

## QUANTUM ANT LION OPTIMIZATION AND SUPPORT VECTOR MACHINE FOR THE FEATURE SELECTION AND GENE CLASSIFICATION

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### Abstract

Gene selection for cancer prediction is a required model for the medical domain to effectively treat cancer patients. The presence of large information related to genes makes the existing model difficult to analyze the relationship between the features for gene classification. The existing models have the limitations of local optima trap, lower convergence and overfitting. To improve gene classification performance this research proposes the Quantum Ant Lion (QAL) optimization for feature selection. The Quantum search process is applied in the Ant Lion method to increase the search efficiency which helps to increase the exploration and overcome the local optima trap. The Archimedes spiral search is applied in the QAL method to increase exploitation in the feature selection based on the fitness function. The QAL method increases exploration and exploitation which helps to improve the convergence rate of the QAL method. The QAL method has 97.4 % accuracy and DNN-CNN model has 93.5 % accuracy for gene classification.

**Keywords:** Archimedes Spiral, Exploration, Gene Selection, Quantum Ant Lion, Quantum Search.

### 1 Introduction

Generally, two essential phases of Gene expression are translation and transcription. Gene information encodes of translation process into an end gene product such as snRNA or tRNA, rRNA, and protein in gene expression. Similar to translation and transcription, a gene is a sequence of the process that collects various sub-processes like post-translation, termination, translation, and initiation processing. Gene expression is the basis for the various life-developing process, specialized functions, develop their shape and essential cells grow [1]. Microarray datasets have a high potential for disease prediction and diagnosis that are high dimensional datasets. The microarray dataset consists of thousands of genes and many genes are irrelevant, noisy, and redundant. The irrelevant genes in the dataset degrade the performance of the machine learning techniques and therefore, dimensionality needs to be reduced. Imbalanced datasets, low sample-sized, and high dimensional datasets are other reasons for dimensionality reduction that result in high computational cost and poor performance of machine learning methods [2, 3]. for handling large dimensional data many algorithms are available. The irrelevant gene not only affects the learning of the machine learning algorithms and also causes the overfitting problem in the training. One solution is to apply the feature selection methods to select high dimensional small sample data for gene selection [4]. Recently, several metaheuristic algorithms were applied for cancer classification problems and gene selection. Continuous optimization problems are solved using

these metaheuristic methods. Gene selection is a discrete optimization problem that applies some transform functions to transform the continuous optimization into a binary optimization problem [5].

Feature selection methods are applied to select the optimal subsets of features from the original feature set that helps in marking the prime features and improves the efficiency of Machine learning models. The optimal method is the easiest way to select the features from a subset of every possible permutation and select the subset that maximizes model performance [6, 7]. Most of the pattern recognition methods have lower efficiency in handling the high dimensional data and combining the feature selection method with the pattern recognition method helps to improve the efficiency of the model [8]. Gene expression data of high-dimensional is a common problem in that many of the genes are not relevant and high correlations among genes are present across the gene. Gene selection is an efficient way to increase the many classification results for the prediction of cancer. A crossover operator is an ineffective way to lead the search process to escape from local optima [9, 10]. The objectives and contributions of this research are discussed as follows.

1. The QAL model is proposed to improve efficiency in feature selection for gene classification and overcome the local optima trap. The quantum bits of a quantum search in the QAL model help to increase the exploitation and overcome the local optima trap.
2. The QAL model is applied with Archimedes spiral to increase the exploitation of the search process. The QAL model increases exploration and exploitation which helps to increase the convergence rate of the model.
3. The SVM model is applied as a classifier due to its efficiency in handling the high-dimensional data. The QAL-SVM model has higher efficiency in gene classification compared to existing methods.

The Organization of this paper is given as follows: Recent gene selection research were discussed in Section 2 and the QAL-SVM model explanation is mentioned at Section 3. The simulation setup details are clearly stated at Section 4 and the results of QAL-SVM for gene classification are given at Section 5. The conclusion of this research paper is labelled at Section 6.

## 2 Literature Review

Classification of the gene is important for the diagnosis and prediction of cancer on gene data. Some of the recent research in gene classification based on soft computing was reviewed in this section.

Lee, *et al.* [11] proposed a multi-variate feature ranking method to increase the efficiency of gene classification and improve micro-array data classification. A Markov Blanket (MB) feature ranking method was embedded in the method and efficiently handle the high-dimensional data. The MB method outperforms the univariate ranking methods and another multi-variate ranking method due to the advantages of data efficiency.

Dabba, *et al.* [12] applied Modified Moth Flame Algorithm (MMFA) and Mutual Information Maximization (MIM) to do data classification using the gene selection in microarray. The MIM filtering technique was applied to find the amount of the relevancy and insufficiency of

genes. To assess the fitness function of the gene subset MMFA was applied. Leave One Out Cross Validation (LOOCV) and SVM were applied to selected genes for cancer prediction. The dataset was pre-processed using normalization and number of genes reduction using MIM. Various gene datasets were used to assess the MIM-MMFA method for the prediction of cancer. The model shows efficient performance of gene classification by using binary and multi-class.

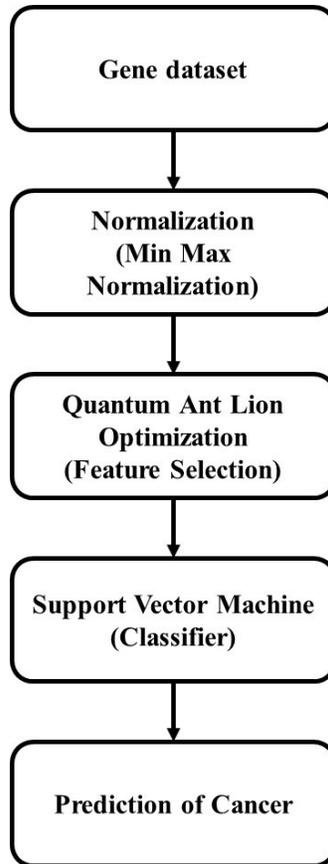
Dabba, *et al.* [13] applied the Quantum Moth Flame Optimization Algorithm (QMFOA) for gene selection. The QMFOA method was used to select a small set of genes that were used to classify samples with high accuracy. The QMFOA method has two-phase methods: pre-processing is the first phase and the hybrid method was the second phase. The pre-processing method measures the redundancy and relevancy of genes to select the gene subset and handle the high-dimensional data. The second phase combines the LOOCV-SVM, quantum computing, and MFOA method. The back and forth of search space among analysis is ensured by Quantum computing. Archimedes spiral and Hamming distance are added in the MFOA method for efficient exploration of gene-subset.

Liu, *et al.* [14] proposed a hybrid deep learning method of Deep Neural Network (DNN) and Convolutional Neural Network (CNN) for the prediction of breast cancer. The multi-modal fusion framework was established with data from patient gene modality and image modality. Feature extraction networks were applied for forms and states. Two feature networks output were fused on the idea of weighted linear aggregation and fused features are applied to predict the breast cancer sub-types. Gene modality which is having the high-dimension was reduced using the Principal Component Analysis (PCA) method and image modality was applied with a filter. The hybrid deep learning method has higher efficiency in breast cancer prediction than existing methods.

Alomari, *et al.* [15] applied Maximum Relevancy Minimum Redundancy (MRMR) of hybrid filter-wrapper method to find top-ranked genes. A wrapper method of Modified Gray Wolf Optimizer (MGWO) was applied for selecting the small sets of genes. The TRIZ-inventive solution of optimization operator was applied in MGWO to the diversity of the population. The SVM model was applied for the classification task on a selected subset of genes. To test the MGWO method for gene classification the dataset with microarray data was used. The combined way of performance of GWO with the TRIZ method was analysed. This MGWO method has higher efficiency in classification than the existing method in gene selection.

### **3 Proposed Method**

The normalization method was employed for gene dataset to reduce the difference in the original data and to increase the learning efficiency of classification. Normalized data is applied to the QAL model for the feature selection process and selected features are applied to SVM classifier. The SVM model performs classification and compares the performance with existing methods in gene selection. The flow of QAL-SVM in gene classification is given in Figure 1.



**Figure 1. The flow of Quantum Ant Lion Optimization in prediction of cancer**

4 Normalization

Min Max normalization method reduces the differences in the feature range of original data. The Min Max normalization equation is given in equations (1 & 2).

$$x_{std} = \frac{x - x_{min}}{x_{max} - x_{min}} \quad (1)$$

$$x_{scaled} = x_{std} \times (max - min) + min \quad (2)$$

The normalized data is applied to QAL for feature selection.

5 Quantum Ant Lion Optimization

The Ant Lion Optimization (ALO) method [16 – 18] is applied to search for parametric values and optimal feature weights of feature selection. Antlions hunting behaviour are mimicked to develop this method by line cone-shaped pit in the sand and catching their prey (ants). Antlion hunger level is the size of the trap, if hunger is high, then pit is larger and vice-versa. Antlion hunting process nature is mathematically modelled for lowering the optimization problem and pre owned for feature subsets searching, classifier parameter and training of the model.

Consider  $P$  antlions method with ants in  $d$  dimensional problem space which is described as  $ALO = \{AL_i, A_i | i \in P$ , where the population of antlions and ant are denoted as  $P$ . Antlions initial positions are randomly determined in given search space. Consider ant movement nature for the discovery of food at the available search space as vague and random walk is modelled. Equation (3) provides a random variable.

$$s = \begin{cases} 1 & \text{if } (r > 0.5) \\ 0 & \text{else} \end{cases} \quad (3)$$

Where the value of  $r$  lies in the range of  $[0, 1]$  at random. The ants' random walk is measured as normalization to the total iteration of increasing sum in the following equation (4).

$$X^t = [0, \text{cumsum}(2s(t_1) - 1)\text{cumsum}(2s(t_2) - 1), \dots, \text{cumsum}(2s(t_T) - 1)] \quad (4)$$

Where current iteration is denoted as  $t$  and maximum iteration is denoted as  $T$ . To keep ants' position in a predefined search space, the Min-max normalization method is applied. The newer calculated position is surpassing the boundary conditions due to the relationship among the aftermath value of equation (5) and barrier conditions. The Ant new location is calculated using equation (5).

$$X^t = \frac{(X^t - a_i) \times (d_i^t - c_i^t)}{b_i - a_i} + c_i^t \quad (5)$$

Where upper bound of the  $i^{\text{th}}$  dimension at  $t^{\text{th}}$  iteration is denoted as  $d_i^t$ , lower bound is denoted as  $c_i^t$ ,  $i^{\text{th}}$  dimension of upper bound random walk is denoted as  $b_i$  and lower bound is denoted as  $a_i$ . Antlion's pit of ants trapping is reflecting the dimensions update of lower and upper bounds. The current iteration of ant  $A_h^t$ , are given as in equation (6).

$$c_i^t = AL_m^t + c_i^t \text{ and } d_i^t = AL_m^t + d_i^t \quad (6)$$

Where  $m^{\text{th}}$  antlion selection position is represented as  $AL_m^t$  around which ants are trapping. Sliding it down inside the pit of the prey catching process is applied using an adaptive decrease in ants' random walk radius and a mathematical model is given in equation (7).

$$c_i^t = \frac{c_i}{I} \text{ and } d_i^t = \frac{d_i}{I} \quad (7)$$

Where  $i^{\text{th}}$  dimension upper bound is  $d_i$  and lower bound is  $c_i$  for given problem and ratio represents  $I$ , as given in equation (8).

$$I = L \frac{t}{T} \quad (8)$$

Where the level of exploitation is controlled by constant parameter  $L$ . Feature weights requirement is modified for this parameter appropriate to minute decimal place. The fitness value is used to present antlion's ant consumption. If ant consumption is better for the newer position when compared with older position of antlion, the antlion's new position is updated to ant current position update that is given as follows: the level of exploitation controls is constant parameter is  $L$ . Feature weights requirements modification is met in the parameter and this is required up to a few decimal places. Antlion's ant's consumption is denoted in terms of fitness value and fitness value calculation is given as in equation (9).

$$AL_m^{t+1} = A_h^t \text{ if } \text{fit}(AL_m^t) < \text{fit}(A_h^t) \quad (9)$$

The classification accuracy fitness function is given in equation (10).

$$\text{fit} = \frac{\text{correctly classified instances}}{\text{Total instances}} \quad (10)$$

The finest antlion is measured from the entire antlions in each iteration based on best fitness value. In each iteration movements of ants are affected by elite antlion and ants lean close to elite antlion. This might cause antlions trapping into local optima and elitism is applied for protecting the surpass result in any iteration in the process of optimization. The elitism is measured by elite antlion

and antlion is selected using the Roulette Wheel method. Ant lion's newer position is the average of both antlions, as in equation (11).

$$A_h^t = \frac{AL_{ET}^t + AL_{RW}^t}{2} \quad (11)$$

Where best antlion is denoted as  $AL_{ET}^t$  and roulette wheel selected antlion at  $t^{\text{th}}$  iteration is denoted as  $AL_{RW}^t$ . The solution vector is integers type, real values and continuous. Selected training functions ( $p_2$ ) and the number of neurons ( $p_1$ ) are integer whereas features weights ( $x_d$ ) are real.

Archimedes spiral of logarithmic spiral is used to define antlions next position and ant movement operation. The following conditions are applied for the movement:

Ant is used to start a spiral of an initial point

The position of antlion should be the spiral final point

Search space limit is should present for the spiral fluctuation range.

Archimedes spiral is applied for the QALO method, as given in equation (12).

$$S(Qm_i; QF_j) = Distance(Bm_i, Bf_j) \times \alpha \quad (12)$$

The distance of  $i^{\text{th}}$  binary ant for  $j^{\text{th}}$  binary antlion is denoted as  $Distance(Bm_i, Bf_j)$ , as in equation (12), and a random angle  $\alpha$  is in the range of  $[0, 2k\pi] / k \in \mathbb{N}$ .

Ants in  $QM(t)$  are modified by Archimedes spiral.

Antlion movement to the ant is applied where  $i^{\text{th}}$  antlion selected gene subset has lower importance than  $j^{\text{th}}$  ant chosen gene subset, i.e., binary antlion fitness function  $Bm_i$  is less than binary ant fitness function  $Bf_j$ . Quantum update is denoted as (Update\_Q) and binary antlion  $Bm_i$  movement moves towards another position considers binary ant  $Bf_j$ .

## 6 Support Vector Machine

Support Vector Machine (SVM) is developed to solve the problems of regression and classification analysis based on supervised learning techniques to train various groups of data from distinct data samples [19, 20]. Multi-class classification problem is used for this model based on non-linear and linear data classification tasks. SVM develops multiple hyperplanes in high-dimensional space and the best hyperplane optimally divides various classes with the largest separation between classes. Margins are used to estimate various kernel functions in non-linear classification and the main objectives of kernel functions are sigmoid, radial basis, polynomial and linear which is to maximize margins between hyper-planes. Researchers have developed many highly promising applications from increasing interest in SVMs. The SVM model has been widely applied in pattern recognition and image processing applications.

SVM architecture of classification model is applied for gene classification process and Radial Basis Function (RBF) is applied for implementation of SVM model in the proposed model. Euclidean distance of maps input data and two numeric vectors to a high dimensional space to optimally separate the given data into respective classes. Kernel RBF is specifically applied for data separating sets to share complex boundaries. Simulations have been conducted using LibSVM package. Multi-class classification problem uses the features for classification. The RBF kernel is applied in this study, as given in equation (13).

$$K(x, y) = e^{-\gamma \|x-y\|^2}, \gamma > 0 \quad (13)$$

Consider training samples  $(x_i, y_i), i = 1, 2, \dots, n$ , where maximum samples of training data are denoted as  $i, y_i \in \{1, -1\}$  and  $x_i \in R_n$ . The positive class is denoted as 1 and the negative class is denoted as -1. The solution to the following problem using SVM is given in equation (14).

$$\min_{w, b, \xi} \frac{1}{2} w^T w + C \sum_{i=1}^n \xi_i \quad (14)$$

Subject to  $y_i(w^T w \phi(x_i) + b) \geq 1 - \xi$ .

The training vector  $x_i$  transforms  $\phi$  to high dimensional space. SVM provides hyper-plane that has a maximum margin to separate different classes of data.

## 7 Results

The research proposes the Quantum Ant Lion Optimization method to improve the efficiency of gene classification. Quantum Ant Lion Optimization performance was verified using various gene datasets. Quantum Ant Lion Optimization selected features were applied to SVM for the classification process.

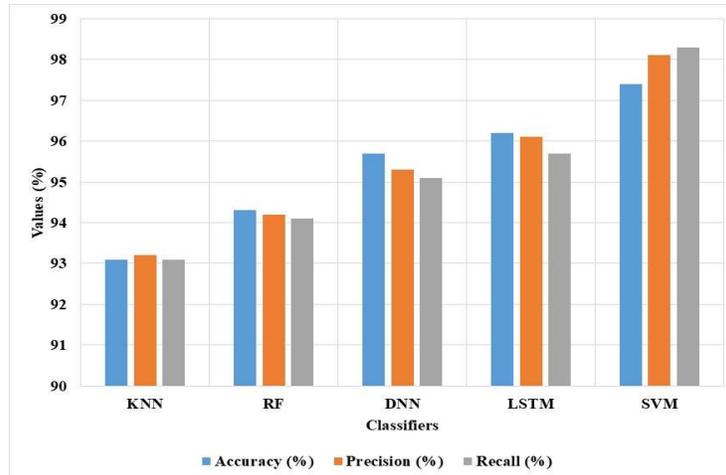
**Table 1. QAL and AL performance on gene classification**

Methods	Accuracy (%)	Precision (%)	Recall (%)
AL	86.2	85.3	85.4
QAL	97.4	98.1	98.3

The Ant Lion (AL) and Quantum Ant Lion (QAL) methods are compared for the gene classification, as shown in Table 1. The Ant Lion method has lower convergence in the feature selection due to its lower performance in learning. The QAL method provides effective learning using a quantum method that helps to improve learning performance and convergence. The QAL method adaptively performs the exploration and exploitation in the search process for feature selection based on a fitness function. The QAL method has 97.4 % accuracy and the AL method has 86.2 % accuracy for gene classification. The QAL method shows significant performance improvement in the gene classification process.

**Table 2. QAL of classifier performance**

Methods	Accuracy (%)	Precision (%)	Recall (%)
KNN	93.1	93.2	93.1
RF	94.3	94.2	94.1
DNN	95.7	95.3	95.1
LSTM	96.2	96.1	95.7
SVM	97.4	98.1	98.3

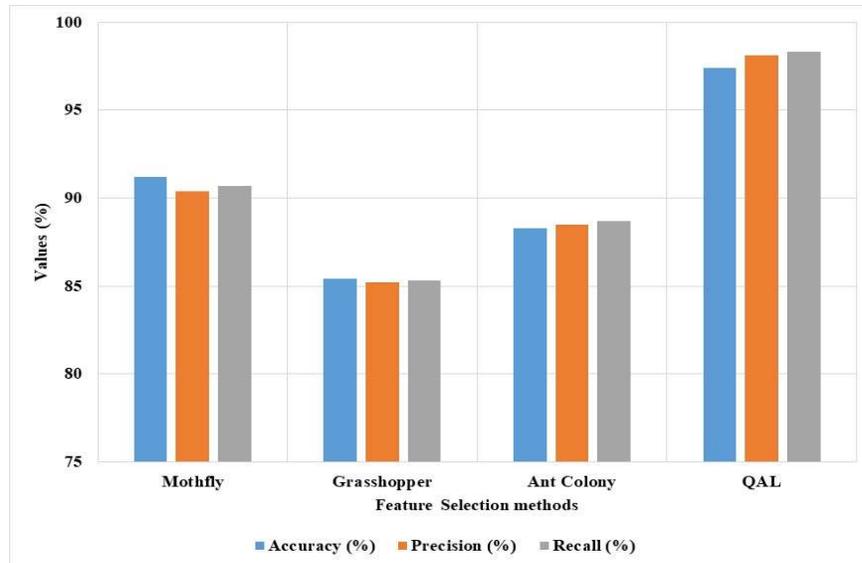


**Figure 2. Classifier performance on QAL method for gene classification**

The QAL feature selection method is tested with various classifier models to select the suitable classifier for gene classification, as given in Table 1 and Figure 2. The SVM model shows significant performance in gene classification compared to other classifiers such as LSTM, and DNN models. The LSTM, Random Forest (RF) and DNN models have the limitations of overfitting problems in the training process. The KNN model is sensitive to outlier data instances that degrade the efficiency of the model. The SVM model has the advantages of effectively handling the high dimensional data and QAL selected relevant performance improves the efficiency of the model. The QAL-SVM model has an accuracy of 97.4 % and the QAL-LSMT model has the accuracy of 96.2 % on gene classification.

**Table 3. Feature selection comparison of QAL method**

Methods	Accuracy (%)	Precision (%)	Recall (%)
Mothfly	91.2	90.4	90.7
Grasshopper	85.4	85.2	85.3
Ant Colony	88.3	88.5	88.7
QAL	97.4	98.1	98.3

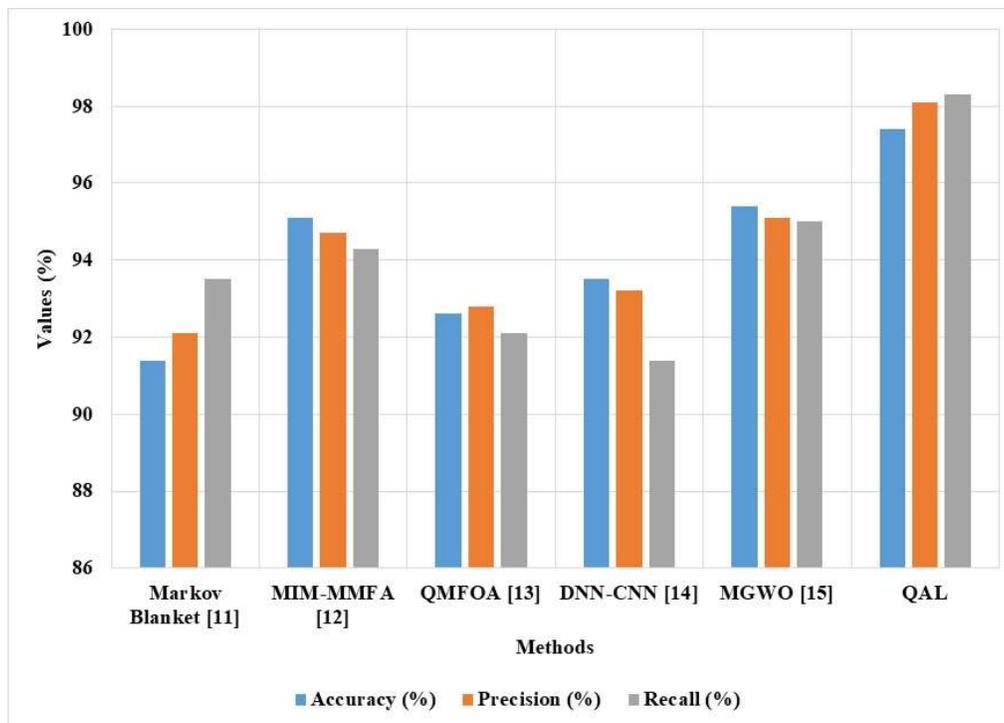


**Figure 3. Feature selection comparison for gene classification**

The QAL feature selection method is compared with existing feature selection methods on gene classification for efficiency analysis, as given in Figure 3 and Table 3. The QAL method increases the exploration process using quantum bits and an effective search process. The QAL exploitation is improved by applying Archimedes spiral method based on fitness function to select suitable features for the classification. The QAL increases in the exploration and exploitation search process which helpsto increase the convergence rate of the feature selection process. The existing feature selection methods such as Ant colony, Grasshopper, and Mothfly algorithms have the limitations of local optima trap and lower convergence in feature learning. The QAL-SVM method has 97.4 % accuracy and Ant Colony-SVM has 88.3 % accuracy in the gene classification process.

**Table 4. Comparative analysis of QAL**

Methods	Accuracy (%)	Precision (%)	Recall (%)
Markov Blanket [11]	91.4	92.1	93.5
MIM-MMFA [12]	95.1	94.7	94.3
QMFOA [13]	92.6	92.8	92.1
DNN-CNN [14]	93.5	93.2	91.4
MGWO [15]	95.4	95.1	95
QAL	97.4	98.1	98.3



**Figure 4. Comparison analysis of QAL method on gene classification**

The QAL method of gene classification is compared with existing methods, as given in Figure 4 and Table 4. The QAL method has the advantages of increasing the exploration by quantum bits and increasing the exploitation by Archimedes spiral in the search process. The QAL increases in exploration and exploitation which helps to improve the convergence rate of the model. The MGWO method has a limitation of local optima trap and DNN-CNN [14] has a limitation of overfitting problem. The QMFOA [13] method has a lower convergence rate and the MIM-MMFA [12] method has a local optima trap. The Markov Blanket [11] has the limitation of imbalance data problem in the classification. The QAL method has 97.4 % accuracy and MGWO [15] method has 95.4 % accuracy in gene classification.

## 8 Conclusion

Gene selection is a difficult task for cancer prediction due to the presence of a large number of gene information. The existing methods in gene selection have the limitation of local optima trap, lower convergence, and overfitting problems. This research proposes the QAL method to increase the exploration and exploitation process that helps to overcome local optima trap and lower convergence rate. The quantum bits in the quantum search process helps to increase the exploration of the search and escape from the local optima trap. The Archimedes spiral is applied in QAL based on the fitness function to increase the exploitation and convergence rate of the model. The QAL method increases the exploration and exploitation and helps to select the relevant features for gene classification. The SVM model is applied as a classifier due to its efficiency in handling the high-dimensional dataset. The QAL method has 97.4 % accuracy and the MIM-MMFA method has 95.1 % accuracy in gene classification. The future work of this research involves applying the hybrid method to improve the efficiency of gene classification.

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