

# Reusability of deep neural network for human functional networks

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## Introduction

Human brain networks receive an increasing attention as potential biomarkers to characterize individuals and brain diseases. Since human brain networks contain a large number of variables, such as nodes, edges, modules and other topological features, dimensional reduction or efficient feature extraction is essentially needed. This study is to answer a question on the reusability of features for different classification of human brain networks. For this purpose, we used deep neural network (DNN) approaches to functional brain networks based on resting-state fMRI. DNN plays as a dimensional reduction scheme by utilizing autoencoders. The autoencoder is an artificial neural network used for learning efficient codings [1]. Starting with random weights in the input and output network of a layer, they can be trained together by minimizing the discrepancy between the original data and its reconstruction. The required gradients are easily obtained by using the chain rule to backpropagate error derivatives first through the decoder network and then through the encoder network [2]. [fig.1]

It is hard to optimize the weights in nonlinear auto-encoders that have multiple hidden layers.

An ensemble of binary vectors can be modeled using a two-layer network called a 'restricted Boltzmann machine' (RBM) [3] in which time and computationally-demand stochastic procedure. Since hyperparameter and parameter in DNN have common optimized value option with target data which has same feature, we assumed that fully optimized deep neural network model from target data can be reused for efficient time and cost consumption. To evaluate reusability of brain features for different classification problem, we used a set of neuroimaging data to solve gender and pathology classification.

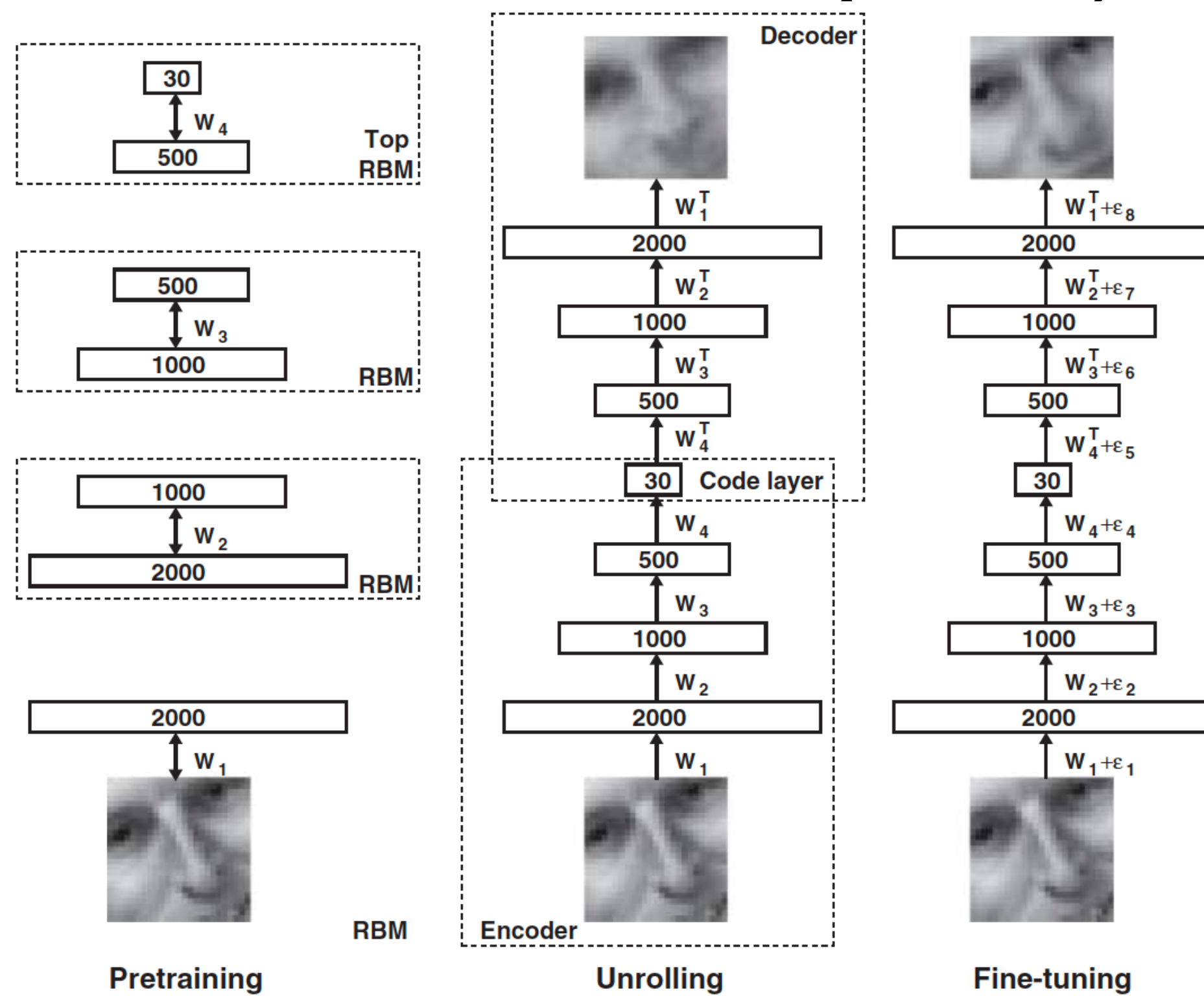


Fig 1. Process of autoencoder system [2]

## Materials and Methods

### Data and Preprocessing

We applied the proposed method to resting state functional MRI (rsfMRI) data from the Human Connectome Project (HCP) database[4]. Scans were acquired on each subject; during four runs with 1200 time points per each run from 820 subjects, with a spatial resolution of  $2 \times 2 \times 2$  mm and a temporal resolution of 0.72 seconds. All fMRI data were first preprocessed in the HCP pipeline using FSL (FMRIB Software Library, <http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/>) to remove several distortion and head motion artifact. After correction process, all data was registered to a common reference atlas space (MNI152) and 100-dimensional independent component analysis (ICA) was conducted to separate brain activity signals to 100 independent component node sets. We calculated functional connectivity matrix group independent components using Pearson correlation and converted by Fisher r-to-z transformation. These functional connectivity procedure were performed by MNET (<http://neuroimage.yonsei.ac.kr/mnet>).

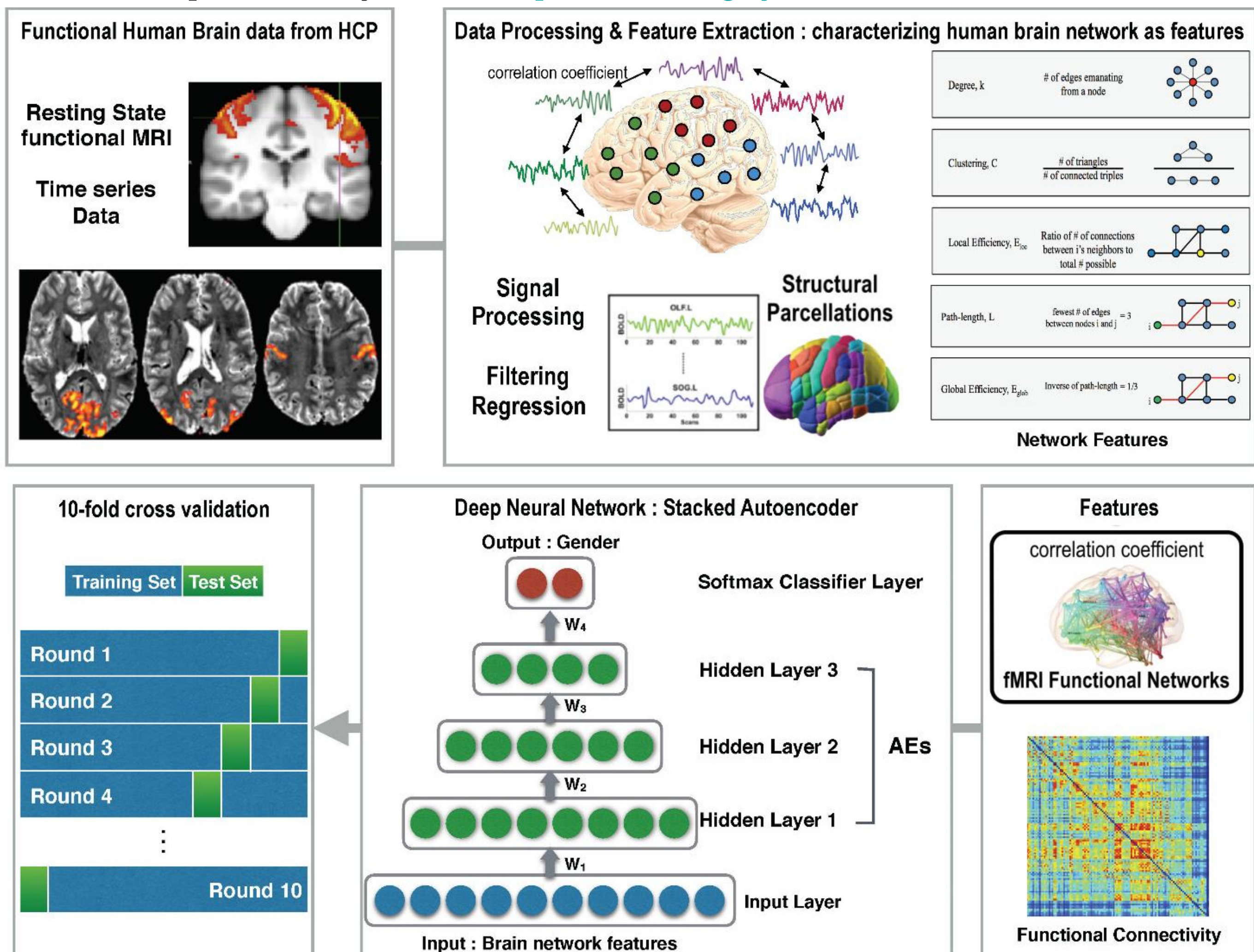


Fig 2. Deep neural network classification process from human functional MRI

Pathology subgroup of HCP data analysis was performed by pathology group or not which was identified by cannabis or alcohol abuse by DSM criteria.

### Stacked Autoencoder for functional brain network

Total 820 functional networks with 100 nodes were used to solve gender classification problem. We optimized the classifier with respect to (1) input data size, (2) the number of hidden layers/nodes, (3) training method and (4) sparsity regularization. For DNN, we used three hidden layered stacked autoencoders [5] which were controlled weight sparsity values in each hidden layer using the L1-norm regularization. The DNN weights were derived from a scaled conjugate gradient and the maximum epoch number was set to 1,000 for every training process. DNN weights were derived from a scaled conjugate gradient. We first evaluated DNN parameter by 10-fold cross validation process using subset of 700 subjects network data and the performance was validated by rest 120 subjects. We then performed training process with previous parameter to solve pathology classification problem, and validation is also completed with same procedure. To check the reproducibility in each condition, a set of training and test process was done 10 times. After optimizing the parameters of DNN, we chose the best and the worst models among tested models in the classification of the gender. Then, we reused fully trained weights of the best and worst models in the classification of the pathology by initialize softmax output layer weight and performed fine tuning.

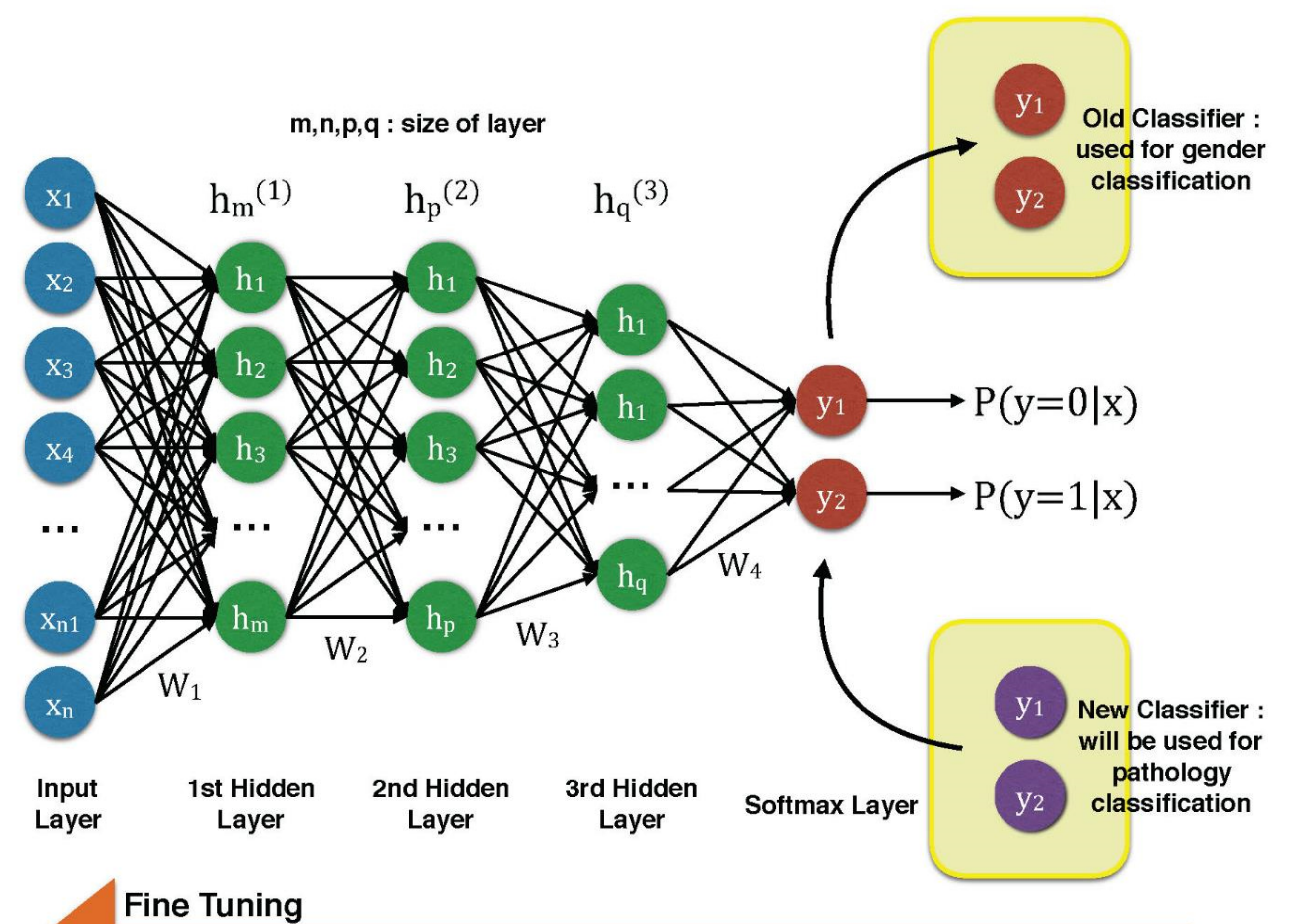


Fig 3. Stacked autoencoder for evaluation of feature reusability

## Results

The average error rate of the best model for the gender classification was 10.95% by 10-fold cross validation. The train parameters of the best model were: number of hidden layers, 3; size of hidden layers, 500-100-20; sparsity regularization, 0.10.; 1<sup>st</sup> weight sparsity, 0.65; 2<sup>nd</sup> weight sparsity, 0.85; number of epoch, 1,000. We also performed classification of pathology subgroup under the same condition and the best average error rate was 13.45%. We then evaluate reusability of the hidden layer which was shown best accuracy for the gender classification in the classification of the pathology. The newly trained model showed the best average error rate of 10.94%.

## Conclusion

This result suggests that a well-trained DNN shows possibility to extract common characteristics for functional brain network, may provide basic modules for general classification, and thus could be reused with many applications with specific fine-tuning. Besides, not only for functional brain networks, multimodal neuroimaging network data is also able to provide brain characteristics with different perspective, integrating multimodal neuroimaging data and constructing best deep neural network model with fully optimized parameters will be remained further study.

## References

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