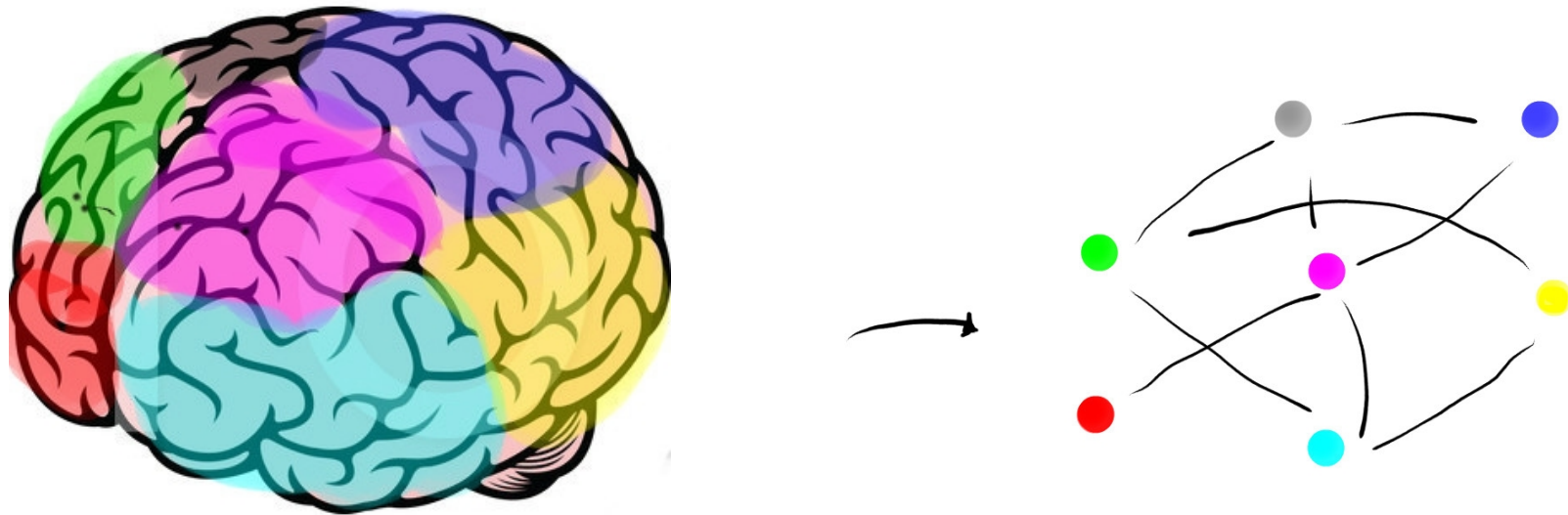


# Classification of normal and pathological brain networks based on similarity of graph partitions

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# What is connectome ? (spoiler connectome = brain network)



In a macro-scale view connectome is a graph in which nodes correspond to different brain regions (**Regions Of Interest**), while the edges are connections between those areas.

# Tasks to solve

1. ROI definition
2. Time series extraction / Tractography
3. **Connectivity matrix**
4. **Supervised learning**

# How to classify graphs?

1. Global graph characteristics (diameter, radius, node degree distribution)
2. Local graph characteristics (degree centrality, closeness centrality, betweenness centrality, eigenvector centrality, average path length, clustering coefficient)
3. Graph's Laplacian spectra
4. Simple distance between adjacency matrices ( $l_1$ ,  $l_2$ )
5. Bag of edges
6. And more, much more

Brain networks  
( $K$  weighted graphs  
with  $n$  nodes)



Adjacency matrices  
( $K$  matrices  $n \times n$ )



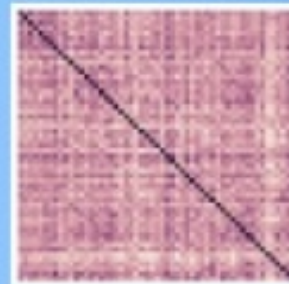
Single graph partition



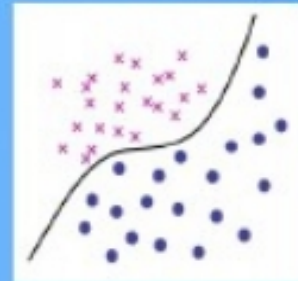
Clustering labels  
Matrix ( $K \times n$ )



ARI / AMI based kernels  
Matrix ( $K \times K$ )



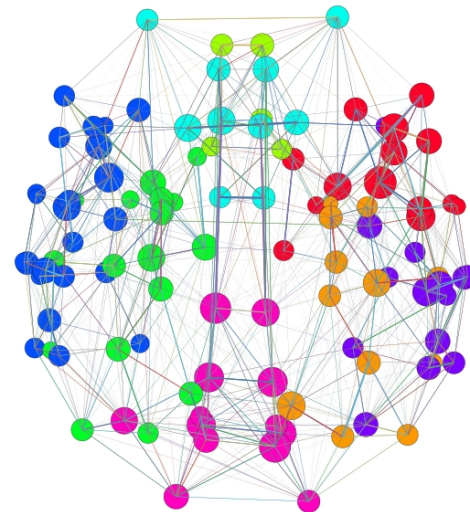
SVM  
classification



Classification pipeline

# Obtaining partitions

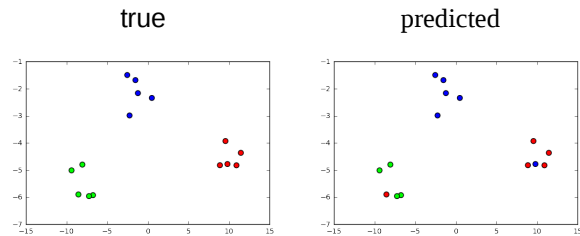
1. Newman eigenvector
2. Louvain
3. Greedy modularity optimization



1. Newman, M. E. J. (2006) Finding community structure in networks using the eigenvectors of matrices, *Phys. Rev. E*, 74, 036104.
2. Blondel, V.D., Guillaume, J.-L., Lambiotte, R., Lefebvre, R. (2008) Fast unfolding of communities in large networks, *Journal of Statistical Mechanics: Theory and Experiment*, 10, P10008.
3. Clauset, A., Newman, M. E. J., Moore, C. (2004) Finding community structure in very large networks. *Phys Rev E*, 70, 066111 .

# Similarity between partitions

1. **Random Index**
2. **Adjusted Rand Index**
3. **Adjusted Mutual Information**



true = [0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 2, 2, 2, 2, 2]

predicted = [0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 2, 2, 2, 2]

ARI (true, predicted) = 0.792

AMI (true, predicted) = 0.804

# Computing kernel from similarity

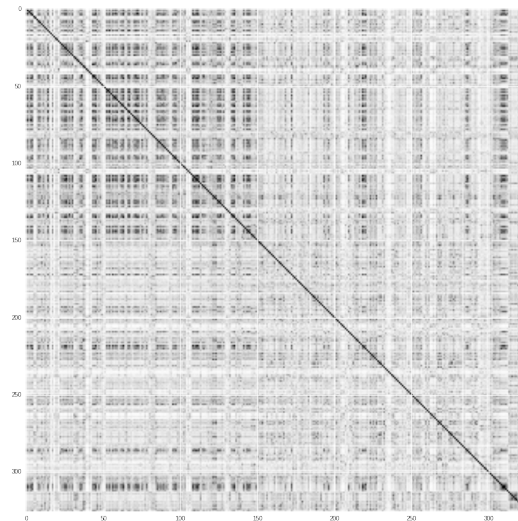
There are no constraints on the structure of the input data  $\mathbb{X}$ . Let  $G$  and  $G'$  be the networks and  $\omega(G, G')$  be a distance between these networks. We build a graph kernel  $K$  using the distance  $\omega$  as follows:

$$K(G, G') = e^{-\alpha\omega(G, G')}$$

Since ARI and AMI measure similarity of two partitions and both vary from 0 to 1 we define distance as follow:

$$\omega(G, G') = 1 - \text{sim}(G, G'),$$

where *sim* stands for either ARI or AMI

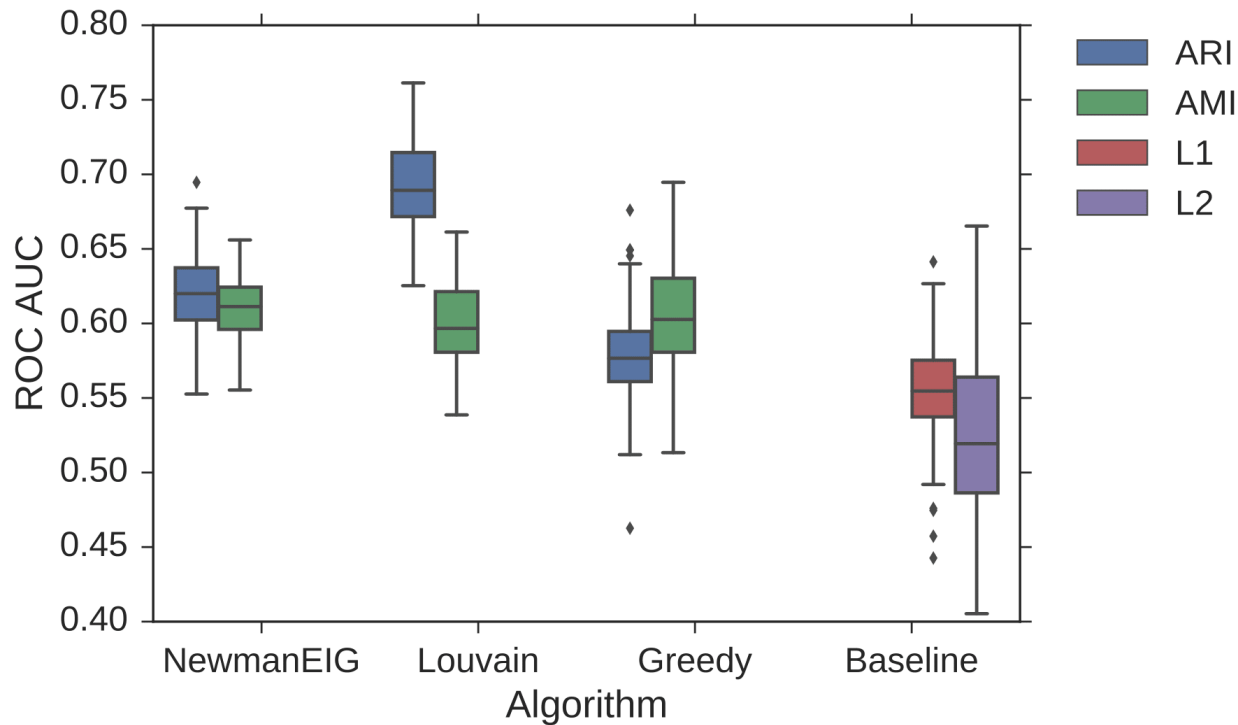




# Data description

We use a publicly available UCLA APOE-4 dataset (UCLA Multimodal Connectivity Database ) that includes precomputed matrices of structural connectomes. These are DTI-based connectivity matrices of carriers and non carriers of the APOE-4 allele associated with the higher risk of Alzheimer's disease. The sample includes 30 APOE-4 non carriers, mean age (age standard deviation) is 63.8 (8.3), and 25 APOE-4 carriers, mean age (age standard deviation) is 60.8 (9.7).

# Results



Q ?