International Journal of Pure and Applied Mathematics
Volume 117 No. 15 2017, 683-697
ISSN: 1311-8080 (printed version); ISSN: 1314-3395 (on-line version)
url: http://www.ijpam.eu
Special Issue
ijpam.eu

CLASSIFICATION SCHEME FOR DETECTING AUTISM USING THREE TIER FEATURE SELECTION AND SINGLE TIER GENE SELECTION

M.Pushpa,
Assistant Professor, VLB Janakiammal College of Arts and Science, Coimbatore
pushy.govind@gmail.com

Dr.Soranamageshwari, Assistant Professor, Government Arts College, Coimbatore
swarnakannappan@gmail.com

ABSTRACT
This paper aims to achieve the primary goal of feature selection, classification and optimize feature subset from a Microarray gene expression data domain. This process has been used in autism selection and prediction that is characterized by large samples. The asymmetric in dimensionality of the Microarray data have the high-dimensional datasets, this data population cause accurate diagnosis autism. To improve the diagnosis of autism, various process tiersare proposed such as multi-tier feature selection, single tier gene selection and classification.Therefore, selecting a small set of marker genes can lead to improve classification accuracy. In this research works, the first stage on the powerful meta-heuristics schema to select the feature by using the Particle Swarm Optimization (PSO), Artificial Bee Colony Algorithm (ABC)andCuckoo Search Algorithm. In the second stage, the appropriate genes are selected based on the gene selection algorithmnamelyAnt Colony Optimization (ACO). SVM classifier is done to classify the autism in dataset. This technology predicts to monitor the wholegenomehigh-dimensional datasets. Furthermore weanalyze the performance of proposed work on autism datasets to estimate the high classification accuracy. In addition to this, we compare the resultant performance with existing well-known optimization algorithms. The proposed work is shown to be effective for detecting high-dimension data and autism detection.

INDEX TERMS: Particle Swarm Optimization, meta-heuristics schema, Artificial Bee Colony, Ant Colony Optimization, support vector machine, high-dimension data.

1. INTRODUCTION

Autism is a child psychiatric neurodevelopment disorder, it is one of the major constitutes from the last decade. Now a day the autism spectrum [29] disorders are identified based on only physical abnormal behavior and observable deficits. But this communication and social functioning based Autism constitutes [29] are difficult to analyze the exact solution as per the real time environment. To fulfill the above constrain the patterns of gene expression are observed and form the microarrays across many different conditions [3] [13]. The two different conditions such as above entropy [8] based kernel point and below entropy based kernel points are useful to detecting the autism [29] [31] with respect to the microarray technology [13]. The proposed technology used to analyze the high dimensional dataset based on above kernel point condition with high speed. The feature selections have become the concentration of attention of proposed research in the domain medical autism datasets even the thousands of variables are available in the dataset.

It aims to select a feature subset to build a pattern classifier with reduced complexity for improving classification performance [16]. Particularly the Gene selection [30] plays the major role in classification of autism using high-dimensional gene expression data. C4.5 and a support vector machine (SVM) [1] [34] [21] to the classification of autism symptoms based input dataset.

The main purpose of this paper is to select the particular autism genes from the autism dataset which is shown in the above architecture diagram (Figure 1). The various process groups are used to identify the gene and classify same in to the particular types. The above processing aspects are done by using the three stages. In first stage, the meta-heuristics schema is used to select the feature by using the Particle Swarm Optimization (PSO) [4] [9] [12] [21],Artificial Bee Colony Algorithm (ABC) [23] [24] [25] and Cuckoo Search Algorithm [17] [32].

In the second stage, the appropriate genes are select based on the Ant Colony Optimization (ACO) [2] [5] [6] [18] with respect to gene selection algorithm. In order to enhance the classification ability, the most consistent steps namely C4.5 and SVM classifier[7] [14] [34] based classification process are done. We demonstrate experimentally, the genes selected by our techniques [17] yield better classification performance and are biologically relevant to autism. The main task of the C4.5 and SVM [1] is to overcome the highest class discriminative ability of the features and it is used in the final recognition and classification of autism. The accuracy of the gene selection is proved by feature selection and gene selection [30] and classification [16].

In this research article, the algorithm [11]SVMis introduced, this includes a new approach to the classification performed and a measure based on kernel point is used to select the appropriate result. This proposed work is used PSO, ABC and cuckoo search [17] [13] for feature selection moreover the gene selection process developed by ACO [30]. The remainder section topics of this paper are structured as follows. Section 2discusses about the literature review. Section III explains the proposed three tier feature selection algorithm. Section IV describes the single tier gene selection algorithm. In order to introduce our hybrid model of classification scheme are presented in Section V. Section VIreports the experimental design with discussions. Article conclusion is provided in the final section with the reference.

2. LITERATURE REVIEW

Bello et al. (2007) proposed new Particle Swarm Optimization called Two-Step PSO which is used for heuristic search on heuristic dataset. They use Rough Set Theory and PSO model for reduction concept. Their proposed system is useful to improving the speed of data manipulation, classification rate by reducing the influence of noise. In addition to this, an improvement of the Particle Swarm Optimization to solve the feature selection problem **Bilal et al. (2009)** proposed the"Text Feature Selection using Particle Swarm Optimization Algorithm". This proposed Feature Selection used to reduce features dimensionality from the huge number of text datasets. This Feature Selection is applied to the multi-objective approach classification [9].

Xue, B et al. (2012) proposed the New Fitness Functions for binary particle swarm optimization (BPSO). It achieves the high classification accuracy features selection by using single and two stage fitness function. Additionally the K-nearest neighbour (KNN) is used to evaluate the classification performance on ten datasets.**Xue et al. (2013)** proposed thefeature selection in classification by using two particle swarm optimization based multi-objective feature selection [9]. The irrelevant and redundant features large number of features is reduced from the large dataset.

Babu et al. (2011)discussed about theSheep and Goat diagnoses the diseases Expert System. They use the dynamic input diseasessymptoms of animalsforrecognizecomplexpatterns and make intelligent decisions of finding the diseases affected or not. This was executed and tested based on the machine-learningalgorithmsnamelyABC and PSO.

Alam et al. (2011) proposed continuous function optimization based on artificial bee colony with exponentially distributed mutation(ABC-EDM). This method used for the various techniques such as Genetic Algorithm (GA), Original ABCalgorithm, Particle Swarm InspiredEvolutionary Algorithm (PS-EA) and Particle Swarm Optimization (PSO), the above listed techniques are returns the higher dimensionality and low optimization compare with the ABC-EDM.

Quanzhou et al. (2011)proposed the Modified Artificial Bee Colony namely guided ABC (GABC)for Numerical Function Optimization on the sixhigh dimensional numerical benchmark functions. They improve the exploitation on the searching, increase diversity and noise and also mitigatestagnation problem. The proposed results returns the GLABC can outperform ABC and GABCalgorithms in most of the experiments with the balance between exploitation and exploration.

Shunmugapriya et al. (2013) proposed the enhanced artificial bee colony for feature selection and optimization with respect to the training and testing. They use swarm intelligent namely Artificial Bee Colony in the enhanced form with the meta-heuristic search algorithm. The numerical optimizationproblems are resolved by the feature selection (EABC-FS). This optimization provides optimal subset offeatures from the ten different medicaldatasets. This proposed EABC-FS affords the better classification and feature selection. To hybridize the originalABC algorithm by improving accuracy, **Alqattan et al. (2015)** proposed the hybrid particle-movement ABC algorithm for optimization performance in different data sets. The research on the classification shows the comparison result of classical ABCand PSO algorithms on six benchmark functions. The final result shows the efficiently in the numerical functions alone.

Yang et al (2009) explain the cuckoo search via Lévy flights [27]. This algorithm is solving optimization problem by using the Cuckoo Search. The Cuckoo Search (CS) performance is better than the genetic algorithms and particle swarm optimization. The Cuckoo Search is another method of PSO and ABC, but the optimization fine turned by the Cuckoo Search algorithm. **Tawfik et al. (2013)** discussed the Trading Systems Optimization for exploring and exploitation to finding the solutions by using cuckoo search along with Lévy flights random walks. This proposed system is used to improve convergence rate and performance of the financial markets with respect to the ten standard benchmark functions. **Adnan et al. (2013)** compare the particle swarmoptimization and cuckoo search techniques in terms of problem-specific distance function. This study return the cuckoo search outperforms particle swarmoptimization and efficiency and quality more in the cuckoo searchbecause it uses less number of parametersthan the PSO.

Mutsubayashi et al. (2008) find thegene selection for disease classification by using statistic of forward variable gene selection method (FSM). The gene selections are made from microarray or DNA chip to find a discriminative subset of genes by the greedy search. The various microarray datasets are examined by the leave-one-out cross validation analysis. This approach is returns the very high accuracy and also perfect classification with the error rate.

Alter et al. (2011) proposed the Autism detection by using the gene expression regulation by the following preprocessing steps. They judge and designed the experiments of gene expression analysis and the experiments are performed with respect to the gene-centered approaches. The pathway analysis is maintained for reduce the risk for autism.

Esteban et al. (2011) detect genes involved in Autism by using game theory. This detection process detects only two genes as differentially regulated in individualswithASD. This analysis are used to detect the most suitable candidates, with the involvement of microarray game wascarried out only on those genes having a raw p-value < 0.01 using the Student's t-test.The resultantsdetectionshows a relevant combination of 78 genes, including one of thetwo genes that survived multiple test correction using standard analysis of microarray data.

Alba et al. (2008), Wang et al. (2010), Zhenget al. (2011), Wilin´ski et al. (2009), Aarøe et al. (2010) discussed about the cancerclassification based on the gee selection. **Aarøe et al. (2010)** discussedthebreast cancer detection, which was detected based on the early detection and profiling of peripheral blood cells. **Wilinski et al. (2009)** also proposed thecancer classification by Hybrid Algorithms of PSO andGA with SVM. **Zhenget al. (2011)** discussed the gene selection method by by Lasso and Dantzig selector for cancer classification. **Wang et al. (2010),**exposethegene selection method for microarraybasedcancer classification.

Civicioglu et al. (2013) and **Kumar et al. (2013)** are compare the three algorithm namely particle swarm optimization, differential evolution, artificial bee colony and cuckoo search for analyze the feature selection in the efficient manner. **Kumar et al. (2013)**finalizedifferential evolution perform the image segmentationof waste wood compare to other techniques. **Civicioglu et al. (2013)**finalizethecuckoo-search algorithm are works on the numerical optimization problem solving in 50 differentbenchmark functions as in the effective manner.

Gabrilovich et al. (2004) verify the feature selection by using the SVMs competitive with C4.5. Their process resolves the categorization problems by using featuresredundancy. This combination of SVMs with C4.5 is while keeping all of themhas substantially detrimental effect on categorization accuracy. They finalize, the C4.5 is significantly superior to that ofSVM. Their work establishes the findings text categorization feature selection with feature redundancy and relevancy.

Krasser et al. (2007) proposed low-cost feature extraction and multi-tierclassificationframework for extract from imagefiles in a very fast fashion on the large amounts of imagespam. They demonstratea classification performance result for C4.5 decision tree and support vector machine [17] classifiers is able to detect a large amount ofmalicious images while being computationally inexpensive.

3. PROPOSED METHODOLOGY

In proposed methodology, each gene is treated as the diagnostic feature and used for feature validation methods to provide the solution to selection problem. The Particle Swarm Optimization (PSO), Artificial Bee Colony Algorithm (ABC) and Cuckoo Search Algorithm are used to produce the different set of genebecause working principle of these technique are different that allows selection problem from different points.Ant Colony optimization (ACO) is used to identify an optimal population sizesofgenes that will assurance that the best performance in the classificationstage. The Support vector machine is used to classify the autism result. The Proposed scheme of autism data classification is given in the figure 1.

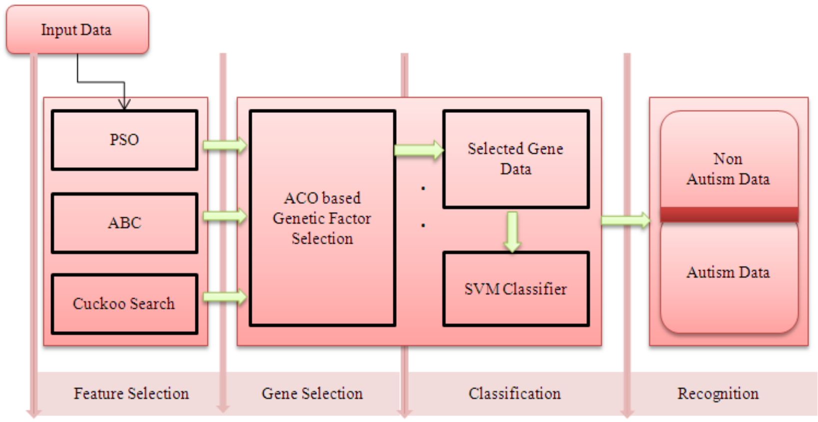

Figure 1.Proposed schemeof autism data classification.

3.1. THREE TIER FEATURE SELECTIONS

In the critical dataset, the high dimensional space reduction is the important criteria in data preprocessingtechnique such as bioinformatics, medical pattern recognition and text categorization. Feature selection techniques are playing the major role to select the appropriate features from the input dataset. This will useful to reduce the classification problems for faster and better searchcapability. Feature selection uses, select the subset of featuresfrom the dataset. These selection processes mainly contribute to theimprovement of accuracy and efficiency. To avoid the difficultiesin the selection process further the three tier feature selection such as particle swarm optimization [4] [21] [20], artificial beecolony algorithm, cuckoo search algorithm are used [17] [25]. All three methodsareoptimization techniques toachieve better solutions by extracting knowledge from previous iterations of each technique. By considering the performance of the selected above feature selection techniques achieve better results than filter approaches. Particularly from the last decade, application of feature selection (FS) techniques in bioinformatics has become a real requirementformodel building. Especially in the high dimensional nature of manyan impairment of health or a condition of abnormal functioning tasks in medical domain, going from sequence analysisover microarray analysis [3] [13] to spectral analysis and literature mininghas given rise to a wealth of feature selection techniques. This process consists of optimization of high dimensional nature data, which reduces the number of features by removes irrelevant, noisy and redundant data, for improving increasing accuracy and performance.

TIER 1: PARTICLE SWARM OPTIMIZATION (PSO)

In this work, we havecarryout,most generalized feature selection algorithm based on Particle Swarm Optimization (PSO) [9] toimprove the performance of autism dataset for feature extraction. This PSO-based feature selection algorithm applied to the autism dataset, the small number of features is picked out form the dataset. This model shows the simulation of the behavior of autism indications. The large amount of dataset symptoms are solved and optimized by applying the PSO in particular the wide range ofoptimization problems are reduced by the smaller number of constrain. Here the Particle Swarm Optimization [12] is used in this research to develop an efficient algorithm to optimize FS problem oriented to autism indications. In this initial stage of Feature selection of PSOaims to find the minimal feature subset of performance rather than better classification of input data. Therefore, it is necessary to develop a PSO based feature selection method to optimize both the classification performance and the number of features.

To accomplish this classification performance, we examine the initialization strategy and the pbest and gbest updating mechanism in PSO for feature selection. By considering the number of features when updating pbest and gbest, which are the leaders of particles, the number of features was significantly reduced and the classification performance was maintained or even increased. This PSO based feature selection outperforms the better result compare to the traditional feature selection algorithms. Meanwhile this reducing mechanism is maintain the computational time, that canalso be reduced. The pbest and gbestupdatingmechanism mange the computational time on the classification process in a smaller number of features cost, less time for each classification process.

From the above consideration,PSOhad not been used to cluster gene expression data in the past.Genefeature selection like better clusteringof gene datasets is done with particle swarm optimization (PSO). Gene Clustering

PSO Methods [12] are essential to the analysis of gene expression data too. The PSO [21]method is essential to update current solution using entire population of solutions by using the near optimal solution. Each particle has set of attributes: current velocity andposition, best position discovered by particle andneighbors.

Randomly initialized velocity and position is Updated by using following description:

Velocity_i,best position (t+1) =inertia weight *Velocity_i,best position (t) +random numbers 1*(best particle (t)-Xi,best position (t)) +random numbers 2*(li,best position (t)-Xi,best position (t)).

Xi,best position (t+1) = Xi,best position (t) + Velocity_i ,best position (t +1).

In addition to this, many methods that are proposed for FS, artificial beecolony algorithm, and cuckoo search algorithm [17][20] [32]haveattracted a lot of attention in the optimization process. This will be applied to the autism dataset the feature selection is fine-tuned with respect to the relevant behavior of autism indications.

Particle Swarm Optimization (PSO) Algorithm for Autism classification

```
Initialize particle as autism dataset input data
    Select particles from the training data
        Assign random number to each data
In search region (find the autism data)
    Do
        Find fitness value as entropy
        If fitness entropy limit is best
            Return new pbest as autism detected
        Else
            Find all the particles as gbest maximum relevant
    End
    Do
        Calculate particle velocity as count of minimum relevant:
            Return new velocity are above range;
        Calculate particle position confirmed:
            Return new position above entropy;
    While move toward the new position as detected autism data
Until Error criteria not attained.
```

Figure 2.: Algorithm for Particle Swarm Optimization

The above algorithm clearly represents the feature selection based on PSO algorithm, where the feature selection always return the optimized appropriate feature, or better than the previous result cases, as it can clearly seen in Figure 2.

TIER 2: ARTIFICIAL BEE COLONY ALGORITHM (ABC)

To select optimal subset offeatures, many techniques are provided by the various researchers, specially Artificial Bee Colony algorithm is a right techniques to draws out the more informativefeatures from all dataset especially autism dataset. The ABC algorithm was introduced by Karaboga (2005). Sincethis technique is used to solving numerical optimizationproblemsimprovetheclassification accuracy by the swarm intelligent, meta-heuristic search algorithm such as Genetic Algorithm, Ant Colony Optimization [2],ParticleSwarm Optimization [9] and Artificial Bee Colonyalgorithm (ABC) [20] have been widely used in optimizingFeatureSelection.TheABCalgorithmworks based on accommodation and manage the history of thepreviouslyresultsand the global best solutions for feature selection optimization. The ABC algorithmhas been tested on autism datasets and experimentalresults show the feature selection behavior of the proposedalgorithm as in the efficient manner. These extracted features are very important because it is applied to the next tier of feature selection called Feature Selection based on cuckoo search [26] [27].

In Artificial Bee Colony algorithm [25], the employ beesand the onlooker bees are form the bee swarm for producing the solutions of anoptimization problem. The employed beesshareexploring new food sources. Theonlookers based on the information received from theemployed bees, exploits the food sources until it getsexhausted. The employed bees of the exhausted foodsources become scouts and the scouts search for newfood sources. The number of food sources is equal tothe number of employed bees and the onlooker bees.Hence the colony is double the size of the food sources.Food sources represent the possible solutions of anoptimization problem [18].However, there is still an A lack of competence adequacy in the ABCalgorithm regarding its solution search equation, whichis good at exploration but poor at exploitation [15]. This research proposed system overcomes the above deficiency by complementing thebees with a memory to record the global best andpreviouslytakensolutions. This process returns the result of exploration and exploitation with efficiency. The performance of ABC feature selection has established theusefulness of additional memory enhancement to ABC.

Pseudo-codeforArtificial Bee Colony Algorithm

Initializationparameters
Begin
Employee bees:
Start Construct solutions:
Assign to each employed bee:
Feature subset configurations as form of binary bit string;
Recordx_{ibest}
Produce new feature subsets s v_i
Pass the produced feature subset to the classifier
Feature subset:
Findfitness (fit_i)
Calculate the probability p_i
EndConstruct solutions
Onlooker's bees:
Start Construct solutions:
Select the probability p_i
Read x_i,x_j, x_{ibest}, x_{aban}
Computev_i
End Construct solutions:
Start Extracted solution:
Findscout bee;
Recordx_{aban}andUpdatex_{ibest}
Return and Store best feature subset
Return and Store best optimal feature subset
Until all extracted input
Generate optimal feature subset configurations
End Extracted solution:
End

Figure 3.Pseudo-code for Artificial Bee Colony Algorithm

The pseudo-code for Artificial Bee Colonyalgorithm [24] is shown in Figure3. ABC with feature selection made based on the autism dataset. The employee bee and onlooker bee construction are useful to make the feature selection with the efficient way. The selected bees are produces the well resultant feature of the autism dataset. These representations are given in figure 3.

TIER 3: CUCKOO SEARCH ALGORITHM

We develop a new recent variant of PSO algorithm is Cuckoo Search algorithm (CS)[27] which is used for solving optimization problems with respect to the breeding behaviors.Thepopulation based optimization technique developed by Xin-She Yang and Suash Deb in 2009 [9].If a Cuckoo's host discovers that the eggs are strange eggs, it will either throw these alien eggs away or simply abandon its nest and build a new nest elsewhere [10].The breeding behaviors of cuckoos is based on the three idealized rules such as

1. Put the Each cuckoo's egg on the randomly chosen nest
2. Barrow nests of eggs with the best quality for the next generations
3. The egg laid by a cuckoo is discovered by the host bird with a probability with respect to the fixed host nests. i.e., $pa \in [0, 1]$.

If the new nest builds,the two cases are available such as.

a. The host bird can throw the egg away

b. The host bird can empty the nest

The last two assumption can be approximated bythe fraction pa of the n nests are replaced by new nests with new random solutions.The ultimate goal is to develop systems that have ability to learn incrementally; of the recent developed bio inspired algorithms is the Cuckoo Search (CS) [28] which is based on style life of Cuckoo bird.

Cuckoo Search Algorithm for Autism Feature Selection

```
Begin
Get dataset as input
Produce initial population of
                    n host nests
while (objective function<Max_Generation)
Get a cuckoo randomly by autism input dataset
Evaluate its fitness
Choose a nest randomly
if (fitness >randomnest),
replacerandomnest by the new solution;
end
A fraction of worse nests
Abandoned and new ones are built;
Keep the best solutions
nests with quality solutions;
Rank the solutions and find the current best
End while
Post process results and visualization
End
```

Figure 4. Pseudo-code Cuckoo Search Algorithm

4. Single Tier Gene Selection

4.1. ACO Based Gene Selection Algorithm

The information extract from the large amount of data through data mining [10] is the challenges in the microarray data autism classification[3] [13]. The ant colony optimization is the technique [2] to solve the keep under surveillance of the whole genome and performs the better monitoring interactions of many genes at the same time. This system is used to achieve those challenges by using multi stage classification method [15] which is helps to manage the gene expression data. In the study, the ant colony optimization (ACO) [2] [22] algorithm is introduced to select genes to reduce problem dimension. ACO is a meta-heuristic approach which simulates the behavior of antcolonies path finding and can beapplied in solving hard combinatorial optimizationproblems [15]. To improve autism classification performance, it isnecessary to remove features that are irrelevant to autism.Inthis research work multi stage classification [15] methods are proposed, PSO, ABC and Cuckoo Search algorithm [17][32] is introduced toselect critical features relevant to autism first, and then the ACO is used for autism categorization and the classification are based on SVM classifier [1] [15] [34]. These three classifiers were chosen as the application tool due to theirpopularity in many applications such as autismcategorization,classification, bio-information analysis and so on.

At presence obstacle between the food sources to the nest, the shortest paths are finding by the real ants. This ant based algorithm called ant colony algorithm produces the positive feedback,distributed computation and constructivegreedy heuristic are used to finding aminimal length on the closed loop of town. From this consideration the town (node) is assign for a gene. The nodes on the closed loop of town generated by the ant colony are the selected genes for autism classification.

This selection of gene indicated based on following algorithms.

```
ACO Algorithm: Optimal Subset of Features
Begin
 | Initialization:
 |   Read pheromone_table, with training_set, test_set;
 | Start constructs solution:
 | |   For each ant:
 | |   |   Select feature subset;
 | |   |  Model creation:
 | |   |    Test training dataset and test_set;
 | |   |  Return classification accuracy
 | |   |    Re-update feature subset
 | |   |      Until termination condition satisfied
 | |   Else
 | Re-constructs solution:
 |        End with best gene selection
End
```

Figure 5. Pseudo code for ACO Based Gene Selection Algorithm

Gene selection is an important step in an autism classification task. The existing study of gene selection [30] was not giving satisfactory outcomes, using the most informative features increased the classification rate. This schema is used to reduce the number of features by the ACO is a solution for better generalization performance. In order to get an optimal subset of features ACO algorithm was employed in figure 5. Experimentalresults show that selecting genes by using ACO algorithm canimprove the accuracy of SVM classifiers [34] which is shown in upcoming section.

5. CLASSIFICATION SCHEME

Classification is a pre-requisite process for the identification and classification of the autism dataset. Classification may have same data type of input and output but different functions. Such a situation arise difficultness in select the autism data during the process of classification. The classifications require outcome of the ACO as an input and returns a set of related group with respect to the availability of autism symptoms.Theproposed process was classified using SVM classifier. TheProposedArchitecture is presented in Figure 6.

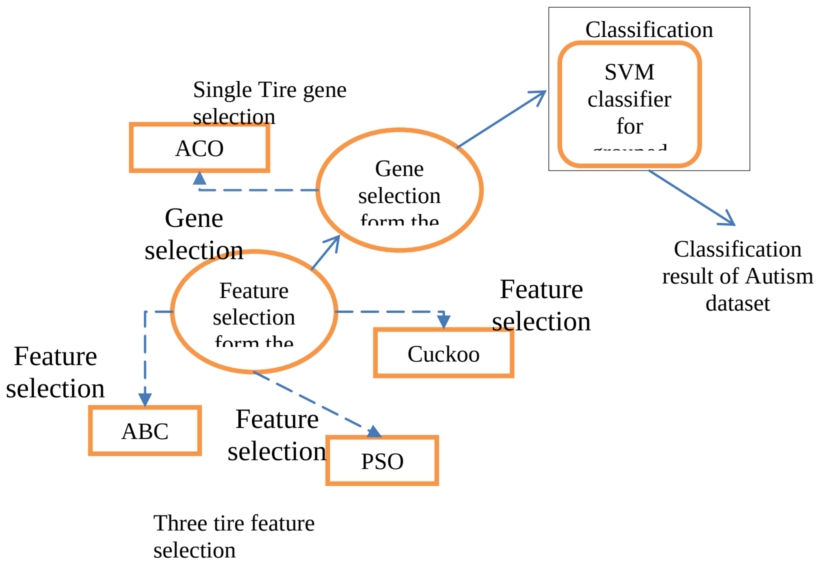

Figure 6.Proposed Architecture

In this classification, first consider N training samples, $\{x_1, y_1\}, \ldots, \{x_N, y_N\}$, here $x^i \in R^m$ is a m-dimensionalfeature vector representing the i[th] training sample, and $y_i \in \{-1,1\}$ is the class label of x_i. In SVM classification, equation $a^T x + b = 0$ is representing the hyperplane. In that equation variable b belongs to scalar and $a \in R^m$. In this classification training and testing the data is needed. Data's are linearly separable in the training, this classification separate into two classes with no error in training condition. SVM maximizes the minimum distance from the training samples to the hyperplane. It is easy to find that the parameter pair (a, b) corresponding to the optimal hyperplane is the solution to the following optimization problem:

$$\text{minimize: } \mathrm{Lin}(a) = \frac{1}{2}\|a\|^2$$

$$\text{subject to: } y_i(a^T x_i + b) \geq 1, i = 1, \ldots, N \qquad (1)$$

There is no hyperplane is needed for nonseparable cases in an linear condition, this type of cases is useful to classify correctly all the training samples. The idea behind the optimization problem is based on the concept of soft margin. The below equation represent the new optimization problem

$$\text{minimize: } \mathrm{Lin}(a, \xi_i) = \frac{1}{2}\|a\|^2 + C\sum_{i=1}^{N} \xi_i$$

$$\text{subject to: } y_i(a^T x_i) + b) \geq 1 - \xi_i, i = 1, \ldots, N \qquad (2)$$

In the above equation slat variables are denoted byξ_i, this variable is related to the soft margin. Balance this margin and training error by using tuning parameter C. Both old and new optimization problems are handled and computed by using Lagrange multipliers $\alpha_i$that transforms them to quadratic programming problems.

The kernel point was used for both SVM training and testing which mapped samples nonlinearly onto a higher dimensional space. For this reason, this kernel is able to handle cases where nonlinear relationship exists between class labels and features. A commonly used radial basis function [3] with respect to the n-dimensional feature vectors such as Vi and Vj. The vector dimensions $\|V_i - V_j\|^2$ the norm of the element Vi and Vj normed vector space is defined as,

$$\|V_i - V_j\|^2 = \left(\left(V_i - V_j\right)^t\right) + \left(V_i - V_j\right)$$

Equation 3

$$\text{Kernal Point}\left(V_i - V_j\right) = e^{\left(-\gamma\|V_i - V_j\|^2 + (V_i - V_j)\right)}$$

Equation 4

The above equation 3 and 4 used to find kernel point in SVM training and testing samples and it requires γ parameters: and a penalization parameter C [19]. Appropriate values of 'C' and 'γ' should be specified to achieve a high accuracy rate in classification.

6. RESULT AND DISCUSSION

In experimental result, classification [11] scheme is used to detecting autism using three tier feature selection and single tier gene selection scheme. The proposed work is evaluated and implemented using JAVA. Theproposed work consists of combination of PSO, ACO, Cuckoo Search [7] [32] and SVM Classifier [11] return the best result in the autism data set.

A. Autism Data Set:

It is a Homo sapiens dataset extracted from the http://www.ncbi.nlm.nih.gov/gene/94313. [33] this dataset contains the Lineage namely Catarrhini; Chordata;Craniata; Euarchontoglires; Eukaryota; Euteleostomi; Eutheria; Haplorrhini; Hominidae; Homo Mammalia; Metazoa; Primates; Vertebrata; this dataset are used to taken as the test dataset.The proposed system returns the following accuracy in terms of precision, recall, which is listed in the following table.

Performance metrics:

The performance metrics used for evaluation are Precision, recall, F-measure and accuracy.

Precision or positive predictive value is defined as the proportion of the true positives against all the positive results (both true positives and false positives)

$$PPV = \frac{TP}{(TP + FP)}$$

Sensitivity (also called the true positive rate, or the recall in some fields) measures the proportion of positives that are correctly identified.

$$TPR = \frac{TP}{P} = \frac{TP}{(TP + FN)}$$

The F1 score (also F-score or F-measure) is a measure of a test's accuracy.F-measure or balanced F-score (F1 score) is the harmonic mean of precision and recall.

$$F1 = \frac{2TP}{(2TP + FP + FN)}$$

The accuracy is the proportion of true results (both true positives and true negatives) among the total number of cases examined.

$$ACC = \frac{(TP + TN)}{(TP + FP + FN + TN)}$$

Table 1: comparison of existing and proposed methods for true positive, true negative, false positive and false negative.

Techniques	True positive	True negative	False positive	False negative
Existing method	0.85	0.88	0.13	0.15
Proposed method	0.98	0.99	0.02	0.04

From Table 1, proposed system has better results in terms of true positive, true negative, false positive and false negative. The proposed methodology yields better true positive result 0.98, true negative 0.99, false positive 0.02 and false negative 0.04.

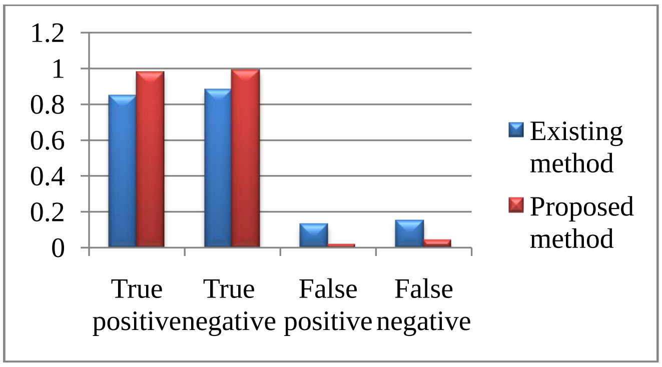

Figure 7: comparison of existing and proposed methods for true positive, true negative, false positive and false negative.

From above figure 7 shows the proposed system has better results in terms of true positive, true negative, false positive and false negative. The proposed methodology yields better true positive result 0.98, true negative 0.99, false positive 0.02 and false negative 0.04.

Table 2: comparison of existing and proposed methods forprecision, Recall and F-measure.

TECHNIQUES	PRECISION	RECALL	F-MEASURE
Existing method	86	85	85
Proposed method	98	98	97

From Table 2,the proposed system has better results in terms of precision, recall and F-measure. The proposed methodology yields better precision result 98%, recall 98% and F-measure 97%.

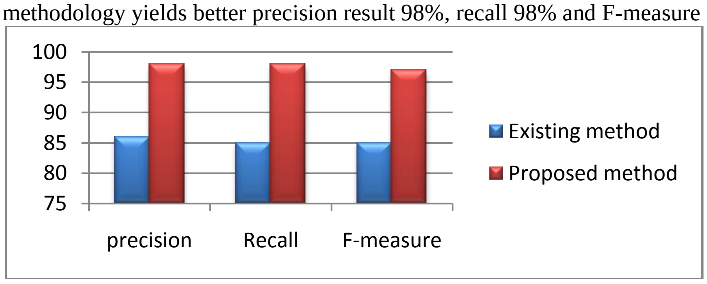

Figure 8: comparison of existing and proposed methods for precision, Recall and F-measure.

From above figure 8 shows the proposed system has better results in terms of precision, recall and F-measure. The proposed methodology yields better precision result 98%, recall 98% and F-measure 97%.

Table 3: comparison of existing and proposed methods for execution time.

Techniques	Execution time in (ms):		
	PSO	ABC	Cuckoo search
Existing method	336000	302000	212000
Proposed method	187000	221000	161000

From Table 3, proposed system has better results in terms of PSO, ABC and Cuckoo search. The proposed methodology yields better result PSO187000, ABC 221000 and Cuckoo search161000.

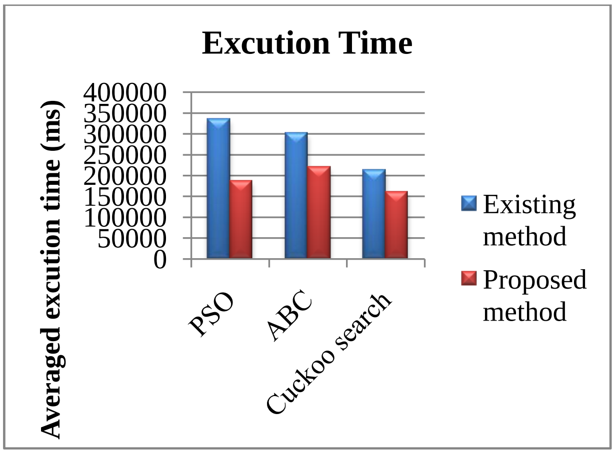

Figure 9: comparison of existing and proposed methods for execution time.
From above figure 9 shows the proposed system has better results in terms of PSO, ABC and Cuckoo search. The proposed methodology yields better result PSO 187000, ABC 221000 and Cuckoo search161000.
Table 4: comparison of existing and proposed methods for execution time.

Techniques	accuracy
Existing method	86
Proposed method	97

From Table 4 the proposed system accuracy achive better result than the existing method. the proposed method accuracy is 97%.

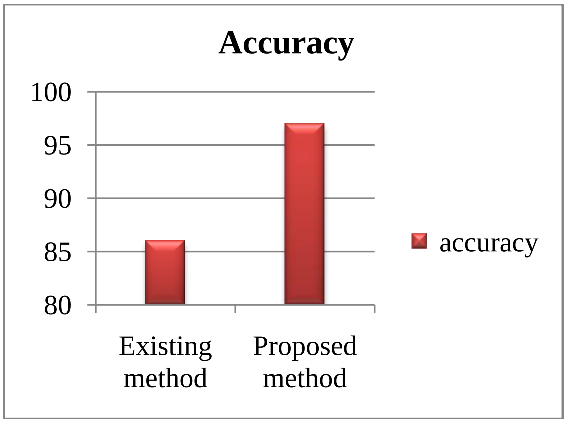

Figure 10: comparison of existing and proposed methods for execution time.
From above figure 10 shows the proposed system accuracy achive better result than the existing method. The proposed method accuracy is 97%.

CONCLUSION

Using real autism data sets, this article returns the performance of proposed method. This method is compare with the other various methods for feature selection and gene selection also the classification through a series of classification experiments. In gene selection, this article are compered the genetic algorithm and random forest with the proposed ACO gene selection techniques. In terms of feature selection, the Fusion-based recursive feature elimination (MCF-RFE) algorithm is compared. In contrast the proposed “hybrid classification scheme for detecting autism using three tier feature selection and single tier gene selection” method eliminates gene redundancy automatically and yields better and more compact gene subsets. The count of 738 probes that discriminated Autism and non-autism samples was identified and also achieved prediction precision of 91.28% with a recall of 90% and an accuracy 94.85%. These approaches are implemented in JAVA Platform with net beans.

REFERENCE

1. Mursalin, M., Hossain, M. M., Noman, M. K., &Azam, M. S. (2013). Performance Analysis among Different Classifier Including Naive Bayes, Support Vector Machine and C4. 5 for Automatic Weeds Classification.Global Journal of Computer Science and Technology, 13(3).
2. Aghdam, M. H., Ghasem-Aghaee, N., &Basiri, M. E. (2009). Text feature selection using ant colony optimization. Expert systems with applications,36(3), 6843-6853.
3. Ding, C., &Peng, H. (2005). Minimum redundancy feature selection from microarray gene expression data. Journal of bioinformatics and computational biology, 3(02), 185-205.
4. Zahran, B. M., &Kanaan, G. (2009). Text Feature Selection using Particle Swarm Optimization Algorithm
5. Chen, Y., Miao, D., & Wang, R. (2010). A rough set approach to feature selection based on ant colony optimization. Pattern Recognition Letters,31(3), 226-233.
6. Li, Y., Wang, G., Chen, H., Shi, L., & Qin, L. (2013). An ant colony optimization based dimension reduction method for high-dimensional datasets. Journal of Bionic Engineering, 10(2), 231-241.
7. Sharma, S., Agrawal, J., & Sharma, S. (2013). Classification through machine learning technique: C4. 5 algorithm based on various entropies. International Journal of Computer Applications, 82(16).
8. Siradeghyan, Y., Zakarian, A., &Mohanty, P. (2008). Entropy-based associative classification algorithm for mining manufacturing data. International Journal of Computer Integrated Manufacturing, 21(7), 825-838.
9. Xue, B., Zhang, M., & Browne, W. N. (2013). Particle swarm optimization for feature selection in classification: A multi-objective approach. Cybernetics, IEEE Transactions on, 43(6), 1656-1671.
10. Yeh, J. Y. (2008). Applying data mining techniques for cancer classification on gene expression data. Cybernetics and Systems: An International Journal, 39(6), 583-602.
11. Alba, E., García-Nieto, J., Jourdan, L., &Talbi, E. G. (2007, September). Gene selection in cancer classification using PSO/SVM and GA/SVM hybrid algorithms.In Evolutionary Computation, 2007. CEC 2007. IEEE Congress on (pp. 284-290). IEEE.
12. Xue, B., Zhang, M., & Browne, W. N. (2012, June). New fitness functions in binary particle swarm optimisation for feature selection. In Evolutionary Computation (CEC), 2012 IEEE Congress on (pp. 1-8). IEEE.
13. Chiang, Y. M., Chiang, H. M., & Lin, S. Y. (2008, July). The application of ant colony optimization for gene selection in microarray-based cancer classification. In Machine Learning and Cybernetics, 2008 International Conference on (Vol. 7, pp. 4001-4006). IEEE.
14. Gabrilovich, E., &Markovitch, S. (2004, July). Text categorization with many redundant features: using aggressive feature selection to make SVMs competitive with C4. 5. In Proceedings of the twenty-first international conference on Machine learning (p. 41). ACM.
15. Krasser, S., Tang, Y. C., Gould, J., Alperovitch, D., & Judge, P. (2007, June). Identifying image spam based on header and file properties using C4. 5 decision trees and support vector machine learning. In Information Assurance and Security Workshop, 2007. IAW'07. IEEE SMC (pp. 255-261). IEEE.
16. Entezari-Maleki, R., Rezaei, A., &Minaei-Bidgoli, B. (2009). Comparison of classification methods based on the type of attributes and sample size.Journal of Convergence Information Technology, 4(3), 94-102.
17. Civicioglu, P., &Besdok, E. (2013). A conceptual comparison of the Cuckoo-search, particle swarm optimization, differential evolution and artificial bee colony algorithms. Artificial Intelligence Review, 39(4), 315-346.
18. Kabir, M., Shahjahan, M., &Murase, K. (2013). Ant Colony Optimization Toward Feature Selection. ANT COLONY OPTIMIZATION-TECHNIQUES AND APPLICATIONS, 1.
19. Uzer, M. S., Yilmaz, N., &Inan, O. (2013). Feature selection method based on artificial bee colony algorithm and support vector machines for medical datasets classification. The Scientific World Journal, 2013.
20. Babu, M. P., Ramjee, M., Narayana, S. S. V. N. L., &Murty, N. R. (2011, July). Sheep and goat expert

system using artificial bee colony (ABC) algorithm and particle swarm optimization (PSO) algorithm. In Software Engineering and Service Science (ICSESS), 2011 IEEE 2nd International Conference on (pp. 51-54). IEEE.
21. Bello, R., Gomez, Y., Nowe, A., & Garcia, M. M. (2007, October). Two-step particle swarm optimization to solve the feature selection problem. InIntelligent Systems Design and Applications, 2007. ISDA 2007. Seventh International Conference on (pp. 691-696). IEEE.
22. Shunmugapriya, P., Kanmani, S., Supraja, R., &Saranya, K. (2013, July). Feature selection optimization through enhanced Artificial Bee Colony algorithm. In Recent Trends in Information Technology (ICRTIT), 2013 International Conference on (pp. 56-61). IEEE.
23. Alqattan, Z. N., & Abdullah, R. (2015). A hybrid artificial bee colony algorithm for numerical function optimization. International Journal of Modern Physics C, 26(10), 1550109.
24. Alam, M. S., Kabir, M. W. U., & Islam, M. M. (2010, December). Self-adaptation of mutation step size in artificial bee colony algorithm for continuous function optimization. In Computer and Information Technology (ICCIT), 2010 13th International Conference on (pp. 69-74). IEEE.
25. Quanzhou, L. J. W. H. W., &Yishui, L. (2011). A Modified Artificial Bee Colony Algorithm for Numerical Function Optimization. 978-1-4244-6448-7/11/$26.00 ©2011 IEEE
26. Tawfik, A. S., Badr, A. A., & Abdel-Rahman, I. F. (2013). One rank cuckoo search algorithm with application to algorithmic trading systems optimization. International Journal of Computer Applications, 64(6).
27. Yang, X. S., & Deb, S. (2009, December). Cuckoo search via Lévy flights. In Nature & Biologically Inspired Computing, 2009. NaBIC 2009. World Congress on (pp. 210-214). IEEE.
28. Adnan, M. A., &Razzaque, M. A. (2013, March). A comparative study of particle swarm optimization and Cuckoo search techniques through problem-specific distance function. In Information and Communication Technology (ICoICT), 2013 International Conference of (pp. 88-92). IEEE.
29. Alter, M. D., Kharkar, R., Ramsey, K. E., Craig, D. W., Melmed, R. D., Grebe, T. A., & Turner, J. B. (2011). Autism and increased paternal age related changes in global levels of gene expression regulation. PloS one, 6(2), e16715.
30. Mutsubayashi, H., Aso, S., Nagashima, T., & Okada, Y. (2008). Accurate and robust gene selection for disease classification using a simple statistic. Bioinformation, 3(2), 68.
31. Esteban, F. J., & Wall, D. P. (2011). Using game theory to detect genes involved in Autism Spectrum Disorder. Top, 19(1), 121-129.
32. Kumar, S., Pant, M. I. L. L. I. E., & Ray, A. K. (2013). A comparison of differential evolution, particle swarm optimization, artificial bee colony and cuckoo search for multilevel thresholding of waste wood. Computer Methods Mater Sci, 13(1), 135-140.
33. http://www.ncbi.nlm.nih.gov/gene/94313.
34. Rajesh, M., and J. M. Gnanasekar. "Annoyed Realm Outlook Taxonomy Using Twin Transfer Learning." International Journal of Pure and Applied Mathematics 116 (2017): 547-558.
35. Rajesh, M. & Gnanasekar, J.M. Wireless Pers Commun (2017),https://doi.org/10.1007/s11277-017-4565-9
36. Rajesh, M., and J. M. Gnanasekar. "GCCover Heterogeneous Wireless Adhoc Networks." Journal of Chemical and Pharmaceutical Sciences (2015): 195-200.
37. Rajesh, M., and J. M. Gnanasekar. "CONGESTION CONTROL IN HETEROGENEOUS WANET USING FRCC." Journal of Chemical and Pharmaceutical Sciences ISSN 974: 2115.
38. Rajesh, M., and J. M. Gnanasekar. "GCCover Heterogeneous Wireless Ad hoc Networks." Journal of Chemical and Pharmaceutical Sciences (2015): 195-200.
39. Rajesh, M., and J. M. Gnanasekar. "CONGESTION CONTROL USING AODV PROTOCOL SCHEME FOR WIRELESS AD-HOC NETWORK." Advances in Computer Science and Engineering 16.1/2 (2016): 19.
40. RAJESH, M. "TRADITIONAL COURSES INTO ONLINE MOVING STRATEGY." The Online Journal of Distance Education and e-Learning 4.4 (2016).
41. Rajesh, M. "Object-Oriented Programming and Parallelism."
42. Rajesh, M., K. Balasubramaniaswamy, and S. Aravindh. "MEBCK from Web using NLP Techniques." Computer Engineering and Intelligent Systems 6.8: 24-26.