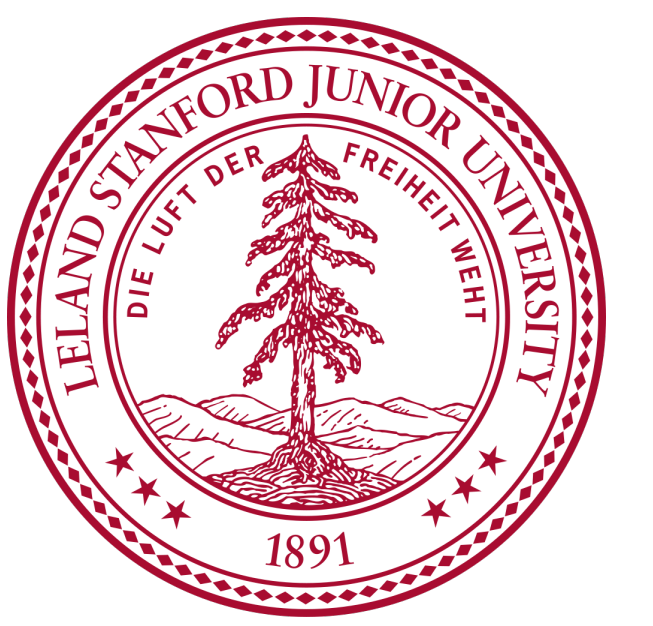


# Subject Measure Prediction from Human rsfMRI Imaging

Zhijie Chen<sup>1</sup>, John Cocjin<sup>2</sup>, Jonathan Fisher<sup>2</sup>

{zcchen, cocjinjb, jofisher}@stanford.edu 1-CS229, 2-CS224W



## Background

Resting-state functional MRI (rsfMRI) measures the brain's intrinsic activity - i.e. the dynamics of the brain when a person is relatively unengaged. In conventional analyses, we look at the relations between the time series of different brain regions, asking: what regions fluctuate together? These regions are thought of as connected in some fundamental way relating not to the context (task) that a subject is in but rather their underlying physiology and individual traits (Mathews 2016). Herein, we examine the Human Connectome Project (HCP) study, which includes rsfMRI and behavioral, cognitive, and demographic measures from 1003 healthy adult subjects. In this project, we investigate the relation of network metrics on rsfMRI graphs to subject-wise non-imaging variables.

## Network Construction and Features

Undirected, weighted graphs for fMRI, referred to as functional connectivity matrices, are computed per subject as follows:

- **Nodes:** Group spatial ICA was applied to the preprocessed rsfMRI data (Smith 2014a, FastICA/MELODIC), yielding 300 spatial ICA maps that represent regions that tend to co-activate.
- **Edges:** The absolute value of partial correlation between node time series with L2 tikhonov regularisation (FSLNets,  $\rho = 0.01$ ) scaled to  $[0,1]$ .

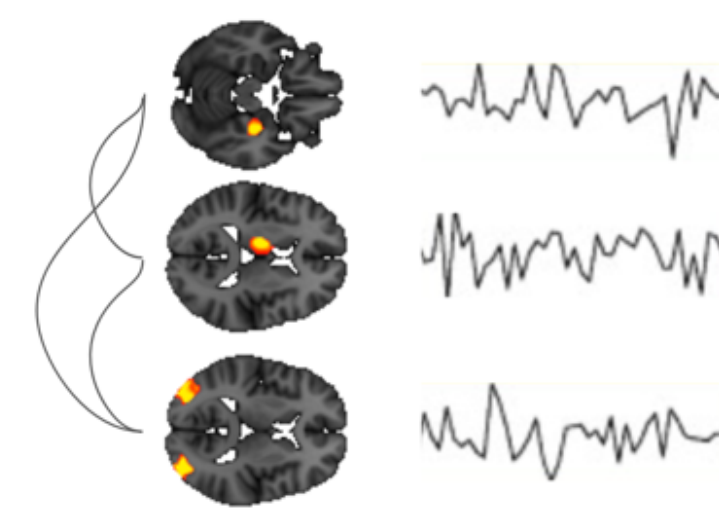


Figure 1: 3/300 independent components (nodes), their time series, and edges.

We consider 23 weighted network metrics. For non-scalar metrics (node-by-node or edge-by-edge), we extract the mean, standard deviation, and max.

|                                    |                                  |                                    |
|------------------------------------|----------------------------------|------------------------------------|
| Strength on absolute               | Negative signed strength         | Positive signed strength           |
| Positive signed clustering coeff   | Negative signed clustering coeff | Transitivity on absolute           |
| Modularity on absolute             | Modularity                       | Assortativity on absolute          |
| Core periphery                     | Weighted distance                | Number edges in distance matrix    |
| Diffusion efficiency               | Node betweenness on absolute     | Edge betweenness on absolute       |
| Eigenvector centrality             | Pagerank centrality on absolute  | Pagerank centrality                |
| Clustering coefficient on absolute | Core periphery                   | Eigenvector centrality on absolute |
| Efficiency on absolute             | Mean first passage on absolute   |                                    |

Table 1: Network features considered.

## Behavioral Measures

Non-imaging data includes scoring in a suite of cognitive/behavioral testing, filtered by category: Alertness, Cognition, Emotion, Motor, Personality, and Sensory. This resulted in 177 different subject wise measures. All subject wise measures are normalised and then input into principal components analysis. The principal component with the largest eigenvalue (PC1) is used to sparsify network edges and as a summary of subject measures.

## Networks of Sparsified Edges

We examine 4 versions of our network. Some weighted edges may be uninformative to the prediction task, and so may introduce noise into network feature calculations. We mask edges out of the network. To construct this mask, we calculate the correlation of each edge weight to the PC1 subject measure. In this manner, we extract which edges more strongly correlate to PC1. We create masks thresholded for the 75th, 85th, and 95th percentiles of the absolute value of the correlation.

## Correlation Analysis

Edge weights exist that correlate more strongly with PC1 than full network features. Strong networks are constructed by keeping 95, 85, and 75th percentile highly correlated edges to PC1. Strong network features correlate more strongly with PC1 than strong edges.

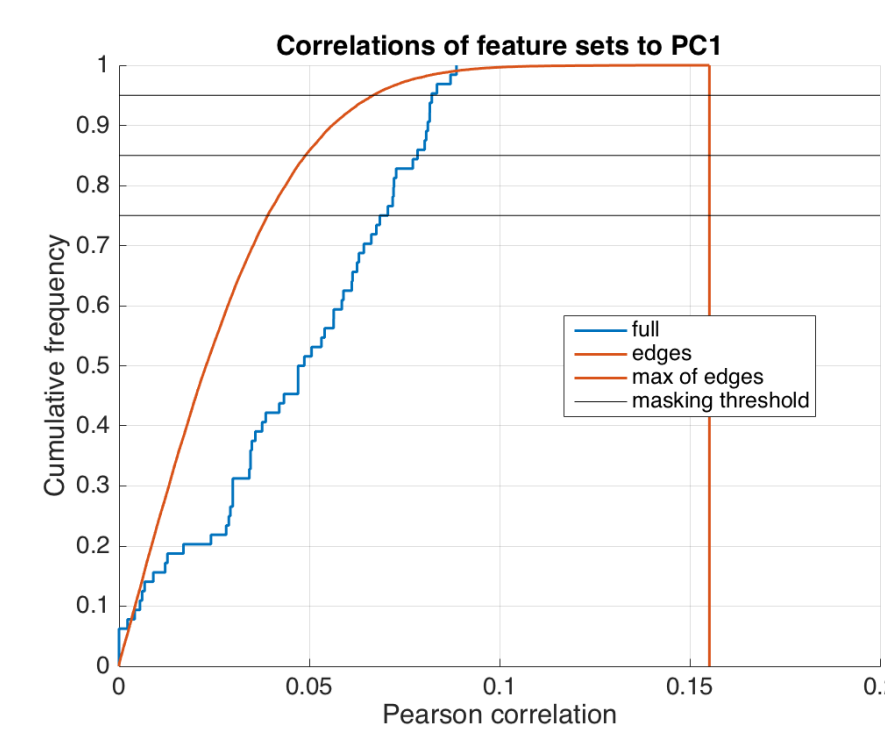


Figure 2: Cumulative histogram of absolute Pearson correlations of either edge weights or full network features.

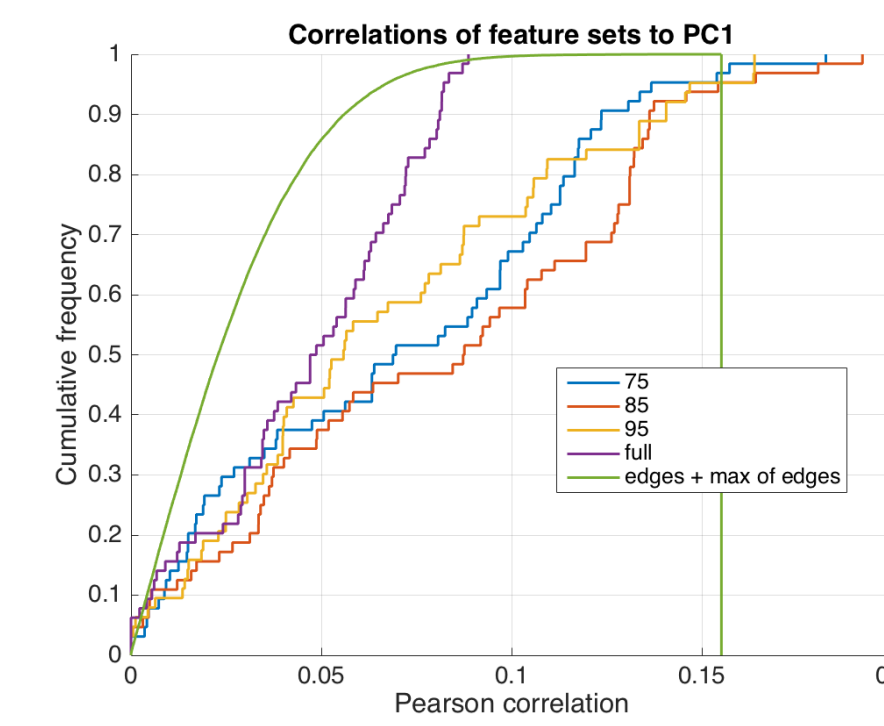


Figure 3: Cumulative histogram of correlations of either edge weights or network features. As can be seen, strong networks yield informative global network features.

Strong networks with different thresholds accentuate different correlative features. We indicate the highest correlated network features here. Notice the lack of overlap among networks.

- **75:** Std of negative signed clustering coefficient, Max negative signed clustering coefficient, Max strength on absolute;
- **85:** Mean diffusion efficiency, Std of distance, Std of negative signed clustering coefficient ;
- **95:** Efficiency, Mean diffusion efficiency, Mean core periphery on absolute.

## Multivariate Prediction

Various regression algorithms perform comparably poorly in predicting PC1. SVM with gaussian kernel performs best of those attempted.

| Model                                 | Dev MSE              | Train MSE |
|---------------------------------------|----------------------|-----------|
| Multivariate linear regression        | 0.8445               | 0.8425    |
| GLM with quadratic terms              | 93.9696 (overfit)    | 1.40E-26  |
| SVMR w. linear kernel                 | 0.8117               | 0.8024    |
| SVMR w. 2nd order polynomial kernel   | 5.9067 (overfit)     | 0.009     |
| SVMR w. 4th order polynomial kernel   | 17920 (not converge) | 17755     |
| SVMR w. gaussian kernel (scale = 100) | 0.8234               | 0.762     |
| SVMR w. gaussian, kernel (scale = 10) | 0.8352               | 0.7454    |
| SVMR w. gaussian, kernel (scale = 1)  | 0.8474 (overfit)     | 0.1988    |

Table 2: (Part of) Regression/classification algorithms attempted on PC1.

We carried out trials on train and dev sets, trying to determine the best scale of Gaussian kernel. With an SVM gaussian kernel, 'strong' edge network features are comparably informative to prediction as the full network features.

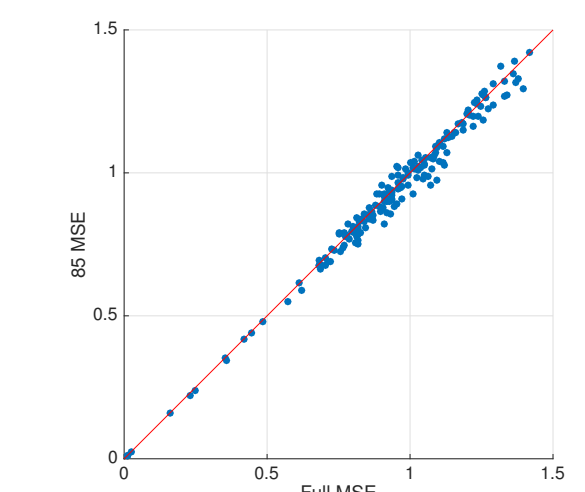
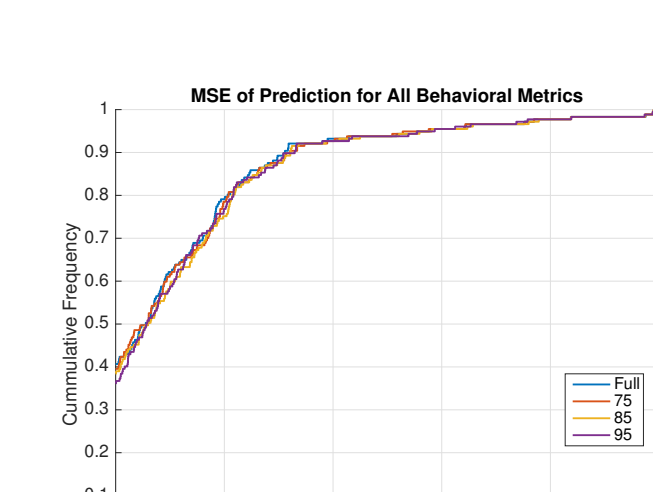
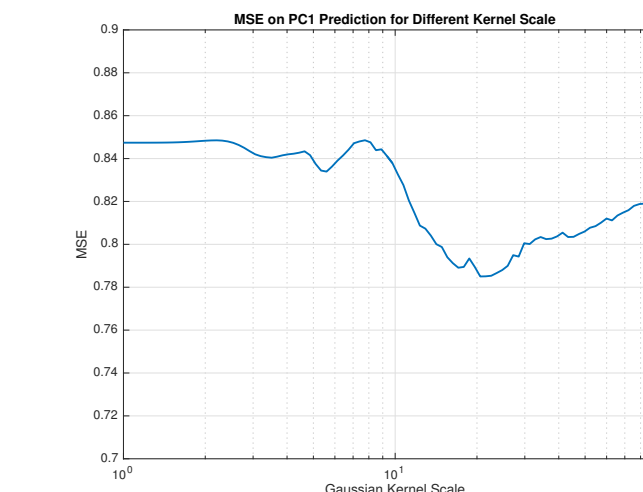


Figure 4: With different Gaussian kernel scale, the model's predictability on dev set varies. The best performance is achieved around 20.

Figure 5: Cumulative histogram of 1-MSE of prediction for all measures using our four networks.

Figure 6: The MSE from full vs. 85% plotted for each metric. The full network and 85% network predict similarly among measures.

The top 5 predictable measures, as well as MSEs on test set, are reported:

| MSE reported              | Full                     | 75                       | 85                       | 95                       |
|---------------------------|--------------------------|--------------------------|--------------------------|--------------------------|
| PC1                       | 0.8826                   | 0.8148                   | 0.7881                   | 0.851                    |
| 1st_Best_Predicted_Metric | Mars_Final<br>0.0099     | Mars_Final<br>0.0102     | Mars_Final<br>0.0103     | Mars_Final<br>0.0099     |
| 2nd_Best_Predicted_Metric | Mars_Log_Score<br>0.0117 | Mars_Log_Score<br>0.0116 | Mars_Log_Score<br>0.0117 | Mars_Log_Score<br>0.0118 |
| 3rd_Predicted_Metric      | SCPT_LRNR<br>0.0248      | SCPT_LRNR<br>0.0225      | SCPT_LRNR<br>0.0258      | SCPT_LRNR<br>0.0268      |
| 4th_Best_Predicted_Metric | ER40HAP<br>0.1624        | ER40HAP<br>0.1617        | ER40HAP<br>0.162         | ER40HAP<br>0.1616        |
| 5th_Best_Predicted_Metric | SCPT_SEN<br>0.2299       | SCPT_SEN<br>0.2305       | SCPT_SEN<br>0.2214       | SCPT_SEN<br>0.242        |

Table 3: Top 5 measures predicted by SVMR from each network.

Previous literature has had corresponding difficulty predicting healthy cognitive/behavioral variables from resting state fMRI (Smith 2015, Shen 2015). Certainly, this poor predictive power calls into question strong interpretations on these network metrics (Rubinov 2010).

## Conclusions and Future Directions

Super network global features correlate more strongly with a latent measure than edge weights or the full network features. However, in multivariate regression, prediction with the strong net is comparable to the full net, and the two share predicted measures. In future work, we would hope that further PCs may capture underlying behavioral factors (intelligence, motor control, etc.) that differentiate from full network prediction. This change may arise from either edge membership or global properties among the different PCs.

Van Essen, D. C., Smith, S. M., Barch, D. M., Behrens, T. E., Yacoub, E., Ugurbil, K., & Wu-Minn HCP Consortium. (2013). The WU-Minn human connectome project: an overview. Neuroimage, 80, 62-79.