The Human Connectome Project aims to build a complete functional and structural map of the human brain. We use their fMRI and structural MRI brain scans to predict sex and age. We use a novel approach by employing ST-GCN. This research project can be used to discover and improve understanding of sex-linked and age-related neurological diseases.

Given a 4D brain scan, classify age and sex of a patient. Regression on age, binary classification of age (old, young adult) and sex (male, female).

Brain regions act as nodes in the graph. Correlation between regions act as edges. Adjacency matrix captures correlations of brain region across timesteps. Feature mapping is computed by using:

\[ f_{out} = D^{-1/2} (A + I) D^{-1/2} f_{in} W \]

ST-GCN Test Accuracies
- Age: 63%, Sex: 78%

Final layer predictions computed with and without Softmax for binary and real-number outputs:

\[ C(y, \hat{y}) = -\frac{1}{m} \sum_{i=1}^{m} \log(\hat{y}(i)) + (1 - \hat{y}(i)) \log(1 - \hat{y}(i)) \] (CE Loss)

\[ C(y, \hat{y}) = \frac{1}{m} \sum_{i=1}^{m} (y(i) - \hat{y}(i))^2 \] (MSE Loss)

Model shows similar accuracies for male and female brains but predicted male more often. Age classification accuracy lower, but model was still able to distinguish age bins.

For full list please checkout github.com/ericksavichay/cs230-final-project


<table>
<thead>
<tr>
<th>Model</th>
<th>Precision</th>
<th>Recall</th>
<th>F1 Score</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age</td>
<td>0.6457</td>
<td>0.8692</td>
<td>0.741</td>
</tr>
<tr>
<td>Sex</td>
<td>0.7563</td>
<td>0.833</td>
<td>0.793</td>
</tr>
</tbody>
</table>

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