

A NOVEL APPROACH BASED ON FEATURE SELECTION AND GENE CLASSIFICATION USING SUPPORT VECTOR MACHINES AND QUANTUM ANT LION OPTIMIZATION

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ABSTRACT

Gene selection for cancer prediction is a crucial model for the medical sector to successfully treat cancer patients. The current model finds it difficult to evaluate the links between the variables used to categorize genes due to the wealth of information available on genes. Local optima traps, slower convergence, and overfitting are drawbacks of the current models. This study suggests using the Quantum Ant Lion (QAL) feature selection optimization to enhance gene classification performance. In the Ant Lion approach, the quantum search process is used to boost search performance, which aids in boosting exploration and avoiding the local optima trap. To maximize utilization of the feature selection based on the fitness function, the Archimedes spiral search is applied in the QAL approach. Exploration and exploitation are increased by the QAL approach, which also serves to raise the method's convergence rate. For classifying genes, the DNN-CNN model and QAL approach both had accuracy of 93.5% and 97.4%, respectively.

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

1. INTRODUCTION

Translation and transcription are typically two crucial stages in gene expression. Gene expression results in the production of end products such as snRNA, tRNA, rRNA, and proteins that are encoded by the translation process. Including translation and transcription, a gene is a sequence of a process that assembles different sub-processes including post-translation, termination, translation, and initiation processing. Gene expression serves as the foundation for the numerous life-development processes, specialized functions, shape development, and growth of vital cells [1]. The high dimensionality of microarray datasets makes them particularly useful for illness detection and prediction. Numerous genes in the micro-array dataset are redundant, useless, and noisy. It contains thousands of genes. It is necessary to minimize dimensionality since the irrelevant genes in the dataset reduce the effectiveness of machine learning approaches. Other causes of dimensionality reduction include imbalanced datasets, small sample sizes, and high-

dimensional datasets, which have a negative impact on machine learning method performance and raise computational costs [2, 3]. Many algorithms are available to handle large-dimensional data. In addition to affecting how machine learning algorithms are learned, the irrelevant gene also contributes to the overfitting issue during training. To pick high dimensional small sample data for gene selection, one way is to use feature selection algorithms [4]. For challenges with cancer categorization and gene selection, a number of meta heuristic algorithms have recently been used. These meta heuristic techniques address challenges in continuous optimization. Gene selection is a discrete optimization problem where some transform functions are used to convert the continuous optimization into a binary optimization problem [5].

In order to improve the effectiveness of machine learning models, feature selection methods are used to choose the best subsets of features from the initial feature set. This helps to identify the key features. The simplest way to

choose features from a set of all possible permutations is to use the optimum technique, which allows you to choose the set of features that will maximize model performance [6,7]. The efficiency of the model is increased by combining the feature selection method with the pattern recognition method because most pattern recognition techniques perform less well when dealing with high dimensional data [8]. As a result of the significant correlations between genes and the large number of irrelevant genes in high-dimensional gene expression data, this issue is frequently encountered. Increased classification outcomes for the cancer prediction can be achieved effectively using gene selection. To guide the search process away from local optima, a crossover operator is useless [9, 10].

The QAL model is suggested to increase feature selection effectiveness for gene classification and avoid the local optima trap. To maximize exploitation and avoid the local optima trap, a quantum search's quantum bits are used in the QAL model. The QAL model is used in conjunction with the Archimedes spiral to maximize the effectiveness of the search procedure. The QAL model increases exploitation and exploration, which aids in speeding up the model's convergence. Considering how well the SVM model handles high-dimensional data, it is used as a classifier. In comparison to existing approaches, the QAL-SVM model is more effective at classifying genes.

This paper is organized as follows: In Section 2, recent studies on gene selection were covered, and Section 3 mentions the QAL-SVM model explanation. Section 4 fully describes the simulation setup, and Section 5 presents the QAL-SVM findings for gene categorization. Section 6 of this research report is designated as the paper's conclusion.

2. LITERATURE REVIEW

For the diagnosis and forecasting of cancer based on gene data, classification of the gene is crucial. This section evaluated several current studies on soft computing-based gene classification.

Lee, *et al.* [11] To boost the effectiveness of gene classification and enhance the

classification of micro-array data, a multi-variate feature ranking method was presented. The method effectively handles the high-dimensional data because it incorporates a Markov Blanket (MB) feature ranking technique. Due to the benefits of data efficiency, the MB technique surpasses univariate ranking methods and another multi-variate ranking method.

Dabba, *et al.* [12] used the gene selection in microarrays to classify the data using the Modified Moth Flame Algorithm (MMFA) and Mutual Information Maximization (MIM). The amount of the relevance and insufficiency of genes was determined using the MIM filtering technique. MMFA was used to evaluate the gene subset's fitness function. SVM and Leave One Out Cross Validation (LOOCV) were used to analyze specific genes for their potential to predict cancer. The dataset was pre-processed using normalization and MIM to reduce the number of genes. The MIM-MMFA technique for cancer prediction was evaluated using several gene datasets. The model demonstrates effective gene classification through the use of binary and multi-class.

Dabba, *et al.* [13] Gene selection was carried out using the Quantum Moth Flame Optimization Algorithm (QMFOA). Using a minimal number of genes, samples were accurately classified using the QMFOA approach. The pre-processing phase of the QMFOA method is the first phase, and the hybrid method is the second. To choose the gene subset and manage the high-dimensional data, the pre-processing method assesses the redundancy and relevance of genes. The MFOA approach is combined with the LOOCV-SVM, quantum computing, and second phase. Quantum computing ensures a continuous search space between analyses. For effective exploration of gene-subset, Archimedes spiral and Hamming distance are added to the MFOA approach.

Liu, *et al.* [14] suggested a hybrid deep learning approach using Deep Neural Networks (DNN) and Convolutional Neural Networks (CNN) for breast cancer prediction. Data from the patient gene modality and the picture modality were used to create the multi-modal fusion framework. For forms and states, feature extraction networks were used. The output of two

feature networks was fused using the concept of weighted linear aggregation, and the fused features were then utilized to forecast the subtypes of breast cancer. Principal Component Analysis (PCA) was used to minimize the high-dimension gene modality, and a filter was used to apply the picture modality. In comparison to other methods, the hybrid deep learning method is more effective at predicting breast cancer.

Alomari, *et al.* [15] employed the hybrid filter-wrapper method's Maximum Relevancy Minimum Redundancy (MRMR) to determine the top-ranked genes. The short sets of genes were chosen using a wrapper approach of the Modified Gray Wolf Optimizer (MGWO). In MGWO, the diversity of the population was addressed by the TRIZ-invented optimization operator solution. A certain subset of genes were subjected to the SVM model's categorization algorithm. The dataset containing microarray data was utilized to evaluate the MGWO approach for gene categorization. Analysis of the GWO and TRIZ method's combined performance was done. Compared to the current method for gene selection, the MGWO method is more efficient in classifying genes.

3. PROPOSED METHOD

For the gene dataset, the normalizing method was used to reduce the disparity in the original data and to boost the classification learning effectiveness. In order to choose the features to use, normalized data is applied to the QAL model, and then the chosen features are applied to the SVM classifier. The classification function of the SVM model is performed, and performance against current gene selection techniques is evaluated. Figure 1 depicts the QAL-SVM categorization process for genes.

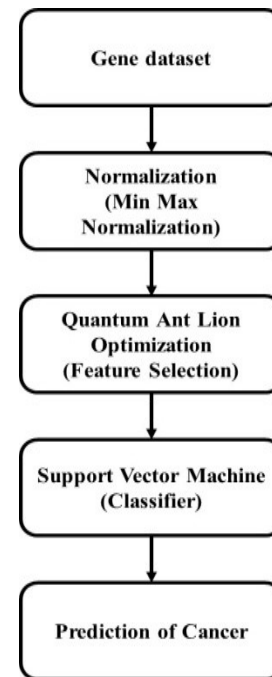


Figure 1. The Flow Of Quantum Ant Lion Optimization In Prediction Of Cancer

Normalization

The discrepancies in the original data's feature range are lessened by the Min Max normalization procedure. Equations (1 & 2) provide the formula for Min Max normalization.

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

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

For feature selection, the normalized data is used with QAL.

Quantum Ant Lion Optimization

In order to find the best feature weights and parametric values for feature selection, the Ant Lion Optimization (ALO) approach [16–18] is used. By lining a cone-shaped pit in the sand and catching their prey (ants), antlions imitate the hunting behavior of other animals to acquire this technique. Ant lion hunger level determines trap size; if hunger is high, pit size is larger, and vice

versa. The mathematical modelling of the ant lion hunting behavior lowers the optimization issue and is pre-owned for feature subset searching, classifier parameter setting, and model training.

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' starting positions in a given search space are chosen at random. Consider the model of the vague and random walk used by ants to find food in the available search space. A random variable is given by equation (3).

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

Where, at random, r 's value falls between $[0, 1]$. The random walk of the ants is quantified in the following equation (4) as normalization to the entire iteration of rising sum.

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

Where T is the maximum iteration and t is the current iteration. The Min-max normalization method is utilized to retain ants at their current location within a predetermined search space. The link between the output value of equation (5) and boundary conditions causes the more recent estimated position to exceed the boundary conditions. Eqn. (5) is used to determine the Ant's new location.

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

Where upper bound of the i^{th} dimension at t^{th} iteration is denoted as d_i^t , lower bound is denoted as c_i^t , i^{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^{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^{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 constant parameter L controls the degree of exploitation. In order to accommodate the parameter's minute decimal place, the criterion for feature weights is adjusted. To display the antlion's ant intake, the fitness value is employed. The new position of the antlion is updated to the current position update, which is provided as follows, if ant consumption is better for the newer position compared to the older position of the antlion: L is a constant parameter for the exploitation control level. Up to a few decimal places are needed to satisfy the feature weights modification criteria. The fitness value used to calculate the consumption of Antlion's ants is provided 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).

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

Each iteration uses the best fitness value to determine which antlion is the best out of all the antlions. The actions of the ants are influenced by the elite antlion in each iteration, and the ants lean against the elite antlion. As a result, elitism is used to defend the superior outcome in every optimization cycle, which may lead to ants being drawn into local optima. Elite ants are used to gauge elitism and are chosen using the Roulette Wheel approach. As seen in equation (11) the

newest position of the ant lion is the average of the two antlions.

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

Where best antlion is denoted as AL_{ET}^t and roulette wheel selected antlion at t^{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.

The next place and method of movement of antlions are defined by the Archimedes spiral of logarithmic spiral. For the movement, the ensuing requirements apply:

When spiraling from a starting position, ant is employed. Antlion should be situated at the center of the spiral. For the range of spiral fluctuations, there should be a search space restriction. Equation (12) states that the Archimedes spiral is used for the QALO approach.

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

The distance of i^{th} binary ant for j^{th} binary antlion is denoted as $\text{Distance}(Bm_i, Bf_j)$, as in equation (12), and a random angle α 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^{th} antlion selected gene subset has lower importance than j^{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 .

Support Vector Machine

Support Vector Machine (SVM) is a tool designed to help with regression and classification analysis problems. It uses supervised learning methods to train different groups of data from diverse data samples [19, 20]. This model uses both non-linear and linear data classification tasks to solve a multi-class classification problem. The best hyperplane

splits different classes with the greatest separation possible according to the SVM's many hyperplanes developed in high-dimensional space. In non-linear classification, margins are used to estimate a variety of kernel functions, with the maximization of margins between hyper-planes being the primary goal of sigmoid, radial basis, polynomial, and linear kernel functions. Because of the growing interest in SVMs, researchers have created a number of extremely interesting applications. Applications for pattern recognition and image processing have made extensive use of the SVM model.

The suggested approach uses SVM architecture of classification models for gene categorization and Radial Basis Function (RBF) for SVM model implementation. To effectively divide the provided data into different classes, Euclidean distance transfers the input data and two numerical vectors to a high dimensional space. For data sets that share complicated boundaries, kernel RBF is specially employed. Using the Lib SVM library, simulations have been run. The features are used to classify problems with many classes. Equation (13), which applies the RBF kernel, is used in this investigation.

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

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

High dimensional space ϕ is transformed by the training vector x_i . SVM offers a hyper-plane with a maximum margin to separate various data classes.

4. RESULTS

In order to increase the effectiveness of gene categorization, the research suggests using the Quantum Ant Lion Optimization approach. Utilizing diverse gene datasets, the effectiveness of the Quantum Ant Lion Optimization was confirmed. SVM was used to classify the data using the characteristics chosen by Quantum Ant Lion Optimization.

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

As indicated in Table 1, the gene classification techniques Ant Lion (AL) and Quantum Ant Lion (QAL) are contrasted. Because it performs less well when learning, the Ant Lion

approach has lower convergence in feature selection. The QAL method offers efficient learning with a quantum approach that enhances learning performance and convergence. Exploration and exploitation steps in the search process for feature selection based on a fitness function are carried out adaptively using the QAL technique. For classifying genes, the QAL technique has an accuracy of 97.4% and the AL method of 86.2%. In the process of classifying genes, the QAL approach exhibits a noticeable performance gain.

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

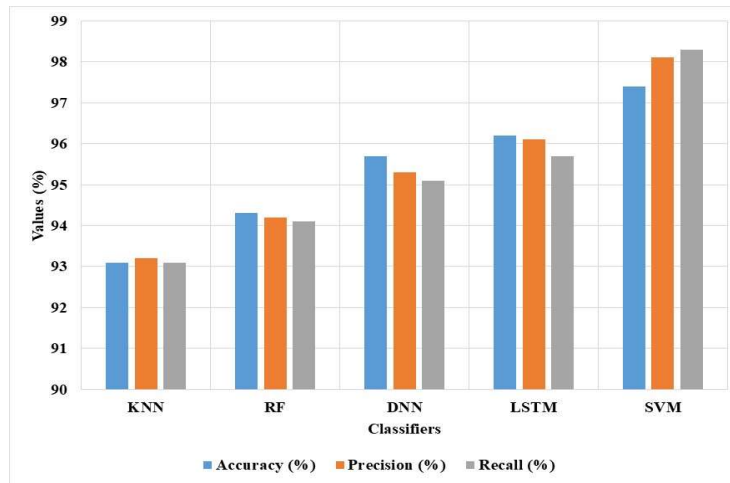


Figure 2. Classifier Performance On QAL Method For Gene Classification

As shown in Table 2 and Figure 2, the QAL feature selection method is evaluated with a variety of classifier models to choose the best classifier for classifying genes. In comparison to other classifiers like LSTM and DNN models, the SVM model performs significantly better in classifying genes. The over fitting issues in the training process are a drawback of the LSTM, Random Forest (RF), and DNN models. The KNN model is susceptible to outlier data examples that

reduce the algorithm's effectiveness. The SVM model has the benefit of processing high dimensional data well, and QAL selected relevant performance increases the model's effectiveness. On gene classification, the QAL-SVM model has an accuracy of 97.4% and the QAL-LSMT model has an accuracy of 96.2%.

Table 3. Feature Selection Comparison Of QAL Method

Methods	Accuracy (%)	Precision (%)	Recall (%)
Moth fly	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

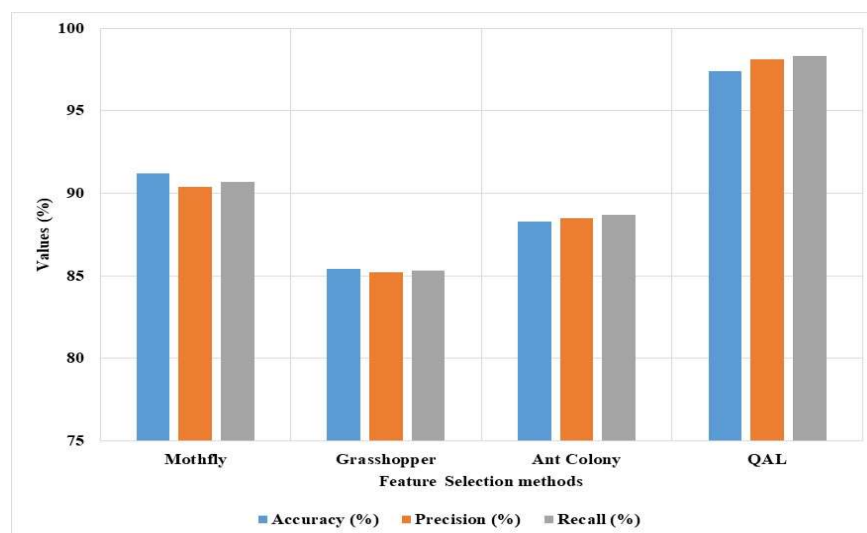


Figure 3. Feature Selection Comparison For Gene Classification

As shown in Figure 3 and Table 3, the efficiency of the QAL feature selection method is compared to other feature selection techniques used for gene classification. Utilizing quantum bits and a successful search strategy, the QAL method speeds up exploration. By using the Archimedes spiral method, which is based on fitness function, to choose appropriate features for the classification, the QAL exploitation is improved. The existing feature selection methods, such as Ant colony, Grasshopper, and Moth fly 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

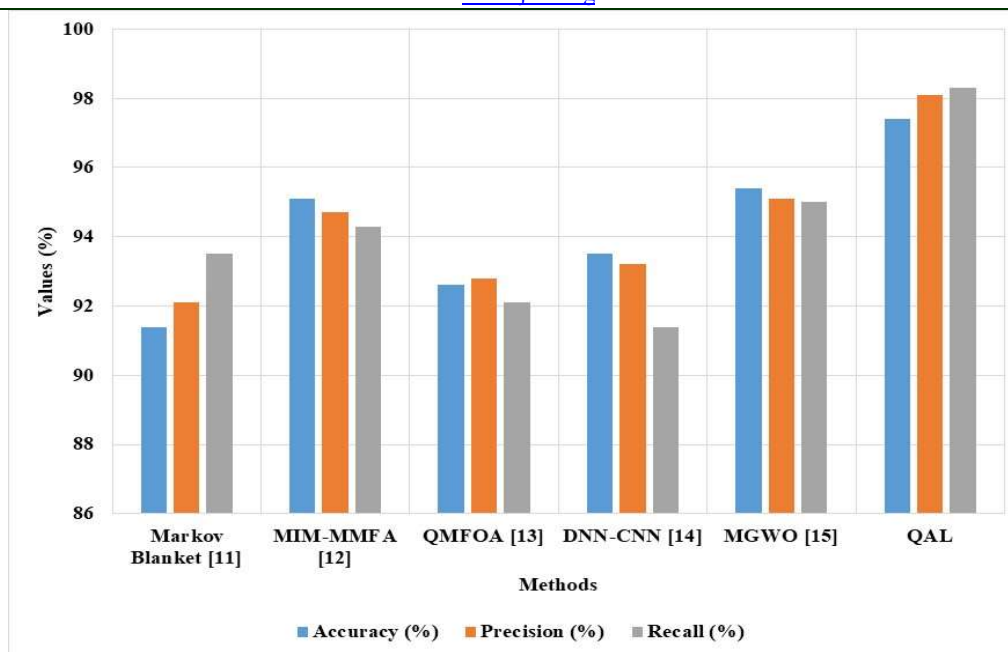


Figure 4. Comparison Analysis Of QAL Method On Gene Classification

Figure 4 and Table 4 compare the QAL method of gene classification with other approaches. The QAL approach has the advantages of enhancing the search process's use of both the Archimedes spiral and quantum bit exploration. Exploration and exploitation of the QAL grow, which boosts the model's convergence rate. A weakness of the MGWO approach is the local optima trap, whereas a limitation of the DNN-CNN [14] method is the overfitting issue. The MIM-MMFA [12] approach features a local optima trap, whereas the QMFOA [13] method converges more slowly. The Markov Blanket's [11] restriction is the classification's imbalance data problem. In terms of classifying genes, the MGWO [15] technique and QAL both have accuracy rates of 97.4% and 95.4%, respectively.

5. CONCLUSION

This passage outlines a research approach for gene selection in cancer prediction, utilizing the Quantum Ant Lion (QAL) approach to overcome challenges associated with existing gene selection. The presence of a wealth of gene information makes gene selection a challenging issue for cancer prediction. The current gene selection techniques are constrained by local optima traps, slower convergence, and over fitting issues. This study suggests a hybrid approach

which aids in avoiding the local optima trap and lowering convergence rates. In the quantum search procedure, the quantum bits aid in extending the search's investigation and assisting in escaping the local optima trap. To speed up the model's exploitation and convergence, the Archimedes spiral is used in QAL and is based on the fitness function. The QAL technique improves aids in choosing the features for gene selection. The QAL technique has a 97.4% accuracy rate and the existing method MIM-MMFA which works on gene selection has 95.1% accuracy rate. The hybrid approach used in this research's can be future work to increase the effectiveness of gene classification in cancer prediction.

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