Supervised Multi-topology Network Cross-diffusion for Population-driven Brain Network Atlas Estimation

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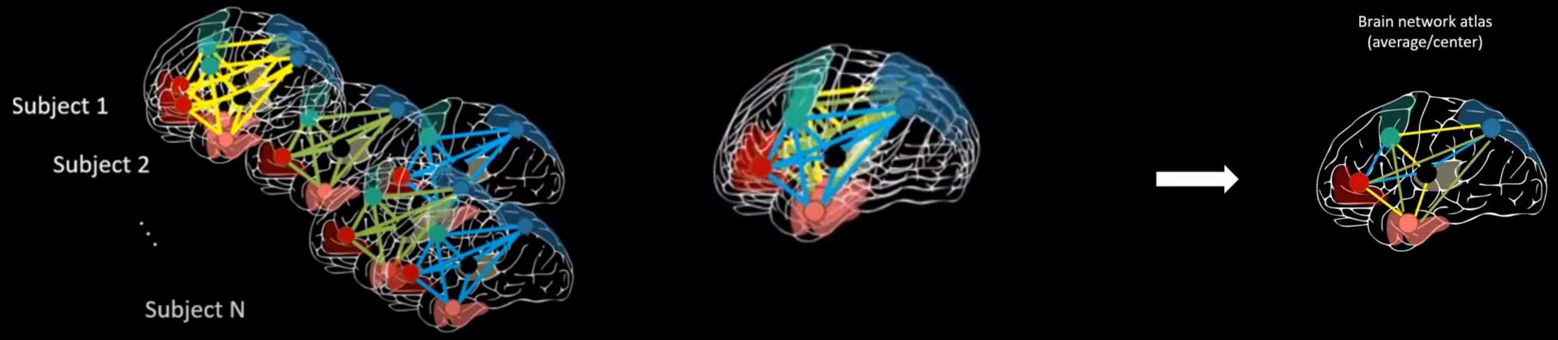
Problem Statement

General Context

- Integrate a set of functional networks to define a unified brain network atlas.



Previous methods

Diffusive shrinking graphs(rekik et al, 2017):

- Introduced a brain network atlas from a population of both morphological and functional brain networks using diffusive-striking graph technique.

netNorm(Dhifallah et al, 2019):

- Designed a sample selection technique followed up by a graph diffusion and fusion step to create a unified brain network atlas.

Brain network atlas-guided feature selection (NAGFS) method (Mihiri et al, 2020):

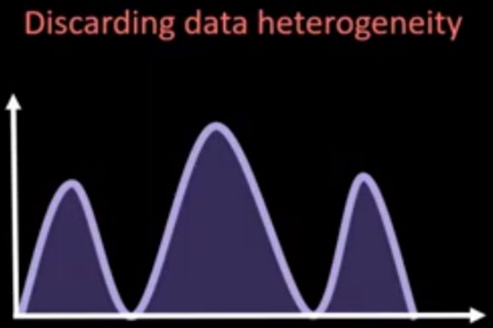
- Estimated a brain network atlas-guided feature selection (NAFGS) method to differentiate the healthy from the disordered brain connectome.

Limitations

-All the methods have relied on Similar network Fusion techniques(SNF)

-Non-linearly diffuses and fuses brain network without considering their heterogeneous distribution.

-Diffusion and Fusion techniques are implemented in fully unsupervised manner.



Proposed SM-netFusion Framework

Supervised network cross-diffusion baked on graph topological measures (SM-netFusion) by enhancing the non-linear fusion process using a weighted mixture of multi-topological measures.

- By clustering similar functional brain networks into non-overlapping subspaces using multiple kernels, we can capture potential data distribution heterogeneity with different bandwidths.

(+) Handles data heterogeneity at different bandwidths.

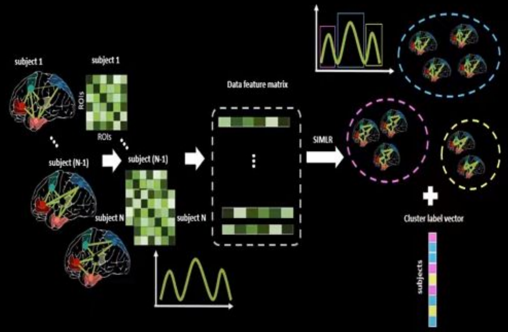
- Supervisedly learn a weighted combination of multi-topological measures which nicely characterize both local and global relationships

(+) preverves the heterogeneous distribution of the data in a specific class.

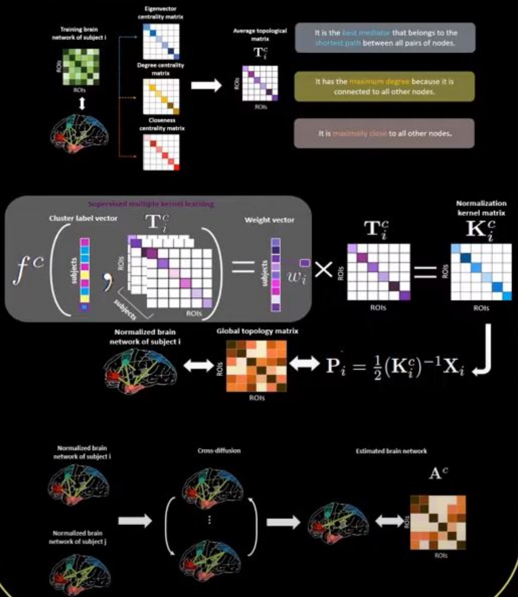
(+) Improves the representativeness and centeredness of the estimated multi-topology BNA

Proposed SM-netFusion Framework

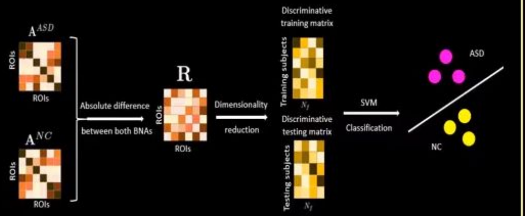
Class-specific feature extraction and clustering



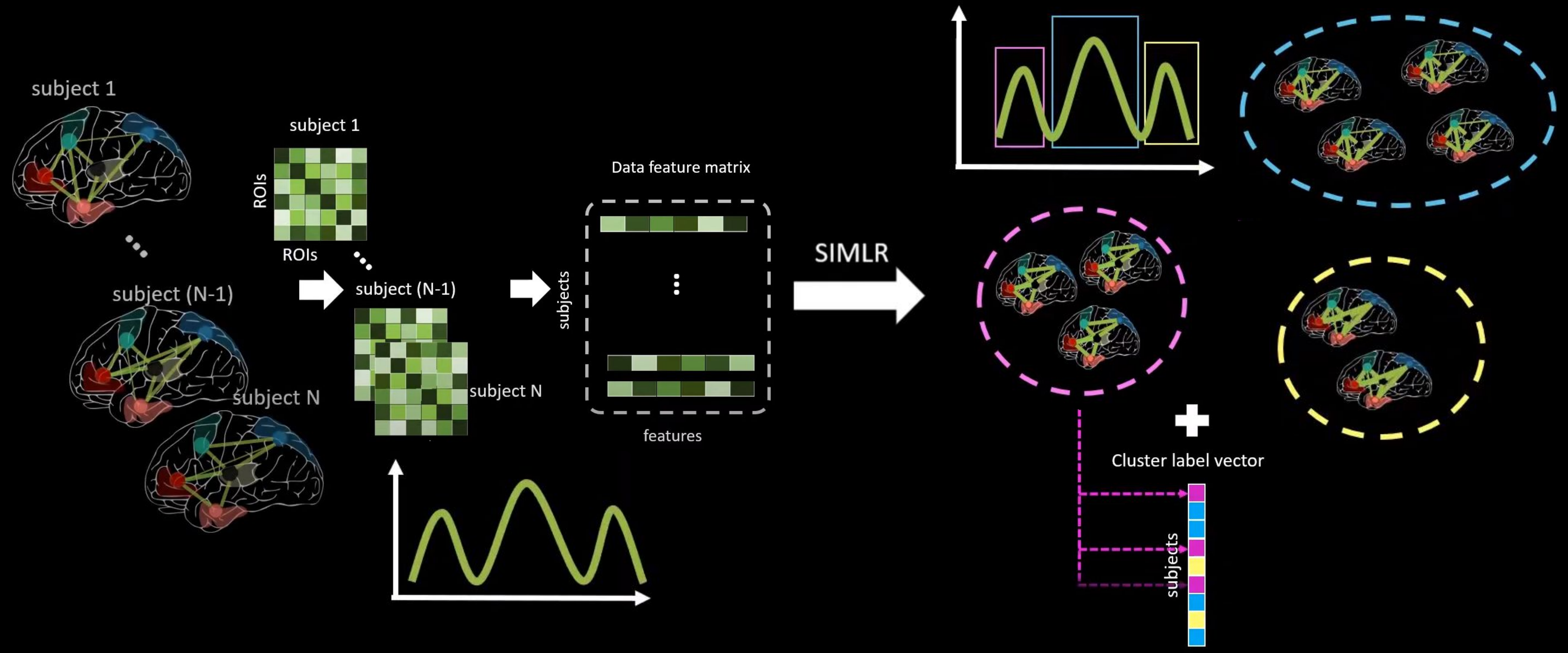
Class-specific supervised multi-topology network cross-diffusion



Identification of the discriminative connectional fingerprint



A) Class-specific feature extraction and clustering



B) Class-specific supervised multi-topology network cross-diffusion

SNF technique

$$\mathbf{P}_i = \frac{1}{2}\mathbf{D}_i^{-1}\mathbf{X}_i$$

Global topology matrix

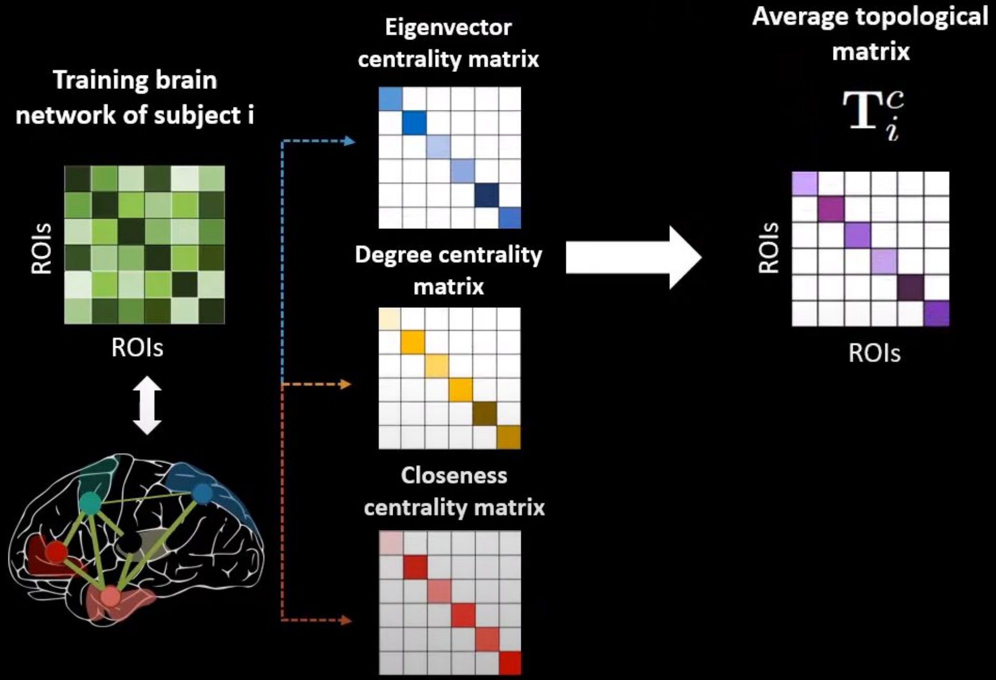
Degree matrix

Brain network matrix of subject i

(-) Cannot capture the full structure of a network.

(-) Captures only the quantitative aspect of a node.

Step 1: Class-specific multi-topology brain network construction



It is the best mediator that belongs to the shortest path between all pairs of nodes.

It has the maximum degree because it is connected to all other nodes.

It is maximally close to all other nodes.

Step-2 Normalization of the global topology for a specific class

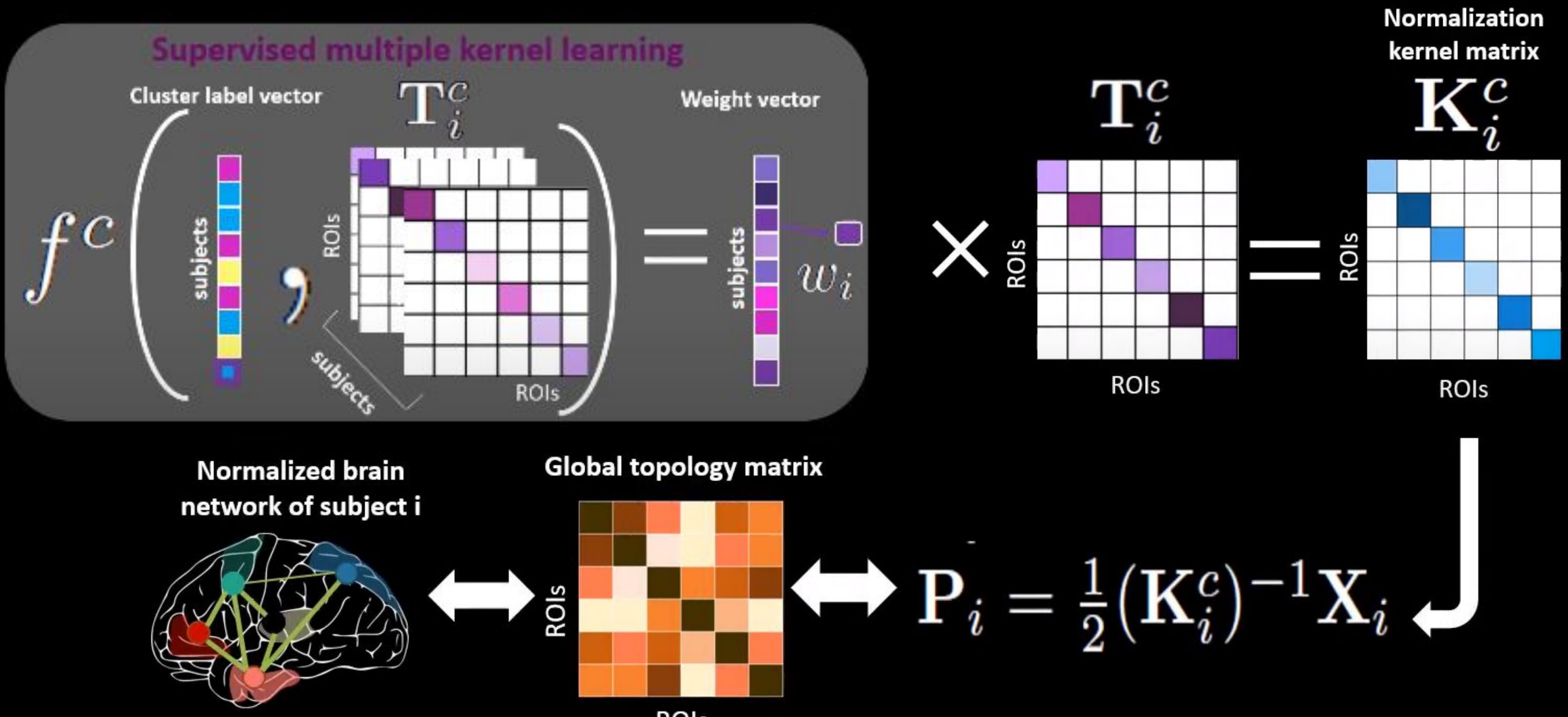
$$\mathbf{P}_i = \frac{1}{2}\boxed{(\mathbf{K}_i^c)}^{-1}\mathbf{X}_i$$

Normalized kernel matrix

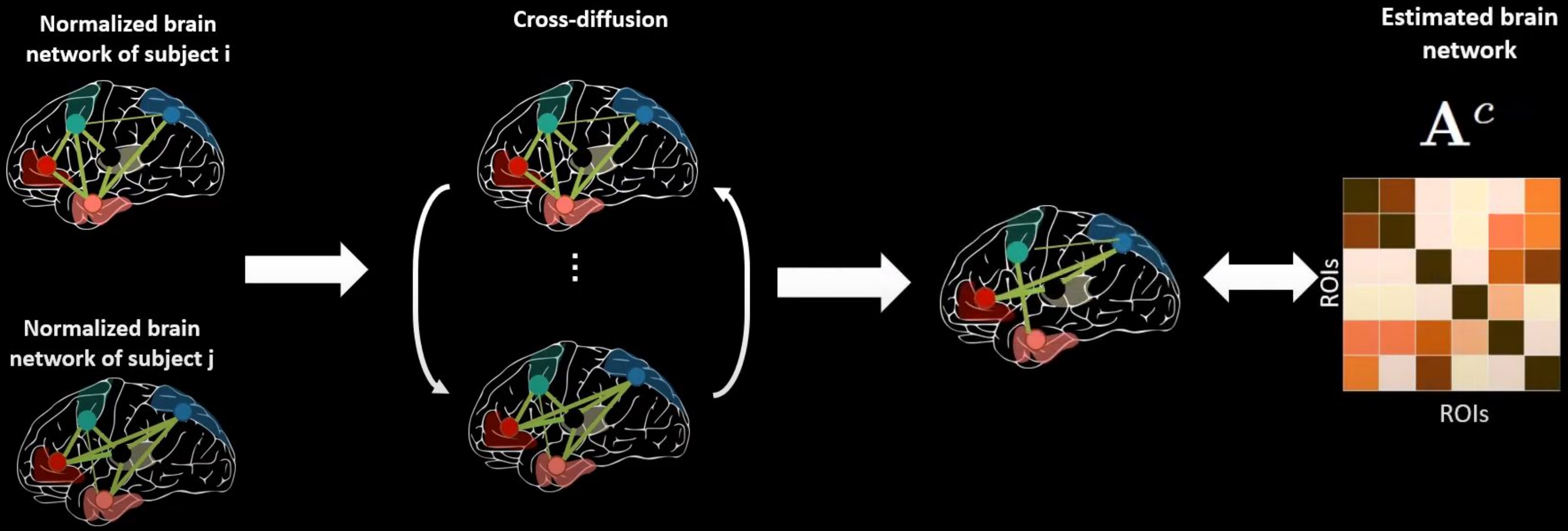
$$\mathbf{P}_i = \frac{1}{2}\cancel{\mathbf{D}_i}^{-1}\mathbf{X}_i$$

Class-specific supervised multi-topology network cross-diffusion

Step 2: Normalization of the global topology matrix for a specific class



Step-3 Class-specific cross diffusion process



Experiments

Dataset

- 505 functional connectomes (266 ASD and 239 NC) from the Autism Brain Imaging Data Exchange (ABIDE[1]) preprocesses public dataset.

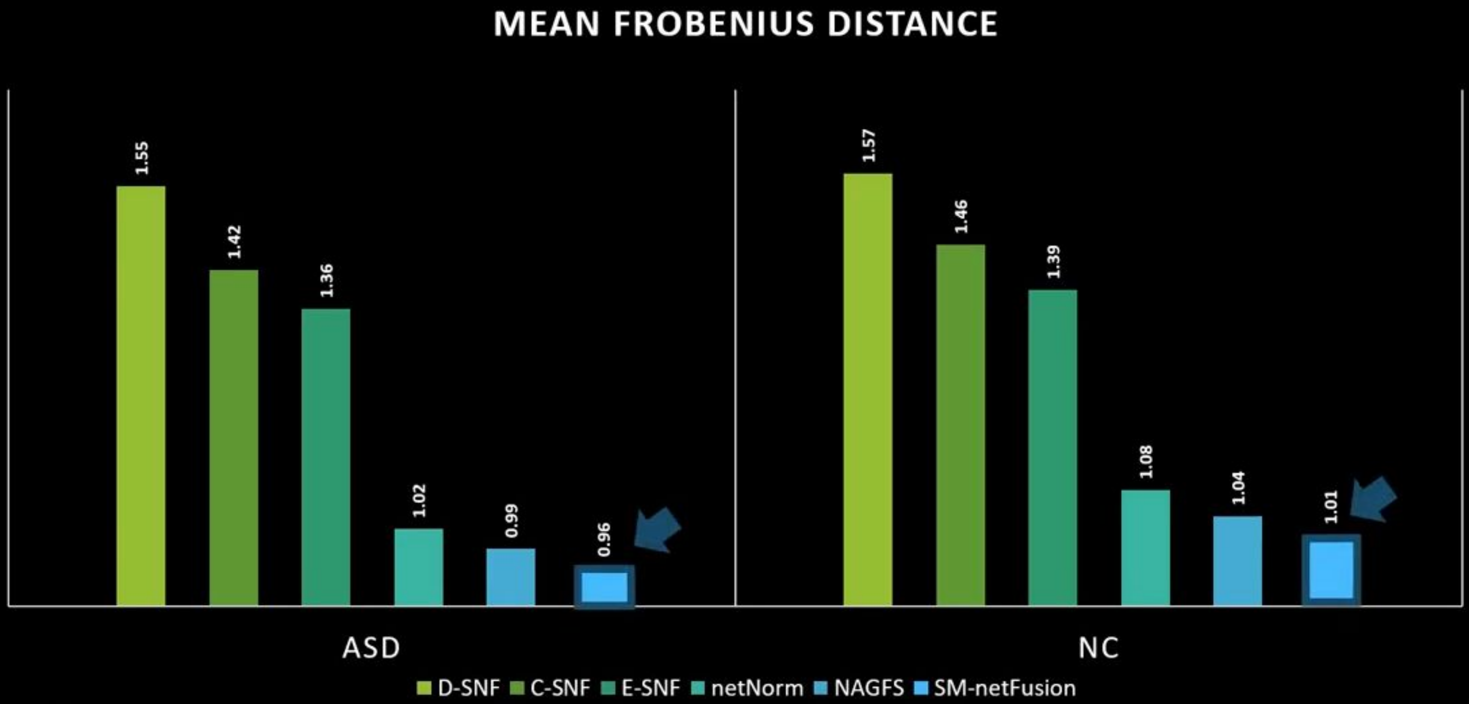
Representativeness evaluation metric

- Frobenius distance d_F between the estimated template *A* and each brain network X_i^c of subject *i* and averaged across subjects:

$$d_F = \frac{1}{N}\sum_i \sqrt{\sum_k \sum_l \left| A^c(k,l) - X_i^c(k,l) \right|^2}$$

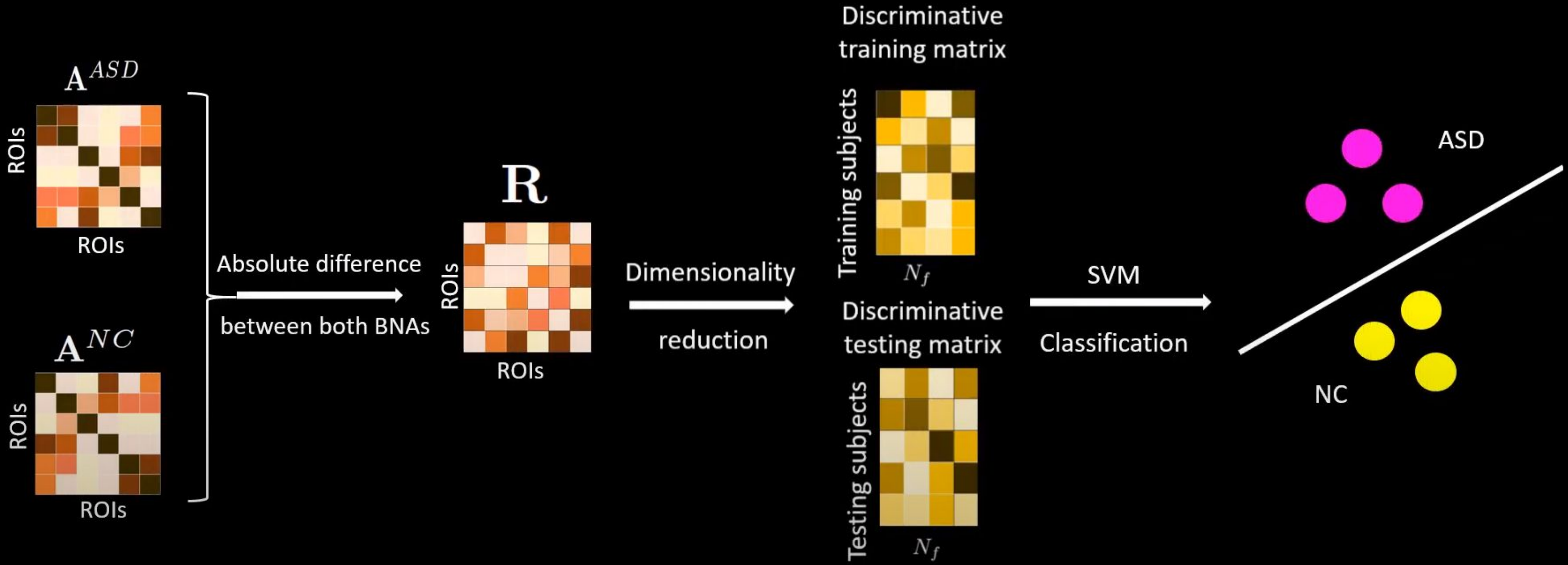
- We evaluated SM-Fusion representativeness using five-fold cross-validation.

Results



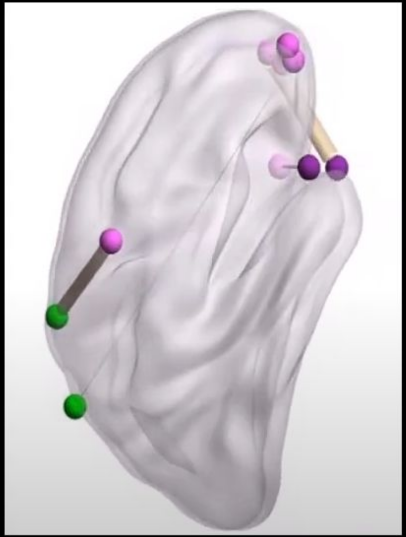
MEAN FROBENIUS DISTANCE
1.55
1.42
1.36
1.02
0.99
0.96
ASD
1.57
1.46
1.39
1.08
1.04
1.01
NC
D-SNF
C-SNF
E-SNF
netNorm
NAGFS
SM-netFusion

C) Identification of the discriminative connectional biomarker



Neuro Biomarkers

Discriminative brain connectivities



The frontal lobe → understanding and reacting to others

The temporal lobe → social language processing and social attention

The parietal lobe → the mediate impairments of social behaviors

Conclusion

Summary

- SM-netFusion is the first framework for supervised network cross-diffusion based on graph topological measures for estimating a representative and discriminative brain network atlas.

➔ Outperformed both baseline and state of-of-the-art methods

Major findings

+ Supervised cross-diffusion process > handles data heterogeneity
+ Can be leveraged to design an efficient feature selection method > training predictive learners in network neuroscience
+ Spot connectional fingerprints of a disorder > helps clinicians better interpret the altered brain connections
+ Can be applied to brain networks derived from any neuroimaging modality > generic method.

Future work

- Evaluate on larger connectomic datasets covering a diverse range of neurological disorders


THANK
YOU!