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**ACO-BASED FEATURE SELECTION ALGORITHM FOR  
CLASSIFICATION**



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Universiti Utara Malaysia

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## Abstrak

Set data dengan bilangan rekod yang kecil tetapi bilangan atribut yang besar mewakili fenomena yang dipanggil “kutukan dimensi”. Pengelasan set data jenis ini memerlukan kaedah pemilihan ciri (FS) untuk pengekstrakan maklumat berguna. Algoritma modified graph clustering ant colony optimisation (MGCACO) ialah kaedah pemilihan ciri yang berkesan yang dibangunkan berdasarkan pengelompokan ciri berkorelasi. Walau bagaimanapun, algoritma MGCACO mempunyai tiga kelemahan utama dalam menghasilkan subset ciri kerana kaedah pengelompokan, kepekaan parameter, dan penentuan subset akhirnya. Algoritma enhanced graf clustering ant colony optimisation (EGCACO) dicadangkan untuk menyelesaikan tiga (3) masalah algoritma MGCACO. Cadangan penambahbaikan termasuk: (i) kaedah pengelompokan ciri ACO untuk mendapatkan kelompok ciri berkorelasi tinggi; (ii) teknik pemilihan penyesuaian untuk pembinaan subset daripada kelompok ciri; dan, (iii) kaedah berdasarkan genetik untuk menghasilkan subset akhir ciri. Kaedah pengelompokan ciri ACO menggunakan keupayaan pelbagai mekanisma seperti pengukuhan dan kepelbagaian untuk pengoptimuman tempatan dan global untuk menyediakan ciri berkorelasi tinggi. Teknik penyesuaian untuk pemilihan semut membolehkan parameter berubah secara adaptif berdasarkan maklum balas ruang carian. Kaedah genetik menentukan subset akhir secara automatik, berdasarkan pengiraan kualiti silang dan subset. Prestasi algoritma yang dicadangkan telah dinilai ke atas 18 set data penanda aras dari repositori University California Irvine (UCI) dan sembilan (9) set data mikroarray asid deoksiribonukleik (DNA) ke atas 15 algoritma metaeuristik penanda aras. Keputusan eksperimen algoritma EGCACO pada dataset UCI adalah lebih baik daripada algoritma pengoptimuman penanda aras lain dari segi bilangan ciri yang dipilih dan kedua terbaik untuk ketepatan pengelasan. Selanjutnya, eksperimen ke atas sembilan (9) set data microarray DNA menunjukkan bahawa algoritma EGCACO adalah lebih unggul daripada algoritma penanda aras dari segi ketepatan klasifikasi dan bilangan ciri yang dipilih. Algoritma EGCACO yang dicadangkan boleh digunakan untuk pemilihan ciri dalam tugas pengkelasian microarray DNA yang melibatkan sebarang saiz set data dan dalam pelbagai domain aplikasi.

**Kata Kunci:** Pemilihan, Pengelompokan Ciri, Genetik, Pengoptimuman Koloni Semut, Microarray

## Abstract

Dataset with a small number of records but big number of attributes represents a phenomenon called “curse of dimensionality”. The classification of this type of dataset requires Feature Selection (FS) methods for the extraction of useful information. The modified graph clustering ant colony optimisation (MGCACO) algorithm is an effective FS method that was developed based on grouping the highly correlated features. However, the MGCACO algorithm has three main drawbacks in producing a features subset because of its clustering method, parameter sensitivity, and the final subset determination. An enhanced graph clustering ant colony optimisation (EGCACO) algorithm is proposed to solve the three (3) MGCACO algorithm problems. The proposed improvement includes: (i) an ACO feature clustering method to obtain clusters of highly correlated features; (ii) an adaptive selection technique for subset construction from the clusters of features; and (iii) a genetic-based method for producing the final subset of features. The ACO feature clustering method utilises the ability of various mechanisms such as intensification and diversification for local and global optimisation to provide highly correlated features. The adaptive technique for ant selection enables the parameter to adaptively change based on the feedback of the search space. The genetic method determines the final subset, automatically, based on the crossover and subset quality calculation. The performance of the proposed algorithm was evaluated on 18 benchmark datasets from the University California Irvine (UCI) repository and nine (9) deoxyribonucleic acid (DNA) microarray datasets against 15 benchmark metaheuristic algorithms. The experimental results of the EGCACO algorithm on the UCI dataset are superior to other benchmark optimisation algorithms in terms of the number of selected features for 16 out of the 18 UCI datasets (88.89%) and the best in eight (8) (44.47%) of the datasets for classification accuracy. Further, experiments on the nine (9) DNA microarray datasets showed that the EGCACO algorithm is superior than the benchmark algorithms in terms of classification accuracy (first rank) for seven (7) datasets (77.78%) and demonstrates the lowest number of selected features in six (6) datasets (66.67%). The proposed EGCACO algorithm can be utilised for FS in DNA microarray classification tasks that involve large dataset size in various application domains.

**Keywords:** Feature Selection, Feature Clustering, Genetic, Ant Colony Optimisation, Microarray

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## List of Abbreviations

ABC	Artificial Bee Colony
ACO	Ant Colony Optimisation
ALO	Ant Lion Optimiser
ASGW	Adaptive Switcher Grey Whale
ASO	Atom Search Optimisation
BA	Bat Algorithm
bALO-QR	Binary Ant Lion Optimiser with the Quickreduct
BGWOPSO	Grey Wolf Optimisation and Particle Swarm Optimisation
CP	Control Parameter
DE	Differential Evolution
DNA	Deoxyribonucleic Acid
ECWSA	Embedded Chaotic Whale Survival Algorithm
FS	Feature Selection
GA	Genetic Algorithm
GCACO	Graph Clustering-Based Ant Colony Optimisation
GCACOELM	Graph Clustering-Based ACO with Extreme Learning Machine
GOA	Grasshopper Optimisation Algorithm
GSA	Gravitational Search Algorithm
GWO	Grey Wolf Optimisation
HHO	Harris Hawks Optimiser
HSGW	Hybrid Serial Grey Whale
k-NN	k-Nearest Neighbor
MGCACO	Modified Graph Clustering-Based Ant Colony Optimisation
MGSACO	Microarray Gene Selection Based on Ant Colony Optimisation
MLACO	Multi-Label Ant Colony Optimisation
MDA	Mean Decrease in Accuracy
PSO	Particle Swarm Optimisation
RRFSACO	Relevance-Redundancy Feature Selection Based on ACO
RSGW	Random Switcher Grey Whale
SI	Swarm Intelligence
SSA	Salp Swarm Algorithm
TGA	Tree Growth Algorithm
UCI	University of California Irvine
UFSACO	Unsupervised Feature Selection-Based Ant Colony Optimisation
UPFS	Unsupervised Probabilistic Feature Selection
WOA	Whale Optimisation Algorithm
WOA-CM	Whale Optimisation Algorithm with Crossover and Mutation
WOASAT	Whale Optimisation Algorithm with Simulated Annealing

## **CHAPTER ONE**

### **INTRODUCTION**

The advancement of deoxyribonucleic acid (DNA) microarray technology has enabled biology researchers to gain the ability to simultaneously track thousands of gene expressions in an elementary examination useful for classifying or detecting a particular tumor gender. The classification of the DNA microarray data requires data mining and machine learning techniques for the extraction of worthy information by developing a model to analyze the samples into diverse categories. The natural structure of DNA microarray data is high-dimensional with a few records and many columns where they represent a well-known phenomenon called “curse of dimensionality” (Naseri & Hasheminejad, 2019). Many studies on tissue classification at the molecular level have indicated that genes with relevant information might significantly contribute to the enhancement of effective disease detection and classification platform. However, these studies agree that not all the genes include relevant information for the classification stage.

Therefore, to achieve reliable, accurate, and effective performance, important preprocessing data should be implemented in DNA microarray classification ( Yuan et al., 2019; Morovvat & Osareh, 2016; Liao et al., 2014; Mirzaei et al., 2014; Najafi et al., 2014; Bolón-Canedo et al., 2014; Lazar et al., 2012; Lee & Leu, 2011; Leung & Hung, 2010). One of the prevailing techniques in the pre-processing of DNA microarray data is gene selection which defines an informational gene subset from the whole gene dataset that reduces computational cost and enhances classification performance (Manbari et al., 2019; Tabakhi et al., 2014; Li et al., 2013).

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