

Machine Learning for Neuroimaging and Neuroscience

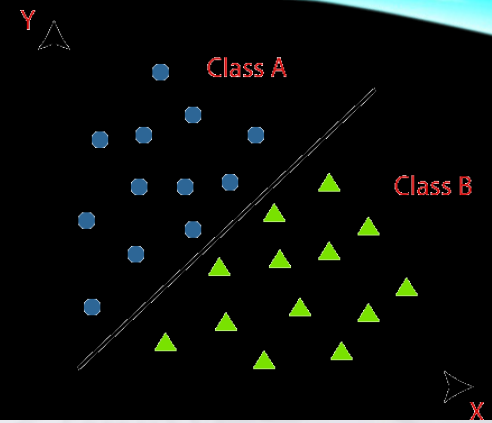


Lesson 3 *Functional* *Connectivity*

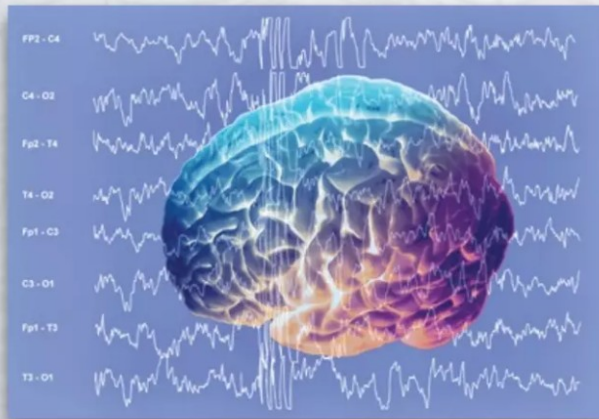


Alessandro Crimi

Functional Connectivity

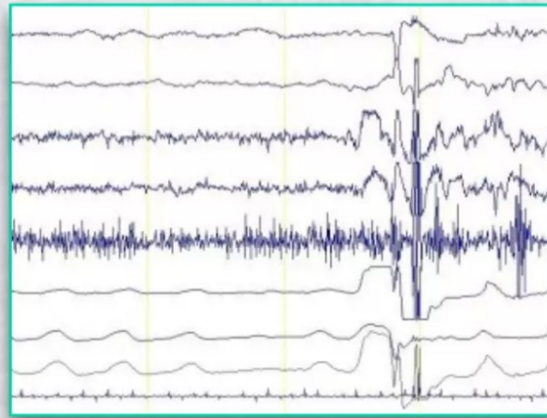


STEP 1



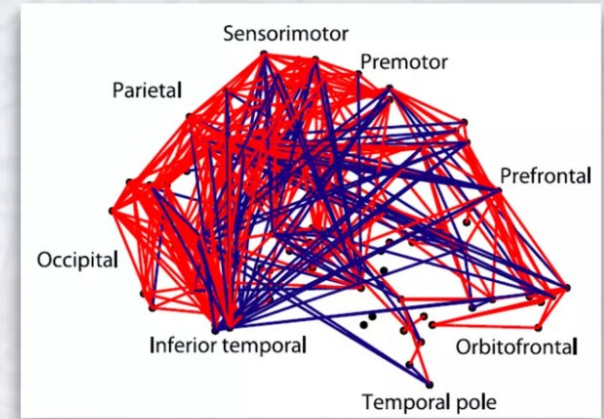
Measuring Brain Activity

STEP 2



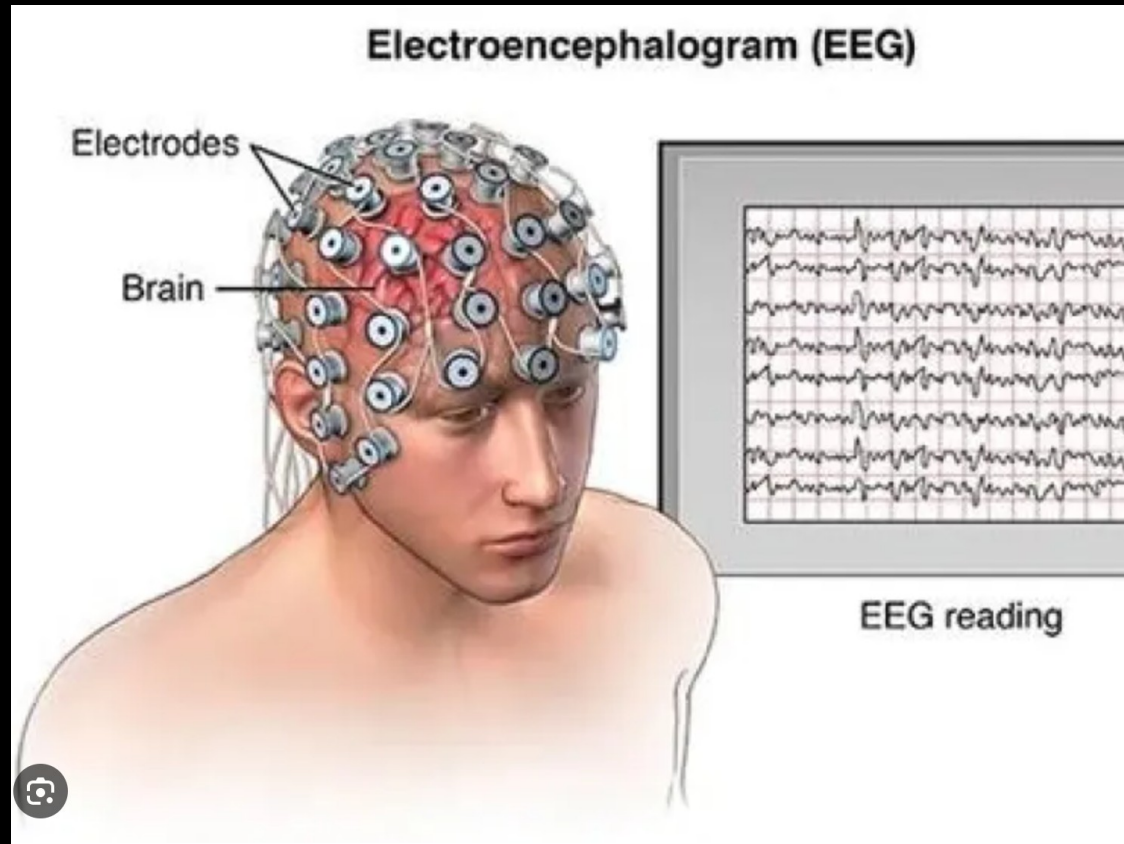
Time Series Analysis &
Network Construction

STEP 3



Network Analysis

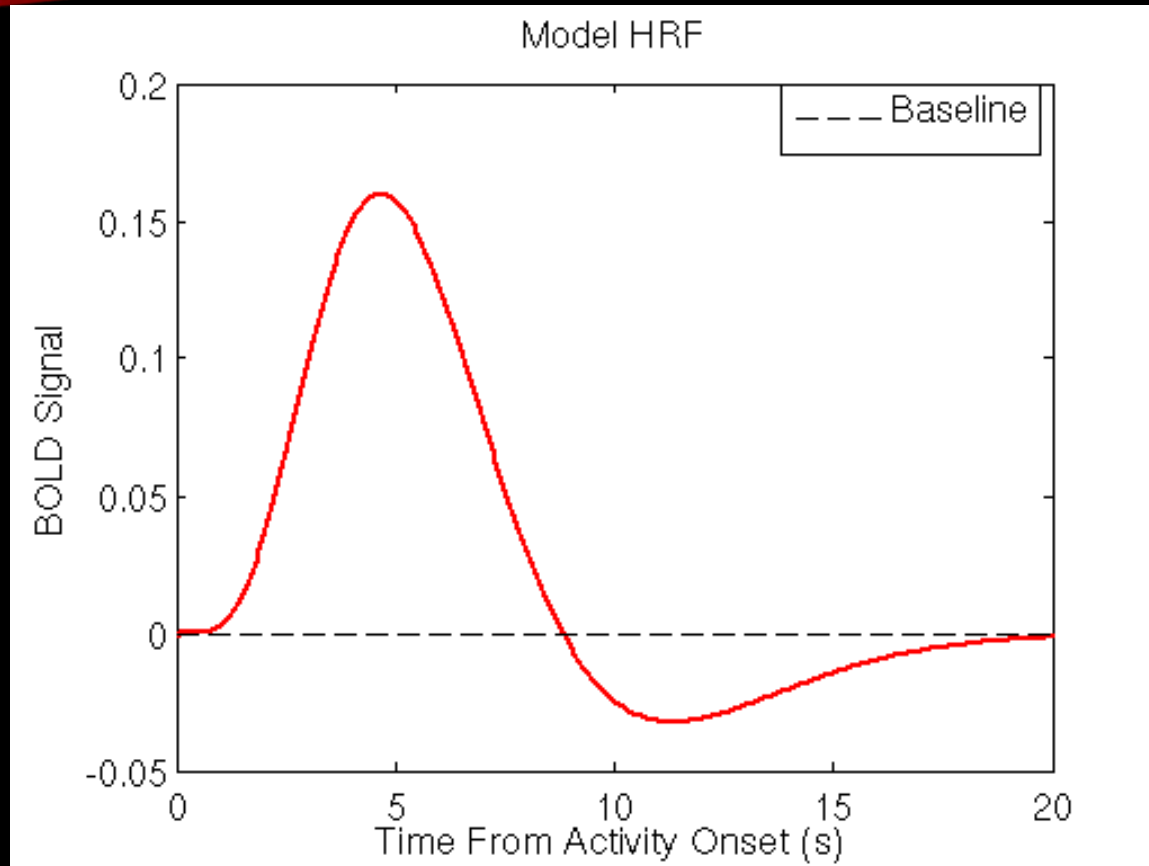
There is also EEG



Hemodynamics



Hemodynamics

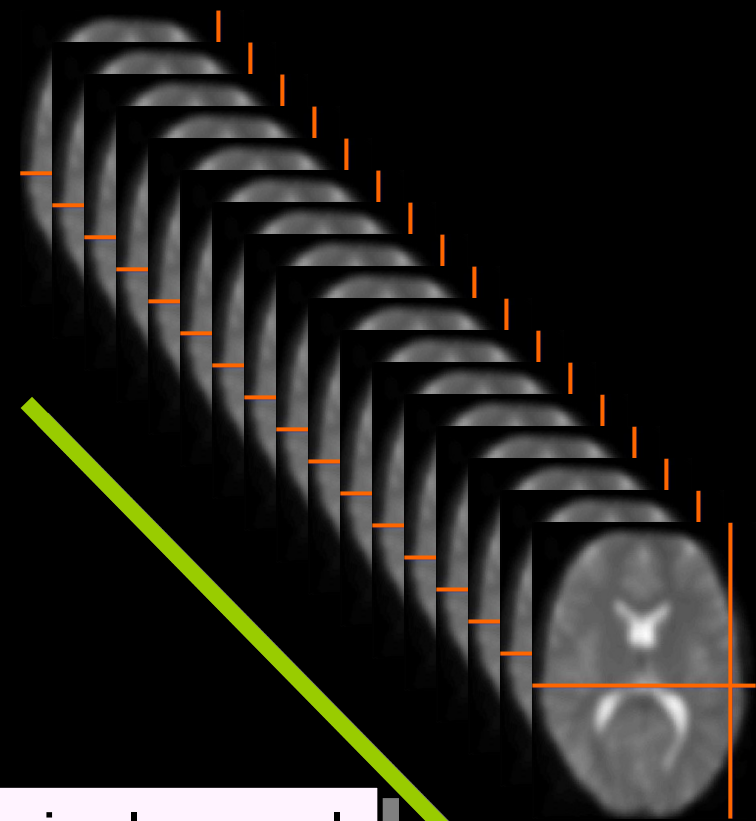


The ability to measure the Blood Oxygen Level Dependent (BOLD) signal allows us assess the hemodynamic response function (HRF) of a region in response to a task/stimulus.

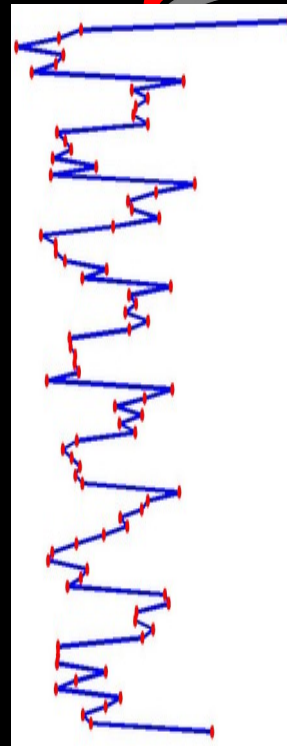
Functional magnetic resonance imaging (fMRI)

- Blood contains oxygenated and deoxygenated haemoglobin, with different magnetic properties
- Paramagnetic deoxyhaemoglobin distorts the magnetic field, leading to faster $T2^*$ decay
- The influx of blood following activity changes the proportion of oxy- and deoxyhaemoglobin, and hence the $T2$ or $T2^*$ -weighted MRI signal
- This Blood Oxygenation Level Dependent (BOLD) effect allows functional imaging with MRI

Voxel-wise time series



single voxel
time series



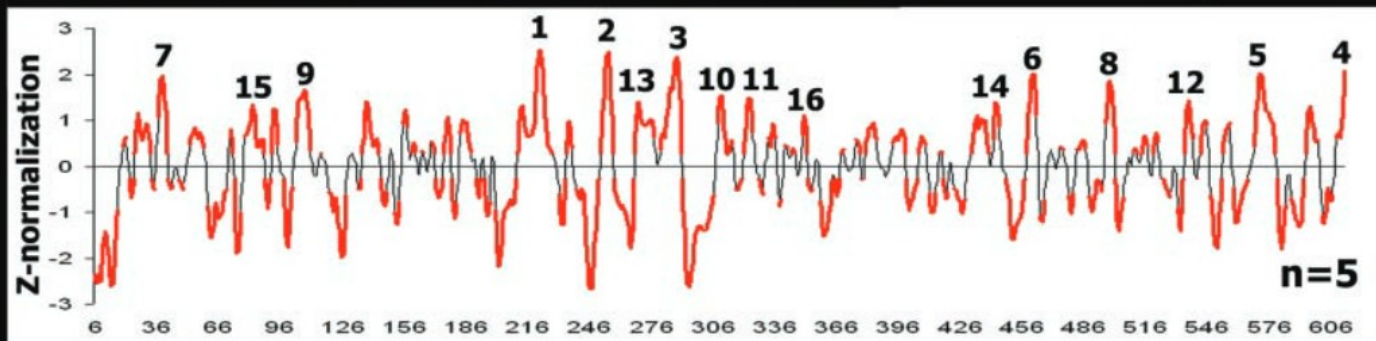
Model
specification

Parameter
estimation

Hypothesis

Statistic

A Fusiform gyrus



Important parameters of fMRI data

Temporal resolution: about one brain volume (TR) every 1-4s

Spatial resolution: typically 2mm^3 - 4mm^3 voxels

Coverage: whole brain or focused on particular portion of brain

Run length: generally ~4-15 minutes

Total scan time (for one task): ~5 minutes to ~ 2 hours

Cost per scan hour: \$500-\$1000

Subjects per study: 15-40

Many (complementary) approaches to correction:

Filtering low frequency noise (deals with scanner drift, etc.)

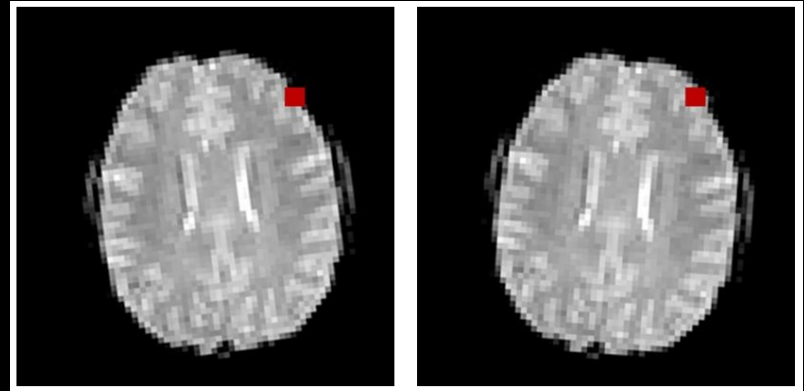
Not appropriate with some designs or concatenated time series

Rigid body realignment
Most commonly applied

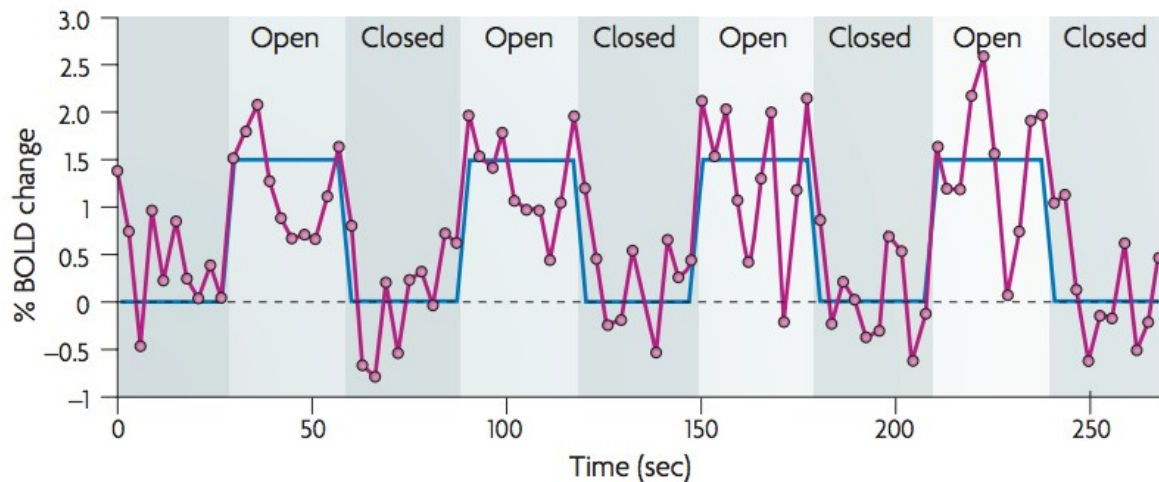
Online motion correction (e.g. PACE)
Utility debated

Modelling motion nuisance regressors/
outlier time points

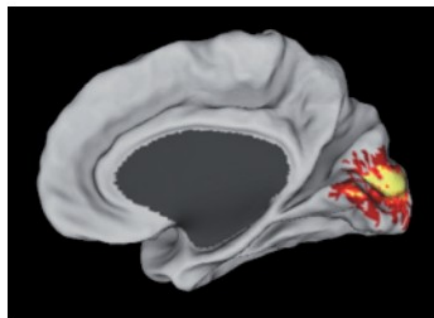
Unwarping
Attempts to correct interactions between head motion and magnetic
field inhomogeneities



“Noise” in the signal is abundant



Open - Closed =



Fox et al. 2007

- Preprocessing

- 'GLM' analysis

 - Creating meaningful regressors

 - Creating nuisance regressors

 - Parallel (voxel-wise) multiple regression

Random effects analysis

Correcting for multiple comparisons

GLM Equation: The GLM equation for each voxel in the brain is as follows:

$$Y = X * \beta + \varepsilon$$

Y represents the fMRI time series data for a specific voxel.

X is the design matrix, which includes predictors for the conditions or tasks.

β is a vector of parameters that the GLM estimates. Each parameter corresponds to the amplitude of the predicted BOLD response for a specific condition.

ε represents the error or noise in the fMRI data.

Estimation: The GLM estimates the β values for each condition using a method like ordinary least squares. These β values represent the strength of activation for each condition in each voxel.

Statistical Inference: You can then perform statistical tests to determine which conditions or tasks evoke significant brain activation. The most common test is the t-test or F-test, comparing the β values to see if they are significantly different from zero. This helps identify which conditions lead to reliable activations in specific brain regions.

Activation Maps: Once you perform statistical tests, you can create activation maps that show regions in the brain where the BOLD response is significantly different from baseline (i.e., activated regions). These maps often use a threshold or false discovery rate (FDR) correction to control for multiple comparisons.

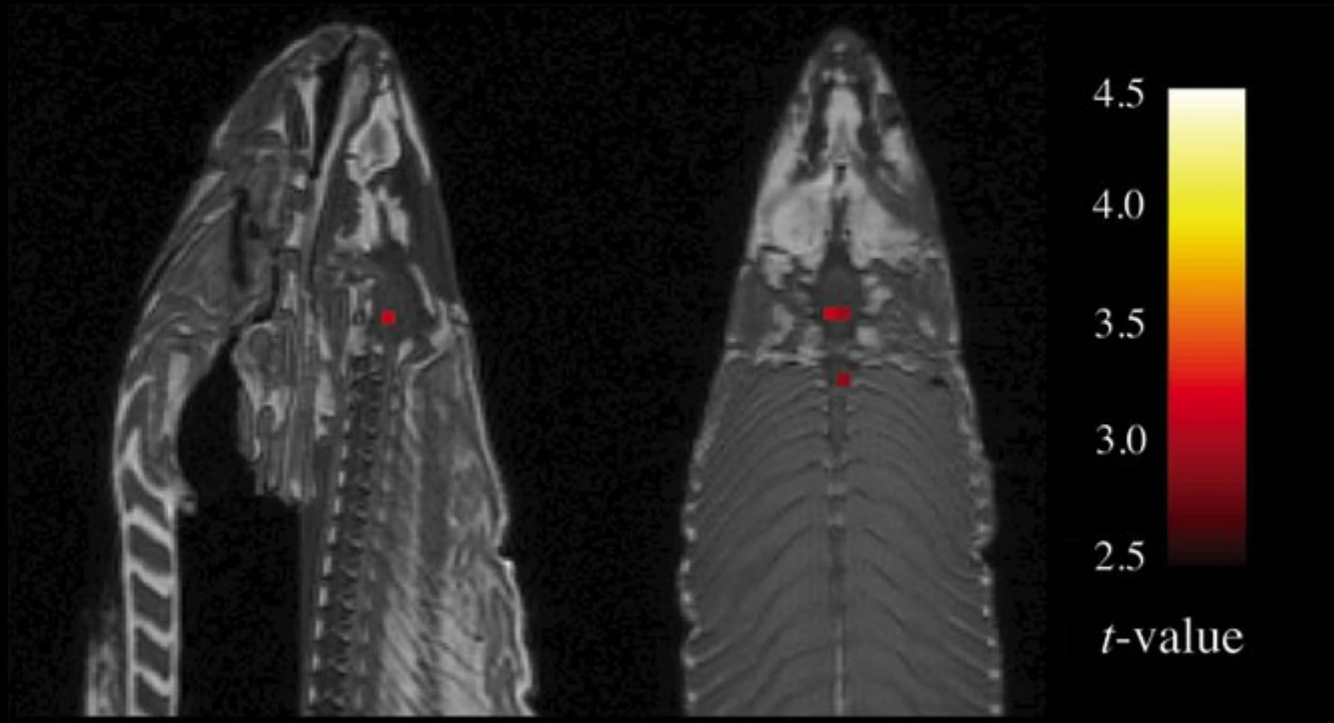
Multiple comparisons

Neural correlates of interspecies perspective taking in the post-mortem Atlantic Salmon: An argument for multiple comparisons correction

Craig M. Bennett¹, Abigail A. Baird², Michael B. Miller¹, and George L. Wolford³

¹ Psychology Department, University of California Santa Barbara, Santa Barbara, CA; ² Department of Psychology, Vassar College, Poughkeepsie, NY;

³ Department of Psychological & Brain Sciences, Dartmouth College, Hanover, NH



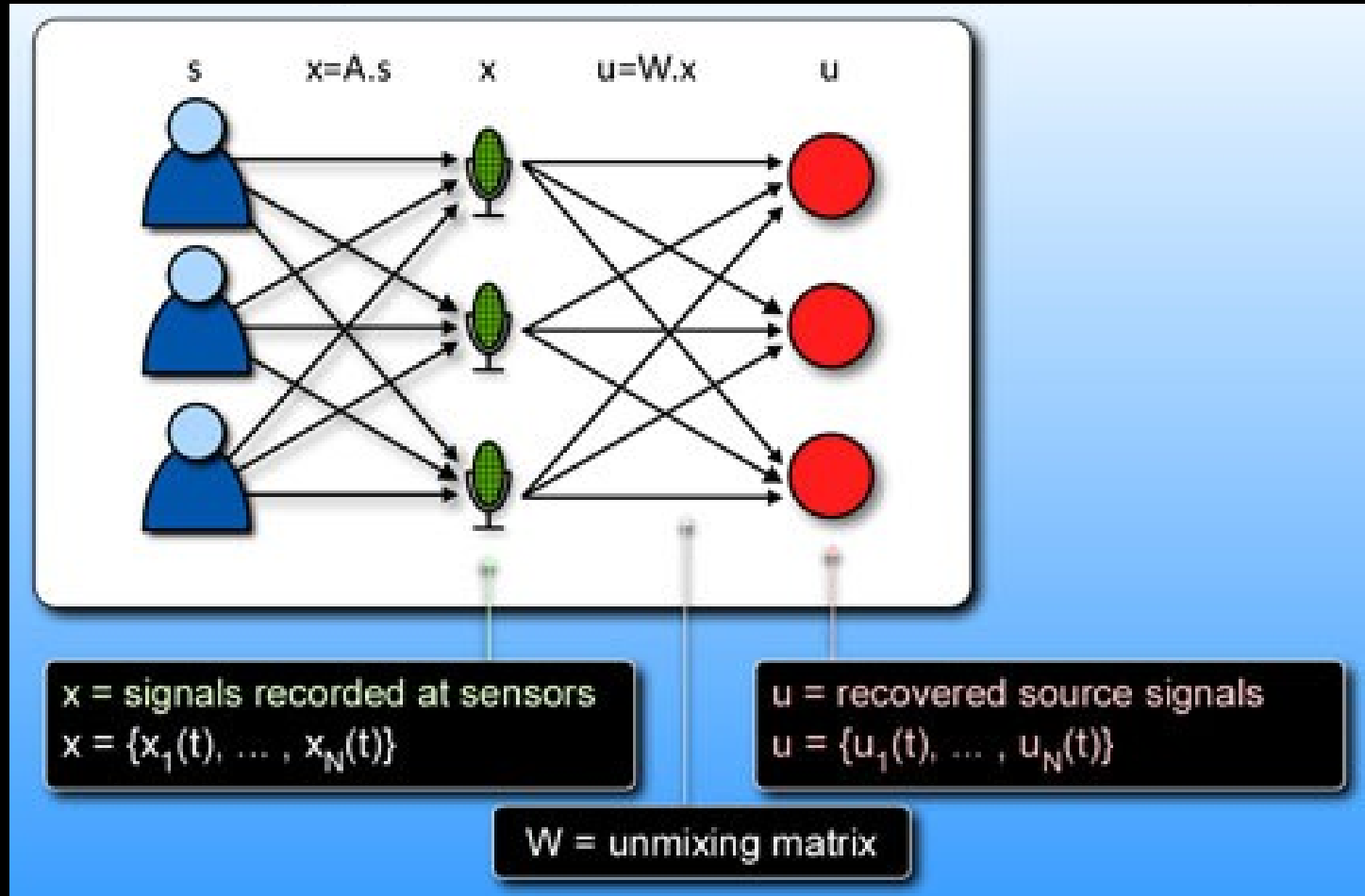
The image features a solid black background. At the top, there is a decorative border consisting of several overlapping, wavy bands of color. From left to right, these bands transition through shades of yellow, orange, red, and finally into a bright cyan or light blue on the far right. The word "Break" is written in a clean, white, sans-serif font, positioned in the upper left quadrant of the image, partially overlapping the colorful border.

Break

The cocktail effect

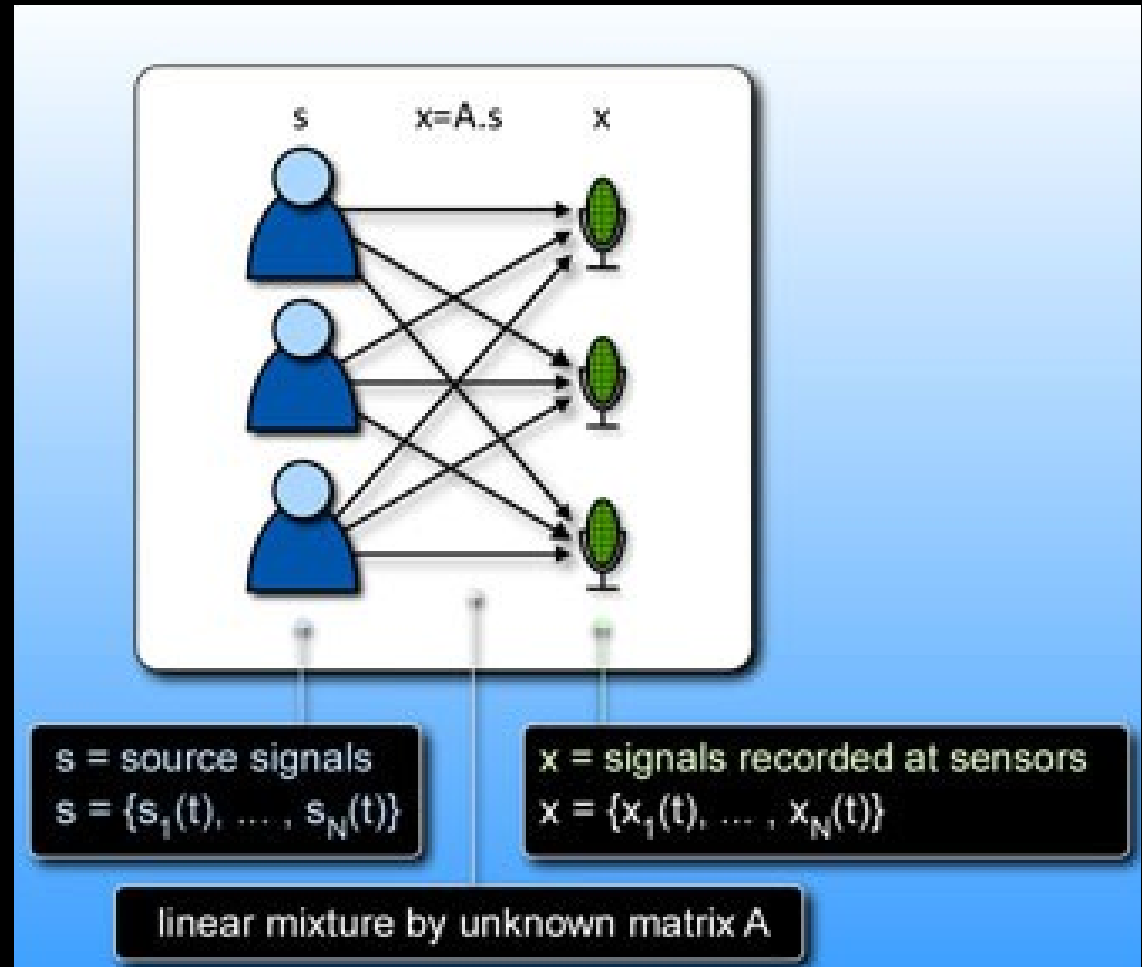


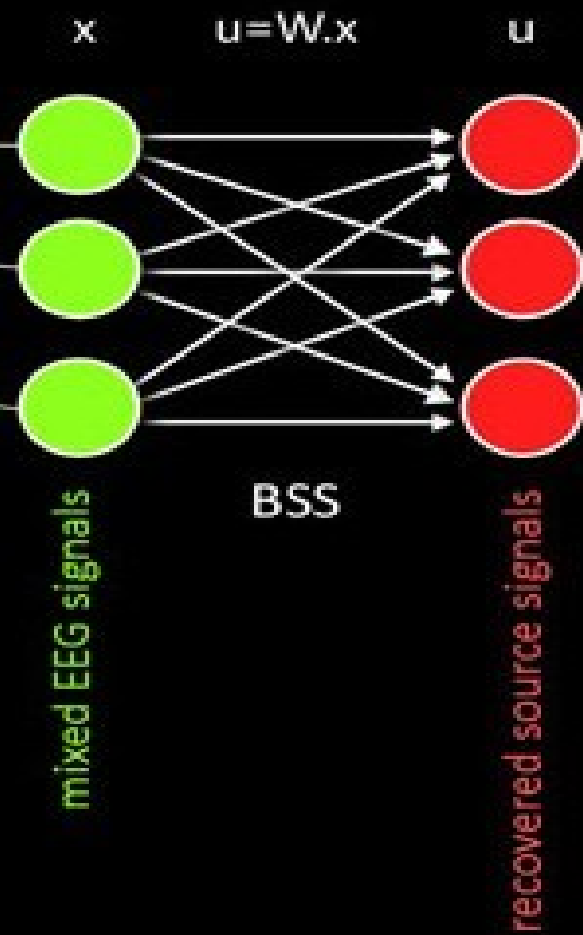
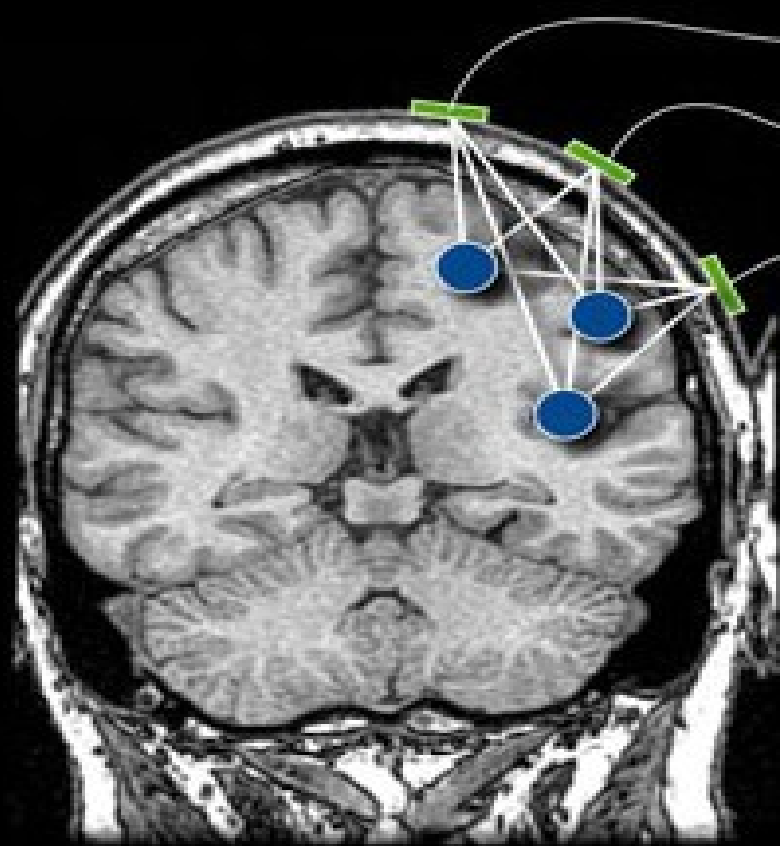
Independent Component Analysis



Independent Component Analysis

Each microphone signal (X) can be modeled as linear superpositions of the recorded source signals (linear mixture by unknown matrix A).





Ok, but what is this ICA?

“Independent component analysis (ICA) is a method for finding underlying factors or components from multivariate (multi-dimensional) statistical data. What distinguishes ICA from other methods is that it looks for components that are both *statistically independent*, and *nonGaussian*.”

A.Hyvarinen, A.Karhunen, E.Oja
'Independent Component Analysis'

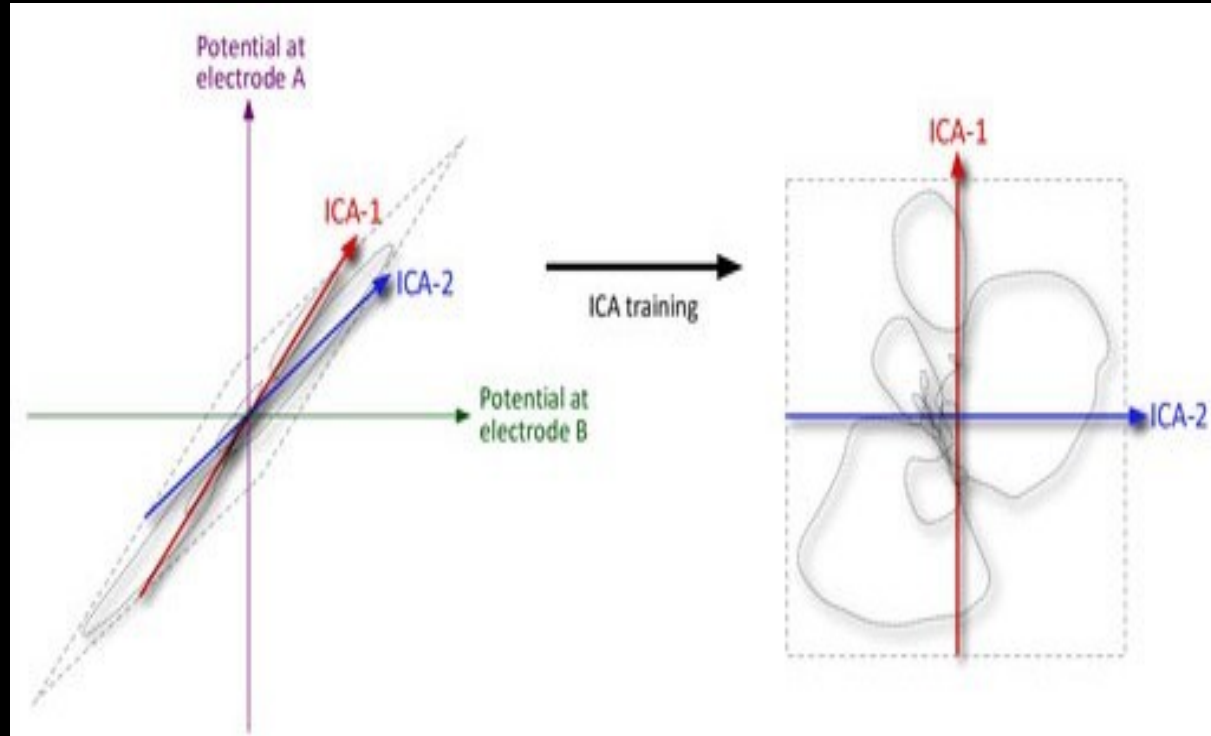
Ok, but what is this ICA?

Principle 1: “Nonlinear decorrelation. Find the matrix W so that for any $i \neq j$, the components y_i and y_j are uncorrelated, *and* the transformed components $g(y_i)$ and $h(y_j)$ are uncorrelated, where g and h are some suitable nonlinear functions.”

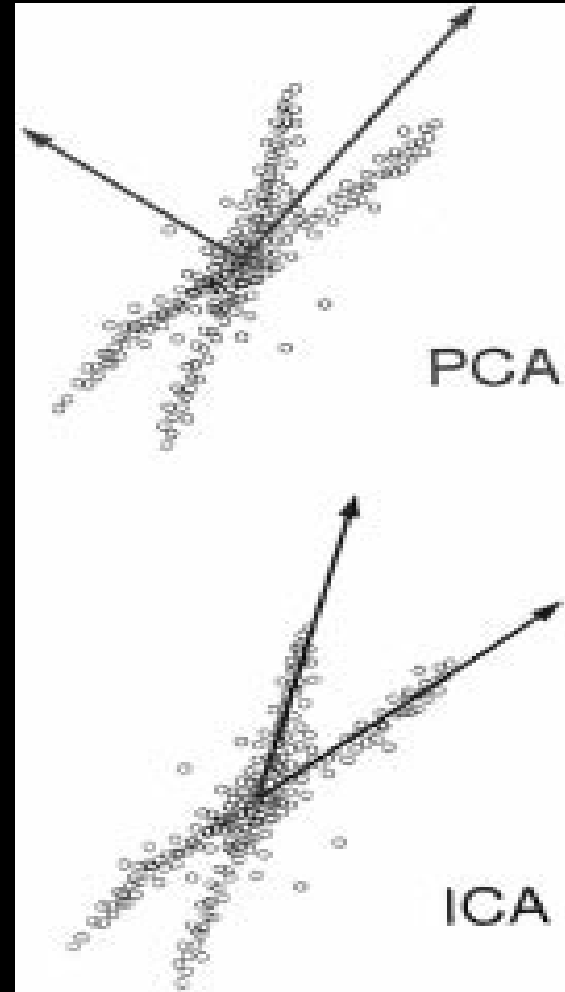
Principle 2: “Maximum nongaussianity”. Find the local maxima of nongaussianity of a linear combination $y=Wx$ under the constraint that the variance of x is constant.

Each local maximum gives one independent component.

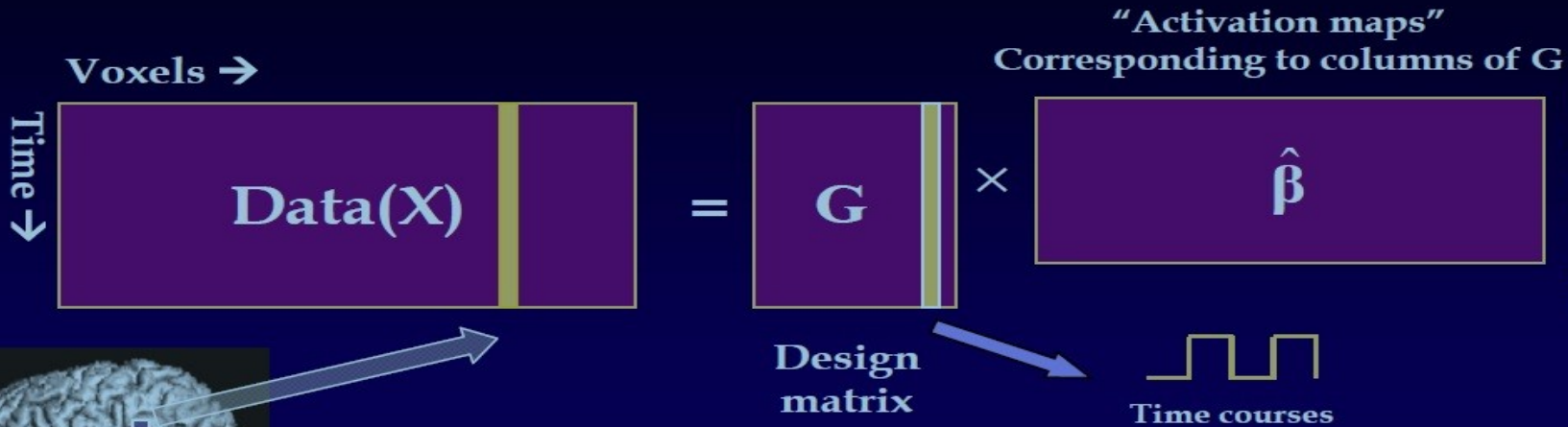
Non-Gaussianity



Difference between PCA and ICA

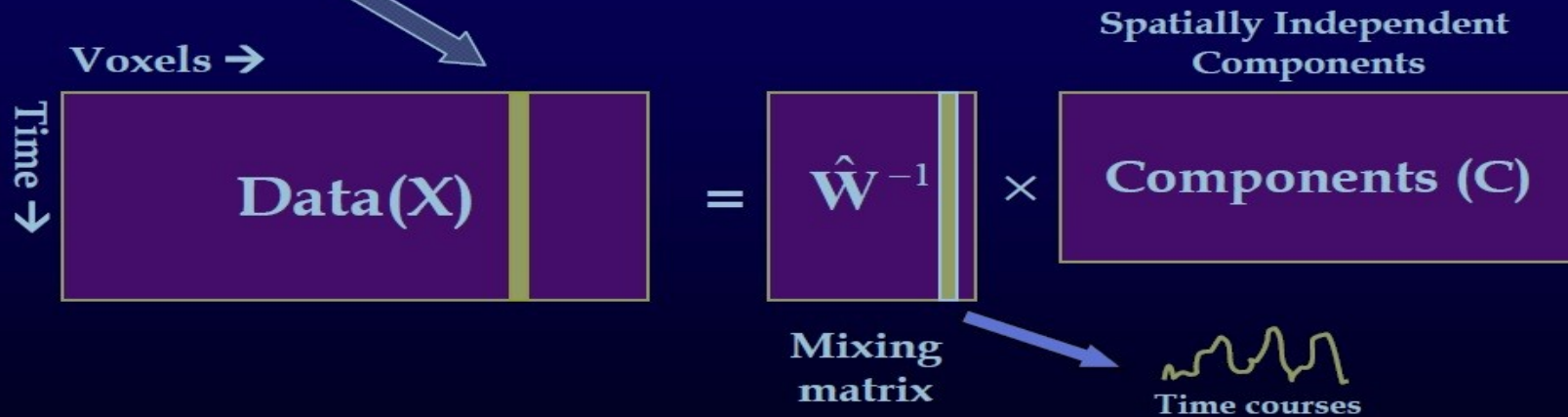


General Linear Model (GLM)



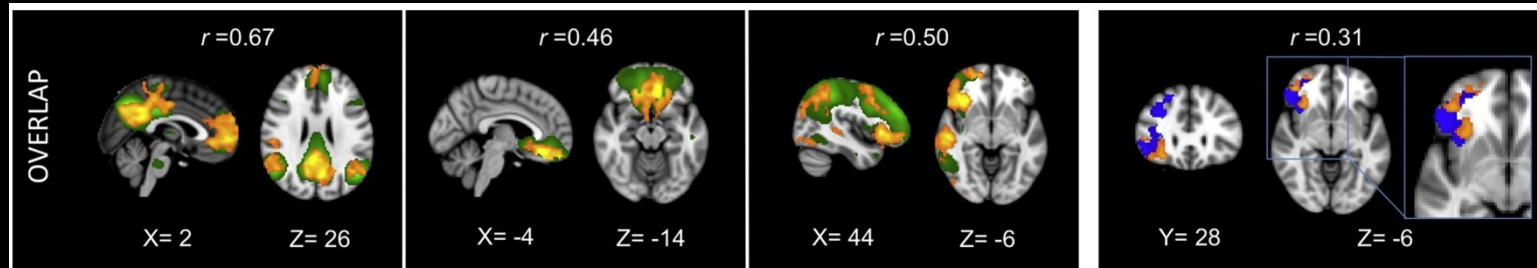
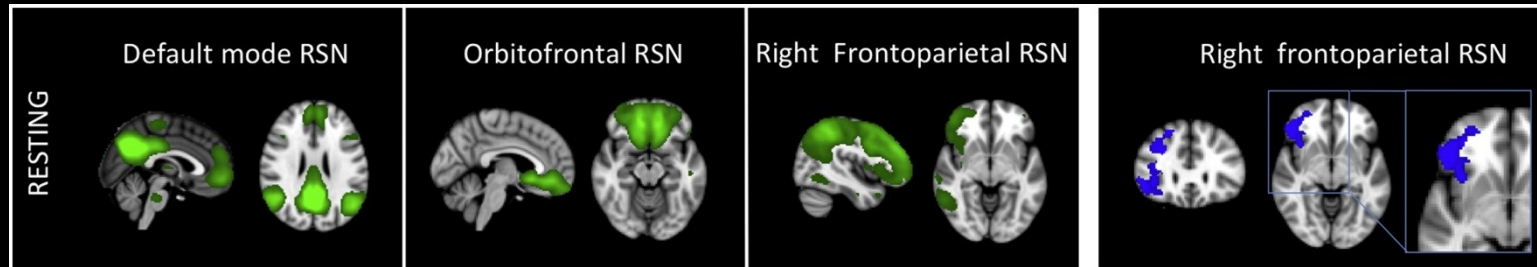
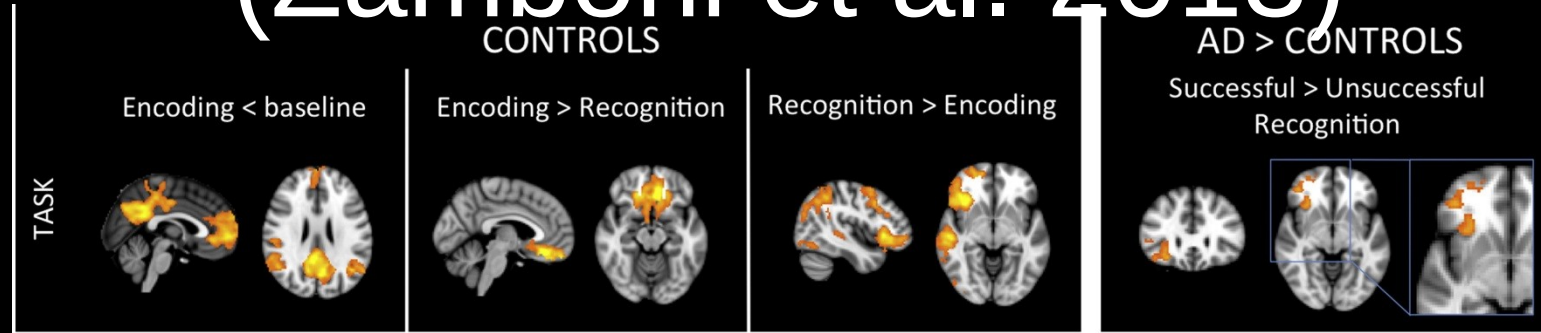
The GLM is by far the most common approach to analyzing fMRI data. To use this approach, one needs a model for the fMRI time course

Independent Component Analysis (ICA)

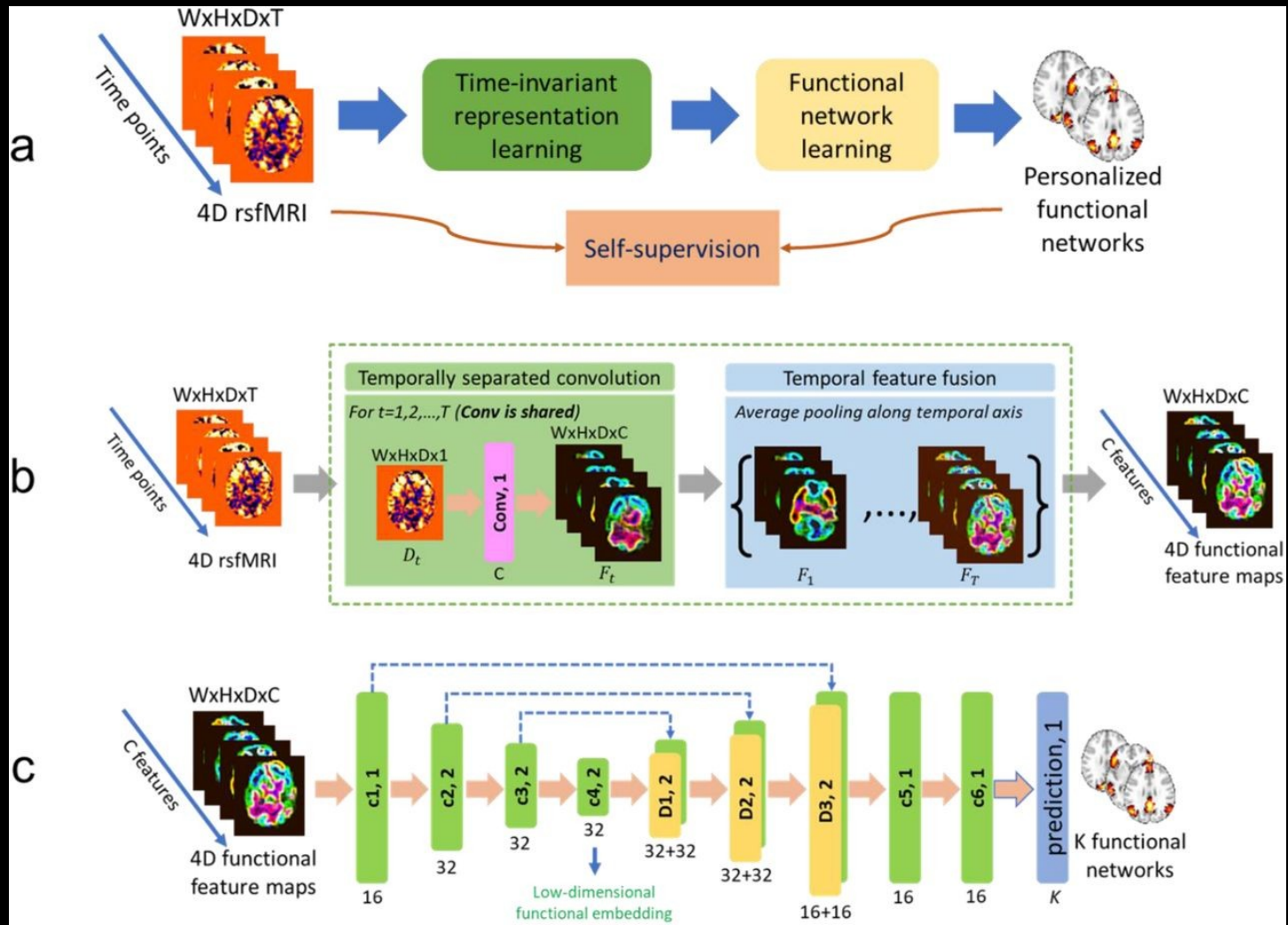


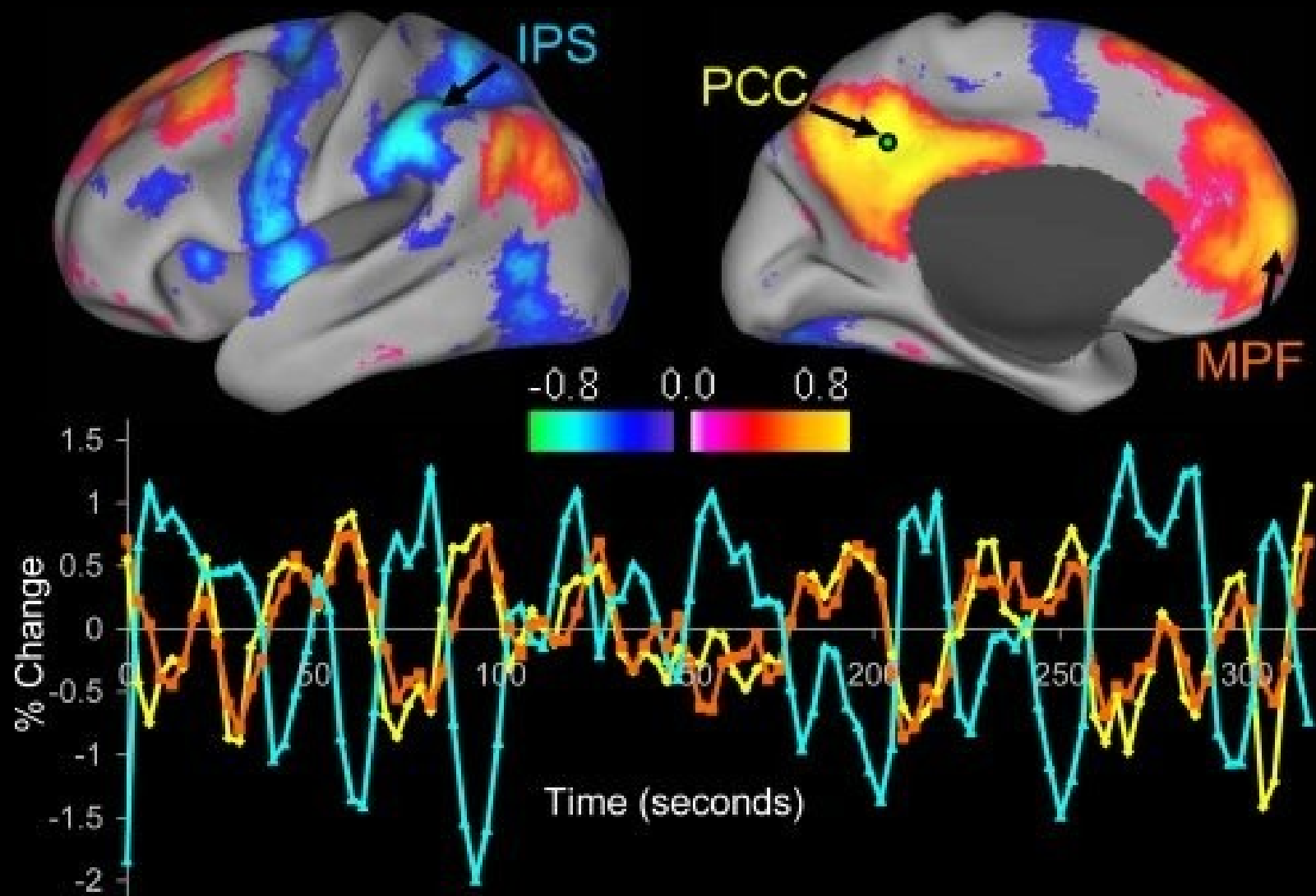
In spatial ICA, there is no model for the fMRI time course, this is estimated along with the hemodynamic source locations

Alzheimer Disease (Zamboni et al. 2013)

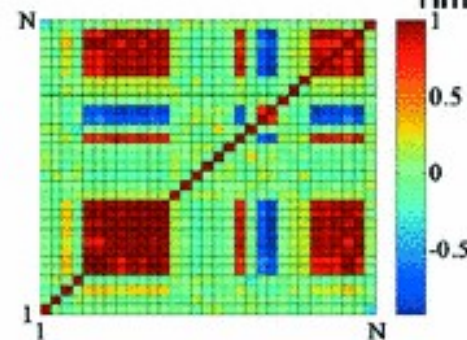
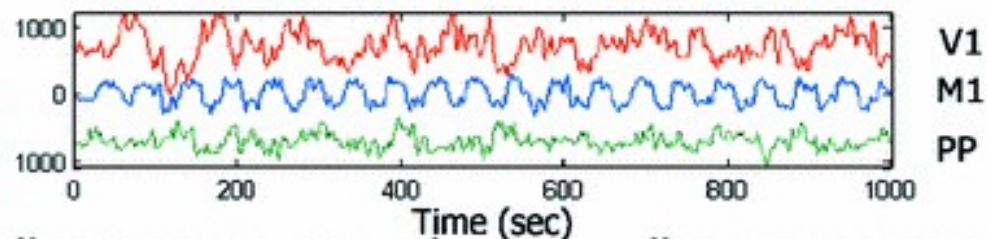
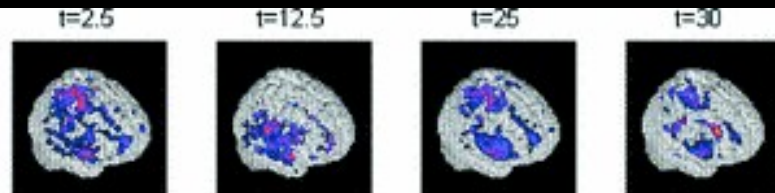


Li et al. Medical Image Analysis 2023

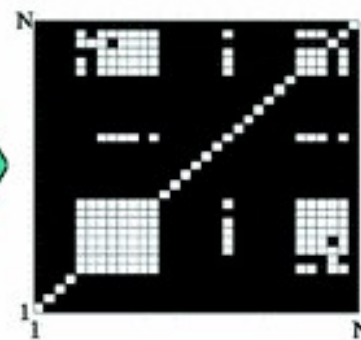




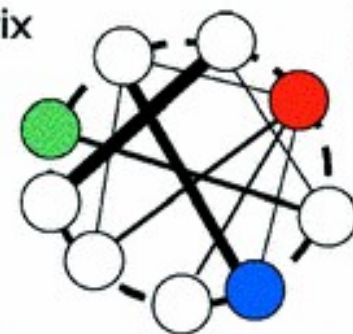
MR
Signal



Correlation Matrix

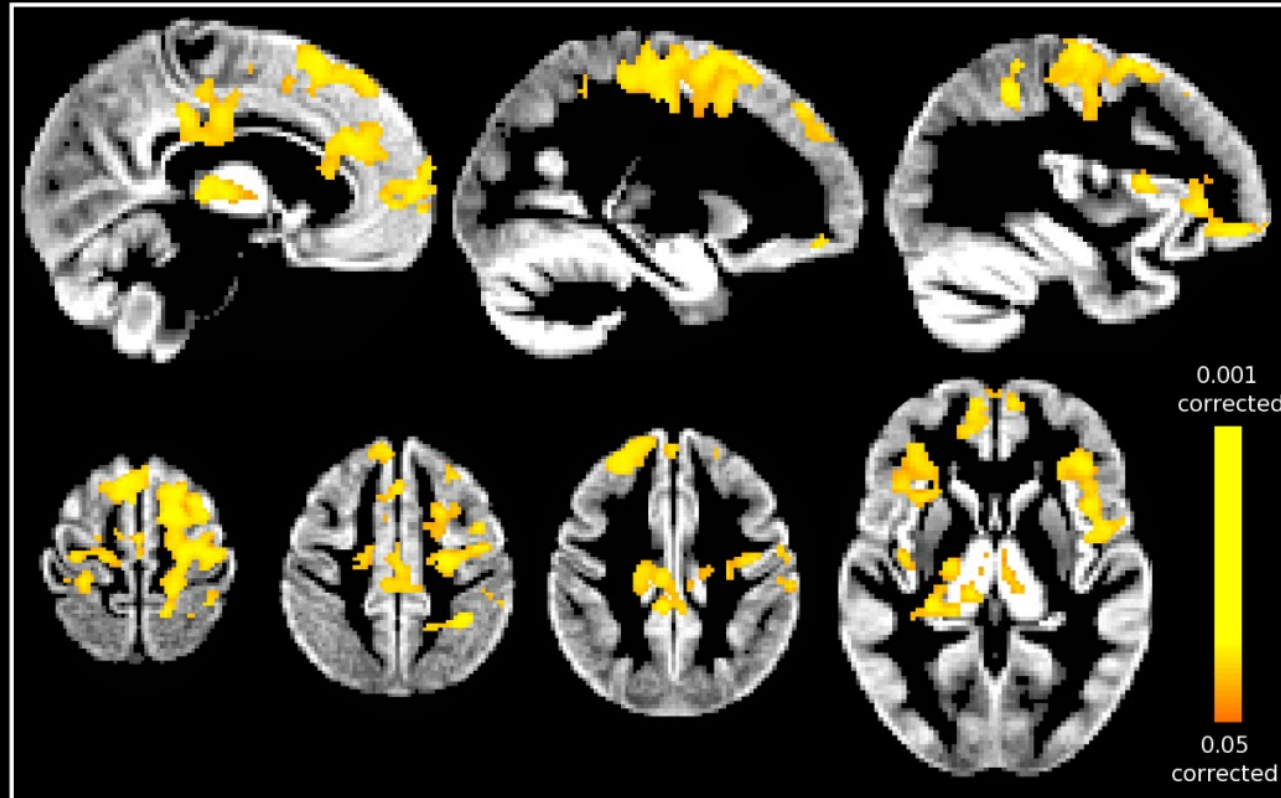


Thresholded
Matrix



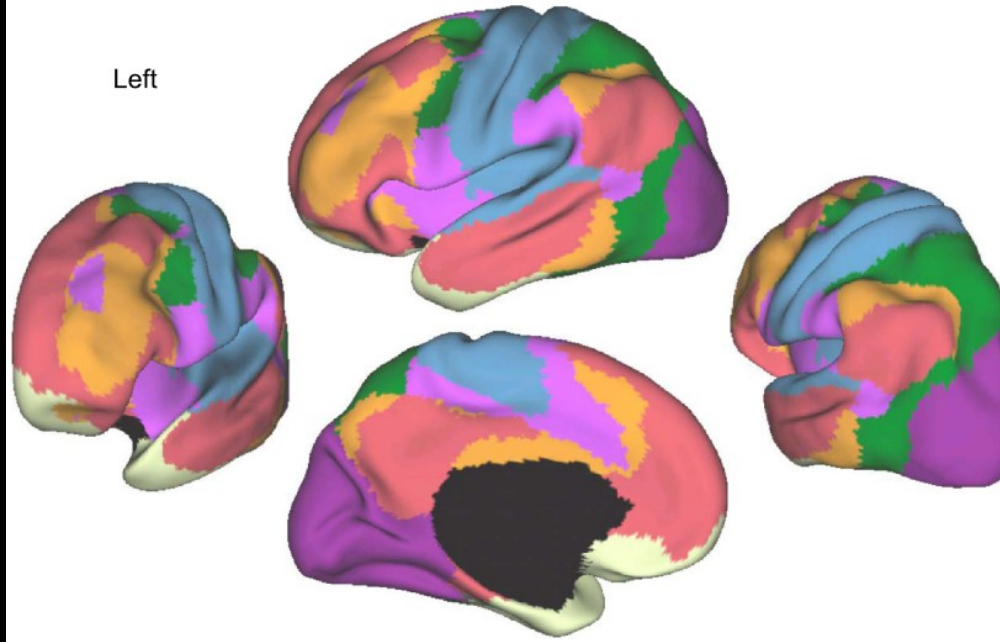
Network Extracted

Amyotrophic Lateral Sclerosis (Filippini et al. 2011)



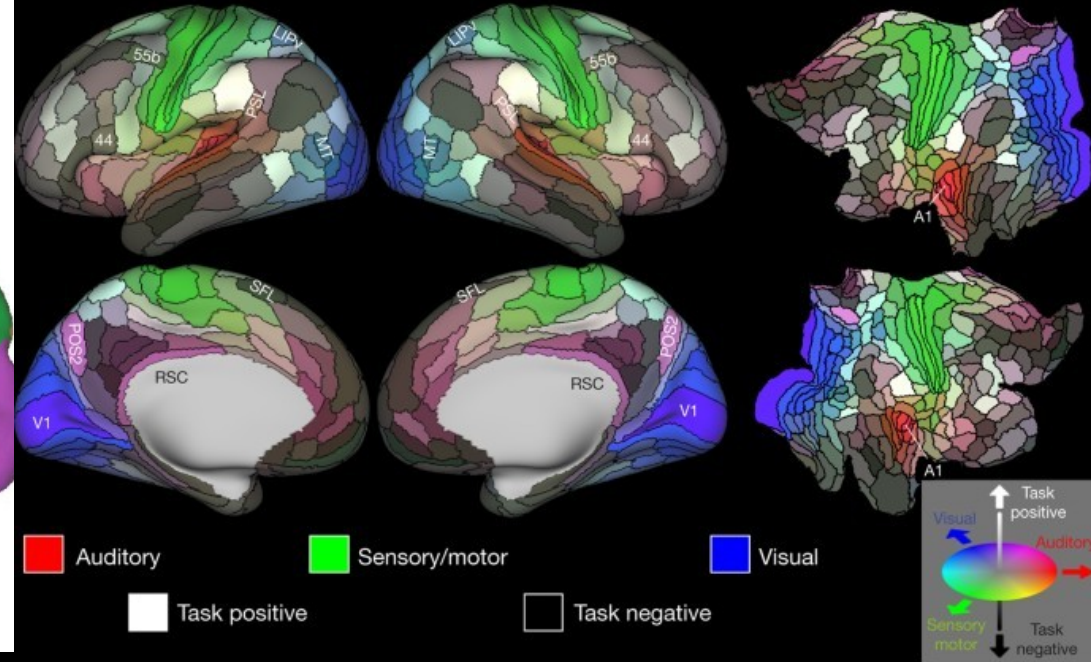
The importance of the atlas

7-Network Parcellation (N=1000)



Yeo & Krienen et al., 2011

The HCP's multi-modal cortical parcellation (HCP_MMP1.0)



Glasser et al., 2016

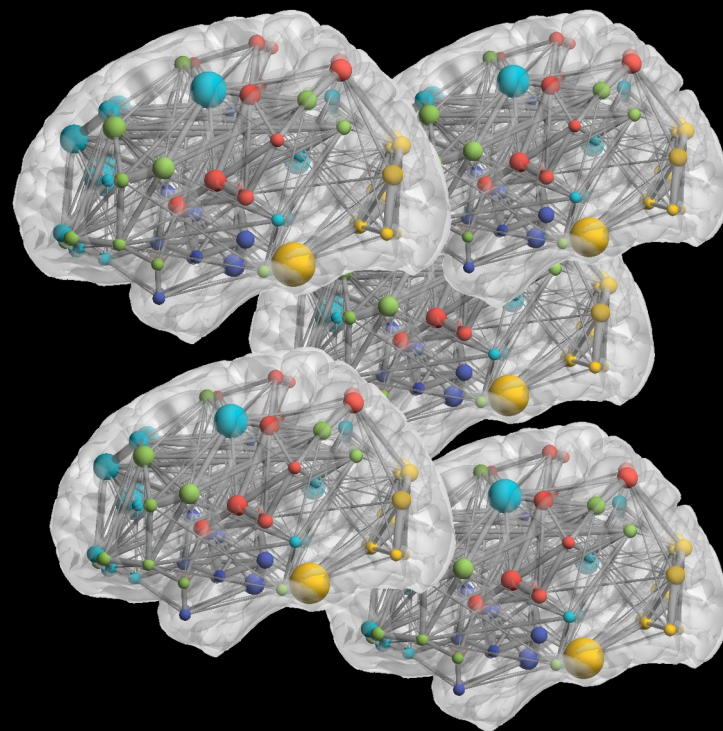
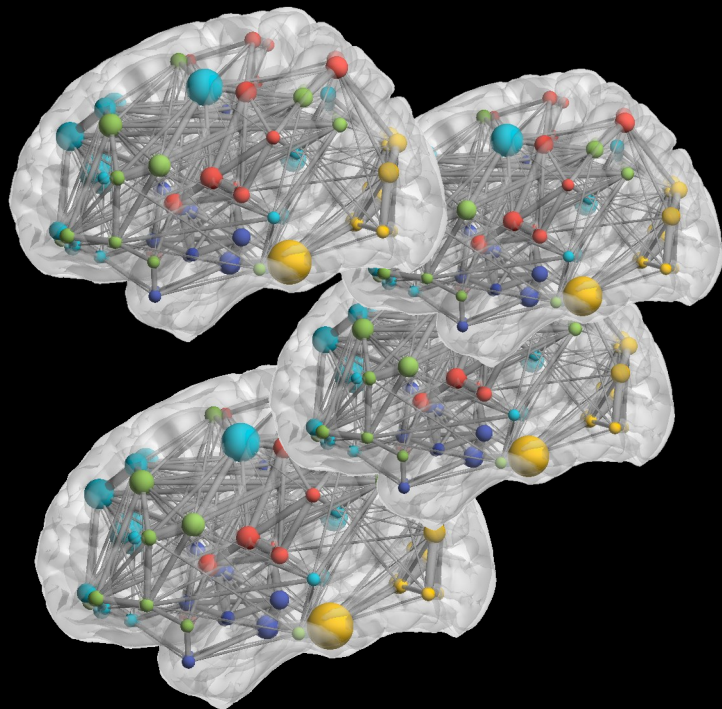
Alzheimer, Schizophrenia,...

Matched healthy control

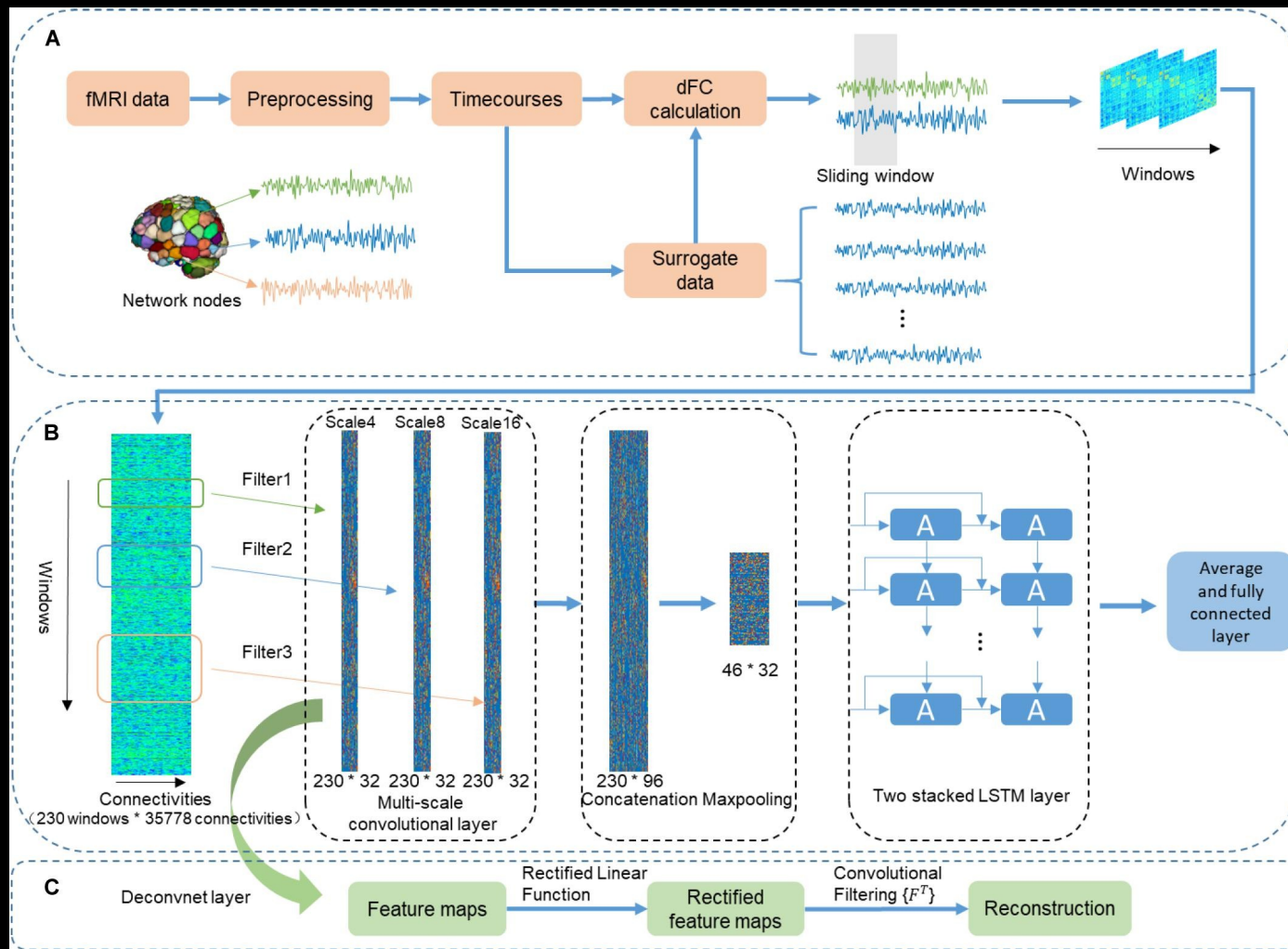
Healthy

vs

Alzheimer



Windowed Functional Connectivity



Questions?

