
**Software Engineering Department**

**Braude College**

**Capstone Project Phase A**

# Classification of MRI imaging of ASD using deep learning methods

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Supervisors:

Assoc. Prof. Miri Weiss-Cohen
Dr. Anat Dahan

Submitters:

Nitzan Ezra
Lior Buzaglo

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## Abstract

Autism spectrum disorder (ASD) is a brain-based disorder characterized by social deficits and repetitive behaviors traditionally diagnosed through behavioral assessments. According to recent Centers for Disease Control data, ASD affects one in 68 children in the United States.
Today there is no unequivocal way to detect ASD, The traditional way is not always accurate and is based on behavioral tests.
Magnetic Resonance Imaging (MRI) is a powerful tool used for investigating brain structural changes in individuals with ASD.
In this project, we investigated ASD patients' brain imaging data from a worldwide multi-site database known as ABIDE (the Autism Brain Imaging Data Exchange) to improve ASD diagnosis accuracy and reliability.
Images will be classified using deep learning and CNN-Inception v4 architecture.
Our model will classify anatomical MRI scans, distinguishing ASD participants from control using brain imaging data, and attempting to unveil the neural patterns that emerged from the classification.
We aim to enhance the accuracy of ASD diagnosis by achieving over 70% accuracy in identifying ASD compared to control patients in the dataset and to offer substantial improvements over traditional methods that rely on behavioral assessments.
Detection of ASD using MRI scans can assist in early detection and allow early suitable treatment.

## 1. Introduction

Autistic disorder and related pervasive developmental disorders (PDDs) are types of neurodevelopmental conditions. The most frequently diagnosed PDD is autism, Asperger's syndrome, and PDD not otherwise specified (NOS) are collectively known as autism spectrum disorders (ASDs). ASD encompass a wide range of symptoms and severities, with common challenges in social communication, social interaction, and sensorimotor skills. The core symptoms of ASD include (1) Impaired social communication and language skills. (2) Repetitive behaviors, restricted interests, or activities. The prevalence of ASD has surged significantly, rising from 4 in 10,000 to 1 in 68 children. Studies show that autism's concordance rate in identical twins ranges from 60% to 90% [1-3].
Historically, the diagnosis of ASD and criteria for clinical trials have been guided by the Diagnostic and Statistical Manual of Mental Disorders or behavioral diagnostic scales. However, disorders like ASD, which involve many genetic and environmental influences, pose a challenge when using symptom-based criteria. The same symptoms can result from diverse underlying biological processes, and only 10% to 38% of cases have identifiable genetic causes, with no clear genetic markers for ASD [2].
To better understand the causes of mental disorders like ASD, researchers are working to identify brain activation patterns and link them to psychological and neural

factors. Noninvasive brain imaging, such as MRI, has advanced this research by identifying objective biomarkers that can aid in diagnosing ASD and addressing social and communication deficits [1].
MRI is the method we decided to use to diagnose (classify) the patient. It is a non-invasive diagnostic technique that offers high spatial resolution and contrast sensitivity without the usage of ionizing radiation. MRI is a powerful tool for investigating changes in the structure, function, maturation, connectivity, and metabolism of the brain. As a result, detailed images of brain development are generated [1,3].
Functional MRI technique is helping to emphasize reduced connectivity, especially between frontal and posterior regions. This technique is helping researchers better understand the neural circuitry in autism, revealing areas of dysfunctional cortical activation and atypical cortical specialization.
Structural MRI techniques are helping researchers determine how the brain develops in autistic individuals. Various cohorts and patients benefit from it since it provides a contrast between gray matter and white matter.
Structural MRI studies found evidence of increased total brain volume, especially in the frontotemporal cortices, and early rapid brain overgrowth in affected individuals [Fig. 1]. In addition, revealed consistent abnormalities in cortical gray and white matter volume in ASDs. Diffusion tensor imaging has been further elucidate the structural integrity and orientation of white matter.
The advances in structural and functional MRI  and structural MRI techniques in the past decades have helped researchers to understand neuropathological differences in ASD and helped to understand the neurobiology of autism [1-3].

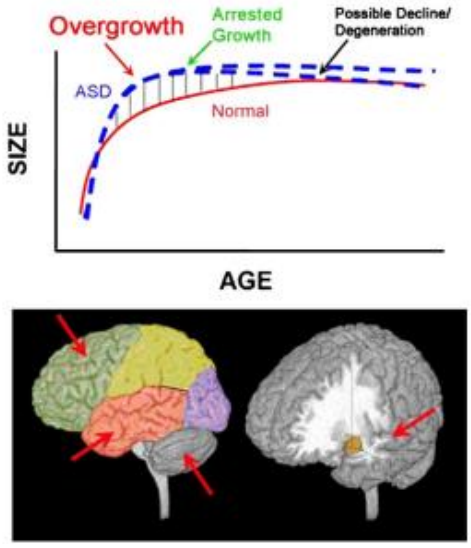


Fig. 1 Regional Early Overgrowth in ASD. (Top) This model illustrates initial rapid brain growth in ASD, depicted by blue lines, followed by a stabilization of growth. In comparison, red lines show the growth patterns of typically developing age-matched individuals. In certain cases and individuals, this plateau in growth may progress to a

mild degeneration, represented by the dashed blue lines that decline slightly. (Bottom) Areas of the brain experiencing early overgrowth in ASD encompass the frontal and temporal cortices, cerebellum, and amygdala[3].

## 2. Literature review

Kimberly A. Stigler a b, Brenna C. McDonald c, Amit Anand b c, Andrew J. Saykin c, Christopher J. McDougle a b [3] focuses on Structural and Functional studies in ASD. Structural MRI has been instrumental in identifying neuroanatomical abnormalities in individuals with autism spectrum disorder (ASD), including atypical increases in total brain volume at an early age and region-specific alterations in both gray and white matter volumes. Contrary to earlier views of ASD as a static condition, recent evidence from head circumference measurements suggests a dynamic, age-dependent pattern [Fig. 2]. Abnormalities in gray and white matter have been observed across various brain regions, highlighting the widespread nature of brain involvement in ASD. There remain, however, inconsistencies related to the precise location and direction of these volumetric changes, as well as the relative contribution of gray matter. Different findings are hypothesized to be due to differences in diagnostic criteria, participant characteristics (e.g., age, IQ, gender), and imaging techniques, as well as the heterogeneity of autism itself.

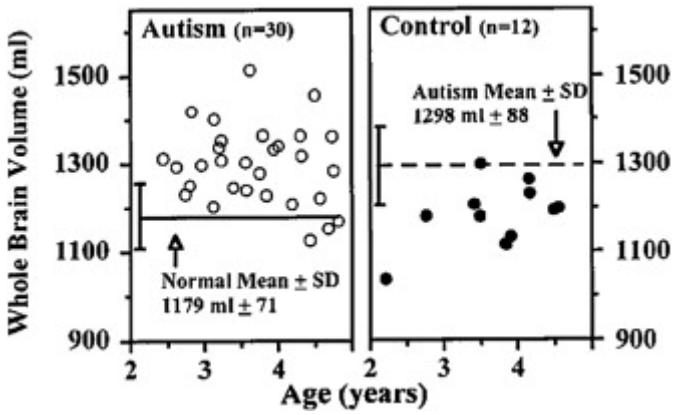


Fig.2 Brain volume by age of Two- to four-year-old autistic and normal boys. The plotted showing overall brain enlargement of the youngest autistic children, 90% of the autistic boys had brain volumes larger than the normal mean, and only one normal boy in this age range exceeded the autism mean.

Functional MRI research in ASD has focused on uncovering the neurobiological basis of social impairments, with particular emphasis on face perception, one of the earliest social deficits in ASDs. Studies have shown that individuals with ASDs display atypical visual scanning of faces, as they tend to avoid the eye region, in contrast to typically-developing individuals. Consistent findings of altered activation

in the fusiform face area (FFA) during face processing suggest the importance of this region in socioemotional functioning. Both task-based and resting-state fMRI have revealed widespread cortical abnormalities, with evidence pointing to reduced connectivity in networks associated with core ASD symptoms. Additionally, disruptions in the default mode network (DMN) during resting states have been identified, which are significant due to the DMN's role in higher-order social cognitive processes like the theory of mind. These deficits in the theory of mind in ASDs may stem from early dysfunction in the mirror neuron system (MNS), which is crucial for action observation, imitation, and emotional understanding [fig.5].

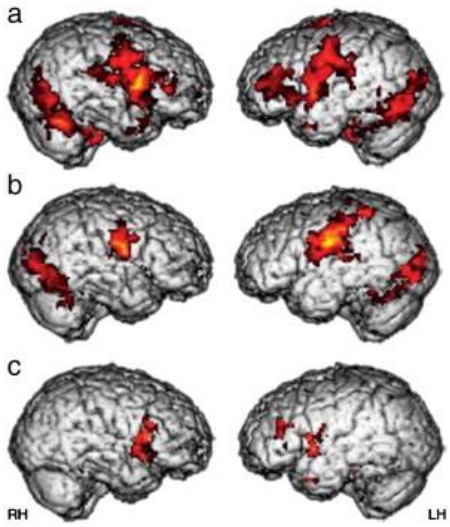


Fig. 3
(a): Significant activity in the bilateral pars opercular is of the inferior frontal gyrus (with stronger activation on the right side) in the typically-developing group.
(b): Demonstrates the absence of such activation in the ASD group.
(c): Illustrates the between-group comparison, revealing that the differences in activity between the two groups were statistically significant ($t > 1.83$, $P < 0.05$), with correction for multiple comparisons at the cluster level.
These findings suggest differences in neural processing of emotional expressions, with the typically developing group showing greater engagement of brain regions related to imitation and emotional understanding.

Dongyun Li, Hans-Otto Karnath and Xiu Xu [2] focuses on identifying potential biomarkers for diagnosing Autism Spectrum Disorder (ASD) in children using various MRI techniques. These biomarkers are crucial for understanding the neurobiological underpinnings of ASD and improving early diagnosis and intervention.
Structural MRI can detect how the brain develops neuroanatomically by determining brain volume and cortex thickness. VBM (voxel-based morphometry) and SBM (surface-based morphometry) are used to analyze tissue density and topological features like curvature. There's been consistent evidence that children with ASD

have bigger brains, even in the frontal and temporal lobes.
Diffusion Tensor Imaging (DTI) evaluates white matter microstructure and connectivity. Fractional anisotropy (FA) and mean diffusivity (MD) are used to measure the directionality and amount of diffusion in white matter. In DTI, tractography, voxel-wise analysis, and tract-based spatial statistics (TBSS) are used. Researchers have found that children with ASD have reduced FA and increased MD in major white matter tracts, indicating microstructural disorganization and altered connectivity.
Resting-state functional MRI (RS-fMRI) examines functional connectivity in the brain during rest by measuring the correlation and anti-correlation between fMRI signals. The use of this technique makes it possible to map large-scale functional networks in the brain and determine how an autism spectrum disorder affects the topology of these networks. In RS-fMRI studies, children with ASD have a decrease in long-range connectivity and an increase in short-range connectivity, suggesting an inability to integrate information.
These MRI techniques show consistent patterns of increased brain volume, altered white matter microstructure, disrupted functional connectivity, and neurochemical imbalances in children with autism. Potentially, these biomarkers can help with early diagnosis and intervention of autism, which could improve outcomes for kids. Developing new, effective biomarkers and integrating them with genetic and phenotypic data will require advances in neuroimaging, cross-disciplinary studies, and large-scale collaborations.[Table 1]

| MRI approaches | Findings |
|---|---|
| Structural MRI | *Cortex* |
| | Increased total GM and WM volumes |
| | Increased GM and WM volumes in frontal and temporal areas |
| | Increased cingulate cortex |
| | Atypical variation of cortical thickness in frontal, temporal, and parietal lobes |
| | *Cerebellum and subcortical areas* |
| | *Cerebellum* |
| | Increased total volume |
| | Increased GM volume |
| | Decreased WM density |
| | *Amygdala* |
| | Increased volumes in younger children bilaterally |
| | Trajectory of development of amygdala follows overall trajectory of TBV |
| | *Corpus callosum* |
| | Decreased overall size |
| | Increased regional volume |
| | *Basal ganglia* |
| | Increased caudate volume |
| | Atypical shapes of the structures |
| | *Hippocampus* |
| | Increased size of hippocampi in young children |
| | Enlargement located especially on the right side |
| | No difference between sides in older children |
| Diffusion tensor imaging | Decreased FA in the whole brain, frontal lobe, arcuate fasciculus, across the entire CC, and in anterior thalamic radiation |
| | Increased FA in arcuate fasciculus and in CC in young children |
| | Increased MD in whole brain, frontal and temporal lobes, and across the entire CC |
| Resting-state fMRI | Altered functional connectivity in the default mode network |
| | Hyper-connectivity in striatal-cortical circuitry, precuneus, cingulate cortex, and temporal-frontal circuity |
| | Under-connectivity in anterior-posterior connections |
| Magnetic resonance spectroscopy | Decreased NAA levels in general GM and WM, especially in frontal, temporal, cingulate, and caudate areas |
| | Decreased Cr+PCr levels in general GM and WM, especially in frontal, parietal, temporal, occipital cortex, and thalamus |
| | Decreased choline levels in cortical areas, temporal lobes, and thalamus |
| | Increased choline levels in caudate, anterior cingulate cortex, and hippocampus-amygdala complex |
| | Decreased Glx in GM of frontal, occipital, temporal cortex, and cerebellar regions |
| | Increased Glx in thalamus and putamen |

Table 1. The findings of each MRI method [2].

Anibal Sólon Heinsfeld, an Alexandre Rosa Franco,b,c,d R. Cameron Craddock,f,g Augusto Buchweitz,b,d,e, and Felipe Meneguzzia,b [1] explores the use of deep learning algorithms to identify autism spectrum disorder (ASD) from brain imaging data.

The researchers utilized a combination of supervised and unsupervised machine learning methods to classify ASD and control participants based on their neural patterns of functional connectivity, leveraging resting-state functional magnetic resonance imaging (Rs-fMRI) data from the ABIDE dataset [7].
They created functional connectivity matrices using Pearson correlation coefficients of time-series data from different brain regions to achieve this. Denoising autoencoders were employed for unsupervised pre-training, extracting lower-dimensional representations of the data. They were then fine-tuned using a multilayer perceptron (MLP) to classify participants as ASD or typically developing

controls. The model's performance was validated through a leave-one-site-out cross-validation approach, testing its generalizability across different imaging sites.
The results showed that the deep learning model achieved a mean classification accuracy of 70%, with a sensitivity of 74% and specificity of 63%, surpassing the state-of-the-art accuracy of up to 67% on the same dataset. Distinct neural patterns associated with ASD were identified, including underconnectivity (anticorrelation) between anterior and posterior brain regions and increased local connectivity in the posterior areas. Key brain regions involved included the Paracingulate Gyrus, Supramarginal Gyrus, Middle Temporal Gyrus, Occipital Pole, and Lateral Occipital Cortex.
The deep learning model outperformed Support Vector Machine (SVM) and Random Forest (RF) classifiers, which achieved mean accuracies of 65% and 63%, respectively. The model demonstrated robustness in handling site-specific variability, a crucial factor for applying machine learning methods to multi-site clinical datasets. However, the study acknowledged the challenges of dealing with multi-site data. It emphasized the need for further refinement to meet biomarker standards for clinical use.
Xin Yang, Paul T. Schrader, Ning Zhang [8] focus on multilayer perceptron's (MLPs), a type of deep neural network (DNN) that is more commonly associated with fully connected layers rather than convolutional layers. The MLPs were designed with various hidden layer configurations to classify Autism Spectrum Disorder (ASD) and typically developing (TD) participants based on functional connectivity features extracted from resting-state functional magnetic resonance imaging (Rs-fMRI) data.

In terms of methodology, the study utilized a large dataset from the Autism Brain Imaging Data Exchange (ABIDE), which comprises Rs-fMRI data from over a thousand subjects, including both ASD patients and TD controls. This data was preprocessed using several pipelines, with the Configurable Pipeline for the Analysis of Connectomes (CPAC) identified as the most effective. The researchers extracted functional connectivity from the Rs-fMRI data using the CC400 brain atlas, generating a large feature set with 77,028 features, and applied various configurations of deep neural networks developed in the TensorFlow framework to classify the subjects based on these features. This approach allowed them to handle the high-dimensional nature of fMRI data effectively. [Fig. 3]

The best-performing DNN model achieved a classification accuracy of 75.27%, with a recall of 74% and a precision of 78.37%. The study shows that deep learning could significantly improve the accuracy of classifying ASD from TD participants using Rs-fMRI data.
Yahoo Konga, Jianliang Gaoa, Yunpei Xua, Yi Pana,b, Jianxin Wanga, Jin Liua [5] focus on approaches enhancing the classification accuracy of ASD through the integration of brain connectivity features and a deep neural network (DNN) classifier. In this study, the researchers constructed individual brain networks from T1-weighted MRI images sourced from ABIDE I [7]. These networks were developed by

parcellating the brain into various regions of interest based on the Destrieux atlas and extracting connectivity features between these regions to form a feature representation for each subject.
To refine the model, features were ranked using the F1-score, which prioritized the most discriminative features for ASD classification. The selected top features were then employed in a DNN classifier that consists of two autoencoders followed by a SoftMax layer[Fig. 4]. This architecture is particularly designed to capture deep, relevant features for distinguishing ASD from typical controls.

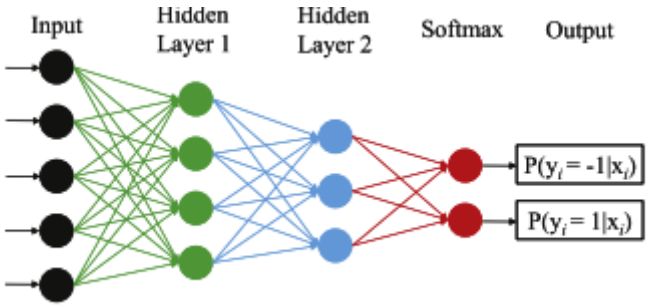


Fig. 4  Proposed DNN classifier.[5]

The effectiveness of this methodology was underscored by the achieved classification accuracy of 90.39% and an area under the receiver operating characteristic curve (AUC) of 0.9738, outperforming several existing methods. Notably, the use of cortical gray matter volume (CGMV) significantly surpassed other morphological features such as cortical thickness and its standard deviation in terms of accuracy, sensitivity, and specificity. When the proposed method was compared with existing techniques using the same dataset, it demonstrated substantial improvements in all evaluated metrics and maintained robust performance across different subsets of the ABIDE dataset[7].
Zeinab Shorthand, Mohammadsadegh Akhondzadeh, Soorena Salari, Mariam Zomorodi-Moghadam, Moloud Abdar, U. Rajendra Achary, Reza Khosrowabadi 9 and Vahid Salari D  [6]  focus on CNN (Convolutional Neural Network) architecture, which processes the brain's functional connectivity matrices. These matrices represent correlations between different regions of the brain, calculated using the CC400 functional parcellation atlas, which divides the brain into 400 regions. The CNN uses these connectivity matrices to classify individuals as either having ASD or being typical controls. The network architecture features convolution layers interspersed with pooling and fully connected layers to extract features from the input connectivity matrices.) to automate the detection of Autism Spectrum Disorder (ASD). This CNN model uses resting-state functional magnetic resonance imaging (fMRI) data from the Autism Brain Imaging Data Exchange (ABIDE) dataset. The model is trained to distinguish between ASD and control subjects by analyzing patterns of functional connectivity within the brain.

The model achieved a promising accuracy of 70.22% on the ABIDE I dataset, surpassing several state-of-the-art techniques while using fewer computational resources, thus enhancing efficiency. The study further explores significant brain regions or regions of interest (ROIs) that contribute to ASD classification. Techniques like saliency mapping highlighted key areas such as the right supramarginal gyrus, fusiform gyrus, and cerebellar vermis—regions known to be associated with neural disruptions in ASD.

## 3. Background

### 3.1 Dataset

We're using the Autism Brain Imaging Data Exchange (ABIDE) dataset [7] for ABIDE initiative is a large-scale brain imaging data from labs worldwide that will be compiled to help understand the neural bases of Autism Spectrum Disorder (ASD). Compiling extensive functional and structural brain imaging data will facilitate discovery science and enable comparisons across diverse samples to address the complexity and heterogeneity of autism spectrum disorders.
The ABIDE dataset comprises two main collections: ABIDE I and ABIDE II. ABIDE I involved 17 international sites and included 1,112 datasets, with 539 from individuals with ASD and 573 from typical controls. The participants' ages range from 7 to 64 years old, with a median age of 14.7 years. Released in August 2012, this collection has demonstrated the feasibility of aggregating resting-state fMRI and structural MRI data across sites, making it a valuable resource for capturing whole-brain and regional properties of the brain connectome in ASD.
ABIDE II, established with support from the National Institute of Mental Health, has aggregated over 1,000 additional datasets, with enhanced phenotypic characterization. This collection includes longitudinal data from 38 individuals at two time points (1-4 year intervals) and involves 19 sites, contributing 1,114 datasets from 521 individuals with ASD and 593 controls. The age range of participants in ABIDE II extends from 5 to 64 years. The data were released to the scientific community in June 2016.
Both ABIDE I and ABIDE II datasets are anonymized according to HIPAA guidelines and the protocols of the 1000 Functional Connectomes Project/International Neuroimaging Data-sharing Initiative (INDI), ensuring no protected health information is included. These datasets, consistent with open science principles, are made available to investigators globally.
For our project, we will focus specifically on the anatomical MRI scans, working with images in size 256x256 pixels to ensure uniformity and facilitate processing. This focus will allow us to harness detailed structural brain data crucial for our ASD classification objectives.[Fig. 5]

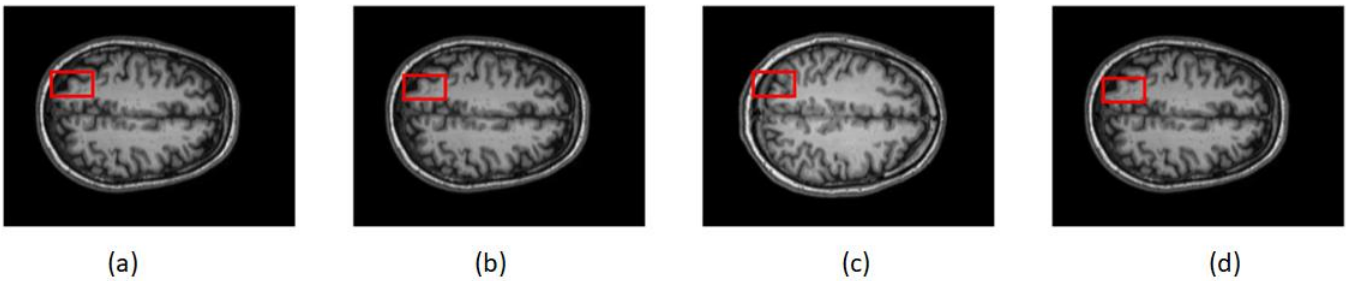


Fig. 5 : Pictures from ABIDE data set[7] The cerebellum is marked with red rectangles. Each rectangle highlights the cerebellum's location in the respective slices. The cerebellum is positioned towards the back and lower part of the brain and is identified by its unique, foliated structure. (a) , (b) are subjects with ASD, and (c ) and (d) are the Typical Controls.

### 3.2 CNN- Inception v4

Inception-v4 is a convolutional neural network (CNN), introduced by researchers from Google in 2016. This architecture advances the development of earlier Inception models such as Inception-V1 (GoogleNet), Inception-V2, and Inception-V3, and is specifically designed for image classification and object detection tasks.Inception-v4 has significantly improved the performance metrics over its predecessors, enhancing both the accuracy and the efficiency of the training process.

The features of Inception-v4 are its unique Inception modules, which are composed of various parallel convolutional layers with different kernel sizes (1x1, 3x3, and 5x5) along with max pooling, This allows the network to effectively capture features at various spatial resolutions. Additionally, Inception-v4 integrates reduction blocks that decrease the spatial size of feature maps while increasing their depth, mainly using 3x3 convolutions combined with max pooling.

To cut down on computational demands, the model employs factorization strategies where a 7x7 convolution is replaced by consecutive 1x7 and 7x1 convolutions, reducing both the parameter count and the computational load. Batch normalization

is also utilized throughout the model to both stabilize and speed up the training phase.

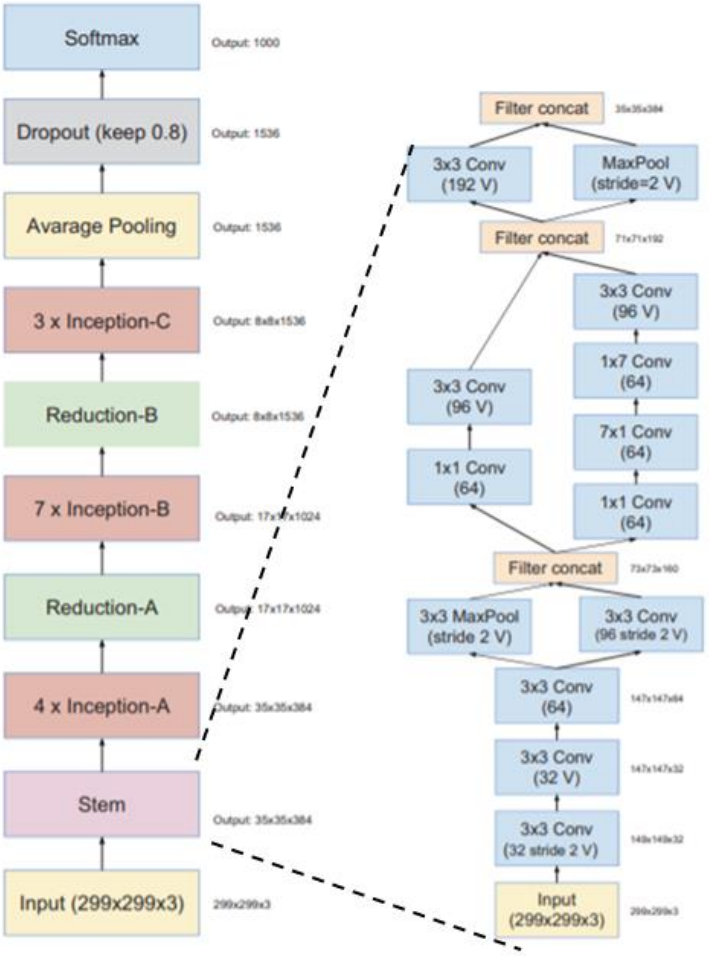


Fig 6: On the left is the overall schema for the pure Inception-v4 network. On the right is the detailed composition of the stem [4].

Stem: Initial convolutional and pooling layers that process the input image, extracting low-level features (e.g., edges, textures).

Inception-A: A module that applies multiple convolutional filters in parallel (1x1, 3x3, 5x5) to capture different feature scales, followed by concatenation.

Reduction-A: A down sampling layer using convolutions and pooling to reduce the spatial dimensions while preserving key features.

Inception-B: A more complex inception module that adds larger filter sizes to capture more abstract features.

Reduction-B: Another down sampling layer, more aggressive than Reduction-A, to further reduce spatial dimensions.

Inception-C: A final inception block with deeper and more intricate filters for the most

abstract and high-level feature extraction.
Average Pooling: A global average pooling layer that reduces the dimensionality by computing the average across each feature map.
Dropout: A regularization technique to prevent overfitting by randomly setting some units to zero during training.
SoftMax: The final layer that generates the class probabilities for classification tasks.

In addition, Inception-v4 incorporates concepts from residual networks (ResNets) by utilizing residual connections between its modules. These connections help improve gradient flow, which simplifies the training process for deeper networks. The architecture is wide, featuring a large number of filters within the convolutional layers, and is also many-layered, making it an exceptionally robust model for image classification tasks.
Finally, Inception-v4's performance is further optimized through techniques such as label smoothing, the use of auxiliary classifiers, and aggressive data augmentation[4].

### 3.3 Transfer learning

Transfer learning is a technique where a model developed for one task is reused for a different, but related, task. It leverages the knowledge gained from solving one problem to improve performance on another, often requiring less data and computational resources. Commonly applied in fields like computer vision and natural language processing, transfer learning enables more efficient training by fine-tuning pre-existing models rather than building new ones from scratch. This approach is particularly valuable when data availability is limited.
TL(Transfer learning) with CNN (convolutional neural networks) is the idea that knowledge can be transferred at the parametric level. CNN models trained in the medical domain utilize the parameters of the convolutional layers to solve a new medical problem. With the use of TL with CNN for medical image classification, it is possible to learn the classification of medical images (target task) using generic features learned from natural image classification (source task), since labels are available in both domains.
There are two transfer learning approaches for utilizing CNN models: using them as feature extractors or through fine-tuning. In the feature extractor approach, the convolutional layers are kept frozen, while in the fine-tuning approach, the parameters are updated during model training.
Each approach can be further divided into two subcategories, resulting in four transfer learning methods, including the feature extractor hybrid.[Fig. 7a], in which the FC layers are removed and the machine learning algorithm is attached to the feature extractor, whereas the structure of the networks remains the same for the other types [Fig. 7b-d]. A fine-tuning process by starting from scratch is the most time-intensive approach because it involves updating the entire ensemble of

parameters during the training process.
Using transfer learning accelerates the development of models for new tasks and significantly reduces the amount of data and computing resources required. Transfer learning improves the efficiency and effectiveness of deep learning applications in various domains by using already trained models, leading to more robust and generalized models[9].

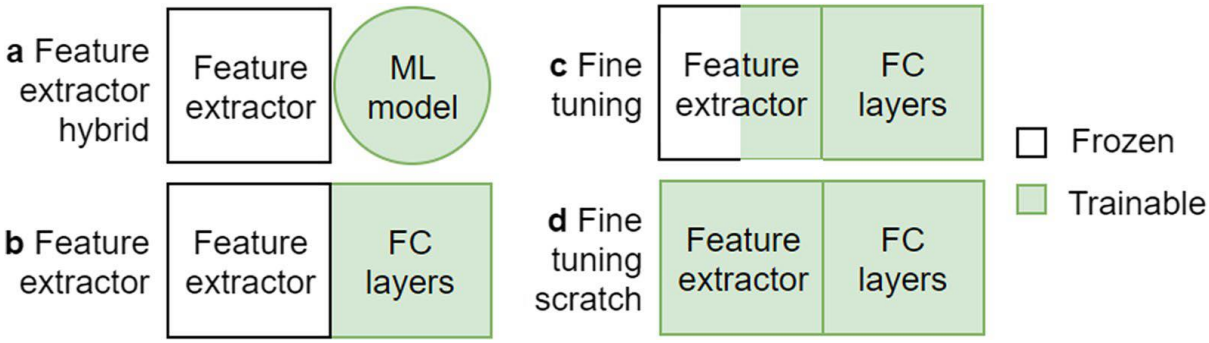


Fig. 7 Four approaches to transfer learning with Convolutional Neural Networks (CNNs):
(a) the "Feature Extractor Hybrid" approach, where the feature extractor is frozen, and the FC layers are replaced with an external machine learning model;
(b) the "Feature Extractor" approach, where only the FC layers are trainable;
(c) the "Fine-tuning" approach, where both the feature extractor and FC layers are trainable;
(d) the "Fine-tuning from Scratch" approach, where the entire network is retrained from scratch.
Frozen parts are shown in white, while trainable parts are shown in green.[9].

## 4. Expected Achievements

We expect to build a system with over 70% accuracy in detecting autism spectrum disorders.
We will create a CNN network and train it with MRI scans from a worldwide multi-site database known as ABIDE (the Autism Brain Imaging Data Exchange) to improve ASD diagnosis accuracy and reliability.
Our CNN model is going to be based on Inception V4 architectures. We will compare the models accuracy and performance for the parameters: learning rate, epochs ,and batch size. We will use transfer learning to help us train the models. We want to build an optimal deep learning system, with loss optimal.
The system will help us identify early whether a person has ASD, Identification of autism allows for timely intervention, which can improve the child's skills and behavior. Accurate diagnosis also prevents incorrect diagnoses and inappropriate treatments.

## 5. Reaches Process

### 5.1. Process:

In the initial phase of our project, we primarily focused on understanding the current state of autism diagnosis and identifying the relevant brain regions that aid in detecting autism. We built the necessary background knowledge by reading articles to fully understand the problem and explore existing solutions. We encountered challenges due to our lack of a medical background, which was crucial for accurately interpreting MRI data. To bridge this gap, we engaged in self-directed learning, reviewing medical articles, and exploring neurological imaging resources. This effort allowed us to understand what relevant areas of the brain were used to identify autism and to acquire the necessary medical insights to work effectively with the MRI data to implement our classification model.

Additionally, we deepened our knowledge of deep neural networks, with emphasis on the Inception v4 architecture and transfer learning and how it can speed up the training process by using general features learned from image classification on the ImageNet dataset to better plan for the next phase.

In the next phase, the key challenge is to develop a system capable of applying what we have learned at this stage and reaching high levels of accuracy classifying whether a person has autism spectrum disorder (ASD) based on MRI scans. Specifically, during the model's training.

### 5.2 Hyperparameters

The hyperparameters of a CNN are settings selected before training that determine how the model will learn. The hyperparameters are optimized in the validation stage and then used in the testing stage. To figure out which combination of these values works best, we'll test different combinations:

**1. Learning rates** - determines the magnitude of steps the model will take during gradient descent, which minimizes the loss function. If the learning rate is too low, the model can take a long time to converge. Learning rates will be tested at 5e-4, 5e-5, and 5e-6.
Loss Function evaluates how the model's predictions align with the actual data.

**2. Epoch** - when all the training data is used at once and is defined as the total number of iterations of all the training data in one cycle for training the model. Epoch sizes range from 50 to 150.

**3. Batch size** - is a technique in which the training data is divided into smaller "batches" and fed to the neural network in separate chunks, rather than all at once. The batch size is 32 vs. 64.

**4. Dropout rate** - A technique involving random deactivation of neurons during training can be used to avoid overfitting in deep learning models.
Overfitting occurs when the model learns not only the underlying patterns in the training data but also the noise, which results in poor performance on new, unseen data. It is caused by training data size is too small or there are not enough samples to represent all possible input data values, which leads to overfitting.
By doing this we are creating a new network architecture out of the parent network. The nodes are dropped by a dropout probability of dropout rate of 0.2 to 0.5.

Based on sensitivity, specificity, precision, and recall, we will evaluate the performance:

- True Positive (TP) - The number of instances that were correctly predicted as positive by the model.
- False Positive (FP) - The number of instances that were incorrectly predicted as positive by the model but are actually negative.
- True Negative (TN) - The number of instances that were correctly predicted as negative by the model.
- False Negative (FN) - The number of instances that were incorrectly predicted as negative by the model but are actually positive.
- Recall - measures the proportion of actual positive cases that are correctly =
  $$\text{Recall} = \frac{TP}{TP + FN}$$
- Sensitivity - is another term for recall, often used in medical testing or diagnostic fields. It refers to the model's ability to correctly identify positive instances out of the actual positives.
  $$\text{Sensitivity} = \frac{TP}{TP + FN}$$
  True Positive Rate (TPR) - is essentially the same as recall and sensitivity. It measures the proportion of actual positives correctly predicted by the model.
  $$\text{TPR} = \frac{TP}{TP + FN}$$
- False Positive Rate(FPR) - The ratio of the number of false positives to the total number of actual negatives. It quantifies how often a model incorrectly labels negative examples as positive.
  $$\text{FPR} = \frac{FP}{TN + FP}$$
- Accuracy - is a metric that measures how often a model correctly predicts the outcome.
  $$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN}$$

- Precision - the quality of a positive prediction made by the model:

$$\text{Precision} = \frac{TP}{TP + FN}$$

- F1 score - is a metric used to evaluate the performance of the model:

$$\text{F1 score} = \frac{2}{\left(\frac{1}{\text{Precision}}\right) + \left(\frac{1}{\text{Recall}}\right)}$$

- Error Rate = 1 – accuracy or $\frac{FP+FN}{TP+TN+FP+FN}$

## 5.3 Product:

In this section, we describe our work process and a first draft of the proposed GUI for the system.
Figure 9 illustrates the screen a doctor will encounter upon accessing a system that utilizes our selected model. Figure 10 shows an example of our system after classification has been performed and how it will assist the doctor in detecting ASD.

Flow chart of system training process:

Before starting the training process, we prepare the dataset. The dataset includes MRI images labeled as either ASD or non-ASD.
The dataset is split, Training set 80%: Used to train the model.
Validation set 15%: Used during training to monitor the model's performance and help prevent overfitting. The test set 5%: Used after training to evaluate the model's final performance.
Images are padded to match the required input size (299x299 for Inception V4).
Loading Inception V4 model pre-trained on ImageNet.
The early layers of the pre-trained model capture general features, which are useful for many tasks. Therefore, these layers are frozen during training to retain their pre-trained weights. Only the deeper layers will be trained to learn task-specific features.
The final layer will have 2 output units with a SoftMax activation function to output probabilities for the two classes.
A batch size of 32 or 64 images per batch.
Training:
Initially, only the new layers added to the model are trained, while the early layers from Inception V4 are frozen.
Validation:
Monitor validation performance after each epoch to check for signs of overfitting or underfitting.
Testing:
To evaluate the final performance, we will measure performance metrics such as accuracy, precision, recall, F1-score, and confusion matrix on the test set to assess how well the model generalizes to completely unseen data.

Once the model performs well on the training, we will fine-tune if necessary (canceling the freeze part or all of the model and continuing training with a smaller learning rate for better performance) [fig. 8].

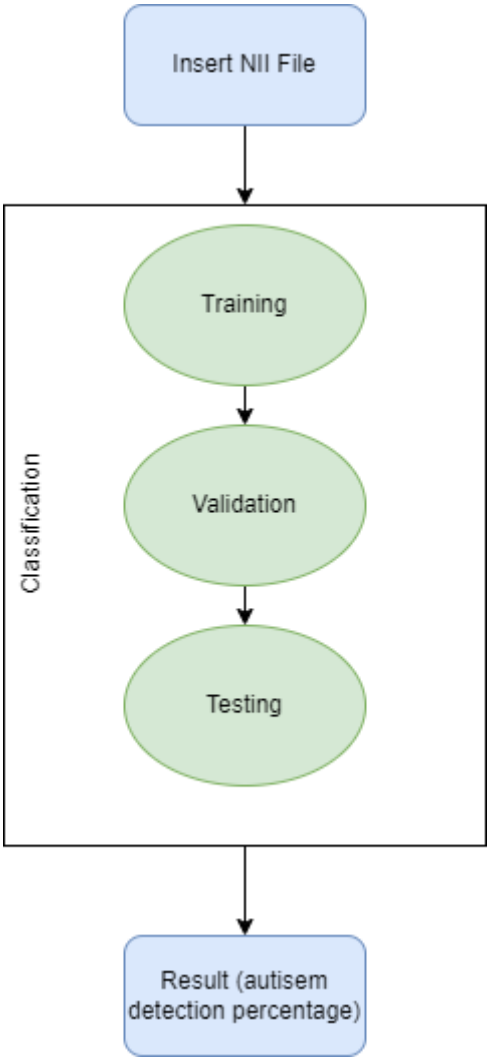


Fig. 8 ASD classification process diagram.

GUI:

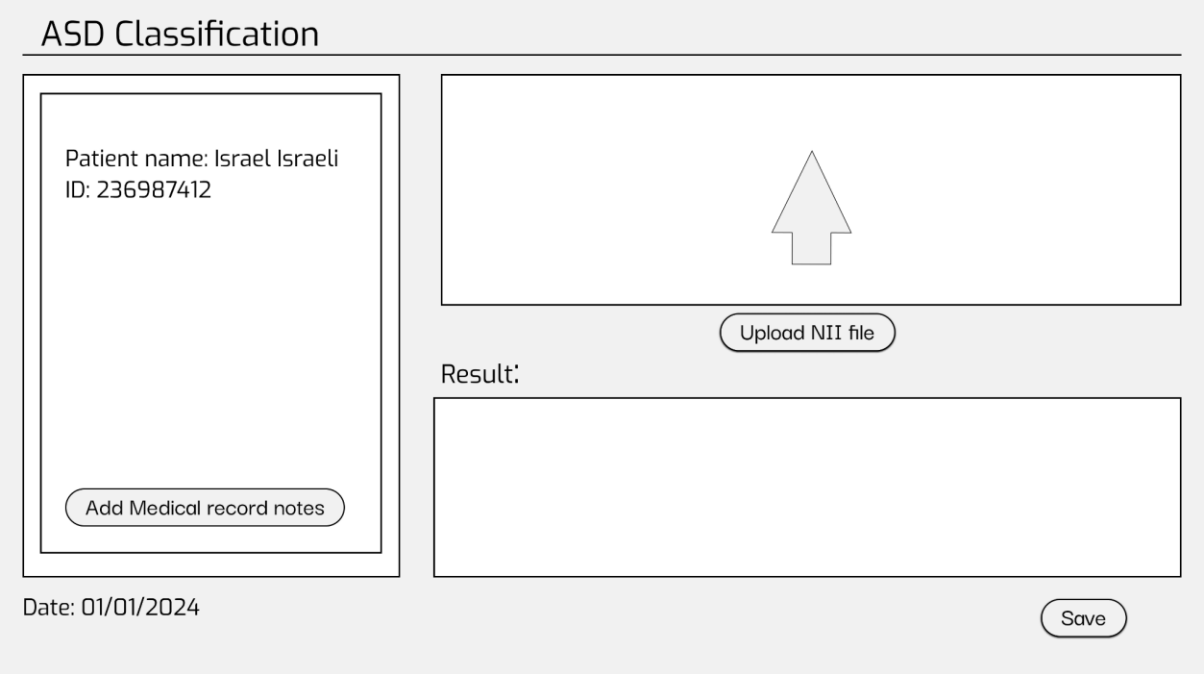


Fig. 9 GUI before classification

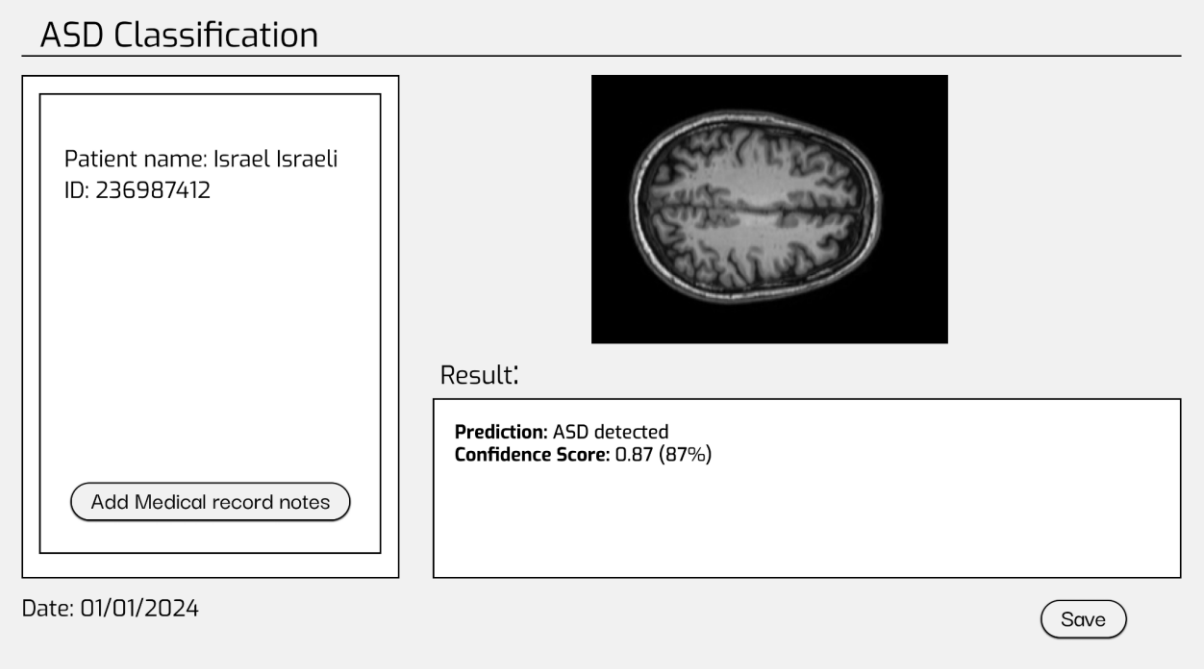


Fig. 10 GUI after classification.

## 6. Evaluation / Verification Plan

| CASE # | Test explanation | Expected result |
|---|---|---|
| 1 | Upload Nii file. | Sends the anatomical MRI scans as input to the model to start the enhancement process. |
| 2 | Press->without uploading anything. | Throw error: “Error! No file has been uploaded”. |
| 3 | Insert the wrong file type. | Throw error: “Error! The file type is not supported”. |
| 4 | Insert empty file. | Throw error: “Error! The file is empty”. |
| 5 | Press save (after uploading the file and receiving results) | Saves the image to the file system. |
| 6 | Press save (before uploading the file and receiving results) | Throw error: “Please upload a file” |
| 7 | Clicking on the "add medical record notes" button | Opening a window for entering information. |

Table 2: Suggested use cases for our program validation.

## 7. Reference

### 7.1 GitHub

https://github.com/NitzanEz/Final-Project

### 7,2 Resources

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