



# Diagnosis of Autism Spectrum Disorder in Adults by Combining Bayes' Law and Genetic Algorithm

**Mohammadali Mohammadi**

Master's degree in Computer Software Engineering, Islamic Azad University, Tehran, IRAN

**Abstract:** Timely diagnosis of diseases is considered vital for treatment. So far, many methods have been created for this purpose; autism spectrum disorder is one of these diseases. In this disease, developmental and developmental disorders will accompany the patient especially since childhood. The range of this disease is wide and it can usually be diagnosed by performing a series of clinical tests. Usually, the symptoms of this disease appear in childhood and before the age of three, and they differ according to the severity of the disease and its symptoms, which may appear in some cases from 5 months of age to two years of age. One of the important and debatable points is the timely diagnosis of this disease in adults, which unfortunately was not diagnosed in childhood, and this causes a series of behavioral problems in the social life of people with autism, and the person, by referring to a neurologist and Nerves and performing a series of clinical evaluations are known to be suspicious of autism spectrum disorder. Therefore, it is important to provide methods that can identify the relationship between different characteristics in contracting this disease. In this research, an attempt is made to predict the effect of each of the parameters on the diagnosis of the disease and also the process of the disease by using Bayes' law and genetic algorithm. In this method, mutual validation technique is used to optimize input and output data. First, the data are pre-processed and in the next step they are classified by Naive Bayes (kernel) which achieves 91% accuracy and then they are optimized with genetic algorithm which reaches 94.06% accuracy. Also, the data were tested with decision tree and Naive Bayes algorithms, and their results were compared.

**Keywords:** autism, Bayes law, Naive Bayes, Naive Bayes (Kernel) genetic algorithm, cross validation

## I. INTRODUCTION

Today, with the progress of all sciences, we are facing an increase in the amount of data. Medical science is no exception to this rule. Medical data is typically obtained through various tests as well as treatment methods and research on patients, especially specific diseases. Recently, data mining and its methods are used for more appropriate use of data. Especially in medical science, which can help the patient's treatment process with timely diagnosis. Autism spectrum disorder is one of these diseases. In this disease, developmental and developmental disorders will accompany the patient especially since childhood. The range of this disease is wide and it can usually be diagnosed by performing a series of clinical tests. Usually, the symptoms of this disease appear in childhood and before the age of three, and they differ according to the severity of the disease and its symptoms, which may appear in some cases from 5 months of age to two years of age. One of the important and debatable points is the timely diagnosis of this disease in adults, which, unfortunately, was not diagnosed in childhood, and this causes a series of behavioral problems in the social life of people with autism.

Nerves and performing a series of clinical evaluations are known to be suspicious of autism spectrum disorder. Considering that the main cause of this disease is genetic disorders, therefore, timely diagnosis and treatment of this disease can prevent its progress to some extent. One of the detection methods can be called using the Bayes law classification method; which is considered one of the common methods in data mining. Using this rule for classification brings good accuracy and speed in large databases.

In this method, it is assumed that the effect of the value of a special attribute on the class label is independent of the values of other special attributes, and this assumption makes calculations easier. One of the important problems of this issue is the increase in the number of patients with autism spectrum disorder in adults, which is diagnosed late in adulthood due to the lack of timely diagnosis of this disorder in childhood. Currently, it is possible to identify this disease through several methods, but the existence of a series of problems creates the motivation to try to solve the problem with a new method.



Considering that autism spectrum disorder for adults is considered an advanced state of neurological disorders of the brain and requires spending time and money for medical care and unfortunately due to the fact that the previous methods which has been done so far, there are no effective methods for the early diagnosis of this disease and it has caused the process of diagnosing the disease to be prolonged, so by using another new method such as the combination of Bayes's law and genetic algorithm, it has been tried that it may be possible to improve. It provided the accuracy of the diagnosis and as a result, the waiting time for the diagnosis of the disease was slightly improved. Finally, with an early diagnosis, it is possible to increase the performance level of patients and also prevent its progress, and also create conditions that may provide access to the primary treatment methods of the disease in order to provide the possibility of better control of the disease in the future. In this research, taking into account the investigated variables, which are 1. accuracy, 2. precision, and 3. recall, at first, data preparation and pre-processing of autistic adult patients is discussed. Data mining techniques are used to diagnose autistic adult patients and determine effective treatment methods for this disease. The characteristics obtained from the algorithms are evaluated and validated by the specialists of this disease. Then, by using Bayes' law and genetic algorithm, the classification and diagnosis model of autistic adult disease is discussed.

The steps of doing the work are as follows, in the first step, the definitions and concepts of autism spectrum disorder, its cause and its difference in children and adults and how it affects the communication, language and cognitive abilities and social behaviors of people with the disease are discussed. It will be in the same way, diagnostic methods and tools and existing challenges are examined. Then, in the second stage, the matching algorithm is investigated using Bayes' rule as a method for classifying the previously prepared data of adult autistic patients. And also, the investigation of how to implement it in order to reach an efficient algorithm is discussed in order to reach the appropriate diagnostic waiting time, and finally, in the last stage, the algorithm is implemented in the environment of Rapid Miner software, where the results obtained are recorded and presented the previous ones are compared and finally the main idea is concluded.

In this thesis, there are two main questions that we intend to answer at the end:

Autism spectrum disorder is a type of psychiatric disorder that prevents communication and social skills as well as language skills in people with autism. Its symptoms are often seen before the age of three. This term was first proposed by Leokaner in 1943 AD.

Diagnostic and statistical manual of mental disorders: It is a diagnostic manual of mental disorders. Recently, the fifth edition of this guide has been prepared, which is known as DSM-5.

The purpose of this research is to provide a suitable and new diagnosis method in autism spectrum disorders in adults, and on the other hand, reaching a timely diagnosis can be considered one of the important challenges in behavioral disorders of autism in adults. Based on this, efforts have been made to improve the accuracy of decisions by using the combination of Bayes' law and genetic algorithm, and then improve the performance of the system. Bayesian networks provide explicit representations of a structure. One of the main advantages of Bayes networks is the ease of mapping many practical problems to such networks, which validates the efficiency of this method compared to other methods. The use of Bayes' law along with the genetic algorithm will be solely for the purpose of better identification and selection of effective features in the damage caused by autism behavioral disorders; that this procedure leads to the emergence of a new and optimal technical approach in the classification of data related to this disease.

## II. RESEARCH BACKGROUND

Debir Vaziri and Tehranizadeh (2017) used artificial neural network to diagnose autism spectrum disorder. The sample included 170 people consisting of 100 autistic children and 70 healthy and cheerful children. Using perceptron multilayer neural network, a clinical decision support system was designed to predict autism based on signs and symptoms. The average accuracy of the designed neural network after 10 executions was 96.11%. As a result, the system designed with proper accuracy can be a reliable assistant and support for experts in this field in distinguishing autistic children from healthy ones [1].

Behnampour et al., (2017) presented their article on the application of fuzzy logistic regression in modeling the severity of autism disorder. He used the fuzzy logistic regression model to obtain a model to determine the severity of autism disorder and its results were analyzed. To fit the model, the subscales of stereotyped movements, communication and social interaction have been used as input variables, as well as the therapist's opinion regarding the severity of the disorder as a fuzzy output variable.



The estimation of the coefficients was done by the two methods of the least squares and the least absolute value of the differences, and the criterion of the goodness of fit was also calculated [2].

Khodami (2017) has published her article on the topic of diagnosis of autism spectrum disorder using data mining techniques in the National Conference of New Technologies in Computer and Medical Engineering. The classification accuracy in nearest neighbor, support vector machine, simple Bayesian and neural network algorithms is 89%, 95%, 97% and 100% respectively. The accuracy value of 100% by the neural network algorithm indicates a better performance than the simple Bayesian, support vector machine and K-nearest neighbor algorithms [3].

Moradi (2015) has conducted research titled A Method for Autism Diagnosis through Blood Test. In this research, by using complex machine learning algorithms, the differences between the blood and urea of healthy and autistic children have been determined, and based on that, the biomarkers (measurable indicators of some biological or biological states and conditions) related to these conditions have been determined. In this study, the blood of 38 children with autism and 31 healthy children between 5 and 12 years old has been analyzed. According to this research, there is a direct relationship between autism and the presence of certain damaged proteins in the plasma, and the level of "d-tyrosine" and "end products of glycation" (AGE) is higher in children with this disorder. The results of this research increase the accuracy of autism diagnosis tests from the current level of 60-70% to 90% [4].

Hashemian has conducted her study on the diagnosis of autism disorder using the analysis of brain signals based on the processing of emotional faces. The mapping process is optimized by assigning weights to the vector components using the genetic algorithm. Finally, the corresponding vectors are entered into the classification stage by processing each of the emotional states of the face, finally, by integrating the information at the decision level of three SVM categories and applying the voting rule, the proposed algorithm is able to identify autistic patterns with 96.66% accuracy. Identify from Salem [5].

An article was compiled by Thabtah in collaboration with the Psychology Department of Huddersfield University in England and published on February 13, 2018. They were able to apply machine learning algorithms such as: support vector machine and decision tree and logistic regression in order to build predictive models on a data set from AGRE genetic database. This dataset contains the medical information of 623 people, 612 of whom are autistic and 11 are not autistic. The whole collection is evaluated by 29 features and only two labels "autism and non-autism" are used to classify them in opinions have been asked. On the other hand, the results showed that the support vector machine algorithm, with an accuracy of 98.2%, has a higher power in diagnosing autism spectrum disorder than the other two algorithms [6].

One of the best classifications done by Feczko et al. (2017) using random forest algorithm was on a statistical sample consisting of 105 children aged 9 to 13 years. Finally, this trained model was able to diagnose 58 children with behavioral disorders similar to autism out of 105 children, of which 31 were female and the rest were male. He also diagnosed those 47 other children definitely have autism spectrum disorder. Among them, 11 are female and the rest are male. On the other hand, in the presented model, sensitivity = 1.63%, specificity = 7.80%, accuracy = 2.72% have been reported [7].

In one of the articles recently published by Rutherford et al (2018), the average total waiting time for the diagnosis of autism spectrum disorder was estimated to be about 162 days, in which about 59% of all these people wait for the diagnosis of their disease. 119 days have been estimated [8].

In one of the articles published on May 28, 2018; Dvornek, N and colleagues stated that reaching a valuable choice can reduce the waiting time for disease diagnosis. Therefore, they looked for a better solution to prove their statements. This technique is based on the medical data set of 19 children with autism spectrum disorder who were subjected to a 19-week trial of the central behavior method; was applied and then by presenting a new validation framework and also using the pipeline method on several standard screening methods, they were finally able to reach a prediction model with the highest accuracy [9].

One of the approaches that has been evaluated by various researchers for several years; Feature selection is based on the cuckoo search algorithm. Thus, in one of the articles published in 2016 by Sudha, M. N. et al., he used this approach to select important features in the data set collected from breast cancer mass tissues. Then he implemented the k-NN classification algorithm according to the selected effective features for K values from 1 to 5. The proposed system calculated the average classification accuracy of 98.75% [10].



In another research conducted in 2017, Alia et al. were able to achieve a new developed algorithm for the classification task by combining binary cuckoo search and rough set theory. He compared the obtained results with the results obtained previously from the genetic algorithm and the PSO algorithm and finally came to the conclusion that the newly developed algorithm is less complicated, simpler to implement and has more effective parameters compared to other selection methods. The feature has higher convergence and better efficiency. On average, the best accuracy among these five data sets was reported for Breast Cancer data. Thus, the values of 93.9% for decision tree classification and 96.1% for simple Bayes classification were obtained [11]. M. Duda et al. (2016) worked on an article entitled "Using machine learning for the behavioral differentiation of autism and hyperactivity". These two disorders still comprise 10% of children today. In this method, by using the selection of forward features as well as testing and cross-validation of K-Fold 6 learning machine models on 65 cases of social responsiveness from 2925 people, 2775 of whom had autism and 150 had hyperactive disease. We found that 5 out of 65 behaviors measured by the screening tool are sufficient to differentiate these two disorders. Finally, a classifier with 96% accuracy was obtained [12].

### III. PROPOSED RESEARCH METHOD

The proposed method is a genetic machine learning system that combines the power of learning machine learning with the power of Naive Bayes inference and optimization of parameters by genetic algorithm so that it can learn from the previous cases with less time and can make the inference correctly. Naive Bayes (Kernel) has been used in learning. This operator produces a KernelNaiveBayes classification model using the estimated kernel density. Setting Naive Bayes (kernel) parameters was explained in the previous section. In the proposed system, K-fold crossvalidation technique should be used for better classification. The goal here is to implement a system that can correctly detect.

The method of work is to collect information and definitions and concepts of autism spectrum disorder, its cause and its difference in children and adults, and how it affects the communication, language and cognitive abilities and social behaviors of people with the disease. It is possible to examine the previous methods in the timely diagnosis of autism spectrum disorder in adults and compare these methods with each other, as well as the specialized examination of the matched algorithm using the combination of Bayes' law and genetic algorithm as a method for data classification. The previously prepared adult autistic patients are treated. And also, the investigation of how to implement it in order to reach an efficient algorithm is discussed in order to reach the appropriate diagnostic waiting time, and finally, the algorithm is implemented in the environment of Rapid Miner software, where the results obtained are recorded in it and with the previous presentations. It is assumed that finally the main idea is concluded.

### IV. RESULTS

In this research, a new dataset related to autism screening in adults is presented, which includes 20 features that are used for further analysis, especially in determining influential autism traits and improving the classification of ASD cases. In this dataset, 10 behavioral characteristics as well as 10 personal characteristics that have been shown to be effective in distinguishing ASD cases from controls in the behavioral sciences have been collected.

Table 1: Features in the input file

Variable name	Data type
Age	Numeric interval
Gender	Field
Nationality	Field
Jaundice	Bolin
Family member with ASD	Bolin
Country of residence	Field
Has used the screening program before	Bolin
Type of screening method	Integer
Question answer code based on the screening method used (10 questions)	Binary
Who completed the test? (Parents, caregivers, medical staff, doctors, etc.)	Field



The number of inputs is 293 lines, each line is related to a person's profile. The last column of the data file is dedicated to the target data. In this file, the input values of the features are measured according to rules, and the last column of the correct answer is generated based on the rules. When a person is healthy, yes is considered as No in case of autism diagnosis.

**4-1 The results of NaivoBiz performance**

It is mainly used to estimate how well a model (implemented by a particular learning operator) will perform in practice. Cross Validation Operator is a nested operator. There are two processes: a training process and a testing process. Subprocessing is used to train a model. Then the trained model is applied in the Testing subtest. The performance of the model is measured in the testing phase. The input sample is divided into k subsets of equal size. Of the k subsets, a single subset is retained as the test data set (ie, the input from the test processing). The remaining k - 1 subsets are used as the training data set (i.e., the input from the training process). Then the cross-validation process is repeated k times, and each of the k subsets is used exactly once as test data. The k results from the iterations are averaged (or otherwise combined) to produce a single estimate. The value of k can be set using the even number parameter. Evaluating the performance of a model in the set of independent tests has a good estimate of the performance in the missing data set. It also indicates whether "overshooting" is occurring. This means that the data model represents the test very well, but does not generalize well to new data. Therefore, performance can be significantly worse on test data.

Table 2: Accuracy of the results obtained from Naive Biz applications

accuracy: 88.33% +/- 5.20% (micro average: 88.30%)

	true NO	true YES	class precision
pred. NO	133	23	85.26%
pred. YES	10	116	92.06%
class recall	93.01%	83.45%	

Table (3) Precision obtained from Naive Biz applications

precision: 92.62% +/- 7.55% (micro average: 92.06%) (positive class: YES)

	true NO	true YES	class precision
pred. NO	133	23	85.26%
pred. YES	10	116	92.06%
class recall	93.01%	83.45%	

Table (4) Recall obtained from Naive Bayes applications

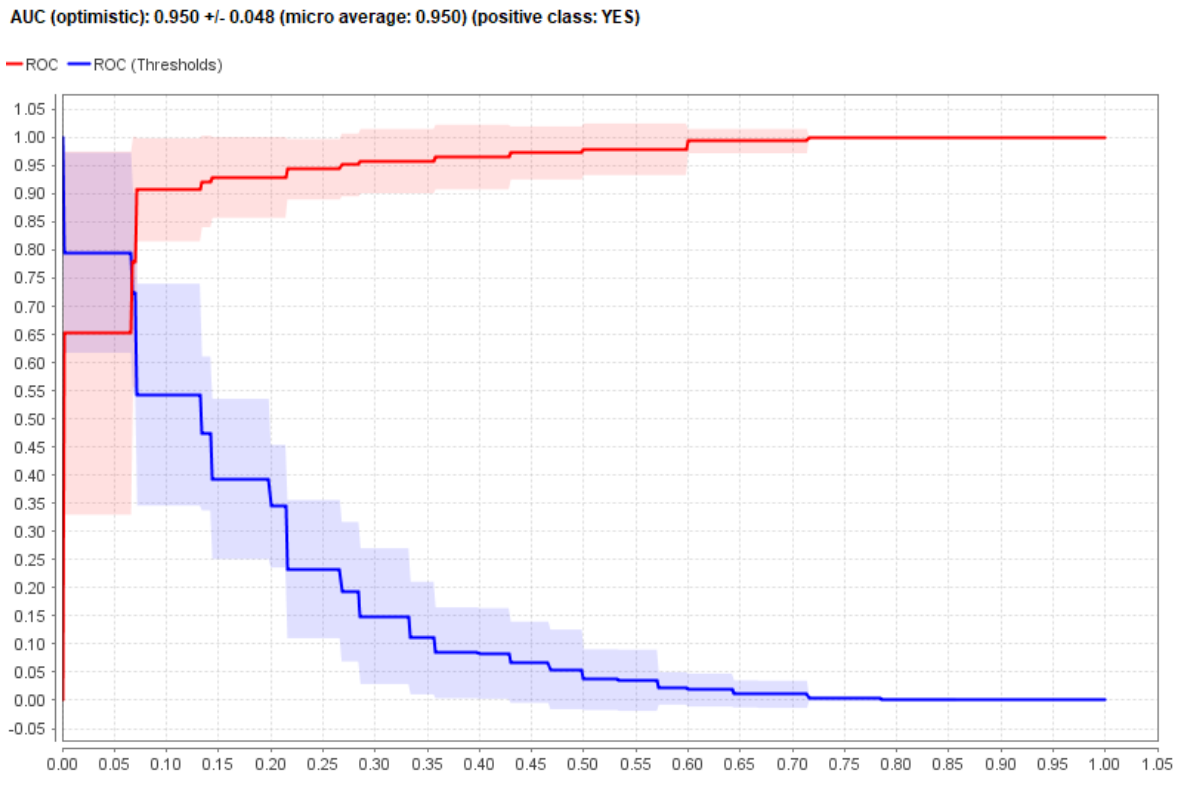
recall: 83.50% +/- 8.23% (micro average: 83.45%) (positive class: YES)

	true NO	true YES	class precision
pred. NO	133	23	85.26%
pred. YES	10	116	92.06%
class recall	93.01%	83.45%	

According to the results, NaiveBiz works with approximately 88.33% accuracy in the detection system.



The optimized AUC diagram is as follows:



Graph (1) of optimized AUC

4-2 The results of the event decision tree function

First, by pre-processing the data values, data with an unknown number of data greater than or equal to 2 have been removed. Then the unknown values are placed with the average value and normalized. At the end, the extraneous data is removed. 282 records have been selected as suitable records for review. These values have been checked with the decision tree as 70% learning and 30% testing as well as cross validation.

Table (5) Precision obtained from applying the decision tree on the data

precision: 90.96% +/- 6.88% (micro average: 90.65%) (positive class: YES)

	true NO	true YES	class precision
pred. NO	130	13	90.91%
pred. YES	13	126	90.65%
class recall	90.91%	90.65%	

Table (6) Recall obtained from applying the decision tree

recall: 90.65% +/- 4.80% (micro average: 90.65%) (positive class: YES)

	true NO	true YES	class precision
pred. NO	130	13	90.91%
pred. YES	13	126	90.65%
class recall	90.91%	90.65%	



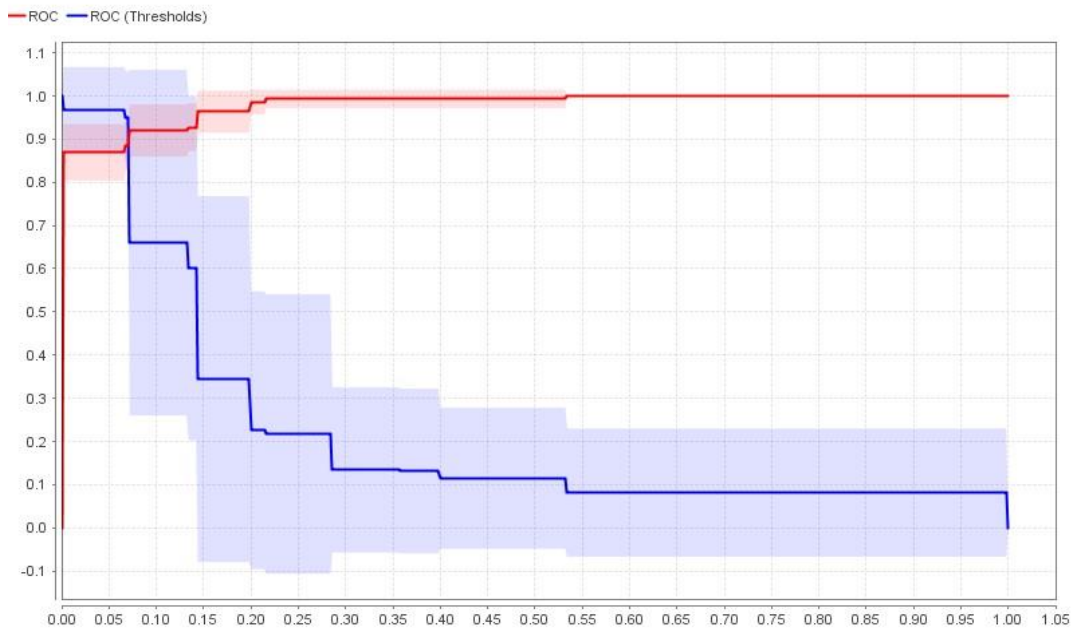
Table (7) Accuracy obtained from applying the decision tree

accuracy: 90.79% +/- 4.41% (micro average: 90.78%)

	true NO	true YES	class precision
pred. NO	130	13	90.91%
pred. YES	13	126	90.65%
class recall	90.91%	90.65%	

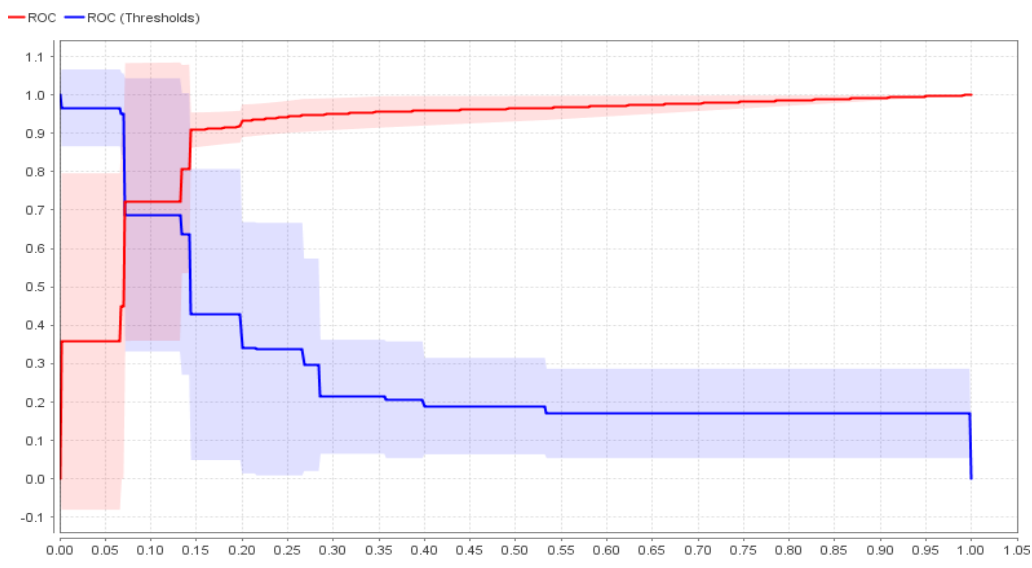
The optimized and normal AUC diagram is as follows:

AUC (optimistic): 0.980 +/- 0.015 (micro average: 0.980) (positive class: YES)



Graph (2) AUC optimized from applying decision tree to data

AUC: 0.908 +/- 0.046 (micro average: 0.908) (positive class: YES)



Graph (3) AUC in a typical way of applying the decision tree to the data



**4-3 Results obtained from NaiveBiz (Kernel)**

In this research, Naive Biz (Kernel) is used. Then the unknown values are placed with the average value and normalized. At the end, the extraneous data is removed. 293 records have been selected as suitable records for review. These values have been checked with support vector machine as 70% learning and 30% testing as well as cross validation. Its results in sensitivity, specificity and accuracy are shown below.

Table (8) four system performance modes in the Naive Bayes (kernel) method

TP=134	FN=16
FP=9	TN=123

**NaivoBiz parameters:**

laplace correction estimation mode: full bandwidth selection: heurisitc

Table (9) Recall obtained by applying Naive Bayes (kernel) on the data

recall: 90.65% +/- 4.80% (micro average: 90.65%) (positive class: YES)

	true NO	true YES	class precision
pred. NO	130	13	90.91%
pred. YES	13	126	90.65%
class recall	90.91%	90.65%	

Table (10) Accuracy obtained from applying Naive Bayes (kernel) on the data

accuracy: 91.15% +/- 6.75% (micro average: 91.13%)

	true NO	true YES	class precision
pred. NO	134	16	89.33%
pred. YES	9	123	93.18%
class recall	93.71%	88.49%	

Table (11) Accuracy obtained from the application of Naive Biz (kernel) on the data

precision: 98.53% +/- 3.40% (micro average: 98.11%) (positive class: NO)

	true yes	true NO	class precision
pred. yes	366	121	75.15%
pred. NO	4	208	98.11%
class recall	98.92%	63.22%	

**4-4 Genetic Algorithm Performance with Naive Bayes (Kernel)**

First, by pre-processing the data values, data with an unknown number of data greater than or equal to 2 have been removed. Then the unknown values are placed with the average value and normalized. At the end, the extraneous data is removed. 699 records have been selected as suitable records for review. These values have been checked with genetic algorithm and support vector machine as 70% learning and 30% testing as well as cross validation. To check and compare the results of combining genetic algorithm and support vector machine, different criteria were selected and checked. These criteria are:





Table (12) results obtained from combining genetic algorithm with Naive Bayes (kernel)

Population size	P Initialize	P Crossover	P Generate	C	Accuracy
5	0.5	0.5	0.1	1.0	99.01 %
10	0.7	0.7	1.0	1.0	99.00%
15	0.5	0.5	1.0	1.0	:99.6%
15	1.1	1.1	1.0	1.0	99.00%

In the adjustment index based on the genetic algorithm, the highest accuracy is obtained with a combination of populationsize = 5, initialize = 0.5, p = 0.5 cross and p = 1.0. The accuracy of the results reaches 99.06%.

Accuracy, sensitivity and accuracy are checked below:

Table (12) accuracy obtained from the combination of genetic algorithm with Nano Bayes (Kernel)

Table (13) Accuracy obtained from combining the algorithm with genetics with Nano Bayes (kernel)

accuracy: 94.25%

	true NO	true YES	class precision
pred. NO	44	4	91.67%
pred. YES	1	38	97.44%
class recall	97.78%	90.48%	

Table (14) Precision obtained from the combination of genetic algorithm with Nano Bayes (kernel)

precision: 97.44% (positive class: YES)

	true NO	true YES	class precision
pred. NO	44	4	91.67%
pred. YES	1	38	97.44%
class recall	97.78%	90.48%	

Table (15) Recall obtained from the combination of genetic algorithm with Nano Bayes (kernel)

recall: 90.48% (positive class: YES)

	true NO	true YES	class precision
pred. NO	44	4	91.67%
pred. YES	1	38	97.44%
class recall	97.78%	90.48%	

4-5 Comparison of results

The optimized and normal AUC diagram is as follows:

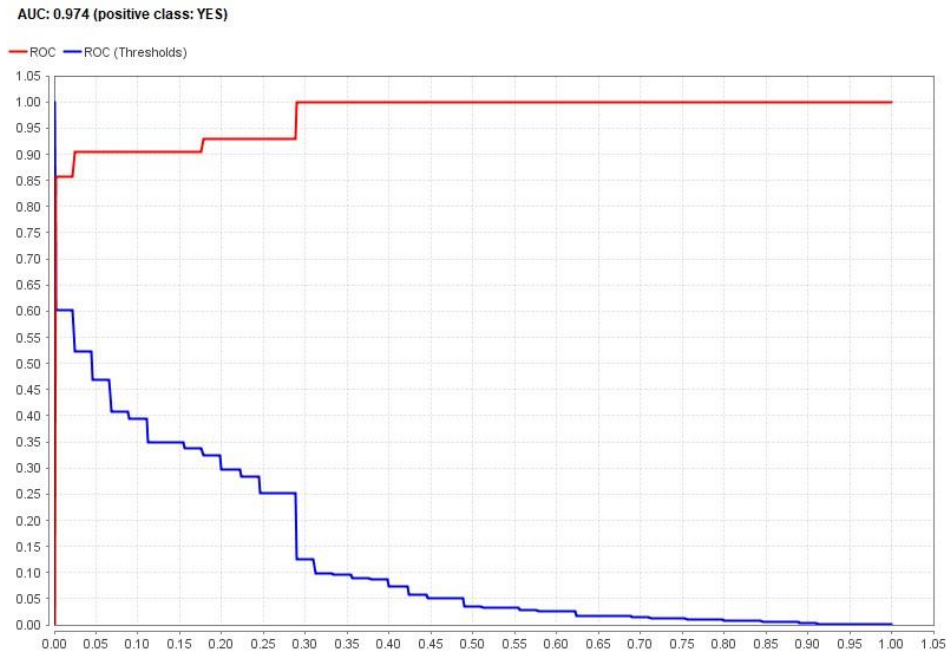


Diagram (4) AUC diagram in the usual way combining genetic algorithm with Naive Bayes (kernel)

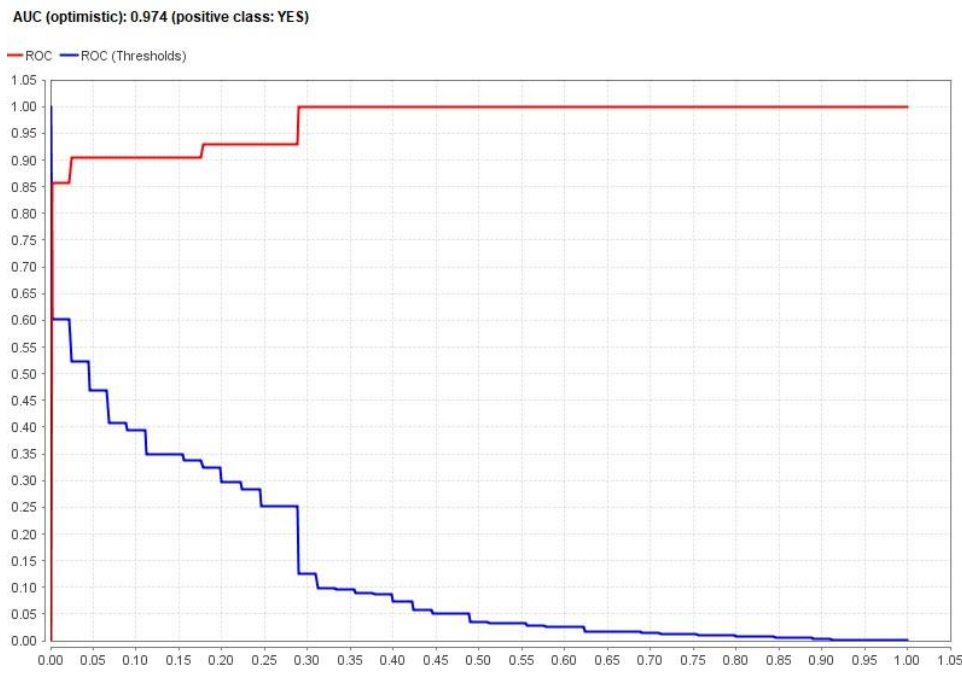


Diagram (5) AUC Diagram optimally combining genetic algorithm with Naive Bayes (kernel)

As can be seen, the combined method of Naive Bayes (kernel) and genetic algorithm has the highest accuracy compared to the rest of the implementation methods. The decision tree gives the best accuracy after the hybrid model. Of course, in the simulations that have been carried out, the hybrid method has a significantly higher training time than the decision tree method, so we can ignore this slight increase in accuracy compared to the huge training time. Ignoring this small amount due to high training time, the support machine with combined training gives the best answer and also has much less training time than other methods.



## V. CONCLUSION

Diagnostic systems play an important role in the treatment and life of the patient. Incorrect and untimely diagnoses in many diseases cause irreparable damage to the patient and the health care system. The aim of this research is to improve the diagnosis of autism spectrum disorder in adults by combining Bayes' rule and genetic algorithm. It has been tried to improve the diagnosis of this disease with the input information by selecting the feature and using Naive Biz. For this, the information of 289 patients was used in the system. In the proposed system, the diagnosis of autism spectrum disorder in adults has been made using the combined training method of Bayes' rule and genetic algorithm. K-fold crossvalidation method was used to optimize input data and optimal diagnosis. These data were used in other methods in addition to the proposed method. The results indicate that the proposed method, the combination system of Bayes' rule and genetic algorithm, gives the best answer with an accuracy of approximately 94.25% due to less time.

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