

Original Article

Prediction of Autism Spectrum Disorder using Reliable Ant Colony Optimisation Based Relevant Vector Machine

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Abstract - Autism spectrum disorder (ASD) is a permanent developmental impairment that impairs a person's capacity to communicate and interact with the outside environment. Social contact and reciprocal communication are consistently impaired in people with ASD. To gain a higher degree of independence, people with ASD require varied amounts of psychosocial assistance, or they may require constant supervision and care at all times. A diagnosis of ASD at an earlier stage leads to more time devoted to individual rehabilitation. This paper proposes a bioinspired optimisation-based classifier, namely Reliable Ant Colony Optimization based Relevant Vector Machine (RACO-RVM), to detect ASD precisely. RACO-RVM performs classification via its heuristic function and pattern evolution. Pheromone update and pattern selection play a vital role in RACO-RVM predicting ASD more accurately. RACO-RVM is evaluated using the benchmark metrics "accuracy" and "F-Measure" on three ASD screening datasets. RACO-RVM is superior in its ability to accurately detect ASD, with an 87.184% averagely compared to other classifiers.

Keywords - Autism, ASD, Optimisation, Classification, ACO, RVM.

1. Introduction

Autism is a lifelong diagnosis, but each ASD person's quality of life will improve intensely with the correct care and support. Autistic persons can improve their social and physical health, gain new skills, and work. As long as they have the proper care, all autistic persons can learn and grow. According to US government statistics, at least one out of every hundred people are diagnosed with autism. It's more frequent in men, but a new study shows that women are underdiagnosed because they try to hide their troubles.[1]. Many people with autism suffer from other disorders, such as anxiety, depression, epilepsy, and attention deficit hyperactivity disorder (ADHD). People with autism have a wide range of intellectual abilities, ranging from significant disability to a high degree of intelligence. Autism is estimated to affect between three and six children in every 1,000. There is a four-to-one male-to-female disparity in the prevalence of autism. Autism is characterised by three basic behaviours, ranging from moderate to profoundly impaired[2].

As a developmental issue, Autism Spectrum Disorder (ASD) is a significant condition that can severely limit an individual's capacity to engage or communicate with others. Individual health is affected by various neurological variables, including heredity or environmental factors such as pollution or a lack of exercise. A wide range of symptoms and varying degrees of severity are present[3]. People with Asperger's syndrome sometimes have difficulties communicating, especially in social

situations, with compulsive hobbies and repeated body language and mannerisms. Detecting ASD necessitates a detailed investigation. Psychiatrists for children and other qualified specialists will also conduct a comprehensive examination and several exams. Default methods of diagnosing ASD include ADOS-R (Autism Diagnostic Observation Schedule Revised) and ADI-R (Autism Diagnostic Interview-Revised). The ADOS-R and ADI-R are extensive and time-consuming, requiring a significant amount of both time and effort. [4, 5]

Even though research into the disorder's aetiology is still underway, it is clear that autism runs in families. Autism is most likely caused by differences in how people's brains grow, but there are many other possible causes. Many people refer to autism as a "hidden handicap" since most autistic persons appear to be no different from the rest of us on the outside. Spectrum disorders, such as autism, impact individuals differently and fluctuate over time[6], [7].

An autistic person may look distant, distant, or otherwise not interested in other people and may have difficulty forming close social connections with others. They have difficulty making friends because of their lack of social skills. However, those diagnosed with Asperger's syndrome frequently have a greater awareness of their issues. For some autistic persons, social settings can be intimidating, making it difficult to connect with others and become part of society. [8, 9]



1.1. Problem Statement

The currently available classifiers are designed to determine whether or not an individual (adolescent, child, or adult) has ASD. Existing classifiers are available for classifying adolescent ASD, child ASD, or adult ASD. There exist no standard classifiers for performing classification in all three types. An improved understanding of the lives of the autistic community can only be achieved by increased field observations and data analysis. This research aims to the standard technique of diagnosing autism and turning it into a machine learning model that uses medical data to generate predictions and observations that will lead to better solutions for finding ASD at the earliest with increased accuracy.

1.2. Motivation

A significant number of children are affected by ASD. Preliminary phases of diagnosis are frequently possible, but the most considerable bottleneck resides in their subjective and laborious character. As a result, it takes 13 to 15 months from when a person first suspects they may have ASD to when they are finally diagnosed. Diagnosis takes a long time, and the demand for visits is expanding faster than the nation's pediatric clinics can keep up. This research work is prompted by the high cost of therapy for ASD-afflicted individuals and the long time it takes to recover from ASD.

1.3. Objective

To speed up autism diagnosis, this paper aims to develop a classification algorithm that employs a bio-inspired optimisation strategy to enhance accuracy in predicting ASD.

1.4. Organization of the Paper

The current section of the paper has provided an overview of ASD and ends with a discussion about the problem statement, motivation and objective. The following section discusses the related literature. Section 3 discusses the proposed classifier for ASD classification. Section 4 provides information about the ASD screening dataset for evaluating the proposed classifier. Section 5 provides the metrics used to assess the proposed classifier against the existing classifiers. Section 6 discusses the results, and Section 7 concludes the paper with a future dimension.

2. Literature Review

"Convolutional Neural Network (CNN) with Stereotypical Motor Movements (SMMs)" [10] is proposed for extracting the features of the ASD dataset. Designing the patterns in sequences with CNN and LSTM attains the increased detection rate of ASD. The transfer learning approach adds an advantage for exact detection. "Risk-based Autism Prediction" [11] is proposed for classifying ASD among children of different ages. The classifier is developed, and the First Year Inventory v.2.0 (FYI) is utilised to evaluate the accuracy of identifying High-familial Risk. "Functional Near-Infrared

Spectroscopy" [12] was applied to calculate and quantify the fluctuation based on entropies. The cluster-based classification model is created, and features are generated for the system for better utilisation. "Interrogative Prediction of Autism" [13] is used to make the investigation on biological pathways of ASD. The standard regression approach is utilised to forecast the connection between autism, genetics, and discovered dysregulations. The results have been compiled, and epigenetic alterations in autism have been detected. "Synergies for ASD Mapping and Categorization" [14] is used to select the characteristics of ASD. Classification algorithms are employed to distinguish between individuals with ASD and everyday individuals. Using this mapping method, the coupling is lowered based on the severity of ASD symptoms. Accuracy is compared to demonstrate the practicality of this approach.

"Computerised Diagnosis System" [15] is introduced to integrate structural MRI characteristics and functional MRI for ASD diagnosis. The division of its areas detects the anomalies present in the brain into areas. The results of neuroimaging are used to conduct training and testing. The characteristics are combined, and precision is achieved. "Pipeline Classification for ASD" [16] is meant to generate features for better prediction of ASD. ASD and TD categorisation is improved using Surface-Based Morphometric (SBM) characteristics. Classifiers with optimisers are utilised to exploit the morphology of brain areas. The properties of the bilateral hippocampus are retrieved, and categorisation is carried out. "Resting-State Network" [17] is applied using Independent Component Analysis with autistic and healthy individuals. The illness related to ASD may be detected and classified using a Support Vector Machine (SVM) classifier. "Feature-based prediction of ASD" [18] is proposed to predict ASD by employing experimental methods, screening tools, and neurofunctional activities. Validation methodologies and a mixture of multi-modal characteristics generate accuracy and measure inconsistency. "Infrared Spectroscopy Signal" [19] was developed to differentiate ASD and its related anomalies. The features of mind-wandering patterns have been found and evaluated. The abnormality's location in the brain is discovered using a machine learning-based classifier. The classification accuracy's efficiency is measured to demonstrate its effectiveness.

"Multi-input Deep Neural Network" [20] is proposed for diagnosing data from neuroimaging studies for ASD. Brain disorder-based features in autistic individuals are classified via a hinge loss function and training of the learnt characteristics. "Hand-crafted feature-based approach" [21] is proposed as an ASD diagnosis method at an early stage. Neural network methods are applied for classifying ASD health records. Acoustic features are developed for utterance level ASD. A cross-validation strategy is used to raise the overall quality of the results. Machine learning methods improve performance when baseline score level and deep learning techniques are used. "Deep Convolutional Neural Network (DCNN)" [22] is

proposed as a machine learning approach to identify ASDs. Facial expressions are classified using electroencephalography data. Individuals' emotions are considered when examining a feature's temporal context. An ASD and a non-ASD population were both accurate in their assessments. "Functional Near-Infrared Spectroscopy" [23] is proposed to identify ASD among children. Multiple activities of the children are used to investigate the brain's activity for ASD, and the results are recorded for further examination. The results show that the tool proposed will be employed in the early stages of ASD exploration. "Support Vector Regression" [24] is proposed to predict the autism diagnostic observation schedule in newborns with ASD. The symptoms of ASD can be anticipated based on measurements of brain connectivity. The regression model predicts early disease detection by watching newborns for signs of illness. In order to get better outcomes, optimisation [25]–[30] procedures are utilised in various fields, and it has just begun to be used in ASD prediction.

"Naturalistic Developmental Behavioral Interventions (NDBI)" [31] is used to describe the virtual reality technology to map the approach. Fusion of NDBI with VR results in a reduction of irrelevant features and an improved prediction of the results. Metrics used to assess the technique's effectiveness are called performance indicators. "Machine Learning in Neuroimaging (MALINI)" [32] is applied as a preprocessing technique to extract the connectivity and functional properties. The impairment caused by Alzheimer's disease neuroimaging initiative is quantified and recorded. The system's accuracy and resilience are evaluated by verifying the classifier's data. "Deep Learning-based framework" [33] is proposed to detect ASD using fMRI scans. Autoencoder and a discriminative restricted Boltzmann machine are used to increase the accuracy of the fMRI classification.

Experiment results have been created, and the accuracy has been determined. "Machine Learning for Asperger's Syndrome (MLAS)" [34] has been tested and included with numerous classifying models. From each family member of ASD-affected persons, a subsample is drawn based on their mental and non-mental health, and these people will be most at risk of contracting the condition. Risk scores and odd ratios are also generated with confidence intervals for diagnosis. "Intelligent Fuzzy Logic Agent System (IFLAS)" [35] is proposed to identify autistic children. Doctors can't make a proper diagnosis without first modelling the system in detail. Machine learning approaches in IFLAS improve the model's resiliency and the efficiency of ASD prediction.

3. Reliable Ant Colony Optimization - Based RVM (RACO-RVM)

RACO-RVM is a biologically plausible algorithm of Swarm Intelligence (SI) for structuring and solving the issues in classifying the health care records to predict

ASD. Swarm Intelligence is an evolving research area of Computational Intelligence grouped by its behaviour through its agents. The working principle of RACO-RVM relies on the behaviour of searching foods of ants. Even though the individual ants in an insect swarm work separately, the swarm works together to solve the most challenging difficulties. The hunting nature of the ants also provides results for real-time global issues that are complex and hard. RACO-RVM delivers a method for sharing the intelligence of real information to predict ASD. Therefore, its cooperative behaviour will solve issues that arise in health care, especially in ASD, which is hard-natured. In RACO-RVM, ants are considered an artificial computational agent that is simple and simulated with the mathematical formula. The pheromone evaporation rate is proportional directly to its path length. Also, the RACO-RVM-based technique gives better results for the optimisation issues in ASD prediction.

RACO-RVM relies upon Ant-Miner methods. Here, the class selection is based upon the growth of evolved patterns, whereas the class in RACO-RVM is fetched, and the rules for classification are defined. The emerging structures are also detected for better classification accuracy. The process is initialised with different terms in the data samples and is followed with the iterative patterns for detecting 1-term jumping structures with the terms initialised. Every term detects whether the individual patterns are enough based on the growth, and the relevance ratio of evolved patterns in the data samples is measured. If the growth ratio is higher or equal to the list of patterns, the lesser threshold value is calculated and appended to the list sorted in descending order. The whole pattern list coverage is measured, and if the range has more secondary threshold coverage, then the pattern search for l -term will be stopped, and the search will end.

The training dataset is loaded at first, and the initialisation of parameters is performed. When the initialisation process gets over, the time convergence evaluation is carried out in which the structures evolve for every interval. After all training requirements are met, the training process is terminated conditions are examined. Patterns for RACO-RVM emerge from the combination of these values and heuristics. The growth rate and relevance rate are measured for every emerging pattern. When patterns are discovered to meet the relevance threshold, the majority class is used to assign the pattern. The fitness value of the pattern is validated, and the value for pheromone is appended. The criteria for convergence are measured to check whether the condition is met. If the condition is met, then the pattern will be selected. The pattern list will be updated to acquire the best patterns, and after this process will stop. The condition is evaluated for its training procedure, and testing data will be provided to calculate the classification technique. In the last phase, the reports for the classifier's accuracy are acquired using the test data samples.

3.1. Initialisation of Pheromone

The pheromone values are initialised at every edge for each class before the loop begins. The initialisation of pheromone is made at edges in equal range for items for every identified pattern. For every term, the value of the initial pheromone (β) is initialised using Eqn. (1).

$$\beta_{s,w}^{(f=1)} = \frac{1}{\sum_{s=1}^d v_s} \quad (1)$$

Here, the attributes are referred to using 'd', and the domain values for attribute 's' are referred to using v_s .

3.2. Heuristic Function

Each phrase has a heuristic value based on the information it provides. To determine information gain, entropy measurements are used. The entropy (H) of the entire dataset (E) is calculated by using Eqn. (2).

$$H(E) = - \sum_u M_u z_j M_u \quad (2)$$

In Eqn. (2), the class label is denoted by u , the $\log_2 m$ probability is z_j for the class u . The information gain j for the term f is measured using Eqn. (3).

$$j(U|D_s = f_{sw}) = - \sum_{\substack{u \in U \\ = f_{sw}}} M(U|D_s = f_{sw}) \cdot z_j m(D_s) \quad (3)$$

In Eqn. (3) the attribute of the dataset is denoted by D_s , the i^{th} attribute of i^{th} value is f_{ij} . The computation of the heuristic function for f term is performed using Eqn. (4).

$$\alpha_{sw} = \frac{z_j(U) - j(u|D_s = f_{sw})}{\sum_{s=1}^d p_s \cdot \sum_{w=1}^{v_s} (z_j(U) - j(u|D_s = f_{sw}))} \quad (4)$$

In Eqn. (4), the set of classes is denoted by U , the total number of attributes in the dataset is denoted by a , and the number of domain values for the attribute s is denoted by v_s . The selection term probability is measured using Eqn. (5).

$$M_{sw} = \frac{\beta_{sw}^\delta \cdot \alpha_{sw}^\gamma}{\sum_{s=1}^d p_s \sum_{w=1}^{v_s} (\beta_{sw} \cdot \alpha_{sw})} \quad (5)$$

The total pheromone among $item_w$ and n $item_s$ is β_{ij} for the current iteration and the heuristic function value for the link among term $item_s$ and $item_w$ is α_{sw} for the class selected. The probability of the chosen item is represented by the constant exponent, δ and γ where the default value is 1.

3.3. Stoppage for Pattern Evolution

The pattern discovered is appended at every generation to the list of patterns. The process ends when the counter generation value is equal to the attributes in the datasets apart from the attributes tested and when the dataset object ranges to the maximum threshold value.

3.4. Update of Pheromone and Pattern Quality

The pattern quality is measured based on the growth ratio measured in Eqn. (6).

$$F = \frac{FM}{Covered} \quad (6)$$

The training samples cover an ant's rule antecedent component in Eqn. (6). FM is the number of training samples with a comparable antecedent to the ant pattern.

RACO-RVM updates the pheromone value at every generation, whereby the ants at subsequent iterations use this same for discovering the emerging pattern. The quantity of pheromone is appended at the links of items that gratify the lesser threshold for the relevant vector ratio, and it is expressed in Eqn. (7).

$$\beta_{sw}^{(j+1)} = \beta_{sw}^{(j)}(1 - \varphi) + \left(1 - \frac{1}{1 + F}\right) \cdot \beta_{sw}^{(j)} \quad (7)$$

Here, the value of the pheromone among $item_s$ and $item_w$ of the current iteration, the rate of evaporation for pheromone is referred to as φ and the pattern quality evolved by an ant is F . The pattern's pheromone value is improved by search space exploration in the upcoming iteration that can be optimised without performing search operations inserted in the pattern set discovered already. In the RACO-RVM, the search discovery is improvised by exploring the search area which is not been discovered before. Once the pattern items are completed, every pheromone value is optimised by segregating with the pheromone summation.

3.5. Process of Pattern Selection

The deterministic method is utilised for pattern selection, which plays a significant role in classification. Other terms related to patterns are selected using the probabilistic mode. Pheromone value and the heuristic value of the terms play a vital role in choosing the probability value.

3.6. Pruning and Pattern Set Discovery

Suppose the pattern set discovery attains the threshold value for coverage. A vast volume of redundant patterns may be present with which no training sample datasets can be avoided. The process stops and is repeated for every class until the pattern list is generated. These repetitious patterns are removed from the list and are ordered based on the growth ratio. Classifications of ASD are performed, and every pattern is tested based on its sorted order. The pruning of unexposed patterns is mined and discarded from the list. This pruning process enhances the classifier's performance and works faster when segregating the pattern.

4. Dataset

This study evaluated the proposed classifier performance for predicting ASD using three different datasets (ASD Screening Dataset for Adults, Children, and Adolescents).[36],[37]. Each dataset has a total of 21 features. The Adults dataset has 704 instances, the Children dataset has 292 instances, and the Adolescents dataset has 104. Table 1 lists 20 common features found in the three datasets.

Table 1. Feature Details

Feature Id	Feature Description
1	Age
2	Gender
3	Ethnicity
4	Jaundice History
5	Family member with Pervasive Development Disorders
6	Who is completing the test
7	Country
8	Whether the Screening App used by the user earlier or not?
9	Screening method type
10 - 19	The answer to 10 questions related to ASD Screening
20	Screening Score

5. Performance Metrics

To calculate performance metrics, four variables are utilised:

- True Positive (*TruPos*): Precise finding of ASD presence
- False Positive (*FalPos*): Imprecise finding of ASD presence
- True Negative (*TruNeg*): Precise finding of ASD absence
- False Negative (*FalNeg*): Imprecise finding of ASD absence

5.1. Classification Accuracy

Classification Accuracy is a measure of how accurate the classifier is in making predictions. Mathematically, Classification Accuracy can be stated as Eqn (8).

$$\begin{aligned}
 \text{Classification Accuracy} &= \frac{\text{TruPos} + \text{TruNeg}}{\text{TruPos} + \text{TruNeg} + \text{FalPos} + \text{FalNeg}} \quad (8)
 \end{aligned}$$

5.2. F-Measure

F-Measure is a better way to quantify erroneously categorised instances and is considered a way of determining their correctness. It is mathematically expressed in Eqn. (9).

$$F - \text{Measure} = \frac{2\text{TruPos}}{2\text{TruPos} + \text{FalPos} + \text{FalNeg}} \quad (9)$$

6. Results and Discussion

6.1. Accuracy Analysis

Figure 1 compares the proposed classification algorithm RACO-RVM with the classification accuracy achieved by the current methods, MLAS and IFLAS. In this graph, the X-axis is marked with ASD Screening Datasets (adults, children, and adolescents), and the Y-axis is marked with accuracy in each classifier. RACO-RVM outperforms MLAS and IFLAS in classification accuracy, as seen in Fig. 1. Optimisation in RACO-RVM leads to greater accuracy than MLAS and IFLAS, which just focus

on classifying data. Heuristic Function and Pattern Evolution of RACO-RVM aid the classification phase to predict ASD better than MLAS and IFLAS, respectively. Table 2 provides the numerical values of Fig. 1.

6.2. F-Measure Analysis

Figure 2 shows a comparison of the proposed classification method RACO-f-measure RVM's accuracy with the accuracy of two current classification algorithms, MLAS and IFLAS. It is possible to see the attained f-measure in Y-Axis in percentage and X-axis with the ASD Screening Dataset names: Adults, Children, and Adolescents. Since pattern selection quality is considered when updating the pheromone, RACO-RVM performs better than the present classifiers (MLAS and IFLAS), as seen in Figure 2. RACO-RVM optimisation has superior performance than MLAS and IFLAS in terms of f-measure. Because of the pruning and discovery of pattern sets, RACO-RVM has a greater f-measure than MLAS and IFLAS. The numerical findings of Figure 2 are shown in Table 3 for better understanding.

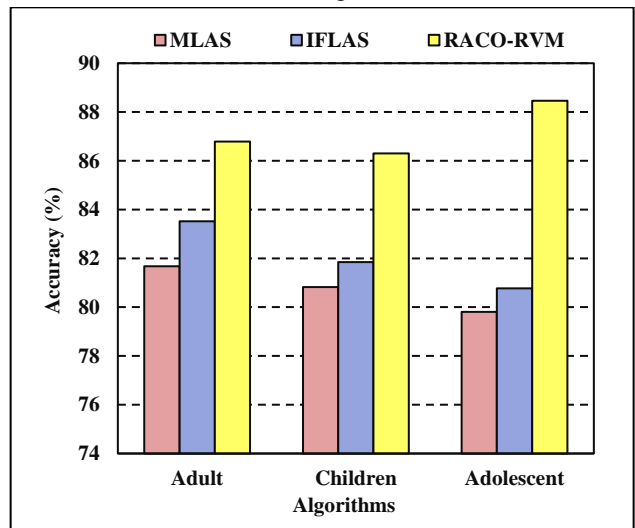


Fig. 1 Classification Accuracy Vs Classifiers

Table 2. Result Values of Classification Accuracy

Algorithms \ Dataset	MLAS	IFLAS	RACO-RVM
Adult	81.676	83.523	86.790
Children	80.822	81.849	86.301
Adolescent	79.808	80.769	88.462

Table 3. Result Values of F-Measure

Algorithms \ Dataset	MLAS	IFLAS	RACO-RVM
Adult	83.137	84.856	87.906
Children	82.390	83.386	87.500
Adolescent	82.353	83.333	90.164

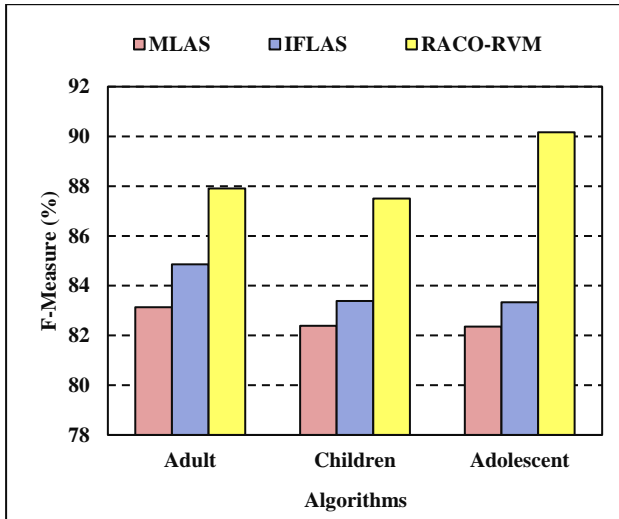


Fig. 2 F-Measures Vs Classifiers

7. Conclusion

People with autism spectrum disorder (ASD) have social and communication difficulties that make it difficult to operate at their highest ability level. There is no known cause or cure for ASD, making an accurate and prompt diagnosis challenging. This paper has proposed a bio-inspired classification strategy, Reliable Ant Colony Optimization based Relevant Vector Machine (RACO-RVM), to predict ASD more accurately. Pheromone update, selection and discovery of patterns present in RACO-RVM assist in predicting ASD more accurately than other classifiers. RACO-RVM is tested on three distinct ASD screening datasets. To analyse RACO-RVM performance, this research chose two standard metrics: classification accuracy and f-measure. RACO-RVM has an average classification accuracy of 87.184%. Using a mix of bioinspired optimisation and machine learning approaches, this research work aspires to increase the classification accuracy even more in the future.

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