AN OPTIMAL CLASSIFICATION MODEL FOR MICROARRAY CANCER DISEASE PREDICTION

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Received: 06.04.2020  Revised: 08.05.2020  Accepted: 03.06.2020

Abstract
As the size of the biomedical databases is increasing day-by-day, finding an essential featureset for classification problem is complex due to large data size and sparsity problems. Microarray feature ranking and classification is one of the major challenges to scientific and medical researchers due to its high dimensional feature space and limited number of samples. Feature transformation, feature ranking and data classification are the essential components to improve the microarray cancer prediction on high dimensional datasets. In this work, a novel framework is designed and implemented to classify the high dimensional data with high true positive rate. In the proposed work, a hybrid feature transformation, hybrid feature selection and advanced classification approach is implemented to improve the true positive rate and error rate of the disease prediction. A novel principal component ranking approach is integrated to find the subset of features for classification. Finally, an extreme decision tree classifier is used to predict the classification accuracy on the selected features set. Experimental results proved that the present framework has better performance compared to the traditional models for variable microarray datasets.

Keyword: Microarray data, feature selection, data transformation and classification.

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DOI: http://dx.doi.org/10.31830/jcr.07.14.02

INTRODUCTION
Micro array data generally contains a set of genes and its disease associations. Most of the traditional approaches are inappropriate and computationally infeasible to find patterns on high dimensional datasets. Hence, it is difficult to process all of the genes that are not required during the process of classification. Also, the overall computational overhead also increases significantly. Unwanted noise is resulted during the process of classification. Hence, it is very much required to select few numbers of genes those usually take part during the classification process. All of the traditional gene selection techniques involve a perfect combination of filter and wrapper schemes[1]. Filtering approaches have the responsibility to rank every individual feature according to their goodness. During the process of ranking, the relationship among every individual gene with respective class label is considered. Univariate scoring metric play a significant role in the above ranking process. The top ranked genes are selected prior to the execution of classification schemes. On the contrary, wrapper schemes require the gene selection approach in order to integrate with a classifier. The prime objective of this technique is to evaluate the classification performance of every individual gene subset. The optimal subset of genes is detected according to the ranking of performance. Traditional filtering schemes are incapable and inefficient to measure the relationship in between different genes. The gene expression data play significant role during the process of biomedical diagnosis. According to the latest research concepts, limited numbers of genes may result high prediction accuracy during the diagnosis process of cancer disease[2]. Large numbers of genes are not relevant to the disease of interest. Therefore, the gene selection procedure is very complicated task during the medical data processing. Feature selection is considered as the most powerful tool in order to decrease the size of available data.

Extreme classification model is an extension of traditional neural network model for data classification. It partitions the whole problem into numbers of sub-problems and merges them to find an optimal solution. The parameters of hidden layer contain training data samples are mapping to output layer. In the traditional SLFN approach, the adjustments of parameters are iterative in nature and results some issues. These issues are overcome by the suggested extreme classifier approach [3]. Hence, ELM approach achieves better generalization performance as well as good learning speed. Most of the traditional learning models for training SLFNs are comparatively slower than that of non-parametric approaches. This approach operates slowly because parameters are required to be tuned iteratively. Moreover, these models require high computational memory and also increase the overall computation time of the mapping process. An extended and slightly modified version of traditional SLFNs approach is developed as extreme classifier [4]. This method is used to enhance the efficiency and performance of conventional SLFNs. Also, most of the Neural network-based learning schemes perform manual tuning of control parameters [such as learning rate, learning epochs etc.] as well as local minima. But, extreme classifier is applied automatically and there is no need of manual iterative tuning. The classification boundary is not optimal in ELM and the boundary is constant throughout the training phase. Hence, there are chances of misclassification of samples closer to boundary. This approach requires a large number of hidden neurons as compared to other traditional tuning-based approaches.

Machine learning allows a classifier to learn a set of rules, or the decision criterion, from a set of labelled data that has been annotated by an expert. This approach allows for better scaling and a reduced cost in classifying medical data when compared to a system that relies on manual input only. Most of the research in the field of machine learning based medical data classification has been done on binary classifiers. That is, building a classifier from a set of positive and negative examples to then deduce a medical data's membership in a class. Classification can take many forms, from fully automated systems with limited human intervention [4] to semi-automatic systems that employ a hybrid human machine approach.

Most of the traditional ensemble classification models are processed with limited feature space and small data size. As the size of the feature space increases, traditional ensemble classifiers select a predefined number of features for classification. Learning classification models with all the high dimensional features may result serious issues such as performance and scalability. Feature selection measures can be categorized into three types: wrappers, filters and embedded models. Learning classification models with all the high dimensional features may result serious issues such as performance and scalability. The main problems in the existing models are:
1. Problem of feature selection on high dimensional datasets.
2. Problem of predicting disease with high mis-classification rate.
3. Problem of handling high dimensional and large datasets using the parallel processing model.

RELATED WORKS
A multi-scale filter bank is used in order to present the characteristics of local data texture and structure. Different efficient and effective classification schemes are implemented to train the system. In the subsequent time, another generalization system is developed which has the responsibility of regional lung classification. Feature subset selection can improve the classification accuracy by creating optimal subset features from the high dimensional feature space. A forward feature selection approach has been used for the selection of limited features from the original feature space [5]. AdaBoost(Adaptive Boosting) is a meta learning based approach from the ensemble learning group. The main objective of the AdaBoost is to improve the strong classifier using the group of base weak classifiers. AdaBoost approach is an iterative method, and in each iteration, a weak base classifier is selected to minimize the error rate of the model. High dimensionality poses a severe issue for machine learning models. In order to optimize the precision of the classification algorithm, most of the classification approaches use feature selection measures such as mutual information, correlation coefficient, rough-set, chi-square test etc. to select subset of features from the high dimensional space. They implemented a PCA based spectral filtering model to high dimensional features of the original training data. Two reconstruction methods are used, one is the principle component analysis and the other is Maximum likelihood estimation. Several distribution algorithms were used in randomization models. Most of these approaches Bayesian analysis is used to predict the original data distribution using the randomization operator and the randomization data.

Most of the traditional approaches detect inappropriate and computationally infeasible patterns on high dimensional datasets. Hence, it is difficult to process all of the cancer patterns that are not required during the process of classification. Hence, the overall computational overhead also increases significantly. Unwanted noise is resulted during the process of classification. Hence, it is very much required to select essential cancer patches during the classification process. All of the traditional cancer selection techniques involve a perfect combination of filter and wrapper schemes. Filtering approaches have the responsibility to rank every individual feature according to their goodness. During the process of ranking, the relationship among every individual cancer with respective class label is considered. Univariate scoring metric play a significant role in the above ranking process. The top ranked cancer patches are selected prior to the execution of classification schemes. On the contrary, wrapper schemes require the cancer selection approach in order to integrate with a classifier. The prime objective of this technique is to evaluate the classification performance of every individual cancer subset. The optimal subset of disease patterns is detected according to the ranking of each feature. Traditional filtering schemes are incapable and inefficient to measure the relationship in between different genes. The cancer patches data play significant role during the process of biomedical diagnosis. A medical instance includes a large number of features or characteristics. Large numbers of cancer features are not relevant to the disease of interest. Therefore, the cancer selection procedure is very complicated task during the medical data processing. Feature selection is considered as the most powerful tool in order to decrease the size of available data. In the cancer classification process, feature selection models are generally divided into two types, wrapper approaches and filter approaches. Wrapper approach evaluates search feature or feature subset to optimize the classification accuracy. Filter method evaluates each feature independent from the classification algorithm, ranks the cancer features after evaluation and considers the superior one. This evaluation is performed using information, dependency, distance and consistency. In general, the speed of wrapper model is lower than the filter model because of cross validation and repeated iteration to evaluate the feature subsets. Traditional wrapper model is more efficient because classification technique affects the overall accuracy, although the subset selection is an NP-hard. However, if the number of features involved in complex data increases, finding new disease patterns can become difficult due to the complex relationships among features. Feature ranking methods compute the measure for each feature and rank them accordingly. These ranking methods select the top-k features based on highest rank and eliminate those having lower feature ranks [6]. Information gain is one of the attribute selection measures which are based on entropy value. Good sub-sets of attributes contain class-related and non-related attributes. The method is used to determine how closely the characteristic vectors are linked. When the coefficient of correlation between the two vectors is above "0," the characteristics are said to have a highly positive correlation. Likewise, the functions are said to be negatively correlated if the correlation coefficient between these two characteristic vectors is less than "0." The features are said not to be correlated if the correspondence coefficient of the two characteristic vectors is equal to "0." Chi-Square is based on the analysis of statistics. The functional vector measures the independence. The strength of the relationship between two random variables is tested with observed and anticipated values. Feature descriptors are the pixels behind so that the classification performance is optimized and a sparse representation is given. The descriptors should ideally be invariant to operations like scale, rotation and illumination changes. This invariance enables descriptors to be matched across videos which have differences in these parameters.

Each medical data is scanned and transformed into normalized continuous data. The main issues of the medical datasets are high dimensionality and imbalance nature. Traditional machine learning classifiers consider subset of features for classification and disease prediction with high true negative rate and error rates. Attribute selection is used to compute the measure for each feature and rank them accordingly. These ranking methods select the top-k features based on highest rank and eliminate those having lower feature ranks. Information gain is one of the attribute selection measures which is based on entropy value. Information gain approach is the mutual information of a target random variable say P and independent random variable Q. The main limitation of this approach is, it chooses features having large distinct values over the features having less distinct values. Table summarizes the different attribute selection measures used in decision tree construction for pattern construction. Table 0, describes the comparison of different machine learning approaches for medical imbalance detection on different parameters [7].
Table 0 summarizes the various attribute selection measures used in decision tree construction for medical intrusion detection.

| Measure Name          | Formula                                                                 |
|-----------------------|-------------------------------------------------------------------------|
| Entropy               | $\text{Entropy} = \sum p_i \log_2(p_i)$                               |
| Information Gain      | $\text{Gain} = \sum p_i \log_2(p_i) - \frac{\sum |D_x| \log |D_x|}{|D|}$     |
| Gain Ratio            | $\text{GainRatio} = \text{Gain} / \left( \sum \frac{|D_x|}{|D|} \log \frac{|D_x|}{|D|} \right)$ |
| Pearson Correlation   | $\text{CorrelationFS} = \frac{m_r c - m(m-1) r_i}{\sqrt{m + m(m-1) r_i}}$ |
| Improved Correlation  | $\arg \max \left[ \frac{\text{cov(Vec}(A_{c}, c), \text{Vec}(D))}{\sqrt{\text{var(Vec}(A_{c}, c) + \text{Vec}(D))}} \right]$ |

Lu and Yan et al., proposed an advanced feature reduce based intrusion detection system [8][9]. In this model, a feature ranking measures such as information gain and correlation are used to filter the feature space. After successful completion of the feature ranking, feature reduction approach is implemented. The feature reduction technique is implemented through the integration of ranks generated from the process of information gain and correlation. The reduced features are given as input to feed forward neural medical to train and test the medical features in cancer dataset. In this method, the preprocessing is carried out manually which is a severe drawback of this model. Liu, et al., proposed knowledge-maximized ensemble approach for various kinds of concept drift [10]. In this work, they presented an advanced data stream classifier which is known as knowledge maximized ensemble. Hence, it becomes hard and complicated to restrict the amount of training data. This technique can be influenced by different kinds of concept drift through integration of various imbalance detection approaches. Decision tree induction is a simple and powerful classification process that produces a tree and a set from a specific dataset[11] representing a model for different classes. The choice tree is a tree structure like a flow chart, in which each inner knot is a test on a single attribute, each branch is a test result and every node in the leaf is a class. The root node is the highest node of a tree. ID3 algorithm and Quinlan’s successor C4.5 algorithm are commonly used for DT induction. In classifying unknown data records, the structure is widely applied. At every inner node of the tree, the impurity measures are applied to the best split decision. The tree leaves consist of the class labels of the data items. Two phases are implemented in the decision tree classification technique: tree building and tree pruning. They introduced CART (Classification and Regression Trees). Different statistical measures are used to select the attribute from the list of feature space. For building a decision tree, CART utilizes both numerical and categorical attributes and includes features dealing with missing attributes[12]. In determining the best partition and data is sorted at all the nodes to determine the best fractional point, it uses a large number of single fractional criteria, such as a gini index, gini ratio etc, and one multivariable linear combination.

Class-imbalanced data are common in the domain of data categorization. It generally categorizes many irrelevant documents, but some articles are categorized under interesting category. BN approaches are mostly implemented as standard classifiers. These approaches give rise to exact results along with the capability for representing relationships in between variables. This approach is unable to resolve the traditional class-imbalanced problem [5]. In order to overcome the class-imbalanced problem, many advanced approaches are developed to gain enhanced accuracy rate of standard classification approaches. These generalized classification approaches involve the following schemes—sampling approaches, cost-sensitive approaches, recognition-based methods and active learning approaches. Sampling approaches have been developed in order to resolve the issues due to class imbalance through removing certain data from majority class. This approach is also known as under sampling approach. Sometimes few additional artificially produced data are included into the minority class and this phenomenon is also called as over-sampling. Cost sensitive learning method generally involves cost-matrix for all categories of errors or instances. It has main objective of facilitating learning mechanism out of imbalanced data sets. The above mechanism has equivalent influence on the process of oversampling the minority class. It can end with over specific rules or rules overfitting training [16]. Random under sampling approach involves the process of randomly removing elements of the over-sized class. The above process continues executing till it matches the size of other class and cost-sensitive learning scheme. It includes the modifications of relative cost associated with misclassification of positive and negative class. The outcomes of both methods are analyzed and compared with performance achieved without balancing.

**PROPOSED MODEL**

The overall architecture of the proposed model is represented in fig 1. Initially, each microarray gene disease dataset is filtered to fill the sparsity problem and missing values of the gene featured. Here, a hybrid data transformation approach is used to transform the feature values using the gaussian transformation measure. Each value is normalized to improve the balancing property of each feature and its class. In the initial phase, each feature is transformed using the gaussian transformation process. In the second phase, essential features are extracted using the hybrid PCA approach. Finally, an optimized decision tree classifier is designed to find the essential cancer patterns for prediction process.
Figure 1: Proposed Gaussian filter based feature selection and classification model

Each microarray training dataset is pre-processed using the data transformation function to remove the variation among the data distribution. In the proposed work, a gaussian based data transformation function is used to normalize the input training data for clustering and wrapper feature ranking process in the mapper phase.

**Gaussian based Data Pre-processing**

**Input**: Training microarray dataset D, P(D): Feature space of D.

**Output**: Gaussian Filtering or Transformed data K.D.

**Procedure**:
1. Read input data D.
2. For each feature F[i] in feature space P(D)
3. Do
4. Apply Gaussian transformation on each feature as
5. \[ \text{GeneKernelTransform}(F[i]) = \phi = \left( \sum \left( \frac{F[i]}{\max\{F[i]\}} \right) \right)^{\frac{1}{2}} e^{-\frac{(F[i] - \mu(F[i]))}{\sigma(F[i])}} \]
6. If \( \phi > 0 \)
7. Then
8. Normalize F[i] using Min-max normalization [0, \phi]
9. Else
10. Normalize F[i] using Min-max normalization with [R1,R2]
   \[ x' = \frac{x - \min_-(x)}{\max_-(x) - \min_-(x)} \cdot (R2 - R1) + R1 \]
11. End if
12. Done

Here, gaussian normalization and min-max range normalization are used to improve the data distribution with uncertain values. R1 and R2 represents the minimum and maximum values of each feature. This approach is used to remove the sparsity problem and data normalization problem in high dimensional datasets.
Algorithm: HybridPCA (HPCA):
In the proposed feature ranking model, traditional PCA algorithm is enhanced to find the most essential features in the given feature space.

**Input:** Normalized training data.

**Output:** Ranked features.

**Step 1:** Input Normalized data ND.

**Step 2:** Mean of the normalized data is computed using eq.(1)

\[ \mu_D = \frac{\sum ND[i]}{N} \]  

**Step 3:** Let \( F = \{f[0], f[1], \ldots, f[m]\} \) be the feature space with m features.

Find the candidate features pairs

\[ CF = \{(f[0], f[1]), (f[0], f[2]), (f[0], f[3]), \ldots, (f[m], f[0])\} \]

For m feature space we will get \( \frac{m!}{(m-2)!2!} \) candidate sets.

For each pair of candidate features CF

Do

Compute covariance between features as

\[ \text{Cov}(CF_{x,y}) = \frac{\sum_{i=1}^{n} (CF_{x,i} - \mu_{CF_{x,i}})(CF_{y,i} - \mu_{CF_{y,i}})}{(n-1)} \]  

Done

**Step 4:** Compute the eigen vector and values using the eq.(3) and eq.(4)

\[ \text{EigenValues}[] = \text{Det}(\lambda I - \text{COV}(CF)) = 0 \]  

Here \( I \) is the identity matrix of same dimension as \( \text{COV}(CF) \). The corresponding Eigen vector is given as

\[ (\lambda I - \text{COV}(CF))v = 0 \]  

Here the optimal eigen sum is computed as

\[ \text{OptimalEigenSum} = \sum_{i=1}^{m} \text{EV}[i] \text{MaxProb} \{ \exp(F(\text{EV}[i])), \text{Math.log(C[m])} \} \]  

for m classes

**Step 5:** Finally, features with highest eigen sum values are taken as subset of features for classification problem.

**Proposed Classification Algorithm**

**Step 1:** Partition the given training dataset into ‘m’ classes.

**Step 2:** For each partition

**Step 3:** do

**Step 4:** Apply the decision tree classification feature selection measures one each partition.

Proposed hybrid measure is used to minimize the runtime (ms) and to improve the true positivity and false negative rate on large datasets. Since, network training data have nominal attributes and numerical attributes, proposed measure is used to find the nominal association between the numerical and nominal attributes using the following measures for node selection.

**Hybrid Entropy Measure for Hoeffding Tree Construction**

Let \( ND \) be the normalized selected feature, \( cbrt \) is the cube root, \( \text{chiVal} \) is the chisquare value. The hybrid entropy of the Hoeffding tree is given by

\[ \text{Ent}(D_P) = \frac{\sum_{i=1}^{n} ND[i].\text{log}(ND[i])}{\sqrt{(\sum_{i=1}^{n} (ND[i] - \mu_{ND})^2}}} \]

\[ \text{HCondEntropy}(D_P) = \frac{\text{Math.sqrt(entropyConditional(ND[i]) * total) * n}}{(\text{CramersV}(ND) + \text{chiVal}(ND))} \]

\[ \text{CramersV}(D_P) = \text{Math.sqrt(\text{chiVal}(ND)/(\sum_{i=1}^{n} ND[i] \cdot \text{min \{nrow,ncolumns\}})} \]
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where $m$ represents $m$ classes.

**Proposed Random forest attribute selection measure (RFASM)**

$$\text{Modified Gain} = e^{-n/\sum_{i} \text{entropy(ND)}} + \text{Gain(D)}$$

$$\text{HRTASM} = -n \cdot \frac{\sum_{i} \text{chiVal}(ND)}{\text{entropy(ND)}}$$

**Step 5:** Construct the decision tree using the enhanced attribute selection measure to improve the true positive rate of the classification.

**Step 6:** Apply ensemble learning model on the proposed decision tree and base classifiers.

**EXPERIMENTAL RESULTS**

To evaluate the performance of the proposed model to the existing models, different microarray datasets were selected from the biomedical repository. Different dataset used for experimental evaluation are summarized in Table 1. In the experimental results, 10% of the training data are used as testing data for performance evaluation. Proposed feature selection-based ensemble methods increase the performance of true positive rate and accuracy on entire high dimensional datasets. Proposed model uses the entire training data set for construction of decision patterns; therefore, the prediction accuracy of each cross validation tends to be more accurate than the traditional ensemble classification models. From the experimental results, it is clear that proposed ensemble classification improves the overall true positive and false negative rate. Also, the main advantage of using proposed model is to reduce the error rate on high dimensional features.

From the experimental results, it is clear that proposed ensemble classification improves the overall true positive and false negative rate. Also, the main advantage of using proposed model is to reduce the error rate on high dimensional features.

| Micro array Datasets | Gene sets | Data-Type       |
|----------------------|-----------|-----------------|
| Prostate             | 2136      | Continuous/Numeric |
| Lymphoma             | 5000      | Continuous/Numeric |
| DLBCL- Stanford      | 4000      | Continuous/Numeric |
| Breast cancer        | 24481     | Continuous/Numeric |
| Leukemia             | 7129      | Continuous/Numeric |

Proposed model increase the performance of accuracy and error rate on entire high dimensional microarray datasets. Proposed classification model uses high dimensional data set to generate decision patterns; therefore, the prediction accuracy of each cross validation tends to be more accurate than the traditional ensemble classification models.

**Leukaemia Data Results**

| PROPOSED PATTERNS |
|-------------------|
| -------- |
| AFFX-CreX-5_at <= -202 |
| | AFFX-BioC-5_at <= 88: ALL (3.21) |
| | AFFX-BioC-5_at > 88 |
| | | AFFX-BioC-5_at <= 241: AML (13.5) |
| | | AFFX-BioC-5_at > 241 |
| | | | AFFXBioB_5_st <= -144: AML (2.89) |
| | | | | AFFXBioB_5_st > -144: AML (9.96/1.29) |
| | AFFX-CreX-5_at > -202 |
| | AFFX-BioC-5_at <= 38: AML (8.04/1.29) |
| | AFFX-BioC-5_at > 38 |
| | | AFFXBioB_5_st <= -56: AML (11.25/4.5) |
| | | AFFXBioB_5_st > -56 |
| | | | AFFXBioB_5_st <= 506: ALL (20.25/0.64) |
| | | | | AFFXBioB_5_st > 506: AML (2.89/0.64) |

| Number of Leaves | 8 |
| Size of the tree | 15 |
| Weight: | 2.03 |

| PROPOSED PATTERNS |
|-------------------|
| -------- |
| AFFX-BioC-5_at <= 328 |
| | AFFX-BioDn-5_at <= -246: ALL (58.5/13.27) |
| | AFFX-BioDn-5_at > -246 |
| | | AFFX-BioC-5_at <= 141: AML (5.09) |
**Lung-cancer Michigan**

PROPOSED PATTERNS  
--------------------
AB000114_at <= 91  
|   | AB000220_at <= 616.6: Tumor (24.6)  
|   | AB000220_at > 616.6: Normal (4.09/0.88)  
|   | AB000114_at > 91  
|   | AB000114_at <= 118: Normal (48.33/2.19)  
|   | AB000114_at > 118: Tumor (18.99/3.36)

Number of Leaves: 4

Size of the tree: 7

Weight: 2.64

PROPOSED PATTERNS  
--------------------
AB000114_at <= 91: Tumor (21.44/1.72)  
|   | AB000114_at > 91  
|   |   | AB000460_at <= 942.6  
|   |   |   | AB000449_at <= 99: Tumor (3.9/0.86)  
|   |   |   | AB000449_at > 99  
|   |   |   |   | AB000449_at <= 130.9: Normal (35.18/0.58)  
|   |   |   |   | AB000449_at > 130.9  
|   |   |   |   |   | AB000449_at <= 164.4: Tumor (14.62)  
|   |   |   |   |   | AB000449_at > 164.4: Normal (13.54/0.08)  
|   |   | AB000460_at > 942.6: Tumor (7.32/0.9)

Number of Leaves: 6

Size of the tree: 11

Weight: 3.1

PROPOSED PATTERNS  
--------------------
AB000409_at <= 502.8  
|   | AB000220_at <= 702.8  
|   |   | AB000409_at <= 236.6: Tumor (3.83)  
|   |   | AB000409_at > 236.6: Tumor (23.66)  
|   |   | AB000449_at <= 151.9: Normal (64.06/5.67)  
|   |   | AB000449_at > 151.9: Tumor (3.43/0.48)  
|   | AB000220_at > 702.8  
|   |   | AB000114_at <= 228.3: Tumor (9.61)  
|   |   | AB000114_at > 228.3: Normal (6.56)  
| AB000409_at > 502.8: Tumor (8.51)

Number of Leaves: 6

Size of the tree: 11

Weight: 2.68

PROPOSED PATTERNS  
--------------------
AB000449_at <= 151.5  
|   | AB000409_at <= 248.7: Normal (12.32/1.35)  
|   | AB000409_at > 248.7  
|   |   | AB000220_at <= 523.9: Tumor (38.9/0.51)  
|   |   | AB000220_at > 523.9  
|   |   |   | AB000220_at <= 702.8  
|   |   |   | AB000409_at <= 371.9: Tumor (3.99)  

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|   | AFFX-BioC-5_at > 141: ALL (3.82/1.27)  
|   | AFFX-BioC-5_at > 328: AML (4.59)  

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|   |   | AB000409_at > 371.9 |
|   |   | AB000114_at <= 54.1: Tumor (2.22) |
|   |   | AB000114_at > 54.1: Normal (14.71/0.32) |
|   |   | AB000220_at > 702.8: Tumor (8.43) |
| AB000449_at > 151.5: Normal (15.43/2.86) |

Number of Leaves : 7
Size of the tree : 13
Weight: 2.89

PROPOSED PATTERNS

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| AB000409_at <= 236.6: Tumor (19.46) |
| AB000409_at > 236.6 |
|   AB000460_at <= 578.8 |
|   | AB000114_at <= 53.4: Tumor (2.06) |
|   | AB000114_at > 53.4: Normal (10.72/0.22) |
|   AB000460_at > 578.8 |
|   | AB000449_at <= 118: Tumor (18.67) |
|   | AB000449_at > 118 |
|   | AB000449_at <= 132.2: Normal (9.76/1.99) |
|   | AB000449_at > 132.2 |
|   | AB000449_at <= 599.3: Normal (2.81) |
|   | AB000449_at > 599.3 |
|   | AB000449_at <= 178.3: Tumor (17.65) |
|   | AB000449_at > 178.3 |
|   | AB000449_at <= 188.1: Normal (5.27/1.45) |
|   | AB000449_at > 188.1: Tumor (9.6) |

Number of Leaves : 9
Size of the tree : 17
Average Classification Accuracy : 0.972
Average TP Rate : 0.969
Average Recall : 0.972
Mean Absolute Error : 0.047
Average Runtime of Each partition :2932.13

Table 2: Comparative analysis of present approach to the traditional approaches by using accuracy on different Microarray dataset.

| Model                      | DLBCL | Prostate | Lymphoma | BreastCancer |
|----------------------------|-------|----------|----------|--------------|
| PCA+Ensemble               | 87.45 | 91.43    | 90.54    | 85.35        |
| ACO+Ensemble               | 86.35 | 89.13    | 91.33    | 82.54        |
| Fuzzy PCA+Ensemble         | 83.24 | 87.34    | 89.23    | 84.67        |
| KM+SNR+Ensemble            | 94.65 | 91.43    | 92.53    | 86.75        |
| KM+t-test+Ensemble         | 95.74 | 94.64    | 95.09    | 87.14        |
| KM+SAM+Ensemble            | 91.53 | 89.13    | 87.45    | 91.43        |
| Gaussian based Deep neural network | 98.93 | 96.35 | 97.14 | 94.92 |
| Proposed Model             | 99.23 | 98.45    | 98.71    | 97.93        |

Table 2, describes the performance of the proposed model on all cancer datasets. Here, all the cancer datasets are evaluated using the proposed model to find the average true positive rate and precision rate on the high dimensional datasets. From the table, it is visualized that the present approach has better true positive rate and precision over the existing models.
Table 3: Gene-Disease features extraction using the proposed PCA model on 2000 test instances

| GeneSamples | Chisquare | MI  | IG  | GA  | PCA | ProposedPCA |
|-------------|-----------|-----|-----|-----|-----|-------------|
| GeneDis-50  | 63        | 65  | 63  | 62  | 66  | 45          |
| GeneDis-100 | 63        | 67  | 62  | 67  | 67  | 52          |
| GeneDis-150 | 65        | 65  | 60  | 64  | 60  | 45          |
| GeneDis-200 | 65        | 61  | 60  | 63  | 64  | 53          |
| GeneDis-250 | 61        | 63  | 65  | 68  | 65  | 38          |
| GeneDis-300 | 59        | 61  | 62  | 66  | 65  | 47          |
| GeneDis-350 | 68        | 65  | 60  | 60  | 60  | 48          |
| GeneDis-400 | 64        | 59  | 66  | 60  | 58  | 52          |
| GeneDis-450 | 59        | 65  | 64  | 60  | 59  | 49          |
| GeneDis-500 | 60        | 64  | 58  | 64  | 64  | 40          |
| GeneDis-550 | 61        | 60  | 62  | 64  | 63  | 37          |
| GeneDis-600 | 62        | 67  | 66  | 58  | 62  | 43          |
| GeneDis-650 | 59        | 65  | 63  | 63  | 62  | 41          |
| GeneDis-700 | 60        | 64  | 61  | 59  | 64  | 50          |
| GeneDis-750 | 64        | 67  | 65  | 64  | 66  | 39          |
| GeneDis-800 | 67        | 61  | 67  | 60  | 59  | 37          |
| GeneDis-850 | 59        | 63  | 63  | 65  | 61  | 48          |
| GeneDis-900 | 63        | 64  | 64  | 58  | 60  | 42          |
| GeneDis-950 | 60        | 62  | 61  | 64  | 59  | 50          |
| GeneDis-1000| 62        | 65  | 68  | 64  | 58  | 47          |

Table 3 illustrates the performance of gene-disease feature extraction using the proposed PCA approach on large datasets. From the table, it is clearly shown that the present feature extraction procedure has high filtering rate as compared to the existing approaches.

Table 4: Performance analysis of computational runtime(ms) with different traditional feature selection models

| GeneSamples | Chisquare | MI  | IG  | GA  | PCA | ProposedPCA |
|-------------|-----------|-----|-----|-----|-----|-------------|
| GeneDis-50  | 6658      | 5180| 5153| 6639| 7122| 6511        |
| GeneDis-100 | 5249      | 6220| 7146| 7035| 5392| 7279        |
| GeneDis-150 | 5739      | 6731| 6140| 6861| 6886| 6564        |
| GeneDis-200 | 6869      | 6729| 6010| 6750| 5545| 5973        |
| GeneDis-250 | 5377      | 6886| 6989| 7088| 5154| 6146        |
| GeneDis-300 | 6710      | 5935| 7350| 6345| 7307| 6179        |
| GeneDis-350 | 6708      | 6136| 6805| 7383| 5310| 5904        |
| GeneDis-400 | 6377      | 5462| 5879| 6262| 6900| 5597        |
| GeneDis-450 | 7119      | 6227| 6161| 5699| 6386| 5406        |
| GeneDis-500 | 6151      | 6522| 5643| 6736| 6942| 5219        |
| GeneDis-550 | 7071      | 6287| 5701| 5734| 5872| 5138        |
| GeneDis-600 | 6996      | 6607| 6688| 6952| 5325| 5915        |
| GeneDis-650 | 5344      | 6132| 7086| 7151| 5502| 5559        |
| GeneDis-700 | 5185      | 5369| 6178| 5468| 6126| 6410        |
| GeneDis-750 | 6148      | 6317| 6482| 5613| 6011| 7137        |
| GeneDis-800 | 6020      | 5046| 6739| 5660| 5406| 5294        |
| GeneDis-850 | 6654      | 5173| 6042| 5532| 6210| 5355        |
| GeneDis-900 | 6508      | 5717| 5706| 5775| 5970| 6828        |
| GeneDis-950 | 6568      | 6470| 5600| 6005| 6357| 5680        |
| GeneDis-1000| 6700      | 7251| 6893| 5744| 5407| 7199        |
Table 4, describes the performance of computational runtime(ms) of gene-disease feature extraction using the proposed PCA approach on large datasets. From the table 3, it is clearly shown that the present feature extraction procedure has low computation runtime as compared to the existing approaches.

Recall

| Gene Cancer Samples | SVM  | RF  | NN  | CNN | Proposed Classifier |
|---------------------|------|-----|-----|-----|---------------------|
| GeneDis50           | 0.8  | 0.82| 0.87| 0.93| 0.98               |
| GeneDis100          | 0.78 | 0.83| 0.87| 0.94| 0.98               |
| GeneDis150          | 0.81 | 0.82| 0.88| 0.94| 0.98               |
| GeneDis200          | 0.79 | 0.83| 0.86| 0.93| 0.97               |
| GeneDis250          | 0.82 | 0.84| 0.86| 0.93| 0.97               |
| GeneDis300          | 0.78 | 0.84| 0.87| 0.93| 0.98               |
| GeneDis350          | 0.82 | 0.84| 0.87| 0.93| 0.98               |
| GeneDis400          | 0.82 | 0.83| 0.86| 0.92| 0.98               |
| GeneDis450          | 0.82 | 0.83| 0.87| 0.93| 0.98               |
| GeneDis500          | 0.81 | 0.84| 0.87| 0.94| 0.97               |
| GeneDis550          | 0.81 | 0.82| 0.87| 0.94| 0.98               |
| GeneDis600          | 0.8  | 0.82| 0.86| 0.94| 0.98               |
| GeneDis650          | 0.79 | 0.83| 0.87| 0.92| 0.98               |
| GeneDis700          | 0.8  | 0.83| 0.85| 0.94| 0.98               |
| GeneDis750          | 0.8  | 0.84| 0.86| 0.92| 0.98               |
| GeneDis800          | 0.81 | 0.83| 0.87| 0.95| 0.97               |
| GeneDis850          | 0.78 | 0.82| 0.88| 0.93| 0.98               |
| GeneDis900          | 0.8  | 0.84| 0.85| 0.93| 0.98               |
| GeneDis950          | 0.8  | 0.83| 0.87| 0.93| 0.98               |
| GeneDis1000         | 0.81 | 0.83| 0.87| 0.93| 0.98               |

Table 4, describes the performance of recall of gene-disease classification using the proposed classification framework on large datasets. From the table 4, it is clearly shown that the present framework has high computational recall as compared to the existing frameworks.

Accuracy

| Gene Cancer Samples | SVM  | RF  | NN  | CNN | Proposed Classifier |
|---------------------|------|-----|-----|-----|---------------------|
| GeneDis50           | 0.81 | 0.84| 0.87| 0.95| 0.98               |
| GeneDis100          | 0.78 | 0.83| 0.87| 0.93| 0.98               |
| GeneDis150          | 0.8  | 0.84| 0.86| 0.93| 0.98               |
| GeneDis200          | 0.79 | 0.83| 0.87| 0.92| 0.98               |
| GeneDis250          | 0.8  | 0.82| 0.86| 0.94| 0.97               |
| GeneDis300          | 0.78 | 0.83| 0.87| 0.93| 0.97               |
| GeneDis350          | 0.81 | 0.82| 0.86| 0.92| 0.98               |
| GeneDis400          | 0.81 | 0.83| 0.87| 0.94| 0.98               |
| GeneDis450          | 0.8  | 0.83| 0.88| 0.92| 0.99               |
| GeneDis500          | 0.81 | 0.83| 0.88| 0.92| 0.98               |
| GeneDis550          | 0.8  | 0.84| 0.87| 0.94| 0.97               |
| GeneDis600          | 0.79 | 0.82| 0.85| 0.93| 0.99               |
| GeneDis650          | 0.82 | 0.83| 0.88| 0.95| 0.98               |
| GeneDis700          | 0.82 | 0.83| 0.86| 0.93| 0.98               |
| GeneDis750          | 0.82 | 0.83| 0.87| 0.93| 0.98               |
| GeneDis800          | 0.81 | 0.83| 0.86| 0.93| 0.98               |
Table 5, describes the performance of accuracy of gene-disease classification using the proposed classification frameworks on large datasets. From the table, it is clearly shown that the present framework has high computational accuracy as compared to the existing frameworks.

CONCLUSION

Ensemble classification algorithm with weighted function is used to find the essential feature sets from the large number of feature space. Since, the weights in the deep neural network is optimized using the weighted function and the logistic function, proposed model efficiently classifies the large data with high dimensionality. Most of the traditional feature transformation approaches such as log transformation, min-max normalization etc. are independent of data distribution and outliers. Traditional PSO based ensemble learning and ABC based ensemble learning are improved using the heuristic activation function and ensemble classification measures. To solve these problems effectively, it is therefore essential to develop an algorithm that can identify reliable candidates for disease using existing associations of gene-disease verified by the biological experiment. In the proposed work, a hybrid feature transformation, hybrid feature selection and advance classification approach are implemented to improve the true positive rate and error rate of the disease prediction. A novel principal component ranking measure is integrated in order to find the subset of features for classification problem. Finally, a hybrid decision tree classifier is used to predict the classification accuracy on the selected features set. Experimental results proved that the present framework has better performance compared to the traditional models for variable microarray datasets.

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| GeneDis850 | 0.82 | 0.83 | 0.85 | 0.94 | 0.98 |
| GeneDis900 | 0.81 | 0.84 | 0.86 | 0.95 | 0.98 |
| GeneDis950 | 0.80 | 0.82 | 0.88 | 0.92 | 0.98 |
| GeneDis1000 | 0.81 | 0.83 | 0.87 | 0.92 | 0.98 |