

# Fully connected cascade deep architecture neural networks outperform support vector machines for disease state classification using fMRI data

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**Introduction:** Support Vector Machines (SVMs) have been favored over Neural Networks (NNs) in classification studies involving fMRI. SVMs are capable of handling data of high dimensionality, are easy to train, and can give informative feedback on the significance of each feature to classification. In addition, feature reduction techniques are available to optimize SVM's performance [1]. However, SVMs do not possess good generalizability, which is critical for machine learning to realize its potential for clinical diagnosis. On the other hand NNs have excellent generalizability. However, common NNs based on Error Back Propagation (EBP) and Multi Layer Perceptron (MLP) architecture face convergence issues and are inconvenient to train. Here we propose a fully connected cascade (FCC) deep architecture NN (shown in Fig.2, compared with MLP) which overcomes these limitations and has broad generalizability. We demonstrate that the proposed NN performs better than SVMs for classifying

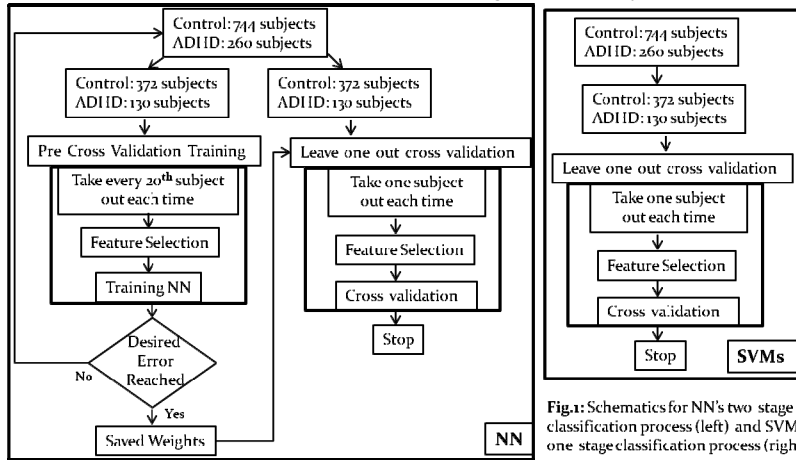


Fig.1: Schematics for NN's two stage classification process (left) and SVMs' one stage classification process (right)

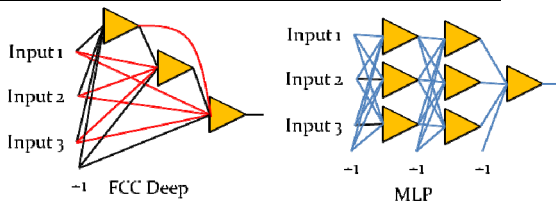


Fig.2: Simplified representation for Fully Connected Cascade Deep NN architecture (left) and Multi Layer Perceptron NN architecture (right)

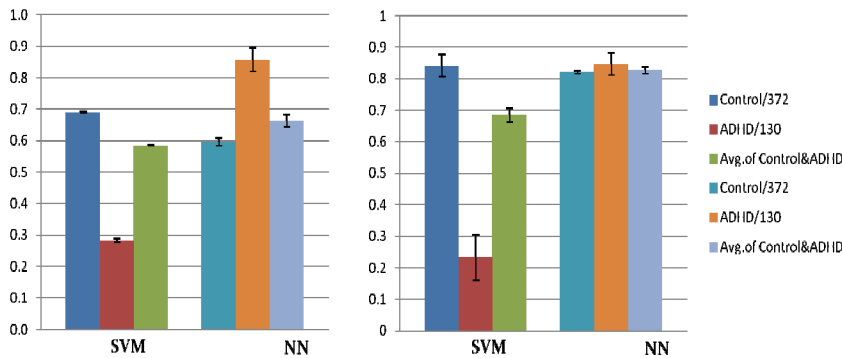


Fig.3: Accuracies for top 15 latent variables Fig.4: Accuracies for top 200 ANOVA ranked principal components

bias caused by the unbalanced data and better generalization. It is noteworthy that the classification accuracy obtained by us beats the winning average accuracy of 61.54% and ADHD classification accuracy of 21%, reported by ADHD-200 Competition [4].

## References:

- [1] Craddock et al, *Magnetic Resonance in Medicine*, 62(6):1619-28, 2009.
- [2] All Releases, from [http://fcon\\_1000.projects.nitrc.org/indi/adhd200/](http://fcon_1000.projects.nitrc.org/indi/adhd200/).
- [3] Wilamowski et al, *IEEE Trans Neural Networks*, 21(11): 1793-1803, 2010.
- [4] Imaging-Based Diagnostic Classification Contest, from [http://fcon\\_1000.projects.nitrc.org/indi/adhd200/results.html](http://fcon_1000.projects.nitrc.org/indi/adhd200/results.html).

http://fcon\_1000.projects.nitrc.org/indi/adhd200/results.html

healthy individuals from patients with attention deficit hyperactivity disorder (ADHD).  
**Methods:** Pre-processed (head motion correction, noise reduction, etc.) fMRI times series from 190 brain regions of 744 control subjects and 260 ADHD subjects were obtained from the ADHD-200 Competition database [2]. Latent variables (Eigen values) and principal components of each time series were obtained using principal component analysis in MATLAB. Two different feature sets were derived from this. First, we chose the top 15 latent variables, which explained most of the variance in the data, as feature inputs to the classifiers. Second, we performed an ANOVA to find principal components which were significantly different between the groups and chose 200 most significant ones as features. Fig.1 illustrates a schematic of the training and cross-validation using the NN and SVM classifiers. The NN we used consisted of only bipolar neurons and formed a FCC deep architecture. It was trained using NBN software [3]. In the Pre-Cross-Validation-Training stage, we trained our NN by taking every 20th subject out each time. We saved the NN's weights and used them for cross validation. In the cross validation process, the root mean square error was restricted to  $\leq 0.75$  (assuming +1 and -1 represent the two classes) on the training data while the error was restricted to  $\leq 90\%$  of the root mean square error on testing data. However, each cross validation started with the saved weights from the Pre-Cross-Validation-Training stage, not the weights from the previous cross validation iteration. ANOVA-based ranking was done inside each cross validation iteration. These steps ensured complete separation of training and testing datasets.  
**Results:** Figs.3 and 4 show the cross validation accuracies using latent variables and ANOVA ranked principal components as input features, respectively. Since SVM's cross validation accuracies are heavily biased by the data sizes, we have calculated the average accuracies separately for each group. In Figs.3 and 4, NN outperforms SVM by 8% and 14% on average accuracy, respectively. Looking at the accuracy for each group individually, our NN reduced the bias caused by the unbalanced data size. NN's accuracy for ADHD group was higher than that for control group, and generally, the NN gives uniformly high accuracies for both groups.  
**Discussion:** The proposed deep architecture NN has two advantages over SVMs: the capability to overcome the