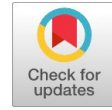# Optimal Classification of Lung Cancer Related Genes using Enhanced reliefF Algorithm and Multiclass Support Vector Machine

Ashok K Patil, Siddanagouda S Patil, M Prabhakar

Abstract: Currently, the automatic lung cancer classification remains a challenging issue for the researchers, due to noisy gene expression data, high dimensional data, and the small sample size. To address these problems, an enhanced gene selection algorithm and multiclass classifier are developed. In this research, the lung cancer-related genes (GEO IDs: GSE10245, GSE19804, GSE7670, GSE10072, and GSE6044) were collected from Gene Expression Omnibus (GEO) dataset. After acquiring the lung cancer-related genes, gene selection was carried out by using enhanced reliefF algorithm for selecting the optimal genes. In enhanced reliefF gene selection algorithm, earthmover distance measure and firefly optimizer were used instead of Manhattan distance measure for identifying the nearest miss and nearest hit instances, which significantly lessens the "curse of dimensionality" issue. These optimal genes were given as the input for Multiclass Support Vector Machine (MSVM) classifier for classifying the sub-classes of lung cancer. The experimental section showed that the proposed system improved the classification accuracy up to 3-10% related to the existing systems in light of accuracy, False Positive Rate (FPR), error rate, and True Positive Rate (TPR).

Index Terms: Enhanced reliefF algorithm, firefly optimizer, gene selection, microarray gene expression, multiclass support vector machine.

I. BACKGROUND

In present decades, lung cancer is the common cause of death among people. So, the early recognition of lung cancer increases the chance of survival rate [1-2]. Presently, gene-level treatment is a promising technique, which effectively identifies the normal and abnormal patients [3]. The available microarray gene expression data are noisier, high dimensional and small sample size, whereas only some genes plays a crucial role in the detection of lung cancer [4]. In present scenario, several methods are developed for gene level lung cancer detection, which is majorly sub-divided into two categories such as, filtering and wrapper methods [5]. Generally, the filtering methodologies are feature ranking methodologies, which works on the basis of gene selection. Some of the common methods used for gene selection are

adaptive genetic algorithm [6], Bayesian lasso quantile regression [7], learning automata-based genetic algorithm [8], reliefF algorithm [9], etc. Similarly, the wrapper methods find effective gene subsets on the basis of classifier like random forest [10], nearest neighbour classifier [11], etc. Though, the above-mentioned methods have their own limitations such as, consumes more processing time, unable to solve complex technological and scientific problems, etc. In order to overcome these problems, an efficient system is developed to determine lung cancer in an early stage. In this research paper, a new automated system has been developed for improving the performance of lung cancer detection. Initially, the input data were collected from GEO dataset (GEO IDs: GSE10245, GSE19804, GSE7670, GSE10072, and GSE6044). After collecting the input data, gene selection was carried out using enhanced reliefF algorithm on individual GEO IDs. In enhanced reliefF, earthmover distance was used instead of Manhattan distance measure for identifying the nearest miss and nearest hit instances. Here, earthmover distance measure uses only a limited number of genes for representing the data that effectively reduces the "curse of dimensionality" issue. Additionally, firefly optimizer was included in conventional reliefF algorithm to select the user defined parameter. Since, firefly optimization algorithm requires only a minimum number of iterations to select the user defined parameter, so the computational complexity was very low compared to other optimization algorithms. Then, the output of gene selection was given as the input for MSVM classifier for classifying the sub-classes of lung cancer such as, normal, small cell lung cancer, adenocarcinoma, and squamous cell carcinoma. At last, the proposed system performance was compared with the existing systems in light of accuracy, FPR, error rate, and TPR. This research paper is pre-arranged as follows. In section II, numerous research papers on gene level lung cancer detection are evaluated. Explanation about the proposed system is given in section III. Section IV illustrates the quantitative analysis of the proposed system. The conclusion is made in section V.

II. RELATED WORK

In recent decades, several methods by the researchers in lung cancer detection using microarray data. In this segment, some major contributions to the earlier research papers are presented. S. Wu, H. Jiang, H. Shen, and Z. Yang, [12] developed a new methodology for gene selection named as L1/2 logistic regression model.

In this research work, the developed method uses new univariate half thresholding for updating the estimated coefficients. In experimental phase, the developed system was tested on three online available datasets such as, GSE10072, GSE19804, and GSE4115. The developed system outperformed the existing methods (L1 and LEN) by means of classification accuracy. The developed system was not advisable to use gene selection algorithms for analytical issues, because the developed system consumes more time to find the solutions with a few computational steps.

H. Azzawi, J. Hou, R. Alanni, Y. Xiang, R. Abdu-Aljabar and A. Azzawi, [13] utilized a new Gene selection programming (GSP) methodology for selecting the appropriate genes for effective lung cancer classification. The GSP method comprises of three main phases such as, recombination mechanism, defining fitness function and improved mutation. After selecting the appropriate genes, classification was carried out by using SVM classifier. In this research work, the experimental result was tested on ten microarray datasets. The comparison valuation states that the developed methodology performed well related to the existing methods in light of computational cost, number of selected genes and classification accuracy. The developed method consumes more processing time, which was considered as one of the major issues. M. Sun, K. Liu, Q. Wu, Q. Hong, B. Wang and H. Zhang, [14] developed a binary decomposition method and Gene Expression Programming (GEP) system for determining the lung cancer genes from microarray data. The prediction performance of the developed system was compared with three traditional classifiers; nearest neighbour, SVM and C4.5 on a real microarray lung cancer dataset. The experimental outcome showed that the developed system outperformed the existing classifiers by means of standard deviation, and accuracy. Since, the developed method was unable to solve complex problems in both technically and scientifically.

R. Al-Anni, J. Hou, R.D.A Abdu-aljabar and Y. Xiang, [15] utilized GEP method for detecting the non-small cell lung carcinoma. The developed method chooses the informative genes to construct an effective prediction model in order to achieve higher accuracy. The developed method was validated on two microarray datasets (GSE 68465, and GSE 8894) in order to show the effectiveness of developed system. In this research work, all the genes were treated equally, so the necessary genes were varied in dissimilar biological activities, which was considered as one of the major problems in the developed methodology.

H. Azzawi, J. Hou, Y. Xiang, and R. Alanni, [16] developed a new GEP model for detecting the lung cancer from microarray data. In this research, two gene selection algorithms were utilized to extract the lung cancer related genes. Here, the performance of the developed system was compared with three traditional classifiers; multi-layer perceptron, SVM and radial basis function neural network on a real micro-array lung cancer dataset (GSE10245). The experimental result showed that the developed system outperformed the existing classifiers by means of accuracy, sensitivity and specificity. The developed algorithm imposes a greater computational demand that leads to longer training times.

In order to overcome the above-mentioned problems, a new enhanced gene selection algorithm is developed for improving the performance of lung cancer classification.

III. PROPOSED METHODOLOGY

In present scenario, microarray dataset is an emerging tool for representing the cell state at the molecular level. Usually, the available microarray databases are larger in size compared to other datasets, which leads to curse of dimensionality issues. So, optimal gene selection is a promising technique to address this problem and also it plays a crucial role in the development of effective classification. In addition, gene selection and classification address several issues such as, choosing the most relevant genes to improve the classification outcome, and eliminate the noisy and irrelevant genes. In this research paper, the proposed system comprises of three phases; data collection, gene selection and optimization, and classification. Fig. 1 represents the working procedure of proposed system. The detailed explanation about the proposed system is given below.
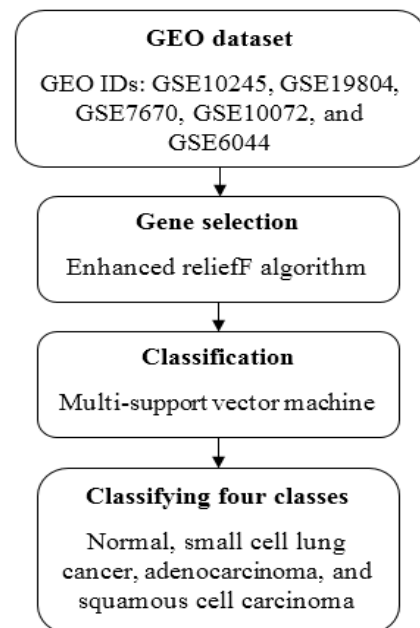

Fig. 1. Working procedure of proposed system

A. Data collection

In this paper, GEO dataset is undertaken to assess the performance of proposed system in lung cancer detection. GEO dataset is an online available dataset that comprises of original submitter supplied records like sample, series and platform. A few series related to lung cancer are considered in this research work such as GSE10245, GSE10072, GSE6044, GSE7670, and GSE19804.

GSE10245 ID: It contains more than 54675 genes and 58 lung cancer cases. Among these cases, 40 patients are lung cancer patients and the remaining 18 patients are healthy patients.

GSE10072 ID: It contains 22283 genes, 58 adenocarcinoma samples (24 current smokers, 18 former smokers, and 16 non-smokers) and 49 non-tumour samples (16 current smokers, 15 non-smokers and 18 former smokers).

GSE6044 ID: It comprises of 8793 genes, 47 samples and 4 classes (ten adenocarcinoma patients, five squamous cell carcinoma patients, five normal patients and nine small cell lung cancer patients).

GSE7670 ID: It contains 22283 genes and 62 adjacent normal-tumour matched lung cancer (adenocarcinoma) samples.

GSE19804 ID: It contains 54676 genes and120 lung cancer cases. Among these cases, 60 are female smoker samples and the remaining 60 are non-smoker female samples.

B. Gene selection using enhanced reliefF algorithm

After collecting the data, enhanced reliefF algorithm is utilized to choose the optimal genes, which are effective to perform better classification. In conventional reliefF algorithm, Manhattan distance measure is used to identify the nearest hit and miss values. In most of the circumstances, conventional reliefF algorithm is very effective. While using large datasets, reliefF algorithm leads to "curse of dimensionality" problem. In order to address this issue, a minor modification is done in the conventional reliefF algorithm. In this research, earthmover distance and firefly optimization algorithm are utilized instead of using. Manhattan distance for identifying the nearest miss and nearest hit instances. The major benefit of earthmover distance measure is that it needs only limited time for deciding the distances between the instances I_i. Although, earthmover distance measure utilizes only limited number of genes to represent the data that is enough to attain accurate neighborhood selection and better prediction and also it completely reduces the "curse of dimensionality" problem.

At first, reliefF gene selection algorithm randomly chooses the instances I_i and then searches for k nearest neighbor in the same class is named as nearest hit h_j and in the dissimilar classes is named as nearest miss m_j. Here, earthmover distance measure is utilized to identify the nearest miss m_j and nearest hit h_j instances. Then, update the quality estimation $Q[a]$ for all the attributes a that mainly depends on the values of I_i, h_j and m_j. If the instances h_j and I_i have similar values, then the attribute a is separated into two instances with the similar classes that minimizes the quality estimation $Q[a]$. Correspondingly, if the instances h_j and I_i have dissimilar values, then the attribute a is separated into two instances with the dissimilar classes that maximizes the quality estimation $Q[a]$. The entire mechanism is repeated for M times, where M is denoted as user defined parameter. In this research work, the user defined parameter is fixed by using firefly optimization algorithm. Since, the firefly optimization algorithm has good efficiency for certain issues and also it needs only a minimum number of iterations. In enhanced reliefF algorithm, the quality estimation $Q[a]$ is updated using the Eq. (1), (2), and (3).

$$Q[a] = Q[a] + (\bar{h} + \bar{m}) \tag{1}$$

Where,

$$\bar{h} = -\sum_{j=1}^{k} d(a, I_i, h_j) / k \tag{2}$$

$$\bar{m} = \Sigma_{C \neq cl(I_i)} \left[\left(\frac{P(C)}{1 - P(I_i)} \right) \Sigma_{j=1}^{k} d(a, I_i, m_j(C)) \right] / k \tag{3}$$

Where, C is denoted as total number of classes, d is specified as distance between the selected instances $I_i, P(C)$ is denoted as prior class, and $cl(I_i)$ is stated as class of the ith sample.

1) Firefly optimization algorithm

Firefly optimization algorithm is very superior in dealing with multimodal and global optimization concerns. The fire-fly optimization algorithm comprises of three idealized rules; attractiveness, unisex and brightness. Usually, all fire-fly insects are unisex, so it is attracted to other fire-flies on the basis of their sex. Brightness of the fire-flies are evaluated by the land-scape of the objective function. For a maximization issue, the brightness is directly proportional to the objective function. In addition, attractiveness is directly proportional to the brightness of a fire-fly, whereas the less bright fire-flies are attracted by the brighter fire-flies.

In addition, attractiveness between the two fire-flies are automatically decreased, if the distance between the two fire-flies are increased. The two major issues in fire-fly optimization algorithm are formulating the amount of absorbency and the difference in light intensity. For simplicity purpose, consider fire-fly absorbency β with luminosity that depends on the target functions. Since, fire-fly absorbency is proportional to the light intensity of adjacent fire-fly. The absorbency from fire-fly β is mathematically defined in the Eq. (4).

$$\beta(r) = \beta_0 e^{-\gamma r^2} \tag{4}$$

Where, β_0 is denoted as attractiveness at $r = 0$ and γ is represented as coefficients of light absorption at the source. The distance between the fire-flies j and i in the points x_j and x_i is evaluated using the Eq. (5) on the basis of Cartesian distance measure.

$$r_{ij} = \|x_i - x_j\| = \sqrt{\sum_{k=1}^{d} (x_{i,k} - x_{j,k})^2} \tag{5}$$

Where, x_i and x_j are represented as spatial coordinates of the fire-flies i and j, and $x_{i,k}$ is denoted as k portion of spatial coordination x_i of fire-fly i in the two dimensional state, which is mathematically rewritten in the Eq. (6).

$$r_{ij} = \sqrt{(x_i - x_j)^2 + (y_i + y_j)^2} \tag{6}$$

In addition, the firefly movement and absorption of j moves luminously determined in the Eq. (7).

$$x_i = x_i + \beta_0 e^{-\gamma r^2_{ij}} \left(x_i - x_j\right) + \alpha\left(rand - \frac{1}{2}\right) \tag{7}$$

Where, the second term $\beta_0 e^{-\gamma r^2_{ij}}$ is denoted as attractiveness, third term $\alpha\left(rand - \frac{1}{2}\right)$ is indicated as randomization with a parameter α, and $rand$ is specified as random number generator, which ranges from $[0,1]$ interval.

In most of the cases, β_0 is equal to one and $\alpha \in [0,1]$. The parameter γ determines the variations in attractiveness and also its objective function value is essential in evaluating the speed of convergences and fire-fly optimization algorithm behavior. Ideally, the parameter γ is evaluated on the basis of absorbency changes that ranges within $[0,\infty]$. Table 1 details about the number of genes exists in the GEO IDs and the number of genes selected after employing enhanced reliefF algorithm. The pseudo code of enhanced reliefF gene selection algorithm is described below.

Table I. Genes selected after enhanced reliefF algorithm

GEO IDs	Number of genes	Selected genes
GSE10072	22283	AGER, CA4, FABP4, GPM6A and SFTPC
GSE19804	54676	AGER, NCKAP5, RTKN2, GPM6A, and SERTM1
GSE7670	22283	CAV2, GPM6A, HIGD1B, SFTPC, and CLEC3B
GSE10245	54675	DSC3, DSG3, KRT5, CLCA2, and FAT2
GSE6044	8793	CALML5, F2RL2, FOXG1, EXOG, and SFTPB

2) Pseudo code of enhanced reliefF algorithm

Input: Vector of class values and attribute values are assigned to each training instances.

Output: Quality estimation Q of the attributes.

1. Assign all weights $Q[a] := 0,0$;
2. **For** $i = 1$ to M do begin
3. Randomly choose the instances I_i
4. Identify k nearest hits h_j; using earthmover distance measure
5. For every class $C \neq class(I_i)$ **do**
6. From class identify the k nearest misses $m_j(C)$; using earthmover distance measure
7. **For** $a : 1$
8. $$Q[a] = Q[a] + \left(= - \sum_{j=1}^{k} d\left(a, I_i, h_j\right)\right)/k +$$
   $$\Sigma_{C \neq cl(I_i)}\left[\left(\frac{P(C)}{1-P\left(cl(I_i)\right)}\right)\sum_{j=1}^{k} d\left(a, I_i, m_j(C)\right)\right]$$

9. User defined parameter is assigned using firefly optimization algorithm.
10. **End**

C. Classification using non-linear MSVM classifier

After obtaining the optimal genes, classification is carried-out using MSVM classifier. Usually, binary SVM is a two-class classification method. Hence, it is essential to concentrate on the multi binary classification issues for extending the normal SVM classifier to multi-class SVM classifier. In SVM classification method, the multi-class classification is rehabilitated into n^{th} two class and i^{th} two-class issues, where class i is distinct from the remaining classes. The two important methodologies in SVM classifier are One-Against-All (1-a-a) and One-Against-One (1-a-1). In this scenario, 1-a-a method gives solution to create a binary classifier for every class that helps to separate the objects in the same classes. In n^{th} class, 1-a-a method generates n^{th} binary classifiers, and the ith classifier is trained with the data samples in i^{th} class with the positive labels and the residual data samples are trained with the negative labels. The result of nth class in 1-a-a method relates with the 1-a-1 method for obtaining the highest output value. In addition, the 1-a-1 method is the resultant of previous researches on two class classifier.

The MSVM classifier generates all possible two class classifiers from the training sets of nth classes, and it trains only two out of nth classes that results in $n \times (n-1)/2$ classifiers. In MSVM, decision function is an active way to moderate the multi-class problems that is constructed by assuming all the nth classes. The M-SVM classification technique is an extension of SVM, which is mathematically represented in the Eq. (8), (9), and (10).

$$\min \Phi\left(w, \xi\right) = 1/2 \sum_{m=1}^{k}\left(w_m . w_m\right) + c\sum_{i=1}^{l}\sum_{m \neq y_i} \xi_i^m \tag{8}$$

Subjected to,

$$\left(w_{yi} . x_i\right) + b_{yi} \geq \left(w_{yi} . x_i\right) + b_m + 2 - \xi_i^m \tag{9}$$

$$\xi_i^m \geq 0, i = 1,2,3...l, m, yi \in \{1,2,3...k\}, m \neq yi \tag{10}$$

Where, ξ_i^m is specified as slack variables, is represented as training data point, is denoted as user's positive constant, yi is indicated as class of training data vectors, and k is identified as number of classes. At last, the decision function is represented in Eq. (11).

$$f(x) = \arg\max\left[\left(w_i . x\right) + b_i\right], i = 1,2,3..k \tag{11}$$

IV. EXPERIMENTAL RESULT AND DISCUSSION

In this research work, MATLAB (version 2018a) was used for experimental simulation with i5 processor and 3.2 GHz. In order to estimate the effectiveness of proposed system, the performance of proposed system was compared with a few existing systems such as, sparse logistic regression with L1/2 regularization [12], GEP multi classification using decomposition schemes [14], and GEP models [16] on GEO dataset. The proposed system performance was evaluated by means of TPR, accuracy, FPR and error rate.

A. Performance measure

Performance measure is determined as the measurement of experimental outcome that develops reliable information about the effectiveness of proposed system. The relationship between the input values and output values of the proposed system was understood by utilizing the performance measures such as TPR, accuracy, FPR and error rate. The formula to evaluate TPR, accuracy, FPR and error rate are given in the Eq. (12), (13), (14), and (15).

$$TPR = \frac{TP}{TP+FN} \times 100 \qquad (12)$$

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \times 100 \qquad (13)$$

$$FPR = \frac{FP}{FP+TN} \times 100 \qquad (14)$$

$$Error\ rate = accuracy - 100 \qquad (15)$$

Where, FP is stated as false positive, TN is specified as true negative, TP is indicated as true positive, and FN is denoted as false negative.

B. Quantitative analysis

In this research work, GEO dataset is used for assessing the performance of proposed system in order classify the sub-stages of lung cancer genes such as, squamous cell carcinoma, small cell lung cancer, normal and adenocarcinoma. In this work, 70% data is used for training and 30% data is used for testing. Table 2 validates the performance of proposed system in light of TPR, accuracy, FPR and error rate. In GEO ID: GSE7670, the proposed system achieved 96.66% of TPR, 98.33% of accuracy, 2.33% of FPR and 1.667% of error rate. Correspondingly, the proposed system attains 98.34% of TPR, 98.99% of accuracy, 2.04% of FPR, and 1.01% of error rate in GEO ID: GSE10072. In addition, the TPR, accuracy, FPR and error rate of the proposed system is 98.59%, 97.64%, 3.47% and 1.41% for GEO ID: GSE19804. In GEO ID: GSE10245, the proposed system achieved 97.61% of TPR, 96.667% of accuracy, 6.67% of FPR and 3.33% of error rate. Similarly, the proposed system attains 96% of TPR, 91.12% of accuracy, 6.42% of FPR, and 8.88% of error rate in GEO ID: GSE6044. The graphical depiction of the proposed system is denoted in the Fig. 2 and 3.

Table II. Performance valuation of the proposed system

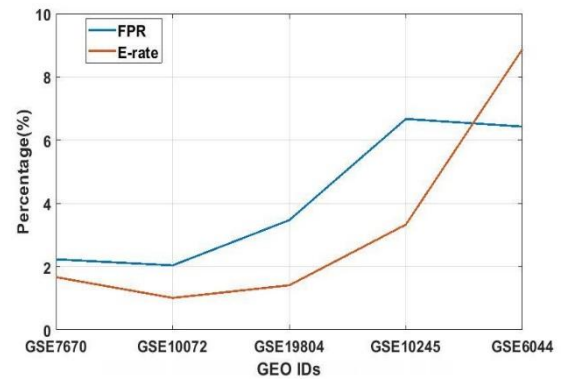| GEO IDs	TPR (%)	Accuracy (%)	FPR (%)	E-rate (%)
GSE7670	96.66	98.33	2.23	1.667
GSE10072	98.34	98.99	2.04	1.01
GSE19804	98.59	97.64	3.47	1.41
GSE10245	97.61	96.667	6.67	3.33
GSE6044	96	91.12	6.42	8.88

Fig. 2. Graphical comparison of the proposed system in light of FPR and error rate
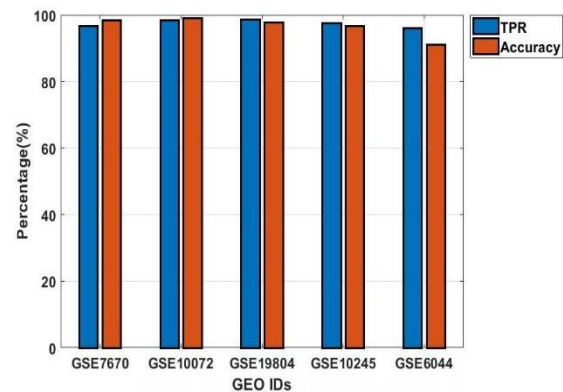

Fig. 3. Graphical comparison of the proposed system in light of TPR and accuracy

Table 3 and Fig. 4 represents the performance of the proposed system with enhanced reliefF and conventional reliefF algorithm for gene selection. In this scenario, the efficiency of gene selection is analyzed with GEO IDs: GSE7670, GSE10072, GSE19804, GSE10245, and GSE6044. In enhanced reliefF algorithm, the MSVM classification methodology averagely improved the accuracy up to 1.5 to 6% compared to conventional reliefF algorithm. In this research, the enhanced reliefF algorithm uses only low number of genes for representing the data, which is enough to attain better prediction and neighborhood selection. By selecting the low number of genes, the proposed system effectively lessens the "curse of dimensionality" problem. Table 3 and Fig. 4 confirms that the enhanced reliefF algorithm performs well in lung cancer detection compared to conventional reliefF algorithm.

Table III. Performance valuation of the proposed system using gene selection algorithms

GEO IDs	Gene selection	Classifier	Accuracy (%)
GSE7670	ReliefF	MSVM	91.667
	Enhanced ReliefF		**98.34**
GSE10072	ReliefF		97.43
	Enhanced ReliefF		**98.99**
GSE19804	ReliefF		96.23
	Enhanced ReliefF		**8.59**
GSE10245	ReliefF		90.78
	Enhanced ReliefF		**96.667**
GSE6044	ReliefF		84.474
	Enhanced ReliefF		**91.12**

In table 4, the performance of proposed system was validated with dissimilar classifiers in light of TPR, accuracy, FPR and error rate. The average accuracy of MSVM classifier is 96.74% and the comparative classification methodologies: Deep Neural Network (DNN) and Random Forest (RF) delivers 86.16% and 89.95% of average accuracy. The average TPR value of MSVM classifier is 97.44% and the comparative classification methods attains 81.76% and 86.15% of average TPR value. Similarly, the average FPR value of MSVM classifier is 4.16% and the comparative classification methods delivers 17.71% and 11.97% of average FPR value. In addition, the average error rate of MSVM classifier is 3.25% and the existing classification methods: DNN and RF delivers 13.83% and 10.05% of average error rate. Tables 2, 3 and 4 clearly shows that the enhanced reliefF algorithm with MSVM classifier performs effectively compared to other existing gene selection and classification algorithms on GEO dataset. The graphical depiction of the proposed system is denoted in the Fig. 5 and 6.
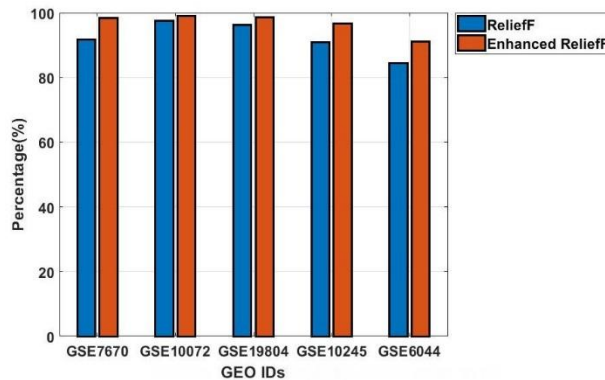

Fig. 4. Graphical comparison of the proposed system using gene selection algorithms

Table IV. Performance analysis of the proposed system using dissimilar classifiers

| GEO IDs	Classifier	Accuracy (%)	TPR (%)	FPR (%)	E-rate (%)
GSE7670	DNN	88.34	90	13.33	11.66
	RF	95	94.77	14.15	5
	MSVM	**98.34**	**96.66**	**2.23**	**1.66**
GSE10072	DNN	97	94.2	2.79	3
	RF	94	97.52	3.83	6
	MSVM	**98.99**	**98.34**	**2.04**	**1.01**
GSE19804	DNN	95.89	94.15	3.74	4.11
	RF	93.03	93.16	5.12	6.97
	MSVM	**98.59**	**98.59**	**3.47**	**1.41**
GSE10245	DNN	95.37	86.67	13.33	4.63
	RF	86.667	73.33	26.67	13.333
	MSVM	**96.667**	**97.61**	**6.67**	**3.333**
GSE6044	DNN	54.211	43.79	55.36	45.789
	RF	81.053	72	10.1	18.947
	MSVM	**91.12**	**96**	**6.42**	**8.88**
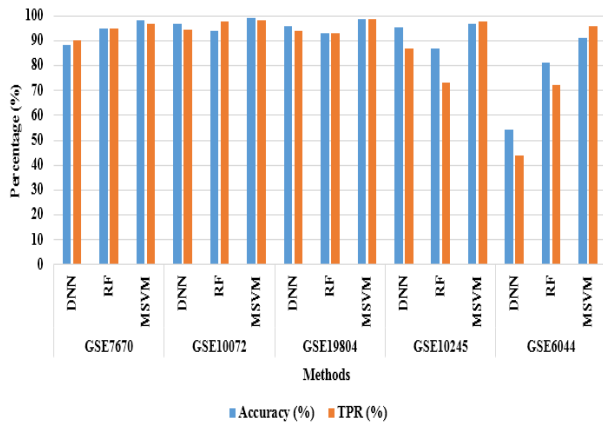
Fig. 5. Graphical comparison of the proposed system using dissimilar classifiers in light of accuracy and TPR
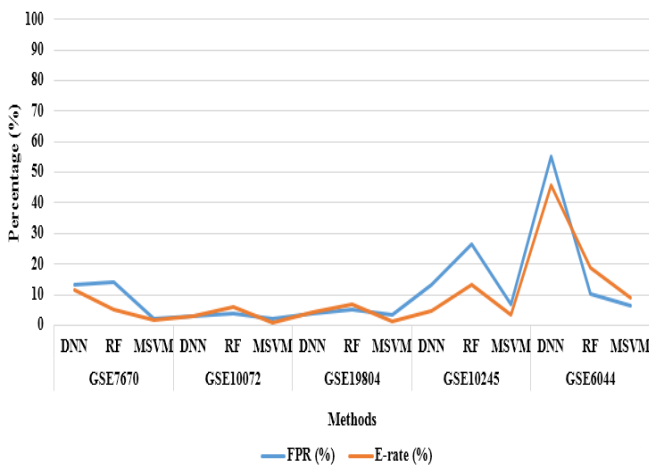

Fig. 6. Graphical comparison of the proposed system using dissimilar classifiers in light of FPR and error rate

Table 5 analysis the performance of proposed and existing systems. S. Wu, H. Jiang, H. Shen, and Z. Yang, [12] developed a new methodology (L1/2 regularized logistic regression) to select the optimal genes for classification. In this research, GEO dataset (GEO IDs: GSE10072 and GSE19804) is utilized to evaluate the performance of the developed system. From the experimental phase, the developed system almost attained 97% and 87% of classification accuracy in GSE10072 and GSE19804. Similarly, M. Sun, K. Liu, Q. Wu, Q. Hong, B. Wang and H. Zhang, [14] used GEP method for achieving better performance in the gene classification. In this paper, GEO ID: GSE6044 is used as a benchmark dataset. From this work, the developed system attained 88.96% of classification accuracy.

H. Azzawi, J. Hou, Y. Xiang, and R. Alanni, [16] developed GEP method to detect the lung cancer from microarray data (GEO ID: GSE10245). Here, the developed system achieved 93.36% of accuracy in gene classification. Compared to these existing papers, the proposed system achieved better performance in light of classification accuracy. In this research work, feature selection is a major part that effectively optimizes the genes, which is appropriate for better classification.

Table V. Performance evaluation of Proposed and existing systems

Methods	GEO IDs	Accuracy (%)
Sparse logistic regression with $L_{1/2}$ regularization [12]	GSE10072	97
	GSE19804	87
GEP multi classification using decomposition schemes [14]	GSE6044	88.96
GEP models [16]	GSE10245	93.36
Proposed work	**GSE7670**	**98.33**
	GSE10072	**98.99**
	GSE19804	**97.64**
	GSE10245	**96.667**
	GSE6044	**91.12**

V. CONCLUSION

In this research, a new feature selection algorithm is proposed (enhanced reliefF algorithm) to select the informative genes for lung cancer classification. The enhanced reliefF algorithm effectively eliminates the several irrelevant genes in the high dimensional gene data. Then, the selected optimal genes are classified by using a multiclass classifier: MSVM. The MSVM classifier reduces the size of resulting dual issue by developing a relaxed classification error bound. In addition, it quickly speed up's training process by maintaining a competitive classification accuracy. Related to other existing systems, the proposed system delivered an effective performance by means of TPR, accuracy, FPR and error rate. From the experimental analysis, the proposed system improved the classification accuracy upto 3-10% compared to the existing papers. In the future, a new dimensionality reduction technique can be developed for further enhancing the performance of lung cancer classification.

REFERENCES

1. Y. Liang, C. Liu, X.Z. Luan, K.S. Leung, T.M. Chan, Z.B. Xu, and H. Zhang. (2013). Sparse logistic regression with a $L_{1/2}$ penalty for gene selection in cancer classification. *BMC bioinformatics*, *14(1),* pp. 198.
2. S. Sayed, M. Nassef, A. Badr and I. Farag. (2019). A Nested Genetic Algorithm for feature selection in high-dimensional cancer Microarray datasets. *Expert Systems with Applications, 121,* pp. 233-243.
3. P. He, B. Fan, X. Xu, J. Ding, Y. Liang, Y. Lou, Z. Zhang, and X. Chang. (2019). Group K-SVD for the classification of gene expression data. *Computers & Electrical Engineering, 76,* pp. 143-153.
4. H. Salem, G. Attiya, and N. El-Fishawy. (2017). Classification of human cancer diseases by gene expression profiles. *Applied Soft Computing, 50,* pp. 124-134, 2017.
5. L. Gao, M. Ye, X. Lu, and D. Huang. (2017). Hybrid method based on information gain and support vector machine for gene selection in cancer classification. *Genomics, proteomics & bioinformatics*, *15(6),* pp. 389-395, 2017.
6. A. K. Shukla, P. Singh, and M. Vardhan. (2018). A two-stage gene selection method for biomarker discovery from microarray data for cancer classification. *Chemometrics and Intelligent Laboratory Systems, 183,* pp. 47-58.
7. Z. Y. Algamal, R. Alhamzawi, and H. T. M. Ali. (2018). Gene selection for microarray gene expression classification using Bayesian Lasso quantile regression. *Computers in biology and medicine, 97,* pp. 145-152, 2018.

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8. H. Motieghader, A. Najafi, B. Sadeghi, and A. Masoudi-Nejad. (2017). A hybrid gene selection algorithm for microarray cancer classification using genetic algorithm and learning automata. *Informatics in Medicine Unlocked, 9,* pp. 246-254.

9. Y. He, J. Zhou, Y. Lin, and T. Zhu. (2019). A class imbalance-aware Relief algorithm for the classification of tumors using microarray gene expression data. *Computational Biology and Chemistry*.

10. C. Arunkumar, and S. Ramakrishnan. (2018). Attribute selection using fuzzy roughset based customized similarity measure for lung cancer microarray gene expression data. *Future Computing and Informatics Journal, 3(1),* pp. 131-142.

11. R. Alanni, J. Hou, H. Azzawi and Y. Xiang. A novel gene selection algorithm for cancer classification using microarray datasets. *BMC medical genomics*, *12(1),* pp. 10.

12. S. Wu, H. Jiang, H. Shen, and Z. Yang. (2018). Gene Selection in Cancer Classification Using Sparse Logistic Regression with L1/2 Regularization. *Applied Sciences*, *8(9),* pp. 1569, 2018.

13. H. Azzawi, J. Hou, R. Alanni, Y. Xiang, R. Abdu-Aljabar and A. Azzawi. (2017). Multiclass lung cancer diagnosis by gene expression programming and microarray datasets, *In International Conference on Advanced Data Mining and Applications*, pp. 541-553, 2017.

14. M. Sun, K. Liu, Q. Wu, Q. Hong, B. Wang and H. Zhang. (2017). A novel ECOC algorithm for multiclass microarray data classification based on data complexity analysis. *Pattern Recognition*, *90*, pp. 346-362.

15. R. Al-Anni, J. Hou, R. D. A Abdu-aljabar and Y. Xiang. (2017). Prediction of NSCLC recurrence from microarray data with GEP", *IET systems biology*, *11(3),* pp. 77-85.

16. H. Azzawi, J. Hou, Y. Xiang, and R. Alanni. (2016). Lung cancer prediction from microarray data by gene expression programming. *IET systems biology*, *10(5),* pp. 168-178.

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