Bootstrapping Graph Convolutional Neural Networks for Autism Spectrum Disorder Classification

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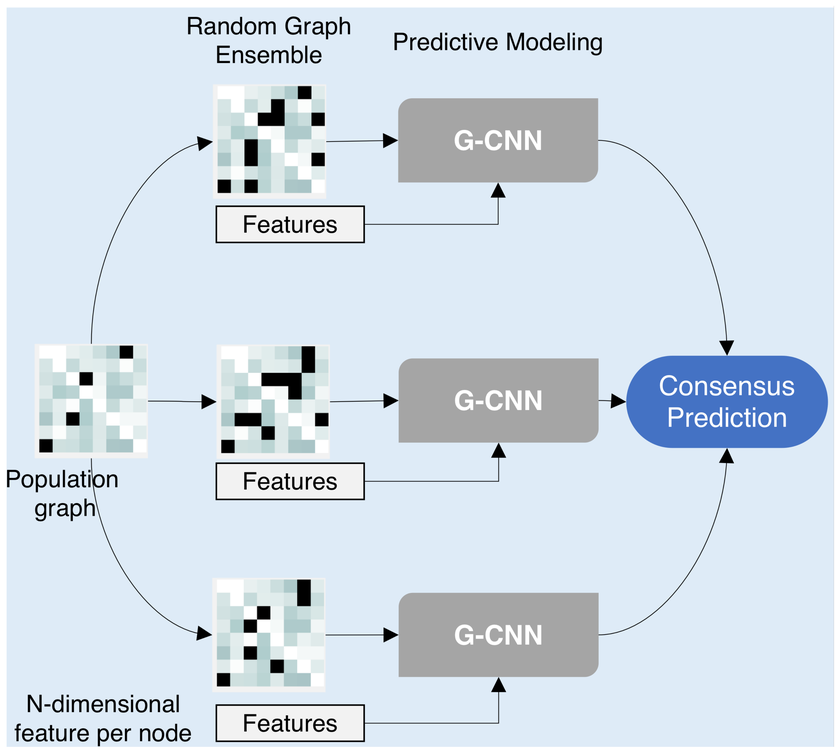
Motivation

- Predictive models can be use to identify patterns that can act as bio-markers for different neuropathological conditions.
- **Autism Spectrum Disorder (ASD)**: Prediction improves significantly by including meta features such as social-cultural traits, in addition to imaging based features [1].
- Encoding meta features into predictive modeling is difficult – Use graph based representation, e.g. an edge between patients of the same gender, and employ graph convolutional neural networks (GCNNs).
- **Challenge:** In practice, such graphs can be uncertain, contain missing links, or be random in the worst case – Can impact prediction significantly.
- **Proposed Work:** We present a bootstrapped version of GCNNs, that utilizes an ensemble of weakly trained models to reduce the sensitivity of the final prediction on the choice of the graph.
- **Impact:** We obtain State of the Art results on ASD classification with the challenging Autism Brain Imaging Data Exchange (ABIDE) dataset, on different graph choices



Graph Construction

- Choice of graph construction is crucial for success of graph based predictive modeling.
- To demonstrate this idea, we study performance variation across a different graph designs:

$\mathcal{G}_0$	$\mathcal{G}_1$	$\mathcal{G}_2$
Imaging feature-based graph, weighted by patient gender and geographical location	*Naïve graph, where the adjacency matrix is identity equivalent to using only imaging features.*	*Noisy version of previous graph -- 30% of edges are randomly dropped*

Bootstrapping GCNNs

- Graph Convolutional Neural Networks (GCNNs) utilize a spectral representation of the graph defined using the eigenvectors of the graph Laplacian.
- Since explicitly computing the spectrum is expensive, GCNNs use localized first-order approximations of spectral graph convolutions.
- **Ensemble Learning –** build robust models by infering an ensemble of weak learners from data and then fuses their decisions using a consensus strategy.
- We generalize this idea by presenting different graphs to every predictive model in the ensemble.

Approach:

- *Graph Dropout*: Randomly drop off *k*% of the edges from a graph, followed by fitting the GCNN on this "noisy graph".
- *Decision Fusion*: Use an average consensus strategy to fuse the softmax predictions obtained from each of the graphs.

The ABIDE Dataset

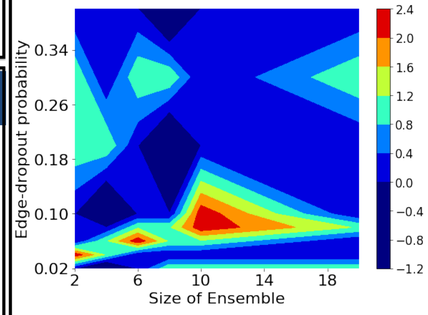
- We follow the C-PAC pipeline and Harvard atlases as in [1] – 872 patients.
- **Goal**: Classify a patient into Autism Spectrum Disorder (ASD) or Typical Control (TC) classes.
- **Data**: Mean time series, obtained from rs-fMRI from each of the 111 ROIs.
- 10-fold cross validation and measure mean accuracy.

Experiments

Implementation details

- We use Kipf et al.'s GCNN code, in Tensorflow: 3 layers of 16 units each. Learning rate of 0.005, dropout of 0.3, Chebychev poynomial of degree 3.
- The features at each node are obtained as the vectorized connectivity matrices.

Hyperparameter Study



We observe a significant boost in performance with no additional data.

When graphs are very unreliable, we see that even a small perturbation of ~0.05 edge drop out boosts classification performance

Classification Performance

We achieve the best prediction performance for a graph based technique on ABIDE.

Even when there is no meta information (naïve graph), we observe improvements using bootstrapping.

Population Graph	Predictive Model	Accuracy
-	Linear SVM[16]	66.8
$\mathcal{G}_0$	G-CNN [7]	69.50
	Proposed	**70.86**
$\mathcal{G}_1$	G-CNN [7]	66.93
	Proposed	**67.85**
$\mathcal{G}_2$	G-CNN [7]	66.35
	Proposed	**67.39**

References

1. Abraham et al., "Deriving reproducible biomarkers from multisite resting-state data: An autism-based example," NeuroImage, 2017.
2. Parisot et al. "Spectral graph convolutions on population graphs for disease prediction," MICCAI 2017
3. Kipf et al., "Semi-supervised classification with graph convolutional networks,". ICLR 2017.

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