

Convolutional Neural Networks for the Prediction of ASD and Biomarker Identification

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1. Introduction

Autism Spectrum Disorder (ASD) is a neurodevelopmental disorder that is characterized by social and communication deficits as well as restricted, repetitive behaviors. Early diagnosis and intervention are critical for improving long-term outcomes; however, the current gold standard assessment tools are limited in their ability to accurately and efficiently diagnose ASD, particularly in young children. Typically, ASD diagnoses are based on behavioral criteria, but there is growing interest in the identification of objective biomarkers to aid in the diagnoses ([Shen et al., 2019](#)). Biomarkers are measurable characteristics that can be used to indicate the presence or severity of a disease. In the case of ASD, biomarkers could be used to improve and validate diagnoses, especially in young children, and potentially before the emergence of symptoms.

Due to advancements in multimodal neuroimaging in recent years, neuroscience has gained unprecedented opportunities to interrogate the living human brain at multiple scales in both health and disease ([Hong et al., 2019](#)), and these advancements have been especially useful in the study of neurodevelopmental disorders ([Nunes et al., 2019](#)).

Several studies have been conducted to examine changes in functional connectivity in individuals with ASD relative to typically developing controls ([Lau et al., 2019](#); [Williams et al., 2013](#)). However, less is known about changes in structural connectivity in individuals with ASD. By capitalizing on diffusion-weighted magnetic resonance imaging (dMRI), previous studies were able to identify abnormalities in the connectivity strength of several inter-regional fiber pathways in individuals with ASD ([d’Albis et al., 2018](#)). Despite the identification of these abnormalities, the diagnosis of ASD based on brain imaging remains a challenge. One reason for this challenge is that the abnormalities associated with ASD are often subtle and are often difficult to detect. This calls for the application of sophisticated computational methods to aid in the diagnoses.

In recent years, there has been an explosion of interest in the potential of machine learning to revolutionize different aspects of neuroscience ([Abós et al., 2017](#); [Vogt, 2018](#)). However, given the complex and high-dimensional nature of connectomes, traditional machine learning approaches are not well-suited for connectome classification problems. Recent advances in deep learning, specifically Convolutional Neural Networks (CNNs), have shown promise in the prediction of clinical neurodevelopmental outcomes from brain networks (connectomes). For example, *BrainNetCNN* was developed for the prediction of cognitive and motor scores from the connectomes of infants born preterm ([Kawahara et al., 2017](#)).

2. Methods

In this paper, we seek to develop and validate a deep-learning based connectome classification model to distinguish between the structural connectomes of individuals with ASD and typically developing controls. By utilizing a combination of different feature selection techniques, we also hope to identify potential biomarkers that could aid in the diagnosis of ASD. Figure 1 provides an outline of the project.

For this purpose we will utilize a collection dMRI-derived structural connectomes from a large collection of individuals with ASD, as well as typically developing controls obtained from collaborators at the University of Pennsylvania. This data will be utilized for the training and validation of the model.

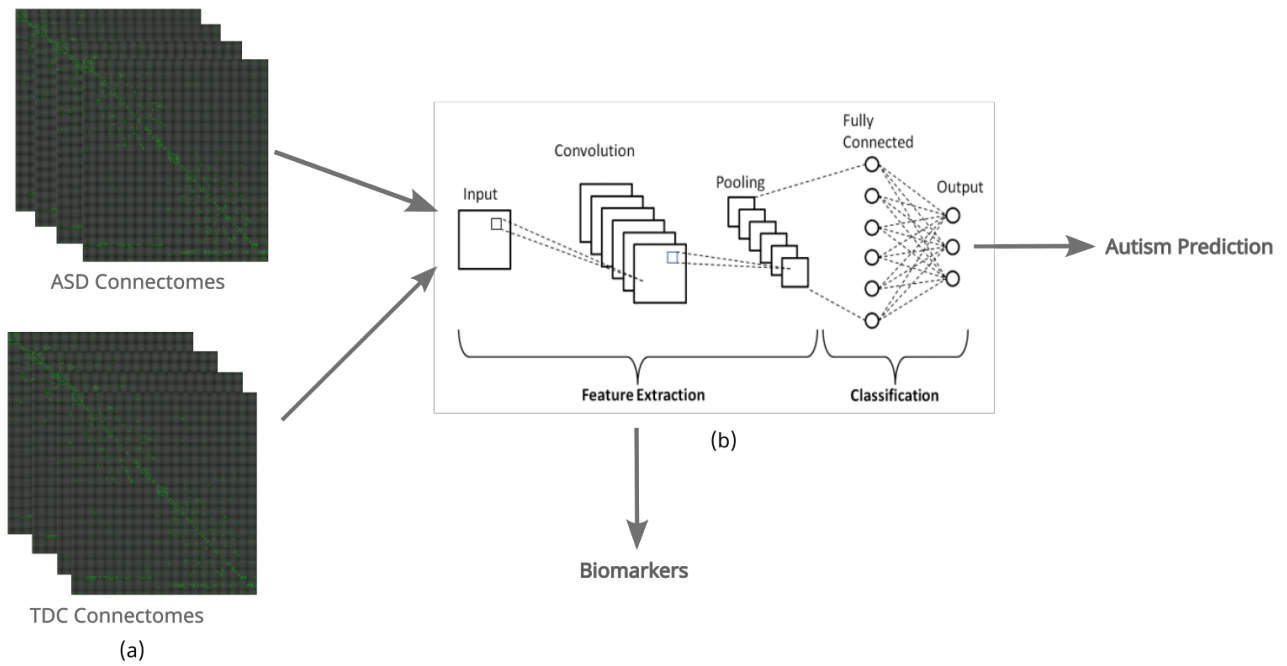


Figure 1. Overview of autism prediction and biomarker identification using a Convolutional Neural Network based classifier. (a) (top) Structural connectomes of patients with Autism Spectrum Disorder. (bottom) Structural connectomes of Typically Developing Controls. (b) Schematic diagram for convolutional neural network.

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