Autism Spectrum Disorder Diagnosis Using Sparse Graph Embedding of Morphological Brain Networks

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Introduction

- Autism Spectrum Disorder (ASD) is a complex neurodevelopmental disorder
- It is widely distributed across the brain, affecting both gray and white matter, and involves atypical brain connectivity
- It is difficult to diagnose (i.e., changes can be subtle)
- Recent research focuses on applying machine learning (ML) techniques to brain networks of structural or functional connectivity, derived from MRI scans.





Features for Machine Learning

- Limitations of Previous Work
 - Structural and functional connectomes are extensively studied whereas
 morphological features are largely ignored (77 studies identified in Brown *et al.* 2016)
 - Acquiring fMRI and dMRI sequences is more time-consuming than conventional
 T1-w MRI
 these are prolonged and can be stressful for subject and family
 - Current measures, involving 2 ROIs, may be too fine-grained and specific to capture the larger scale, cross-brain atypical connectivity suspected of ASD.





Features for Machine Learning

- Proposed connectomic data representation
 - + Explore the use of morphological features by constructing graphs of multiple morphological "views" of the brain (e.g., cortical thickness)
 - + Construct a high order network (HON) for each subject incorporating all morphological views → better captures more widespread, higher order connectivity and the relationships between the views.
 - HONs are too large and computationally expensive





Feature Reduction Methods

- Limitations of Some Previous Works
 - Statistical test based methods (e.g., t-test) cannot leverage the graph structure of connectomes in selecting features
 - Graph-based dimensionality reduction methods (e.g., Local Linear Embedding (LLE)) explore the data distribution using a fixed number of neighbors to each data point
 - overlooks cases where data points have different density distribution on the manifold
 - → Does not allow to tease apart close manifolds (for classification or clustering)





- Proposed feature embedding method
 - + Use a dimensionality reduction method that leverages the data graph structure.
 - + Can handle the potentially very close manifolds (i.e., subpopulations) involved in connectomic morphological data representation.
 - + Can automatically learn neighbourhoods of varying sizes for a better, more representative connectomic feature embedding.
 - + Can learn a similarity matrix for encoding the relationship between different connectomic features and can be easily integrated into a supervised classification framework.
 - Based on (Elhamifar and Rene, 2011), we propose a sparse graph embedding (SGE) of connectomic data for ASD diagnosis.





Connectomic data representation

Low Order Networks

- 2 connectomes are constructed for each morphological view of the brain (1 for each hemisphere), for every subject



- Nodes represent cortical ROIs; edges represent the absolute difference between a morphological measure's average for a region (taken across all vertices in a specific region), and the connected region's average.





Connectomic data representation

High Order Networks

- For each hemisphere of each subject all views are integrated into a single HON
- A node of the HON represents a <u>pair</u> of ROIs. An edge is calculated by first constructing a vector (for each node) of the <u>connectivity strength</u> values between the given pair of ROIs, from every LON:



- ROI pair 1 connectivity strength vector
- ROI pair 2 connectivity strength vector
- The edge then represents the correlation between these two vectors.





Proposed Method

Feature Extraction

HON Feature Vectors

As connectomes are symmetrical, the elements of the upper triangles are extracted and vectorized, excluding the diagonal.



CON Feature Vectors

 All LONs are also vectorized, then all of a subject's vectors are concatenated into 1 feature vector, including both hemispheres of every view.



Subject 1 HON



Proposed Method

Sparse Graph Embedding

- Build a Similarity Matrix
 - Build the similarity matrix W from the learned graph of the relationship between

data points lying in different connectomic manifolds.







Proposed Method

Sparse Graph Embedding

- Generate Low-Dimensional Embedding
 - Eigen-decomposition of the normalized Laplacian matrix of the learned similarity matrix W.



Training and Test Data

- Train SVM- SGE is conducted on the training data to obtain the training features

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- Test SVM- SGE is conducted on the full dataset, and the test partition extracted from the result.





$$\begin{aligned} & \underset{\alpha_i}{\operatorname{min}} \lambda || \mathbf{Q}_i \alpha_i ||_1 + \frac{1}{2} || \mathbf{\tilde{D}}_i \alpha_i ||_2^2 \ s.t. \ \mathbf{1}^T \alpha_i = 1, \\ & \underset{\sum_{t \neq i} || \mathbf{h}_t - \mathbf{h}_i ||_2}{\bigcup} \in]0, 1] \\ & \underset{[|\mathbf{h}_1 - \mathbf{h}_i||_2}{\overset{|\mathbf{h}_1 - \mathbf{h}_i||_2}{\bigcup}} \in]0, 1] \end{aligned}$$

- + Encourages a sparse selection of nearby connectomic points that lie in the same manifold and span a low-dimensional affine subspace passing near point i.
- + The number of sparsely selected neighbors for each datapoint depends on the datapoint and its local neighborhood and ideally would belong to the same manifold → This better handles variation in the density of data points on the manifold.



$$\begin{aligned} & \underset{\alpha_i}{\operatorname{Graph Learning}} \\ & \underset{\alpha_i}{\min} \lambda || \mathbf{Q}_i \alpha_i ||_1 + \frac{1}{2} || \mathbf{\check{D}}_i \alpha_i ||_2^2 \ s.t. \ \mathbf{1}^T \alpha_i = 1, \\ & \underset{\alpha_i}{\operatorname{I}} \end{aligned}$$

$$& \underset{\alpha_i j}{\operatorname{Fhe learned similarity matrix}} \\ & w_{ij} \triangleq \frac{\alpha_{ij} / || \mathbf{h}_j - \mathbf{h}_i ||_2}{\sum_{t \neq i} \alpha_{it} / || \mathbf{h}_t - \mathbf{h}_i ||_2}; \ j \neq i \end{aligned}$$

+ Perform dimensionality reduction using the learned matrix W.





Dataset

- 102 Subjects from the Autism Brain Imaging Data Exchange (59 ASD, 43 NC)
- Leave-one-out cross-validation scheme
- FREESURFER was used to reconstruct both hemispheres for every subject, which were then parcellated into 35 ROIs using Desikan-Killiany Atlas.
- Morphological views:
 - 1) C1 = Maximum principal curvature
 - 2) C2 = Mean cortical thickness
 - 3) C3 = Mean sulcal depth
 - 4) C4 = Mean of average curvature





Parameters

- A nested grid search approach was used to find the intrinsic dimension of the manifold for feature embedding (LLE = 50, SGE = 9)
- We estimate W_{tr} to train SVM, then rebuild W_{ts} (including both training and testing subjects), and classify the testing subject.

Comparison Methods

- RAW Feature vectors are classified with no feature reduction employed
- T-test T-tests are used to select a number of the most discriminative features
- LLE A local linear embedding of the features is carried out reduce the dimensionality of the features for classification



Feature Types

- CON Simple, concatenated, low order features vector
- HON High order feature vector
- CC(HON) Clustering coefficient of the HONs, as another preliminary feature reduction method





Features	Accuracy (%)	Sensitivity (%)	Specificity (%)
View 1	51.9608	48.8372	54.2373
View 3	53.9216	44.1860	61.0169
View 5	47.0588	37.2093	54.2373
View 6	47.0588	41.8605	50.8475
CON	52.9412	37.2093	64.4068
HON	52.9412	44.1860	59.3220
CC(HON)	46.0784	32.5581	55.9322
HON + CON	53.9216	46.5116	59.3220
CC(HON) + CON	51.9608	39.5349	61.0169
CC(HON) (T-Test)	47.0588	32.5581	57.6271
HON + CON (T-test)	55.8824	37.2093	69.4915
CC(HON) + CON (T-test)	52.9412	37.2093	64.4068
CC(HON) (LLE)	58.8235	60.4651	57.6271
HON + CON (LLE)	50.9804	55.8140	47.4576
CC(HON) + CON (LLE)	43.1373	32.5581	50.8475
CC(HON) (SGE)	52.9412	62.7907	45.7627
HON + CON (SGE)	50	51.1628	49.1525
CC(HON) + CON (SGE)	61.7647	62.7907	61.0169



■Raw ■T-Test ■LLE ■SGE





On-going Work

Whole-Brain HONs

- As the corpus callosum has been implicated in ASD, we might expect crosshemisphere connectivity to be affected and therefore more discriminative
- Incorporating both hemispheres in HONs could produce better accuracies; preliminary work found **63.16%** accuracy for raw, whole-brain HONs.







Conclusion

Summary

- High-order networks using cortical morphological attributes.
- > Jointly integrated multiple cortical morphological network for autism identification
- > Utilized sparse graph embedding for high-dimensional connectomic data reduction.

Future work

- > Evaluation of the method on the whole ABIDE dataset (for more powerful statistical analysis)
- Instead of decoupling sparse graph learning and classification, we can extend SGE into a semi-supervised graph learning method for higher classification accuracy.
- Compare morphological networks with functional and structural networks in performance



Thank you for your attention!

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