Imaging for Neuroscience

HOMEWORK – GROUP 2

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HOMEWORK'S GOAL

- Investigate the relationship between dynamic positron emission tomography (PET) and resting-state functional MRI data

DATA

- The scans were simultaneously acquired with a hybrid PET/MRI system on a healthy subject with an **irreversible** tracer

AIMS OF THE STUDY:

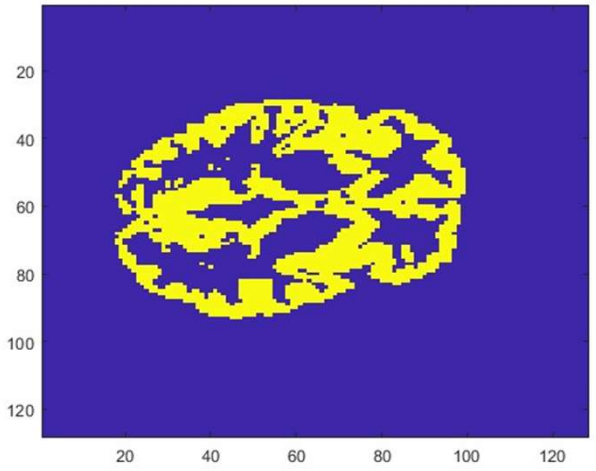
- Using a graphical approach, to quantify the PET dynamic at the region of interest (ROI) and voxel-level
- Analyze fMRI signal to compute the subject's functional connectivity (FC) matrix and the related cluster coefficents
- Investigate at the ROI level whether there is a relationship between the PET estimates and the computed connectivity measures

PET ANALYSIS - DATA

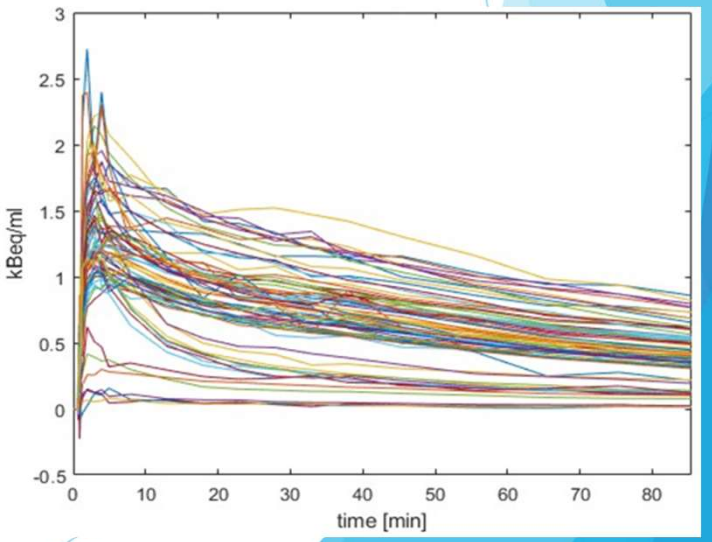
- $C_{b\ new}$ = plasmatic tracer concentration, corrected for metabolites [kBq/ml] *{5439x1}*
- mask = Hammers anatomical atlas resampled in the PET images space *{128x128x95}*
- PET = 4D dynamic PET data *{128x128x95x24}*
- time = PET hemi-scan times [min] *{24x1}*
- t_{new} = arterial sampling acquisition timing [min] *{5439x1}*

Computed variables:

Grey matter mask *{128x128x95}*



Time Activity Curve at ROI level



PET ANALYSIS

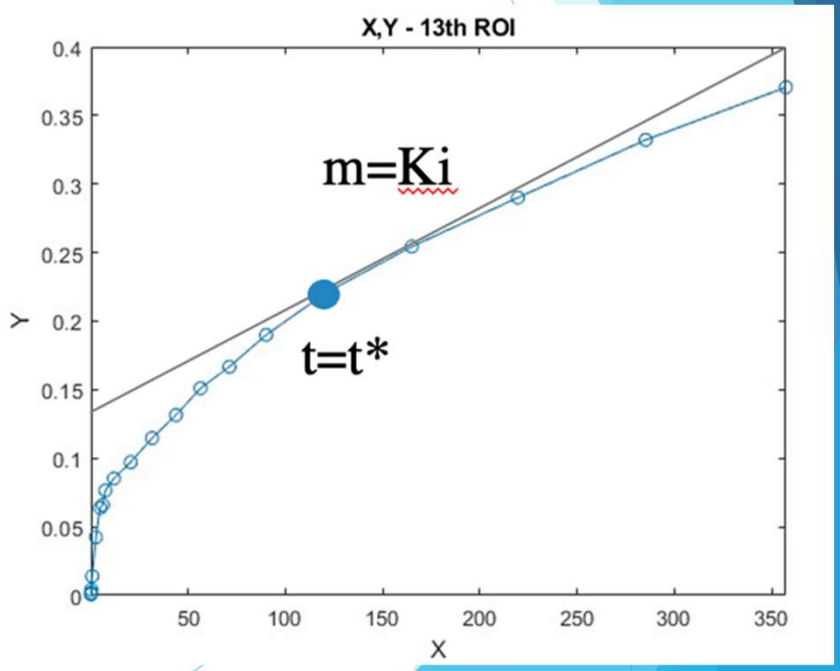
The tracer is **irreversible** → Patlak's graphical method

Calculation of Ki (fractional rate of irreversible tracer binding to specific receptor sites) at ROI and voxel levels as the slope of the curve after t*

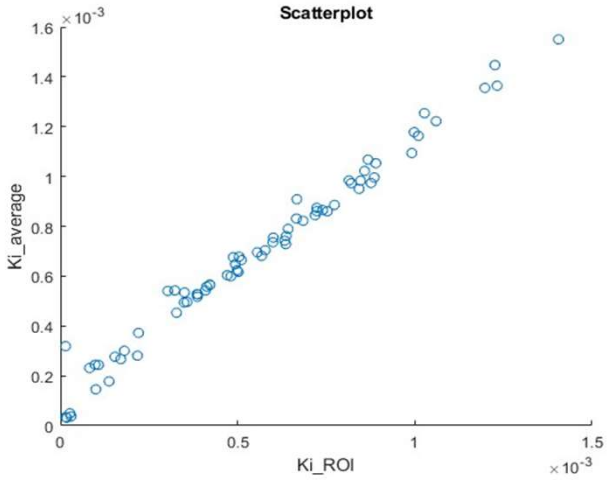
1) $$x = \frac{\int_0^t C_p(\tau)\,d\tau}{C_P(t)} \qquad y = \frac{C_{measured}(t)}{C_P(t)}$$

2) Choice of **t*** at ROI level as the instant after which the relationship between x and y is linear

3) Ki calculation using unweighted linear least square method



PET ANALYSIS

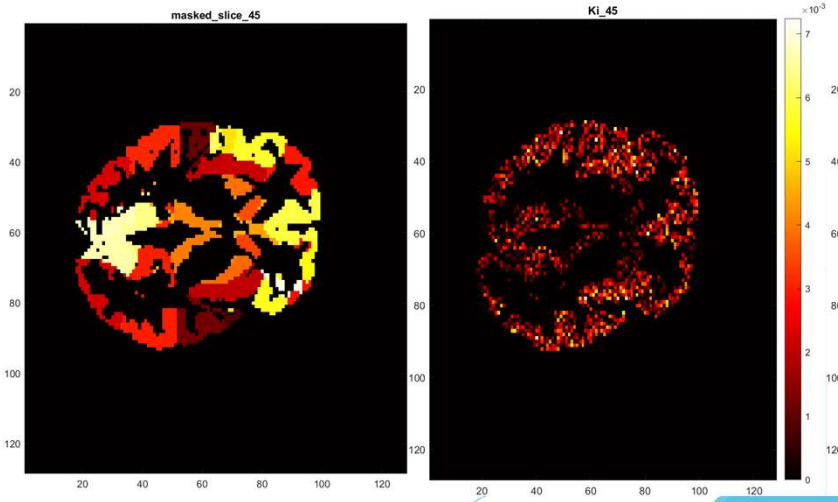


Correlation between Ki at ROI level and the average of Ki values of the voxels contained within each ROI

r = Pearson's coefficient = 0.99047

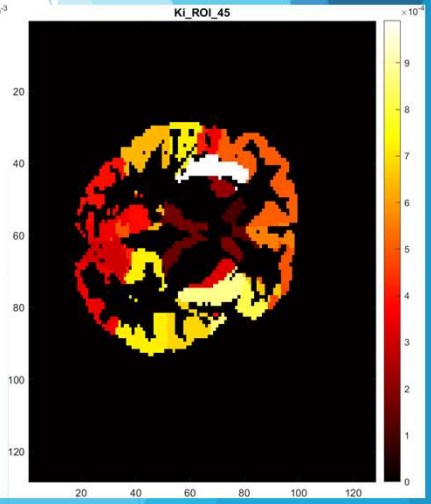
It is possible to say that the activation is not homogeneous among regions, infact it is possible to identify regions with a higher level of activity.

Atlas slice 45



Ki voxel level

Ki roi level

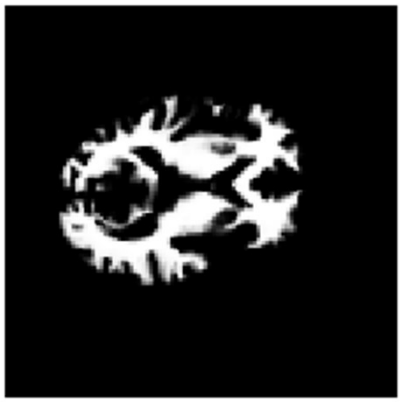


fMRI ANALYSIS - DATA

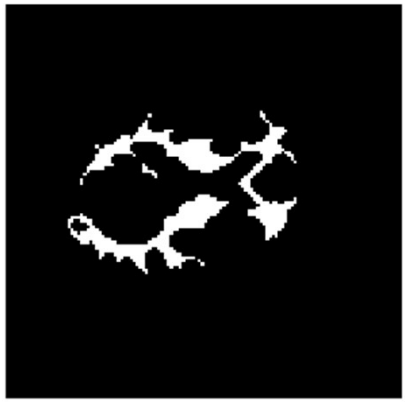
- WM_{Pmap} CSF_{Pmap} = probability maps of white matter and crebrospinal fluid
- ATLAS = PET.mask = Hammer Atlas reference *{128x128x95}*
- fMRI = 4D matrix sequence of volumes *{128x128x95}*
- TR = time resolution
- reg_mov = six regressor for motion correction

Looking at the histogramm, thresholds are applied to WM_pmap (75%) and CSF_pmap (40%) to obtain binary mask, then both the binary mask are eroded using a disk of radius 1.

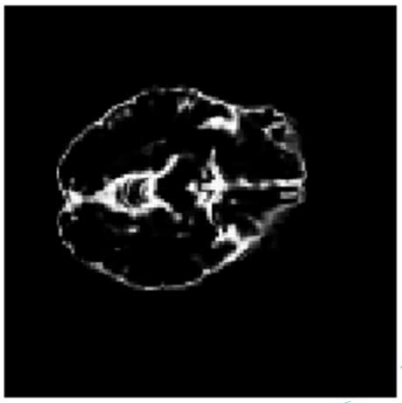
WM_pmap sl 46



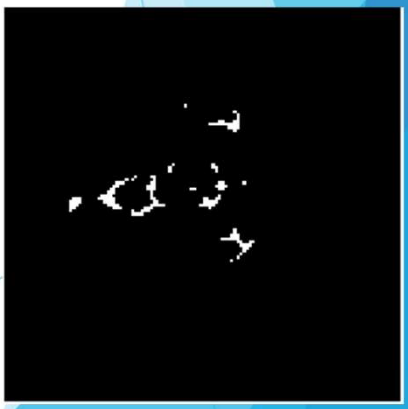
WM eroded mask sl 46



CSF_pmap sl 40



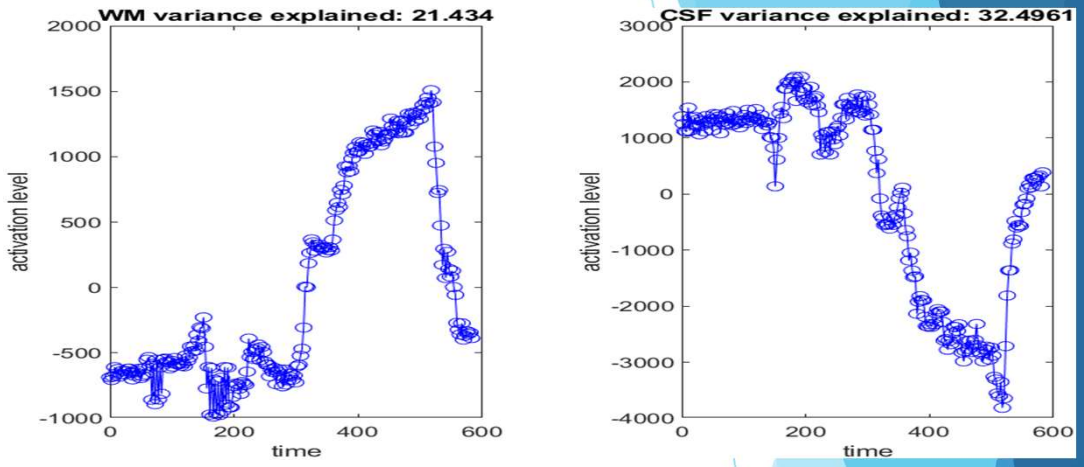
CSF eroded mask sl 40

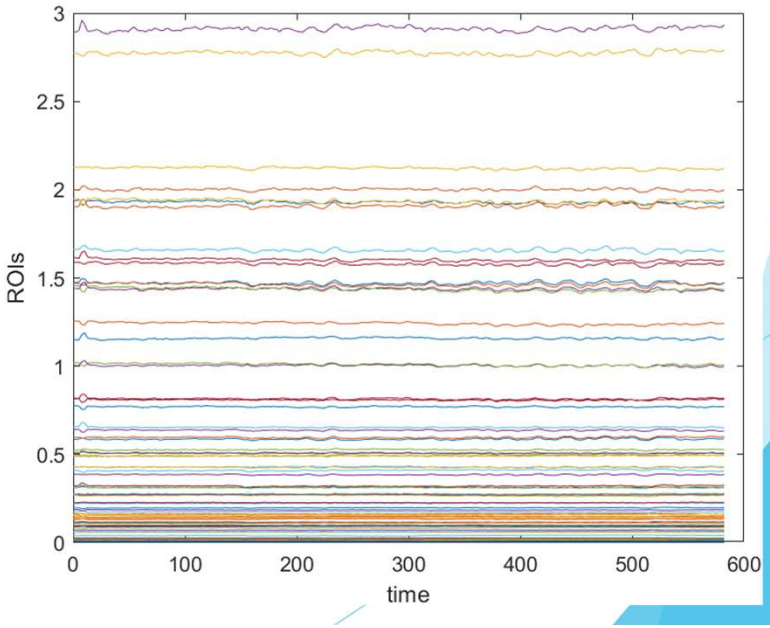


fMRI ANALYSIS

The masks are applied to all the volumes of fMRI and for both WM and CSF the data are organized in matrix in whitch each column represent the time serie of a certain voxel. PCA is applied to these matrix to extract the first principal component of WM and CSF.

The average activation curve of each roy is extracted using the Atlas reference and the grey_mask

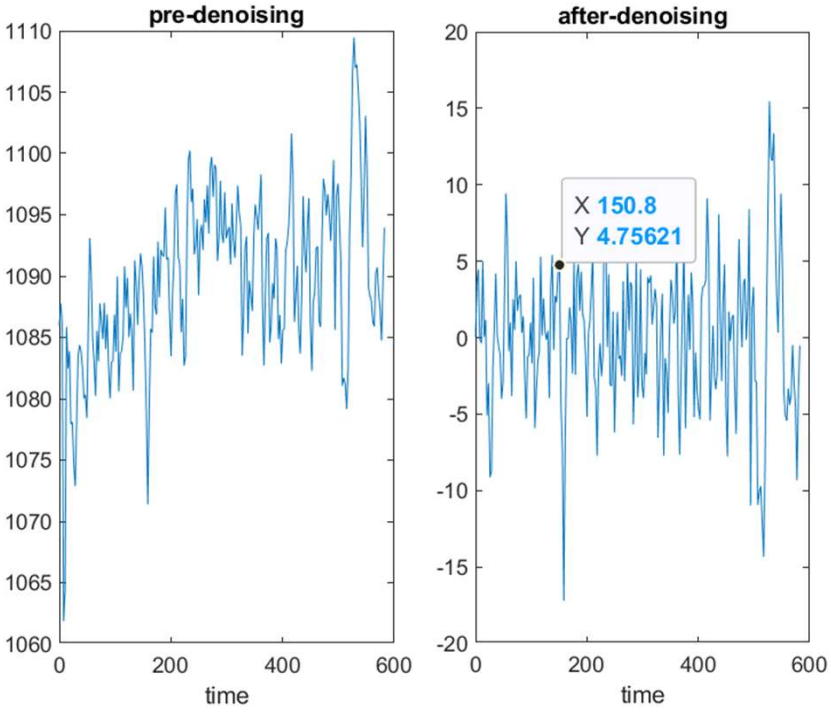


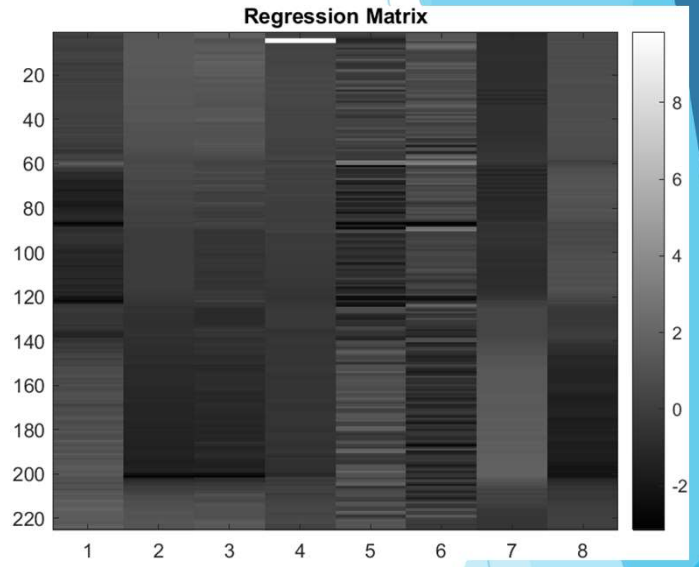


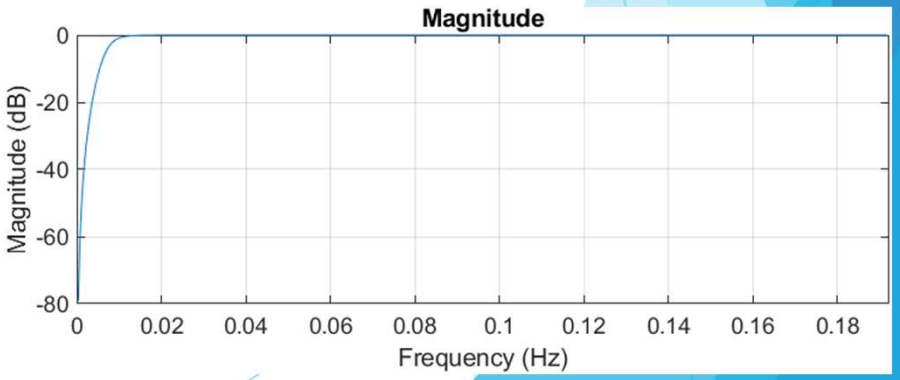
fMRI ANALYSIS

Each roy signal is filtered at the voxel level computing a linear regression with 8 regressor (6 from reg_mov and the 2 first components of WM and CSF) and an Butterworth High-pass filter (f_cutoff = 1/128 = standard SPM12, order = 3)

Efffects of the denoising step on the Hippocampus



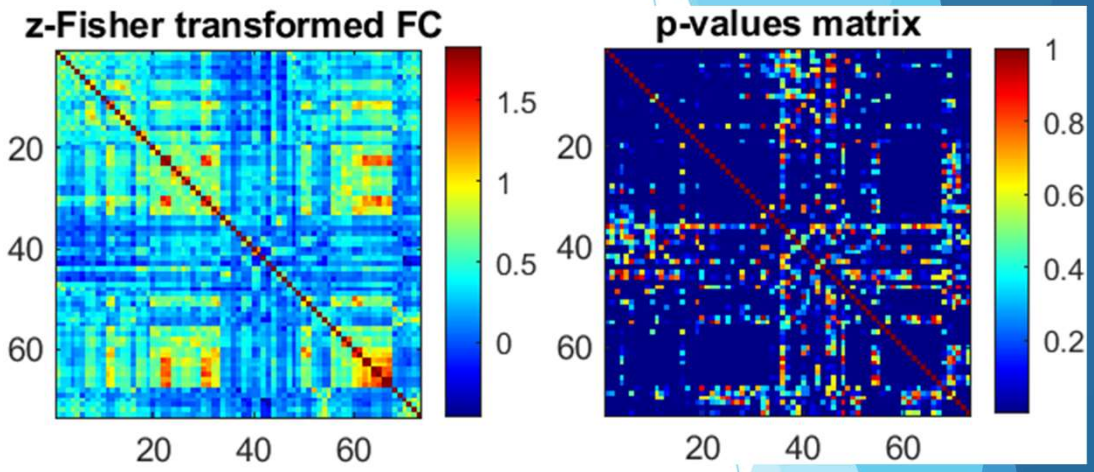


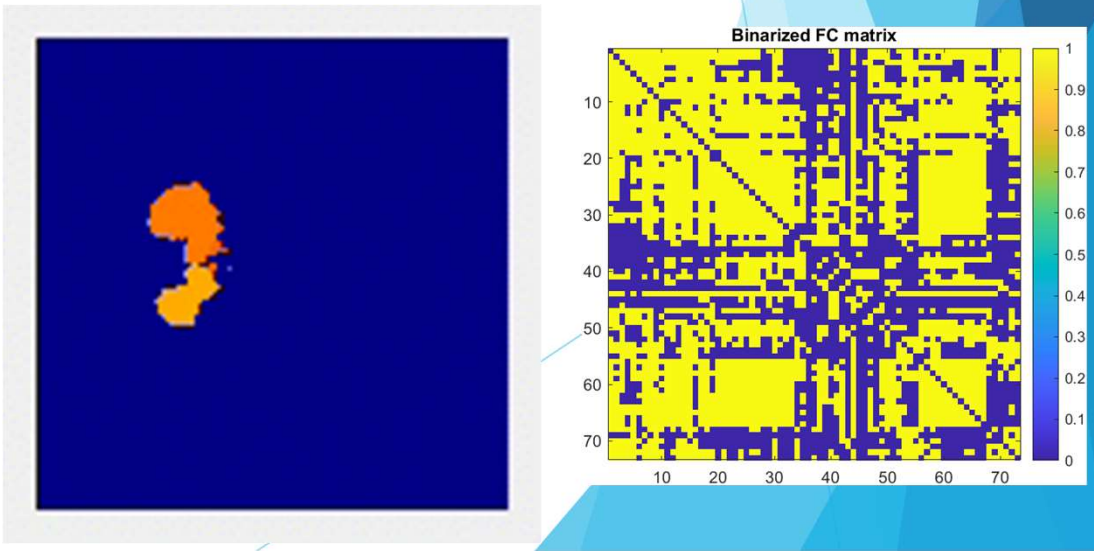


fMRI ANALYSIS

The Functional connectivity matrix is generated computing the correlation between the mean activity time serie of the rois, then is applied the Fisher z-trasform so that the correlation coefficent became normally distributed.

The Clustering coefficent for each roi is calculated on the binarized functional connectivity matrix, only correlations with a p_value<0.05/n_roi are considered valid.





PET/fMRI INTEGRATION

Correlation between PET Ki and fMRI clustering coefficient

Looking at the graphs we can say that there's not correlation between the clustering coefficient and the Ki. Our though is that they represent somenthing different: Ki is related to the activation/consumption of a certain area, while the clustering coefficient is related to how much the activation of that area is linked to the activation of the near areas. Therefore some areas can have an high Ki and a low clustering coefficient. For example in case of tasks that demand the activation of segregated areas instead of diffuse activation of the brain the activated area will show an high Ki but a low clustering coefficient.