Sensors & Transducers, Vol. 159, Issue 11, November 2013, pp. 174-178

Sensors & Transducers

http://www.sensorsportal.com

Solution to Degree Diameter-2 Graph Problem in Parallel Machine Tools Control Network Based on Genetic Algorithm

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Received: 25 July 2013 /Accepted: 25 October 2013 /Published: 30 November 2013

Abstract: Parallel Machine Tools (PMT) is a mechanical and electrical integration product with good technique additional value, the control network of which is usually represented with graphs as parallel network or local network. Address to degree diameter problem in PMT control network graph, the paper used genetic algorithm (GA) to solve graph with maximum node number in different degree and diameter 2. Three evaluation functions as tree structure, recursive five loop and greedy five loop were designed and used for solving corresponding degree diameter-2 problem with genetic evolutionary. Experimental results show that evaluation function with tree structure has low time complexity and good adaptability, which has a certain reference for design and analysis on parallel computing environment constituted by multiple PMTs. *Copyright © 2013 IFSA.*

Keywords: Parallel machine tool control network, Genetic algorithm, Degree-diameter problem.

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1. Introduction

Parallel Machine Tool, namely Virtual Axis Machine Tool is a combination product of robotics and machine tool. Compared with traditional CNC machine tools, PMT has advantages of large stiffness specific gravity, fast response, high machining precision, environmental adaptability and etc. PMT is mechanical and electrical integration product with good technique additional value, which is also cross-application of disciplinary as parallel robots, CNS machine tool, computer control and precision measurement. The control issue in MPT is usually equivalent to parallel computing network problem constituted of multiple interconnected processors. Generally, network topology of parallel computing network or local area network that made of communication network or interconnected processors can be represented by graphs. Nodes in the graph can be regarded as processor or workstation of machine tool. Edges in graph show interconnections among processors. The degree of graph represents the number of channel connected from processor to outside. The diameter of graph means maximum intermediate node number along randomly interconnected processors. Majority tasks of reliability, maximum delay as well as workflow network analyzing and design of PMTs can refer to graph theory for assisted analysis. For example, the interconnect problem of multiple processor parallel computing system can be converted into degree-diameter problem of graph, which can solve maximum graph with maximum node number under given degree and diameter [1-3]. Currently, researches on degree-diameter mainly use combination method, namely substituting nodes in the graph with one or more graphs constantly to form larger graph. The theoretical upper limit of node number contained in a graph with δ degree and D diameter is named Moore upper limit $n(\delta, D)$ [4] as:

$$n(\delta, D) \le (\delta(\delta-1)^p - 2), \delta > 2 \tag{1}$$

Petersen graph with degree 3 and Hoffman-Singleton graph with degree 7 [4] are two graphs with diameter 2 that reaches Moore upper limit. A parallel sorting algorithm in [5, 6] is based on multiple processor interconnected network established from topology. In this paper, genetic algorithm is used to solve given degree problem with diameter 2. Three kinds of evaluation functions are designed and compared. The paper is organized as follows: Section 2 discusses on method to solve degree-diameter problem with genetic algorithm; Section 3 provides experiment result and Section 4 concludes our work.

2. Degree-diameter Problem Solving with Genetic Algorithm

2.1. Degree-diameter 2 Problem Expression

Let G be a graph that represented as $G = < V(G), E(G) >$. To random given $u, v \in V(G)$, the length of short diameter between u and v is the length of shortest path that connect u and v in G. When $u, v \in V(G)$ is not connected, $dist_G < u, v >$ is defined as infinity. The diameter *diam*(*G*) of *G* is defined as $diam(G) = \max dist_G < u, v > (u, v \in V(G))$. The degree-diameter 2 problem is to solve graph problem ensuring diameter between random two nodes is 2, including undirected graph and directed graph. Here we only discuss on undirected graph.

2.2. Encoding and Fitness Computing

A chromosome individual is one solution of degree-diameter problem. The solution of degree-diameter problem is an undirected graph with same degree of each vertex. If the undirected graph has *n* vertices and the degree of each vertex is *degree*. Generally, *degree*=*sqr*(*n*-1), so there is totally $n \times degree$ edges. The solution of degree-diameter 2 problem can be regarded as undirected graph constituted by $n \times degree$ edges. This chromosome individual is encoded according to $n \times degree$ edges among n vertices, which is now represented with one-dimensional array. The length of array is $width(width = n \times degree)$, marked as $p[0], p[1], \cdots, p[j], \cdots, p[width-1]$. In the graph, *degree* nodes connect to the *j*-th node $(j = 0, 1, 2, \cdots, width-1)$ are $p[j \times degree + 0]$, $p[j \times degree + 1]$, $\cdots$, $p[j \times degree + (degree-1)]$.

Let $C = (c_1, c_2, \cdots, c_n)$ be set of n nodes. $E = e_{11}, e_{12}, \cdots, e_{21}, e_{22}, \cdots, e_{nn}$ is the set of connection edges among n nodes. The distance of direct connection edge between any two nodes is 1. If not connected, it is marked as *max*. *R*[*i*. *j*] denotes two-dimensional matrix of shortest paths from node *i* to node *j*. *R*[*i*, *j*]=1 means there is edge from node c_i to c_j in R_{ij}, the shortest distance of which is 1; *R*[*i*, *j*]=2 means there is edge from node c_i to c_k and then to c_j in R_{ij}, the shortest distance of which is 2, and so forth. $E = e_{11}, e_{12}, \cdots, e_{21}, e_{22}, \cdots, e_{nn}$ is a solution set constituted by $n \times n$ paths. The fitness function *f*(*R*) is defined as following:

$$f(R) = \sum_{i=0}^{n-1} \frac{1}{1 + (bestscore - \sum_{j=1}^{n} \text{sgn}(R[i,j]))} \tag{2}$$

$$\text{sgn}(R[i,j]) = \begin{cases} 1, & R[i,j] = 1 \\ 2, & R[i,j] = 2 \\ 3, & else \end{cases} \tag{3}$$

$$bsetscore = d + (n - d - 1) \times 2 \tag{4}$$

2.3. Evaluation Function

1) Tree Structure Method.

Algorithm idea is as follows. Ensure connection between each node and others shows two-layer tree structure. When the connections among *n* nodes and other node are complete tree structure, the evolution completes.

The two-layer complete tree structure in case of *n*=10 and *degree*=3 is shown in Fig. 1. At this moment, the diameter from root node to others is less than or equal to 2.

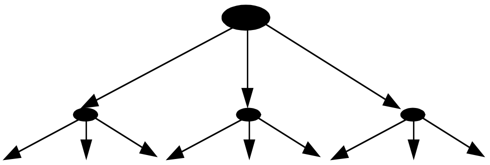

Fig. 1. Two-layer trigeminal complete tree.

Step 1: Initialization. Start from the *j*-th node (*j*=0), $score[i][j] = 3(i, j = 0, 1, 2, \cdots, n-1)$.

Step 2: Directly connect from *j* to *m* and score path length from *j* to *m*. As to *degree* nodes $m = p[j * s\_pop.degree + k]$ $(k = 0, 1, 2, \cdots, degree-1)$ connecting with node *j*, if $m \ne j$ and $score[j][m] = 1$, go to Step 3. Otherwise, *k* increases itself. After all nodes connected to *j* has been traversed, go to Step 5.

Step 3: Determine whether there is back edge from *j* directly connects to *m*. As to *degree* nodes

$n_1 = [m * s\_pop.\deg ree + n]$ $(n = 0,1,2,\cdots,\deg ree - 1)$ connected to node *m*, if n_1=*j*, go to Step4. Otherwise, go to Step 2.

Step 4: If there is back edge from *m* directly connect to node *j*, connect *m* directly to n_1 and score the length of path from *j* to n_1. As to $n_1 = p[m * s\_pop.\deg ree + n]$ $(n = 0,1,2,\cdots,\deg ree - 1)$, the situation as $p[m * s\_pop.\deg ree + n] = j$ should be deleted in case of $n_1 \neq j$ and $score[j][n_1] = 2$. After all nodes connected to *m* has been traversed, go to Step 2.

Step 5: *j*++. When *j*=*n*, the scoring on path length of all vertices complete and go to Step 6.

Step 6: Calculate sum of all score and go to Step 7.

Step 7: End. The evaluation on a chromosome completes.

In the early period of algorithm operation and then the node number is *degree*+1, the connection path length from these *degree*+1 nodes and others are less than or equal to 2. The moment is a cut-off point. Before this point, each node can rapidly find topology that promote it connect to other nodes and the shortest path length less than or equal to 2. After it, the speed is very slow and easy to fall into local optimum.

2) Recursive Five Loop Method.

The method uses mathematical proof from recursive five loop calculation methods. Obviously, when the joined edge can generate triangle or quadrilateral (Fig. 2), it means the finite edge connect has not been fully utilized so that the distance from it to each vertex be short as possible. If the joined edge is one of pentagon, each vertex on five loop cannot reach random other vertex with distance less than or equal to 2. The polygon with 5 edges is a critical point. Then the joined edge is one from hexagon, the diameter from vertices 1 and 3, 2 and 4, 3 and 6 are 3.

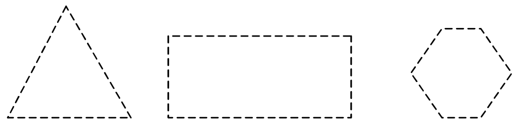

Fig. 2. One edge from triangle, quadrilateral and hexagon to being joined.

The algorithm idea is as follows. The selection of random five node uses recursive to ensure the connection from each node and other *i* nodes has 5 loops or more. In case of node increment each time, when there are no three loops or five loops exist in *n* nodes and others, the evolution completes. The algorithm flow to determine five loops is as following:

Step 1: Initialization. Select five nodes *comb*[*j*] and set traversal number of each node as cc[j]=0($j = 0,1,\cdots,4$).

Step 2: Determine whether there are edges connected of two nodes. Randomly select two nodes *comb*[*j*] and *comb*[*m*], directly connect *comb [j] to comb [m], cc[j]*++, *cc[m]*++ and go to Step 2. After selection ends, go to Step 3.

Step 3: Determine whether the loop number should be increases. If all *cc*[*j*]=2($j = 0,1,\cdots,4$), the loop number increase 1 and go to Step 2. Otherwise, the loop number remains unchanged and go to Step 4.

Step 4: Algorithm ends.

The obvious shortcoming of this algorithm is the time complexity is relatively large and has slow operation speed, but it has good stability. This is determined by inherent natures of increasing loops number searching difficulty and non-sensitive to topology. The relatively better stability means difference between every successful operation time and average operation time is not obvious. Secondly, the fluctuation of population evaluation function value in the evolution process is also not large.

3) Greedy Five Loop Method.

Firstly let all nodes in disconnect state and gradually add edges and nodes, the condition of which is there is no triangular or quadrilateral. The algorithm flow is shown in Fig. 3.

2.4. Degree-diameter Problem Genetic Algorithm

Here we give the steps for solving degree-diameter problem based on genetic algorithm:

Step 1: Generate a group of chromosomes and divide into multiple sub-groups. Each one represents a kind of topology according to a set of randomly generated integer. Then, compute and evaluate robustness of each chromosome, namely fitness.

Step 2: Select and remain chromosomes with better robustness, namely chromosomes with larger fitness. The remaining acts as parent chromosomes.

Step 3: Parent chromosome exchange or shift to generate next generation chromosomes.

Step 4: Go to Step1 on the basis of next generation chromosome.

Step 5: Traverse whole procedure multiple times and record best chromosome of each generation, followed by iteration.

Step 6: Select the best chromosome as optimal solution. The selection operator in genetic algorithm uses roulette operator; crossover operator using single-point crossover and mutation operator using single point mutation.

After a comparatively short period of evolution, the chromosome has sharp of chromosome in latter part of evolution with general genetic algorithm, which can rapidly reduce evolution generation number. However, it is not easy to escape from local convergence.

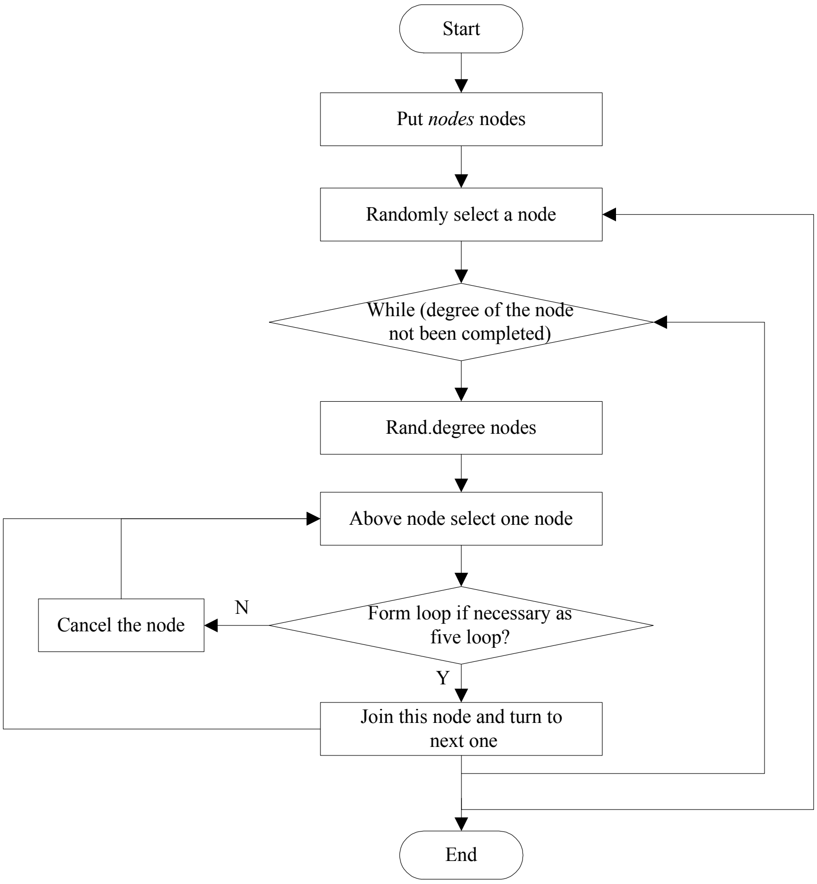

Fig. 3. Algorithm flow of greedy five loop method.

3. Experiment Result

3.1. Comparison of Three Evaluation Functions

Construct undirected graph under the condition of node number and degree d with minimum edges for given diameter 2. Solve the problem with genetic algorithm T (Tree Structure), R (Recursive Five Loop) and G (Greedy Five Loop).

The parameters are as follows: mutation probability *pmut* 0.001; crossover probability *pcross* 0.9. The experiment results are shown in Table 1 and Table 2.

3.2. Parameter Selection and Improvement

It is appropriate that population size *popsize*=8. Larger population size greatly increase computation amount, but evolution speed still remains unchanged. The right way is to change crossover and mutation probability adaptively.

In the early period:

f(f<f_{av})pmut=0.1-0.09*(best_val-f)/(f_{max}-f_{av});
else pmut=0.1;
if(f≥f_{av})pcross=0.9-0.09*(best_val-f)/(f_{max}-f_{av});
else pcross=0.9;

In the latter period:

if(f<f_{av})pmut=0.001;
else pmut=0.001*(best_val-f)/(f_{max}-f_{av});
if(f≥f_{av})pcross=0.9;
else pcross=0.9*(best_val-f)/(f_{max}-f_{av});

The improvement effect is as follows. To graph with 24 nodes and degree 5, the evolution can achieve node number of local optimum. Among them, the connection between any node and other 24 nodes meet the condition that shortest path length less than or equal to 2 and keeps 10 to 16.

Table 1. Algorithms comparison.

Method	**Time complexity**	**Convergence**	**Stability**
T	$P \times n \times d^3$	Good	General
G	$P \times n \times d^4$	Poor	Good
R	$P \times n^4 \times 4 \times d \times d$	General	Good
TG	$P \times n \times d^3$	Good	Good

Table 2. Experiment result comparison.

Method	**Best solution**	**Average evolution generation number**
T	15	20000
G	15	—
R	10	20000
TG	15	2000

The solution of degree-diameter is represented with $n \times degree = 2$ to generate an undirected graph. The evolution speeds slows and becomes unstable. The main reason is versatile solution space decreasing and its spatial structure dissimilarity widening. These operations just slightly improve on jumping from local convergence. The experiment result shows that it is fundamental that finding an algorithm appropriate to this structure.

4. Conclusions

The paper proposed a genetic algorithm to solve degree-diameter problem. The strategy is based on multi-tree structure. Algorithm is encoded using connection matrix of undirected graph according to integer but not binary coding, which effectively reduces time complexity of optimal chromosome searching. In three evaluation functions, it is most likely of greedy five loop algorithm to enter into evolution middle period that other general genetic algorithm should consume more time. Thus, it can be used for pre-processing before population evolution. The tree structure function is simple and easy to understand, time complexity of which is the lowest. It can promote rapid convergence population evolution. Therefore, the tree structure is most suitable for acting as evaluation function. The recursive rings method has the largest time complexity, but best stability, so it can be used for latter work after jump from local convergence. Due to huge computation amount in the latter usage of genetic algorithm, we have to discard it. After comparison using, the iteration on topology with degree 4 and 15 nodes only about 2000 times, which indicates that the algorithm can rapidly find optimal solution. The researches in the future will focus on detection strategy with heuristic algorithm to find the optimal algorithm suitable to this structure.

Acknowledgements

The research is supported by Scientific Research Program Funded by Shaanxi Provincial Education Department (Program No. 12JK0073).

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