

Microarray Gene Expression Data Classification using a Hybrid Algorithm: MRMRAGA



Rabindra Kumar Singh, M. Sivabalakrishnan

Abstract: In the field of microarray gene expression research, the high dimension of the features with a comparatively small sample size of these data became necessary for the development of a robust and efficient feature selection method in order to perform classification task more precisely on gene expression data. We propose the hybrid feature selection (mRMRAGA) approach in this paper, which combines the minimum redundancy and maximum relevance (mRMR) with the adaptive genetic algorithm (AGA). The mRMR method is frequently used to identify the characteristics more accurately for gene and its phenotypes. Then their relevance is narrowed down which is described in pairing with its relevant feature selection. This approach is known as Minimum Redundancy and Maximum Relevance. The Genetic Algorithm (GA) has been propelled with the procedure of natural selection and it is based on heuristic search method. And the adaptive genetic algorithm is improvised one which gives better performance. We have conducted an experiment on four benchmarked dataset using our proposed approach and then classified using four well-known classification approaches. The accuracy was measured and observed that it gives better performance compared to the other conventional feature selection methods.

Index Terms: Feature selection, classification, mRMR, AGA, hybrid feature selection

I. INTRODUCTION

The microarray technology has become a benchmark technique for prognosis and diagnosis of cancer. Prognosis and diagnosis of cancer is nothing but a classification of microarray dataset [1, 2]. The microarray dataset (gene expression dataset) contains information about the way genes are expressed. It has become possible to locate altered genes by means of analyzing these data. Hence better diagnosis and classification can be facilitated to medical science for the gene-related disease. Accordingly, cost-effective and efficient analysis can be performed by a biologist on the altered genes with few selected genes [3]. Still, the prediction and classification for the types of cancer remain a great challenge for medical science.

Profiles of gene expression data become very important for this purpose. However, due to the presence of small sample size in comparison to a large number of features (genes), many computational approaches used to fail in order to identify small important subset from microarray data. This eventually makes more challenging for microarray data

analysis [4]. Moreover, normally microarray data contain irrelevant features (genes) and redundant data. Hence, there will be a considerable increase in computational complexity [5]. Actually, when we build a better predictor model then these redundant features do not contribute since this information is basically already available with other feature(s) [6]. $N \times M$ matrix shown in Figure 1 is an example of microarray dataset. Where N represents the samples number, M represents the genes number and $\{l_i | i = 1, 2, \dots, N\}$ is the class labels.

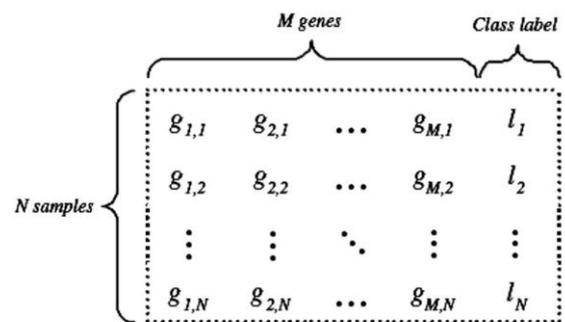


Figure 1: $N \times M$ microarray dataset

It is a well-known fact that redundant feature will have an adverse effect on the performance of the classification model therefore, it is necessary to reduce feature in order to get good performance using feature selection approach. The main aim of the feature selection is to identify the subset of important features. This is very essential and has been recognized as one of the focused areas in bioinformatics and machine learning [7]. There are three main methods have been used in the area of feature selection, which is categorized as filter-based, wrapper-based and hybrid-based [8]. All these mentioned approaches have been classified depending on their used criterion in the learning algorithm. The filter selection approach used to select features irrespective of the classifier model used. In this method, the feature(s) used to be selected which are of least interest and suppressed. The remaining feature(s) will be used for the classification by classification or regression model [9]. Since the filter method is not used in order to build classifier [10], the performance of the predictor will not be up to mark, if the learning algorithm considers the results of the filter directly. Taking into the consideration data are distributed and filters are categorized in two namely parametric and non-parametric approaches [11]. A parametric filter is based on the identical distribution of samples among different classes, such as chi-squared, Bayesian and ANOVA [12]. However, the assumption made in parametric cannot be assured in all datasets.

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Hence, a non-parametric approach may be a suitable option when dataset distribution is uncertain. Information gain, Relief-F, Gain ratio, and Pearson Correlation coefficient are the examples of non-parametric filters. Correlation Coefficient (PCC) is used to determine the relationships among the features in order to find the relation among classes. The evaluation on the subset of features is performed in a wrapper-based approach, by doing so the possible relation between the features can be detected. Wrapper method used to choose the subset of variables which gives the best accuracy for the model. Less number of variables is selected with the discriminative approach in this method [13]. We also know that the wrapper-based methods are classifier dependent and therefore the same performance may not be obtained if another classifier is used [10, 14]. Moreover, the overall performance of this approach is not upto the mark and also if they are directly utilized then there is a chance of overfitting on the data without pre-processing is performed [15].

Maximum Relevance and Minimum Redundancy (mRMR) has been designed for microarray dataset feature selection [16]. It is a special type of feature selection method which works based on filter approach tends to select uncorrelated high predictive features. In this approach subset of features are selected having a high correlation with a class (relevance) with the minimum correlation among themselves (redundancy). Here, the features used to get ranked as per the maximum-relevance-minimum-redundancy criteria in this algorithm. The relevance of the features is calculated with the use of F-statistic and mutual information for continuous and discrete features simultaneously. The feature's redundancy is computed with the use of the Pearson correlation coefficient (PCC) and mutual information for continuous and discrete features simultaneously. MIFS-ND algorithm has been proposed in [17], wherein features are selected based on the maximum-relevance-minimum-redundancy criteria. Here an optimization algorithm has been utilized which is known as No-dominated Sorting Genetic Algorithm-II [18]. Here authors have used domination count for the rank of calculated relevance and dominant count for the rank of calculated redundancy, and then both of them have been arranged in the sorted form [19], then one representative gene was selected from each group in such a way that selected genes are jointly distinct. Before using this approach, features have to be clustered on the basis of domain knowledge or correlation (e.g., gene ontology, molecular function, etc.). Redundant feature selection can be prevented by the clustering of genes by this algorithm.

Genetic Algorithm (GA) has been known as a stochastic optimization technique which works based on population. This is propelled with the procedure of natural selection and basic genetic concepts [20]. There are operations has been carried out i.e. crossover and mutation in genetic algorithm. Here the crossover and mutation probability is represented by P_c and P_m respectively. This algorithm has two common problems i.e. premature convergence or non-convergent. This may result because of inappropriate fixing the value of P_c and P_m . The Crossover probability (P_c) and mutation probability (P_m) values can be adjusted to improve the conventional GA, which is known as the Adaptive Genetic Algorithm (AGA). The robustness of the AGP is proven because of the adaptability capacity and hence, improves the likelihood in order to find the global optima solution. Combing two or more well-proven algorithm is known as a

hybrid approach in order to design a new method to solve a problem. The hybrid algorithm is normally built on the benefits of the existing approaches and hence becomes more robust than the traditional approach. Hybrid feature selection approach has been proposed here combing the mRMR and AGP in order to achieve minimum redundancy and maximum relevance among the features of the microarray dataset. We have demonstrated the efficiency of the proposed mRMRAGA feature selection approach using the comparison of the classification accuracy with other existing methods. We have applied three well-known classifiers on the four benchmarked datasets in order to test the accuracy of the proposed method. And we have found that our classification accuracy is comparable with the existing one.

II. MATERIALS AND METHODS

A. System Architecture

The system architecture is illustrated in Figure 2. In our system input data are microarray gene expression data. First data are normalized and preprocessed in order to take care of noise and inconsistency. After that feature selection is performed using correlation coefficient methods are used in order to find the dependency of features i.e. genes. Then we mRMR feature selection method for considering the important features, subsequently, we used AGA algorithm to optimize the result. Finally, different classifiers are used and efficiency and effectiveness are measured.

We divided the system into three parts

Feature selection by mRMR

Optimization by AGA

Classification

The detailed explanation will follow in below subsection

B. Relevance and redundancy for mutual information

In gene expression data analysis finding the features which are most relevant is very important. Identification of features (genes) w. r. t. the class labels that contain maximum information is the main goal of the feature selection procedure.

Feature entropy is an ideal metric in order to identify these features (genes). The entropy is nothing but the early improbability of the resulting class [21]. Equation 1 describes the entropy as below:

$$H(X) = \sum_{x=1}^{N_x} P_x(x) \log(P_x(x)) \quad (1)$$

Where, $\{P_x(x) \mid x = 1, 2, \dots, N_x\}$ is the class probabilities. Then, the conditional entropy for the feature vector is computed as average uncertainty, that has been shown in Equation 2 as below:

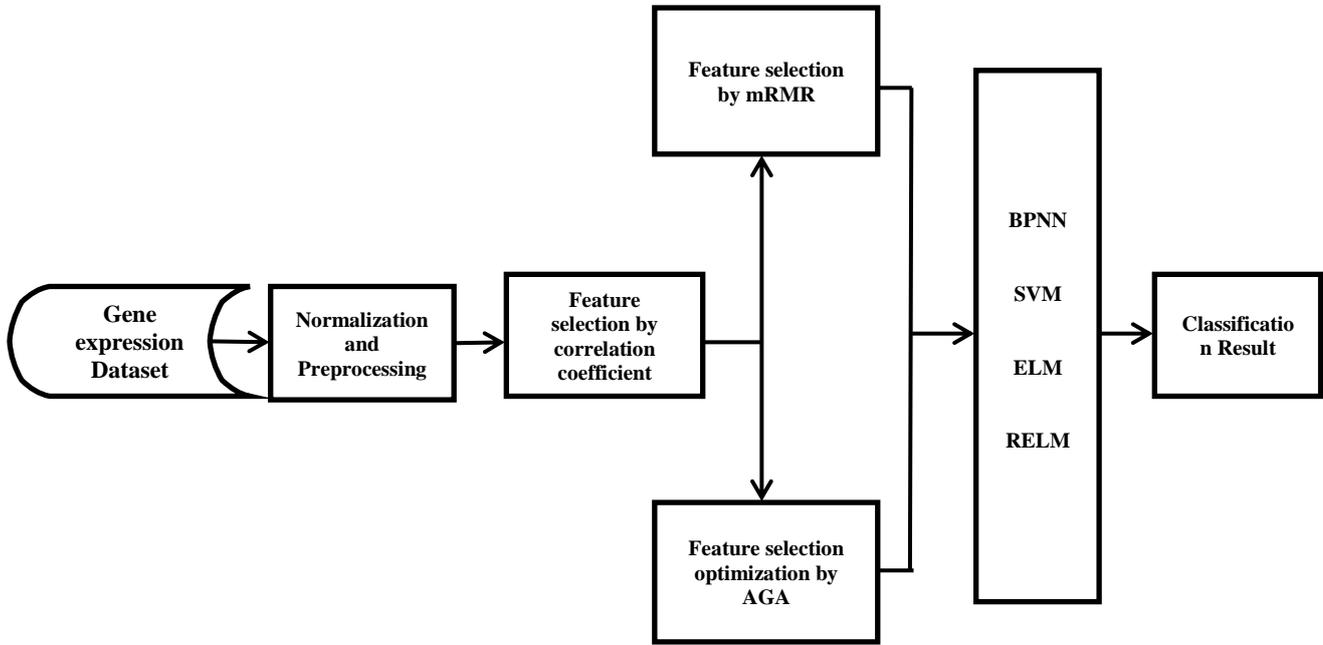


Figure 2: System Architecture

$$H(X|S) = \sum_{s=1}^{N_s} P(s) \left(\sum_{x=1}^{N_x} P_x(x|s) \log(P_x(x|s)) \right) \quad (2)$$

Here, s is known as input feature vector with N_s samples number. $P_x(x|s)$ is known as the conditional probability of class x . Normally, the value of conditional entropy should be \leq initial entropy. If conditional entropy value becomes equal to initial entropy then we can conclude that features are independent of the classes. Therefore, the amount of uncertainty reduced is known as mutual information [21, 22]. $I(X; S)$ the mutual information varies among x and s which is described as below:

$$I(X; S) = H(X) - H(X|S) \quad (3)$$

Equation 3 can be re-written as:

$$I(X; S) = I(S; X) = \sum P(x, s) \log \frac{P(x, s)}{P(x)P(s)} \quad (4)$$

Since the mutual information function is symmetric w. r. t. S and X , therefore $I(S; X) = I(X; S)$.

C. mRMR method:

A well-known feature selection method minimum redundancy and maximum relevance (mRMR) with MID (mutual information difference) and MIQ (mutual information quotient) [23] are defined in this section. The genes have different expression in two or more classes significantly are known as differentially expressed genes. The levels of differential expression of genes are termed as the relevance of genes. With the help of mutual expression, the relevance of genes can be determined. When the expression of the genes has a uniform distribution of the subset among the different classes then their mutual information is zero with these classes. But when genes

differential expression is strongly related to classes, then their mutual information is high. We have considered a discrete variable for mutual information calculation in our study. The mutual information (I) for discrete data having 2 variables S and X is shown in Equation (4). Principle of minimizing the redundancy is nothing but to select features (genes) in such a way that their mutual information is having maximum dissimilarity w. r. t. other genes. Here, s is referred to as the subset of genes which we like to find. In Equation (5) the average minimum redundancy is described:

$$MinimumW = \frac{1}{|S|^2} \sum I(i, j) \quad (5)$$

Where,

Mutual information is represented as $I(i, j)$ between the i th and j th feature (gene) and a number of features (genes) in subset S is $|s|$. Mutual information technique is used in order to select the gene which is differentially expressed. The discriminant controls of genes are computed with the help of mutual information $I(h, g_i)$ as described in Equation (6). The relevance of gene is measured as the mutual information between target class (h_1, h_2, \dots, h_k) and gene expression (g_i). Hence, maximizing the average relevance is nothing but the maximum relevance for all genes in subset s that is defined in Equation (6) as below:

$$MinimumV = \frac{1}{|S|^2} \sum_{i \in S} I(h, i) \quad (6)$$

Thus, it has become necessary that the gene redundancy should be minimized and the gene's relevance should be maximized. It means that these two conditions are not apart perhaps they are combined and formed single criteria in mRMR. Though these two criteria are equally significant. Therefore we have two simple combined criteria which are defined as: $Max(V/M)$, $Max(V - W)$.



At this moment mRMR has been described for discrete data which is in the form of mRMRMID and mRMRMIQ. The mRMRMID (mutual information difference) and mRMRMIQ (mutual information quotient) are formulated as shown in equation (7) and (8) respectively.

$$mRMR_{MID} = \max_{i \in \Omega_s} \left[I(i, h) - \frac{1}{|S|} \sum_{j \in S} i(i, j) \right] \quad (7)$$

$$mRMR_{MIQ} = \max_{i \in \Omega_s} \left\{ I(i, h) / \left[\frac{1}{|S|} \sum_{j \in S} i(i, j) \right] \right\} \quad (8)$$

Algorithm for mRMR is defined as follows:

Algorithm 1: Feature selection with mRMR

Input: n – number of features to be selected, d - discretized data, g - number of features in d, c - class,.

Output: F - feature set.

- Step 1: *idle ft* ← [1 :g]
 Step 2: repeat **for** *i* ← 1 to *g*
 Step 3: *relevance(i)* ← *mutualinfo(d(:, i), c)*;
 Step 4: [R, *id*] ← *Max(relevance)*;
 Step 5: *F[1]* ← *id*;
 Step 6: *idle ft* ← *idle ft* - *F*;
 Step 7: repeat **for** *i* ← 2 to *ndo*
 Step 8: *obj1* ← *relevance(idle ft)*;
 Step 9: repeat **for** *j* ← 1 to |*idle ft*| **do**
 Step 10: *sum* ← $\sum_{k=1}^F (\text{mutual} - \text{info}(d(:, k), d(:, \text{idle ft})))$
 Step 11: *redun(j)* ← *sum* / |*F*|;
 Step 12: **end for** (step 9)
 Step 13: *obj2* ← *relevance(idle ft) / (redun + 0.0001)*;
 Step 14: [*newid*, *obj2*]
 ← *Nondominated-FeatureSelection(obj1, obj2, idle ft)*;
 Step 15: [R, *id*] ← *Max(obj2)*;
 Step 16: *F[i]* ← *id*;
 Step 17: *idle ft* ← *idle ft* - *F*;
 Step 18: **end for** (step 7)

D. Adaptive genetic algorithm

Normally, the Genetic Algorithm (GA) has two critical operations which are known as crossover and mutation. The new individuals are generated with the help of crossover globally and the new individuals are generated with the help of mutation locally. The GA has been granted with global and local search because of these two operations. The GA convergence in order to determine the optimal solution is determined by the probability of crossover (P_c) and the probability of mutation (P_m). P_c and P_m are predefined fixed variables in any standard GA. If P_c is too high then the optimal solution will miss out because of the granular global search. And if P_c happens to be very small, then searching will be lost with local minima. But if P_m happens to be very large, then there is no difference between GA and random search. And if P_m is very small, then the exploratory ability of searching will be suppressed. Therefore, multiple cross-validations are necessary in order to achieve an appropriate value of P_c and P_m . If GA is allowed to adjust P_c

and P_m value throughout the searching space, that can be a more suitable approach. This approach is known as AGA (adaptive genetic algorithm). P_c and P_m values are adjusted as per the given formula 9 and 10.

$$P_c = \begin{cases} K_1 \frac{(f_{max} - f')}{(f_{max} - f_{avg})}, & f' \geq f_{avg} \\ K_2, & f' < f_{avg} \end{cases} \quad (9)$$

$$P_m = \begin{cases} K_3 \frac{(f_{max} - f)}{(f_{max} - f_{avg})}, & f \geq f_{avg} \\ K_4, & f < f_{avg} \end{cases} \quad (10)$$

Where,

f_{max} is a maximum fitness of all individuals, f_{avg} is the average fitness, f' is the bigger parents fitness in chromosome crossover [24]. There are four control variables k_1, k_2, k_3 and k_4 which ranged between (0, 1). The optimization process of AGA is shown in figure 3 and has been explained subsequently.

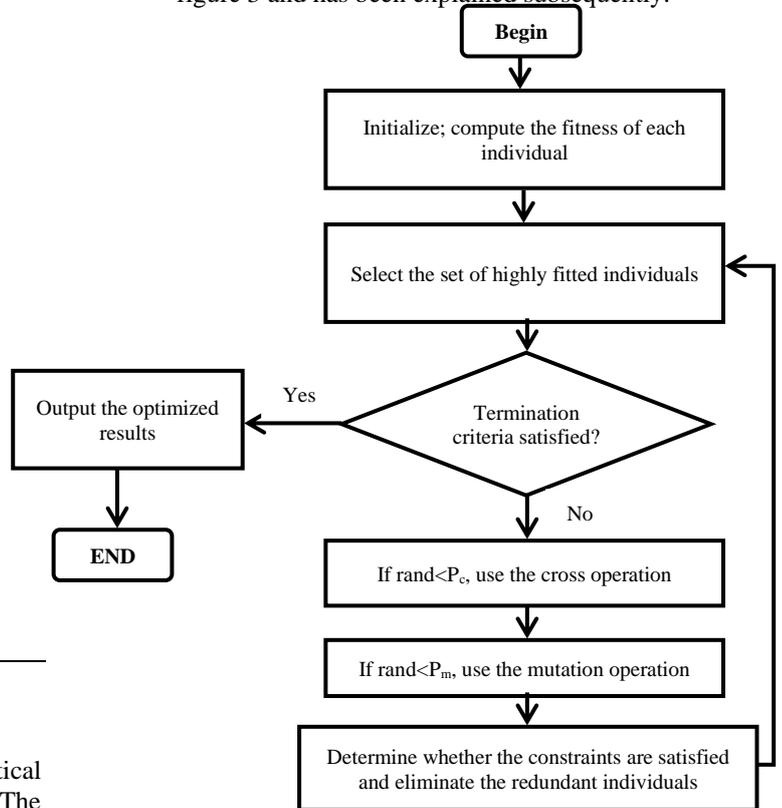


Figure 3: AGA Optimization Process

E. mRMRAGA selection

We propose a gene selection approach with after mRMR and AGA, named as mRMRAGA – selection. The AGA fitness has been set to ELM’s classification accuracy with the use of ELM (extreme learning machine) as a classifier. We have set the value of K_1, K_2, K_3 , and K_4 as 0.9, 0.6, 0.1 and 0.001 respectively, and the number of maximum iteration = 600 in formula (9) and (10).

Assume that A is gene expression dataset that contains samples a1 and genes a2.

The mRMRAGA-selection approach is elaborated as below:

- i. Mutual information is computed for all genes of dataset A. The subset B of A is obtained by applying mRMR multiple times. Let the B feature number is 300.
- ii. AGA population is initialized, and for all individuals, fitness is computed. As per the problem space, the population size is determined. If the size is large, the AGA search will be easier for an optimal solution but will consume a long time. Here, the population size $M=30$. Each individual contains many features of B, and the sample size of each gene is equal to a1.
- iii. 30 individuals are encoded in a population by using binary coding. After that, each individual resembles a chromosome having a length of 300.
- iv. All fitness values are computed for f_{avg}, f_{max}, f' .
- v. By setting a threshold, chose a set of individuals who are highly fitted.
- vi. In step (5) the individuals are paired randomly, with the use of cross over operation as per the P_c value for generating a new population.
- vii. In order to generate a new population, mutation operation is used as per the P_m value.
- viii. Check if the value of current optimal fitness or termination criteria is met. When true, go to step (9); else, go to step (4).
- ix. The gene's optimal subsets are obtained as per the decoding rules.

III. EXPERIMENTS

In this section we emphasis on the experimental verification of the proposed methods. We have chosen the four most frequently used benchmarked datasets. The descriptions of datasets are presented in section 3.1. Experimental settings and other items are described in the subsequent section.

A. Datasets

We have selected four benchmarked gene expression microarray datasets, in order to conduct extensive experiments. All of them are widely used by many researchers in this field and available online. They are Breast cancer, Lung cancer, Lymphoma cancer and Small-round-blue-cell tumor (SRBCT) which are shown in table 1. Breast and Lung datasets have been achieved from [25]. Breast cancer dataset contains samples of 97 patients. In this dataset, there are 24481 features and two class labels (46 – normal and 51-tumour). Lung cancer datasets contain samples of 181 patients. In this dataset, there are 12533 features and 5 class labels (139-AD, 17-NL, 6-SMCL, 21-SQ and 20- COID). Where AD represents adenocarcinoma, NL represents normal lung, SMCL represents small cell lung cancer, SQ represents squamous cell carcinoma and COID represents pulmonary carcinoid. Lymphoma microarray dataset has been obtained from [26]. This dataset contains 4026 features and 62 samples. These samples are from 3 different adult lymphoid malignancies (42- DLBCL, 9-FL, and 11-CLL). Where DLBCL represents the diffuse large

B-cell lymphoma, FL represents Follicular Lymphoma and CLL represents Chronic Lymphocytic Leukemia. SRBCT dataset was obtained from [27]. This dataset contains 2308 features and 63 samples. These samples belong to 4 classes (23 - EWS, 8- NHL, 12- NB and 20- RMS).

Table 1: The characteristics of the four utilized datasets

S.No	Datasets	No of Features	No of Samples	No of Classes
1	Breast	24481	97	2(46- 51)
2	Lung	12600	203	5(139-17-6-21-20)
3	Lymphoma	4026	62	3(42-9-11)
4	SRBCT	2308	63	4(23-8-12-20)

B. Classifiers

In this paper, well-known four classifiers are deployed. The reason for choosing these classifiers is because any specific approach does not work perfectly on all datasets and at the same time, all the classifiers do not work on the same way on a dataset. Here, the deployed classifiers are support vector machine (SVM), back propagation neural network (BPNN), regularized extreme learning machine (RELM) and extreme learning machine (ELM).

IV. RESULTS

Use either SI (MKS) or CGS as primary units. (SI units are strongly encouraged.) English units may be used as secondary units (in parentheses). **This applies to papers in data storage.** For example, write “15 Gb/cm² (100 Gb/in²).” An exception is when English units are used as identifiers in trade, such as “3½ in a disk drive.” Avoid combining SI and CGS units, such as current in amperes and magnetic field in oersteds. This often leads to confusion because equations do not balance dimensionally. If you must use mixed units, clearly state the units for each quantity in an equation.

The SI unit for magnetic field strength H is A/m. However, if you wish to use units of T, either refer to magnetic flux density B or magnetic field strength symbolized as $\mu_0 H$. Use the center dot to separate compound units, e.g., “A·m².”

We have performed mRMRAGA-selection 10 times for each of the four chosen microarray datasets with a number of selected genes (different target genes). Table 2 demonstrates the results.

Table 2 The number of genes with the application of mRMRAGA selection to the four microarray datasets

Dataset	Number of genes									
	1	2	3	4	5	6	7	8	9	10
Breast	6	23	59	80	125	140	158	168	216	220
Lung	3	42	74	89	122	151	170	186	216	220
Lymphoma	22	28	90	105	120	150	175	203	210	215
SRBCT	27	31	77	96	114	146	168	195	208	215

The accuracy rates of classification are demonstrated in table 3 for each subset of the dataset using ELM. This classification accuracy has been obtained after finding an average result of the classification process after repeating 30 times.

Table 3 mRMRAGA-Selection and ELM classification accuracy rates.

Dataset	Classification accuracy rates %									
	1	2	3	4	5	6	7	8	9	10
Breast	82.47	84.32	87.19	85.12	84.39	86.73	92.31	94.37	95.21	95.55
Lung	97.80	92.00	93.57	92.78	94.43	94.89	93.22	93.33	94.67	95.00
Lymphoma	95.34	94.80	94.00	92.88	92.00	91.50	90.00	89.32	88.50	88.24
SRBCT	94.66	95.80	90.11	89.09	86.36	87.16	88.07	88.98	88.64	88.52

We have used three existing feature selection approach in order to demonstrate the effectiveness of the mRMRAGA-Selection approach. These algorithms are mRMR, SFS (sequential forward selection) and ReliefF for the targeted gene on the same datasets. The ELM is applied with the same setting of the three algorithms to the selected feature subsets. Tables 4-6 demonstrate the classification accuracy rate for the same.

Table 4 ReliefF and ELM classification accuracy rates.

Dataset	Classification accuracy rates %									
	1	2	3	4	5	6	7	8	9	10
Breast	50.71	51.67	52.33	54.33	53.44	52.81	51.25	50.94	50.31	50.21
Lung	50.54	51.54	53.08	54.23	59.25	58.57	57.50	54.29	50.71	50.24
Lymphoma	52.34	53.12	55.30	56.00	57.40	56.70	55.32	54.38	52.86	51.76
SRBCT	58.32	59.87	68.04	62.51	65.39	64.24	63.44	60.39	59.63	58.61

Table 5 SFS and ELM classification accuracy rates.

Dataset	Classification accuracy rates %									
	1	2	3	4	5	6	7	8	9	10
Breast	70.22	73.58	74.48	76.38	77.28	78.59	78.94	70.29	74.22	74.67
Lung	83.27	84.21	81.77	83.27	86.90	87.27	82.38	84.29	89.57	90.76
Lymphoma	82.65	84.32	83.21	85.12	84.73	83.45	84.00	86.88	85.35	85.12
SRBCT	81.48	86.77	85.28	86.68	82.08	79.27	80.26	83.43	80.33	79.12

Table 6 mRMR and ELM classification accuracy rates.

Dataset	Classification accuracy rates %									
	1	2	3	4	5	6	7	8	9	10
Breast	80.00	70.59	73.56	72.31	75.65	73.21	76.33	73.89	73.43	72.89
Lung	79.52	77.94	77.22	77.14	78.33	77.22	78.50	77.61	77.62	77.61
Lymphoma	75.64	78.22	77.43	75.23	79.88	78.70	77.12	76.21	76.00	75.89
SRBCT	86.82	87.30	77.78	79.37	85.71	80.95	79.36	79.68	78.73	78.76

Therefore we can say that the classification accuracy rate is higher by mRMRAGA selection compared to the existing algorithm. The classification accuracy comparison is demonstrated for Breast, Lung, Lymphoma and SRBCT datasets in Figure 4-7 accordingly.

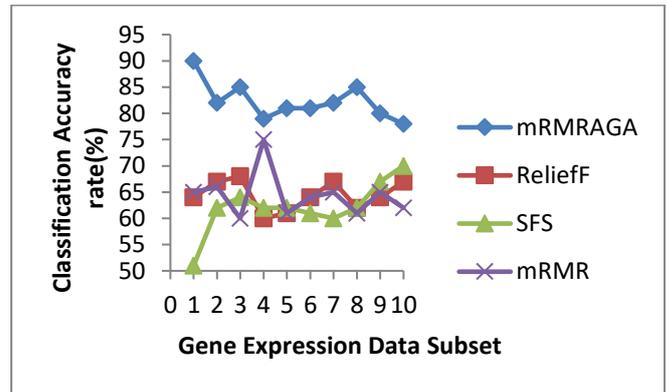


Figure 4. Classification accuracy rates on the Breast dataset with the use of feature selection algorithms.

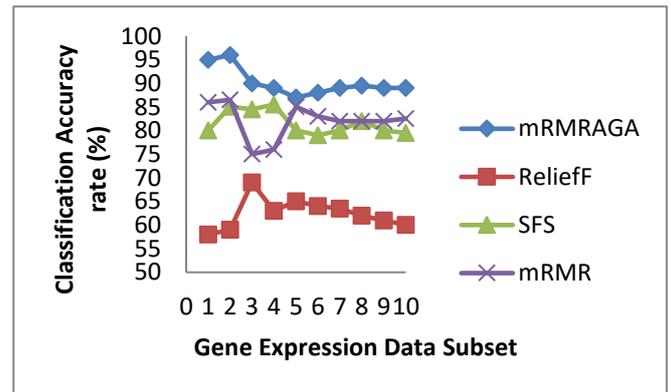


Figure 5. Classification accuracy rates on the Lung dataset with the use of feature selection algorithms.

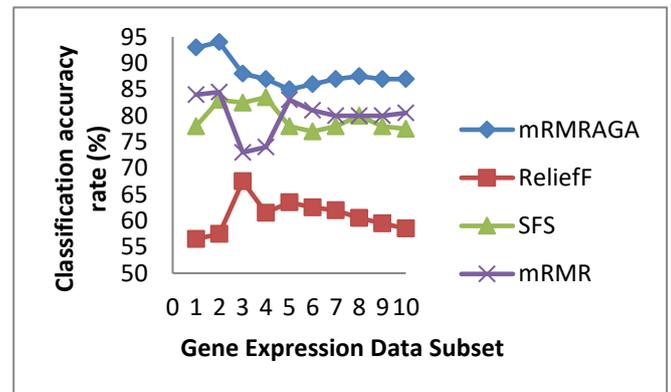


Figure 6. Classification accuracy rates on the Lymphoma dataset with the use of feature selection algorithms.

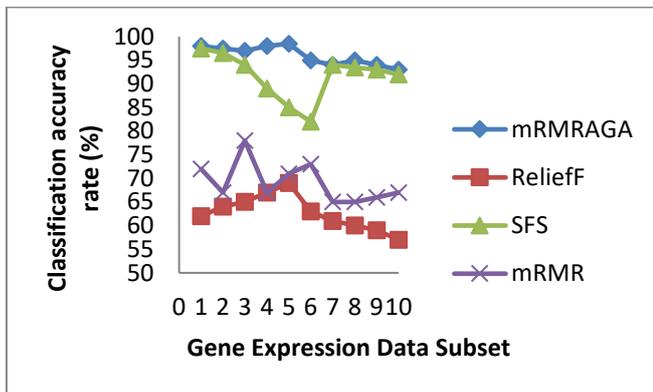


Figure 7. Classification accuracy rates on the SRBCT dataset with the use of feature selection algorithms.

The selected genes effectiveness with the use of mRMRA-selection approach, it has demonstrated further. The four well-known classifiers have been used to classify the selected genes by mRMRA-selection approach. These four well-known classifiers are support vector machine (SVM), back propagation neural network (BPNN), regularized extreme learning machine (RELM) and extreme learning machine (ELM). The classification accuracy for Breast, Lung, Lymphoma, and SRBCT are demonstrated in Figure 8, 9, 10 and 11 respectively.

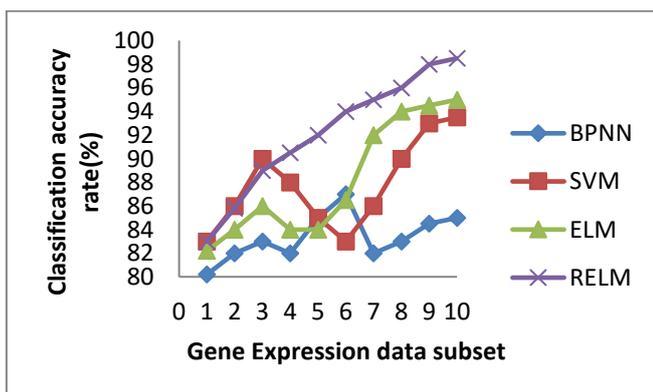


Figure 8. Classification accuracy rates on Breast dataset using different classifiers.

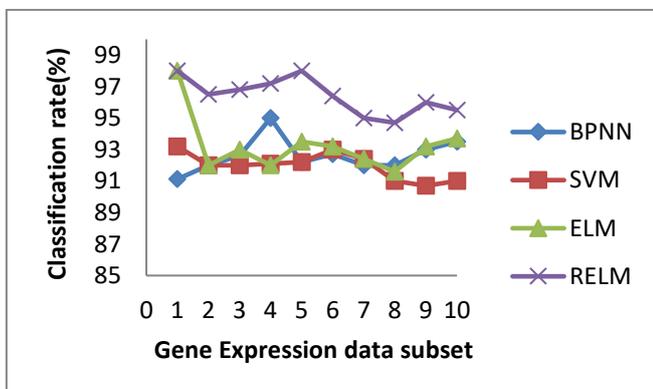


Figure 9. Classification accuracy rates on the Lung dataset using different classifiers.

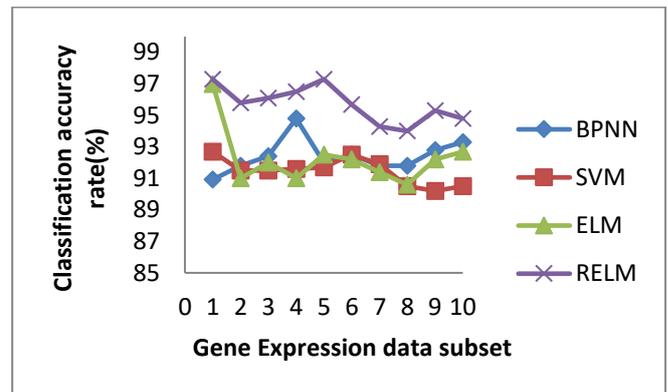


Figure 10. Classification accuracy rates on the Lymphoma dataset using different classifiers.

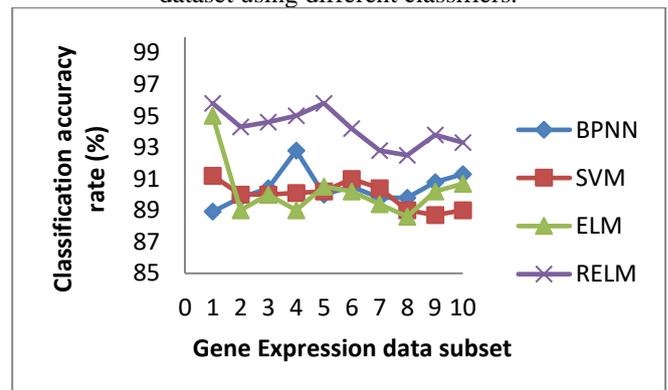


Figure 12. Classification accuracy rates on the SRBCT dataset using different classifiers.

It has been observed that the accuracy of the classification may not increase all the time with the increase in gene numbers. The only advantage may be, mapping of genes to class labels will be easier if the numbers of genes are less. The classification rate does not depend on the number of genes. The classification rate depends on the correlation complexity among the genes. The accuracy curve of classification will be more stable if the feature selection approach has a close agreement with the classifier in order to correlation identification. We have observed the RELM is more ideal classifier in this experiment for mRMRA-selection approach.

V. CONCLUSION

We propose the hybrid feature selection (mRMRA) approach in this paper, which combines mRMR and AGA and named as mRMRA-selection. This approach is successfully tested with four well-known classifiers on four benchmarked gene expression dataset. The mRMRA-selection approach is able to reduce the dimension effectively and reduce the redundancy of the dataset, hence improve the classification accuracy. For example, the dataset having the genes approximately 20000, the mRMRA-selection has the capability to reduce the number of genes less than 300 with high classification accuracy.



The classification accuracy rate was compared with four classifiers as shown in the previous section.

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