189 is 921.5 2662.75
Best chromosome for g = 1395 is center 190 is 768.7777777777778
2745.222222222222
Best chromosome for g = 1395 is center 191 is 516.2727272727273
3160.7272727272725
Best chromosome for g = 1395 is center 192 is 1694.0 1888.0
Best chromosome for g = 1395 is center 193 is 1150.7777777777778
2495.4444444444443
Best chromosome for g = 1395 is center 194 is 1314.2857142857142
2558.714285714286
Best chromosome for g = 1395 is center 195 is 1634.3 2067.7
Best chromosome for g = 1395 is center 196 is 1456.4 2217.2
Best chromosome for g = 1395 is center 197 is 1630.625 2224.375
Best chromosome for g = 1395 is center 198 is 1428.0 2368.25
Best chromosome for g = 1395 is center 199 is 902.3333333333334
2862.3333333333335
Best chromosome for g = 1395 is center 200 is 1116.0 2724.6
Best chromosome for g = 1395 is center 201 is 1328.6666666666667 2721.0
Best chromosome for g = 1395 is center 202 is 1478.3333333333333
2541.3333333333335
Best chromosome for g = 1395 is center 203 is 704.125 3144.25
Best chromosome for g = 1395 is center 204 is 824.2857142857143
3029.285714285714
Best chromosome for g = 1395 is center 205 is 693.6666666666666
3276.3333333333335
Best chromosome for g = 1395 is center 206 is 1109.9 2871.0
Best chromosome for g = 1395 is center 207 is 968.4285714285714
3068.8571428571427
Best chromosome for g = 1395 is center 208 is 1338.125 2868.5
Best chromosome for g = 1395 is center 209 is 522.4545454545455
3340.3636363636365
Best chromosome for g = 1395 is center 210 is 1247.0 2999.1666666666665
Best chromosome for g = 1395 is center 211 is 702.25 3428.625
Best chromosome for g = 1395 is center 212 is 871.1 3244.4
Best chromosome for g = 1395 is center 213 is 403.8888888888889
3511.3333333333335
Best chromosome for g = 1395 is center 214 is 329.9 3653.7
Best chromosome for g = 1395 is center 215 is 1117.0 3140.6666666666665
Best chromosome for g = 1395 is center 216 is 549.8333333333334
3581.3333333333335
Best chromosome for g = 1395 is center 217 is 720.125 3569.25

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Best chromosome for g = 1395 is center 218 is 1109.375 3299.75
Best chromosome for g = 1395 is center 219 is 951.6666666666666 3402.0
Best chromosome for g = 1395 is center 220 is 1999.75 1581.0
Best chromosome for g = 1395 is center 221 is 1866.2 1777.6
Best chromosome for g = 1395 is center 222 is 1999.125 1736.5
Best chromosome for g = 1395 is center 223 is 1807.2857142857142
2025.5714285714287
Best chromosome for g = 1395 is center 224 is 1820.875 2179.75
Best chromosome for g = 1395 is center 225 is 1644.0 2379.1111111111113
Best chromosome for g = 1395 is center 226 is 1808.5 2334.8
Best chromosome for g = 1395 is center 227 is 1650.8 2530.2
Best chromosome for g = 1395 is center 228 is 1530.8333333333333
2722.1666666666665
Best chromosome for g = 1395 is center 229 is 1527.2222222222222
2875.222222222222
Best chromosome for g = 1395 is center 230 is 1417.125 3063.875
Best chromosome for g = 1395 is center 231 is 1298.8333333333333 3211.5
Best chromosome for g = 1395 is center 232 is 144.0 3849.777777777778
Best chromosome for g = 1395 is center 233 is 487.6 3717.6
Best chromosome for g = 1395 is center 234 is 710.2857142857143
3688.5714285714284
Best chromosome for g = 1395 is center 235 is 303.2 3813.8
Best chromosome for g = 1395 is center 236 is 909.6 3567.6
Best chromosome for g = 1395 is center 237 is 504.25 3860.0
Best chromosome for g = 1395 is center 238 is 703.625 3822.75
Best chromosome for g = 1395 is center 239 is 1325.857142857143
3353.5714285714284
Best chromosome for g = 1395 is center 240 is 901.6 3707.5
Best chromosome for g = 1395 is center 241 is 1110.090909090909
3597.7272727272725
Best chromosome for g = 1395 is center 242 is 1122.357142857143
3801.714285714286
Best chromosome for g = 1395 is center 243 is 1291.0 3631.0833333333335
Best chromosome for g = 1395 is center 244 is 883.6363636363636
3837.5454545454545
Best chromosome for g = 1395 is center 245 is 1333.25 3810.8333333333335
Best chromosome for g = 1395 is center 246 is 2668.1428571428573
47.857142857142854
Best chromosome for g = 1395 is center 247 is 2668.0 206.16666666666666
Best chromosome for g = 1395 is center 248 is 2810.8 114.9
Best chromosome for g = 1395 is center 249 is 2612.75 383.0
Best chromosome for g = 1395 is center 250 is 2810.8 307.7
Best chromosome for g = 1395 is center 251 is 2509.8888888888887
565.2222222222222
Best chromosome for g = 1395 is center 252 is 2654.1666666666665 549.0
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Best chromosome for g = 1395 is center 254 is 2779.3636363636365
543.3636363636364
Best chromosome for g = 1395 is center 255 is 2371.3333333333335
884.1666666666666
Best chromosome for g = 1395 is center 256 is 2547.4285714285716 867.0
Best chromosome for g = 1395 is center 257 is 2643.8 726.4
Best chromosome for g = 1395 is center 258 is 2285.0 1062.6666666666667
Best chromosome for g = 1395 is center 259 is 2323.0 1176.8181818181818
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Best chromosome for g = 1395 is center 260 is 2510.1111111111113
1053.3333333333333
Best chromosome for g = 1395 is center 261 is 2506.1 1212.9
Best chromosome for g = 1395 is center 262 is 2302.4285714285716
1314.4285714285713
Best chromosome for g = 1395 is center 263 is 2201.875 1520.0
Best chromosome for g = 1395 is center 264 is 2174.875 1655.375
Best chromosome for g = 1395 is center 265 is 2361.714285714286 1504.0
Best chromosome for g = 1395 is center 266 is 2037.857142857143
1874.5714285714287
Best chromosome for g = 1395 is center 267 is 2183.777777777778
1811.111111111111
Best chromosome for g = 1395 is center 268 is 2000.3333333333333
2089.5555555555557
Best chromosome for g = 1395 is center 269 is 1980.5454545454545
2263.181818181818
Best chromosome for g = 1395 is center 270 is 1839.5714285714287 2481.0
Best chromosome for g = 1395 is center 271 is 1745.7 2727.2
Best chromosome for g = 1395 is center 272 is 1561.5 3151.7
Best chromosome for g = 1395 is center 273 is 2781.1 732.1
Best chromosome for g = 1395 is center 274 is 2758.8571428571427
1021.5714285714286
Best chromosome for g = 1395 is center 275 is 2648.6 1107.6
Best chromosome for g = 1395 is center 276 is 2485.0 1377.5833333333333
Best chromosome for g = 1395 is center 277 is 2638.0 1257.7142857142858
Best chromosome for g = 1395 is center 278 is 2789.1666666666665
1212.4166666666667
Best chromosome for g = 1395 is center 279 is 2635.0 1517.375
Best chromosome for g = 1395 is center 280 is 2772.4444444444443
1394.7777777777778
Best chromosome for g = 1395 is center 281 is 2348.5 1656.625
Best chromosome for g = 1395 is center 282 is 2521.6 1637.9
Best chromosome for g = 1395 is center 283 is 2234.3333333333335
1981.3333333333333
Best chromosome for g = 1395 is center 284 is 2349.5555555555557
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Best chromosome for g = 1395 is center 287 is 2773.7272727272725
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Best chromosome for g = 1395 is center 288 is 2169.75 2260.8333333333335
Best chromosome for g = 1395 is center 289 is 2354.1428571428573
2077.5714285714284
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Best chromosome for g = 1395 is center 291 is 2510.222222222222
2039.5555555555557
Best chromosome for g = 1395 is center 292 is 2525.1 2220.5
Best chromosome for g = 1395 is center 293 is 2660.3333333333335
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Best chromosome for g = 1395 is center 294 is 2662.6 1977.6
Best chromosome for g = 1395 is center 295 is 1979.5555555555557
2404.5555555555557
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2408.6666666666665
Best chromosome for g = 1395 is center 297 is 1742.6363636363637
2885.181818181818
Best chromosome for g = 1395 is center 298 is 1958.2727272727273
2661.7272727272725
Best chromosome for g = 1395 is center 299 is 2158.3636363636365
2635.090909090909
Best chromosome for g = 1395 is center 300 is 2357.8888888888887
2420.777777777778
Best chromosome for g = 1395 is center 301 is 2511.8888888888887
2456.4444444444443
Best chromosome for g = 1395 is center 302 is 1949.8 2856.0
Best chromosome for g = 1395 is center 303 is 2347.0 2618.5
Best chromosome for g = 1395 is center 304 is 2152.1111111111113
2798.3333333333335
Best chromosome for g = 1395 is center 305 is 1733.7 3112.9
Best chromosome for g = 1395 is center 306 is 1952.2857142857142
3035.1428571428573
Best chromosome for g = 1395 is center 307 is 2154.714285714286
2951.8571428571427
Best chromosome for g = 1395 is center 308 is 1530.142857142857
3299.285714285714
Best chromosome for g = 1395 is center 309 is 2323.6666666666665
2759.1111111111113
Best chromosome for g = 1395 is center 310 is 2334.0 2925.5555555555557
Best chromosome for g = 1395 is center 311 is 1950.125 3183.375
Best chromosome for g = 1395 is center 312 is 2145.6 3146.9
Best chromosome for g = 1395 is center 313 is 1760.1666666666667
3286.8333333333335
Best chromosome for g = 1395 is center 314 is 1639.625 3422.25
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Best chromosome for g = 1395 is center 316 is 2670.3333333333335 2186.0
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Best chromosome for g = 1395 is center 318 is 2508.75 2601.25
Best chromosome for g = 1395 is center 319 is 2761.5 2337.785714285714
Best chromosome for g = 1395 is center 320 is 2704.375 2481.0
Best chromosome for g = 1395 is center 321 is 2693.1666666666665 2655.5
Best chromosome for g = 1395 is center 322 is 2493.777777777778
2782.8888888888887
Best chromosome for g = 1395 is center 323 is 2511.8571428571427
2987.714285714286
Best chromosome for g = 1395 is center 324 is 2330.4 3130.3
Best chromosome for g = 1395 is center 325 is 1439.375 3540.0
Best chromosome for g = 1395 is center 326 is 1967.6 3344.9
Best chromosome for g = 1395 is center 327 is 2140.3333333333335
3311.777777777778
Best chromosome for g = 1395 is center 328 is 2337.5555555555557
3281.8888888888887
Best chromosome for g = 1395 is center 329 is 2550.8888888888887
3131.8888888888887
Best chromosome for g = 1395 is center 330 is 1608.8333333333333
3607.8333333333335

```
Best chromosome for g = 1395 is center 331 is 1531.888888888889
3714.4444444444443
Best chromosome for g = 1395 is center 332 is 1741.111111111111
3638.1111111111113
Best chromosome for g = 1395 is center 333 is 1462.0 3854.2
Best chromosome for g = 1395 is center 334 is 1651.1818181818182
3852.4545454545455
Best chromosome for g = 1395 is center 335 is 1807.5 3799.1666666666665
Best chromosome for g = 1395 is center 336 is 1941.0 3641.0
Best chromosome for g = 1395 is center 337 is 2108.3333333333335
3646.3333333333335
Best chromosome for g = 1395 is center 338 is 1960.2857142857142
3829.714285714286
Best chromosome for g = 1395 is center 339 is 2391.5 3435.3333333333335
Best chromosome for g = 1395 is center 340 is 2142.3333333333335 3825.5
Best chromosome for g = 1395 is center 341 is 2664.0 2905.3333333333335
Best chromosome for g = 1395 is center 342 is 2779.6666666666665
3068.1666666666665
Best chromosome for g = 1395 is center 343 is 2534.75 3272.25
Best chromosome for g = 1395 is center 344 is 2729.5714285714284
3194.1428571428573
Best chromosome for g = 1395 is center 345 is 2563.777777777778
3390.222222222222
Best chromosome for g = 1395 is center 346 is 2781.777777777778
3350.4444444444443
Best chromosome for g = 1395 is center 347 is 2793.3333333333335
3517.3333333333335
Best chromosome for g = 1395 is center 348 is 2444.5 3754.0
Best chromosome for g = 1395 is center 349 is 2733.1666666666665
3877.8333333333335
Time Elapsed: 1.049536134E9 Seeding Time: 483647.0
The seeding percentage time is : 0.000461
```

TSP-LIB-3038, *k* = 400: Separation, Deterministic

```
Random = 0
Density = 0
Separation = 200
Selection Method = 2
Number of centers = 400
After 0 generations new best SSE for g = 0 is 1.068845454798537E7
After 2 generations new best SSE for g = 2 is 1.0654812868002804E7
After 1 generations new best SSE for g = 3 is 1.0652183927995587E7
After 1 generations new best SSE for g = 4 is 1.0633267075572595E7
After 1 generations new best SSE for g = 5 is 1.0559460887001889E7
After 2 generations new best SSE for g = 7 is 1.0528077602207504E7
After 1 generations new best SSE for g = 8 is 1.0514253012143414E7
After 2 generations new best SSE for g = 10 is 1.0511371395873258E7
After 1 generations new best SSE for g = 11 is 1.0447297248124098E7
After 2 generations new best SSE for g = 13 is 1.0425276360017762E7
After 1 generations new best SSE for g = 14 is 1.0414891956468549E7
After 2 generations new best SSE for g = 16 is 1.0400177280662362E7
After 1 generations new best SSE for g = 17 is 1.0396444828282865E7
After 1 generations new best SSE for g = 18 is 1.0335127894189158E7
After 1 generations new best SSE for g = 19 is 1.0324348573357226E7
After 1 generations new best SSE for g = 20 is 1.030394138358031E7
After 4 generations new best SSE for g = 24 is 1.0287379849439468E7
After 1 generations new best SSE for g = 25 is 1.0277094644821817E7
After 2 generations new best SSE for g = 27 is 1.0251835798834505E7
After 2 generations new best SSE for g = 29 is 1.0241024575804759E7
After 1 generations new best SSE for g = 30 is 1.0204811295720952E7
After 2 generations new best SSE for g = 32 is 1.0164850312653998E7
After 5 generations new best SSE for g = 37 is 1.01446397344017E7
After 3 generations new best SSE for g = 40 is 1.0088730232088527E7
After 4 generations new best SSE for g = 44 is 1.0076759832520261E7
After 2 generations new best SSE for g = 46 is 1.0027725337215535E7
After 1 generations new best SSE for g = 47 is 1.0025126587215535E7
After 6 generations new best SSE for g = 53 is 1.0011265351531792E7
After 8 generations new best SSE for g = 61 is 1.0001337605228087E7
After 1 generations new best SSE for g = 62 is 9980569.956876451
After 8 generations new best SSE for g = 70 is 9948202.400990678
After 5 generations new best SSE for g = 75 is 9932152.19553498
After 4 generations new best SSE for g = 79 is 9915102.94686141
After 8 generations new best SSE for g = 87 is 9914817.596717162
After 1 generations new best SSE for g = 88 is 9914369.792254958
After 1 generations new best SSE for g = 89 is 9914274.915270831
After 1 generations new best SSE for g = 90 is 9904007.05756465
After 3 generations new best SSE for g = 93 is 9902088.140104333
After 1 generations new best SSE for g = 94 is 9897077.984575363
After 7 generations new best SSE for g = 101 is 9880389.447291577
After 2 generations new best SSE for g = 103 is 9870232.391555646
After 2 generations new best SSE for g = 105 is 9860387.367857115
After 3 generations new best SSE for g = 108 is 9855517.150011055
After 4 generations new best SSE for g = 112 is 9849861.02883782
After 2 generations new best SSE for g = 114 is 9836600.380463956
After 8 generations new best SSE for g = 122 is 9834965.187703928
After 1 generations new best SSE for g = 123 is 9829767.882281583
```

```
After 1 generations new best SSE for g = 124 is 9823671.012026858
After 2 generations new best SSE for g = 126 is 9794373.45090463
After 5 generations new best SSE for g = 131 is 9752357.619092003
After 6 generations new best SSE for g = 137 is 9740664.185156515
After 12 generations new best SSE for g = 149 is 9736264.50343823
After 1 generations new best SSE for g = 150 is 9731772.753438229
After 10 generations new best SSE for g = 160 is 9704548.993811756
After 5 generations new best SSE for g = 165 is 9704003.89828506
After 7 generations new best SSE for g = 172 is 9700871.761671668
After 9 generations new best SSE for g = 181 is 9699706.678268937
After 4 generations new best SSE for g = 185 is 9693588.398579182
After 1 generations new best SSE for g = 186 is 9692550.83815906
After 4 generations new best SSE for g = 190 is 9670328.909293473
After 4 generations new best SSE for g = 194 is 9668793.818023633
After 7 generations new best SSE for g = 201 is 9667996.889868455
After 4 generations new best SSE for g = 205 is 9655069.586729925
After 8 generations new best SSE for g = 213 is 9652961.50260294
After 4 generations new best SSE for g = 217 is 9646927.371245416
After 5 generations new best SSE for g = 222 is 9644684.224198021
After 8 generations new best SSE for g = 230 is 9627334.112803845
After 4 generations new best SSE for g = 234 is 9627221.08550337
After 3 generations new best SSE for g = 237 is 9626328.954223542
After 8 generations new best SSE for g = 245 is 9623367.069225205
After 4 generations new best SSE for g = 249 is 9605468.579220777
After 1 generations new best SSE for g = 250 is 9604223.77121213
After 5 generations new best SSE for g = 255 is 9592649.802849913
After 8 generations new best SSE for g = 263 is 9590545.755264182
After 21 generations new best SSE for g = 284 is 9584678.258150177
After 8 generations new best SSE for g = 292 is 9577677.737684535
After 6 generations new best SSE for g = 298 is 9572637.830042172
After 1 generations new best SSE for g = 299 is 9568945.495951261
After 6 generations new best SSE for g = 305 is 9564712.047660673
After 12 generations new best SSE for g = 317 is 9563460.61995504
After 2 generations new best SSE for g = 319 is 9562586.392538015
After 7 generations new best SSE for g = 326 is 9560039.236105543
After 2 generations new best SSE for g = 328 is 9548867.069918966
After 13 generations new best SSE for g = 341 is 9546702.69307359
After 3 generations new best SSE for g = 344 is 9540226.12629591
After 11 generations new best SSE for g = 355 is 9538495.837667866
After 4 generations new best SSE for g = 359 is 9536469.820226975
After 2 generations new best SSE for g = 361 is 9534860.564177474
After 1 generations new best SSE for g = 362 is 9525595.777672315
After 10 generations new best SSE for g = 372 is 9525504.529148614
After 6 generations new best SSE for g = 378 is 9520487.658477614
After 11 generations new best SSE for g = 389 is 9518023.885106528
After 6 generations new best SSE for g = 395 is 9516541.465084894
After 2 generations new best SSE for g = 397 is 9516189.729659209
After 4 generations new best SSE for g = 401 is 9515760.391275367
After 1 generations new best SSE for g = 402 is 9514210.93084136
After 6 generations new best SSE for g = 408 is 9504811.086158259
After 8 generations new best SSE for g = 416 is 9502335.520790294
After 3 generations new best SSE for g = 419 is 9500779.9432595
After 5 generations new best SSE for g = 424 is 9498217.087595724
After 3 generations new best SSE for g = 427 is 9494368.166924726
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After 23 generations new best SSE for g = 450 is 9482870.62038793
After 3 generations new best SSE for g = 453 is 9480663.970959593
After 10 generations new best SSE for g = 463 is 9476987.402958153
After 4 generations new best SSE for g = 467 is 9476508.562085137
After 8 generations new best SSE for g = 475 is 9476296.64541847
After 6 generations new best SSE for g = 481 is 9472401.77248029
After 4 generations new best SSE for g = 485 is 9471057.042424245
After 7 generations new best SSE for g = 492 is 9463945.857720034
After 6 generations new best SSE for g = 498 is 9463189.613672415
After 4 generations new best SSE for g = 502 is 9462654.91327559
After 3 generations new best SSE for g = 505 is 9462075.395418447
After 16 generations new best SSE for g = 521 is 9460215.117646223
After 5 generations new best SSE for g = 526 is 9459139.578571405
After 6 generations new best SSE for g = 532 is 9455164.74221055
After 4 generations new best SSE for g = 536 is 9454044.627131186
After 4 generations new best SSE for g = 540 is 9453567.63109944
After 8 generations new best SSE for g = 548 is 9453317.8151848
After 7 generations new best SSE for g = 555 is 9451944.619153056
After 9 generations new best SSE for g = 564 is 9451017.852522459
After 5 generations new best SSE for g = 569 is 9442291.680844143
After 26 generations new best SSE for g = 595 is 9439619.947222194
After 1 generations new best SSE for g = 596 is 9437247.130952349
After 5 generations new best SSE for g = 601 is 9434064.682683952
After 5 generations new best SSE for g = 606 is 9433487.466810938
After 7 generations new best SSE for g = 613 is 9433370.176692732
After 7 generations new best SSE for g = 620 is 9430172.939787963
After 10 generations new best SSE for g = 630 is 9429675.84545174
After 5 generations new best SSE for g = 635 is 9427580.433943804
After 29 generations new best SSE for g = 664 is 9422369.372963138
After 5 generations new best SSE for g = 669 is 9421075.500740916
After 21 generations new best SSE for g = 690 is 9417857.916594502
After 26 generations new best SSE for g = 716 is 9417128.232212214
After 15 generations new best SSE for g = 731 is 9416805.15793649
After 2 generations new best SSE for g = 733 is 9415652.773482053
After 2 generations new best SSE for g = 735 is 9415642.940315219
After 1 generations new best SSE for g = 736 is 9414200.359126965
After 3 generations new best SSE for g = 739 is 9414020.896500701
After 1 generations new best SSE for g = 740 is 9412981.70382394
After 1 generations new best SSE for g = 741 is 9412657.380591616
After 3 generations new best SSE for g = 744 is 9407820.67487511
After 2 generations new best SSE for g = 746 is 9403777.717568528
After 7 generations new best SSE for g = 753 is 9402721.909632023
After 17 generations new best SSE for g = 770 is 9401185.15977355
After 21 generations new best SSE for g = 791 is 9400805.330011645
After 22 generations new best SSE for g = 813 is 9398363.956021747
After 14 generations new best SSE for g = 827 is 9396590.786363618
After 12 generations new best SSE for g = 839 is 9394948.855300244
After 6 generations new best SSE for g = 845 is 9392827.272435883
After 23 generations new best SSE for g = 868 is 9391849.998951038
After 8 generations new best SSE for g = 876 is 9387348.75303029
After 1 generations new best SSE for g = 877 is 9387168.60541124
After 8 generations new best SSE for g = 885 is 9387167.59350648
After 21 generations new best SSE for g = 906 is 9386403.370779207
After 24 generations new best SSE for g = 930 is 9381391.671933599
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After 18 generations new best SSE for g = 948 is 9379817.446717149
After 19 generations new best SSE for g = 967 is 9379054.537445864
After 22 generations new best SSE for g = 989 is 9377200.389502143
After 4 generations new best SSE for g = 993 is 9376787.644660873
After 16 generations new best SSE for g = 1009 is 9376417.491089443
After 1 generations new best SSE for g = 1010 is 9376302.725613253
After 8 generations new best SSE for g = 1018 is 9376169.990223644
After 15 generations new best SSE for g = 1033 is 9376084.226442976
After 3 generations new best SSE for g = 1036 is 9375702.492712827
After 13 generations new best SSE for g = 1049 is 9375273.611144388
After 3 generations new best SSE for g = 1052 is 9374133.345382376
After 13 generations new best SSE for g = 1065 is 9373886.72712841
After 10 generations new best SSE for g = 1075 is 9373659.504509361
After 7 generations new best SSE for g = 1082 is 9373646.253460417
After 19 generations new best SSE for g = 1101 is 9373516.57355698
After 4 generations new best SSE for g = 1105 is 9373497.060461743
After 2 generations new best SSE for g = 1107 is 9371826.430699838
After 38 generations new best SSE for g = 1145 is 9370650.03466809
After 35 generations new best SSE for g = 1180 is 9369999.07633475
After 6 generations new best SSE for g = 1186 is 9369579.84148627
After 26 generations new best SSE for g = 1212 is 9369407.636688279
After 15 generations new best SSE for g = 1227 is 9368830.953787854
After 12 generations new best SSE for g = 1239 is 9367798.98863634
After 29 generations new best SSE for g = 1268 is 9367576.886616135
After 12 generations new best SSE for g = 1280 is 9367278.282359282
After 9 generations new best SSE for g = 1289 is 9367012.363275586
After 4 generations new best SSE for g = 1293 is 9365883.781962456
After 64 generations new best SSE for g = 1357 is 9365658.060894633
After 33 generations new best SSE for g = 1390 is 9364045.162878761
After 78 generations new best SSE for g = 1468 is 9363686.310497807
After 20 generations new best SSE for g = 1488 is 9363190.548989872
After 74 generations new best SSE for g = 1562 is 9361285.922005748
Best SSE for g = 1662 is 9361285.922005748
Best chromosome for g = 1662 is center 0 is 31.5 90.33333333333333
Best chromosome for g = 1662 is center 1 is 189.8 91.6
Best chromosome for g = 1662 is center 2 is 160.0 199.71428571428572
Best chromosome for g = 1662 is center 3 is 42.888888888888886
342.3333333333333
Best chromosome for g = 1662 is center 4 is 184.0 324.875
Best chromosome for g = 1662 is center 5 is 374.3333333333333 48.0
Best chromosome for g = 1662 is center 6 is 320.75 184.125
Best chromosome for g = 1662 is center 7 is 489.1111111111111
183.33333333333334
Best chromosome for g = 1662 is center 8 is 336.0 317.14285714285717
Best chromosome for g = 1662 is center 9 is 674.2727272727273
128.72727272727272
Best chromosome for g = 1662 is center 10 is 509.5 330.625
Best chromosome for g = 1662 is center 11 is 833.8333333333334 101.0
Best chromosome for g = 1662 is center 12 is 691.7 311.1
Best chromosome for g = 1662 is center 13 is 933.1666666666666
151.83333333333334
Best chromosome for g = 1662 is center 14 is 889.8571428571429
264.2857142857143
Best chromosome for g = 1662 is center 15 is 1107.2 129.9
```

```
Best chromosome for g = 1662 is center 16 is 1285.0 108.22222222222223
Best chromosome for g = 1662 is center 17 is 1461.8 119.2
Best chromosome for g = 1662 is center 18 is 860.5 373.25
Best chromosome for g = 1662 is center 19 is 1086.125 279.625
Best chromosome for g = 1662 is center 20 is 1163.8 402.2
Best chromosome for g = 1662 is center 21 is 1285.090909090909
263.90909090909093
Best chromosome for g = 1662 is center 22 is 1415.875 273.125
Best chromosome for g = 1662 is center 23 is 1689.2857142857142
115.28571428571429
Best chromosome for g = 1662 is center 24 is 1687.8181818181818
257.45454545454544
Best chromosome for g = 1662 is center 25 is 1518.7777777777778
282.1111111111111
Best chromosome for g = 1662 is center 26 is 1823.25 149.875
Best chromosome for g = 1662 is center 27 is 1940.4285714285713
132.28571428571428
Best chromosome for g = 1662 is center 28 is 1903.111111111111
294.77777777777777
Best chromosome for g = 1662 is center 29 is 2103.4285714285716
120.42857142857143
Best chromosome for g = 1662 is center 30 is 2109.9 259.8
Best chromosome for g = 1662 is center 31 is 2249.285714285714
100.42857142857143
Best chromosome for g = 1662 is center 32 is 2291.090909090909
279.8181818181818
Best chromosome for g = 1662 is center 33 is 2366.777777777778
150.33333333333334
Best chromosome for g = 1662 is center 34 is 2504.0 108.75
Best chromosome for g = 1662 is center 35 is 2655.8571428571427
64.42857142857143
Best chromosome for g = 1662 is center 36 is 2508.2727272727275
255.8181818181818
Best chromosome for g = 1662 is center 37 is 2801.1428571428573
67.71428571428571
Best chromosome for g = 1662 is center 38 is 2670.0 220.6
Best chromosome for g = 1662 is center 39 is 2811.0 192.5
Best chromosome for g = 1662 is center 40 is 447.7142857142857
485.2857142857143
Best chromosome for g = 1662 is center 41 is 45.875 535.875
Best chromosome for g = 1662 is center 42 is 270.57142857142856
493.42857142857144
Best chromosome for g = 1662 is center 43 is 637.2 512.0
Best chromosome for g = 1662 is center 44 is 984.8333333333334
511.3333333333333
Best chromosome for g = 1662 is center 45 is 1299.3333333333333
529.7777777777778
Best chromosome for g = 1662 is center 46 is 1471.3333333333333 488.0
Best chromosome for g = 1662 is center 47 is 1760.0 433.1666666666667
Best chromosome for g = 1662 is center 48 is 2066.2 466.0
Best chromosome for g = 1662 is center 49 is 93.0 671.6666666666666
Best chromosome for g = 1662 is center 50 is 266.22222222222223
710.3333333333334
Best chromosome for g = 1662 is center 51 is -61.0 801.0
```

```
Best chromosome for g = 1662 is center 52 is 119.25 824.0
Best chromosome for g = 1662 is center 53 is 412.1666666666667 665.5
Best chromosome for g = 1662 is center 54 is 272.625 864.0
Best chromosome for g = 1662 is center 55 is 571.25 679.125
Best chromosome for g = 1662 is center 56 is 78.875 1024.625
Best chromosome for g = 1662 is center 57 is 222.28571428571428
1008.2857142857143
Best chromosome for g = 1662 is center 58 is 50.333333333333336
1133.6666666666667
Best chromosome for g = 1662 is center 59 is 158.25 1137.0
Best chromosome for g = 1662 is center 60 is 49.666666666666664
1244.3333333333333
Best chromosome for g = 1662 is center 61 is 46.125 1362.0
Best chromosome for g = 1662 is center 62 is 142.66666666666666
1274.111111111111
Best chromosome for g = 1662 is center 63 is 43.6 1501.5
Best chromosome for g = 1662 is center 64 is 135.5 1420.9
Best chromosome for g = 1662 is center 65 is 133.11111111111111
1582.888888888889
Best chromosome for g = 1662 is center 66 is 50.888888888888886
1640.3333333333333
Best chromosome for g = 1662 is center 67 is 38.857142857142854
1754.142857142857
Best chromosome for g = 1662 is center 68 is 139.42857142857142
1710.7142857142858
Best chromosome for g = 1662 is center 69 is 23.25 1979.5
Best chromosome for g = 1662 is center 70 is 311.85714285714283
1165.2857142857142
Best chromosome for g = 1662 is center 71 is 319.25 1270.375
Best chromosome for g = 1662 is center 72 is 284.09090909090907
1416.6363636363637
Best chromosome for g = 1662 is center 73 is 287.375 1572.5
Best chromosome for g = 1662 is center 74 is 300.75 1724.0
Best chromosome for g = 1662 is center 75 is 180.8 1839.6
Best chromosome for g = 1662 is center 76 is 316.55555555555554
1870.4444444444443
Best chromosome for g = 1662 is center 77 is 174.5 2051.0
Best chromosome for g = 1662 is center 78 is 49.888888888888886 2177.0
Best chromosome for g = 1662 is center 79 is 170.2 2157.0
Best chromosome for g = 1662 is center 80 is 49.888888888888886
2296.1111111111113
Best chromosome for g = 1662 is center 81 is 411.0 817.1666666666666
Best chromosome for g = 1662 is center 82 is 523.5 824.0
Best chromosome for g = 1662 is center 83 is 442.85714285714283 1044.0
Best chromosome for g = 1662 is center 84 is 566.75 987.75
Best chromosome for g = 1662 is center 85 is 789.0 626.5
Best chromosome for g = 1662 is center 86 is 669.625 837.0
Best chromosome for g = 1662 is center 87 is 482.9 1161.9
Best chromosome for g = 1662 is center 88 is 472.5 1297.75
Best chromosome for g = 1662 is center 89 is 686.625 1126.625
Best chromosome for g = 1662 is center 90 is 693.375 1254.375
Best chromosome for g = 1662 is center 91 is 478.8888888888889
1427.5555555555557
Best chromosome for g = 1662 is center 92 is 632.2 1395.2
```

```
Best chromosome for g = 1662 is center 93 is 442.75 1572.5
Best chromosome for g = 1662 is center 94 is 463.8888888888889
1730.2222222222222
Best chromosome for g = 1662 is center 95 is 615.8333333333334 1548.0
Best chromosome for g = 1662 is center 96 is 607.0 1712.0
Best chromosome for g = 1662 is center 97 is 452.2 1865.2
Best chromosome for g = 1662 is center 98 is 333.1 2027.4
Best chromosome for g = 1662 is center 99 is 329.0 2155.6
Best chromosome for g = 1662 is center 100 is 597.25 1880.0
Best chromosome for g = 1662 is center 101 is 160.6 2275.6
Best chromosome for g = 1662 is center 102 is 46.36363636363637
2425.3636363636365
Best chromosome for g = 1662 is center 103 is 630.8571428571429
2032.2857142857142
Best chromosome for g = 1662 is center 104 is 499.3333333333333 2073.5
Best chromosome for g = 1662 is center 105 is 922.8571428571429
691.2857142857143
Best chromosome for g = 1662 is center 106 is 1108.8181818181818
596.6363636363636
Best chromosome for g = 1662 is center 107 is 1284.3333333333333
653.7777777777778
Best chromosome for g = 1662 is center 108 is 1464.0 600.4285714285714
Best chromosome for g = 1662 is center 109 is 1697.2222222222222
601.6666666666666
Best chromosome for g = 1662 is center 110 is 1519.5714285714287 708.0
Best chromosome for g = 1662 is center 111 is 1680.75 750.125
Best chromosome for g = 1662 is center 112 is 1910.875 568.125
Best chromosome for g = 1662 is center 113 is 1892.6363636363637
717.7272727272727
Best chromosome for g = 1662 is center 114 is 1093.2727272727273
752.1818181818181
Best chromosome for g = 1662 is center 115 is 897.7777777777778
852.4444444444445
Best chromosome for g = 1662 is center 116 is 836.5714285714286
1018.8571428571429
Best chromosome for g = 1662 is center 117 is 1054.8333333333333 917.0
Best chromosome for g = 1662 is center 118 is 1229.25 848.0
Best chromosome for g = 1662 is center 119 is 1331.2857142857142
800.5714285714286
Best chromosome for g = 1662 is center 120 is 1481.0 832.3333333333334
Best chromosome for g = 1662 is center 121 is 1203.2857142857142
1007.7142857142857
Best chromosome for g = 1662 is center 122 is 852.375 1161.125
Best chromosome for g = 1662 is center 123 is 830.6666666666666
1319.3333333333333
Best chromosome for g = 1662 is center 124 is 759.0 1573.7142857142858
Best chromosome for g = 1662 is center 125 is 872.5 1512.3333333333333
Best chromosome for g = 1662 is center 126 is 1039.2 1127.7
Best chromosome for g = 1662 is center 127 is 1202.0 1162.7777777777778
Best chromosome for g = 1662 is center 128 is 1026.1666666666667 1254.0
Best chromosome for g = 1662 is center 129 is 1209.875 1291.125
Best chromosome for g = 1662 is center 130 is 1053.6666666666667
1379.3333333333333
```

Best chromosome for g = 1662 is center 131 is 1421.857142857143 1064.5714285714287
Best chromosome for g = 1662 is center 132 is 1386.8 1197.6
Best chromosome for g = 1662 is center 133 is 1210.5 1399.6666666666667
Best chromosome for g = 1662 is center 134 is 1055.875 1503.375
Best chromosome for g = 1662 is center 135 is 1256.6666666666667 1529.1666666666667
Best chromosome for g = 1662 is center 136 is 1403.125 1346.625
Best chromosome for g = 1662 is center 137 is 1567.5 1160.75
Best chromosome for g = 1662 is center 138 is 1560.1666666666667 1321.5
Best chromosome for g = 1662 is center 139 is 1720.0 1049.8333333333333
Best chromosome for g = 1662 is center 140 is 1731.6 1189.4
Best chromosome for g = 1662 is center 141 is 1735.5 1347.1666666666667
Best chromosome for g = 1662 is center 142 is 709.2222222222222 1882.0
Best chromosome for g = 1662 is center 143 is 851.125 1842.375
Best chromosome for g = 1662 is center 144 is 996.2 1664.0
Best chromosome for g = 1662 is center 145 is 1425.5 1567.2
Best chromosome for g = 1662 is center 146 is 1897.6 869.6
Best chromosome for g = 1662 is center 147 is 1915.5555555555557 1046.7777777777778
Best chromosome for g = 1662 is center 148 is 1900.4444444444443 1200.0
Best chromosome for g = 1662 is center 149 is 2060.8333333333335 744.6666666666666
Best chromosome for g = 1662 is center 150 is 2245.125 481.75
Best chromosome for g = 1662 is center 151 is 2424.8 404.8
Best chromosome for g = 1662 is center 152 is 2128.4 615.3
Best chromosome for g = 1662 is center 153 is 2313.75 607.625
Best chromosome for g = 1662 is center 154 is 2612.75 383.0
Best chromosome for g = 1662 is center 155 is 2509.8888888888887 565.2222222222222
Best chromosome for g = 1662 is center 156 is 2298.8888888888887 730.6666666666666
Best chromosome for g = 1662 is center 157 is 2160.1428571428573 858.4285714285714
Best chromosome for g = 1662 is center 158 is 2654.1666666666665 549.0
Best chromosome for g = 1662 is center 159 is 2504.25 711.0
Best chromosome for g = 1662 is center 160 is 2371.3333333333335 884.1666666666666
Best chromosome for g = 1662 is center 161 is 2547.4285714285716 867.0
Best chromosome for g = 1662 is center 162 is 2079.75 1057.0
Best chromosome for g = 1662 is center 163 is 2246.5 1085.0
Best chromosome for g = 1662 is center 164 is 2643.8 726.4
Best chromosome for g = 1662 is center 165 is 2810.75 326.875
Best chromosome for g = 1662 is center 166 is 2781.0 498.8333333333333
Best chromosome for g = 1662 is center 167 is 2778.5714285714284 613.4285714285714
Best chromosome for g = 1662 is center 168 is 2781.0 751.375
Best chromosome for g = 1662 is center 169 is 322.1111111111111 2274.8888888888887
Best chromosome for g = 1662 is center 170 is 41.7 2583.2
Best chromosome for g = 1662 is center 171 is 176.44444444444446 2393.8888888888887
Best chromosome for g = 1662 is center 172 is 140.7 2510.9
Best chromosome for g = 1662 is center 173 is 447.0 2270.0

```
Best chromosome for g = 1662 is center 174 is 321.8888888888889
2390.8888888888887
Best chromosome for g = 1662 is center 175 is 462.4 2444.4
Best chromosome for g = 1662 is center 176 is 327.5 2573.75
Best chromosome for g = 1662 is center 177 is 49.333333333333336
2718.1111111111113
Best chromosome for g = 1662 is center 178 is 152.11111111111111
2638.6666666666665
Best chromosome for g = 1662 is center 179 is 56.083333333333336
2852.5833333333335
Best chromosome for g = 1662 is center 180 is -66.0 3134.0
Best chromosome for g = 1662 is center 181 is 169.3 2753.3
Best chromosome for g = 1662 is center 182 is 173.0 2893.8
Best chromosome for g = 1662 is center 183 is 310.77777777777777
2738.5555555555557
Best chromosome for g = 1662 is center 184 is 300.25 2890.25
Best chromosome for g = 1662 is center 185 is 137.77777777777777
3170.222222222222
Best chromosome for g = 1662 is center 186 is 124.75 3330.5
Best chromosome for g = 1662 is center 187 is 1869.6 1348.0
Best chromosome for g = 1662 is center 188 is 2045.625 1251.25
Best chromosome for g = 1662 is center 189 is 1965.8 1401.4
Best chromosome for g = 1662 is center 190 is 1581.5555555555557
1528.3333333333333
Best chromosome for g = 1662 is center 191 is 617.2222222222222
2179.6666666666665
Best chromosome for g = 1662 is center 192 is 780.8333333333334 2120.0
Best chromosome for g = 1662 is center 193 is 1000.7142857142857
1885.2857142857142
Best chromosome for g = 1662 is center 194 is 905.875 2000.5
Best chromosome for g = 1662 is center 195 is 1139.857142857143
1865.2857142857142
Best chromosome for g = 1662 is center 196 is 1387.4 1744.2
Best chromosome for g = 1662 is center 197 is 1264.6666666666667
1887.3333333333333
Best chromosome for g = 1662 is center 198 is 1720.3333333333333
1521.888888888889
Best chromosome for g = 1662 is center 199 is 1712.1666666666667
1700.8333333333333
Best chromosome for g = 1662 is center 200 is 1877.25 1605.625
Best chromosome for g = 1662 is center 201 is 2167.4285714285716
1170.857142857143
Best chromosome for g = 1662 is center 202 is 2361.0 1099.4
Best chromosome for g = 1662 is center 203 is 2136.714285714286
1334.4285714285713
Best chromosome for g = 1662 is center 204 is 2310.6666666666665
1216.6666666666667
Best chromosome for g = 1662 is center 205 is 1999.75 1581.0
Best chromosome for g = 1662 is center 206 is 2301.2 1334.2
Best chromosome for g = 1662 is center 207 is 2201.875 1520.0
Best chromosome for g = 1662 is center 208 is 2409.8333333333335
1443.8333333333333
Best chromosome for g = 1662 is center 209 is 499.57142857142856
2619.714285714286
```

```
Best chromosome for g = 1662 is center 210 is 627.125 2334.5
Best chromosome for g = 1662 is center 211 is 626.3333333333334 2484.5
Best chromosome for g = 1662 is center 212 is 919.3333333333334
2136.1111111111113
Best chromosome for g = 1662 is center 213 is 1153.111111111111 2051.0
Best chromosome for g = 1662 is center 214 is 1433.8 1883.0
Best chromosome for g = 1662 is center 215 is 915.2222222222222
2294.6666666666665
Best chromosome for g = 1662 is center 216 is 1193.4545454545455
2190.7272727272725
Best chromosome for g = 1662 is center 217 is 502.125 2765.875
Best chromosome for g = 1662 is center 218 is 626.6666666666666
2648.4444444444443
Best chromosome for g = 1662 is center 219 is 624.8571428571429 2784.0
Best chromosome for g = 1662 is center 220 is 509.0 2916.714285714286
Best chromosome for g = 1662 is center 221 is 1191.4 2329.1
Best chromosome for g = 1662 is center 222 is 894.7 2458.6
Best chromosome for g = 1662 is center 223 is 1150.7777777777778
2495.4444444444443
Best chromosome for g = 1662 is center 224 is 861.0 2650.6666666666665
Best chromosome for g = 1662 is center 225 is 739.7142857142857 2725.0
Best chromosome for g = 1662 is center 226 is 727.8 2865.4
Best chromosome for g = 1662 is center 227 is 962.7142857142857
2683.5714285714284
Best chromosome for g = 1662 is center 228 is 419.7142857142857
3047.1428571428573
Best chromosome for g = 1662 is center 229 is 622.625 2911.75
Best chromosome for g = 1662 is center 230 is 302.55555555555554 3185.0
Best chromosome for g = 1662 is center 231 is 275.125 3318.5
Best chromosome for g = 1662 is center 232 is 569.4285714285714
3169.4285714285716
Best chromosome for g = 1662 is center 233 is 897.25 2834.375
Best chromosome for g = 1662 is center 234 is 1116.0 2724.6
Best chromosome for g = 1662 is center 235 is 819.8333333333334 2987.0
Best chromosome for g = 1662 is center 236 is 456.85714285714283 3247.0
Best chromosome for g = 1662 is center 237 is 704.125 3144.25
Best chromosome for g = 1662 is center 238 is 978.6 3007.8
Best chromosome for g = 1662 is center 239 is 903.2857142857143 3136.0
Best chromosome for g = 1662 is center 240 is 1109.9 2871.0
Best chromosome for g = 1662 is center 241 is 1428.0 2368.25
Best chromosome for g = 1662 is center 242 is 1319.0 2546.0
Best chromosome for g = 1662 is center 243 is 1440.2222222222222
2060.6666666666665
Best chromosome for g = 1662 is center 244 is 1456.4 2217.2
Best chromosome for g = 1662 is center 245 is 1478.3333333333333
2541.3333333333335
Best chromosome for g = 1662 is center 246 is 1324.875 2695.25
Best chromosome for g = 1662 is center 247 is 1305.6666666666667 2823.0
Best chromosome for g = 1662 is center 248 is 1571.2857142857142
1846.5714285714287
Best chromosome for g = 1662 is center 249 is 1694.0 1888.0
Best chromosome for g = 1662 is center 250 is 1999.125 1736.5
Best chromosome for g = 1662 is center 251 is 1866.2 1777.6
Best chromosome for g = 1662 is center 252 is 1634.3 2067.7
```

```
Best chromosome for g = 1662 is center 253 is 1807.2857142857142
2025.5714285714287
Best chromosome for g = 1662 is center 254 is 2037.857142857143
1874.5714285714287
Best chromosome for g = 1662 is center 255 is 1820.875 2179.75
Best chromosome for g = 1662 is center 256 is 1630.625 2224.375
Best chromosome for g = 1662 is center 257 is 2000.3333333333333
2089.5555555555557
Best chromosome for g = 1662 is center 258 is 1644.0 2379.1111111111113
Best chromosome for g = 1662 is center 259 is 1808.5 2334.8
Best chromosome for g = 1662 is center 260 is 1650.8 2530.2
Best chromosome for g = 1662 is center 261 is 1980.5454545454545
2263.181818181818
Best chromosome for g = 1662 is center 262 is 2174.875 1655.375
Best chromosome for g = 1662 is center 263 is 2183.777777777778
1811.111111111111
Best chromosome for g = 1662 is center 264 is 2349.5 1559.3333333333333
Best chromosome for g = 1662 is center 265 is 2348.75 1695.625
Best chromosome for g = 1662 is center 266 is 2344.5 1843.125
Best chromosome for g = 1662 is center 267 is 2224.875 1988.125
Best chromosome for g = 1662 is center 268 is 2152.875 2122.0
Best chromosome for g = 1662 is center 269 is 1839.5714285714287 2481.0
Best chromosome for g = 1662 is center 270 is 1241.4 2982.0
Best chromosome for g = 1662 is center 271 is 1530.8333333333333
2722.1666666666665
Best chromosome for g = 1662 is center 272 is 1393.8333333333333
2907.3333333333335
Best chromosome for g = 1662 is center 273 is 1536.0 2873.375
Best chromosome for g = 1662 is center 274 is 1979.5555555555557
2404.5555555555557
Best chromosome for g = 1662 is center 275 is 1745.7 2727.2
Best chromosome for g = 1662 is center 276 is 2169.75 2260.8333333333335
Best chromosome for g = 1662 is center 277 is 1995.6 2615.8
Best chromosome for g = 1662 is center 278 is 1742.6363636363637
2885.181818181818
Best chromosome for g = 1662 is center 279 is 2354.1428571428573
2077.5714285714284
Best chromosome for g = 1662 is center 280 is 2181.3333333333335
2408.6666666666665
Best chromosome for g = 1662 is center 281 is 2327.090909090909
2231.181818181818
Best chromosome for g = 1662 is center 282 is 864.5 3259.875
Best chromosome for g = 1662 is center 283 is 1117.0 3140.6666666666665
Best chromosome for g = 1662 is center 284 is 1335.1666666666667
3106.8333333333335
Best chromosome for g = 1662 is center 285 is 1473.6666666666667
3091.8333333333335
Best chromosome for g = 1662 is center 286 is 1293.7 3224.6
Best chromosome for g = 1662 is center 287 is 2510.1111111111113
1053.3333333333333
Best chromosome for g = 1662 is center 288 is 2506.1 1212.9
Best chromosome for g = 1662 is center 289 is 2648.6 1107.6
Best chromosome for g = 1662 is center 290 is 2638.0 1257.7142857142858
```

Best chromosome for g = 1662 is center 291 is 2499.3333333333335 1359.4444444444443
Best chromosome for g = 1662 is center 292 is 2525.5714285714284 1588.4285714285713
Best chromosome for g = 1662 is center 293 is 2647.4285714285716 1516.4285714285713
Best chromosome for g = 1662 is center 294 is 2521.3333333333335 1715.5
Best chromosome for g = 1662 is center 295 is 2529.375 1845.75
Best chromosome for g = 1662 is center 296 is 2510.222222222222 2039.5555555555557
Best chromosome for g = 1662 is center 297 is 2750.6 991.0
Best chromosome for g = 1662 is center 298 is 2787.714285714286 1140.7142857142858
Best chromosome for g = 1662 is center 299 is 2786.4444444444443 1269.0
Best chromosome for g = 1662 is center 300 is 2769.8571428571427 1413.142857142857
Best chromosome for g = 1662 is center 301 is 2772.3333333333335 1566.0
Best chromosome for g = 1662 is center 302 is 2659.75 1718.375
Best chromosome for g = 1662 is center 303 is 2780.5 1697.6666666666667
Best chromosome for g = 1662 is center 304 is 1932.75 2719.5
Best chromosome for g = 1662 is center 305 is 2357.8888888888887 2420.777777777778
Best chromosome for g = 1662 is center 306 is 2155.0 2610.75
Best chromosome for g = 1662 is center 307 is 1949.875 2875.5
Best chromosome for g = 1662 is center 308 is 2158.2 2757.7
Best chromosome for g = 1662 is center 309 is 1658.142857142857 3073.285714285714
Best chromosome for g = 1662 is center 310 is 1559.142857142857 3208.4285714285716
Best chromosome for g = 1662 is center 311 is 1952.0 3055.0
Best chromosome for g = 1662 is center 312 is 1760.2857142857142 3156.1428571428573
Best chromosome for g = 1662 is center 313 is 2752.0 1826.875
Best chromosome for g = 1662 is center 314 is 2517.8888888888887 2208.0
Best chromosome for g = 1662 is center 315 is 2662.6 2023.8
Best chromosome for g = 1662 is center 316 is 2671.0 2202.4
Best chromosome for g = 1662 is center 317 is 2780.8888888888887 2129.0
Best chromosome for g = 1662 is center 318 is 2347.0 2618.5
Best chromosome for g = 1662 is center 319 is 2780.8333333333335 2260.0
Best chromosome for g = 1662 is center 320 is 2668.2 2343.4
Best chromosome for g = 1662 is center 321 is 2511.8888888888887 2456.4444444444443
Best chromosome for g = 1662 is center 322 is 2709.714285714286 2493.4285714285716
Best chromosome for g = 1662 is center 323 is 2508.75 2601.25
Best chromosome for g = 1662 is center 324 is 2779.285714285714 2374.5714285714284
Best chromosome for g = 1662 is center 325 is 2323.6666666666665 2759.1111111111113
Best chromosome for g = 1662 is center 326 is 2149.625 2917.75
Best chromosome for g = 1662 is center 327 is 2334.0 2925.5555555555557
Best chromosome for g = 1662 is center 328 is 2493.777777777778 2782.8888888888887

Best chromosome for g = 1662 is center 329 is 2133.714285714286 3101.5714285714284
Best chromosome for g = 1662 is center 330 is 2504.0 2963.6
Best chromosome for g = 1662 is center 331 is 2334.222222222222 3122.0
Best chromosome for g = 1662 is center 332 is 2545.5 3108.8
Best chromosome for g = 1662 is center 333 is 2693.1666666666665 2655.5
Best chromosome for g = 1662 is center 334 is 2664.0 2905.3333333333335
Best chromosome for g = 1662 is center 335 is 2779.6666666666665 3068.1666666666665
Best chromosome for g = 1662 is center 336 is 95.5 3511.375
Best chromosome for g = 1662 is center 337 is 114.3 3621.1
Best chromosome for g = 1662 is center 338 is 0.5 3893.75
Best chromosome for g = 1662 is center 339 is 394.77777777777777 3393.4444444444443
Best chromosome for g = 1662 is center 340 is 249.0 3493.4
Best chromosome for g = 1662 is center 341 is 396.375 3521.0
Best chromosome for g = 1662 is center 342 is 699.8888888888889 3291.4444444444443
Best chromosome for g = 1662 is center 343 is 567.3333333333334 3353.8333333333335
Best chromosome for g = 1662 is center 344 is 706.0 3438.5714285714284
Best chromosome for g = 1662 is center 345 is 96.66666666666667 3736.5555555555557
Best chromosome for g = 1662 is center 346 is 144.0 3849.777777777778
Best chromosome for g = 1662 is center 347 is 312.375 3614.875
Best chromosome for g = 1662 is center 348 is 311.875 3743.25
Best chromosome for g = 1662 is center 349 is 300.4 3861.8
Best chromosome for g = 1662 is center 350 is 567.0 3576.4
Best chromosome for g = 1662 is center 351 is 440.42857142857144 3676.0
Best chromosome for g = 1662 is center 352 is 720.125 3569.25
Best chromosome for g = 1662 is center 353 is 536.0 3766.875
Best chromosome for g = 1662 is center 354 is 476.75 3867.625
Best chromosome for g = 1662 is center 355 is 708.6666666666666 3705.6666666666665
Best chromosome for g = 1662 is center 356 is 690.2857142857143 3855.8571428571427
Best chromosome for g = 1662 is center 357 is 951.6666666666666 3402.0
Best chromosome for g = 1662 is center 358 is 909.6 3567.6
Best chromosome for g = 1662 is center 359 is 901.6 3707.5
Best chromosome for g = 1662 is center 360 is 883.6363636363636 3837.5454545454545
Best chromosome for g = 1662 is center 361 is 1109.375 3299.75
Best chromosome for g = 1662 is center 362 is 1325.857142857143 3353.5714285714284
Best chromosome for g = 1662 is center 363 is 1536.1666666666667 3327.6666666666665
Best chromosome for g = 1662 is center 364 is 1110.7142857142858 3559.285714285714
Best chromosome for g = 1662 is center 365 is 1061.0 3705.5
Best chromosome for g = 1662 is center 366 is 1200.1 3704.8
Best chromosome for g = 1662 is center 367 is 1313.625 3595.25
Best chromosome for g = 1662 is center 368 is 1647.857142857143 3429.285714285714

```
Best chromosome for g = 1662 is center 369 is 1449.2857142857142
3535.8571428571427
Best chromosome for g = 1662 is center 370 is 1695.8 3280.8
Best chromosome for g = 1662 is center 371 is 1807.6666666666667
3305.8333333333335
Best chromosome for g = 1662 is center 372 is 1949.5 3222.0
Best chromosome for g = 1662 is center 373 is 1110.75 3838.875
Best chromosome for g = 1662 is center 374 is 1608.8333333333333
3607.8333333333335
Best chromosome for g = 1662 is center 375 is 1317.7777777777778
3830.8888888888887
Best chromosome for g = 1662 is center 376 is 1531.888888888889
3714.4444444444443
Best chromosome for g = 1662 is center 377 is 1746.375 3627.5
Best chromosome for g = 1662 is center 378 is 1462.0 3854.2
Best chromosome for g = 1662 is center 379 is 1972.375 3361.375
Best chromosome for g = 1662 is center 380 is 2166.714285714286
3221.1428571428573
Best chromosome for g = 1662 is center 381 is 2131.8333333333335
3340.8333333333335
Best chromosome for g = 1662 is center 382 is 1939.5 3624.2
Best chromosome for g = 1662 is center 383 is 2333.4 3274.2
Best chromosome for g = 1662 is center 384 is 2538.222222222222
3263.6666666666665
Best chromosome for g = 1662 is center 385 is 1640.888888888889
3868.222222222222
Best chromosome for g = 1662 is center 386 is 1758.625 3787.375
Best chromosome for g = 1662 is center 387 is 1925.3333333333333
3781.3333333333335
Best chromosome for g = 1662 is center 388 is 2108.3333333333335
3646.3333333333335
Best chromosome for g = 1662 is center 389 is 1985.375 3852.0
Best chromosome for g = 1662 is center 390 is 2391.5 3435.3333333333335
Best chromosome for g = 1662 is center 391 is 2142.3333333333335 3825.5
Best chromosome for g = 1662 is center 392 is 2729.5714285714284
3194.1428571428573
Best chromosome for g = 1662 is center 393 is 2563.777777777778
3390.222222222222
Best chromosome for g = 1662 is center 394 is 2781.777777777778
3350.4444444444443
Best chromosome for g = 1662 is center 395 is 2793.3333333333335
3517.3333333333335
Best chromosome for g = 1662 is center 396 is 2444.5 3754.0
Best chromosome for g = 1662 is center 397 is 2701.0 3919.25
Best chromosome for g = 1662 is center 398 is 2797.5 3795.0
Best chromosome for g = 1662 is center 399 is 1377.5 3733.75
Time Elapsed: 8.19008786E8 Seeding Time: 226777.0
The seeding percentage time is : 0.000277
```

TSP-LIB-3038, *k* = 450: Separation, Deterministic

```
Random = 0
Density = 0
Separation = 200
Selection Method = 2
Number of centers = 450
After 0 generations new best SSE for g = 0 is 9413370.34094239
After 1 generations new best SSE for g = 1 is 9380725.692962553
After 1 generations new best SSE for g = 2 is 9363081.110669887
After 2 generations new best SSE for g = 4 is 9296523.187168395
After 1 generations new best SSE for g = 5 is 9249175.688791772
After 2 generations new best SSE for g = 7 is 9205618.740631595
After 1 generations new best SSE for g = 8 is 9186034.740698196
After 1 generations new best SSE for g = 9 is 9148024.644144744
After 2 generations new best SSE for g = 11 is 9083269.053746244
After 4 generations new best SSE for g = 15 is 9052444.585076055
After 1 generations new best SSE for g = 16 is 9047756.1870546
After 1 generations new best SSE for g = 17 is 9030558.831499046
After 3 generations new best SSE for g = 20 is 9007720.0053974
After 3 generations new best SSE for g = 23 is 8963894.71649185
After 4 generations new best SSE for g = 27 is 8962607.983699642
After 1 generations new best SSE for g = 28 is 8955247.521289824
After 1 generations new best SSE for g = 29 is 8923156.969175274
After 2 generations new best SSE for g = 31 is 8911621.426742699
After 1 generations new best SSE for g = 32 is 8884579.385503408
After 6 generations new best SSE for g = 38 is 8881417.302211696
After 1 generations new best SSE for g = 39 is 8878974.195027215
After 1 generations new best SSE for g = 40 is 8875665.024328468
After 1 generations new best SSE for g = 41 is 8871263.83754302
After 1 generations new best SSE for g = 42 is 8863736.864468884
After 1 generations new best SSE for g = 43 is 8855779.155416816
After 1 generations new best SSE for g = 44 is 8842308.367501955
After 1 generations new best SSE for g = 45 is 8838878.88937174
After 1 generations new best SSE for g = 46 is 8834137.419230767
After 1 generations new best SSE for g = 47 is 8785647.77435065
After 10 generations new best SSE for g = 57 is 8777815.381640581
After 1 generations new best SSE for g = 58 is 8767028.898629138
After 2 generations new best SSE for g = 60 is 8762458.006096682
After 1 generations new best SSE for g = 61 is 8758955.88435454
After 1 generations new best SSE for g = 62 is 8742554.680880226
After 2 generations new best SSE for g = 64 is 8726690.437101796
After 1 generations new best SSE for g = 65 is 8716058.577308794
After 2 generations new best SSE for g = 67 is 8690923.163009211
After 3 generations new best SSE for g = 70 is 8686255.792460322
After 3 generations new best SSE for g = 73 is 8666272.482178953
After 1 generations new best SSE for g = 74 is 8650698.667640714
After 1 generations new best SSE for g = 75 is 8649897.128355
After 13 generations new best SSE for g = 88 is 8625439.223989924
After 9 generations new best SSE for g = 97 is 8609439.667640718
After 6 generations new best SSE for g = 103 is 8590174.773376612
After 10 generations new best SSE for g = 113 is 8585697.413492082
After 3 generations new best SSE for g = 116 is 8578423.780436216
After 3 generations new best SSE for g = 119 is 8572588.727317141
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After 8 generations new best SSE for g = 127 is 8565375.110392377
After 1 generations new best SSE for g = 128 is 8545352.95362417
After 3 generations new best SSE for g = 131 is 8540574.505303046
After 7 generations new best SSE for g = 138 is 8537218.202816647
After 6 generations new best SSE for g = 144 is 8530847.957178922
After 4 generations new best SSE for g = 148 is 8530061.355130991
After 6 generations new best SSE for g = 154 is 8513084.055092115
After 1 generations new best SSE for g = 155 is 8501877.989901775
After 2 generations new best SSE for g = 157 is 8500859.563816754
After 6 generations new best SSE for g = 163 is 8490342.807398176
After 4 generations new best SSE for g = 167 is 8478380.579223543
After 6 generations new best SSE for g = 173 is 8477969.488564214
After 5 generations new best SSE for g = 178 is 8463186.856277054
After 3 generations new best SSE for g = 181 is 8462158.707706183
After 2 generations new best SSE for g = 183 is 8460625.189610388
After 5 generations new best SSE for g = 188 is 8446672.249458881
After 6 generations new best SSE for g = 194 is 8440370.70977634
After 4 generations new best SSE for g = 198 is 8426309.344336217
After 8 generations new best SSE for g = 206 is 8422810.616269838
After 8 generations new best SSE for g = 214 is 8413779.26836219
After 2 generations new best SSE for g = 216 is 8412846.919369517
After 9 generations new best SSE for g = 225 is 8412530.005083803
After 4 generations new best SSE for g = 229 is 8411731.453715723
After 3 generations new best SSE for g = 232 is 8375152.184235223
After 9 generations new best SSE for g = 241 is 8368780.289393951
After 11 generations new best SSE for g = 252 is 8364835.481457443
After 22 generations new best SSE for g = 274 is 8359363.872727277
After 4 generations new best SSE for g = 278 is 8348852.963170152
After 8 generations new best SSE for g = 286 is 8347636.545598854
After 8 generations new best SSE for g = 294 is 8346896.179220789
After 7 generations new best SSE for g = 301 is 8342549.583405495
After 3 generations new best SSE for g = 304 is 8338642.144985563
After 2 generations new best SSE for g = 306 is 8338567.076695539
After 3 generations new best SSE for g = 309 is 8323573.185101002
After 4 generations new best SSE for g = 313 is 8321057.287448664
After 1 generations new best SSE for g = 314 is 8318762.674531027
After 13 generations new best SSE for g = 327 is 8317410.957362076
After 4 generations new best SSE for g = 331 is 8306116.0277805505
After 13 generations new best SSE for g = 344 is 8304252.4145770855
After 4 generations new best SSE for g = 348 is 8303157.285281384
After 4 generations new best SSE for g = 352 is 8295022.177780541
After 10 generations new best SSE for g = 362 is 8285446.050796413
After 4 generations new best SSE for g = 366 is 8279403.022224984
After 7 generations new best SSE for g = 373 is 8276924.410569977
After 25 generations new best SSE for g = 398 is 8274856.168109663
After 2 generations new best SSE for g = 400 is 8272929.035894669
After 1 generations new best SSE for g = 401 is 8267229.5185064925
After 11 generations new best SSE for g = 412 is 8267172.506818196
After 1 generations new best SSE for g = 413 is 8263913.012554119
After 9 generations new best SSE for g = 422 is 8262110.653246752
After 4 generations new best SSE for g = 426 is 8253353.1319264015
After 5 generations new best SSE for g = 431 is 8248450.717424242
After 13 generations new best SSE for g = 444 is 8246872.580519482
After 4 generations new best SSE for g = 448 is 8244982.956132766
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After 10 generations new best SSE for g = 458 is 8240558.774025978
After 9 generations new best SSE for g = 467 is 8231372.042712846
After 1 generations new best SSE for g = 468 is 8227180.992748928
After 18 generations new best SSE for g = 486 is 8221070.196500713
After 1 generations new best SSE for g = 487 is 8220019.220490624
After 1 generations new best SSE for g = 488 is 8219792.55263348
After 7 generations new best SSE for g = 495 is 8217175.1880591735
After 1 generations new best SSE for g = 496 is 8216562.207900444
After 20 generations new best SSE for g = 516 is 8216467.330916317
After 6 generations new best SSE for g = 522 is 8216162.307106792
After 2 generations new best SSE for g = 524 is 8209433.585281394
After 5 generations new best SSE for g = 529 is 8206920.34310967
After 15 generations new best SSE for g = 544 is 8204756.273520935
After 4 generations new best SSE for g = 548 is 8200695.011616173
After 14 generations new best SSE for g = 562 is 8198137.243759028
After 2 generations new best SSE for g = 564 is 8195600.075685437
After 20 generations new best SSE for g = 584 is 8189631.532106794
After 5 generations new best SSE for g = 589 is 8188947.641342003
After 2 generations new best SSE for g = 591 is 8188827.64054835
After 1 generations new best SSE for g = 592 is 8187873.992532484
After 16 generations new best SSE for g = 608 is 8186686.92745312
After 8 generations new best SSE for g = 616 is 8182514.522005785
After 18 generations new best SSE for g = 634 is 8181661.465548343
After 5 generations new best SSE for g = 639 is 8175588.948809542
After 2 generations new best SSE for g = 641 is 8174396.675937971
After 35 generations new best SSE for g = 676 is 8174067.585858604
After 3 generations new best SSE for g = 679 is 8172394.847258313
After 6 generations new best SSE for g = 685 is 8171500.886507948
After 4 generations new best SSE for g = 689 is 8169877.283477649
After 4 generations new best SSE for g = 693 is 8169226.433261191
After 12 generations new best SSE for g = 705 is 8166529.019408384
After 7 generations new best SSE for g = 712 is 8164883.449927863
After 1 generations new best SSE for g = 713 is 8163781.365331898
After 8 generations new best SSE for g = 721 is 8162889.0288239615
After 8 generations new best SSE for g = 729 is 8162560.374242443
After 2 generations new best SSE for g = 731 is 8157445.006746039
After 8 generations new best SSE for g = 739 is 8154677.653030303
After 34 generations new best SSE for g = 773 is 8150097.263383859
After 9 generations new best SSE for g = 782 is 8146645.198701319
After 13 generations new best SSE for g = 795 is 8146360.986904772
After 37 generations new best SSE for g = 832 is 8143247.089610404
After 29 generations new best SSE for g = 861 is 8141803.980808082
After 23 generations new best SSE for g = 884 is 8140870.9210317675
After 5 generations new best SSE for g = 889 is 8139956.521500735
After 8 generations new best SSE for g = 897 is 8139882.899458882
After 9 generations new best SSE for g = 906 is 8139068.8636003025
After 7 generations new best SSE for g = 913 is 8138148.966486307
After 11 generations new best SSE for g = 924 is 8136336.6755050635
After 10 generations new best SSE for g = 934 is 8135423.858838393
After 6 generations new best SSE for g = 940 is 8134911.319696975
After 10 generations new best SSE for g = 950 is 8133654.6974747535
After 17 generations new best SSE for g = 967 is 8132415.923015876
After 4 generations new best SSE for g = 971 is 8127272.8199855825
After 27 generations new best SSE for g = 998 is 8127083.135930749
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After 2 generations new best SSE for g = 1000 is 8126640.75028861
After 6 generations new best SSE for g = 1006 is 8125783.882359316
After 18 generations new best SSE for g = 1024 is 8125452.456601742
After 4 generations new best SSE for g = 1028 is 8124923.0073953895
After 12 generations new best SSE for g = 1040 is 8124191.529617611
After 13 generations new best SSE for g = 1053 is 8124061.311075053
After 6 generations new best SSE for g = 1059 is 8122997.835173166
After 9 generations new best SSE for g = 1068 is 8122984.746284277
After 1 generations new best SSE for g = 1069 is 8122437.365331897
After 7 generations new best SSE for g = 1076 is 8122408.6685065
After 8 generations new best SSE for g = 1084 is 8121263.60541126
After 2 generations new best SSE for g = 1086 is 8121212.904906214
After 8 generations new best SSE for g = 1094 is 8120713.168903336
After 4 generations new best SSE for g = 1098 is 8120225.350865818
After 1 generations new best SSE for g = 1099 is 8120058.031204923
After 5 generations new best SSE for g = 1104 is 8119471.879978368
After 6 generations new best SSE for g = 1110 is 8119395.409379525
After 1 generations new best SSE for g = 1111 is 8119155.947655138
After 3 generations new best SSE for g = 1114 is 8118447.4357503755
After 3 generations new best SSE for g = 1117 is 8118280.116089482
After 44 generations new best SSE for g = 1161 is 8117546.5433261255
After 2 generations new best SSE for g = 1163 is 8116791.839898998
After 3 generations new best SSE for g = 1166 is 8116377.05894662
After 33 generations new best SSE for g = 1199 is 8116335.5157287335
After 10 generations new best SSE for g = 1209 is 8116287.361544031
After 28 generations new best SSE for g = 1237 is 8116275.367243885
After 20 generations new best SSE for g = 1257 is 8115624.934271299
After 7 generations new best SSE for g = 1264 is 8115452.328354993
After 1 generations new best SSE for g = 1265 is 8115308.847402614
After 5 generations new best SSE for g = 1270 is 8115190.949025988
After 16 generations new best SSE for g = 1286 is 8114615.359523825
After 12 generations new best SSE for g = 1298 is 8114555.211038977
After 7 generations new best SSE for g = 1305 is 8113903.784199148
After 11 generations new best SSE for g = 1316 is 8113581.631601746
After 65 generations new best SSE for g = 1381 is 8113552.576731617
After 1 generations new best SSE for g = 1382 is 8113368.148665233
After 2 generations new best SSE for g = 1384 is 8113173.526767696
After 2 generations new best SSE for g = 1386 is 8112743.755880245
After 11 generations new best SSE for g = 1397 is 8112179.8110750485
After 5 generations new best SSE for g = 1402 is 8111938.181998571
After 27 generations new best SSE for g = 1429 is 8111914.8398629315
After 16 generations new best SSE for g = 1445 is 8111507.968217909
After 6 generations new best SSE for g = 1451 is 8111436.892460327
After 13 generations new best SSE for g = 1464 is 8111241.48156567
After 7 generations new best SSE for g = 1471 is 8111089.8666306045
After 24 generations new best SSE for g = 1495 is 8110787.388275627
After 11 generations new best SSE for g = 1506 is 8110691.547366538
After 14 generations new best SSE for g = 1520 is 8110201.339826853
After 3 generations new best SSE for g = 1523 is 8109951.228968264
After 15 generations new best SSE for g = 1538 is 8109772.052164512
After 80 generations new best SSE for g = 1618 is 8109496.864862929
After 13 generations new best SSE for g = 1631 is 8109468.137157304
After 12 generations new best SSE for g = 1643 is 8109159.258189049
After 18 generations new best SSE for g = 1661 is 8108763.05386004
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After 52 generations new best SSE for g = 1713 is 8107357.846717184
After 84 generations new best SSE for g = 1797 is 8107324.763383851
After 50 generations new best SSE for g = 1847 is 8106706.330050517
After 13 generations new best SSE for g = 1860 is 8105966.2205267055
After 23 generations new best SSE for g = 1883 is 8105779.528860036
After 12 generations new best SSE for g = 1895 is 8105072.646717185
After 42 generations new best SSE for g = 1937 is 8104470.239971154
After 19 generations new best SSE for g = 1956 is 8104403.61219337
After 4 generations new best SSE for g = 1960 is 8104392.55981242
After 6 generations new best SSE for g = 1966 is 8104106.462590205
After 2 generations new best SSE for g = 1968 is 8103696.730050519
After 3 generations new best SSE for g = 1971 is 8103218.059415596
After 12 generations new best SSE for g = 1983 is 8103060.44671719
After 8 generations new best SSE for g = 1991 is 8102366.037590197
After 4 generations new best SSE for g = 1995 is 8102172.04354258
After 43 generations new best SSE for g = 2038 is 8101832.09711401
After 35 generations new best SSE for g = 2073 is 8101601.269733058
Best SSE for g = 2173 is 8101601.269733058
Best chromosome for g = 2173 is center 0 is 31.5 90.33333333333333
Best chromosome for g = 2173 is center 1 is 374.3333333333333 48.0
Best chromosome for g = 2173 is center 2 is 189.8 91.6
Best chromosome for g = 2173 is center 3 is 833.8333333333334 101.0
Best chromosome for g = 2173 is center 4 is 1285.0 108.22222222222223
Best chromosome for g = 2173 is center 5 is 1461.7142857142858
98.71428571428571
Best chromosome for g = 2173 is center 6 is 1656.25 104.75
Best chromosome for g = 2173 is center 7 is 1900.1666666666667
97.66666666666667
Best chromosome for g = 2173 is center 8 is 2246.8333333333335
89.33333333333333
Best chromosome for g = 2173 is center 9 is 2504.0 108.75
Best chromosome for g = 2173 is center 10 is 2655.8571428571427
64.42857142857143
Best chromosome for g = 2173 is center 11 is 2801.1428571428573
67.71428571428571
Best chromosome for g = 2173 is center 12 is 42.888888888888886
342.3333333333333
Best chromosome for g = 2173 is center 13 is 160.0 199.71428571428572
Best chromosome for g = 2173 is center 14 is 88.0 511.25
Best chromosome for g = 2173 is center 15 is 10.166666666666666 590.0
Best chromosome for g = 2173 is center 16 is 128.0 683.0
Best chromosome for g = 2173 is center 17 is -61.0 801.0
Best chromosome for g = 2173 is center 18 is 320.75 184.125
Best chromosome for g = 2173 is center 19 is 489.1111111111111
183.33333333333334
Best chromosome for g = 2173 is center 20 is 677.5 120.8
Best chromosome for g = 2173 is center 21 is 933.1666666666666
151.83333333333334
Best chromosome for g = 2173 is center 22 is 1104.2222222222222
121.66666666666667
Best chromosome for g = 2173 is center 23 is 184.0 324.875
Best chromosome for g = 2173 is center 24 is 270.57142857142856
493.42857142857144
```

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Best chromosome for g = 2173 is center 25 is 266.22222222222223
710.3333333333334
Best chromosome for g = 2173 is center 26 is 336.0 317.14285714285717
Best chromosome for g = 2173 is center 27 is 669.8333333333334
265.8333333333333
Best chromosome for g = 2173 is center 28 is 889.8571428571429
264.2857142857143
Best chromosome for g = 2173 is center 29 is 1091.4444444444443
271.22222222222223
Best chromosome for g = 2173 is center 30 is 509.5 330.625
Best chromosome for g = 2173 is center 31 is 433.3333333333333
487.3333333333333
Best chromosome for g = 2173 is center 32 is 412.1666666666667 665.5
Best chromosome for g = 2173 is center 33 is 411.0 817.1666666666666
Best chromosome for g = 2173 is center 34 is 602.0 519.2
Best chromosome for g = 2173 is center 35 is 708.3333333333334
360.1666666666667
Best chromosome for g = 2173 is center 36 is 530.0 673.8
Best chromosome for g = 2173 is center 37 is 860.5 373.25
Best chromosome for g = 2173 is center 38 is 640.0 707.5
Best chromosome for g = 2173 is center 39 is 984.8333333333334
511.3333333333333
Best chromosome for g = 2173 is center 40 is 789.0 626.5
Best chromosome for g = 2173 is center 41 is 523.5 824.0
Best chromosome for g = 2173 is center 42 is 922.8571428571429
691.2857142857143
Best chromosome for g = 2173 is center 43 is 1280.7 258.2
Best chromosome for g = 2173 is center 44 is 1163.8 402.2
Best chromosome for g = 2173 is center 45 is 1462.3333333333333
205.22222222222223
Best chromosome for g = 2173 is center 46 is 1394.6666666666667
308.1666666666667
Best chromosome for g = 2173 is center 47 is 1530.3333333333333
308.3333333333333
Best chromosome for g = 2173 is center 48 is 1108.8181818181818
596.6363636363636
Best chromosome for g = 2173 is center 49 is 1299.3333333333333
529.7777777777778
Best chromosome for g = 2173 is center 50 is 1458.0 478.8
Best chromosome for g = 2173 is center 51 is 1433.8 604.0
Best chromosome for g = 2173 is center 52 is 1284.3333333333333
653.7777777777778
Best chromosome for g = 2173 is center 53 is 1537.5 591.0
Best chromosome for g = 2173 is center 54 is 1754.0 117.8
Best chromosome for g = 2173 is center 55 is 1687.8181818181818
257.45454545454544
Best chromosome for g = 2173 is center 56 is 1843.4285714285713
222.14285714285714
Best chromosome for g = 2173 is center 57 is 1781.6 429.8
Best chromosome for g = 2173 is center 58 is 1954.25 202.25
Best chromosome for g = 2173 is center 59 is 2103.4285714285716
120.42857142857143
Best chromosome for g = 2173 is center 60 is 1921.0 325.4
Best chromosome for g = 2173 is center 61 is 2109.9 259.8
```

Best chromosome for g = 2173 is center 62 is 2378.1428571428573 136.71428571428572
Best chromosome for g = 2173 is center 63 is 2300.285714285714 210.85714285714286
Best chromosome for g = 2173 is center 64 is 1686.4 534.2
Best chromosome for g = 2173 is center 65 is 2288.285714285714 309.2857142857143
Best chromosome for g = 2173 is center 66 is 2508.2727272727275 255.8181818181818
Best chromosome for g = 2173 is center 67 is 2670.0 220.6
Best chromosome for g = 2173 is center 68 is 119.25 824.0
Best chromosome for g = 2173 is center 69 is 71.42857142857143 1020.2857142857143
Best chromosome for g = 2173 is center 70 is 273.1666666666667 842.1666666666666
Best chromosome for g = 2173 is center 71 is 230.57142857142858 970.4285714285714
Best chromosome for g = 2173 is center 72 is 673.8571428571429 847.1428571428571
Best chromosome for g = 2173 is center 73 is 156.57142857142858 1094.142857142857
Best chromosome for g = 2173 is center 74 is 1093.2727272727273 752.1818181818181
Best chromosome for g = 2173 is center 75 is 548.4 986.0
Best chromosome for g = 2173 is center 76 is 897.7777777777778 852.4444444444445
Best chromosome for g = 2173 is center 77 is 50.333333333333336 1133.6666666666667
Best chromosome for g = 2173 is center 78 is 49.666666666666664 1244.3333333333333
Best chromosome for g = 2173 is center 79 is 296.4 1125.6
Best chromosome for g = 2173 is center 80 is 159.14285714285714 1216.7142857142858
Best chromosome for g = 2173 is center 81 is 132.0 1319.875
Best chromosome for g = 2173 is center 82 is 43.4 1386.2
Best chromosome for g = 2173 is center 83 is 46.125 1516.25
Best chromosome for g = 2173 is center 84 is 139.57142857142858 1439.142857142857
Best chromosome for g = 2173 is center 85 is 292.85714285714283 1357.857142857143
Best chromosome for g = 2173 is center 86 is 276.42857142857144 1461.0
Best chromosome for g = 2173 is center 87 is 326.0 1235.3333333333333
Best chromosome for g = 2173 is center 88 is 451.44444444444446 1075.111111111111
Best chromosome for g = 2173 is center 89 is 482.7 1200.7
Best chromosome for g = 2173 is center 90 is 475.7 1321.5
Best chromosome for g = 2173 is center 91 is 1060.4 900.8
Best chromosome for g = 2173 is center 92 is 1235.2 831.4
Best chromosome for g = 2173 is center 93 is 1343.3333333333333 806.5
Best chromosome for g = 2173 is center 94 is 1507.857142857143 724.8571428571429
Best chromosome for g = 2173 is center 95 is 1703.625 663.5
Best chromosome for g = 2173 is center 96 is 686.625 1126.625

Best chromosome for g = 2173 is center 97 is 816.6666666666666
963.3333333333334
Best chromosome for g = 2173 is center 98 is 852.375 1091.875
Best chromosome for g = 2173 is center 99 is 1026.0 1063.2
Best chromosome for g = 2173 is center 100 is 693.375 1254.375
Best chromosome for g = 2173 is center 101 is 1899.5714285714287 567.0
Best chromosome for g = 2173 is center 102 is 2067.25 448.0
Best chromosome for g = 2173 is center 103 is 133.11111111111111
1582.888888888889
Best chromosome for g = 2173 is center 104 is 50.888888888888886
1640.3333333333333
Best chromosome for g = 2173 is center 105 is 38.857142857142854
1754.142857142857
Best chromosome for g = 2173 is center 106 is 1487.0 845.8
Best chromosome for g = 2173 is center 107 is 1662.4 777.4
Best chromosome for g = 2173 is center 108 is 632.2 1395.2
Best chromosome for g = 2173 is center 109 is 852.1666666666666 1220.0
Best chromosome for g = 2173 is center 110 is 1203.2857142857142
1007.7142857142857
Best chromosome for g = 2173 is center 111 is 824.1428571428571
1335.7142857142858
Best chromosome for g = 2173 is center 112 is 1049.5714285714287 1167.0
Best chromosome for g = 2173 is center 113 is 1021.4285714285714
1282.5714285714287
Best chromosome for g = 2173 is center 114 is 1188.5 1141.6666666666667
Best chromosome for g = 2173 is center 115 is 1417.1666666666667
1053.3333333333333
Best chromosome for g = 2173 is center 116 is 1197.4285714285713
1253.2857142857142
Best chromosome for g = 2173 is center 117 is 1348.75 1191.875
Best chromosome for g = 2173 is center 118 is 1606.0 1084.6
Best chromosome for g = 2173 is center 119 is 1462.8 1194.4
Best chromosome for g = 2173 is center 120 is 1578.2 1210.6
Best chromosome for g = 2173 is center 121 is 1343.2 1341.4
Best chromosome for g = 2173 is center 122 is 469.1111111111111
1441.4444444444443
Best chromosome for g = 2173 is center 123 is 302.125 1577.125
Best chromosome for g = 2173 is center 124 is 455.625 1607.125
Best chromosome for g = 2173 is center 125 is 139.42857142857142
1710.7142857142858
Best chromosome for g = 2173 is center 126 is 180.8 1839.6
Best chromosome for g = 2173 is center 127 is 300.75 1724.0
Best chromosome for g = 2173 is center 128 is 615.8333333333334 1548.0
Best chromosome for g = 2173 is center 129 is 846.3333333333334 1512.5
Best chromosome for g = 2173 is center 130 is 1065.625 1400.25
Best chromosome for g = 2173 is center 131 is 1209.25 1382.125
Best chromosome for g = 2173 is center 132 is 753.8333333333334
1582.1666666666667
Best chromosome for g = 2173 is center 133 is 1451.25 1346.25
Best chromosome for g = 2173 is center 134 is 1558.8 1335.6
Best chromosome for g = 2173 is center 135 is 1476.5714285714287
1529.5714285714287
Best chromosome for g = 2173 is center 136 is 23.25 1979.5
Best chromosome for g = 2173 is center 137 is 174.5 2051.0

Best chromosome for g = 2173 is center 138 is 316.55555555555554
1870.4444444444443
Best chromosome for g = 2173 is center 139 is 333.1 2027.4
Best chromosome for g = 2173 is center 140 is 465.57142857142856
1748.857142857143
Best chromosome for g = 2173 is center 141 is 607.0 1712.0
Best chromosome for g = 2173 is center 142 is 452.2 1865.2
Best chromosome for g = 2173 is center 143 is 597.25 1880.0
Best chromosome for g = 2173 is center 144 is 709.2222222222222 1882.0
Best chromosome for g = 2173 is center 145 is 499.3333333333333 2073.5
Best chromosome for g = 2173 is center 146 is 1010.6666666666666
1508.3333333333333
Best chromosome for g = 2173 is center 147 is 849.5 1754.0
Best chromosome for g = 2173 is center 148 is 996.2 1664.0
Best chromosome for g = 2173 is center 149 is 1156.75 1523.0
Best chromosome for g = 2173 is center 150 is 1304.0 1530.8
Best chromosome for g = 2173 is center 151 is 1417.3333333333333
1644.1666666666667
Best chromosome for g = 2173 is center 152 is 852.125 1891.75
Best chromosome for g = 2173 is center 153 is 49.888888888888886 2177.0
Best chromosome for g = 2173 is center 154 is 170.2 2157.0
Best chromosome for g = 2173 is center 155 is 329.0 2155.6
Best chromosome for g = 2173 is center 156 is 1856.0 713.0
Best chromosome for g = 2173 is center 157 is 1945.3333333333333 725.0
Best chromosome for g = 2173 is center 158 is 2046.0 590.8
Best chromosome for g = 2173 is center 159 is 2245.125 481.75
Best chromosome for g = 2173 is center 160 is 2424.8 404.8
Best chromosome for g = 2173 is center 161 is 2810.875 211.875
Best chromosome for g = 2173 is center 162 is 2158.0 616.1428571428571
Best chromosome for g = 2173 is center 163 is 1897.6 869.6
Best chromosome for g = 2173 is center 164 is 2090.5714285714284
763.5714285714286
Best chromosome for g = 2173 is center 165 is 2313.75 607.625
Best chromosome for g = 2173 is center 166 is 1749.25 1038.5
Best chromosome for g = 2173 is center 167 is 2612.75 383.0
Best chromosome for g = 2173 is center 168 is 2810.8333333333335
345.8333333333333
Best chromosome for g = 2173 is center 169 is 1865.25 1038.75
Best chromosome for g = 2173 is center 170 is 2298.8888888888887
730.6666666666666
Best chromosome for g = 2173 is center 171 is 2172.6 879.8
Best chromosome for g = 2173 is center 172 is 1964.6666666666667
1049.6666666666667
Best chromosome for g = 2173 is center 173 is 2371.3333333333335
884.1666666666666
Best chromosome for g = 2173 is center 174 is 2509.8888888888887
565.2222222222222
Best chromosome for g = 2173 is center 175 is 2654.1666666666665 549.0
Best chromosome for g = 2173 is center 176 is 2781.0 498.8333333333333
Best chromosome for g = 2173 is center 177 is 2499.0 702.4285714285714
Best chromosome for g = 2173 is center 178 is 2557.375 833.625
Best chromosome for g = 2173 is center 179 is 2778.5714285714284
613.4285714285714
Best chromosome for g = 2173 is center 180 is 2659.5 715.5

```
Best chromosome for g = 2173 is center 181 is 2781.0 751.375
Best chromosome for g = 2173 is center 182 is 2097.0 1066.375
Best chromosome for g = 2173 is center 183 is 1731.6 1189.4
Best chromosome for g = 2173 is center 184 is 1900.4444444444443 1200.0
Best chromosome for g = 2173 is center 185 is 2246.5 1085.0
Best chromosome for g = 2173 is center 186 is 2512.8333333333335
1005.6666666666666
Best chromosome for g = 2173 is center 187 is 2361.0 1099.4
Best chromosome for g = 2173 is center 188 is 1735.5 1347.1666666666667
Best chromosome for g = 2173 is center 189 is 1604.75 1537.25
Best chromosome for g = 2173 is center 190 is 1869.6 1348.0
Best chromosome for g = 2173 is center 191 is 2045.625 1251.25
Best chromosome for g = 2173 is center 192 is 1965.8 1401.4
Best chromosome for g = 2173 is center 193 is 1727.875 1517.25
Best chromosome for g = 2173 is center 194 is 2167.285714285714
1192.857142857143
Best chromosome for g = 2173 is center 195 is 2135.1666666666665
1346.6666666666667
Best chromosome for g = 2173 is center 196 is 2310.6666666666665
1216.6666666666667
Best chromosome for g = 2173 is center 197 is 2502.3333333333335
1116.8333333333333
Best chromosome for g = 2173 is center 198 is 2750.6 991.0
Best chromosome for g = 2173 is center 199 is 49.888888888888886
2296.1111111111113
Best chromosome for g = 2173 is center 200 is 160.6 2275.6
Best chromosome for g = 2173 is center 201 is 630.8571428571429
2032.2857142857142
Best chromosome for g = 2173 is center 202 is 50.0 2411.777777777778
Best chromosome for g = 2173 is center 203 is 171.4 2399.3
Best chromosome for g = 2173 is center 204 is 447.0 2270.0
Best chromosome for g = 2173 is center 205 is 322.1111111111111
2274.8888888888887
Best chromosome for g = 2173 is center 206 is 617.2222222222222
2179.6666666666665
Best chromosome for g = 2173 is center 207 is 1000.7142857142857
1885.2857142857142
Best chromosome for g = 2173 is center 208 is 1139.857142857143
1865.2857142857142
Best chromosome for g = 2173 is center 209 is 1346.0 1771.0
Best chromosome for g = 2173 is center 210 is 49.111111111111114
2525.222222222222
Best chromosome for g = 2173 is center 211 is 919.5 2033.125
Best chromosome for g = 2173 is center 212 is 321.8888888888889
2390.8888888888887
Best chromosome for g = 2173 is center 213 is 780.8333333333334 2120.0
Best chromosome for g = 2173 is center 214 is 1264.6666666666667
1887.3333333333333
Best chromosome for g = 2173 is center 215 is 49.333333333333336
2641.777777777778
Best chromosome for g = 2173 is center 216 is 49.77777777777778
2758.222222222222
Best chromosome for g = 2173 is center 217 is 158.28571428571428
2521.1428571428573
```

```
Best chromosome for g = 2173 is center 218 is 160.0 2638.125
Best chromosome for g = 2173 is center 219 is 336.0 2539.8571428571427
Best chromosome for g = 2173 is center 220 is 169.3 2753.3
Best chromosome for g = 2173 is center 221 is 311.2857142857143
2637.8571428571427
Best chromosome for g = 2173 is center 222 is 49.75 2874.25
Best chromosome for g = 2173 is center 223 is 168.54545454545453
2888.3636363636365
Best chromosome for g = 2173 is center 224 is 310.6666666666667
2772.5555555555557
Best chromosome for g = 2173 is center 225 is 462.4 2444.4
Best chromosome for g = 2173 is center 226 is 313.85714285714283
2915.5714285714284
Best chromosome for g = 2173 is center 227 is 499.57142857142856
2619.714285714286
Best chromosome for g = 2173 is center 228 is 627.125 2334.5
Best chromosome for g = 2173 is center 229 is 626.3333333333334 2484.5
Best chromosome for g = 2173 is center 230 is 907.6666666666666
2160.1666666666665
Best chromosome for g = 2173 is center 231 is 1060.0 2096.25
Best chromosome for g = 2173 is center 232 is 915.2222222222222
2294.6666666666665
Best chromosome for g = 2173 is center 233 is 1177.3333333333333
2042.3333333333333
Best chromosome for g = 2173 is center 234 is 626.6666666666666
2648.4444444444443
Best chromosome for g = 2173 is center 235 is 894.7 2458.6
Best chromosome for g = 2173 is center 236 is 867.5 2617.25
Best chromosome for g = 2173 is center 237 is 502.125 2765.875
Best chromosome for g = 2173 is center 238 is 1201.5 2162.375
Best chromosome for g = 2173 is center 239 is 1191.875 2272.875
Best chromosome for g = 2173 is center 240 is 1177.8333333333333
2392.6666666666665
Best chromosome for g = 2173 is center 241 is 1331.0 2348.75
Best chromosome for g = 2173 is center 242 is 731.1666666666666 2716.0
Best chromosome for g = 2173 is center 243 is 960.625 2695.25
Best chromosome for g = 2173 is center 244 is 1143.0 2513.714285714286
Best chromosome for g = 2173 is center 245 is 624.8571428571429 2784.0
Best chromosome for g = 2173 is center 246 is -66.0 3134.0
Best chromosome for g = 2173 is center 247 is 502.6666666666667
2901.1666666666665
Best chromosome for g = 2173 is center 248 is 836.4 2760.4
Best chromosome for g = 2173 is center 249 is 137.77777777777777
3170.222222222222
Best chromosome for g = 2173 is center 250 is 333.2 3106.8
Best chromosome for g = 2173 is center 251 is 622.625 2911.75
Best chromosome for g = 2173 is center 252 is 727.8 2865.4
Best chromosome for g = 2173 is center 253 is 124.75 3330.5
Best chromosome for g = 2173 is center 254 is 95.5 3511.375
Best chromosome for g = 2173 is center 255 is 114.3 3621.1
Best chromosome for g = 2173 is center 256 is 96.66666666666667
3736.5555555555557
Best chromosome for g = 2173 is center 257 is 1066.6 2726.2
```

Best chromosome for g = 2173 is center 258 is 300.7142857142857 3218.5714285714284
Best chromosome for g = 2173 is center 259 is 477.8 3052.8
Best chromosome for g = 2173 is center 260 is 545.3333333333334 3147.6666666666665
Best chromosome for g = 2173 is center 261 is 251.33333333333334 3326.0
Best chromosome for g = 2173 is center 262 is 913.5 2873.6666666666665
Best chromosome for g = 2173 is center 263 is 819.8333333333334 2987.0
Best chromosome for g = 2173 is center 264 is 704.125 3144.25
Best chromosome for g = 2173 is center 265 is 455.6666666666667 3261.0
Best chromosome for g = 2173 is center 266 is 358.2857142857143 3382.0
Best chromosome for g = 2173 is center 267 is 590.3333333333334 3278.5
Best chromosome for g = 2173 is center 268 is 249.0 3493.4
Best chromosome for g = 2173 is center 269 is 511.8333333333333 3395.0
Best chromosome for g = 2173 is center 270 is 396.375 3521.0
Best chromosome for g = 2173 is center 271 is 312.375 3614.875
Best chromosome for g = 2173 is center 272 is 311.875 3743.25
Best chromosome for g = 2173 is center 273 is 440.42857142857144 3676.0
Best chromosome for g = 2173 is center 274 is 711.8571428571429 3284.714285714286
Best chromosome for g = 2173 is center 275 is 567.0 3576.4
Best chromosome for g = 2173 is center 276 is 671.6666666666666 3426.8333333333335
Best chromosome for g = 2173 is center 277 is 896.3333333333334 3124.8333333333335
Best chromosome for g = 2173 is center 278 is 1165.4 2723.0
Best chromosome for g = 2173 is center 279 is 1109.9 2871.0
Best chromosome for g = 2173 is center 280 is 987.25 3026.75
Best chromosome for g = 2173 is center 281 is 838.0 3260.3333333333335
Best chromosome for g = 2173 is center 282 is 709.0 3591.0
Best chromosome for g = 2173 is center 283 is 1121.4285714285713 3090.5714285714284
Best chromosome for g = 2173 is center 284 is 944.75 3260.25
Best chromosome for g = 2173 is center 285 is 1108.0 3203.0
Best chromosome for g = 2173 is center 286 is 1109.1666666666667 3319.1666666666665
Best chromosome for g = 2173 is center 287 is 810.0 3479.25
Best chromosome for g = 2173 is center 288 is 952.8 3418.2
Best chromosome for g = 2173 is center 289 is 912.5 3601.6666666666665
Best chromosome for g = 2173 is center 290 is 1110.7142857142858 3559.285714285714
Best chromosome for g = 2173 is center 291 is 0.5 3893.75
Best chromosome for g = 2173 is center 292 is 144.0 3849.777777777778
Best chromosome for g = 2173 is center 293 is 532.5714285714286 3756.5714285714284
Best chromosome for g = 2173 is center 294 is 300.4 3861.8
Best chromosome for g = 2173 is center 295 is 464.7142857142857 3866.0
Best chromosome for g = 2173 is center 296 is 710.4285714285714 3722.714285714286
Best chromosome for g = 2173 is center 297 is 1061.0 3705.5
Best chromosome for g = 2173 is center 298 is 576.6666666666666 3886.0
Best chromosome for g = 2173 is center 299 is 703.8333333333334 3841.8333333333335
Best chromosome for g = 2173 is center 300 is 902.75 3722.625

Best chromosome for g = 2173 is center 301 is 883.6363636363636 3837.5454545454545
Best chromosome for g = 2173 is center 302 is 1104.2857142857142 3844.285714285714
Best chromosome for g = 2173 is center 303 is 1877.25 1605.625
Best chromosome for g = 2173 is center 304 is 1999.8333333333333 1561.1666666666667
Best chromosome for g = 2173 is center 305 is 2301.2 1334.2
Best chromosome for g = 2173 is center 306 is 2201.875 1520.0
Best chromosome for g = 2173 is center 307 is 2412.1428571428573 1431.5714285714287
Best chromosome for g = 2173 is center 308 is 2507.0 1226.875
Best chromosome for g = 2173 is center 309 is 2648.6 1107.6
Best chromosome for g = 2173 is center 310 is 2508.5 1359.625
Best chromosome for g = 2173 is center 311 is 2638.0 1257.7142857142858
Best chromosome for g = 2173 is center 312 is 2787.714285714286 1140.7142857142858
Best chromosome for g = 2173 is center 313 is 2786.4444444444443 1269.0
Best chromosome for g = 2173 is center 314 is 1433.8 1883.0
Best chromosome for g = 2173 is center 315 is 1580.125 1849.625
Best chromosome for g = 2173 is center 316 is 1712.1666666666667 1700.8333333333333
Best chromosome for g = 2173 is center 317 is 1999.375 1697.875
Best chromosome for g = 2173 is center 318 is 2174.875 1655.375
Best chromosome for g = 2173 is center 319 is 2349.5 1559.3333333333333
Best chromosome for g = 2173 is center 320 is 1866.2 1777.6
Best chromosome for g = 2173 is center 321 is 2348.75 1695.625
Best chromosome for g = 2173 is center 322 is 1708.6666666666667 1907.1666666666667
Best chromosome for g = 2173 is center 323 is 1835.857142857143 2031.0
Best chromosome for g = 2173 is center 324 is 2028.0 1833.142857142857
Best chromosome for g = 2173 is center 325 is 2183.777777777778 1811.111111111111
Best chromosome for g = 2173 is center 326 is 1820.875 2179.75
Best chromosome for g = 2173 is center 327 is 2054.8 1976.2
Best chromosome for g = 2173 is center 328 is 1428.0 2009.75
Best chromosome for g = 2173 is center 329 is 1452.2857142857142 2117.714285714286
Best chromosome for g = 2173 is center 330 is 1456.0 2231.875
Best chromosome for g = 2173 is center 331 is 1634.3 2067.7
Best chromosome for g = 2173 is center 332 is 1453.5555555555557 2373.1111111111113
Best chromosome for g = 2173 is center 333 is 1630.625 2224.375
Best chromosome for g = 2173 is center 334 is 1319.0 2546.0
Best chromosome for g = 2173 is center 335 is 1324.875 2695.25
Best chromosome for g = 2173 is center 336 is 1464.4 2539.0
Best chromosome for g = 2173 is center 337 is 1644.0 2379.1111111111113
Best chromosome for g = 2173 is center 338 is 1321.8333333333333 2817.0
Best chromosome for g = 2173 is center 339 is 1611.4 2527.2
Best chromosome for g = 2173 is center 340 is 1544.142857142857 2689.714285714286
Best chromosome for g = 2173 is center 341 is 2349.4285714285716 1831.142857142857
Best chromosome for g = 2173 is center 342 is 2268.25 1934.0

```
Best chromosome for g = 2173 is center 343 is 2221.4 2045.6
Best chromosome for g = 2173 is center 344 is 1999.875 2141.875
Best chromosome for g = 2173 is center 345 is 1808.5 2334.8
Best chromosome for g = 2173 is center 346 is 2525.5714285714284
1588.4285714285713
Best chromosome for g = 2173 is center 347 is 2521.3333333333335 1715.5
Best chromosome for g = 2173 is center 348 is 2647.4285714285716
1516.4285714285713
Best chromosome for g = 2173 is center 349 is 2769.8571428571427
1413.142857142857
Best chromosome for g = 2173 is center 350 is 2658.8571428571427
1707.5714285714287
Best chromosome for g = 2173 is center 351 is 2772.3333333333335 1566.0
Best chromosome for g = 2173 is center 352 is 2151.8888888888887
2143.3333333333335
Best chromosome for g = 2173 is center 353 is 1976.2222222222222
2276.8888888888887
Best chromosome for g = 2173 is center 354 is 2529.375 1845.75
Best chromosome for g = 2173 is center 355 is 2354.1428571428573
2077.5714285714284
Best chromosome for g = 2173 is center 356 is 1979.5555555555557
2404.5555555555557
Best chromosome for g = 2173 is center 357 is 1839.5714285714287 2481.0
Best chromosome for g = 2173 is center 358 is 1777.4 2649.0
Best chromosome for g = 2173 is center 359 is 1508.3333333333333
2775.1666666666665
Best chromosome for g = 2173 is center 360 is 2168.8 2273.3
Best chromosome for g = 2173 is center 361 is 2327.8 2222.7
Best chromosome for g = 2173 is center 362 is 2181.3333333333335
2408.6666666666665
Best chromosome for g = 2173 is center 363 is 1995.6 2615.8
Best chromosome for g = 2173 is center 364 is 2340.285714285714
2386.5714285714284
Best chromosome for g = 2173 is center 365 is 2510.222222222222
2039.5555555555557
Best chromosome for g = 2173 is center 366 is 2517.8888888888887 2208.0
Best chromosome for g = 2173 is center 367 is 2780.5 1697.6666666666667
Best chromosome for g = 2173 is center 368 is 2665.75 1859.5
Best chromosome for g = 2173 is center 369 is 2780.6666666666665
1817.6666666666667
Best chromosome for g = 2173 is center 370 is 2662.0 2046.0
Best chromosome for g = 2173 is center 371 is 2671.0 2202.4
Best chromosome for g = 2173 is center 372 is 2394.6 2489.8
Best chromosome for g = 2173 is center 373 is 2521.25 2450.375
Best chromosome for g = 2173 is center 374 is 2668.2 2343.4
Best chromosome for g = 2173 is center 375 is 2780.8888888888887 2129.0
Best chromosome for g = 2173 is center 376 is 2780.8333333333335 2260.0
Best chromosome for g = 2173 is center 377 is 2779.285714285714
2374.5714285714284
Best chromosome for g = 2173 is center 378 is 1260.6 2955.0
Best chromosome for g = 2173 is center 379 is 1438.142857142857
2897.8571428571427
Best chromosome for g = 2173 is center 380 is 1740.4444444444443
2763.5555555555557
```

```
Best chromosome for g = 2173 is center 381 is 2155.0 2610.75
Best chromosome for g = 2173 is center 382 is 1944.0 2730.1428571428573
Best chromosome for g = 2173 is center 383 is 2709.714285714286
2493.4285714285716
Best chromosome for g = 2173 is center 384 is 2337.222222222222
2644.8888888888887
Best chromosome for g = 2173 is center 385 is 1405.8 3034.8
Best chromosome for g = 2173 is center 386 is 1252.8333333333333
3150.3333333333335
Best chromosome for g = 2173 is center 387 is 1584.0 2873.5
Best chromosome for g = 2173 is center 388 is 1361.6 3187.2
Best chromosome for g = 2173 is center 389 is 1480.6 3139.2
Best chromosome for g = 2173 is center 390 is 1592.5714285714287
3147.1428571428573
Best chromosome for g = 2173 is center 391 is 1302.2857142857142
3282.714285714286
Best chromosome for g = 2173 is center 392 is 1741.5555555555557
2900.5555555555557
Best chromosome for g = 2173 is center 393 is 1949.875 2875.5
Best chromosome for g = 2173 is center 394 is 2166.625 2733.75
Best chromosome for g = 2173 is center 395 is 1703.0 3059.75
Best chromosome for g = 2173 is center 396 is 1760.2857142857142
3156.1428571428573
Best chromosome for g = 2173 is center 397 is 1930.5714285714287 3073.0
Best chromosome for g = 2173 is center 398 is 2066.25 2977.25
Best chromosome for g = 2173 is center 399 is 2158.125 2859.125
Best chromosome for g = 2173 is center 400 is 2140.0 3109.25
Best chromosome for g = 2173 is center 401 is 2508.75 2601.25
Best chromosome for g = 2173 is center 402 is 2337.25 2801.125
Best chromosome for g = 2173 is center 403 is 2493.777777777778
2782.8888888888887
Best chromosome for g = 2173 is center 404 is 2319.375 2950.125
Best chromosome for g = 2173 is center 405 is 2693.1666666666665 2655.5
Best chromosome for g = 2173 is center 406 is 2511.8571428571427
2987.714285714286
Best chromosome for g = 2173 is center 407 is 2664.0 2905.3333333333335
Best chromosome for g = 2173 is center 408 is 2342.1666666666665
3095.6666666666665
Best chromosome for g = 2173 is center 409 is 2326.4444444444443 3219.0
Best chromosome for g = 2173 is center 410 is 1949.5 3222.0
Best chromosome for g = 2173 is center 411 is 1316.75 3388.25
Best chromosome for g = 2173 is center 412 is 1336.857142857143
3556.285714285714
Best chromosome for g = 2173 is center 413 is 1478.3333333333333
3560.3333333333335
Best chromosome for g = 2173 is center 414 is 1530.142857142857
3299.285714285714
Best chromosome for g = 2173 is center 415 is 1695.8 3280.8
Best chromosome for g = 2173 is center 416 is 1807.6666666666667
3305.8333333333335
Best chromosome for g = 2173 is center 417 is 1639.625 3422.25
Best chromosome for g = 2173 is center 418 is 1638.4444444444443
3607.6666666666665
Best chromosome for g = 2173 is center 419 is 1949.6666666666667 3364.0
```

```
Best chromosome for g = 2173 is center 420 is 2159.25 3247.625
Best chromosome for g = 2173 is center 421 is 2096.8333333333335
3359.3333333333335
Best chromosome for g = 2173 is center 422 is 1240.857142857143
3656.5714285714284
Best chromosome for g = 2173 is center 423 is 1169.1666666666667
3751.1666666666665
Best chromosome for g = 2173 is center 424 is 1317.7777777777778
3830.8888888888887
Best chromosome for g = 2173 is center 425 is 1375.8 3716.2
Best chromosome for g = 2173 is center 426 is 1542.5555555555557 3732.0
Best chromosome for g = 2173 is center 427 is 1462.0 3854.2
Best chromosome for g = 2173 is center 428 is 1795.0 3628.25
Best chromosome for g = 2173 is center 429 is 1698.0 3742.75
Best chromosome for g = 2173 is center 430 is 2550.8888888888887
3131.8888888888887
Best chromosome for g = 2173 is center 431 is 2422.6666666666665
3473.3333333333335
Best chromosome for g = 2173 is center 432 is 2534.75 3272.25
Best chromosome for g = 2173 is center 433 is 2563.777777777778
3390.222222222222
Best chromosome for g = 2173 is center 434 is 2347.4285714285716
3355.285714285714
Best chromosome for g = 2173 is center 435 is 2779.6666666666665
3068.1666666666665
Best chromosome for g = 2173 is center 436 is 2729.5714285714284
3194.1428571428573
Best chromosome for g = 2173 is center 437 is 2782.4285714285716
3331.1428571428573
Best chromosome for g = 2173 is center 438 is 2803.3333333333335
3459.3333333333335
Best chromosome for g = 2173 is center 439 is 2749.5 3592.0
Best chromosome for g = 2173 is center 440 is 1795.0 3802.6
Best chromosome for g = 2173 is center 441 is 1648.125 3876.625
Best chromosome for g = 2173 is center 442 is 1939.5 3624.2
Best chromosome for g = 2173 is center 443 is 2108.3333333333335
3646.3333333333335
Best chromosome for g = 2173 is center 444 is 1925.3333333333333
3781.3333333333335
Best chromosome for g = 2173 is center 445 is 2444.5 3754.0
Best chromosome for g = 2173 is center 446 is 1985.375 3852.0
Best chromosome for g = 2173 is center 447 is 2142.3333333333335 3825.5
Best chromosome for g = 2173 is center 448 is 2797.5 3795.0
Best chromosome for g = 2173 is center 449 is 2701.0 3919.25
Time Elapsed: 7.67514116E8 Seeding Time: 302765.0
The seeding percentage time is : 0.000394
```

TSP-LIB-3038, *k* = 500: Separation, Deterministic

```
Random = 0
Density = 0
Separation = 200
Selection Method = 2
Number of centers = 500
After 0 generations new best SSE for g = 0 is 8337798.146933599
After 1 generations new best SSE for g = 1 is 8331023.084967787
After 1 generations new best SSE for g = 2 is 8265801.693842253
After 1 generations new best SSE for g = 3 is 8202105.353288382
After 3 generations new best SSE for g = 6 is 8181695.27792209
After 2 generations new best SSE for g = 8 is 8149520.557070697
After 1 generations new best SSE for g = 9 is 8145543.608730165
After 1 generations new best SSE for g = 10 is 8134328.082101234
After 1 generations new best SSE for g = 11 is 8108303.081593403
After 1 generations new best SSE for g = 12 is 7968779.349675321
After 9 generations new best SSE for g = 21 is 7952985.145526674
After 5 generations new best SSE for g = 26 is 7931202.3150072275
After 1 generations new best SSE for g = 27 is 7921632.084054847
After 2 generations new best SSE for g = 29 is 7839519.911580098
After 6 generations new best SSE for g = 35 is 7802567.35880233
After 10 generations new best SSE for g = 45 is 7801098.120238113
After 1 generations new best SSE for g = 46 is 7798556.579509402
After 1 generations new best SSE for g = 47 is 7796892.9229076505
After 3 generations new best SSE for g = 50 is 7785090.363347783
After 3 generations new best SSE for g = 53 is 7774243.150829737
After 2 generations new best SSE for g = 55 is 7770427.836075048
After 1 generations new best SSE for g = 56 is 7761042.575757579
After 5 generations new best SSE for g = 61 is 7737909.715692622
After 1 generations new best SSE for g = 62 is 7733517.254617618
After 6 generations new best SSE for g = 68 is 7732203.773556999
After 2 generations new best SSE for g = 70 is 7726496.4574314635
After 1 generations new best SSE for g = 71 is 7710082.252322696
After 3 generations new best SSE for g = 74 is 7709297.896212096
After 5 generations new best SSE for g = 79 is 7704474.432165046
After 1 generations new best SSE for g = 80 is 7699123.222582985
After 2 generations new best SSE for g = 82 is 7695307.023340548
After 2 generations new best SSE for g = 84 is 7694931.799841822
After 1 generations new best SSE for g = 85 is 7676725.736147189
After 5 generations new best SSE for g = 90 is 7655125.317138426
After 7 generations new best SSE for g = 97 is 7650118.988422703
After 1 generations new best SSE for g = 98 is 7629095.590256965
After 5 generations new best SSE for g = 103 is 7618170.470313033
After 4 generations new best SSE for g = 107 is 7612145.015551133
After 1 generations new best SSE for g = 108 is 7611028.808116896
After 3 generations new best SSE for g = 111 is 7600266.441428018
After 4 generations new best SSE for g = 115 is 7591543.349062064
After 3 generations new best SSE for g = 118 is 7588645.26572873
After 4 generations new best SSE for g = 122 is 7574216.815656566
After 7 generations new best SSE for g = 129 is 7574081.051492954
After 2 generations new best SSE for g = 131 is 7563531.851515158
After 1 generations new best SSE for g = 132 is 7557013.721176052
After 4 generations new best SSE for g = 136 is 7551754.370670997
```

```
After 1 generations new best SSE for g = 137 is 7530451.335894657
After 8 generations new best SSE for g = 145 is 7530087.388672431
After 2 generations new best SSE for g = 147 is 7528341.09837664
After 1 generations new best SSE for g = 148 is 7524460.848376639
After 3 generations new best SSE for g = 151 is 7522246.025180381
After 3 generations new best SSE for g = 154 is 7522126.785894667
After 6 generations new best SSE for g = 160 is 7509860.146572872
After 2 generations new best SSE for g = 162 is 7500025.356168832
After 4 generations new best SSE for g = 166 is 7489802.758946611
After 4 generations new best SSE for g = 170 is 7464950.819660888
After 15 generations new best SSE for g = 185 is 7437432.999639266
After 24 generations new best SSE for g = 209 is 7434675.908261206
After 5 generations new best SSE for g = 214 is 7428692.691969134
After 3 generations new best SSE for g = 217 is 7423122.311871455
After 3 generations new best SSE for g = 220 is 7417396.760497825
After 2 generations new best SSE for g = 222 is 7414723.083730162
After 2 generations new best SSE for g = 224 is 7407131.554906208
After 3 generations new best SSE for g = 227 is 7404064.873376626
After 3 generations new best SSE for g = 230 is 7401877.173520943
After 4 generations new best SSE for g = 234 is 7400898.040945166
After 8 generations new best SSE for g = 242 is 7397023.412518034
After 5 generations new best SSE for g = 247 is 7384420.836796529
After 1 generations new best SSE for g = 248 is 7373387.483116885
After 18 generations new best SSE for g = 266 is 7366489.655699854
After 8 generations new best SSE for g = 274 is 7366264.192785
After 3 generations new best SSE for g = 277 is 7366262.690331894
After 2 generations new best SSE for g = 279 is 7361880.301443012
After 2 generations new best SSE for g = 281 is 7360321.838314466
After 1 generations new best SSE for g = 282 is 7358381.484812421
After 1 generations new best SSE for g = 283 is 7355515.632611841
After 1 generations new best SSE for g = 284 is 7350268.245021635
After 4 generations new best SSE for g = 288 is 7338484.301443015
After 3 generations new best SSE for g = 291 is 7337522.967316034
After 4 generations new best SSE for g = 295 is 7330673.650360762
After 12 generations new best SSE for g = 307 is 7318510.920562773
After 6 generations new best SSE for g = 313 is 7318048.552705632
After 22 generations new best SSE for g = 335 is 7314205.923268415
After 2 generations new best SSE for g = 337 is 7309083.06814575
After 6 generations new best SSE for g = 343 is 7307614.7474026065
After 10 generations new best SSE for g = 353 is 7291663.431024544
After 17 generations new best SSE for g = 370 is 7290985.971500734
After 4 generations new best SSE for g = 374 is 7278830.48849208
After 1 generations new best SSE for g = 375 is 7278056.679725844
After 8 generations new best SSE for g = 383 is 7275754.4659812525
After 7 generations new best SSE for g = 390 is 7273204.79375903
After 1 generations new best SSE for g = 391 is 7271833.515836952
After 2 generations new best SSE for g = 393 is 7264141.929437235
After 24 generations new best SSE for g = 417 is 7263515.576262634
After 2 generations new best SSE for g = 419 is 7261261.051948061
After 4 generations new best SSE for g = 423 is 7261136.8841991415
After 4 generations new best SSE for g = 427 is 7257393.131782107
After 1 generations new best SSE for g = 428 is 7255543.50519481
After 4 generations new best SSE for g = 432 is 7254143.448051956
After 11 generations new best SSE for g = 443 is 7250719.182900442
```

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After 10 generations new best SSE for g = 453 is 7246285.394191926
After 4 generations new best SSE for g = 457 is 7243328.159559876
After 12 generations new best SSE for g = 469 is 7237382.9690837115
After 15 generations new best SSE for g = 484 is 7237185.389321803
After 1 generations new best SSE for g = 485 is 7232895.980591643
After 5 generations new best SSE for g = 490 is 7222667.230808095
After 5 generations new best SSE for g = 495 is 7221232.078030317
After 25 generations new best SSE for g = 520 is 7220499.956998558
After 12 generations new best SSE for g = 532 is 7219153.750360744
After 6 generations new best SSE for g = 538 is 7218332.83517317
After 9 generations new best SSE for g = 547 is 7216831.542640694
After 4 generations new best SSE for g = 551 is 7213655.137265514
After 4 generations new best SSE for g = 555 is 7211897.0944083715
After 5 generations new best SSE for g = 560 is 7211732.056782114
After 5 generations new best SSE for g = 565 is 7207603.904545461
After 2 generations new best SSE for g = 567 is 7206792.661652249
After 3 generations new best SSE for g = 570 is 7206001.497077926
After 8 generations new best SSE for g = 578 is 7203157.613888897
After 1 generations new best SSE for g = 579 is 7203136.798665228
After 1 generations new best SSE for g = 580 is 7198736.432972594
After 3 generations new best SSE for g = 583 is 7195062.541305935
After 19 generations new best SSE for g = 602 is 7192944.206277067
After 22 generations new best SSE for g = 624 is 7192162.348448775
After 5 generations new best SSE for g = 629 is 7191884.102705636
After 1 generations new best SSE for g = 630 is 7191345.853427135
After 1 generations new best SSE for g = 631 is 7180641.684487747
After 7 generations new best SSE for g = 638 is 7179966.2916306
After 9 generations new best SSE for g = 647 is 7179804.645562778
After 4 generations new best SSE for g = 651 is 7173734.801154408
After 2 generations new best SSE for g = 653 is 7171752.061038966
After 11 generations new best SSE for g = 664 is 7171195.05263349
After 12 generations new best SSE for g = 676 is 7169446.066919205
After 2 generations new best SSE for g = 678 is 7169208.0986652365
After 7 generations new best SSE for g = 685 is 7167614.18246754
After 1 generations new best SSE for g = 686 is 7166730.190800874
After 11 generations new best SSE for g = 697 is 7165918.626515158
After 15 generations new best SSE for g = 712 is 7163609.59130592
After 16 generations new best SSE for g = 728 is 7163128.916197698
After 22 generations new best SSE for g = 750 is 7161204.747546899
After 11 generations new best SSE for g = 761 is 7160981.9515151605
After 3 generations new best SSE for g = 764 is 7156150.905880236
After 16 generations new best SSE for g = 780 is 7153182.5527056325
After 2 generations new best SSE for g = 782 is 7153128.077705633
After 4 generations new best SSE for g = 786 is 7152622.760245315
After 25 generations new best SSE for g = 811 is 7151945.763131317
After 13 generations new best SSE for g = 824 is 7150428.855194805
After 10 generations new best SSE for g = 834 is 7150338.647258298
After 5 generations new best SSE for g = 839 is 7150247.988924964
After 6 generations new best SSE for g = 845 is 7148178.242099569
After 9 generations new best SSE for g = 854 is 7147726.99448052
After 9 generations new best SSE for g = 863 is 7145529.505988458
After 9 generations new best SSE for g = 872 is 7145332.000432906
After 15 generations new best SSE for g = 887 is 7145016.495671
After 13 generations new best SSE for g = 900 is 7142282.329292936
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After 5 generations new best SSE for g = 905 is 7142227.854292937
After 1 generations new best SSE for g = 906 is 7141715.555880235
After 13 generations new best SSE for g = 919 is 7140996.004292941
After 3 generations new best SSE for g = 922 is 7138675.026190488
After 38 generations new best SSE for g = 960 is 7138309.861111122
After 33 generations new best SSE for g = 993 is 7134536.741125546
After 3 generations new best SSE for g = 996 is 7134221.236363641
After 19 generations new best SSE for g = 1015 is 7133229.712554117
After 1 generations new best SSE for g = 1016 is 7132646.117316022
After 23 generations new best SSE for g = 1039 is 7131853.62936509
After 15 generations new best SSE for g = 1054 is 7131152.617460327
After 22 generations new best SSE for g = 1076 is 7130151.790909101
After 6 generations new best SSE for g = 1082 is 7129416.165728722
After 1 generations new best SSE for g = 1083 is 7126247.151515161
After 6 generations new best SSE for g = 1089 is 7124878.562229447
After 42 generations new best SSE for g = 1131 is 7124563.00667389
After 27 generations new best SSE for g = 1158 is 7124355.449458883
After 2 generations new best SSE for g = 1160 is 7124247.501911985
After 18 generations new best SSE for g = 1178 is 7124191.525865809
After 21 generations new best SSE for g = 1199 is 7122951.797474757
After 5 generations new best SSE for g = 1204 is 7122613.413347771
After 2 generations new best SSE for g = 1206 is 7122527.559379518
After 4 generations new best SSE for g = 1210 is 7122495.9966811035
After 7 generations new best SSE for g = 1217 is 7121932.325252533
After 12 generations new best SSE for g = 1229 is 7120473.036038971
After 18 generations new best SSE for g = 1247 is 7120062.151118337
After 8 generations new best SSE for g = 1255 is 7119868.311832622
After 4 generations new best SSE for g = 1259 is 7119768.503499288
After 3 generations new best SSE for g = 1262 is 7118844.338744598
After 15 generations new best SSE for g = 1277 is 7118501.723268407
After 18 generations new best SSE for g = 1295 is 7118377.356277064
After 1 generations new best SSE for g = 1296 is 7118244.620887454
After 3 generations new best SSE for g = 1299 is 7117925.89707793
After 31 generations new best SSE for g = 1330 is 7117049.309776343
After 24 generations new best SSE for g = 1354 is 7116456.70382396
After 24 generations new best SSE for g = 1378 is 7115644.830014437
After 29 generations new best SSE for g = 1407 is 7115240.24040405
After 20 generations new best SSE for g = 1427 is 7115075.512157298
After 18 generations new best SSE for g = 1445 is 7114820.676443012
After 6 generations new best SSE for g = 1451 is 7114469.212157301
After 4 generations new best SSE for g = 1455 is 7113953.858585869
After 23 generations new best SSE for g = 1478 is 7112326.721681108
After 81 generations new best SSE for g = 1559 is 7111862.013347773
After 13 generations new best SSE for g = 1572 is 7111685.909595971
After 20 generations new best SSE for g = 1592 is 7111291.441919202
After 17 generations new best SSE for g = 1609 is 7110845.9871572945
After 75 generations new best SSE for g = 1684 is 7110259.815728726
After 16 generations new best SSE for g = 1700 is 7110209.170490629
After 2 generations new best SSE for g = 1702 is 7110138.929834063
Best SSE for g = 1802 is 7110138.929834063
Best chromosome for g = 1802 is center 0 is 31.5 90.33333333333333
Best chromosome for g = 1802 is center 1 is 189.8 91.6
Best chromosome for g = 1802 is center 2 is 160.0 199.71428571428572
Best chromosome for g = 1802 is center 3 is 374.3333333333333 48.0
```

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Best chromosome for g = 1802 is center 4 is 320.75 184.125
Best chromosome for g = 1802 is center 5 is 489.0 166.14285714285714
Best chromosome for g = 1802 is center 6 is 643.8333333333334
118.16666666666667
Best chromosome for g = 1802 is center 7 is 750.3333333333334 106.0
Best chromosome for g = 1802 is center 8 is 886.25 126.25
Best chromosome for g = 1802 is center 9 is 1036.4 150.8
Best chromosome for g = 1802 is center 10 is 1132.142857142857
130.85714285714286
Best chromosome for g = 1802 is center 11 is 1283.857142857143
92.14285714285714
Best chromosome for g = 1802 is center 12 is 1425.5 124.16666666666667
Best chromosome for g = 1802 is center 13 is 1516.25 111.75
Best chromosome for g = 1802 is center 14 is 1656.25 104.75
Best chromosome for g = 1802 is center 15 is 42.888888888888886
342.3333333333333
Best chromosome for g = 1802 is center 16 is 10.166666666666666 590.0
Best chromosome for g = 1802 is center 17 is 175.0 316.7142857142857
Best chromosome for g = 1802 is center 18 is 88.0 511.25
Best chromosome for g = 1802 is center 19 is 470.0 288.14285714285717
Best chromosome for g = 1802 is center 20 is 675.4 254.4
Best chromosome for g = 1802 is center 21 is 311.7142857142857
331.14285714285717
Best chromosome for g = 1802 is center 22 is 270.57142857142856
493.42857142857144
Best chromosome for g = 1802 is center 23 is 545.5 349.75
Best chromosome for g = 1802 is center 24 is 433.3333333333333
487.3333333333333
Best chromosome for g = 1802 is center 25 is 602.0 519.2
Best chromosome for g = 1802 is center 26 is -61.0 801.0
Best chromosome for g = 1802 is center 27 is 128.0 683.0
Best chromosome for g = 1802 is center 28 is 280.8 678.6
Best chromosome for g = 1802 is center 29 is 256.3333333333333
767.1666666666666
Best chromosome for g = 1802 is center 30 is 419.0 635.0
Best chromosome for g = 1802 is center 31 is 405.14285714285717
781.7142857142857
Best chromosome for g = 1802 is center 32 is 530.0 673.8
Best chromosome for g = 1802 is center 33 is 119.25 824.0
Best chromosome for g = 1802 is center 34 is 272.5 884.8333333333334
Best chromosome for g = 1802 is center 35 is 94.5 1014.1666666666666
Best chromosome for g = 1802 is center 36 is 222.28571428571428
1008.2857142857143
Best chromosome for g = 1802 is center 37 is 45.75 1099.75
Best chromosome for g = 1802 is center 38 is 53.7 1213.9
Best chromosome for g = 1802 is center 39 is 45.875 1323.25
Best chromosome for g = 1802 is center 40 is 45.875 1439.125
Best chromosome for g = 1802 is center 41 is 147.5 1118.8333333333333
Best chromosome for g = 1802 is center 42 is 154.5 1256.25
Best chromosome for g = 1802 is center 43 is 137.125 1387.0
Best chromosome for g = 1802 is center 44 is 283.3333333333333
1157.6666666666667
Best chromosome for g = 1802 is center 45 is 432.6666666666667
946.3333333333334
```

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Best chromosome for g = 1802 is center 46 is 331.625 1240.0
Best chromosome for g = 1802 is center 47 is 31.666666666666668
1559.3333333333333
Best chromosome for g = 1802 is center 48 is 124.0 1518.625
Best chromosome for g = 1802 is center 49 is 292.85714285714283
1357.857142857143
Best chromosome for g = 1802 is center 50 is 39.285714285714285
1675.2857142857142
Best chromosome for g = 1802 is center 51 is 129.0 1629.6666666666667
Best chromosome for g = 1802 is center 52 is 133.57142857142858
1738.7142857142858
Best chromosome for g = 1802 is center 53 is 28.4 1795.4
Best chromosome for g = 1802 is center 54 is 24.0 2012.0
Best chromosome for g = 1802 is center 55 is 698.8571428571429
354.85714285714283
Best chromosome for g = 1802 is center 56 is 889.5714285714286
247.71428571428572
Best chromosome for g = 1802 is center 57 is 875.0 362.8
Best chromosome for g = 1802 is center 58 is 789.0 626.5
Best chromosome for g = 1802 is center 59 is 640.0 707.5
Best chromosome for g = 1802 is center 60 is 523.5 824.0
Best chromosome for g = 1802 is center 61 is 458.375 1087.5
Best chromosome for g = 1802 is center 62 is 1092.142857142857
290.14285714285717
Best chromosome for g = 1802 is center 63 is 1282.0 212.0
Best chromosome for g = 1802 is center 64 is 1291.6 307.2
Best chromosome for g = 1802 is center 65 is 1472.142857142857
227.28571428571428
Best chromosome for g = 1802 is center 66 is 1407.8 305.6
Best chromosome for g = 1802 is center 67 is 1754.0 117.8
Best chromosome for g = 1802 is center 68 is 1900.1666666666667
97.66666666666667
Best chromosome for g = 1802 is center 69 is 1530.4 321.0
Best chromosome for g = 1802 is center 70 is 1687.8181818181818
257.45454545454544
Best chromosome for g = 1802 is center 71 is 1843.4285714285713
222.14285714285714
Best chromosome for g = 1802 is center 72 is 929.6666666666666
572.3333333333334
Best chromosome for g = 1802 is center 73 is 1189.0 373.6666666666667
Best chromosome for g = 1802 is center 74 is 1012.25 490.75
Best chromosome for g = 1802 is center 75 is 1120.0 488.0
Best chromosome for g = 1802 is center 76 is 1300.1666666666667
508.3333333333333
Best chromosome for g = 1802 is center 77 is 1054.6 626.4
Best chromosome for g = 1802 is center 78 is 1458.0 478.8
Best chromosome for g = 1802 is center 79 is 1781.6 429.8
Best chromosome for g = 1802 is center 80 is 1954.25 202.25
Best chromosome for g = 1802 is center 81 is 2103.4285714285716
120.42857142857143
Best chromosome for g = 1802 is center 82 is 2246.8333333333335
89.33333333333333
Best chromosome for g = 1802 is center 83 is 2065.6 259.4
Best chromosome for g = 1802 is center 84 is 1921.0 325.4
```

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Best chromosome for g = 1802 is center 85 is 673.8571428571429
847.1428571428571
Best chromosome for g = 1802 is center 86 is 921.8333333333334 704.5
Best chromosome for g = 1802 is center 87 is 1158.4285714285713 628.0
Best chromosome for g = 1802 is center 88 is 1297.375 606.125
Best chromosome for g = 1802 is center 89 is 1433.8 604.0
Best chromosome for g = 1802 is center 90 is 1092.6666666666667
766.1111111111111
Best chromosome for g = 1802 is center 91 is 1289.6 720.6
Best chromosome for g = 1802 is center 92 is 566.75 987.75
Best chromosome for g = 1802 is center 93 is 897.7777777777778
852.4444444444445
Best chromosome for g = 1802 is center 94 is 816.6666666666666
963.3333333333334
Best chromosome for g = 1802 is center 95 is 1060.4 900.8
Best chromosome for g = 1802 is center 96 is 482.7 1200.7
Best chromosome for g = 1802 is center 97 is 686.625 1126.625
Best chromosome for g = 1802 is center 98 is 470.44444444444446
1315.3333333333333
Best chromosome for g = 1802 is center 99 is 276.42857142857144 1461.0
Best chromosome for g = 1802 is center 100 is 291.2857142857143
1580.857142857143
Best chromosome for g = 1802 is center 101 is 693.375 1254.375
Best chromosome for g = 1802 is center 102 is 852.375 1091.875
Best chromosome for g = 1802 is center 103 is 852.1666666666666 1220.0
Best chromosome for g = 1802 is center 104 is 478.8888888888889
1427.5555555555557
Best chromosome for g = 1802 is center 105 is 438.5 1554.6666666666667
Best chromosome for g = 1802 is center 106 is 632.2 1395.2
Best chromosome for g = 1802 is center 107 is 1537.5 591.0
Best chromosome for g = 1802 is center 108 is 1229.25 848.0
Best chromosome for g = 1802 is center 109 is 1344.6 821.2
Best chromosome for g = 1802 is center 110 is 1026.0 1063.2
Best chromosome for g = 1802 is center 111 is 1686.4 534.2
Best chromosome for g = 1802 is center 112 is 1507.857142857143
724.8571428571429
Best chromosome for g = 1802 is center 113 is 824.1428571428571
1335.7142857142858
Best chromosome for g = 1802 is center 114 is 2154.2 260.2
Best chromosome for g = 1802 is center 115 is 2292.0 205.33333333333334
Best chromosome for g = 1802 is center 116 is 2378.1428571428573
136.71428571428572
Best chromosome for g = 1802 is center 117 is 2504.0 108.75
Best chromosome for g = 1802 is center 118 is 2647.2 40.2
Best chromosome for g = 1802 is center 119 is 1703.625 663.5
Best chromosome for g = 1802 is center 120 is 2067.25 448.0
Best chromosome for g = 1802 is center 121 is 1899.5714285714287 567.0
Best chromosome for g = 1802 is center 122 is 2248.25 312.75
Best chromosome for g = 1802 is center 123 is 1487.0 845.8
Best chromosome for g = 1802 is center 124 is 2249.0 450.0
Best chromosome for g = 1802 is center 125 is 2355.0 298.2
Best chromosome for g = 1802 is center 126 is 2677.6 164.0
Best chromosome for g = 1802 is center 127 is 2508.2727272727275
255.8181818181818
```

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Best chromosome for g = 1802 is center 128 is 2658.6666666666665 286.0
Best chromosome for g = 1802 is center 129 is 2801.1428571428573
67.71428571428571
Best chromosome for g = 1802 is center 130 is 2811.0 192.5
Best chromosome for g = 1802 is center 131 is 1173.0 1000.4
Best chromosome for g = 1802 is center 132 is 1049.5714285714287 1167.0
Best chromosome for g = 1802 is center 133 is 1279.0 1026.0
Best chromosome for g = 1802 is center 134 is 1021.4285714285714
1282.5714285714287
Best chromosome for g = 1802 is center 135 is 1192.625 1159.0
Best chromosome for g = 1802 is center 136 is 2431.0 422.75
Best chromosome for g = 1802 is center 137 is 2810.75 326.875
Best chromosome for g = 1802 is center 138 is 1662.4 777.4
Best chromosome for g = 1802 is center 139 is 2046.0 590.8
Best chromosome for g = 1802 is center 140 is 1856.0 713.0
Best chromosome for g = 1802 is center 141 is 1945.3333333333333 725.0
Best chromosome for g = 1802 is center 142 is 2159.3333333333335
629.8333333333334
Best chromosome for g = 1802 is center 143 is 2225.6 541.8
Best chromosome for g = 1802 is center 144 is 2090.5714285714284
763.5714285714286
Best chromosome for g = 1802 is center 145 is 2321.1428571428573
612.8571428571429
Best chromosome for g = 1802 is center 146 is 2509.8888888888887
565.2222222222222
Best chromosome for g = 1802 is center 147 is 2298.8888888888887
730.6666666666666
Best chromosome for g = 1802 is center 148 is 2504.3333333333335 692.0
Best chromosome for g = 1802 is center 149 is 2606.1428571428573
391.2857142857143
Best chromosome for g = 1802 is center 150 is 2654.1666666666665 549.0
Best chromosome for g = 1802 is center 151 is 2781.0 498.8333333333333
Best chromosome for g = 1802 is center 152 is 2778.5714285714284
613.4285714285714
Best chromosome for g = 1802 is center 153 is 1348.75 1191.875
Best chromosome for g = 1802 is center 154 is 1417.1666666666667
1053.3333333333333
Best chromosome for g = 1802 is center 155 is 1197.5714285714287
1287.142857142857
Best chromosome for g = 1802 is center 156 is 1065.625 1400.25
Best chromosome for g = 1802 is center 157 is 1897.6 869.6
Best chromosome for g = 1802 is center 158 is 1462.8 1194.4
Best chromosome for g = 1802 is center 159 is 1606.0 1084.6
Best chromosome for g = 1802 is center 160 is 1749.25 1038.5
Best chromosome for g = 1802 is center 161 is 1578.2 1210.6
Best chromosome for g = 1802 is center 162 is 2172.6 879.8
Best chromosome for g = 1802 is center 163 is 1865.25 1038.75
Best chromosome for g = 1802 is center 164 is 1731.6 1189.4
Best chromosome for g = 1802 is center 165 is 1964.6666666666667
1049.6666666666667
Best chromosome for g = 1802 is center 166 is 1860.2 1198.2
Best chromosome for g = 1802 is center 167 is 2093.5 1047.0
Best chromosome for g = 1802 is center 168 is 2659.5 715.5
Best chromosome for g = 1802 is center 169 is 2449.5 827.25
```

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Best chromosome for g = 1802 is center 170 is 2343.0 898.5
Best chromosome for g = 1802 is center 171 is 2569.1428571428573
833.7142857142857
Best chromosome for g = 1802 is center 172 is 2243.0 1073.4
Best chromosome for g = 1802 is center 173 is 2512.8333333333335
1005.6666666666666
Best chromosome for g = 1802 is center 174 is 2781.0 751.375
Best chromosome for g = 1802 is center 175 is 2750.6 991.0
Best chromosome for g = 1802 is center 176 is 604.0 1553.4
Best chromosome for g = 1802 is center 177 is 713.25 1532.75
Best chromosome for g = 1802 is center 178 is 846.3333333333334 1512.5
Best chromosome for g = 1802 is center 179 is 1010.6666666666666
1508.3333333333333
Best chromosome for g = 1802 is center 180 is 300.5 1704.1666666666667
Best chromosome for g = 1802 is center 181 is 184.25 1854.25
Best chromosome for g = 1802 is center 182 is 456.5 1665.1666666666667
Best chromosome for g = 1802 is center 183 is 309.7142857142857
1824.2857142857142
Best chromosome for g = 1802 is center 184 is 49.888888888888886 2177.0
Best chromosome for g = 1802 is center 185 is 174.5 2051.0
Best chromosome for g = 1802 is center 186 is 170.2 2157.0
Best chromosome for g = 1802 is center 187 is 469.4 1766.6
Best chromosome for g = 1802 is center 188 is 316.2857142857143 1938.0
Best chromosome for g = 1802 is center 189 is 452.2 1865.2
Best chromosome for g = 1802 is center 190 is 296.2 2086.6
Best chromosome for g = 1802 is center 191 is 390.2 2040.2
Best chromosome for g = 1802 is center 192 is 607.0 1712.0
Best chromosome for g = 1802 is center 193 is 49.888888888888886
2296.1111111111113
Best chromosome for g = 1802 is center 194 is 160.6 2275.6
Best chromosome for g = 1802 is center 195 is 50.0 2411.777777777778
Best chromosome for g = 1802 is center 196 is 49.111111111111114
2525.222222222222
Best chromosome for g = 1802 is center 197 is 176.44444444444446
2393.8888888888887
Best chromosome for g = 1802 is center 198 is 156.83333333333334
2494.1666666666665
Best chromosome for g = 1802 is center 199 is 49.333333333333336
2641.777777777778
Best chromosome for g = 1802 is center 200 is 299.0 2196.6666666666665
Best chromosome for g = 1802 is center 201 is 328.85714285714283
2286.4285714285716
Best chromosome for g = 1802 is center 202 is 384.4 2162.0
Best chromosome for g = 1802 is center 203 is 49.77777777777778
2758.222222222222
Best chromosome for g = 1802 is center 204 is 321.8888888888889
2390.8888888888887
Best chromosome for g = 1802 is center 205 is 597.25 1880.0
Best chromosome for g = 1802 is center 206 is 512.4 2075.8
Best chromosome for g = 1802 is center 207 is 781.6666666666666
1627.6666666666667
Best chromosome for g = 1802 is center 208 is 709.2222222222222 1882.0
Best chromosome for g = 1802 is center 209 is 630.8571428571429
2032.2857142857142
```

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Best chromosome for g = 1802 is center 210 is 849.5 1754.0
Best chromosome for g = 1802 is center 211 is 449.25 2313.75
Best chromosome for g = 1802 is center 212 is 160.5 2608.75
Best chromosome for g = 1802 is center 213 is 336.0 2539.8571428571427
Best chromosome for g = 1802 is center 214 is 953.0 1640.3333333333333
Best chromosome for g = 1802 is center 215 is 613.8571428571429
2162.714285714286
Best chromosome for g = 1802 is center 216 is 852.125 1891.75
Best chromosome for g = 1802 is center 217 is 780.8333333333334 2120.0
Best chromosome for g = 1802 is center 218 is 627.6666666666666
2276.8333333333335
Best chromosome for g = 1802 is center 219 is 165.22222222222223
2722.777777777778
Best chromosome for g = 1802 is center 220 is 159.875 2830.5
Best chromosome for g = 1802 is center 221 is 469.25 2462.25
Best chromosome for g = 1802 is center 222 is 311.2857142857143
2637.8571428571427
Best chromosome for g = 1802 is center 223 is 310.6666666666667
2772.5555555555557
Best chromosome for g = 1802 is center 224 is 499.57142857142856
2619.714285714286
Best chromosome for g = 1802 is center 225 is 626.8333333333334 2392.5
Best chromosome for g = 1802 is center 226 is 626.5 2511.25
Best chromosome for g = 1802 is center 227 is 919.5 2033.125
Best chromosome for g = 1802 is center 228 is 907.6666666666666
2160.1666666666665
Best chromosome for g = 1802 is center 229 is 917.2857142857143
2277.8571428571427
Best chromosome for g = 1802 is center 230 is 907.5 2391.5
Best chromosome for g = 1802 is center 231 is 626.6666666666666
2648.4444444444443
Best chromosome for g = 1802 is center 232 is 502.125 2765.875
Best chromosome for g = 1802 is center 233 is 624.8571428571429 2784.0
Best chromosome for g = 1802 is center 234 is 886.3333333333334
2490.6666666666665
Best chromosome for g = 1802 is center 235 is 731.1666666666666 2716.0
Best chromosome for g = 1802 is center 236 is 863.8 2633.6
Best chromosome for g = 1802 is center 237 is 836.6 2791.4
Best chromosome for g = 1802 is center 238 is 1210.5 1399.6666666666667
Best chromosome for g = 1802 is center 239 is 1156.75 1523.0
Best chromosome for g = 1802 is center 240 is 1061.0 1699.5
Best chromosome for g = 1802 is center 241 is 1343.2 1341.4
Best chromosome for g = 1802 is center 242 is 1451.25 1346.25
Best chromosome for g = 1802 is center 243 is 1558.8 1335.6
Best chromosome for g = 1802 is center 244 is 1304.0 1530.8
Best chromosome for g = 1802 is center 245 is 1000.7142857142857
1885.2857142857142
Best chromosome for g = 1802 is center 246 is 1139.857142857143
1865.2857142857142
Best chromosome for g = 1802 is center 247 is 1056.0 2062.3333333333335
Best chromosome for g = 1802 is center 248 is 1735.5 1347.1666666666667
Best chromosome for g = 1802 is center 249 is 1960.6 1202.8
Best chromosome for g = 1802 is center 250 is 1869.6 1348.0
```

```
Best chromosome for g = 1802 is center 251 is 1476.5714285714287
1529.5714285714287
Best chromosome for g = 1802 is center 252 is 1604.75 1537.25
Best chromosome for g = 1802 is center 253 is 1727.875 1517.25
Best chromosome for g = 1802 is center 254 is 1417.3333333333333
1644.1666666666667
Best chromosome for g = 1802 is center 255 is 1346.0 1771.0
Best chromosome for g = 1802 is center 256 is 1264.6666666666667
1887.3333333333333
Best chromosome for g = 1802 is center 257 is 1177.3333333333333
2042.3333333333333
Best chromosome for g = 1802 is center 258 is 1162.4285714285713
2165.5714285714284
Best chromosome for g = 1802 is center 259 is 1265.0 2193.0
Best chromosome for g = 1802 is center 260 is 1183.857142857143
2277.4285714285716
Best chromosome for g = 1802 is center 261 is 1965.8 1401.4
Best chromosome for g = 1802 is center 262 is 1869.2857142857142
1600.4285714285713
Best chromosome for g = 1802 is center 263 is 1712.1666666666667
1700.8333333333333
Best chromosome for g = 1802 is center 264 is 1866.2 1777.6
Best chromosome for g = 1802 is center 265 is 2049.5 1270.5
Best chromosome for g = 1802 is center 266 is 1999.8333333333333
1561.1666666666667
Best chromosome for g = 1802 is center 267 is 1989.857142857143
1673.7142857142858
Best chromosome for g = 1802 is center 268 is 2129.8571428571427
1159.7142857142858
Best chromosome for g = 1802 is center 269 is 2361.0 1099.4
Best chromosome for g = 1802 is center 270 is 2253.125 1199.0
Best chromosome for g = 1802 is center 271 is 2358.5 1225.75
Best chromosome for g = 1802 is center 272 is 2136.714285714286
1334.4285714285713
Best chromosome for g = 1802 is center 273 is 2301.2 1334.2
Best chromosome for g = 1802 is center 274 is 2201.875 1520.0
Best chromosome for g = 1802 is center 275 is 2174.5 1635.5
Best chromosome for g = 1802 is center 276 is 1433.8 1883.0
Best chromosome for g = 1802 is center 277 is 1571.2857142857142
1846.5714285714287
Best chromosome for g = 1802 is center 278 is 1428.0 2009.75
Best chromosome for g = 1802 is center 279 is 1694.0 1888.0
Best chromosome for g = 1802 is center 280 is 1452.2857142857142
2117.714285714286
Best chromosome for g = 1802 is center 281 is 1634.3 2067.7
Best chromosome for g = 1802 is center 282 is 2016.6666666666667
1790.8333333333333
Best chromosome for g = 1802 is center 283 is 1801.8 2002.2
Best chromosome for g = 1802 is center 284 is 2502.3333333333335
1116.8333333333333
Best chromosome for g = 1802 is center 285 is 2507.0 1226.875
Best chromosome for g = 1802 is center 286 is 2188.625 1770.125
Best chromosome for g = 1802 is center 287 is 2648.6 1107.6
Best chromosome for g = 1802 is center 288 is 2349.5 1559.3333333333333
```

Best chromosome for g = 1802 is center 289 is 2409.8333333333335
1443.8333333333333
Best chromosome for g = 1802 is center 290 is 2499.3333333333335
1359.4444444444443
Best chromosome for g = 1802 is center 291 is 2638.0 1257.7142857142858
Best chromosome for g = 1802 is center 292 is 1177.8333333333333
2392.6666666666665
Best chromosome for g = 1802 is center 293 is 1143.0 2513.714285714286
Best chromosome for g = 1802 is center 294 is 1331.0 2348.75
Best chromosome for g = 1802 is center 295 is 1456.0 2231.875
Best chromosome for g = 1802 is center 296 is 2787.714285714286
1140.7142857142858
Best chromosome for g = 1802 is center 297 is 2787.8571428571427
1251.4285714285713
Best chromosome for g = 1802 is center 298 is 1630.625 2224.375
Best chromosome for g = 1802 is center 299 is 1821.3333333333333
2121.8333333333335
Best chromosome for g = 1802 is center 300 is 1820.1666666666667
2237.6666666666665
Best chromosome for g = 1802 is center 301 is 1453.5555555555557
2373.1111111111113
Best chromosome for g = 1802 is center 302 is 2016.0 1905.75
Best chromosome for g = 1802 is center 303 is 2153.6666666666665
1882.3333333333333
Best chromosome for g = 1802 is center 304 is 2001.0 2048.0
Best chromosome for g = 1802 is center 305 is 1999.6666666666667 2161.5
Best chromosome for g = 1802 is center 306 is 1976.2222222222222
2276.8888888888887
Best chromosome for g = 1802 is center 307 is 2300.25 1921.75
Best chromosome for g = 1802 is center 308 is 2221.4 2045.6
Best chromosome for g = 1802 is center 309 is 2151.8888888888887
2143.3333333333335
Best chromosome for g = 1802 is center 310 is 962.7142857142857
2683.5714285714284
Best chromosome for g = 1802 is center 311 is 1066.6 2726.2
Best chromosome for g = 1802 is center 312 is 1319.0 2546.0
Best chromosome for g = 1802 is center 313 is 1644.0 2379.1111111111113
Best chromosome for g = 1802 is center 314 is 1464.4 2539.0
Best chromosome for g = 1802 is center 315 is 1808.2 2365.9
Best chromosome for g = 1802 is center 316 is 1165.4 2723.0
Best chromosome for g = 1802 is center 317 is 1275.5 2684.25
Best chromosome for g = 1802 is center 318 is 1611.4 2527.2
Best chromosome for g = 1802 is center 319 is 1773.0 2522.6666666666665
Best chromosome for g = 1802 is center 320 is 1373.4 2721.4
Best chromosome for g = 1802 is center 321 is 1544.142857142857
2689.714285714286
Best chromosome for g = 1802 is center 322 is 1979.5555555555557
2404.5555555555557
Best chromosome for g = 1802 is center 323 is 2168.8 2273.3
Best chromosome for g = 1802 is center 324 is 1903.75 2514.5
Best chromosome for g = 1802 is center 325 is 2181.3333333333335
2408.6666666666665
Best chromosome for g = 1802 is center 326 is 2319.6666666666665
2268.6666666666665

Best chromosome for g = 1802 is center 327 is 2348.3333333333335
1676.3333333333333
Best chromosome for g = 1802 is center 328 is 2353.0 1806.625
Best chromosome for g = 1802 is center 329 is 2356.2 2056.8
Best chromosome for g = 1802 is center 330 is 2339.714285714286 2170.0
Best chromosome for g = 1802 is center 331 is 2650.8333333333335
1481.8333333333333
Best chromosome for g = 1802 is center 332 is 2781.0 1389.5
Best chromosome for g = 1802 is center 333 is 2525.5714285714284
1588.4285714285713
Best chromosome for g = 1802 is center 334 is 2521.3333333333335 1715.5
Best chromosome for g = 1802 is center 335 is 2675.5 1596.0
Best chromosome for g = 1802 is center 336 is 2780.875 1563.875
Best chromosome for g = 1802 is center 337 is 2529.375 1845.75
Best chromosome for g = 1802 is center 338 is 2658.714285714286
1729.5714285714287
Best chromosome for g = 1802 is center 339 is 2507.1428571428573
2021.857142857143
Best chromosome for g = 1802 is center 340 is 2520.6666666666665
2139.6666666666665
Best chromosome for g = 1802 is center 341 is 2665.6666666666665
1881.3333333333333
Best chromosome for g = 1802 is center 342 is 2780.5 1697.6666666666667
Best chromosome for g = 1802 is center 343 is 2780.6666666666665
1817.6666666666667
Best chromosome for g = 1802 is center 344 is 2662.0 2046.0
Best chromosome for g = 1802 is center 345 is 2515.8 2247.4
Best chromosome for g = 1802 is center 346 is 2671.0 2202.4
Best chromosome for g = 1802 is center 347 is 2780.8888888888887 2129.0
Best chromosome for g = 1802 is center 348 is -66.0 3134.0
Best chromosome for g = 1802 is center 349 is 49.75 2874.25
Best chromosome for g = 1802 is center 350 is 178.33333333333334
2920.3333333333335
Best chromosome for g = 1802 is center 351 is 313.85714285714283
2915.5714285714284
Best chromosome for g = 1802 is center 352 is 502.6666666666667
2901.1666666666665
Best chromosome for g = 1802 is center 353 is 727.8 2865.4
Best chromosome for g = 1802 is center 354 is 622.625 2911.75
Best chromosome for g = 1802 is center 355 is 945.8 2854.8
Best chromosome for g = 1802 is center 356 is 349.0 3102.5
Best chromosome for g = 1802 is center 357 is 123.33333333333333 3266.5
Best chromosome for g = 1802 is center 358 is 145.71428571428572
3153.714285714286
Best chromosome for g = 1802 is center 359 is 266.6 3188.0
Best chromosome for g = 1802 is center 360 is 477.8 3052.8
Best chromosome for g = 1802 is center 361 is 839.0 2965.5
Best chromosome for g = 1802 is center 362 is 562.5 3130.5
Best chromosome for g = 1802 is center 363 is 710.0 3088.0
Best chromosome for g = 1802 is center 364 is 1109.9 2871.0
Best chromosome for g = 1802 is center 365 is 1273.5 2834.75
Best chromosome for g = 1802 is center 366 is 119.5 3375.25
Best chromosome for g = 1802 is center 367 is 95.5 3511.375
Best chromosome for g = 1802 is center 368 is 114.3 3621.1

```
Best chromosome for g = 1802 is center 369 is 251.33333333333334 3326.0
Best chromosome for g = 1802 is center 370 is 356.4 3258.2
Best chromosome for g = 1802 is center 371 is 352.3333333333333
3415.8333333333335
Best chromosome for g = 1802 is center 372 is 249.0 3493.4
Best chromosome for g = 1802 is center 373 is 450.0 3367.8
Best chromosome for g = 1802 is center 374 is 468.4 3230.6
Best chromosome for g = 1802 is center 375 is 587.0 3242.8
Best chromosome for g = 1802 is center 376 is 703.3333333333334 3202.0
Best chromosome for g = 1802 is center 377 is 896.3333333333334
3124.8333333333335
Best chromosome for g = 1802 is center 378 is 987.25 3026.75
Best chromosome for g = 1802 is center 379 is 709.1666666666666
3312.3333333333335
Best chromosome for g = 1802 is center 380 is 569.0 3368.8
Best chromosome for g = 1802 is center 381 is 838.0 3260.3333333333335
Best chromosome for g = 1802 is center 382 is 403.14285714285717
3527.285714285714
Best chromosome for g = 1802 is center 383 is 670.8 3440.4
Best chromosome for g = 1802 is center 384 is 312.375 3614.875
Best chromosome for g = 1802 is center 385 is 96.66666666666667
3736.5555555555557
Best chromosome for g = 1802 is center 386 is 567.0 3576.4
Best chromosome for g = 1802 is center 387 is 440.42857142857144 3676.0
Best chromosome for g = 1802 is center 388 is 1241.4 2982.0
Best chromosome for g = 1802 is center 389 is 1112.3333333333333 3101.0
Best chromosome for g = 1802 is center 390 is 1252.8333333333333
3150.3333333333335
Best chromosome for g = 1802 is center 391 is 1108.0 3203.0
Best chromosome for g = 1802 is center 392 is 944.75 3260.25
Best chromosome for g = 1802 is center 393 is 1109.1666666666667
3319.1666666666665
Best chromosome for g = 1802 is center 394 is 791.0 3465.0
Best chromosome for g = 1802 is center 395 is 952.8 3418.2
Best chromosome for g = 1802 is center 396 is 1377.2 2877.8
Best chromosome for g = 1802 is center 397 is 1508.3333333333333
2775.1666666666665
Best chromosome for g = 1802 is center 398 is 1710.0 2742.8571428571427
Best chromosome for g = 1802 is center 399 is 1480.0 2892.5
Best chromosome for g = 1802 is center 400 is 1584.0 2873.5
Best chromosome for g = 1802 is center 401 is 1405.8 3034.8
Best chromosome for g = 1802 is center 402 is 1714.1666666666667
2903.6666666666665
Best chromosome for g = 1802 is center 403 is 1361.6 3187.2
Best chromosome for g = 1802 is center 404 is 1291.1666666666667 3277.0
Best chromosome for g = 1802 is center 405 is 1480.6 3139.2
Best chromosome for g = 1802 is center 406 is 1595.0 3105.0
Best chromosome for g = 1802 is center 407 is 1703.0 3059.75
Best chromosome for g = 1802 is center 408 is 1588.0 3217.0
Best chromosome for g = 1802 is center 409 is 1760.2857142857142
3156.1428571428573
Best chromosome for g = 1802 is center 410 is 1327.2 3374.0
Best chromosome for g = 1802 is center 411 is 1521.1666666666667
3306.1666666666665
```

Best chromosome for g = 1802 is center 412 is 709.0 3591.0
Best chromosome for g = 1802 is center 413 is 909.6 3567.6
Best chromosome for g = 1802 is center 414 is 1695.8 3280.8
Best chromosome for g = 1802 is center 415 is 1808.0 2706.6
Best chromosome for g = 1802 is center 416 is 1807.2 2897.8
Best chromosome for g = 1802 is center 417 is 2007.25 2631.5
Best chromosome for g = 1802 is center 418 is 1944.0 2730.1428571428573
Best chromosome for g = 1802 is center 419 is 1949.875 2875.5
Best chromosome for g = 1802 is center 420 is 1943.8333333333333
3086.8333333333335
Best chromosome for g = 1802 is center 421 is 2352.5714285714284
2402.5714285714284
Best chromosome for g = 1802 is center 422 is 2155.0 2610.75
Best chromosome for g = 1802 is center 423 is 2391.75 2505.25
Best chromosome for g = 1802 is center 424 is 2342.714285714286
2628.714285714286
Best chromosome for g = 1802 is center 425 is 2521.25 2450.375
Best chromosome for g = 1802 is center 426 is 2154.4285714285716 2733.0
Best chromosome for g = 1802 is center 427 is 2310.0 2734.1666666666665
Best chromosome for g = 1802 is center 428 is 2154.0 2848.714285714286
Best chromosome for g = 1802 is center 429 is 2345.2 2829.2
Best chromosome for g = 1802 is center 430 is 2508.75 2601.25
Best chromosome for g = 1802 is center 431 is 2488.1666666666665
2754.8333333333335
Best chromosome for g = 1802 is center 432 is 2066.25 2977.25
Best chromosome for g = 1802 is center 433 is 2194.6666666666665
2983.6666666666665
Best chromosome for g = 1802 is center 434 is 2126.8333333333335
3113.6666666666665
Best chromosome for g = 1802 is center 435 is 2333.285714285714
2944.4285714285716
Best chromosome for g = 1802 is center 436 is 2501.5 2854.75
Best chromosome for g = 1802 is center 437 is 2668.2 2343.4
Best chromosome for g = 1802 is center 438 is 2780.8333333333335 2260.0
Best chromosome for g = 1802 is center 439 is 2779.285714285714
2374.5714285714284
Best chromosome for g = 1802 is center 440 is 2709.714285714286
2493.4285714285716
Best chromosome for g = 1802 is center 441 is 2693.1666666666665 2655.5
Best chromosome for g = 1802 is center 442 is 2664.0 2905.3333333333335
Best chromosome for g = 1802 is center 443 is 144.0 3849.777777777778
Best chromosome for g = 1802 is center 444 is 0.5 3893.75
Best chromosome for g = 1802 is center 445 is 311.875 3743.25
Best chromosome for g = 1802 is center 446 is 300.4 3861.8
Best chromosome for g = 1802 is center 447 is 532.5714285714286
3756.5714285714284
Best chromosome for g = 1802 is center 448 is 464.7142857142857 3866.0
Best chromosome for g = 1802 is center 449 is 576.6666666666666 3886.0
Best chromosome for g = 1802 is center 450 is 710.4285714285714
3722.714285714286
Best chromosome for g = 1802 is center 451 is 901.6 3707.5
Best chromosome for g = 1802 is center 452 is 1110.7142857142858
3559.285714285714
Best chromosome for g = 1802 is center 453 is 1340.875 3567.5

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Best chromosome for g = 1802 is center 454 is 1061.0 3705.5
Best chromosome for g = 1802 is center 455 is 1240.857142857143
3656.5714285714284
Best chromosome for g = 1802 is center 456 is 703.8333333333334
3841.8333333333335
Best chromosome for g = 1802 is center 457 is 922.3333333333334
3835.8333333333335
Best chromosome for g = 1802 is center 458 is 837.2 3839.6
Best chromosome for g = 1802 is center 459 is 1169.1666666666667
3751.1666666666665
Best chromosome for g = 1802 is center 460 is 1104.2857142857142
3844.285714285714
Best chromosome for g = 1802 is center 461 is 1949.5 3222.0
Best chromosome for g = 1802 is center 462 is 1807.6666666666667
3305.8333333333335
Best chromosome for g = 1802 is center 463 is 1639.625 3422.25
Best chromosome for g = 1802 is center 464 is 1478.3333333333333
3560.3333333333335
Best chromosome for g = 1802 is center 465 is 1638.4444444444443
3607.6666666666665
Best chromosome for g = 1802 is center 466 is 1354.5714285714287 3756.0
Best chromosome for g = 1802 is center 467 is 1314.6666666666667 3853.5
Best chromosome for g = 1802 is center 468 is 1542.5555555555557 3732.0
Best chromosome for g = 1802 is center 469 is 1972.375 3361.375
Best chromosome for g = 1802 is center 470 is 1795.0 3628.25
Best chromosome for g = 1802 is center 471 is 1462.0 3854.2
Best chromosome for g = 1802 is center 472 is 1698.0 3742.75
Best chromosome for g = 1802 is center 473 is 2166.714285714286
3221.1428571428573
Best chromosome for g = 1802 is center 474 is 2342.1666666666665
3095.6666666666665
Best chromosome for g = 1802 is center 475 is 2515.3333333333335 3002.0
Best chromosome for g = 1802 is center 476 is 1648.125 3876.625
Best chromosome for g = 1802 is center 477 is 1929.8 3585.8
Best chromosome for g = 1802 is center 478 is 1949.0 3680.4285714285716
Best chromosome for g = 1802 is center 479 is 1795.0 3802.6
Best chromosome for g = 1802 is center 480 is 1908.0 3813.714285714286
Best chromosome for g = 1802 is center 481 is 2131.8333333333335
3340.8333333333335
Best chromosome for g = 1802 is center 482 is 2326.4444444444443 3219.0
Best chromosome for g = 1802 is center 483 is 2550.8888888888887
3131.8888888888887
Best chromosome for g = 1802 is center 484 is 2534.75 3272.25
Best chromosome for g = 1802 is center 485 is 2108.3333333333335
3646.3333333333335
Best chromosome for g = 1802 is center 486 is 1994.75 3837.75
Best chromosome for g = 1802 is center 487 is 2117.2 3828.0
Best chromosome for g = 1802 is center 488 is 2347.4285714285716
3355.285714285714
Best chromosome for g = 1802 is center 489 is 2422.6666666666665
3473.3333333333335
Best chromosome for g = 1802 is center 490 is 2563.777777777778
3390.222222222222
```

```
Best chromosome for g = 1802 is center 491 is 2779.6666666666665
3068.1666666666665
Best chromosome for g = 1802 is center 492 is 2718.1666666666665 3187.5
Best chromosome for g = 1802 is center 493 is 2782.5714285714284 3309.0
Best chromosome for g = 1802 is center 494 is 2802.4285714285716
3449.285714285714
Best chromosome for g = 1802 is center 495 is 2268.0 3813.0
Best chromosome for g = 1802 is center 496 is 2444.5 3754.0
Best chromosome for g = 1802 is center 497 is 2749.5 3592.0
Best chromosome for g = 1802 is center 498 is 2797.5 3795.0
Best chromosome for g = 1802 is center 499 is 2701.0 3919.25
Time Elapsed: 2.378459297E9 Seeding Time: 489078.0
The seeding percentage time is : 0.000206
```

Appendix C: Genetic Algorithm Source Code

```
package dissertation;

//* import java.awt.Point;
import java.io.BufferedReader;
import java.io.FileNotFoundException;
import java.io.FileOutputStream;
import java.io.FileReader;
import java.io.IOException;
import java.io.PrintStream;
import java.util.Random;
import java.util.Arrays;
public class GeneticAlgorithm {
   public static void main(String[] args) {
//* This program requires seven arguments, all integers.
//*     The first argument is the number of initial chromosomes selected at random. Number must be between 0 and number of total chromosomes.
//*     The second argument is the number of initial chromosomes selected with the Density algorithm. Number must be between number of total
chromosomes.
//*     The third argument is the number of initial chromosomes selected at with the Separation algorithm. Number must be between number of total
chromosomes.
//* NOTE: The sum of the first three arguments must equal number of total chromosomes.
//*     The fourth argument is the method by which chromosomes are selected for the mating buffer.  Number must be between 0 and 4.
//*     Selection method: Roulette Wheel = 0, Probabilistic = 1, Deterministic = 2, Parent Favored Hybrid = 3, Roulette Wheel by Rank = 4
//*             The fifth argument is the K value.
//*             The sixth argument is the dimensionality of the data.
//*             The seventh argument is the number of data points in the dataset.
        try
                {
                        FileOutputStream fout= new FileOutputStream("T10K30DPFH10.log");        //* output file
                        FileOutputStream ferr= new FileOutputStream("stderr.log");
                        MultiOutputStream multiOut= new MultiOutputStream(System.out, fout);
                        MultiOutputStream multiErr= new MultiOutputStream(System.err, ferr);
                        PrintStream stdout= new PrintStream(multiOut);
                        PrintStream stderr= new PrintStream(multiErr);
                        System.setOut(stdout);
                        System.setErr(stderr);
                }
                catch (FileNotFoundException ex)
                {
                        //*           Could not create/open the file
                }
        boolean goodArguments;
        //*           Set goodArguments to "true"
        goodArguments = true;
        int randomChromosomes = 0;
        int densityChromosomes = 0;
        int separationChromosomes = 0;
        int selectionMethod = 0;
        int dim = 10;
        int numCenters = 50;
        int numPoints = 10000;
        int chromosomes = 100;          //* number of chromosomes
        //*  Read input arguments
        int numArgs = args.length;
      if (numArgs != 7) {
         System.out.println("Seven input arguments required");
         goodArguments = false;
      }
       else {
                randomChromosomes = (Integer.valueOf(args[0]) ).intValue();
                densityChromosomes = (Integer.valueOf(args[1]) ).intValue();
                separationChromosomes = (Integer.valueOf(args[2]) ).intValue();
                selectionMethod = (Integer.valueOf(args[3]) ).intValue();
                numCenters = (Integer.valueOf(args[4])).intValue();
                dim = (Integer.valueOf(args[5])).intValue();
                numPoints = (Integer.valueOf(args[6])).intValue();
         if (randomChromosomes > chromosomes  || randomChromosomes < 0) {
```

```
                    System.out.println ("First argument must be between 0 and " +chromosomes);
                    goodArguments = false;
            }
            if (densityChromosomes > chromosomes  || densityChromosomes < 0) {
                    System.out.println ("Second argument must be between 0 and " +chromosomes);
                    goodArguments = false;
            }
            if (separationChromosomes > chromosomes  || separationChromosomes < 0) {
                    System.out.println ("Third argument must be between 0 and " +chromosomes);
                    goodArguments = false;
            }
            if (selectionMethod < 0  || selectionMethod > 4) {
                    System.out.println ("Fourth argument must be between 0 and 4" );
                    goodArguments = false;
            }
            if (chromosomes != randomChromosomes + densityChromosomes + separationChromosomes) {
                    System.out.println ("Density, Random and Separation Chromosomes must equal total Chromosomes");
                    goodArguments = false;
            }
          }
            String [] data;
            data = new String [numPoints * dim];
            BufferedReader br = null;
//* Read input file of data points
                    try {
                            String sCurrentLine;
                            br = new BufferedReader(new FileReader("C:\\Users\\william\\workspace\\BillMcGarvey \\TSP1060.txt"));  //input data set
                            int p = 0;
                            while ((sCurrentLine = br.readLine()) != null) {
                                    data[p] = sCurrentLine;
                                    p = p + 1;
                            }
                    } catch (IOException e) {
                            e.printStackTrace();
                    } finally {
                            try {
                                    if (br != null)br.close();
                            } catch (IOException ex) {
                                    ex.printStackTrace();
                            }
                    }
            double [] dataPoints;
            dataPoints = new double [numPoints * dim];
            int p = 0;
            while (p < numPoints * dim) {
                    dataPoints[p] = Double.parseDouble(data[p]);
                    p = p + 1;
            }
            double start_time, end_time;
                    start_time=System.currentTimeMillis();
          double[][][] childBuffer;
          childBuffer = new double[chromosomes][numCenters][dim];
          double[][][] matingBuffer;
          matingBuffer = new double[chromosomes][numCenters][dim];
          double[][][] parentBuffer;
          parentBuffer = new double[chromosomes][numCenters][dim];
          if (goodArguments == true) {
            System.out.println ("Random = " +randomChromosomes );
            System.out.println ("Density = " +densityChromosomes );
            System.out.println ("Separation = " +separationChromosomes );
            System.out.println ("Selection Method = " +selectionMethod );
            System.out.println ("Number of centers = " +numCenters );
            Random generator = new Random();
            double[] sortPoints;
            sortPoints = new double[numPoints];
            double[] minDim;
            minDim = new double[dim];
            double[] maxDim;
            maxDim = new double[dim];
            int i = 0;
```

```
while (i < dim) {
		int j = 0;
		while (j < numPoints) {
				sortPoints[j] = dataPoints[i + (j * dim)];
				j = j + 1;
		}
		Arrays.sort(sortPoints);
		minDim[i] = sortPoints[0];
		maxDim[i] = sortPoints[numPoints - 1];
		i = i + 1;
}
//* Create chromosomes
		int n = 0;
		while (n < chromosomes) {
//*		Select randomChromosomes chromosomes at random
		int r = 0;
		while (r < randomChromosomes) {
				int k = 0;
				while (k < numCenters) {
						int iRandom = generator.nextInt( numPoints);
						i = 0;
						while (i < dim) {
								childBuffer[n][k][i] = dataPoints[(iRandom * dim) + i];
								i = i + 1;
						}
						k = k + 1;
				}		//* end k loop
				r = r + 1;
				n = n + 1;
		} //* end randomChromosomes loop
		int d = 0;
		if (d < densityChromosomes) {
		//*		Select densityCenters chromosomes using Density algorithm
				double[] tempCenter;
				tempCenter = new double [dim];
				double[] distance;
		distance = new double[numPoints];
		double[] sortDistance;
		sortDistance = new double[numPoints];
				int radius = numPoints / numCenters;
				//* Determine centroid of data set
				i = 0;
				double [] sumPoints;
				sumPoints = new double [dim];
				while (i < dim) {
						sumPoints[i] = 0;
						i = i + 1;
				}
				i = 0;
				while (i < numPoints) {
						int j = 0;
						while (j < dim) {
								sumPoints[j] = sumPoints[j] + dataPoints[(i * dim) + j];
								j = j + 1;
						}
						i = i + 1;
				}
				double [] cent;
				cent = new double [dim];
				i = 0;
				while (i < dim) {
						cent[i] = sumPoints[i] / numPoints;
						i = i + 1;
				}
				//* Determine data set density (area is circle about centroid where radius is distance from centroid to farthest point)
				i = 0;
				while (i < numPoints) {
						distance[i] = 0;
						int j = 0;
						while (j < dim) {
```

```
						distance[i] = distance [i] + (Math.pow(cent[j] - dataPoints[(i * dim) + j], 2));
						j = j + 1;
					}
					i = i + 1;
				}
				System.arraycopy(distance, 0, sortDistance, 0, numPoints);
				Arrays.sort(sortDistance);
				double maxLength = sortDistance[numPoints - 1];
				double maxArea = Math.PI * maxLength;
				double maxDensity = numPoints / maxArea;
				while (d < densityChromosomes) {
					//*		Do until densityCenters cluster centers are chosen
					int k = 0;
					while (k < numCenters) {
						int iRandom = generator.nextInt( numPoints);
						i = 0;
					while (i < dim) {
						tempCenter[i] = dataPoints[(iRandom * dim) + i];
						i = i + 1;
					}
					//*			Determine density of area of space within radiusLength of tempCenter
					i = 0;
					while (i < numPoints) {
						distance[i] = 0;
						int j = 0;
						while (j < dim) {
							distance[i] = distance [i] + (Math.pow(tempCenter[j] - dataPoints[(i * dim) + j], 2));
							j = j + 1;
						}
						i = i + 1;
					}
					System.arraycopy(distance, 0, sortDistance, 0, numPoints);
					Arrays.sort(sortDistance);
					double radiusLength = sortDistance[radius];
					double area = Math.PI * radiusLength;
					double tempDensity = radius / area;
					//*			Select tempCenter as center with proportional probability
					double dRandom = generator.nextDouble();
					if ((tempDensity / (tempDensity + maxDensity)) >= dRandom) {
						i = 0;
						while (i < dim) {
							childBuffer[n][k][i] = tempCenter[i];
							i = i + 1;
						}
					k = k + 1;
					}
					}		//* end k loop
					d = d + 1;
					n = n + 1;
				} //* end d loop
			}		//* end Density section
			//*		Select separationCenters chromosomes using Separation algorithm
			int s = 0;
			while (s < separationChromosomes) {
				// *			Select a data point at random from the set of data points in the data set.
				double[][] kDistance;
			kDistance = new double[numCenters][numPoints];
			double[] shortestkDistance;
			shortestkDistance = new double[numPoints];
			double shortestkSum;
			shortestkSum = 0;
				int k = 0;
				int iRandom = generator.nextInt(numPoints);
				i = 0;
				while (i < dim) {
					childBuffer[n][k][i] = dataPoints[(iRandom * dim) + i];
					i = i + 1;
				}
				int j = 0;
				while (j < numPoints) {		//*			Determine distance of each data point to center already chosen
```

```
                    kDistance[k][j] = 0;
                    i = 0;
                    while (i < dim) {
                        kDistance[k][j] = kDistance[k][j] + (Math.pow(childBuffer[n][k][i] - dataPoints[(j * dim) + i], 2));
                        i = i + 1;
                    }
                    shortestkDistance[j] = kDistance[k][j];
                    shortestkSum = shortestkSum + shortestkDistance[j];
                    j = j + 1;
                }

                while (k < numCenters - 1) {
                    iRandom = generator.nextInt(numPoints);
                    double dRandom = generator.nextDouble();
                    if ((shortestkDistance[iRandom] / shortestkSum) >= dRandom) {
//*         Select tempCenter as next center with proportional probability
                        k = k + 1;
                        i = 0;
                    while (i < dim) {
                        childBuffer[n][k][i] = dataPoints[(iRandom * dim) + i];
                        i = i + 1;
                    }
                        shortestkSum = 0;
                        j = 0;
                        while (j < numPoints) {
//*         Determine distance of each data point to closest center already chosen
                            kDistance[k][j] = 0;
                        i = 0;
                        while (i < dim) {
                            kDistance[k][j] = kDistance[k][j] + (Math.pow(childBuffer[n][k][i] - dataPoints[(j * dim) + i],
2));

                            i = i + 1;
                        }
                            if (kDistance[k][j] < shortestkDistance[j]) {

                                shortestkDistance[j] = kDistance[k][j];

                            }
                            shortestkSum = shortestkSum + shortestkDistance[j];
                            j = j + 1;
                        }

                    }
                }
                s = s + 1;
                n = n + 1;
            }
            }
            //*   Do for g generations
            end_time=System.currentTimeMillis();
                double seedingTime = (end_time - start_time);
            int g = 0;
            double bestSSE = 9.99999999E99;
            int genCount = 0;
            int genMax = 100;  //* number of generations without improvement of best SSE before GA terminates
            double[] SSE;
        SSE = new double[chromosomes];
        double[] sortedSSE;
        sortedSSE = new double[chromosomes];
        double[][] bestChromosome;
        bestChromosome = new double[numCenters][dim];
        double[] parentSSE;
        parentSSE = new double[chromosomes];
        n = 0;
                //*             make sure parentSSE array is initially zeros
                while (n < chromosomes) {
                    parentSSE[n] = 0;
                    n = n + 1;
                }
        double[] kDistance;
```

```
        kDistance = new double[numCenters];
        double[] shortestkDistance;
        shortestkDistance = new double[numPoints];
        int holdk = 0;
        int [][] closestk;
        closestk = new int [chromosomes][numPoints];
        //* Initialize sumRank and RankSSE for Random Rank selection method
                n = 0;
                int sumRank = 0;
                int[] rankSSE;
          rankSSE = new int[chromosomes];
          i = chromosomes;
                while (n < chromosomes) {
                        rankSSE[n] = i;
                        sumRank = sumRank + rankSSE[n];
                        i = i - 1;
                        n = n + 1;
                }
        while (genCount < genMax) {
//* Run genMax generations without improvement in bestSSE value before terminating
                        n = 0;
                        //*        For each chromosome in ChildBuffer run k-means until partition stability is achieved
                        while (n < chromosomes) {
                                SSE[n] = 0;
                                boolean centersStable;
                        centersStable = true;
                        int j = 0;
                        while (j < numPoints) {
                                int k = 0;
                                while (k < numCenters) {
                                        kDistance[k] = 0;
                                        i = 0;
                                        while (i < dim) {
                                                kDistance[k] = kDistance[k] + (Math.pow(childBuffer[n][k][i] - dataPoints[(j * dim) + i], 2));
                                                i = i + 1;
                                        }
                                        k = k + 1;
                                }
                                shortestkDistance[j] = 9.99999999E99;
                                k = 0;
                                while (k < numCenters) {
                                        if (kDistance[k] < shortestkDistance[j]) {
                                                shortestkDistance[j] = kDistance[k];
                                                holdk = k;
                                        }
                                        k = k + 1;
                                }
                                SSE[n] = SSE[n] + shortestkDistance[j];
                                closestk[n][j] = holdk;
                                j = j + 1;
                        }
                        int k = 0;
                        while (k < numCenters) {
                                double [] kSum;
                                kSum = new double[dim];
                                double [] newCenter;
                                newCenter = new double[dim];
                                j = 0;
                                i = 0;
                                while (j < numPoints) {        //* determine centroid of clusters
                                        if (k == closestk[n][j]) {
                                                int m = 0;
                                        while (m < dim) {
                                                kSum[m] = kSum[m] + dataPoints[(j * dim) + m];
                                                m = m + 1;
                                        }
                                                i = i + 1;
                                        }
                                        j = j + 1;
                                }
```

```
		if (i == 0) {
			int iRandom = generator.nextInt(numPoints);
			int m = 0;
			while (m < dim) {
				newCenter[m] = dataPoints[(iRandom * dim) + m];
				m = m + 1;
			}
		}
		else {
			int m = 0;
			while (m < dim) {
				newCenter[m] = kSum[m] / i;
				m = m + 1;
			}
		}
		int m = 0;
		while (m < dim) {
			if (childBuffer[n][k][m] != newCenter[m]) {
				childBuffer[n][k][m] = newCenter[m];
				centersStable = false;
			}
			m = m + 1;
		}
		k = k + 1;
	}
	if (centersStable == true) {
		n = n + 1;
	}
	}		//* end k-means
	System.arraycopy(SSE, 0, sortedSSE, 0, chromosomes);
	Arrays.sort(sortedSSE);
	//*	Keep track of the best SSE and chromosome found so far
	if (sortedSSE[0] < bestSSE) {
		bestSSE = sortedSSE[0];
		System.out.println ("After " +genCount +" generations new best SSE for g = " +g +" is " +bestSSE);
		genCount = 0;
		n = 0;
		while (n < chromosomes) {
			if (SSE[n] == sortedSSE[0]) {
				int k = 0;
				while (k < numCenters) {
					int m = 0;
			while (m < dim) {
				bestChromosome[k][m] = childBuffer[n][k][m];
				m = m + 1;
			}
					k = k + 1;
				}
				n = chromosomes;
			}
			else {
				n = n + 1;
			}
		}
	}
	if (sortedSSE[0] >= bestSSE) {
		genCount = genCount + 1;
	}
	//*		If fittest parent chromosome more fit than every chromosome in child buffer, Then {
	if ((sortedSSE[0] > bestSSE) & (selectionMethod == 0 || selectionMethod == 4)) {
		int iRandom = generator.nextInt(chromosomes);
	int k = 0;
	//*			Replace random chromosome in child buffer with fittest parent chromosome
	while (k < numCenters) {
		int m = 0;
		while (m < dim) {
			childBuffer[iRandom][k][m] = bestChromosome[k][m];
			m = m + 1;
		}
		k = k + 1;
```

```
}
SSE[iRandom] = bestSSE;
System.arraycopy(SSE, 0, sortedSSE, 0, chromosomes);
Arrays.sort(sortedSSE);
}
if (selectionMethod == 0) {
//*			Select chromosomes of mating buffer using roulette wheel method
	double totalSSE = 0;
	double totalScaledSSE = 0;
	double largestSSE = 1 + sortedSSE[chromosomes - 1];
	double [] scaledSSE;
	scaledSSE = new double[chromosomes];
	double f = 1.8;		//* scaling factor for roulette wheel
	n = 0;
	while (n < chromosomes) {
		totalSSE = totalSSE + largestSSE - SSE[n];
		n = n + 1;
	}
	double scale = (f * (totalSSE / chromosomes)) / (largestSSE - sortedSSE[0]);
	n = 0;
	while (n < chromosomes) {
		scaledSSE[n] = scale * (largestSSE - SSE[n]);
		totalScaledSSE = totalScaledSSE + scaledSSE[n];
		n  = n + 1;
	}
	n = 0;
	while (n < chromosomes) {
		double rouletteSpin = generator.nextDouble() * totalScaledSSE;

		double sumSSE = 0;
		i = 0;
		while (i < chromosomes) {
			sumSSE = sumSSE + scaledSSE[i];
			if (rouletteSpin <= sumSSE) {
				int k = 0;
			    while (k < numCenters) {
				int m = 0;
			        while (m < dim) {
			            matingBuffer[n][k][m] = childBuffer[i][k][m];
			            m = m + 1;
			        }
				k = k + 1;
			    }
				i = chromosomes;
			}
			else {
				i = i + 1;
			}
		}
		n = n + 1;
	}		//* end n loop of chromosomes for matingBuffer

}	//* end Roulette wheel selection method
	if (selectionMethod == 4) {
		//*			Select chromosomes of mating buffer using roulette wheel rank method

			n = 0;
			while (n < chromosomes) {
				int rouletteSpin = generator.nextInt(sumRank);

				int sumSSE = 0;
				i = 0;
				while (i < chromosomes) {
					sumSSE = sumSSE + rankSSE[i];
					if (rouletteSpin < sumSSE) {
						int j = 0;
						while (j < chromosomes) {
							if (SSE[j] == sortedSSE[i]) {
								int k = 0;
								while (k < numCenters) {
```

```
                                                                        int m = 0;
                                                int m = 0;
                                                while (m < dim) {
                                                        matingBuffer[n][k][m] = childBuffer[j][k][m];
                                                        m = m + 1;
                                                }
                                                                        k = k + 1;
                                                                }
                                                                j = chromosomes;
                                                        }
                                                        else {
                                                                j = j + 1;
                                                        }
                                                }
                                                i = chromosomes;
                                        }
                                        else {
                                                i = i + 1;
                                        }
                                }
                                n = n + 1;
                        }       //* end n loop of chromosomes for matingBuffer

                }       //* end Roulette wheel rank selection method
        if (selectionMethod == 1 || selectionMethod == 2 || selectionMethod == 3) {
                //*                     Select via local tournaments
                n = 0;
                while (n < chromosomes) {
                        if (parentSSE[n] == 0) {
                                int k = 0;
                                while (k < numCenters) {
                                        int m = 0;
                                while (m < dim) {
                                        matingBuffer[n][k][m] = childBuffer[n][k][m];
                                        m = m + 1;
                                }
                                        k = k + 1;
                                }
                                n = n + 1;
                        }
                        else {
                                if (selectionMethod == 2) {                     //* use deterministic algorithm
                                        if (parentSSE[n] < SSE[n]) {
                                                SSE[n] = parentSSE[n];
                                                int k = 0;
                                                while (k < numCenters) {
                                                        int m = 0;
                                while (m < dim) {
                                        matingBuffer[n][k][m] = parentBuffer[n][k][m];
                                        m = m + 1;
                                }
                                                        k = k + 1;
                                                }
                                        }
                                        else {
                                                int k = 0;
                                                while (k < numCenters) {
                                                        int m = 0;
                                while (m < dim) {
                                        matingBuffer[n][k][m] = childBuffer[n][k][m];
                                        m = m + 1;
                                }
                                                        k = k + 1;
                                                }
                                        }
                                        n = n + 1;
                                }       //* end deterministic algorithm section
                                if (selectionMethod == 1){      //* use probabilistic algorithm
                                        double dRandom = generator.nextDouble();
                                        if (SSE[n] / (SSE[n] + parentSSE[n]) < dRandom) {
                                                int k = 0;
```

```
                              while (k < numCenters) {
                                    int m = 0;
                  while (m < dim) {
                        matingBuffer[n][k][m] = childBuffer[n][k][m];
                        m = m + 1;
                  }
                                    k = k + 1;
                              }
                        }
                        else {
                              SSE[n] = parentSSE[n];
                              int k = 0;
                              while (k < numCenters) {
                                    int m = 0;
                  while (m < dim) {
                        matingBuffer[n][k][m] = parentBuffer[n][k][m];
                        m = m + 1;
                  }
                                    k = k + 1;
                              }
                        }
                        n = n + 1;
                  }     //* end probabilistic algorithm section
                  if (selectionMethod == 3) {

                        if (parentSSE[n] < SSE[n]) {
                              SSE[n] = parentSSE[n];
                              int k = 0;
                              while (k < numCenters) {
                                    int m = 0;
                  while (m < dim) {
                        matingBuffer[n][k][m] = parentBuffer[n][k][m];
                        m = m + 1;
                  }
                                    k = k + 1;
                              }
                        }
                        else {
                              double dRandom = generator.nextDouble();
                        if (parentSSE[n] / (SSE[n] + parentSSE[n]) < dRandom) {
                              SSE[n] = parentSSE[n];
                              int k = 0;
                              while (k < numCenters) {
                                    int m = 0;
                        while (m < dim) {
                              matingBuffer[n][k][m] = parentBuffer[n][k][m];
                              m = m + 1;
                        }
                                    k = k + 1;
                              }
                        }
                        else {

                              int k = 0;
                              while (k < numCenters) {
                                    int m = 0;
                        while (m < dim) {
                              matingBuffer[n][k][m] = childBuffer[n][k][m];
                              m = m + 1;
                        }
                                    k = k + 1;
                              }
                        }
                        }
                        n = n + 1;
                  }
            }
      }
}     //* end local tournament selection algorithms
//*               Crossover Section
```

```
			int [] randomPair;
		randomPair = new int[chromosomes];
		i = 0;
		while (i < chromosomes) {		//* randomPair is an array of ints 0 to chromosomes - 1
			randomPair[i] = i;
			i = i + 1;
		}
			int randIndex;
			int temp;
			for(i = randomPair.length-1; i > 1 ; i--) {
						randIndex = generator.nextInt(i);
						temp = randomPair[i];
						randomPair[i] = randomPair[randIndex];
						randomPair[randIndex] = temp;
			}
			//* use randomPair to select chromosome pairs from the mating buffer
			double crossoverPercentage = 1.0;		//* percentage of chromosome pairs that undergo crossover
			n = 0;
			while (n < chromosomes) {
				double dRandom = generator.nextDouble();
				if (dRandom > crossoverPercentage) {
//* these chromosomes do not undergo crossover so they go into childBuffer
					parentSSE[n] = SSE[randomPair[n]];
					parentSSE[n + 1] = SSE[randomPair[n + 1]];
					int k = 0;
					while (k < numCenters) {
						int m = 0;
					while (m < dim) {
						childBuffer[n][k][m] = matingBuffer[randomPair[n]][k][m];
						childBuffer[n + 1][k][m] = matingBuffer[randomPair[n + 1]][k][m];
						parentBuffer[n][k][m] = matingBuffer[randomPair[n]][k][m];
						parentBuffer[n + 1][k][m] = matingBuffer[randomPair[n + 1]][k][m];
						m = m + 1;
					}
							k = k + 1;
						}
				}
				else {	//* dRandom <= crossover percentage, so perform crossover
					double [] a;
		a = new double[dim];  //* get random point to be point on random line through data set space
		int m = 0;
				while (m < dim) {
					a[m] = generator.nextDouble()* (maxDim[m] - minDim[m]) + minDim[m];
					m = m + 1;
				}
		double [] normal;	//* get random point from data set space to be normal to random point a.
		normal = new double[dim];
		m = 0;
				while (m < dim) {
					normal[m] = generator.nextDouble()* (maxDim[m] - minDim[m]) + minDim[m];
					while (a[m] == normal[m]) {
			normal[m] = generator.nextDouble()* (maxDim[m] - minDim[m]) + minDim[m];
		}
					m = m + 1;
				}

		double [] d;
		d = new double [dim];
		int p1over = 0;
		int p2over = 0;
		int p1under = 0;
		int p2under = 0;
		double [][] p1O;
		p1O = new double [numCenters][dim];
		double [][] p2O;
		p2O = new double [numCenters][dim];
		int k = 0;
		while (k < numCenters) {
			double dSum = 0;
			m = 0;
```

```
                        while (m < dim) {
                                d[m] = (matingBuffer[randomPair[n]][k][m] - a[m]) * normal[m];
                                dSum = dSum + d[m];
                                m = m + 1;
                        }
        if (dSum >= 0) {
        //* center[n][k] is in crossover region
                m = 0;
                        while (m < dim) {
                                p1O[p1over][m] = matingBuffer[randomPair[n]][k][m];
                                m = m + 1;
                        }
                p1over = p1over + 1;
        }
        else {
                m = 0;
                        while (m < dim) {
                                childBuffer[n][p1under][m] = matingBuffer[randomPair[n]][k][m];
                                m = m + 1;
                        }
                                        p1under = p1under  + 1;
        }
        dSum = 0;
        m = 0;
                        while (m < dim) {
                                d[m] = (matingBuffer[randomPair[n + 1]][k][m] - a[m]) * normal[m];
                                dSum = dSum + d[m];
                                m = m + 1;
                        }
                        if (dSum >= 0) {
                //* center[n + 1][k] is in crossover region
                                m = 0;
                        while (m < dim) {
                                p2O[p2over][m] = matingBuffer[randomPair[n + 1]][k][m];
                                m = m + 1;
                        }
                p2over = p2over + 1;
        }
        else {
                m = 0;
                        while (m < dim) {
                                childBuffer[n + 1][p2under][m] = matingBuffer[randomPair[n + 1]][k][m];
                                m = m + 1;
                        }
                                        p2under = p2under  + 1;
        }
        k = k + 1;
}
i  = p1under;
int j = 0;
while ((i < numCenters) & (j < p2over)) {
        m = 0;
                        while (m < dim) {
                                childBuffer[n][i][m] = p2O[j][m];
                                m = m + 1;
                        }
        i = i + 1;
        j = j + 1;
}
if (i < numCenters) {
        j = 0;
        while (i < numCenters) {
                m = 0;
                        while (m < dim) {
                                childBuffer[n][i][m] = p1O[j][m];
                                m = m + 1;
                        }
        i = i + 1;
        j = j + 1;
        }
```

```
}
i = p2under;
j = 0;
while ((i < numCenters) & (j < p1over)) {
        m = 0;
                        while (m < dim) {
                                childBuffer[n + 1][i][m] = p1O[j][m];
                                m = m + 1;
                        }
        i = i + 1;
        j = j + 1;
}
if (i < numCenters) {
        j = 0;
        while (i < numCenters) {
                m = 0;
                        while (m < dim) {
                                childBuffer[n + 1][i][m] = p2O[j][m];
                                m = m + 1;
                        }
        i = i + 1;
        j = j + 1;
        }
}
if (p1over > p2over) {
        j = p2over;
}
else {
        j = p1over;  //* j contains number of cluster centers swapped
}
if (j < (numCenters / 2)) {             //* parent is pair with most centers in common with child
        parentSSE[n] = SSE[randomPair[n]];
        parentSSE[n + 1] = SSE[randomPair[n + 1]];
        k = 0;
                        while (k < numCenters) {
                                m = 0;
                        while (m < dim) {
                                parentBuffer[n][k][m] = matingBuffer[randomPair[n]][k][m];
                                parentBuffer[n + 1][k][m] = matingBuffer[randomPair[n + 1]][k][m];
                                m = m + 1;
                        }
                                        k = k + 1;
                                }
}
else {  //* j >= numCenters / 2 means the other chromosome in the pair is the parent
        parentSSE[n] = SSE[randomPair[n + 1]];
        parentSSE[n + 1] = SSE[randomPair[n]];
        k = 0;
                        while (k < numCenters) {
                                m = 0;
                        while (m < dim) {
                                parentBuffer[n][k][m] = matingBuffer[randomPair[n + 1]][k][m];
                                parentBuffer[n + 1][k][m] = matingBuffer[randomPair[n]][k][m];;
                                m = m + 1;
                        }
                                        k = k + 1;
                                }
}
                } //* end section where chromosomes undergo crossover
                n = n + 2;
        }       //* end Crossover section
        //*             Mutation Section
        n = 0;
        while (n < chromosomes) {
                int k = 0;
                while (k < numCenters) {
                        double dRandom = generator.nextDouble();
                        if (dRandom < 0.001) {
                                int iRandom = generator.nextInt(numPoints);
                                int m = 0;
```

```
					while (m < dim) {
						childBuffer[n][k][m] = dataPoints[(iRandom * dim) + m];
						m = m + 1;
					}
					}
					k = k + 1;
				}
				n = n + 1;
			}		//* end mutation section
			g = g + 1;
			if (genCount == genMax) {
				//* Run k-means one last time
			n = 0;
				//*			for each chromosome in ChildBuffer run k-means until partition stability is achieved
			while (n < chromosomes) {
				SSE[n] = 0;
				boolean centersStable;
			centersStable = true;
			int j = 0;
			while (j < numPoints) {
				int k = 0;
				while (k < numCenters) {
					kDistance[k] = 0;
					i = 0;
					while (i < dim) {
						kDistance[k] = kDistance[k] + (Math.pow(childBuffer[n][k][i] - dataPoints[(j * dim) + i], 2));
						i = i + 1;
					}
						k = k + 1;
				}
				shortestkDistance[j] = 9.99999999E99;
				k = 0;
				while (k < numCenters) {
					if (kDistance[k] < shortestkDistance[j]) {
						shortestkDistance[j] = kDistance[k];
						holdk = k;
					}
					k = k + 1;
				}
				SSE[n] = SSE[n] + shortestkDistance[j];
				closestk[n][j] = holdk;
				j = j + 1;
			}
			int k = 0;
			while (k < numCenters) {
				double [] kSum;
				kSum = new double[dim];
				double [] newCenter;
				newCenter = new double[dim];
				j = 0;
				i = 0;
				while (j < numPoints) {				//* determine centroid of clusters
					if (k == closestk[n][j]) {
						int m = 0;
					while (m < dim) {
						kSum[m] = kSum[m] + dataPoints[(j * dim) + m];
						m = m + 1;
					}
						i = i + 1;
					}
					j = j + 1;
				}
				if (i == 0) {
					int iRandom = generator.nextInt(numPoints);
					int m = 0;
					while (m < dim) {
						newCenter[m] = dataPoints[(iRandom * dim) + m];
						m = m + 1;
					}
				}
```

```
				else {
					int m = 0;
					while (m < dim) {
						newCenter[m] = kSum[m] / i;
						m = m + 1;
					}
				}
				int m = 0;
				while (m < dim) {
					if (childBuffer[n][k][m] != newCenter[m]) {
						childBuffer[n][k][m] = newCenter[m];
						centersStable = false;
					}
					m = m + 1;
				}
				k = k + 1;
			}
			if (centersStable == true) {
				n = n + 1;
			}
			}		//* end k-means
				System.arraycopy(SSE, 0, sortedSSE, 0, chromosomes);
				Arrays.sort(sortedSSE);
				//*	Keep track of the best SSE and chromosome found so far
				if (sortedSSE[0] < bestSSE) {
					bestSSE = sortedSSE[0];
				System.out.println ("After " +genCount +" generations new best SSE for g = " +g +" is " +bestSSE);
				genCount = 0;
				n = 0;
				while (n < chromosomes) {
					if (SSE[n] == sortedSSE[0]) {
						int k = 0;
						while (k < numCenters) {
							int m = 0;
					while (m < dim) {
						bestChromosome[k][m] = childBuffer[n][k][m];
						m = m + 1;
					}
							k = k + 1;
						}
						n = chromosomes;
					}
					else {
						n = n + 1;
					}
				}
				}
				else {
					System.out.println ("Best SSE for g = " +g +" is " +bestSSE);
				}
			}
		}  //* end g loop (100 generations)
			int k = 0;
			while (k < numCenters) {
				if (dim < 3){
					System.out.println ("Best chromosome for g = " +g +" is center " +k + " is " +bestChromosome[k][0] +" "
+bestChromosome[k][1]);
				}
				else {
					System.out.println ("Best chromosome for g = " +g +" is center " +k + " is ");
					int m = 0;
				while (m < dim) {
					System.out.println(bestChromosome[k][m]);
					m = m + 1;
				}
				}
				k = k + 1;
			}
			end_time=System.currentTimeMillis();
			double timeelapsed = (end_time - start_time);
```

```
            double seedingPercent = seedingTime / timeelapsed;
            System.out.println("Time Elapsed: "+ timeelapsed +" Seeding Time: " + seedingTime );
            System.out.format("The seeding percentage time is : %f%n", seedingPercent);
}
}
}
```

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