

Spectral Graph Convolutions for Population-based Disease Prediction

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Paper overview



Disease prediction



Contribution: Graph Convolution Networks ^[*]



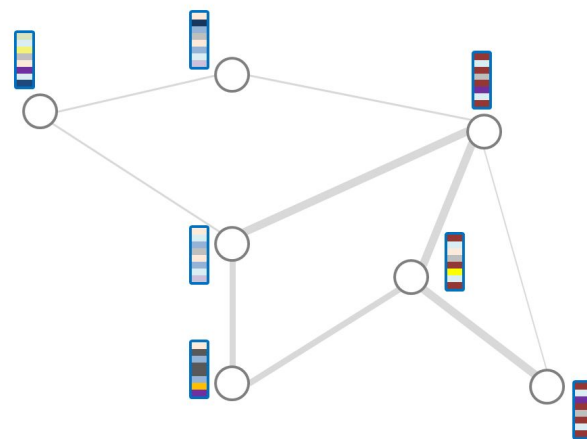
Datasets : ABIDE → Autism | ADNI → Alzheimer

Population graph

○ Nodes = Patients

— Edges = Similarity between patients

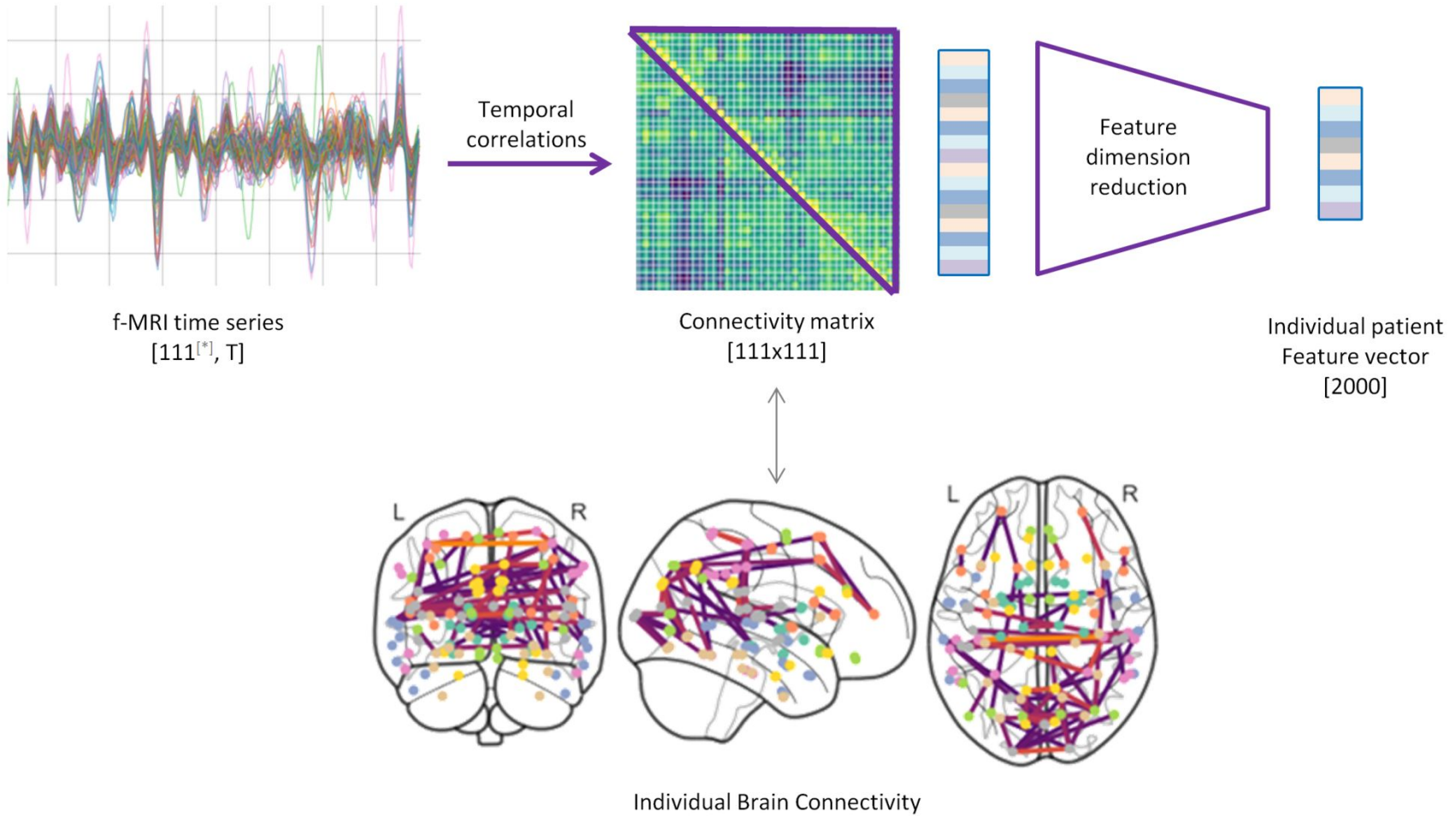
 Feature vector



[*] Semi-Supervised Classification with Graph Convolutional Networks - Thomas N. Kipf, Max Welling ICLR **2017**

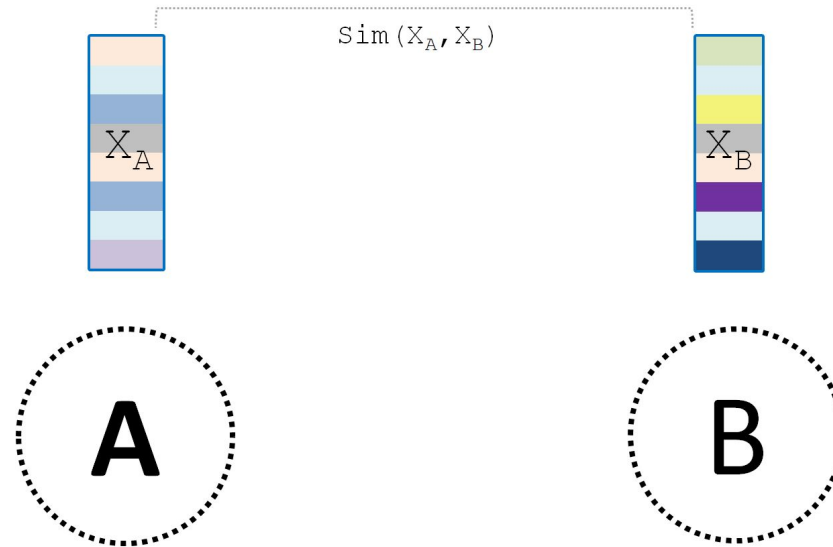
Defining graph nodes

1 patient \leftrightarrow 1 node

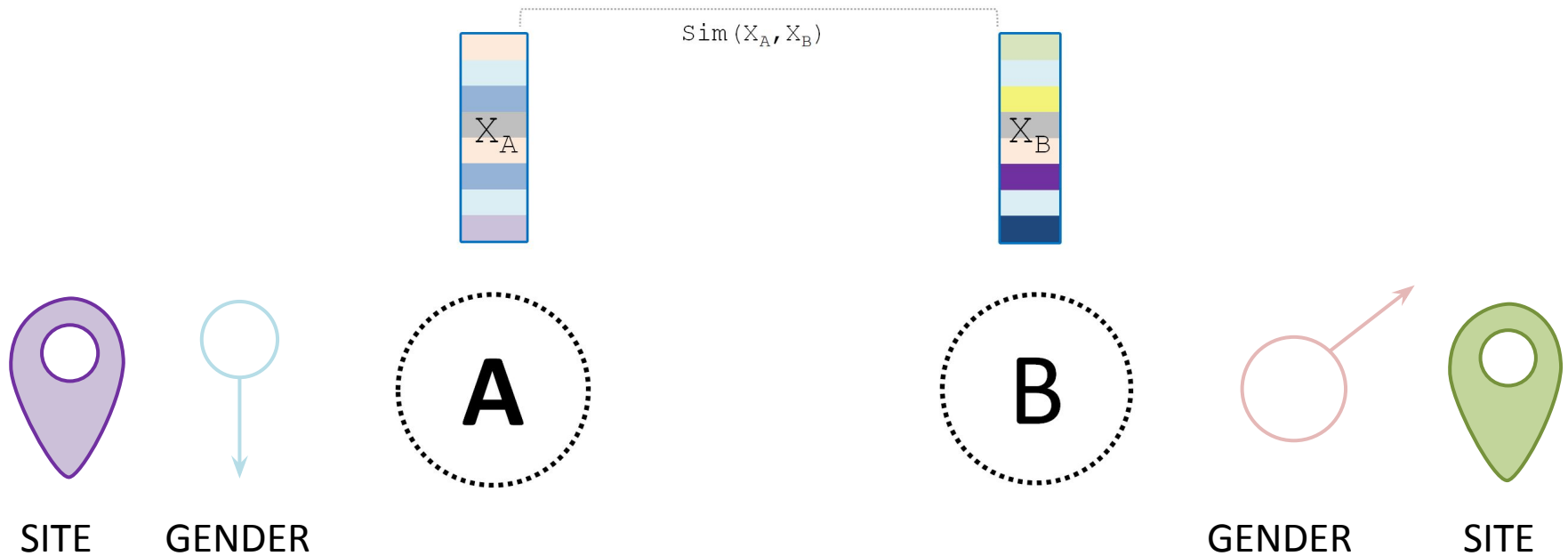


[*] 111: Harvard-Oxford cortical and subcortical structural atlases

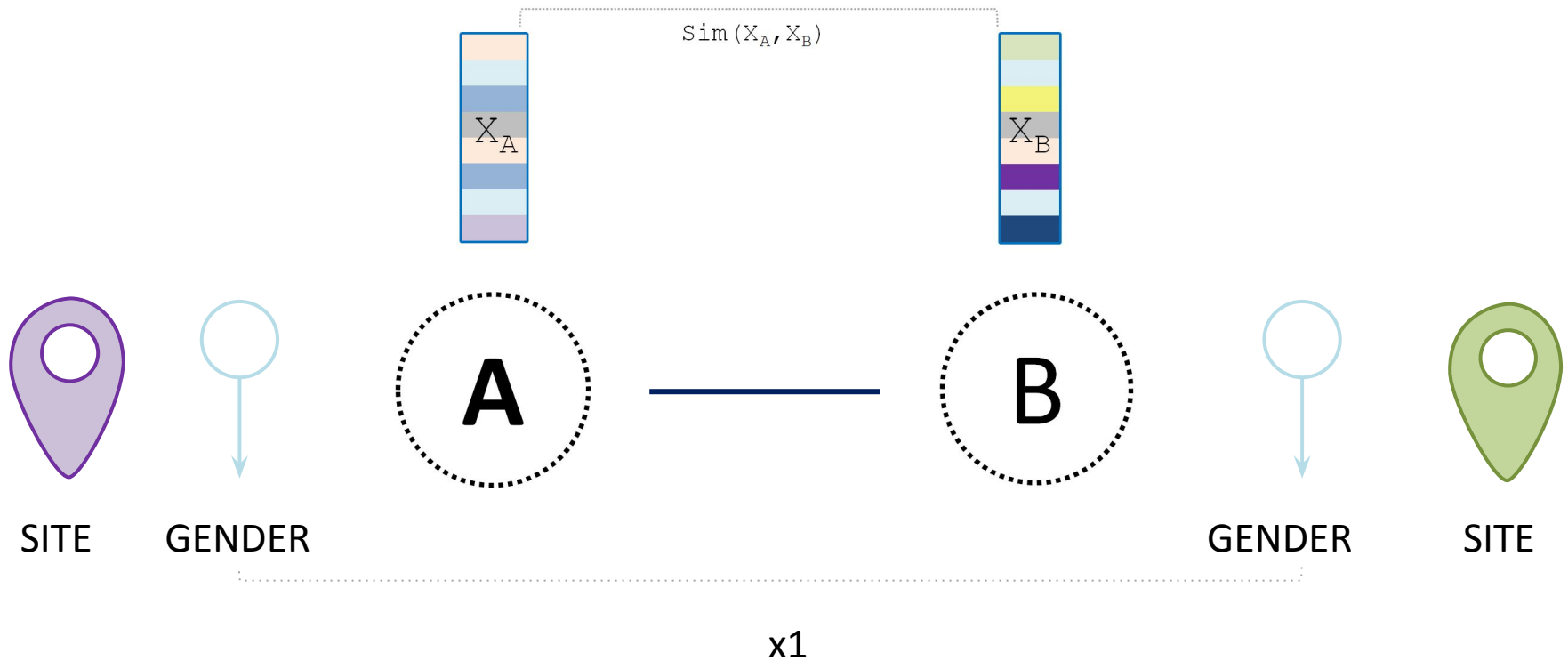
Defining graph edges



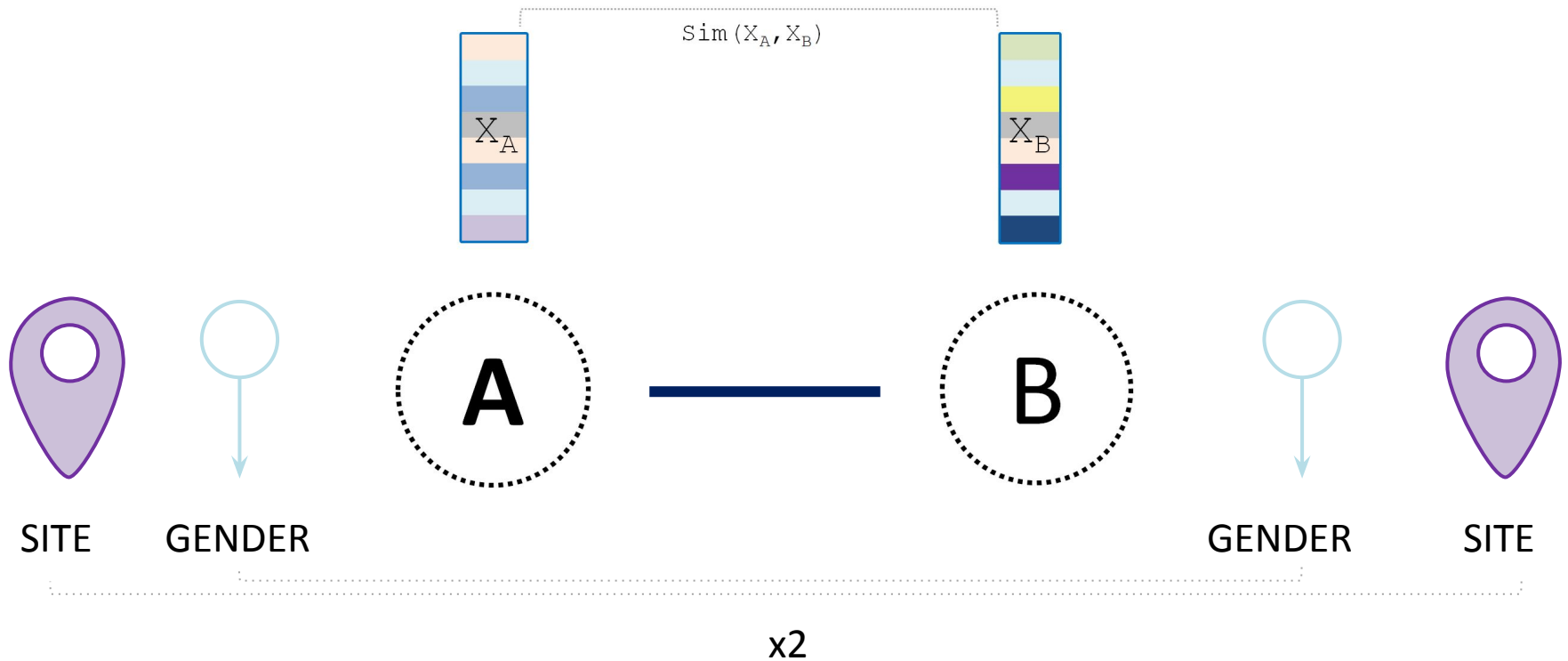
Defining graph edges



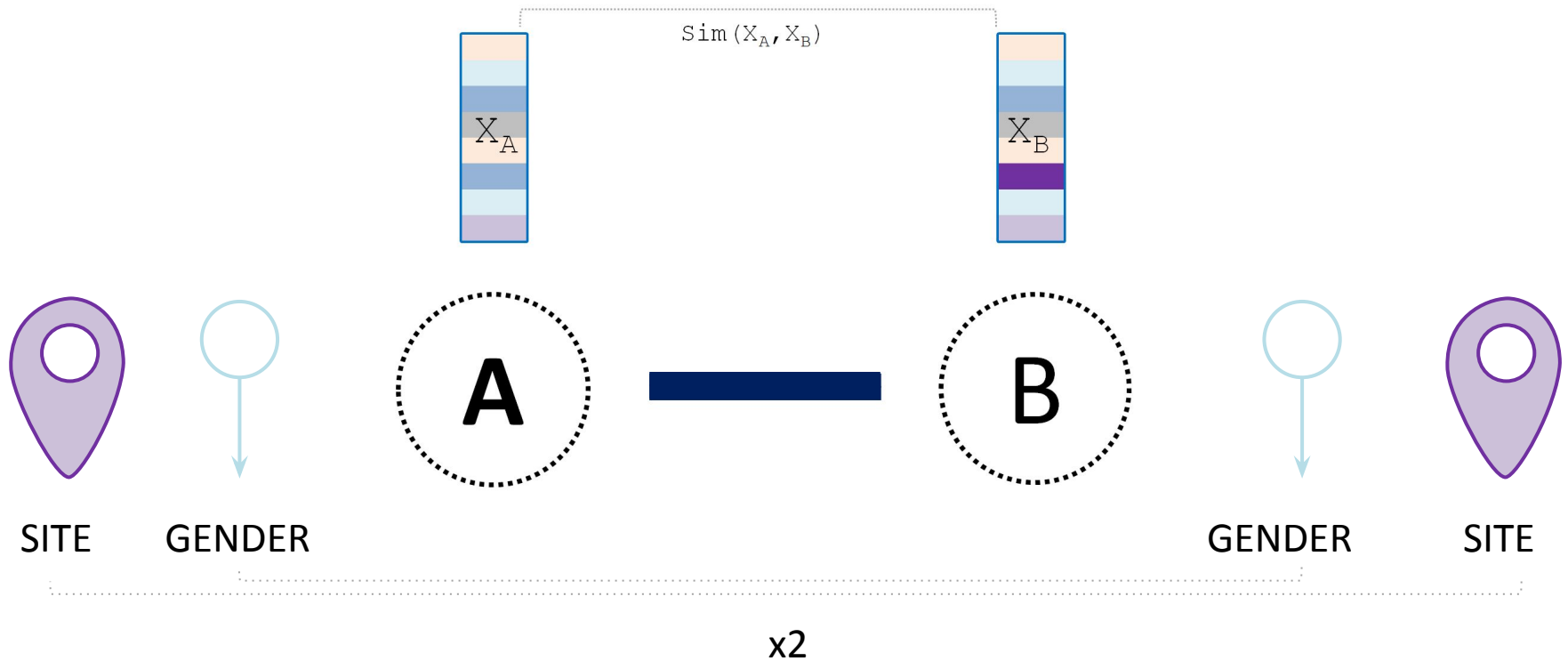
Defining graph edges



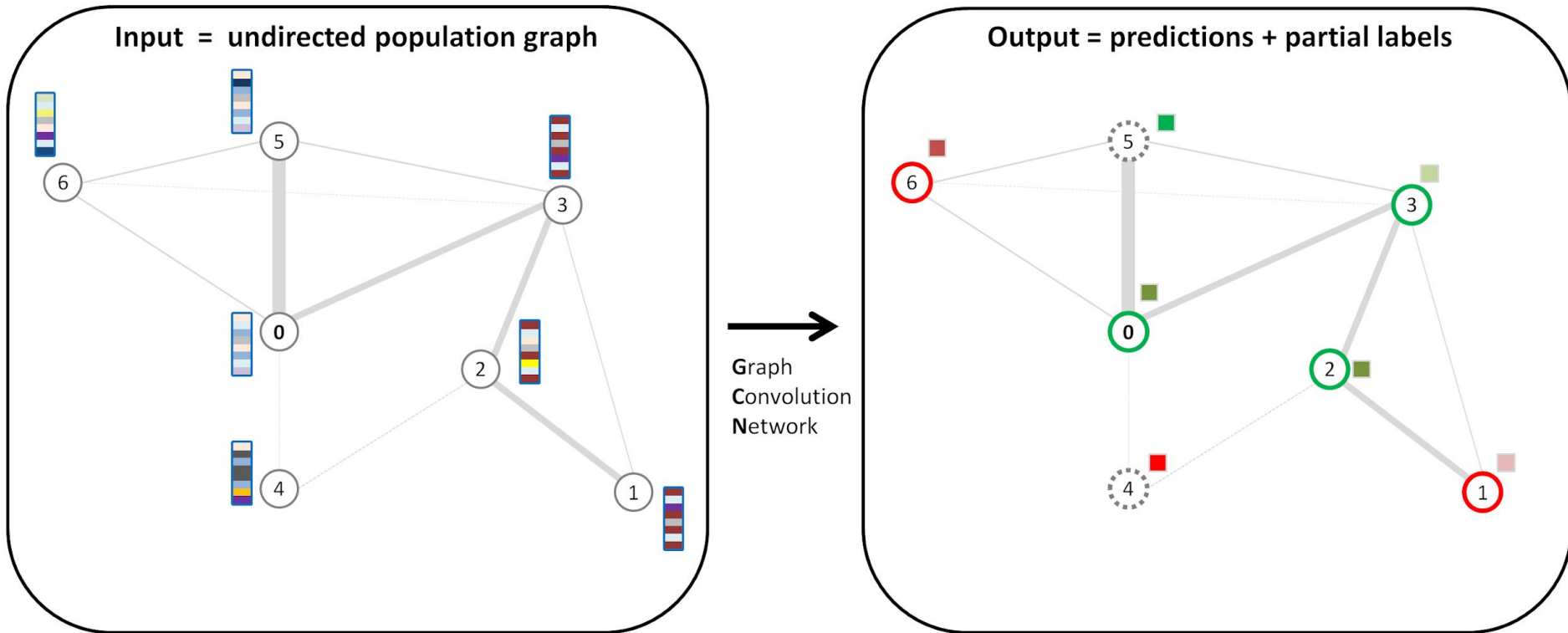
Defining graph edges



Defining graph edges

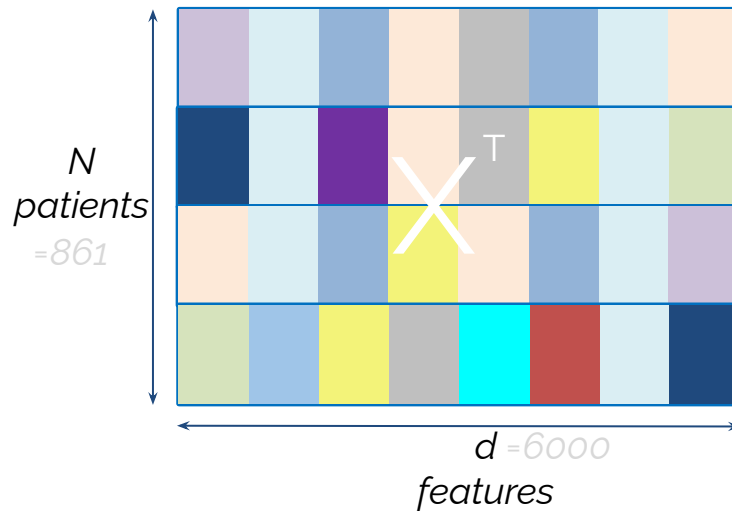
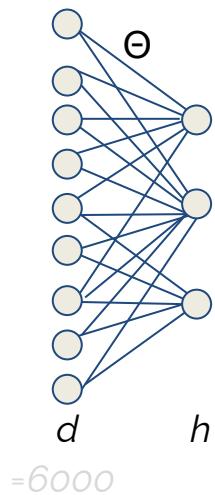


Graph Convolution Network



Graph Convolution Network

$$\underbrace{Y}_{h,N} = \underbrace{\Theta}_{h,d} \underbrace{X^T}_{N,d}$$

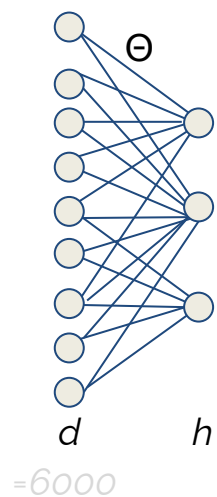


Fully connected $[h, d]$

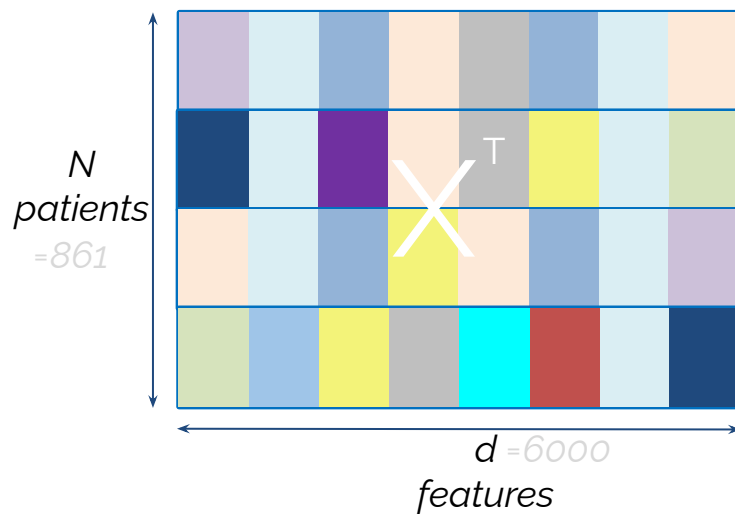
Input features $[N, d]$

Graph Convolution Network

$$\underbrace{Y}_{h,N} = \underbrace{\Theta}_{h,d} \underbrace{X^T}_{N,d} \underbrace{A}_{N,N}$$

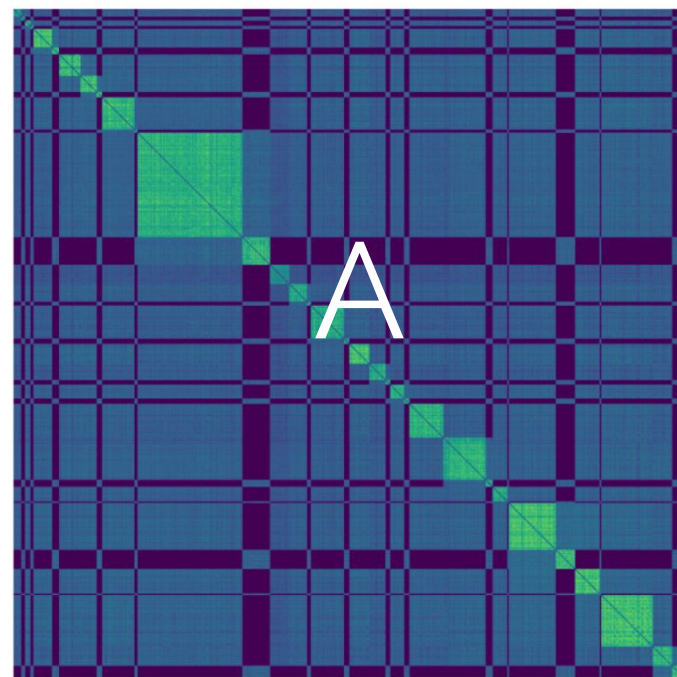


Fully connected $[h, d]$



Input features $[N, d]$

Basic message passing

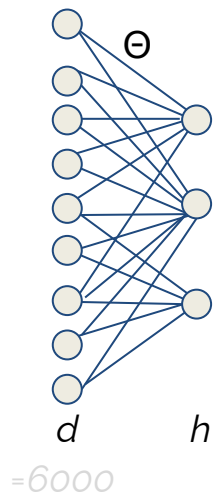


Adjacency matrix $[N, N]$

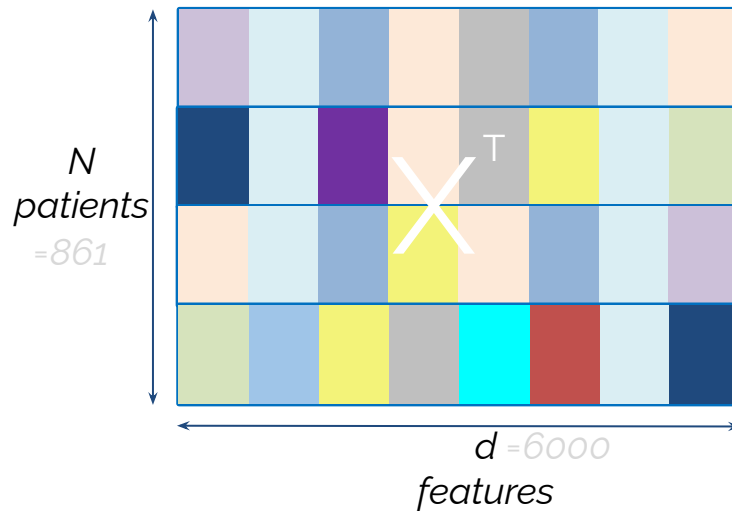
Analogy: Non Local means - denoise similar colors on images

Graph Convolution Network

$$\underbrace{Y}_{h,N} = \underbrace{\Theta}_{h,d} \underbrace{X^T}_{N,d} \underbrace{A}_{N,N}$$

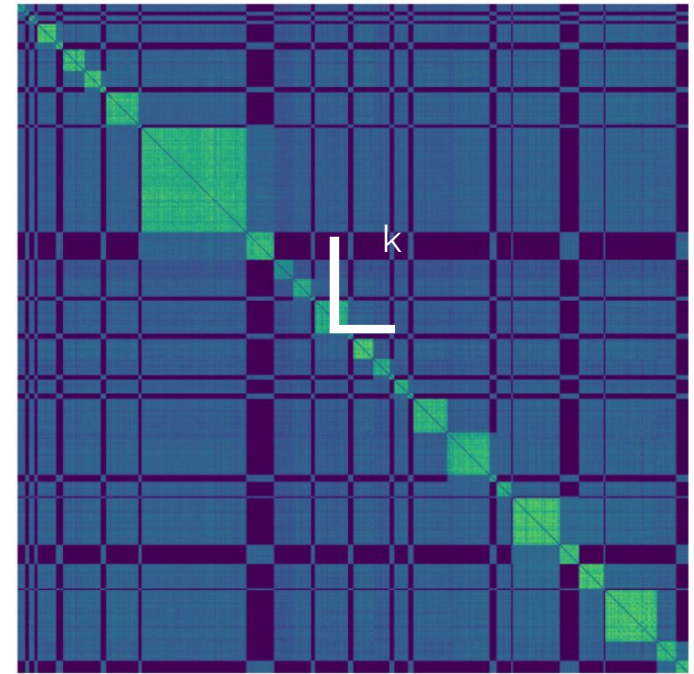


Fully connected $[h,d]$



Input features $[N, d]$

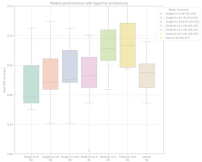
Basic message passing



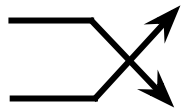
Power of Laplacian matrix $[N, N]$

Variant in the paper : ChebConv - polynomial of the Laplacian $L=I-A$ \rightarrow gives access to a larger neighborhood

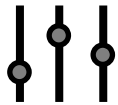
Experimental setup



Accuracy **68.9%** \pm 4% on ABIDE (Autism Disorder Spectrum)
Ability to reproduce results (\sim 69.5%)
→ Compare various models



Cross validation over 10 runs
80% train, 10% validation, 10% test



Frozen hyperparameters
Adam, LR 1E-4, Weight decay 0.1, no LR scheduler, 1000 epochs



Reproducible results



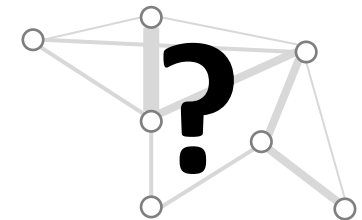
Code from scratch with documentation.

Results

- Is the use of graphs truly relevant?

Compare

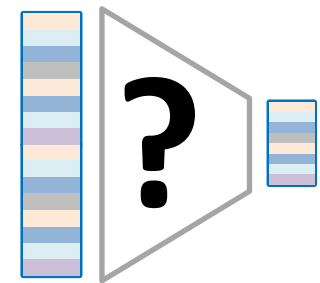
- Dense Neural Networks
- Graph Convolutional Networks **+5%**



- Is input dimension reduction relevant?

No significant differences between

- Raw input features
- Recursive Feature Elimination **+0%**
- Auto Encoders' Latent vector **-3%**

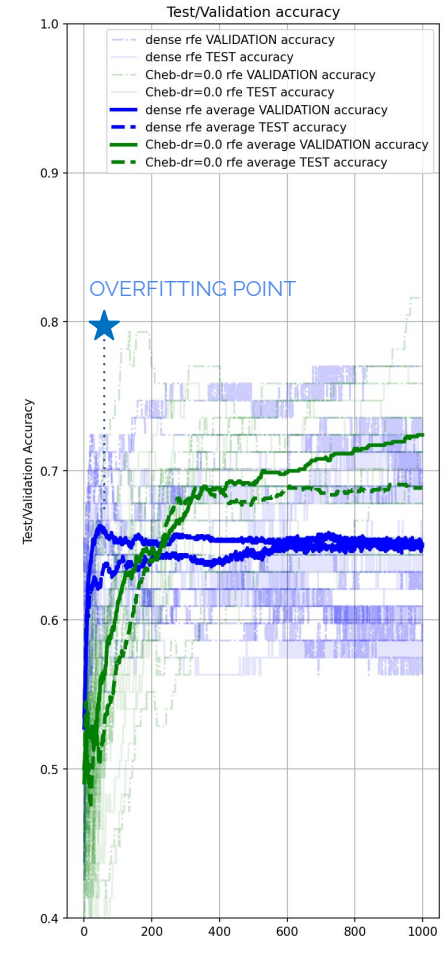
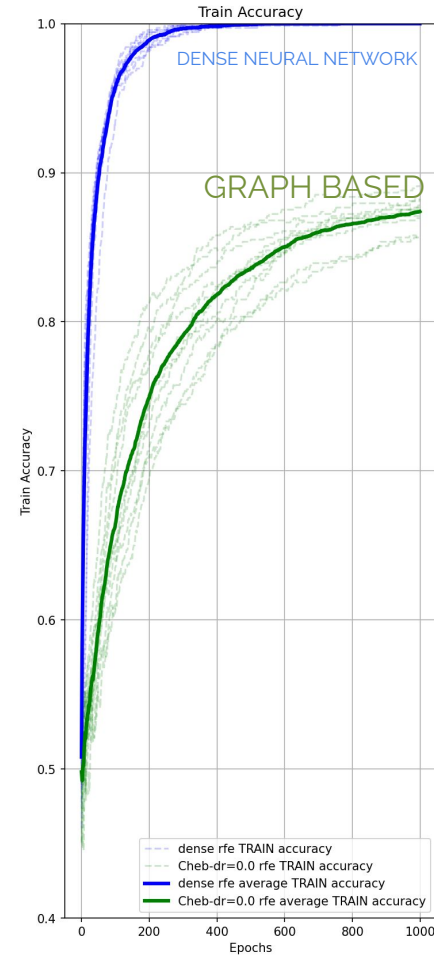
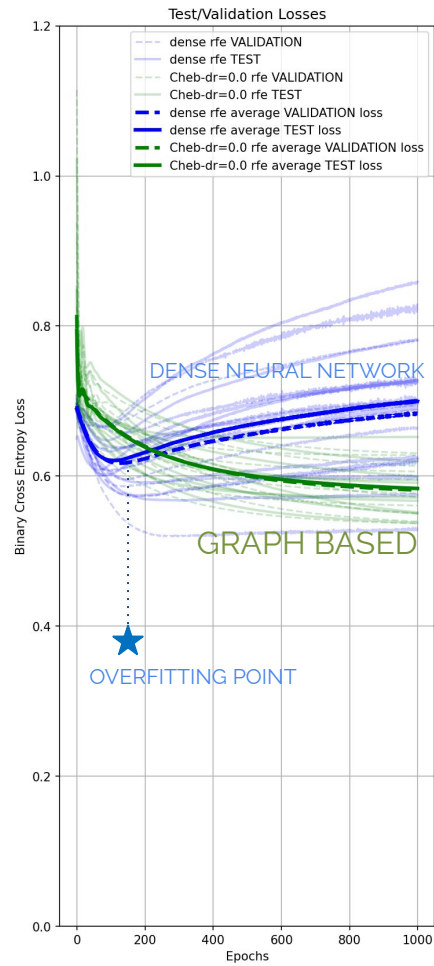
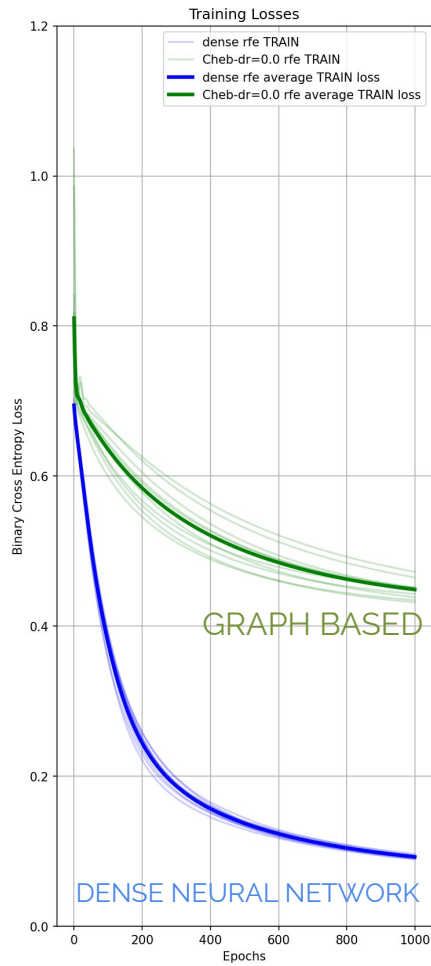


Conclusion

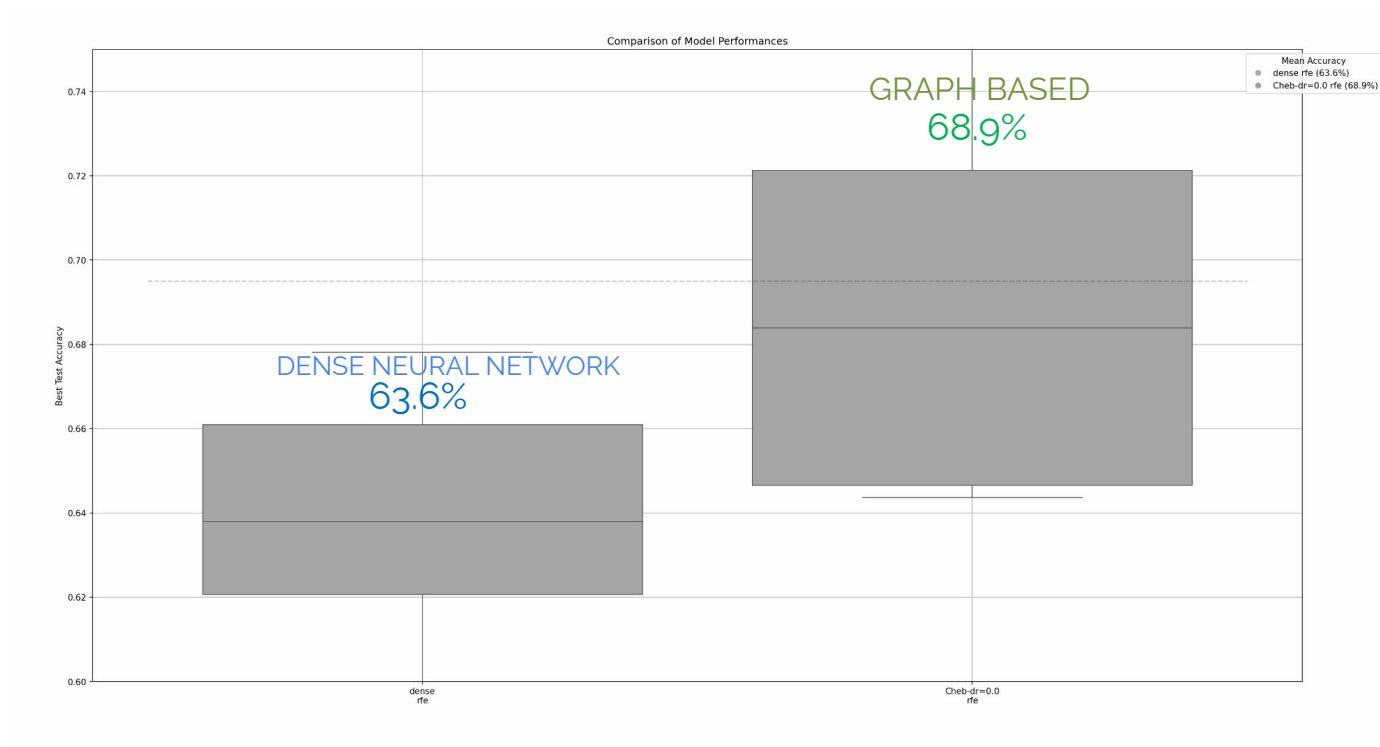
- A good introduction to the difficult domain of medical data analysis
- Curse of dimensionality
- Personal insights
 - Data type : time series , not 4D f-MRI volumes
 - Memory requirements : laptop GPU Nvidia T500 4Gb
 - « Spectral graph convolutions »

Thank you

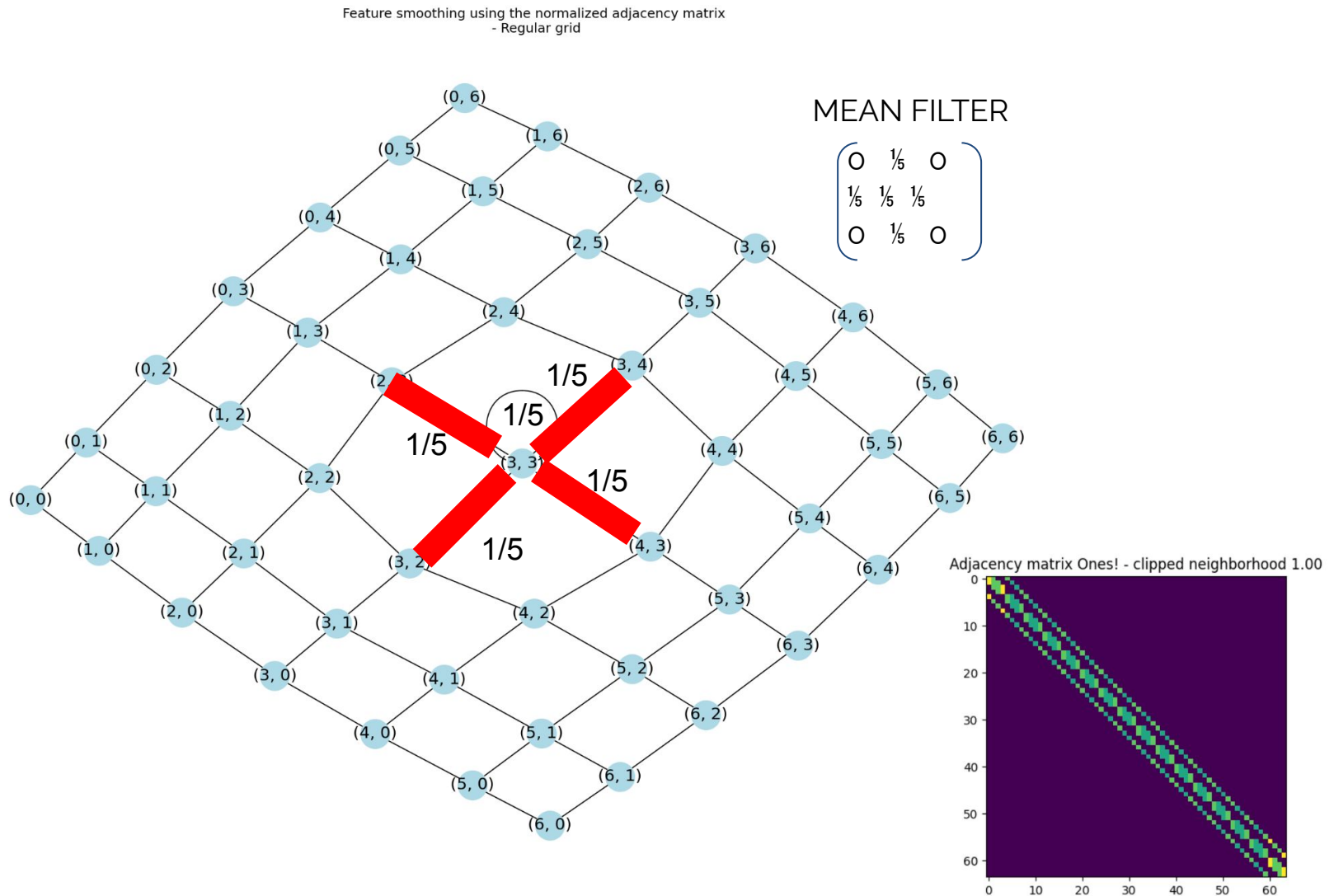
Training curves



Dense Neural Network VS Graph Convolution



Analogy : Graph convolutions and Image denoising



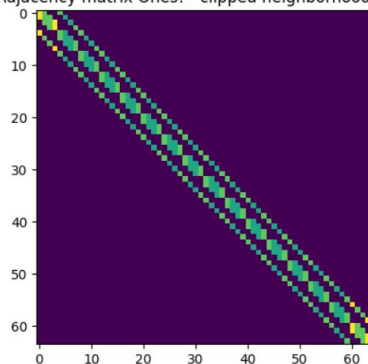
Analogy : Graph convolutions and Image denoising

CONSTANT WEIGHTS ON EDGES

MEAN FILTER

$$\begin{pmatrix} 0 & \frac{1}{5} & 0 \\ \frac{1}{5} & \frac{1}{5} & \frac{1}{5} \\ 0 & \frac{1}{5} & 0 \end{pmatrix}$$

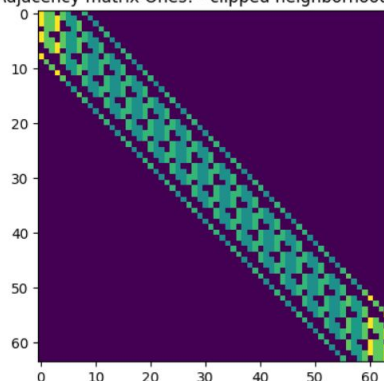
Adjacency matrix Ones! - clipped neighborhood 1.00



BOX FILTER

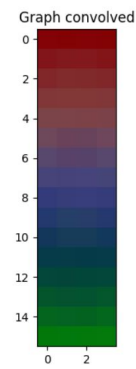
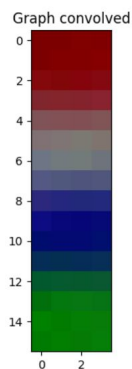
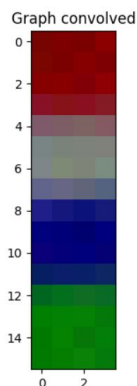
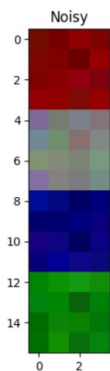
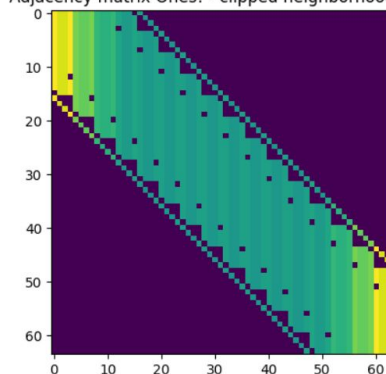
$$\frac{1}{9} \begin{pmatrix} 1 & 1 & 1 \\ 1 & 1 & 1 \\ 1 & 1 & 1 \end{pmatrix}$$

Adjacency matrix Ones! - clipped neighborhood 1.41



$$\frac{1}{13} \begin{pmatrix} 0 & 0 & 1 & 0 & 0 \\ 0 & 1 & 1 & 1 & 0 \\ 1 & 1 & 1 & 1 & 1 \\ 0 & 1 & 1 & 1 & 0 \\ 0 & 0 & 1 & 0 & 0 \end{pmatrix}$$

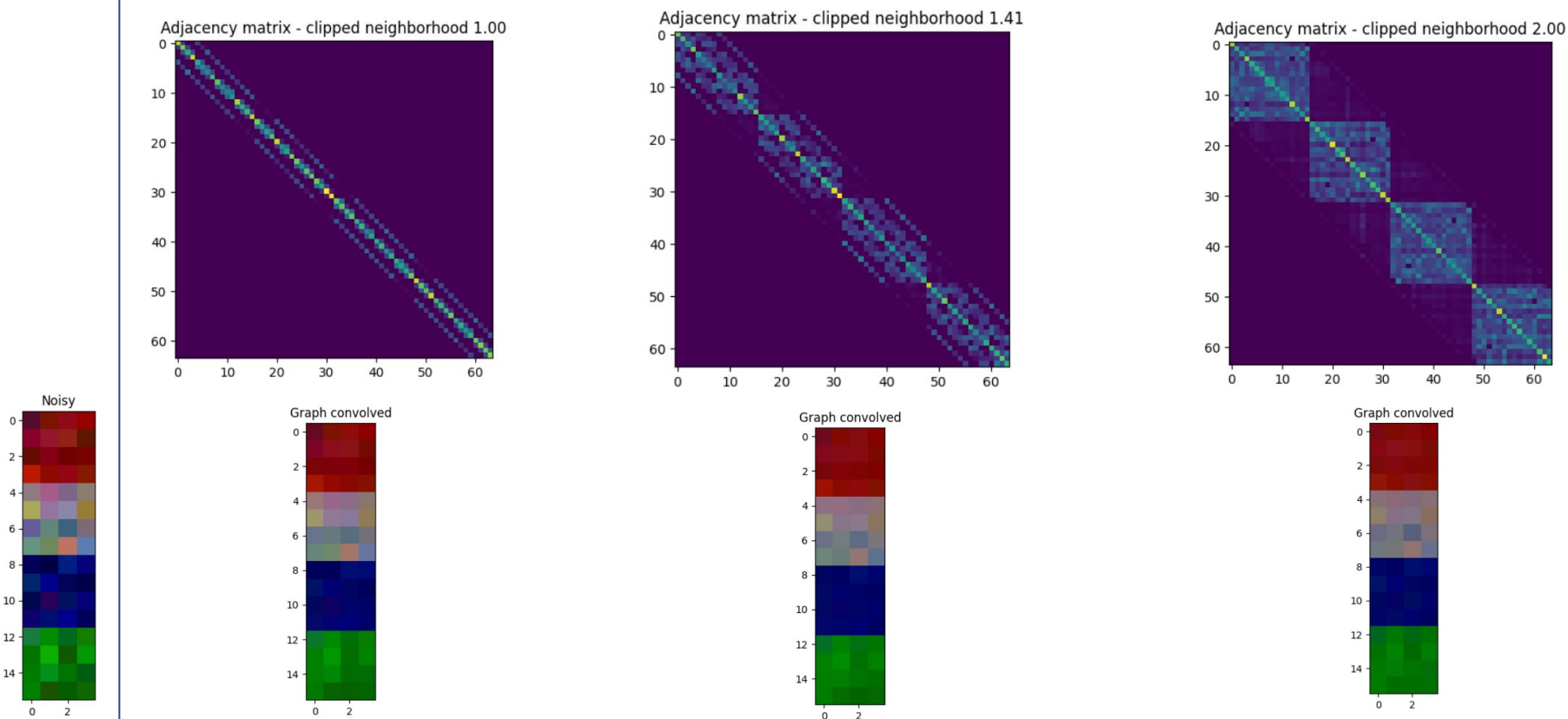
Adjacency matrix Ones! - clipped neighborhood 2.00



Analogy : Graph convolutions and Image denoising

SIMILARITY WEIGHTS ON EDGES

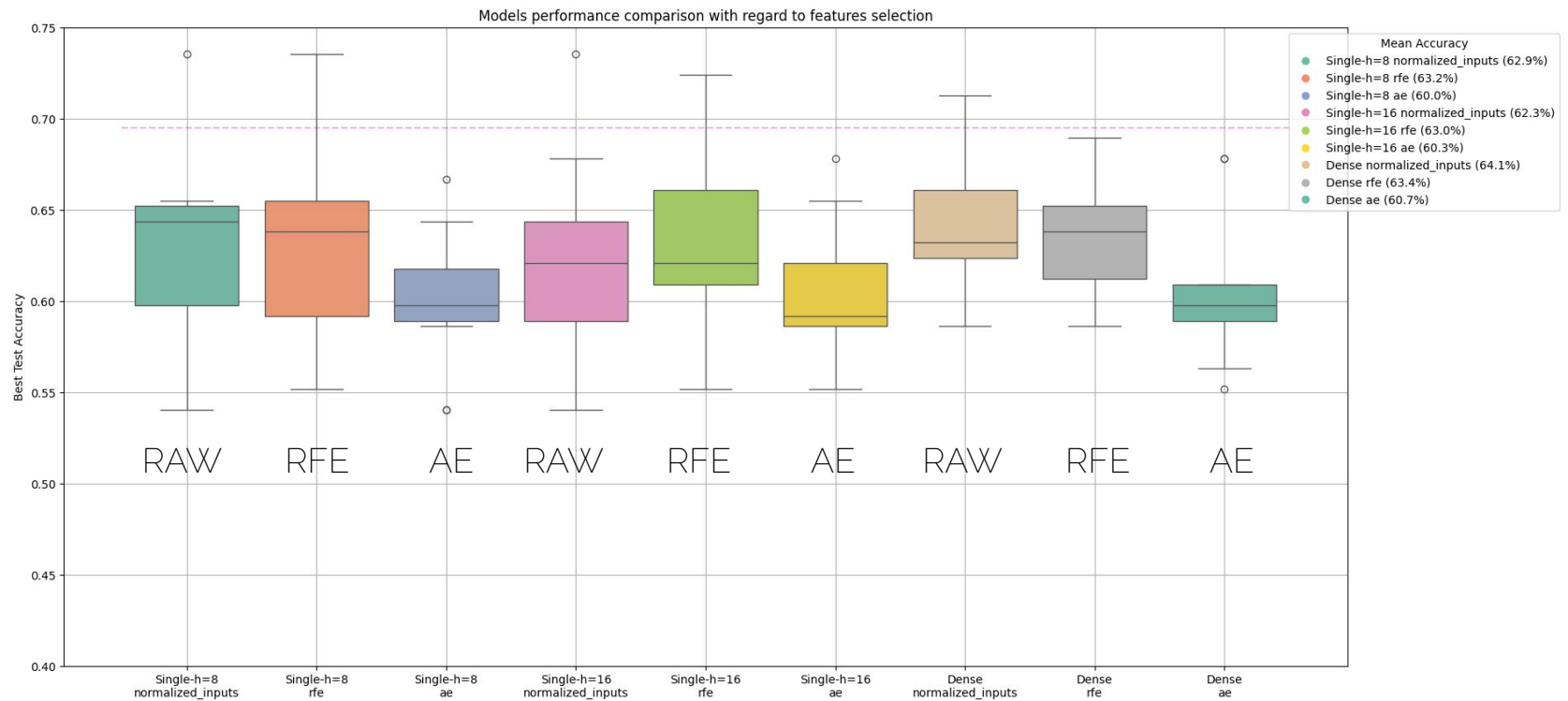
→ BILATERAL FILTER / NON LOCAL MEANS *



[*] ANTONI BUADES, BARTOMEU COLL, AND JEAN-MICHEL MOREL, *Non-Local Means Denoising*, Image Processing On Line, 1 (2011), pp. 208–212.

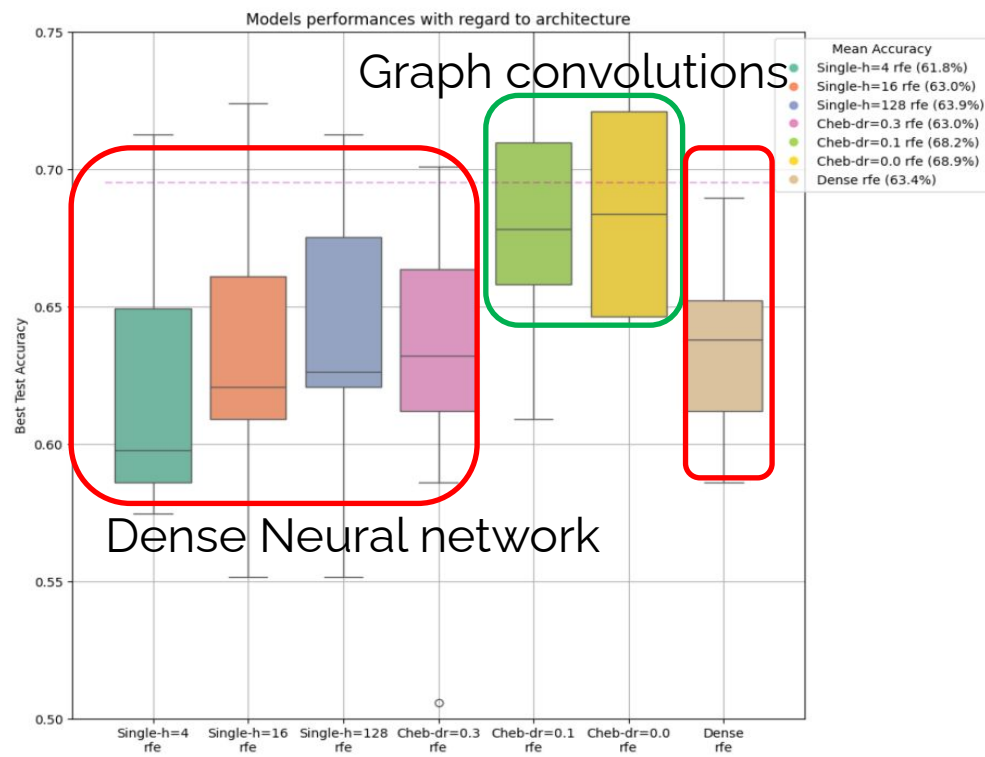
Results

- Relevance of reduce feature dimension?
– **NOT REALLY**



Results

- Relevance of using graph?
 - **YES** ~ +5% accuracy



Extra questions

A the beginning of the project, we asked ourselves a few questions on the paper:

- Does the graph structure bring anything?
-> yes
- What does feature reduction do?
-> nothing significant
- Would adding metadata to the input feature help a dense NN do better?
- How does the research world process MRI?
- Can we think of a toy example?
-> not trivial, focus on ABIDE dataset

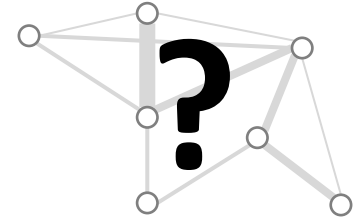
Medical domain

Expectations V.S. Reality

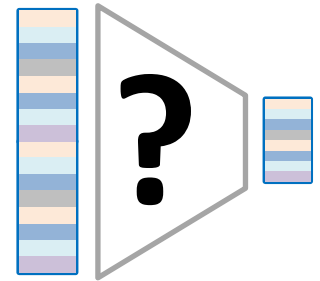
Expectation	Reality
f-MRI 4D volumes	Time series
Graph, big memory requirement	GPU laptop Nvidia T500 4Gb
« Spectral graph convolutions »	Message passing

Investigation

- Is the use of graphs truly relevant?

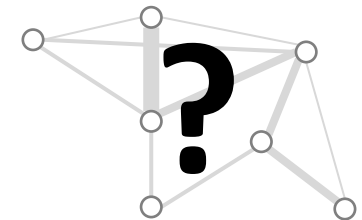


- Is input dimension reduction relevant?



Investigation

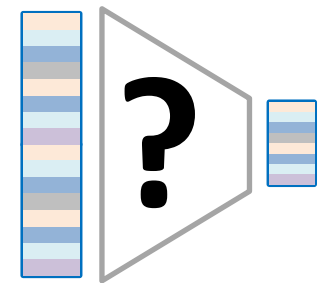
- Is the use of graphs truly relevant?
 - Dense Neural Networks
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- Is input dimension reduction relevant?

No significant differences between

 - Raw input features
 - Recursive Feature Elimination
 - Auto Encoder's Latent vector



Overview

- Paper summary - Overview
 - Node
 - Edges
 - GCN
- Our contributions
 - Graph relevance
 - Feature dimension reduction
- Discussion

Medical domain

Expectations V.S. Reality

Expectation	Reality
MRI 3D volumes ?	Time series
Huge medical dataset	861 patients – curse of dimensionality
Graph, big memory requirement	Nvidia T500 4Gb ~ enough
« Spectral graph convolutions »	Message passing, analogy NL-means