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[Francesca Mainas](#) <sup>\*</sup>, [Bruno Golosio](#), [Alessandra Retico](#), [Piernicola Oliva](#)

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## Article

# Exploring Autism Spectrum Disorder: A Comparative Study of Traditional Classifiers and Deep Learning Techniques to Analyze Functional Connectivity Measures from a Multicentric Dataset

Francesca Mainas <sup>1,2,3,\*</sup>, Bruno Golosio <sup>1,2</sup>, Alessandra Retico <sup>4</sup> and Piernicola Oliva <sup>2,5</sup>

<sup>1</sup> Department of Physics, University of Cagliari, Italy; golosio@unica.it

<sup>2</sup> National Institute for Nuclear Physics (INFN), Cagliari Division, Italy; francesca.mainas@ca.infn.it

<sup>3</sup> Department of Informatic, University of Pisa, Italy

<sup>4</sup> National Institute for Nuclear Physics (INFN), Pisa Division, Italy; alessandra.retico@pi.infn.it

<sup>5</sup> Department of Chemical, Physical, Mathematical and Natural Sciences, University of Sassari, Italy; oliva@uniss.it

\* Correspondence: francesca.mainas@ca.infn.it

**Abstract:** Investigation of functional magnetic resonance imaging (fMRI) data with machine learning (ML) techniques, including also deep learning (DL) methods, have been widely used to study Autism Spectrum Disorder (ASD). This disorder is characterized by symptoms that affect the individual's behavioral aspects and social relationships. Early diagnosis is crucial for intervention, but the complexity of ASD poses challenges for treatment development. This study compares traditional ML techniques with deep learning (DL) methods in the analysis of functional connectivity measures obtained from the time series of multicentric ABIDE dataset. Specifically, Support Vector Machines (SVM) classifiers, with both linear and Radial Basis Function (RBF) kernels, as well as eXtreme Gradient Boosting (XGBoost) classifiers, are compared against the TabNet classifier, which is a DL architecture customized for tabular data analysis and a Multi Layer Perceptron (MLP). The findings suggest that DL classifiers may not be optimal for the type of data analyzed, as their performance trails behind that of standard classifiers. SVMs achieve performances, in terms of AUC, around 75%, compared to the best TabNet and MLP results, which are 65% and 71%, respectively. Additionally, this work investigates the brain regions that contribute most to the classification task, which are found to be those primarily responsible for sensory and spatial perception, as well as attention modulation, known to be altered in ASD.

**Keywords:** ABIDE; multi-site data; deep learning; machine learning; autism spectrum disorder

## 1. Introduction

Autism spectrum disorder (ASD) is a neurodevelopmental disorder characterized by repetitive and stereotyped behaviours as well as deficit in social communication and interaction [1]. ASD affects approximately 1 child out of 59, with strong male prevalence, one in every 37 males and 1 in every 51 females [2]. Currently the diagnosis is based on behavioral criteria that require a team of specialists which can be often time consuming and sometimes does not lead to a conclusive response due to factors such as comorbidity [3,4]. Given the heterogeneous nature of this disorder, it is still studied across different fields and the diagnosis criteria is constantly updated [5,6]. Early diagnosis and intervention is crucial to improve the quality of life and develop effective intervention strategies [7]. Thus far, many studies focus on the analysis of brain images acquired with functional magnetic resonance imaging (fMRI). This is a non-invasive imaging technique that can be used to measure the brain activity through the hemodynamic response associated with the neural activity of a specific brain area (Region of Interest - ROI). Brain activity can be revealed through the Blood Oxygenation Level Dependent (BOLD) signal, whose intensity depends on the oxygenation level of the brain areas involved in neural activity. In particular, resting-state functional magnetic resonance imaging (rs-fMRI) has been regarded as a valuable tool in the ASD studies. This imaging technique involves acquiring functional magnetic resonance images while the patient is not performing specific tasks, i.e. while he/she is at rest. This acquisition technique is often used in the study of brain functional connectivity,

which refers to the study of the correlation between the temporal signals of two anatomically distinct brain areas. By assuming that functional connectivity is a phenomenon involving interactions that occur on time scales shorter than acquisition times, it is possible to evaluate the correlation between the temporal signals of two anatomically distinct brain areas, considering the entire observation time interval, instant by instant. This process, repeated for all brain areas, allows to quantify the functional connection between brain areas, from which researchers can identify neurological distinctions between typically developing (TD) individuals from ASD ones leading to more accurate interventions. Given the abundance of data in neuroimaging, machine learning (ML) and deep learning (DL) techniques have been employed to advance ASD prediction and detection with good accuracy [8,9]. Usually neuroscientists apply traditional machine learning techniques for classification, such as support vector machine [10] and random forest [11,12], DL models like convolutional neural networks [13] and deep neural networks[14]. Deep neural networks have achieved significant success different fields, including image and text processing [15,16]. In practical applications, tabular data is the most common data type, particularly in medicine. Recent studies have shown that deep learning-based methods can have a crucial role in diagnosing of ASD [17,18]. Over the last decade, traditional ML methods have remained dominant when dealing with tabular data and frequently achieved better performance than DL approaches. Usually, ML models are simpler compared to DL ones, which facilitates their understanding and interpretation. While DL complexity, lack of transparency and interpretability [19], limiting their applicability in clinical contexts, leading to the necessity of identify the features that contribute the most to the classification results, emphasizing which are the features involved in identifying ASD subjects.

In this work, we investigated different ML and DL methods to show the differences in classification performances and most important features involved in the classification.

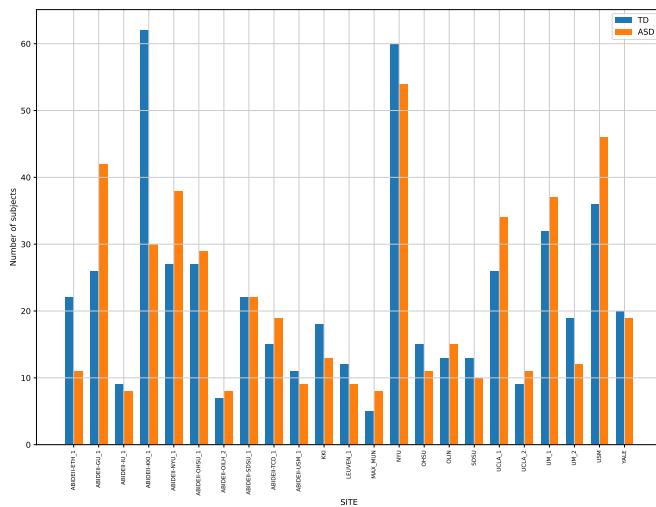
## 2. Materials and Methods

### 2.1. Data Selection

For this work, we used the data obtained with rs-fMRI of the ABIDE archive [20]. The entire ABIDE dataset has been published in two versions: ABIDE I and ABIDE II. Not all sites belonging to ABIDE II are different from those of ABIDE I, but even if some clinical centers are the same, the pipeline and acquisition parameters may have been modified between the two publications. For this reason, they will be considered as different acquisition sites. Furthermore, even within a single collection, such as ABIDE II, there are sites that have released two different data samples. For this reason, some of these samples are labeled with a subscription number (e.g. 1 or 2). Subjects belonging to the ABIDE II collection will have the prefix "ABIDE II" before the site name. When this prefix is missing, it is understood that the collection belongs to ABIDE I.

The data selected for this work have been preprocessed with the Configurable Pipeline for the Analysis of Connectomes (CPAC) pipeline [21]. CPAC applies filters for noise from respiration, heart rate, movements of the subjects' heads, and other smoothing techniques. This pipeline is among the most used, and previous studies have found that, when compared to images preprocessed with other pipelines, those preprocessed with CPAC led to better ASD/TD classification [22]. CPAC also provides the time series of brain areas of interest for patients.

We selected 1001 male subjects aged between 5 and 40 years, with their eyes open during acquisition. The subjects come from 23 different sites. Male subjects were chosen because the sample is larger than the female one and because males have a probability about four times higher of being affected by the disorder [23]. Moreover, the female dataset was insufficiently populated to allow statistically significant studies. The choice of the condition with eyes open was made to avoid including cases with potentially sleeping subjects during the examination. The dataset is equally distributed between ASD and TD, it consists of 506 TD subjects and 495 ASD. Figure 1 shows the distribution of ASD/TD for each site.



**Figure 1.** Dataset composition. Sites without a prefix belong to the ABIDE I collection.

## 2.2. Features Generation

In neuroimaging, Pearson correlation analysis determines the potential correlation between the instantaneous variation in activation state of different brain regions and how these areas are involved in carrying out a specific function. The values, or coefficients, of Pearson correlation are defined as follows:

$$r_{xy} = \frac{\sum_{i=1}^n (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{(\sum_{i=1}^n (x_i - \bar{x})^2)(\sum_{i=1}^n (y_i - \bar{y})^2)}} \quad (1)$$

In the studied case,  $x$  and  $y$  represent the time series of two brain regions and  $n$  is their dimension (number of time points), the coefficient  $r$  represents signals that are fully correlated or anti-correlated [24]. Pearson coefficients were normalized using the Fisher transformation (2) to make them statistically more significant [25].

$$Z = \frac{1}{2} \sqrt{n-3} \ln \left( \frac{1+r}{1-r} \right) \quad (2)$$

In equation (2),  $n$  represents the number of time points of the time series and  $r$  indicates the Pearson coefficient calculated with equation (1). Pearson coefficients will be used as features for classification. The number of features depends on the atlas used. In fact, for  $N$  regions, we will have  $\frac{N(N-1)}{2}$  features. This is because calculating the Pearson correlation between the time series of each of the regions of an atlas generates a square and symmetric connectivity matrix (see equation (1), which is invariant under the interchange of time series indices), thus, the upper triangle of the matrix contains the only elements of interest. In this work we used the Harvard-Oxford anatomical atlas [26], composed of 110 regions, which result in  $\frac{110(110-1)}{2} = 5995$  features.

For this study, out of the initial 110 ROIs, 7 were excluded due to having null time series in a substantial number of patients. This led to a total of 103 ROIs for each patient. The correlation was then computed for each pair of brain areas, resulting in  $N_{\text{comb}} = \frac{103(103-1)}{2} = 5253$  independent combinations of connectivity features for each subject.

### 2.3. Harmonization Procedure

Given that large datasets can be obtained by collecting images from different centers, this brings a heterogeneity of data due to differences in scanners and/or acquisition protocols that requires a harmonization technique to minimize these differences. In this work we used the Neuroharmonize tool proposed by Pomponio et al. [27,28], which is derived from Fortin et al.'s ComBat [29,30].

Neuroharmonize aims to eliminate the site effect while preserving the dependence of the features on biologically significant covariates, like age and sex.

According to Serra et. al [31], in order to avoid a bias due to data leakage, the harmonization parameters were estimated using only the subjects belonging to the control group of the training set. Once the set of covariates is defined, the harmonization model is computed. In this work we used age and site as covariates. Subsequently, the model is used to harmonize both the train and test sets. In a cross-validation scheme, the procedure is repeated for each fold separately.

#### 2.4. Classification Strategy

For this work, traditional classifiers, Support Vector Machine with a Linear kernel (L-SVM), Support Vector Machine with a Gaussian kernel (SVM-RBF) and eXtreme Gradient Boosting (XGBoost) were chosen, alongside deep classifiers, Attentive Interpretable Tabular Learning (TabNet) and Multi Layer Perceptron (MLP). The SVM classifiers are the most commonly used classifiers in these classification problems. SVMs have demonstrated superior performance compared to other classifiers, particularly in scenarios with a small number of samples and a large number of features [32]. XGBoost, was chosen because tree ensemble models are recommended when dealing with tabular data classification problems [33] and offers better generalization capability and is less susceptible to overfitting. TabNet is a deep learning model mostly used when dealing with tabular data, it employs sequential attention to select the most relevant features for reasoning at each decision step enhancing interpretability and optimizes learning efficiency by focusing the learning capacity on the most significant features [34]. MLP consists of fully connected layers where every node of each adjacent layer is connected, is a classifier easy to implement, fast and has shown performances that outperform other classifiers [35]. The L-SVM and SVM-RBF classifiers were implemented using the `sklearn.svm.SVC` module from the Python library `scikit-learn,svmpy,svm2`. For XGBoost, we used the `XGBoostClassifier` from the `xgboost` package in Python [38]. The TabNet model was implemented with the `TabNetClassifier` from the PyTorch library `pytorch_tabnet.tab_model` [39] and the MLP was implemented using the `MLPClassifier` from `sklearn.neural_network` package [40].

Once the features for each subject are obtained, these characteristics, along with the labels (+1 for ASD subjects and -1 for TD subjects), are used for classification. We applied a feature scaling method, the Scikit-learn RobustScaler and a hyperparameters tuning for XGBoost and TabNet classifiers. The classification results are obtained using the Repeated Stratified k-fold cross-validation method, setting the number of folds to 5 and the number of repetitions to 10. The classification performance was evaluated using the area under the ROC curve (AUC) [41,42]. The AUC was calculated for each fold and repetition and the final result is calculated as the mean of the AUC at which we associated the standard deviation as error.

With such a high number of features compared to the number of samples, the analysis, in addition to being more complex, is highly prone to overfitting. For this reason the performances of the classifiers were observed both without Principal Component Analysis (PCA) and with PCA, varying the number of principal components (PCs) from 30 to 300 PCs (30, 50, 100, 200, 300).

#### 2.5. Features Importance

Understanding the most important features that contribute to the classification of ASD and TD individuals is crucial for advancing diagnostic and therapeutic strategies. In order to determine which pairs of regions were discriminating for distinguishing TD from ASD, the permutation importance [43] technique was used for each analyzed classifier because it can be applied uniformly to all of the models tested.

Permutation importance is generally useful for understanding data and interpreting models: by calculating the score for each feature, one can determine which features most influenced the utilized model. Permutation importance is considered as one of the global Explainable Artificial Intelligence (XAI) methods. It provides insights into the overall behavior of a model and offers a comprehensive

view of feature contributions across the entire dataset. Using a global XAI approach, the interpretability and reliability of the model are increased. The basic idea of permutation importance is to observe how much a particular score decreases when a feature is not available. The score thus represents the importance of each feature. A higher score indicates that the feature in question has a greater effect on the utilized model. In principle, one could remove features, retrain the classifier, and check the score. However, this approach can be computationally complex because it would require retraining the classifier for each feature. Additionally, this method demonstrates which features might be important in the dataset rather than which features are important for the classifier. To avoid retraining the classifier, a feature is replaced with noise derived from the same distribution as the original feature values during each permutation. The simplest way to derive this noise is by shuffling the values of one feature using the values of another. In this study, permutation importance was implemented using the method described above. The purpose of the analysis was to determine whether the key features for the classification vary depending on the model used. We used the feature permutation importance implemented in the ELI5 python library [44]. This library offers a function that takes into account a trained model, a validation dataset, a scoring metric and it returns the importance score for each feature. The importance score reflects the decrease in model performance: the greater the drop in performance when a feature is shuffled, the more significant that feature will be considered. We employed the AUC as a scoring metric and computed the permutation importance for each fold of the 5-fold cross-validation and repetition. The final results were obtained as the average importance score across the folds and repetitions. We carried out the feature permutation importance analysis for all classification models.

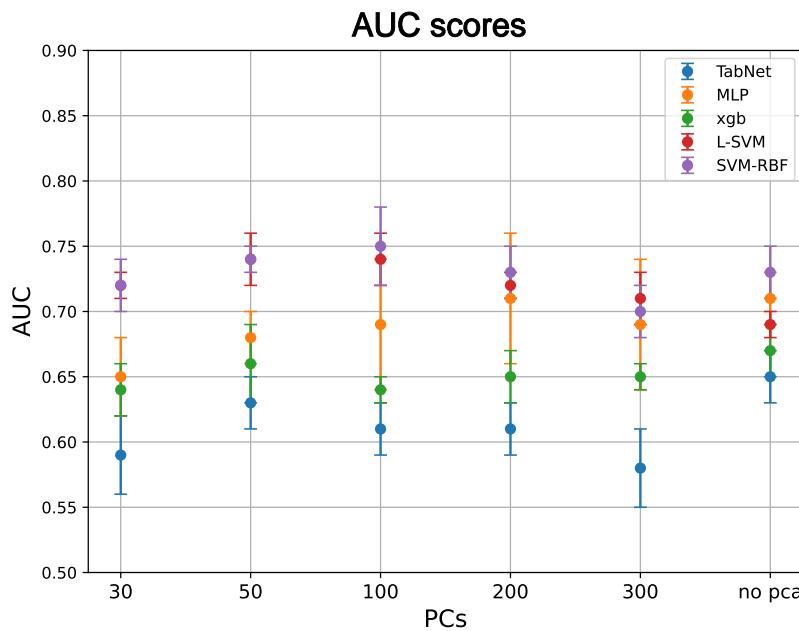
### 3. Results and Discussion

#### 3.1. Classification Performances

In Figure 2 are illustrated the classification performances in discriminating ASD subjects from TD ones. The results are reported for each classifier analyzed (TabNet, MLP, XGBoost, L-SVM, and SVM-RBF) and with different numbers of PCs. The best classification results are obtained for the SVM-RBF classifier with an AUC of  $0.75 \pm 0.03$  (100 PCs), followed by L-SVM with an AUC of  $0.74 \pm 0.02$  (50 and 100 PCs). As for the DL models the classification results fall behind,  $0.71 \pm 0.02$  (200 PCs and no PCA) for MLP and  $0.65 \pm 0.02$  (no PCA) for TabNet. These results are in accordance with the current literature, where performance typically hovers around 70% in multi-site approaches [45–47]. The higher classification performance of standard ML models indicates that the use of deep learning algorithms does not always provide an advantage for this type of data.

**Table 1.** Best classification performances for each classifier.

Classifier	AUC	# of PCs
MLP	$0.71 \pm 0.02$	no PCA
	$0.71 \pm 0.05$	200 PCs
TabNet	$0.65 \pm 0.02$	no PCA
XGBoost	$0.67 \pm 0.02$	no PCA
L-SVM	$0.74 \pm 0.02$	50 PCs
	$0.74 \pm 0.05$	100 PCs
SVM-RBF	$0.75 \pm 0.03$	100 PCs



**Figure 2.** The ASD and TD classification results are reported, for each classifier considered and for different values of PCs.

### 3.2. Feature Importance

Identifying the key features that differentiate ASD from TD subjects is essential for understanding ASD. Given that these features measure the correlation between the temporal signals of ROIs, they provide valuable insight into which aspects most significantly impact the distinction between ASD and TD subjects. In order to compare which regions were most significant in discriminating ASD/TD, we selected the top 50 features with the highest scores for each classifier. Subsequently, we checked for common features among all the top-50 features. From this analysis we didn't find any common feature for all the classifiers but only some features that were in common between two or three classifiers. This difference in the most important features for different classifiers is certainly connected to the high number of features (5253) and the intrinsic multivariate nature of the problem. Hence, a large set of features appears to be relevant in the classification, while no small subset can be defined relevant in the classification. To provide an example, the most important features present a feature importance that is in the range of 0.1%-1% of AUC, depending on the classification method.

However, despite the lack of global common features, we looked for brain regions occurrences in the 50 most relevant correlations by counting the number of times these regions were present in all classifiers. This allowed us to observe which regions had the most significant effect on ASD/TD classification based on their connectivity to other regions. The results are shown in Table 2. Consistent regions can be identified in all classifiers. These regions are those whose correlation with other regions was most significant in discriminating between ASD and TD. We also examined the belonging of these regions in the functional networks of Mesulam [48] catalog. In this way it was possible to highlight how the most significant areas for distinguishing between ASD and TD belong to the heteromodal, unimodal, primary and paralimbic network. The importance of these networks has also been found in literature [49–51]. These highlighted areas are crucial for sensory perception, processing visual and auditory signals, spatial perception, and attention modulation. They are fundamental for understanding social signals that require the integration of complex sensory information such as facial expression, tone of voice and gesture [52]. Therefore, they are important in understanding the mechanisms underlying autism spectrum disorder [53]. Heteromodal networks, involving various cortical areas, are crucial for integrating complex sensory information and processing multisensory knowledge. In contrast,

unimodal networks are specialized in a specific sensory modality. Neuroimaging studies have shown alterations in these areas in autism spectrum disorder, suggesting dysfunction in sensory integration and processing of complex information in this disorder [54].

**Table 2.** ROIs whose connectivity with other regions had the most significant effect on ASD/TD classification. The *Occurrences* column includes the number of times a ROI appears in the five classifiers, while the numbers in the *ROI* column represent the identifiers of the ROIs in the HO atlas. The *Anatomical Part* column lists the corresponding anatomical parts of the brain (according to HO parcellation), while the *Mesulam* column identifies the associated functional networks.

Occurrences	ROI	Anatomical Part	Mesulam
18	3102	L-Precuneous Cortex	Heteromodal
15	1002	L-Superior Temporal Gyrus; posterior division	Unimodal
15	501	R-Inferior Frontal Gyrus; pars triangularis	Heteromodal
14	1302	L-Middle Temporal Gyrus; temporo-occipital	Heteromodal
11	1101	R-Middle Temporal Gyrus; anterior division	Heteromodal
10	1301	R-Middle Temporal Gyrus; temporo-occipital	Heteromodal
8	4301	R- Parietal Operculum Cortex	Unimodal
8	3301	R-Frontal Orbital Cortex	Paralimbic
8	2702	L-Subcallosal Cortex	Paralimbic
8	1102	L-Middle Temporal Gyrus; anterior division	Heteromodal
7	3401	R-Parahippocampal Gyrus; anterior division	Paralimbic
7	2801	R-Paracingulate Gyrus	Heteromodal
7	2302	L-Lateral Occipital Cortex; inferior division	Paralimbic
7	1702	L-Postcentral Gyrus	Primary
6	2201	R-Lateral Occipital Cortex; superior division	Unimodal
6	401	R-Middle Frontal Gyrus	Heteromodal
5	4402	L-Planum Polare	Unimodal

#### 4. Conclusions

In this work we investigated the effectiveness of both traditional ML methods and DL approaches in classifying individuals with ASD against TD controls. Our findings revealed that ML methods achieved state-of-the-art classification performance, outperforming the DL models, TabNet and MLP. These results suggest that DL classifiers may not always provide optimal outcomes for this specific data domain. Moreover, our analysis emphasizes the need to pay attention when interpreting DL models performance, given that optimizing DL models presents greater challenges compared to traditional ML techniques. Additionally, the features that have the most significant impact in the classification task vary across different classifiers. Such diversity could be also related to overfitting. This highlights the challenges posed by the dataset's complexity and the abundance of features in achieving robust model generalization and accurately identifying significant features. Therefore, when employing a classification task to identify brain regions or features which are the most involved in the discrimination of a neurological or neurodevelopmental disease, it is necessary to consider the validity of these findings.

**Author Contributions:** F.M. implemented, analyzed and interpreted the classification procedures and the feature importance and wrote the manuscript with input from all authors. P.O. contributed to the design and implementation of the research, to the analysis of the results and to the writing of the manuscript. A.R. was involved in planning and supervised the work. B.G. was involved in planning and supervised the work. All authors read and approved the final manuscript.

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**Informed Consent Statement:** We used a public database, ABIDE. The ABIDE initiative declared: "This database was created through the aggregation of datasets independently collected across more than 24 international brain imaging laboratories and are being made available to investigators throughout the world, consistent with open science principles, such as those at the core of the International Neuroimaging Data-sharing Initiative. In

accordance with HIPAA guidelines and 1000 Functional Connectomes Project / INDI protocols, all datasets have been anonymized, with no protected health information included."

**Data Availability Statement:** The data used for this work can be found in the ABIDE site for download. We provided all the additional and necessary informations to interpret, replicate and build upon the findings reported in the manuscript.

**Acknowledgments:** Not applicable.

**Conflicts of Interest:** The authors declare no conflicts of interest.

## Abbreviations

The following abbreviations are used in this manuscript:

ABIDE	Autism Brain Imaging Data Exchange
ASD	Three letter acronym
AUC	Area Under the Curve
BOLD	Blood Oxygenation Level Dependent
CPAC	Configurable Pipeline for the Analysis of Connectomes
CV	Cross Validation
DL	Deep Learning
fMRI	Functional Magnetic Resonance Imaging
HO	Harvard Oxford
L-SVM	Support Vector Machine with Linear Kernel
ML	Machine Learning
MLP	Multi Layer Perceptron
PCA	Principal Component Analysis
PCs	Principal Components
RBF-SVM	Support Vector Machine with Gaussian Radial Basis Function
ROC	Receiver Operating Characteristic
ROI	Region of Interest
rs-fMRI	resting-state Functional Magnetic Resonance Imaging
SVM	Support Vector Machine
TabNet	Attentive Interpretable Tabular Learning
TD	Typically Developing
XAI	Explainable Artificial Intelligence
XGBoost	eXtreme Gradient Boosting

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