Dear TAs,

Out team, of 4 PhD students in neurosciences, would like to propose a project on brain networks.

Team 51:
Claudia Bigoni
Giorgia Giulia Evangelista
Emeline Mullier
Joan Rue

Dataset:
The human brain connectome we are going to use is obtained by averaging the individual brain connectomes processed over 80 healthy subjects.
For the nodes features, which are represented by the resting state fMRI, we are going to use the BOLD signal coming from one healthy subject (fMRI resting-state was recorded for 9 minutes – 275 samples).

Here below you can find the description of the dataset (in terms of images that were needed to create it in the first place):
80 healthy subjects:
- Structural: MPRAGE, processed with FreeSurfer and segmented with Desikan atlas into 82 brain regions
- Resting-state fMRI: BOLD signal preprocessed according to a state of the art pipeline
One fMRI signal for each brain region
- Diffusion Spectrum Imaging: Whole-brain tractography performed allowing the construction of weighted network number of streamlines, gFA, ADC...

	Description	Amount
Nodes	Grey matter regions	83
Edges	Average of streamlines over 80 connectomes[1]	N/A
Nodes features	Time series of BOLD signal	275
Labels	Name of brain region (from parcellation)	83

For the milestones we plan to use only the above-described dataset.

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[1] Another option could be to use a weighted average where the weight is the occurrence of the connection along the subjects.

For the second part of the project we would like to use additional datasets to make comparisons with pathological datasets. Indeed, this will be decided along the project and with your suggestions.