Iraqi Journal for Computer Science and Mathematics

Volume 5 | Issue 4 Article 11

2024

Explainable Machine Learning Approach enables Computer-Aided Identification System for Children Autism Spectrum Disorder (C-ASD)

Karrar Hameed Abdulkareem
College of Agriculture, Al-Muthanna University, Samawah 66001, Iraq, khak9784@mu.edu.iq

Zainab Hussein Arif
College of Arts, University of Al-Qadisiyah, Al-Qadisiyah Province, 58002, Iraq, zhussian94@gmail.com

Mazin Abed Mohammed
Department of Artificial Intelligence, College of Computer Science and Information Technology, University of Anbar, Anbar 31001, Iraq, mazinalshujeary@uoanbar.edu.iq

Recommended Citation

Abdulkareem, Karrar Hameed; Arif, Zainab Hussein; and Mohammed, Mazin Abed (2024) "Explainable Machine Learning Approach enables Computer-Aided Identification System for Children Autism Spectrum Disorder (C-ASD)," *Iraqi Journal for Computer Science and Mathematics*: Vol. 5: Iss. 4, Article 11.
DOI: https://doi.org/10.52866/2788-7421.1216
Available at: https://ijcsm.researchcommons.org/ijcsm/vol5/iss4/11

IRAQI JOURNAL FOR COMPUTER SCIENCE AND MATHEMATICS 2024;5:118–130

RESEARCH ARTICLE

Explainable Machine Learning Approach enables Computer-Aided Identification System for Children Autism Spectrum Disorder (C-ASD)

Karrar Hameed Abdulkareem [a,*], **Zainab Hussein Arif** [b], **Mazin Abed Mohammed** [c]

[a] College of Agriculture, Al-Muthanna University, Samawah 66001, Iraq
[b] College of Arts, University of Al-Qadisiyah, Al-Qadisiyah Province, 58002, Iraq
[c] Department of Artificial Intelligence, College of Computer Science and Information Technology, University of Anbar, Anbar 31001, Iraq

ABSTRACT

Neurodevelopmental disorders like autism spectrum disorder (ASD) cause significant cognitive, linguistic, object identification, communication, and social skills deficits. Although there is currently no cure for autism spectrum disorder (ASD), early detection can aid in diagnosis and implementing effective preventative measures. Artificial intelligence (AI) tools allow for an earlier diagnosis of ASD than was previously possible. Furthermore, many clinical and not clinical attributes can be used for identification of ASD but select the most proper ones still challenge. Therefore, in this study we propose a Computer-Aided Identification System based on machine learning concept and feature selection methods to diagnosis Children Autism Spectrum Disorder (C-ASD) cases. Two main feature selection methods namely Gain Ratio (GR) and Chi-squared ($\chi 2$) that used to rank then select best subset C-ASD attributes. In order to identify ASD cases, four machine learning algorithms are used into proposed system for identification purpose namely, Neural Network (NN), Random Forest (RF), K-Nearest Neighbors (KNN), and Support Vector Machine (SVM). A dataset contained 1045 cases with 18 attributes employed for feature selection and C-ASD identification processes. C-ASDs are identified into binary classification approach namely negative and positive C-ASD classes. The results indicate only 10 attributes instead of 18 are significant into identification process. We found that each of RF and NN performed better than other classifiers where both classifiers score accuracy reach to 100 % based selected subset. This supports the idea that these models might be used for screening for C-ASD at an early stage of test-bed applications.

Keywords: Children Autism Spectrum Disorder (C-ASD), Machine learning, Feature ranking, Feature selection, Identification

1. Introduction

Limitations in social interactions, communication, and behavior are hallmarks of autism spectrum disorder (ASD), a neurodevelopmental disorder [1]. Social collaboration, play, creative thinking, repetitive routines, and correspondence are only a few of the non-genetic characteristics linked with behavior used in the fundamental analysis of individuals with ASD [2]. Current estimates show that around 1.5% of the population is on the range, and it is widely assumed that many people on the spectrum go undiscovered [3]. The increasing vigilance of those with ASD necessitates, therefore, the availability of facilities for rapid analysis [4]. Traditional behavioral investigations, however, are inadequate for detecting and diagnosing ASD. Several factors, including the degree of severity of the symptoms, ASD may be diagnosed later than age two. Whereas there are a variety of clinical techniques available for early detection of ASD, they are

Received 13 July 2024; accepted 16 August 2024.
Available online 25 November 2024

* Corresponding author.
E-mail addresses: khak9784@mu.edu.iq (K. H. Abdulkareem), zhussian94@gmail.com (Z. H. Arif), mazinalshujeary@uoanbar.edu.iq (M. A. Mohammed).

https://doi.org/10.52866/2788-7421.1216

frequently not employed until there is a high suspicion or risk of ASD progress.

Only trained medical personnel should make a diagnosis. Healthcare providers will utilize standardized diagnostic tools for determining a child's autism diagnosis. They will also interview the child's parents or primary caregivers to better understand the child's present behavior and past development [5]. The Autism Diagnostic Observation Schedule (ADOS), the Autism Diagnostic Interview-Revised (ADI-R), and the Diagnosing and Statistical Manual of Mental Disorders, Fifth Edition (DSM-5) are the three most common diagnostic tools used to identify autistic individuals today [6]. Doctors use standardized diagnostic methods to make ASD diagnoses. Still, this method has a fundamental problem: the evaluation and interpretation of results take a long time to complete. An intelligent machine-learning strategy has been presented as a remedy for this issue. They minimize diagnostic time while increasing accuracy, a fundamental goal of machine learning studies into autism spectrum disorder. Patients with ASD will benefit from faster diagnosis and subsequent treatments. Another goal of machine learning is to reduce the complexity of each input dataset so that the highest-scoring ASD characteristics may be identified [7].

The rapidly expanding discipline of machine learning aims to build excellent prediction models from the corresponding study datasets. It incorporates several forms of prediction, including search algorithms, AI, mathematical modeling, and more [8]. Support vector machine, rule-based classifiers, decision trees, and Neural networks, are the mainstays of machine learning techniques since they are fully automated and require little to no human intervention when processing data. Diagnosing autism spectrum disorder mainly entails sorting input features into the appropriate class (autism spectrum disorder or other). Intelligent technologies, such as machine learning, can make the process seem like a prediction task [9]. Therefore, experts develop automated methods or classifiers employing machine learning to determine if a child has ASD. The diagnostic class prediction performance of the computerized tool is evaluated by running test instances; the tool's design is informed by the input dataset [7].

Several studies have investigated the feasibility of various ML methods for ASD detection and diagnosis. Support Vector Machines (SVM), Naive Bayes (NB), Logistic Regression (LR), and K-Nearest Neighbors (KNN) were only a few of the models employed in our data by the authors of [10]. Our paper's primary goal is to aid in the early identification of ASD by establishing whether or not the child is at risk. Omar et al. [11] provided a helpful machine learning approach in which they used Random Forest (RF), Regression Trees and Classification (CART), and Random Forest-Iterative Dichotomiser 3 (ID3) to examine the AQ-10 and 250 actual datasets. Using the CFS-greedy stepwise feature selector, Sharma et al. [12] dug into these datasets and employed several methods, including The NB, Stochastic Gradient Descent (SGD), the KNN), Random Tree (RT), and K-Star (KS). Using several tree-based classifiers, Satu et al. [13] analyzed data from children aged 16 to 30 and identified several rules for autism and typical development. Similar datasets were analyzed by Erkan et al. [14], who used KNN, SVM, and RF to determine which was more effective in detecting autism spectrum disorder. Several feature selection methods are discussed in [15], along with the collection of ASD datasets from infants to teenagers. The datasets were then used with several classifiers. They discovered that SVM outperformed other classifiers for the RIPPER-based toddler subgroup, with an accuracy of 97.82%. Finally, in [16], early-detected ASD datasets for toddlers, children, adolescents, and adults were collected and subjected to various feature transformation techniques, such as log, Z-score, and sine functions. These adjusted ASD datasets were then used to test the efficacy of different categorization strategies. For the youngest age group, SVM performed best, followed by Adaboost for the next age group up, Glmboost for the following age up again, and Adaboost for the adult dataset.

All previous studies have presented significant identification performance for ASD cases especially those adapted a specific features selection method. However, most of used feature selection methods have selected different ASD subset attributes and there is a clear different into number of selected features. Therefore, the main challenge which are the feature selection methods that are matched into type and number of ASD selected subset that can be generalize for any identification problem of ASD. Furthermore, some room still available for improvements the identification accuracy of ML algorithms for ASD cases. The contribution of proposed works lays into following points:

- Propose a Computer-Aided Identification System for Children Autism Spectrum Disorder (C-ASD) based on machine learning adapted algorithms.
- Propose two feature ranking and selection methods namely Gain Ratio (GR) and Chi-squared ($\chi 2$) to select best C-ASD attributes that employed for identification of C-ASD cases.
- Implement four machine learning techniques namely, NN, RF, KNN and SVM for identification of identification of C-ASD cases.

- Evaluate and validate the proposed system based on explainable ML techniques to identify the most important features for diagnosing Children with Autism Spectrum Disorder (C-ASD).

The sections of our study are structured as follows. Section 2 includes materials and methods, covering the ASD dataset, feature selection methods, and ML algorithms. Section 3 explains on the study's outcomes and discusses these findings. To end, Section 4 comprises the conclusion and discussion of possible future research opportunities.

2. Methodology

Specialty doctors place a premium on promptly diagnosing autism spectrum disorder. After that, we cover the many clinical screening approaches used to identify individuals with ASD. These include the Joseph Picture Self-Concept Scale, the Social Responsiveness Scale, the Autism Childhood Autism Rating Scale (CARS), the Autism Diagnostic Observation Schedule (ADOS), and the Diagnostic Interview-Revised (ADI-R). Specialist doctors are keenly interested in clinical screening approaches because of their efficacy in diagnosing ASD. Furthermore, these strategies aid in addressing and avoiding the onset of ASD. There are numerous benefits to the listed approaches, but experts will constantly be faced with new obstacles. Many medical professionals have voiced their displeasure with clinical screening processes because of the time and effort required to complete and interpret lengthy questionnaires.

Several feature subsets were created using a variety of feature selection techniques that were employed in this work. Then, key toddler datasets and associated feature subsets were subjected to several machine-learning identification techniques. The effectiveness of several classifiers was studied to identify the best set of characteristics for making the ASD diagnosis over controls. Early detection of ASD using the suggested approach is shown in Fig. 1.

2.1. Dataset and data distribution

Our research relies on a dataset [17] with categorical, continuous, and binary features produced by Dr. Fadi Thabtah [18]. The original dataset contained 1054 instances and 18 characteristics (including a class variable). The Q-CHAT-10 and AQ-10 tools (AQ-10 Child, AQ-10 Adolescent, and AQ-10 Adult) were utilized to create the ASDTests app, which is used for screening and detecting ASD risk factors. A final score more excellent than 6 out of 10 implies an optimistic prediction of ASD using this app's scoring system, which goes from 0 to 10. Values between 1 and 10 are assigned to each item.

2.2. Data preprocessing

Pre-processing is a crucial part of most detection systems, and it is used to prepare the data for the following stage [19]. Due to several category and non-contributing features in the dataset, pre-processing was required. "pre-processing" describes the steps taken before data collection is fed into a model. It is performed to improve raw data quality for subsequent use in instruction and analysis. We got rid of the Case_No characteristics because they were not helping anything. Label encoding is being used for dealing with the category values. To make labels machine-readable, Label encoding turns them into numbers. When a label appears many times, the previous value is used. We have chosen to binary Label encode four characteristics with two classes: sex, jaundice, the family member with autism spectrum disorder (ASD), and class/ASD traits. More than two classes render Label Encoding useless. For more info all details of dataset are displayed into Table 1.

2.3. Feature ranking and selection

One of the most significant difficulties in developing a reliable prediction ML approach from highly dimensional data is overcoming the curse of complexity [20]. If they are used to directly train ML classification algorithms, the resulting model will likely be overfitted, meaning it will do well on the training data and badly in the real world. When a model incorrectly interprets noise and random fluctuations as a learned idea, this is known as overfitting. In addition, having an excessive amount of features causes unnecessary and redundant features to clog up the learning process, significantly extending the learning and computing time [21].

One popular technique for dealing with too many characteristics or ones that are not useful is rating and selecting features. To minimize the dimension of the training data, feature selection techniques often exclude observations that 1) have little to no predictive potential for the phenotypic class and 2) are redundant with other observations [22]. Careful feature selection may increase learning effectiveness, prediction accuracy, and learned output complexity [23]. In addition, it is commonly believed that the illness data included in the prediction model (after feature selection) are linked to loci that are technically or connected functionally to the etiology of the underlying disease [24]. Therefore, getting insight into the disease's underlying biological processes may

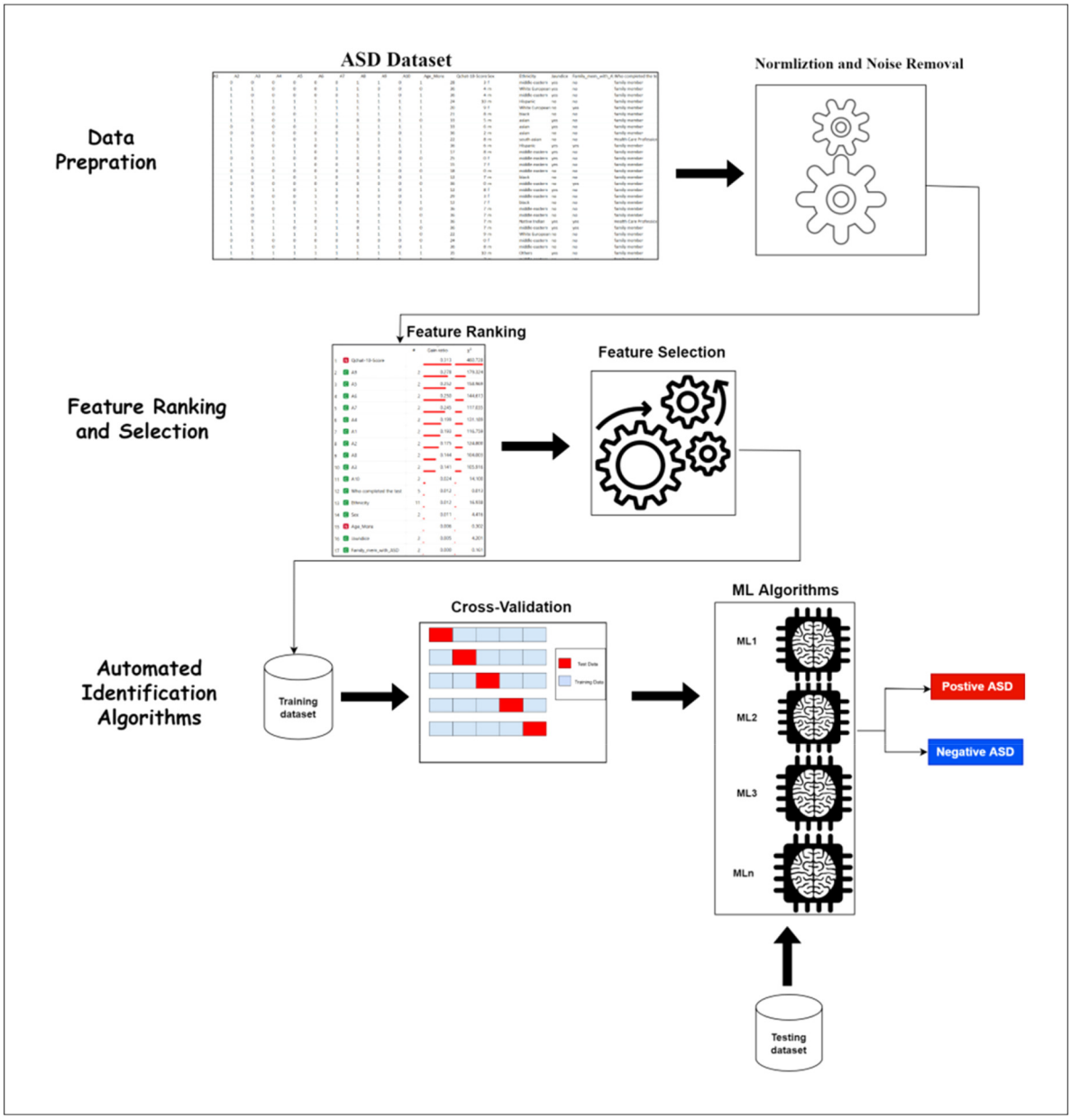

Fig. 1. Proposed system for identification of C-ASD cases.

be possible by selecting a subset of the most critical data (through feature selection) [25]. Feature selection in this setting can be compared to detecting illnesses linked to phenotypes in secondary data [26]. We have selected two main feature ranking and selection methods namely Gain Ratio (GR) and $\chi 2$ statistical methods.

2.3.1. Gain Ratio (GR) method

The GR results when a collection is divided according to its qualities and the best possible candidate is selected. Our research made use of GR [27], which is determined using the formula:

$$GR\,(x) = \frac{H\,(c) - H(c|x)}{H\,(x)} \tag{1}$$

Where

$$H(x) = -p_x log_2(p_x) \tag{2}$$

(with px symbolizing the likelihood of a feature selection x),

$$H\,(c) = -p_c log_2\,(p_c) \tag{3}$$

Table 1. Distribution of dataset per each class.

No	Feature name	Data Type	Data distribution
1	A1	Boolean	460 (0) 591 (1)
2	A2	Boolean	581 (0) 473 (1)
3	A3	Boolean	631 (0) 423 (1)
4	A4	Boolean	514 (0) 540 (1)
5	A5	Boolean	501 (0) 553 (1)
6	A6	Boolean	446 (0) 608 (1)
7	A7	Boolean	369 (0) 685 (1)
8	A8	Boolean	570 (0) 484 (1)
9	A9	Boolean	538 (0) 516 (1)
10	A10	Boolean	436 (0) 618 (1)
11	Age_Mons	Integer	67 (Age_Mons > 13) 18 (Age_Mons=13) 19 (Age_Mons=14) 31 (Age_Mons=15) 13 (Age_Mons=16) 12 (Age_Mons=17) 16 (Age_Mons=18) 21 (Age_Mons=19) 21 (Age_Mons=20) 13 (Age_Mons=21) 27 (Age_Mons=22) 28 (Age_Mons=23) 70 (Age_Mons=24) 26 (Age_Mons=25) 36 (Age_Mons=26) 23 (Age_Mons=27) 42 (Age_Mons=28) 24 (Age_Mons=29) 67 (Age_Mons=30) 30 (Age_Mons=31) 30 (Age_Mons=32) 36 (Age_Mons=33) 34 (Age_Mons=34) 350 (Age_Mons≥35)
12	Qchat-10-Score	Integer	54 (Qchat-10-Score < 1) 88 (Qchat-10-Score=1) 88 (Qchat-10-Score=2) 96 (Qchat-10-Score=3) 110 (Qchat-10-Score=4) 120 (Qchat-10-Score=5) 96 (Qchat-10-Score=6) 135 (Qchat-10-Score=7) 97 (Qchat-10-Score=8) 170 (Qchat-10-Score≥9)
13	Sex	String	735 (Male) 319 (Female)
14	Ethnicity	String	40 (Hispanic) 26 (Latino) 3 (Native Indian) 35 (Others) 8 (Pacifica) 334 (White European) 299 (Asian) 53 (Black) 188 (Middle Eastern) 8 (Mixed) 60 (South Asian)
15	Jaundice	String	766 (No) 288 (Yes)
16	Family_mem_with_ASD	String	884 (No) 170 (Yes)
17	Who completed the test	String	24 (Health care professional) 3 (Others) 4 (Self) 1018 (Family member)

(*continued on next column*)

Table 2. Calculation table for the x^2 test score [30].

	Positive class	Negative class	Total
Feature Xi occurs	P	N	p+n=m
Feature Xi does not occur	Λ	D	λ+d=t-m
Total	p+ λ =c	n+d=t-c	t

The degree of entropy of an instance with feature x, the entropy of class c, and the conditional entropy of feature x given class c are, respectively, H(c|x) and (where pc is the probability of picking an instance in class c). Features are prioritized based on their gain ratio, which considers the chances of every feature value to decide which ones are most important. The data provided for the gain (H(c)-H(c|x)) of a feature is normalized against its entropy using the Gain Ratio, additionally referred to as the uncertainty coefficient [28].

2.3.2. Chi-Squared (χ2):

One way to gather features based on their connection with the projected class is using the chi-squared (2) test. Chi-square statistics are calculated for each feature (Xi) that is not negative to see which characteristics are dependent on the projected attribute. If the chi-square score is high, the feature is susceptible to the projected class [29]. The 13 most popular features are first listed by their two test scores. The following characteristics comprise the two test ranks for a binary classification problem: Let us pretend there are two types of cases, positive and negative, and t cases total. We built Table 2 to compute the two scores.

Where (m) is the total number of occurrences where feature (Xi) is present, (t-m) is the total number of events where feature (Xi) is absent, (c) is the total

number of positive occurrences, and (t-c) is the total number of unfavorable circumstances.

Following a GR and two feature ranking, we sought the highest-scoring subset of features (n). At first, we only considered features with the top 2 scores (n = 1). As a second method, we focused on the two traits with the highest average scores (n = 5). After making this choice, the SVM model was run with the data. We repeated this approach until we found the optimal ranking feature subset (n = 10), significantly improving performance.

2.4. Machine learning algorithms

2.4.1. Support Vector Machine (SVM)

Classification and Regression issues are both amenable to using the SVM [31]. However, the majority of its applications in ML are for classification tasks. To classify fresh data points efficiently in the future, the SVM algorithm seeks to find the optimal line or decision boundary that divides the space into distinct classes. A hyperplane describes this optimal choice boundary. An SVM locates the best possible hyperplane to classify data into two groups. Kernel linear, polynomial, radial basis or quadratic functions are very defining. Optimal functional classification of instance x_0:

$$f\left(s'\right) = Sgn\left[\sum_{i=1}^{z} a_i\, d_i K(s_i, s') + b\right]$$
$$0 \le a_i \le C, \quad (4)$$
$$\sum a_i\, d_i = 0,$$
$$a_i \ge 0, i = 1, 2, \ldots, Z$$

K(s_i,s') is the kernel function that maps the input vectors into a broader feature space [28]. Here, Z is the number of training examples, s_i is the feature vector of a single instance, and d_i is the occurrence's class label.

2.4.2. K-Nearest neighbours

The KNN is a classifier based on supervised learning that makes grouping predictions based on how closely two data points are located to one another. KNN is based on the following premise: The first step is to determine how far away the new sample is from the training sample; the second step is to identify the K nearest neighbours; the third step is to assign each neighbor a score; and the fourth step is to transfer the new sample a score based to the class to which it belongs [32]. First, we must determine a distance in the parameters space using Eq. (5) to identify the nearest neighbours quantitatively.

$$DS_j = \sqrt{\sum_{i=1}^{ndim} (xa_i - ya_i)^2} \quad (5)$$

Where xai and yai are prediction amounts at discovered and unidentified areas, and since DSj is the total length in the space of parameters from the jth noticed datum to the location we are attempting to predict, we use L2normalized (i.e., Euclidean) distance to calculate these distances [33].

2.4.3. Random Forest (RF)

The RF is a well-known ML algorithm part of the supervised learning method. It is put to use in situations requiring classification or regression. It constructs decision trees from many samples and uses the tally with the highest confidence for categorization, or the average in the regression case [34]. For a given collection of training papers containing Dc and Nsf features, the RF method may be defined as [35]:

1. Initial: $Dc1$, $Dc2$,$\ldots\ldots Dc_K$ using a systematic sampling method that includes a replacement component.
2. Second, Dc_K builds a decision tree technique for each text. Using the features supplied, a random sample of training papers is drawn from the subspace of the m-try dimension. Determine every conceivable probability using the m-try features. The optimal data partitioning is achieved at the leaf node. The procedure will be repeated until the saturation condition is met.

Use the highest probability value for a classification decision by combining a random forest ensemble of K unpruned trees $h_1(X_1)$, $h_2(X_2)$, etc.

2.4.4. Artificial Neural Network

Multilayer perceptrons are a popular NN method in visual, auditory, and linguistic recognition systems. The multilayer perceptron has been widely used in recent research for medical diagnostics [36]. The input, hidden, and output layers comprise the multilayer perceptron, a feedforward NN. An input layer receives the data, while an output layer receives the results from a hidden layer.

3. Results and discussions

The selected method is trained using the preprocessed dataset once the hyperparameter settings have been adjusted. During this phase, the algorithm is "taught" to connect the feature values (i.e., see

Table 3. Hyper-parameters of training and validation process.

Algorithm	Hyper-parameters
SVM	Kernel=Polynomial Iteration limit=100 Cost(c)=1.00
KNN	Number of neighbours =5 Metric=Euclidean Weight=uniform
RF	No of trees=10
NN	Neurons in hidden layer=200 Activation function=Relu Maximum no of iterations=200

Table 3, A1–A10) and the positive and negative C-ASD class labels. Predictive performance (accuracy, precision, and AUC) is verified once the trained model has been learned. To evaluate the model's performance on unseen data, K-fold cross-validation is commonly used. Overfitting the training data is avoided by using cross-validation on new data. The training dataset is divided into equal K pieces for use in cross-validation; each of these parts serves as a validation/testing set. For instance, in 5-fold (K = 5) cross-validation, the data set is cut in half five times. The approach is then trained using four components, with the fifth used to evaluate its efficacy. Repeat this procedure five more times to ensure that every possible combination has been tested. The model's overall performance is then assessed by averaging the results from each test set.

Cross-validation's estimated method performance can be utilized to inform further iterations of optimization. Iterative refinement involves reiterating and improving upon various components of the model-building process (steps 1–4). Experimenting with multiple settings, such as hyperparameter tuning, learning methods, feature selection techniques, and quality control criteria, is possible. The identification algorithm is built from the set of options whose average performance is highest after being subjected to cross-validation. Model selection refers to deciding upon an appropriate model development pipeline. An external dataset can verify the model's predictive accuracy before the final identification method is employed for illness identification prediction.

As mentioned before two methods have employed for features ranking then select the most influence subset, the result of this process have presented into Table 4.

According to Table 4, GR and x2 methods have selected only ten features an significant ones for classification process which are (A1, A2, A3, A4, A5, A6, A8, A9, and Q-CHAT-10). However, each of (A10, Who completed the test, Ethnicity, Sex, Age_Mons, Jaundice, and Family_mem_with_ASD) have scored very poor performance under the rules of two mentioned features selection methods.

Table 4. Features ranking and selection results.

		#	Gain ratio	χ^2
1	N Qchat-10-Score		0.313	460.728
2	C A9	2	0.278	179.324
3	C A5	2	0.252	158.969
4	C A6	2	0.250	144.613
5	C A7	2	0.245	117.035
6	C A4	2	0.199	131.189
7	C A1	2	0.193	116.759
8	C A2	2	0.175	124.800
9	C A8	2	0.144	104.003
10	C A3	2	0.141	105.916
11	C A10	2	0.024	14.100
12	C Who completed the test	5	0.012	0.013
13	C Ethnicity	11	0.012	16.938
14	C Sex	2	0.011	4.416
15	N Age_Mons		0.006	0.302
16	C Jaundice	2	0.005	4.201
17	C Family_mem_with_ASD	2	0.000	0.161

Table 5. Identification of ASD results based on machine learning algorithms.

Algorithm	AUC	Accuracy	F1	Precision	Sensitivity
SVM	99.2%	95%	95%	96%	95%
KNN	98.5%	99%	98%	99	98
RF	100%	100%	100%	100%	100%
NN	100%	100%	100%	100%	100%

Q-CHAT-10 features have gained highest score based on calculation procedures into GR and x2.While Family_mem_with_ASD feature have obtained the lowest score followed by each of (Who completed the test, Ethnicity, Sex, Age_Mons, Jaundice, and A10).

The efficiency ten selected subset features must be show significant in terms of identification process based on machine learning algorithms. In this direction, four machine learning algorithms have been used for identify the ASD disease into children which are SVM, KNN, RF, and NN. The performance of four mentioned algorithms have verified based on well-known measurements such as Area Under Curve(AUC),Accuracy,F1-Score,Precision,and Recall as shown into Table 5.

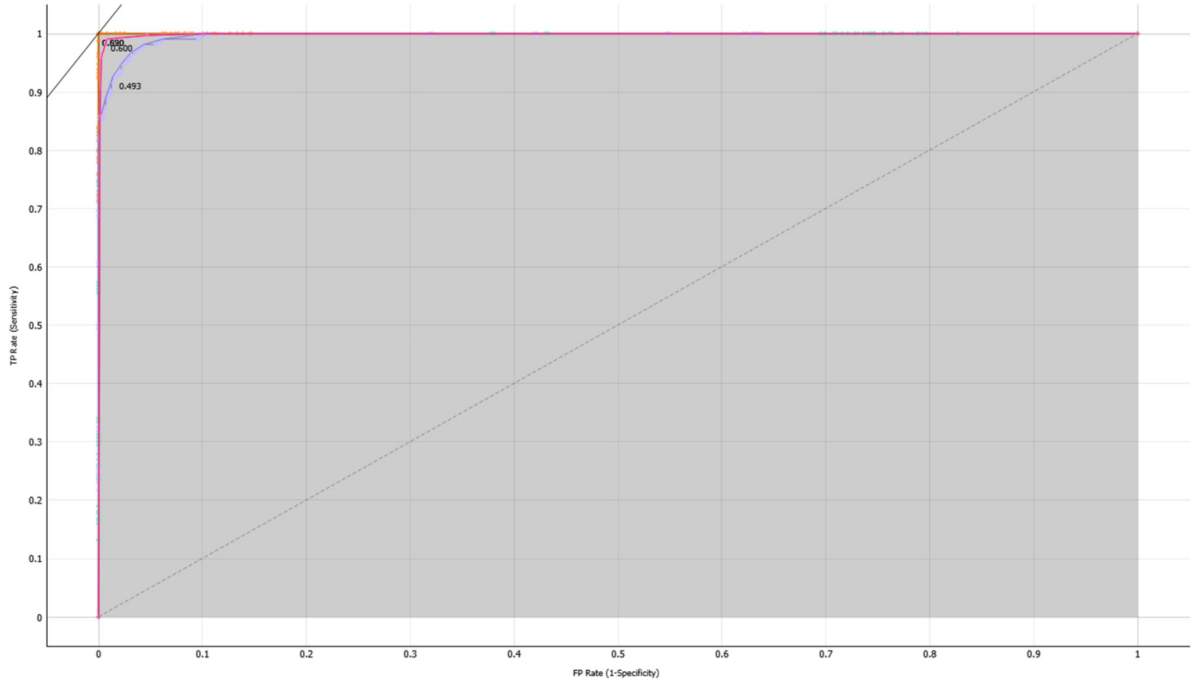

Fig. 2. ROC for negative C-ASD class.

According to Table 5, the performance of classification into all identification algorithms is significant. Thus, the selected ten features have great impact on the classification process without regard to the type of classifier. Each of RF and NN has presented the highest scores in all evaluation metrics. This followed by KNN algorithm with difference only 1%.However, the lowest score have recorded by SVM algorithm with difference reach to 5% from RF and NN in terms accuracy, F1, and Recall. However, according to literature SVM still have significant powerful identification performance for ASD cases.

Figs. 2 and 3 have presented ROC analysis that show the performance of selected algorithm per target classes (Negative C-ASD and Positive C-ASD class). According to mentioned observed results, all algorithms have significant identification performance based on both classes but small portion higher for positive C-ASD class. Thus, this indicate a balance classification performance by four selected algorithm have presented that guaranteed no such over-fitting or under-fitting issue towards distinct class data.

To evaluate the efficacy of the suggested research, we need to emphasize the precision of every class. This is true whether the classification procedure is binary or multi-class. You need to look at its performance to know how effectively a classification model predicts instances and hits its aim. The confusion matrix is a more in-depth look at how well a prediction model works. It is a visual representation of the types of mistakes that have occurred and the classes that have been successfully and wrongly predicted. Every data point can be labeled as either True Positive (TP), True Negative (TN), False Positive (FP), or False Negative (FN) in the confusion matrix [37]. As mentioned above, the information from the four classes is represented in the confusion matrix. Four different ASD diagnosis methods' CM findings are shown in Tables 6 to 9.

Table 6. Confusion Matrix (CM) for SVM.

	Predicted		
Actual	Negative C-ASD	Positive C-ASD	∑
Negative C-ASD	289	37	326
Positive C-ASD	6	722	728
∑	295	759	1054

Table 7. Confusion Matrix (CM) for KNN.

	Predicted		
Actual	Negative C-ASD	Positive C-ASD	∑
Negative C-ASD	323	3	326
Positive C-ASD	6	722	728
∑	329	725	1054

As displayed into Tables 6 to 9, SVM algorithm has the highest misclassification rate where 37 Negative C-ASD cases classified as Positive C-ASD cases. In the same time only 6 Positive C-ASD cases identified as Negative C-ASD this indicate the SVM algorithm

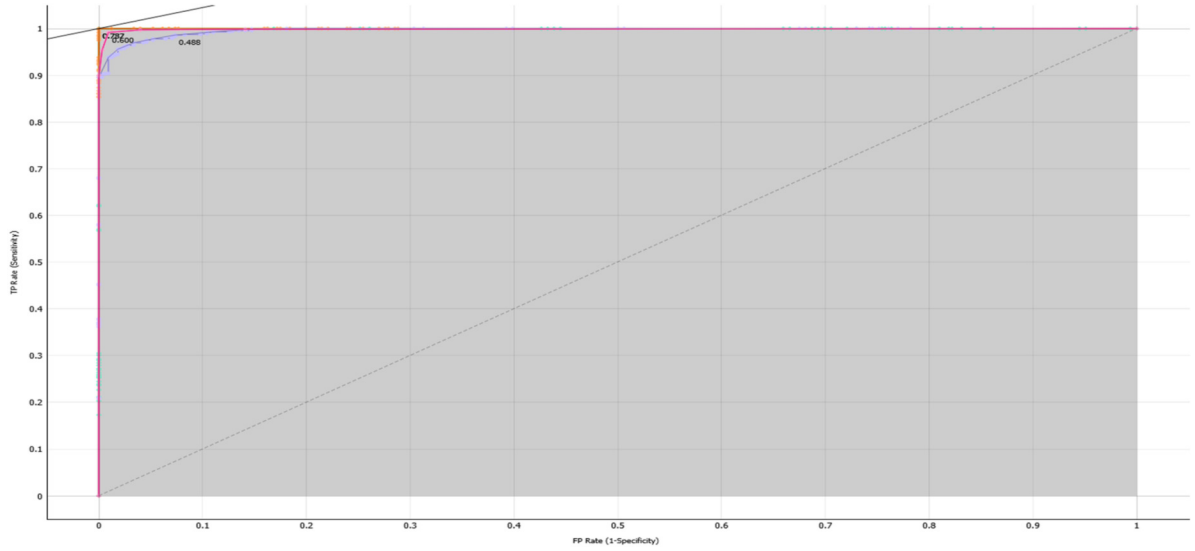

Fig. 3. ROC for positive C-ASD class.

Table 8. Confusion Matrix (CM) for RF.

	Predicted		
Actual	Negative C-ASD	Positive C-ASD	∑
Negative C-ASD	326	0	326
Positive C-ASD	0	728	728
∑	326	728	1054

Table 9. Confusion Matrix (CM) for NN.

	Predicted		
Actual	Negative C-ASD	Positive C-ASD	∑
Negative C-ASD	326	0	326
Positive C-ASD	0	728	728
∑	326	728	1054

have significant identification performance in terms of Positive C-ASD cases while less identification rate for Negative-ASD cases. KNN algorithm have showed less misidentification rate than SVM where only 3 Negative-ASD cases classified as Positive C-ASD cases. On other hand, only 6 Positive C-ASD cases identified as Negative C-ASD this indicate the SVM algorithm have significant identification performance in terms of Negative C-ASD and minor misidentification act towards Positive C-ASD cases. However, we observed that each RF and NN algorithms have momentous performance where zero missing value is presented in terms Positive C-ASD and as Negative C-ASD cases. Thus, these algorithms considered are the best performing ones that can be used for identification of ASD cases.

3.1. Comparisons with state of art works

In the view to generalize the results obtained by our study for more real-test-bed application, we should compare the obtained results with most state of the art studies that proposed recently for ASD identification target. Therefore, we have provided full comparison scenario as shown into Table 10.Two main studies [10, 15] have used same dataset that have been used in our study therefore we have chosen these studies as baseline for performance comparison. The baseline studies are implemented with different algorithms such as SVM, KNN, and RF which most of them used in our studies. The main criteria for comparison is using of feature ranking method, type of identification algorithm, number of used features, and obtained accuracy.

As observed into Table 10, the highest number of used features in study where 16 out of 18 attributes has been used into ASD identification process. Also, this study has used three main algorithms which are SVM, KNN, and RF which the obtained identification accuracy range form 81–93%.

In four features ranking methods have used which are Boruta algorithm, CFS, RIPPER, and RFE. Each method has distinct processes and mathematical representation which may give different selected subset features. However, all features ranking method have preferred different ASD attributes ranging from 13–11. Also, each of SVM and KNN have tested within each distinct features selection method. The obtained identification accuracy is ranging from 88%–98%.Comapring with study, this study have

Table 10. Comparison state of the art C-ASD identification methods.

Study	Feature ranking method	Algorithm	No of features	Accuracy
	–	SVM	16	93.84%
[10]	–	KNN	16	90.52%
[10]	–	RF	16	81.52
[10]	–	SVM	16	98.7%
[16]	Boruta algorithm,	SVM	13	95.87%
[15]	Boruta algorithm,	KNN	13	92.92%
[15]	Correlation-based Feature Selection with Harmony Search (CFS)	SVM	11	89.51%
[15]	(CFS)	KNN	11	91.93%
[15]	Repeated Incremental Pruning to Produce Error Reduction (RIPPER)	SVM	12	94.76%
[15]	RIPPER	KNN	12	91.52%
[15]	Recursive Feature Elimination (RFE)	SVM	11	89.51%
[15]	RFE	KNN	11	88.30%
Proposed study	GR and X2	SVM	10	95%
Proposed study	GR and X2	KNN	10	99%
Proposed study	GR and X2	RF	10	100%
Proposed study	GR and X2	NN	10	100%

scored high average identification accuracy rate and less number of C-ASD features have used into identification process.

Comparing with baseline studies, our study have scored the highest accuracy identification rate which reach to 100% with zero misidentification case. On other hand, the minimum number of C-ASD features are selected by GR and X2 that have used in the classification process. Therefore, less computational load and high classification performance are presented in proposed study.

3.2. Explainable computer-aided identification system for C-ASD

ML has enlarged well-known reputation and has been applied to uncountable domains. However, precise measures are essential to be implemented to guarantee that industrial and other academic community accepts as well as trusts ML-powered schemes. In this direction, it is obligatory to explain and visualize how the decisions are made based on ML models. Explainable C-ASD provides a precise picture for users about processes and data used for training of ML models. In the study we employed Local Interpretable Model-Agnostic Explanations (LIME) to visualize our proposed system based on explainable artificial intelligence approach.

LIME is a commonly used algorithm that provides the ability to interpret machine learning models in healthcare sector by creating a comprehensive explanation for a single prediction [38–40].

LIME's prediction is based on very simple interpretable approach, such as a linear classifier.

LIME model can be summarized into following steps:

- Creating new samples of data then acquires their predictions based on used (original) model.
- Calculating the generated samples' weight based on how close they are to the explanation instance.

Based on the probabilities of output from some of generated samples as the input desired to be clarified, a linear model is constructed. The weights that generated by substitute model used to assess the real value of selected features. Furthermore, LIME is model-agnostic, so that it can be applied to any model of machine learning [41]. To mention, we have used RF model as explainable ML based on LIME approach. Fig. 4 illustrates the results of LIME for a positive and a negative prediction.

The outcomes cover three parts of information from left to right: (1) the model's predictions, (2) contributions of feature for prediction and (3) the real value for distinct feature.

Fig. 4a illuminates a negative C-ASD prediction made by the RF model, in which the negative probability prediction was 100%. It is showed that only A1 and Q-CHAT-10 contributed to the negative C-ASD prediction. In contrast, Fig. 4b clarifies a positive C-ASD prediction based on RF approach, in which the probability for positive C-ASD class prediction was 100%. It is showed that each of A4, A6, A7, A8, A9,

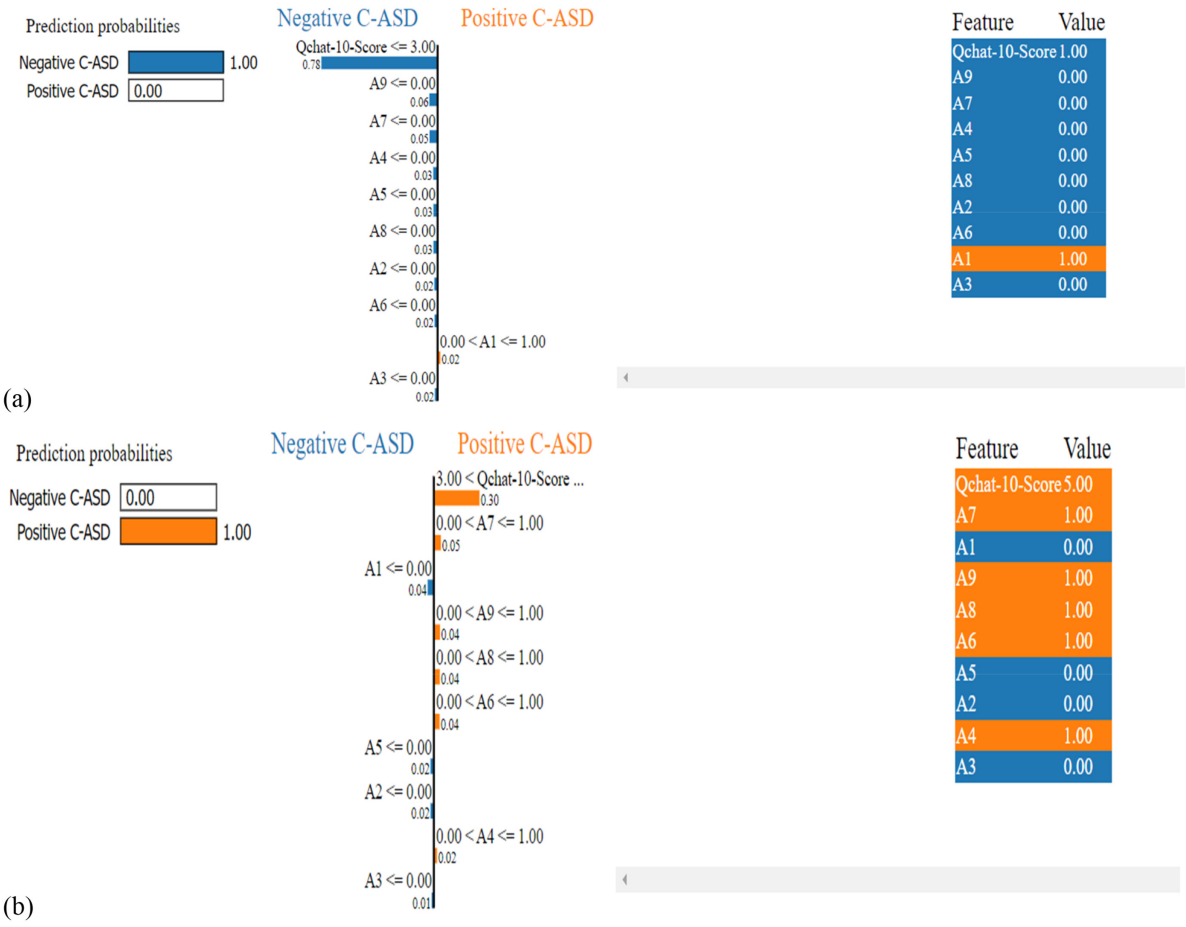

Fig. 4. LIME predictions for the RF model (a) Negative C-ASD (b) Positive C-ASD.

and Q-CHAT-10 contributed to the positive C-ASD class prediction.

4. Conclusion

The primary goal of our research was to establish an efficient and effective basic diagnostic test for C-ASD or an improved and comprehensive screening tool explicitly designed to detect the beginning of ASD. Furthermore, many identified C-ASD attributes can be used into identification process but which subset that is more important and present less computational load into computer aided systems still challenge. Therefore, this study have proposed a system for select best C-ASD attributes then use chosen features into identification process. Each of Gain Ratio (GR) and Chi-squared ($\chi 2$) methods that have used into our proposed system has successfully to select the best C-ASD which are (A1, A2, A3, A4, A5, A6, A8, A9, and Q-CHAT-10). Detailed procedures for the planned identifying system were laid forth. The suggested identification system was created using four machine-learning techniques: SVM, KNN, RF, and NN. An assessment experiment was carried out using various metrics and several machine-learning algorithms to confirm the efficacy of the suggested model. The results confirm that our study has selected the minimal set of features to identify C-ASD cases compared with other feature ranking and selection methods. RF and NN are the best identification machine learning algorithms for C-ASD cases. A balance identification(classification) performance in all machine learning algorithms per class where no under-fitting or over-fitting issue has been presented. Also, compared with state-of-the-art studies, our study has scored a high classification accuracy rate with minimum C-ASD cases, which leads to a quick computer-aided identification approach with less computational load. Furthermore, previous studies showed that the SVM algorithm claim is valid but only for some examined datasets because each dataset has distinct features, and a compromise of misleading results could be presented. The primary limitation of this research is the scarce availability of large and open-source ASD datasets that can be used to identify

deep-learning models. Due to limitation of data, in the future we intend to collect a new secondary dataset to identify C-ASD cases-based deep learning algorithms. Also, there several challenges regrading diagnosis of autism patients such as screening tools to get the data where some data about austim need to obtained from parents as well as child behavior combined with clinical data. Also,data quality is very important issue when using machine learning approach for diagnosis of C-ASD. Finally, as any other system based on ML concept, the proposed system into real-time application need to avoid overlap(bias) between positive C-ASD and negative C-ASD classes.

Funding

This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

Conflicts of interest

The authors report there are no competing interests to declare.

Data availability

The dataset is publicly available by study [17]. Also this data is available on https://www.kaggle.com/fabdelja/datasets.

References

1. E. Ruzich et al., "Measuring autistic traits in the general population: a systematic review of the Autism-Spectrum Quotient (AQ) in a nonclinical population sample of 6,900 typical adult males and females," *Molecular Autism*, vol. 6, no. 1, p. 2, 2015.
2. G. Ramaswami and D. H. Geschwind, "Genetics of autism spectrum disorder," *Handb Clin Neurol.*, vol. 147, pp. 321–329, 2018.
3. T. S. Brugha et al., "Epidemiology of autism spectrum disorders in adults in the community in England," *Arch Gen Psychiatry*, vol. 68, no. 5, pp. 459–465, 2011.
4. A. J. Russell et al., "The mental health of individuals referred for assessment of autism spectrum disorder in adulthood: A clinic report," *Autism*, vol. 20, no. 5, pp. 623–667, 2016.
5. L. D. Wiggins et al., "Using standardized diagnostic instruments to classify children with autism in the study to explore early development," *J Autism Dev Disord.*, vol. 45, no. 5, pp. 1271–1280, 2015.
6. J. A. Christiansz et al., "Autism Spectrum Disorder in the DSM-5: Diagnostic Sensitivity and Specificity in Early Childhood," *J Autism Dev Disord.*, vol. 46, no. 6, pp. 2054–2063, 2016.
7. M. M. Rahman et al., "A Review of Machine Learning Methods of Feature Selection and Classification for Autism Spectrum Disorder," *Brain Sciences*, vol. 10, 2020. doi: 10.3390/brainsci10120949.
8. M. A. Mohammed et al., "Automated waste-sorting and recycling classification using artificial neural network and features fusion: A digital-enabled circular economy vision for smart cities," *Multimedia Tools and Applications*, vol. 82, no. 3, 2022.
9. M. E. Minissi et al., "Assessment of the Autism Spectrum Disorder Based on Machine Learning and Social Visual Attention: A Systematic Review," *Journal of Autism and Developmental Disorders*, vol. 52, no. 5, pp. 2187–2202, 2022.
10. K. Vakadkar, D. Purkayastha, and D. Krishnan, "Detection of Autism Spectrum Disorder in Children Using Machine Learning Techniques," *SN Computer Science*, vol. 2, no. 5, p. 386, 2021.
11. K. S. Omar et al., "A Machine Learning Approach to Predict Autism Spectrum Disorder," in 2019 International Conference on Electrical, Computer and Communication Engineering (ECCE). 2019.
12. M. Sharma, "Improved autistic spectrum disorder estimation using Cfs subset with greedy stepwise feature selection technique," *International Journal of Information Technology*, vol. 14, no. 3, pp. 1251–1261, 2022.
13. M. S. Satu et al., "Early Detection of Autism by Extracting Features: A Case Study in Bangladesh," in 2019 International Conference on Robotics, Electrical and Signal Processing Techniques (ICREST). 2019.
14. U. Erkan and D. N. H. Thanh, "Reviews," *Autism Spectrum Disorder Detection with Machine Learning Methods*, vol. 15, no. 4, pp. 297–308, 2019.
15. M. Bala et al., "Efficient Machine Learning Models for Early Stage Detection of Autism Spectrum Disorder," *Algorithms*, vol. 15, 2022. doi: 10.3390/a15050166.
16. T. Akter et al., "Machine Learning-Based Models for Early Stage Detection of Autism Spectrum Disorders," *IEEE Access*, vol. 7, pp. 166509–166527, 2019.
17. F. Thabtah, F. Kamalov, and K. Rajab, "A new computational intelligence approach to detect autistic features for autism screening," *International Journal of Medical Informatics*, vol. 117, pp. 112–124, 2018.
18. F. Thabtah, "Machine learning in autistic spectrum disorder behavioral research: A review and ways forward," *Inform Health Soc Care*, vol. 44, no. 3, pp. 278–297, 2019.
19. A. M. Dinar et al., "Towards Automated Multiclass Severity Prediction Approach for COVID-19 Infections Based on Combinations of Clinical Data," vol. 2022, 2022.
20. H. K. Bhuyan and C. Chakraborty, "Explainable Machine Learning for Data Extraction Across Computational Social System," *IEEE Transactions on Computational Social Systems*, pp. 1–15, 2022.
21. M. A. Mohammed et al., "Rise of Deep Learning Clinical Applications and Challenges in Omics Data: A Systematic Review," *Diagnostics*, vol. 13, no. 4, p. 664, 2023. doi: 10.3390/diagnostics13040664.
22. S. Okser et al., "Regularized Machine Learning in the Genetic Prediction of Complex Traits," *PLOS Genetics*, vol. 10, no. 11, p. e1004754, 2014.
23. M. A. Hall, Correlation-based feature selection of discrete and numeric class machine learning, in Computer Science Working Papers. 2000, University of Waikato, Department of Computer Science.
24. B. López et al., "Single Nucleotide Polymorphism relevance learning with Random Forests for Type 2 diabetes risk prediction," *Artificial Intelligence in Medicine*, vol. 85, pp. 43–49, 2018.
25. N. Cueto-López et al., "A comparative study on feature selection for a risk prediction model for colorectal cancer,"

Computer Methods and Programs in Biomedicine, vol. 177, pp. 219–222, 2019.
26. N. Pudjihartono et al., "A Review of Feature Selection Methods for Machine Learning-Based Disease Risk Prediction," *Front. Bioinform.*, vol. 2, p. 927312, 2022.
27. S. Gnanambal et al., "Classification algorithms with attribute selection: an evaluation study using WEKA," *Int. J. Advanced Networking and Applications*, vol. 9, no. 6, pp. 3640–3644, 2018.
28. E. Dritsas and M. Trigka, "Data-Driven Machine-Learning Methods for Diabetes Risk Prediction," *Sensors*, vol. 22, no. 14, p. 5304, 2022. doi: 10.3390/s22145304.
29. S. A. Ali et al., "An Optimally Configured and Improved Deep Belief Network (OCI-DBN) Approach for Heart Disease Prediction Based on Ruzzo–Tompa and Stacked Genetic Algorithm," *IEEE Access*, vol. 8, pp. 65947–65958, 2020.
30. L. Ali et al., "An Automated Diagnostic System for Heart Disease Prediction Based on $\{\chi^2\}$ Statistical Model and Optimally Configured Deep Neural Network," *IEEE Access*, vol. 7, pp. 34938–34945, 2019.
31. Y. Yujun, L. Jianping, and Y. Yimei, "The research of the fast SVM classifier method," in 2015 12th International Computer Conference on Wavelet Active Media Technology and Information Processing (ICCWAMTIP). 2015.
32. P. Cunningham and S. J. Delany, "k-Nearest Neighbour Classifiers - A Tutorial," *ACM Computing Surveys (CSUR)*, vol. 54, no. 6, pp. 1–25, 2021.
33. T. R. Lee, W. T. Wood, and B. J. Phrampus, A Machine Learning (kNN) Approach to Predicting Global Seafloor Total Organic Carbon. vol. 33, no. 1, pp. 37–46, 2019.
34. P. Palimkar, R. N. Shaw, and A. Ghosh, "Machine Learning Technique to Prognosis Diabetes Disease: Random Forest Classifier Approach," in *Advanced Computing and Intelligent Technologies*, 2022. Singapore: Springer Singapore.
35. V. Jackins et al., "AI-based smart prediction of clinical disease using random forest classifier and Naive Bayes," *The Journal of Supercomputing*, vol. 77, no. 5, pp. 5198–5219, 2021.
36. M. A. Mohammed et al., "A Multi-agent Feature Selection and Hybrid Classification Model for Parkinson's Disease Diagnosis," *J ACM Trans. Multimedia Comput. Commun. Appl.*, vol. 17, Article 74, 2021.
37. Z. H. Arif et al., "Adaptive Deep Learning Detection Model for Multi-Foggy Images," *International Journal of Interactive Multimedia and Artificial Intelligence*, vol. 7, no. 7, pp. 26–37, 2022.
38. N. B. Kumarakulasinghe et al., "Evaluating local interpretable model-agnostic explanations on clinical machine learning classification models," in 2020 IEEE 33rd International Symposium on Computer-Based Medical Systems (CBMS). 2020. IEEE.
39. A. Alotaibi et al., "Explainable Ensemble-Based Machine Learning Models for Detecting the Presence of Cirrhosis in Hepatitis C Patients," *Computation*, vol. 11, no. 6, p. 104, 2023.
40. M. R. Zafar and N. M. Khan, DLIME: A deterministic local interpretable model-agnostic explanations approach for computer-aided diagnosis systems. 2019.
41. M. T. Ribeiro, S. Singh, and C. Guestrin, "Why should i trust you?" "Explaining the predictions of any classifier," in Proceedings of the 22nd ACM SIGKDD International Conference on Knowledge Discovery and Data Mining. 2016.