UNIVERSITÀ DEGLI STUDI DI PADOVA

DIPARTIMENTO DI INGEGNERIA DELL'INFORMAZIONE

Investigating the relationship between resting state functional MRI and diffusion MRI data

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Academic Year 2021/2022

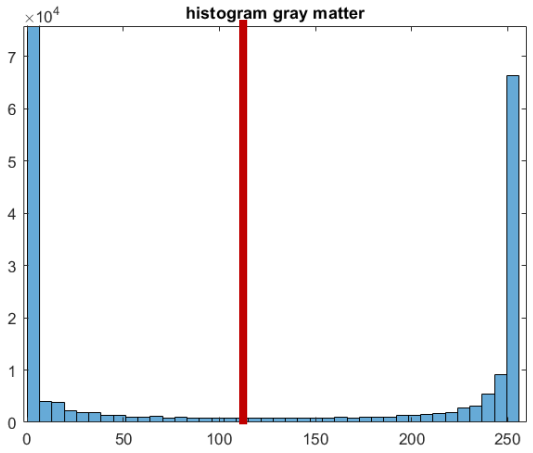
Outline

- Functional MRI data analysis
  - Data pre-processing steps
  - Subject's FC matrix
  - Multiple comparison correction
  - Graph measures
- Diffusion MRI data analysis
  - Understanding of the signal
  - Diffusion tensor computation
  - DTI metrics
- fMRI and dMRI integration

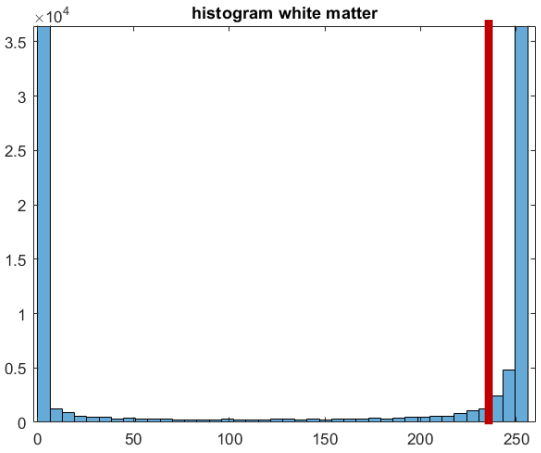
Functional MRI data analysis

Data pre-processing steps → Masks creation

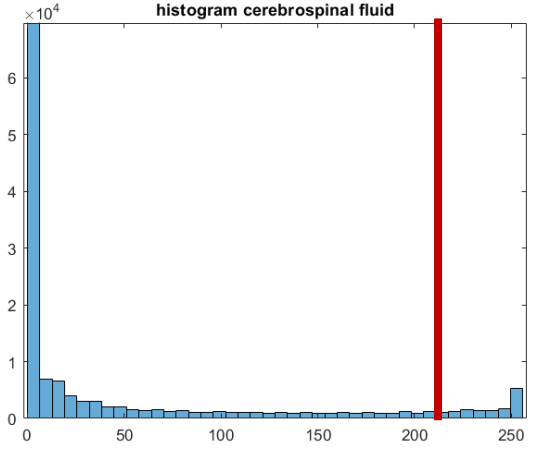
- Using **SPM software**, the T1w structural image has been segmented into **GM, WM and CSF** and their **tissue probability maps** have been obtained
- **Binary masks** for GM, WM and CSF have been retrieved with thresholds of **0.45, 0.95 and 0.85** respectively
- Summing the fourth dimension of the 4D resting state fMRI data, the **sumEPI image** has been obtained and its **binary mask** has been retrieved with a threshold of **10^5**
- We setted these **thresholds**
  - looking at the **histograms of the masks**: these thresholds allow a distinct separation between pixel intensity groups
  - **visualizing the masks**: there wasn't any isolated pixel



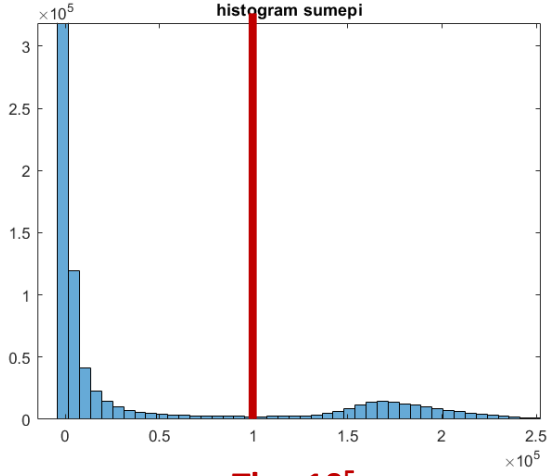
Th = 0.45



Th = 0.95



Th = 0.85



Th = 10^5

Functional MRI data analysis

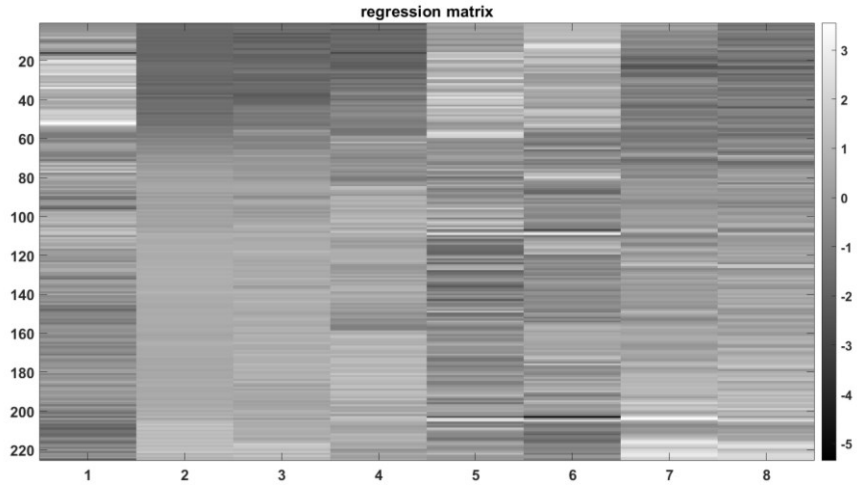
Data pre-processing steps → Mask erosion

- **WM and CSF masks** have been eroded with a **structuring element of dimension 2**
- We opted for this dimension for the structuring element because we saw that it allows a good erosion of isolated pixels without deleting too much
- We did't eroded the GM mask because we saw that it wasn't necessary
- **Mean fMRI signal of WM ad CSF** has been computed

With the GM mask and the sumEPI mask, we **masked the Hammers atlas** and we **extracted the ROI TACs**, excluding from the computations the ROIs with less than 10 voxels and amygdala, cerebellum, brainstem, corpus callosum, substantia nigra, ventricles.

Data pre-processing steps → Noise regression

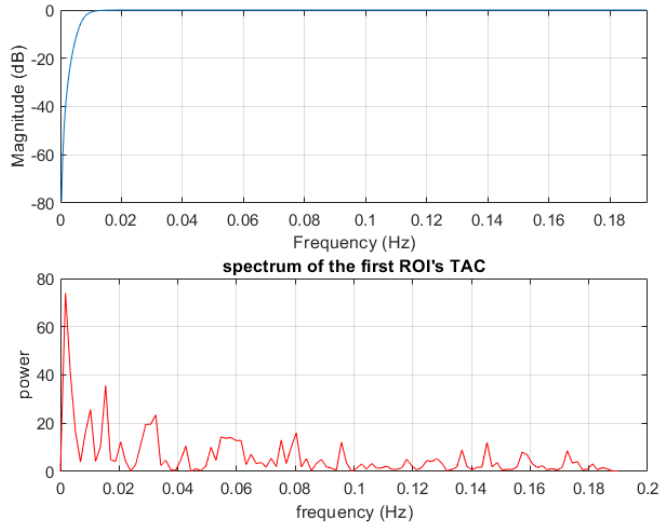
- We used the linear regression approach to remove **non-neural undesidered fluctuations** from the ROI TACs
- The regressors were the six parameters estimated during the motion correction step and the **mean fMRI signals of WM and CSF**
  - Each regressor has been z-scored



Functional MRI data analysis

Data pre-processing steps → Temporal filtering

- A high-pass filter with a cut-off frequency of **1/128 Hz** has been applied to the regressed signal to take the **slow components** out of it
- We set the cut-off frequency to 1/128 Hz because
  - it allows to **preserve the range related to the neuronal activity (0.08-0.1 Hz)**
  - it is the **default cut-off frequency used in SPM**

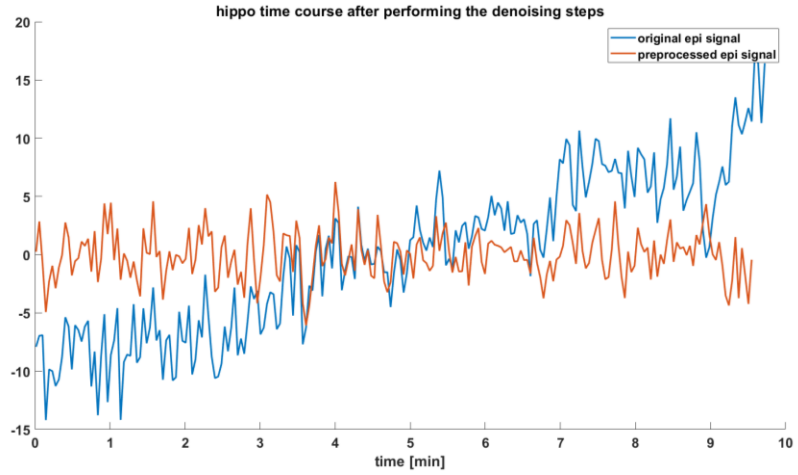


Data pre-processing steps → Volume censoring

- The volume with **frame-wise displacement grater than 3.5 mm** has been discarded
- Since motion artifacts could be presented also in the neighboring volumes, also one volume before and two volume after the affected volume have been discarded
- The censored volume were **4**

Data pre-processing steps → Check

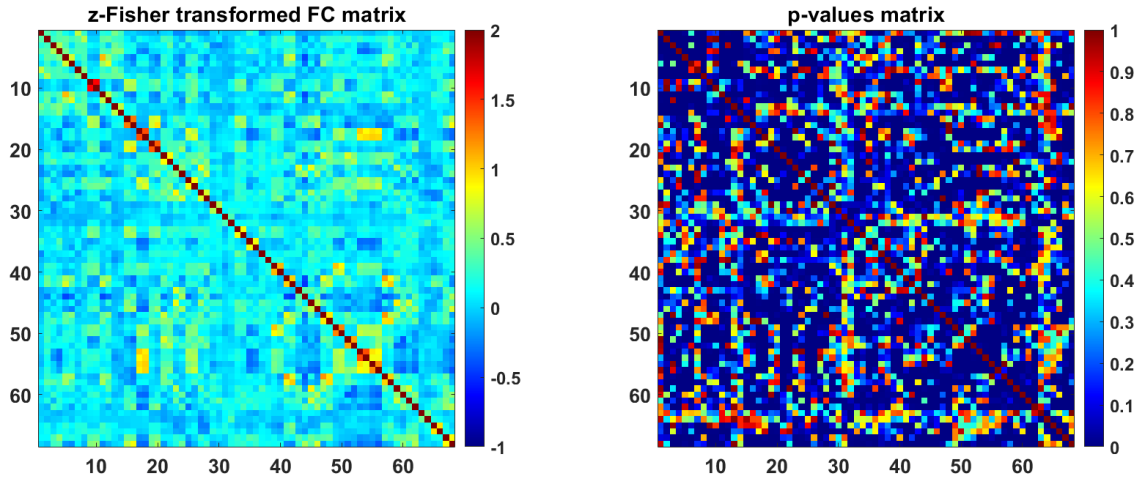
- To check the appropriateness of the preprocessing steps, we plotted the original and the processed TAC of the **right hippocampus region**
- The denoising step has been able to **remove the drift** that were present in the signal



Functional MRI data analysis

Subject's FC matrix

- The **pair-wise Pearson's correlation and associated p-value** has been computed between ROI TACs, in order to get a measure of synchrony between brain's parcels with its associated reliability
- We applied **Fisher's z-transform** to the resulting coefficients



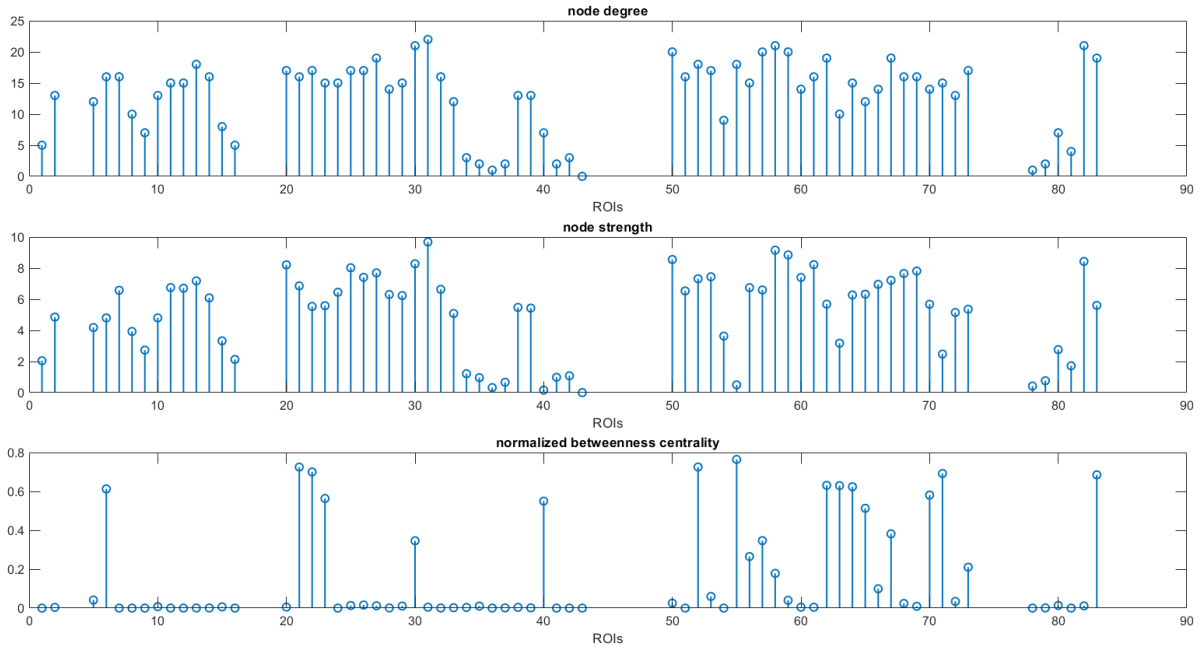
Multiple comparison correction

- Since a lot of statistical tests have been performed, multiple comparison correction was necessary
- We decided to opt for the **Bonferroni correction** because it allows to keep ~**20% of the correlations** (the ones with lowest p-values and so the more reliable ones), which is the sparsification suggested in literature

Functional MRI data analysis

Graph measures

Interpreting the ROIs as nodes of a graph and correlations between ROIs as its edges, it is possible to summarize the functional connectivity in terms of node centrality computing for each ROI:



- **node degree**
  - Highest values (hubs): 31, 30, 58, 82, 50, 57, 59, 27, 62, 67
- **node strength**
  - Highest values: 31, 58, 59, 50, 61, 20, 25, 68, 30, 82
- **normalized betweenness centrality**
  - Highest values: 55, 52, 21, 22, 71, 83, 63, 62, 64, 6

We can clearly see a similar pattern between node degree and node strength ($r = 0.87$, $p = 0$).

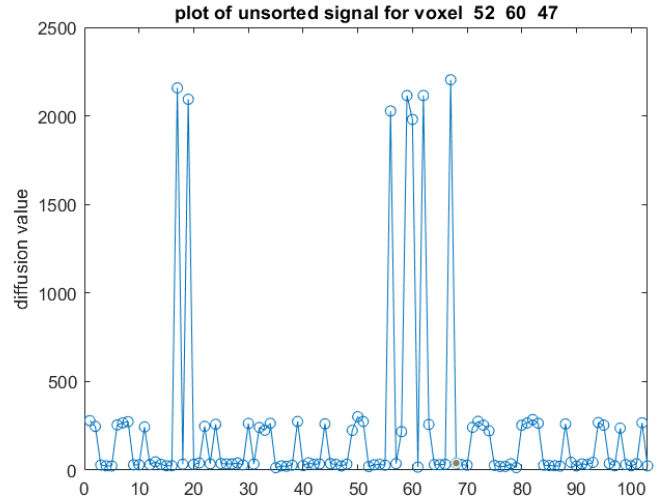
Diffusion MRI data analysis

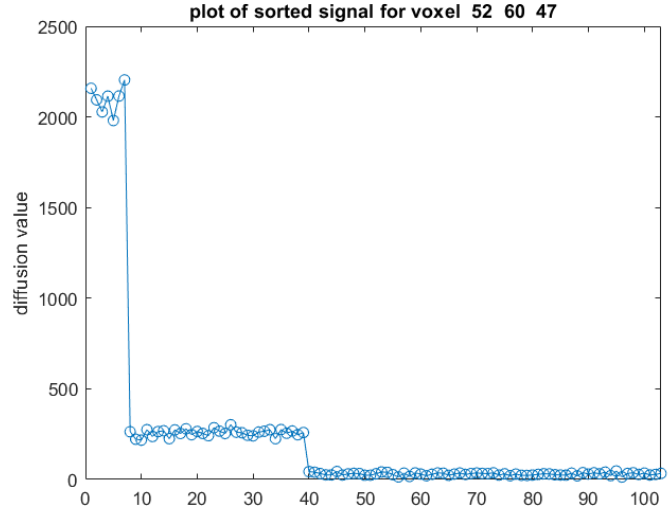
Understanding of the signal

- The Diffusion Weighted Images that have been acquired are **103**
- Excluding b = 0 s/mm^2, we identified two diffusion shells: **b = 700 s/$\mathbf{mm}^2$ and b = 2000 s/$\mathbf{mm}^2$**

- We selected a **voxel populated principally with CSF** (voxel with coordinates [52, 60, 47]) and the selection has been based on
  - **DTI metrics**: FA value at these coordinates is low as expected for a voxel populated principally with CSF
  - **CSF mask** created while analysizing fMRI data
  - **Anatomical atlas**: this voxel has label 45 and so belongs to the lateral ventricle, which is a region where the CSF flows

- The diffusion signal of the selected voxel were **not ordered** by its b-value and so we ordered it
  - The **intra b-value variability** of the signal is probably due to random effects, since the diffusion can be described as a random walk
  - The **inter b-value variability** of the signal is related to the law behind diffusion MRI signal
    - $S = S_0 e^{-bD}$: the higher the b-value, the lower the signal acquired





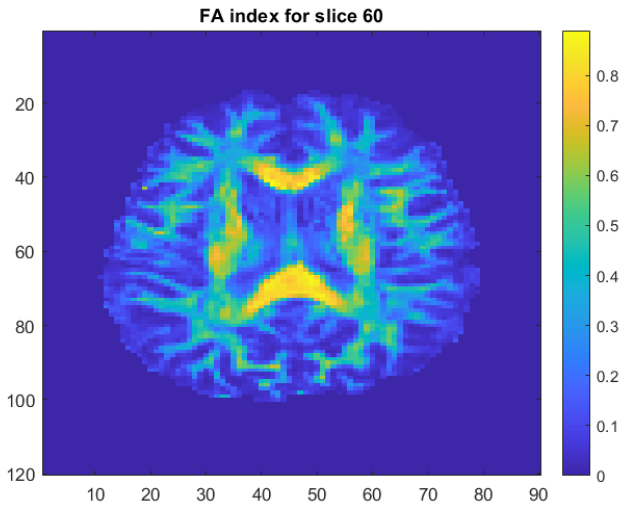
Diffusion MRI data analysis

Diffusion tensor

- From the DTI matrix we created a new 4D matrix containing only the volumes corresponding to b = 0 s/mm^2 and b = 700 s/mm^2
- S_0 image has been retrieved computing the voxel-wise mean value of all b = 0 s/mm^2 volumes
- We removed from the brain diffusion mask the voxels for which there was an error in the acquisition step (S_0 = 0)

For each slice:

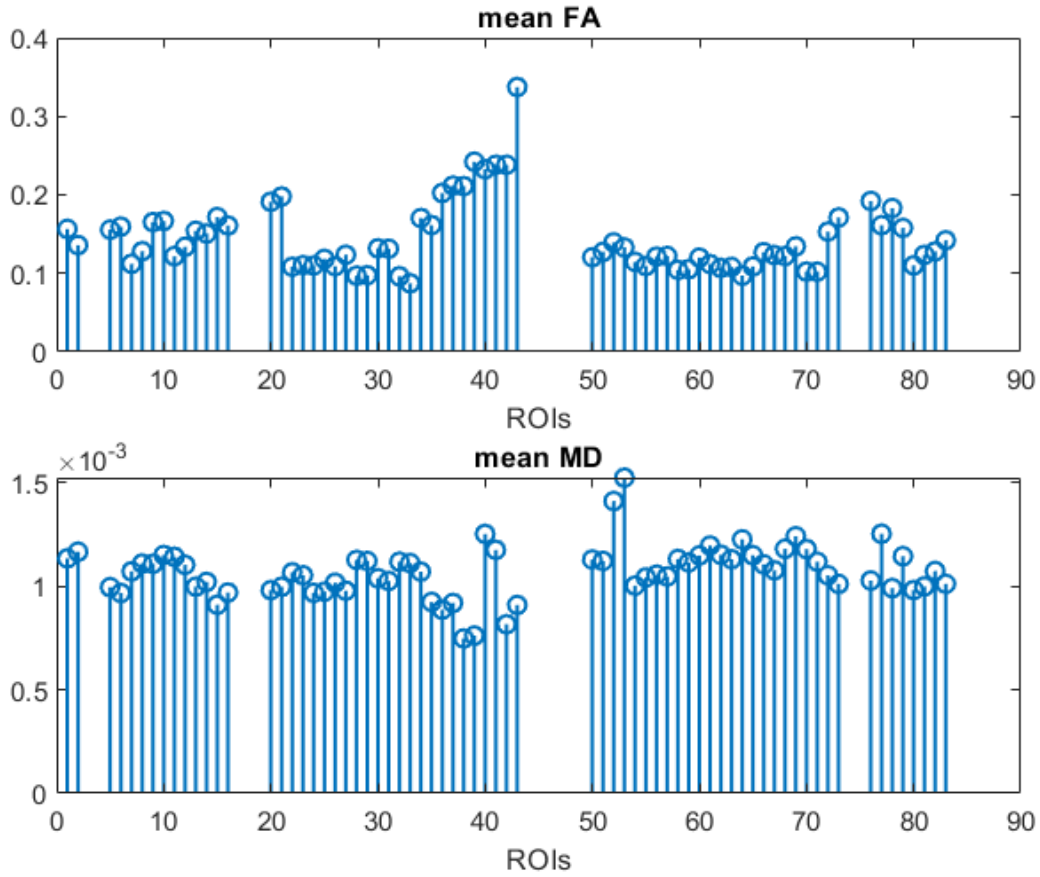
- we fitted the voxel-wise diffusion tensor D, using the linear least square approach
- through the computation of eigenvalues of D, we retrieved
  - **Fractional Anisotropy (FA) index map**
  - **Mean Diffusivity (MD) index map**



Diffusion MRI data analysis

DTI metrics

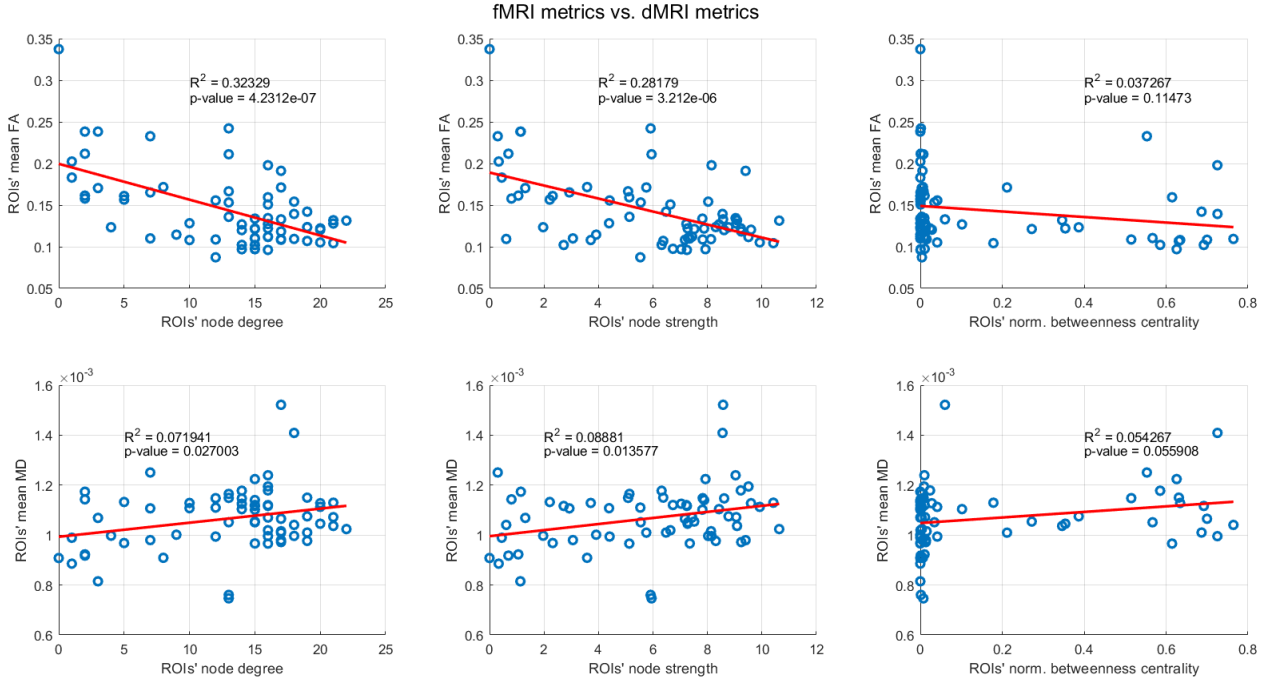
With the GM mask and the brain diffusion mask, we **masked the Hammers atlas** and we **extracted the mean FA and MD of each ROI**, excluding from the computations the ROIs with less than 10 voxels and amygdala, cerebellum, brainstem, corpus callosum, substantia nigra, ventricles.

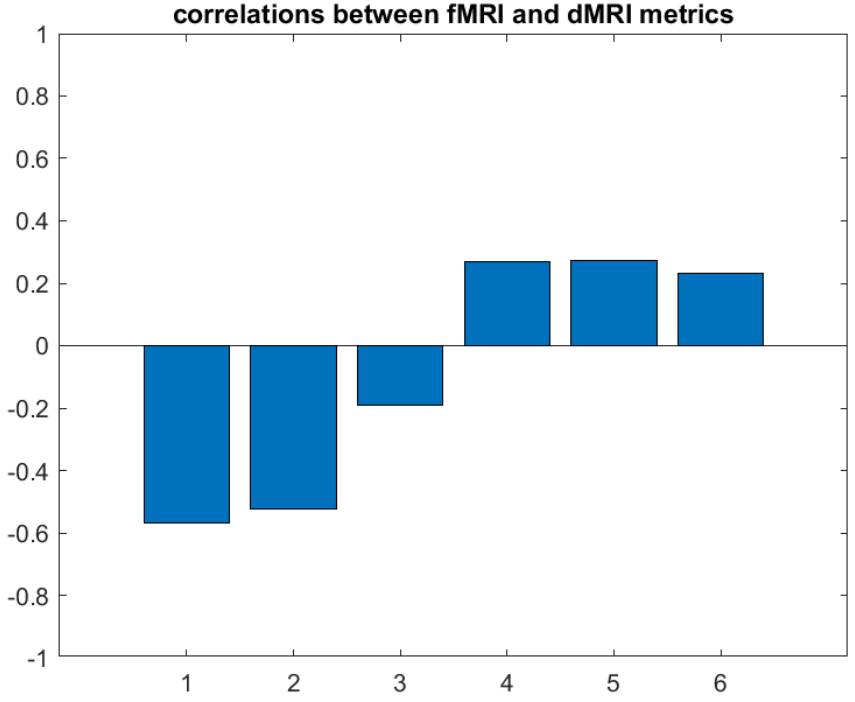


fMRI and dMRI integration

Through **Pearson's correlation analysis**, we found out that:

- mean FA is **significantly negatively correlated** with node degree (r = -0.57) and node strength (r = -0.53)
- mean MD is (weakly) **significantly positively correlated** with node degree (r = 0.27) and node strength (r = 0.3)
- normalized betweenness centrality is **not correlated** with mean FA or mean MD





Thanks for your attention!