### UNIVERSIDAD POLITÉCNICA DE MADRID

ESCUELA TÉCNICA SUPERIOR DE INGENIEROS DE TELECOMUNICACIÓN MÁSTER UNIVERSITARIO EN INGENIERÍA BIOMÉDICA



# Design and development of a novel pipeline for resting-state functional magnetic resonance imaging processing

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### Motivation



- The H2H project is carried out by a CNIC research group that aims to unravel the relationship between cardiovascular and neurocognitive diseases.
- The pipelines must be able to obtain correlation matrices to determine functional connectivity and the degree of correlation between brain regions.
- In collaboration with the project, a versatile tool will be developed, capable of processing R-fMRI data in an automatic and optimized way.
- Two groups of subjects will be analyzed to validate the pipeline.

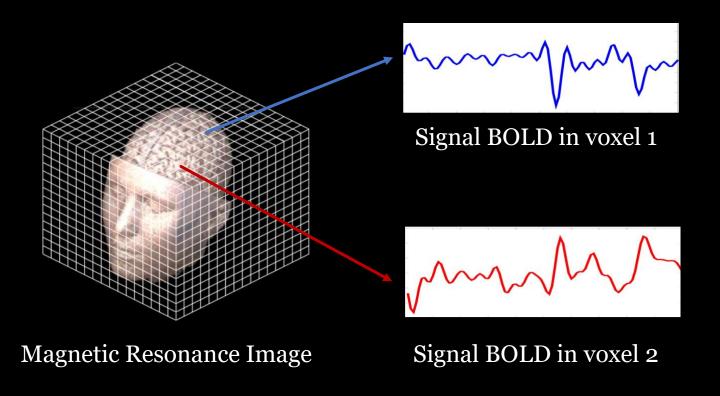
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### Introduction

Resting state – functional Magnetic Resonance Image (R-fMRI)



Synchronization in the activation of voxels.

Functional connectivity

## Preprocessing



### Why fMRI preprocessing is necessary?

- Movements of the subject inside the scanner
- · Inhomogeneities in the magnetic field
- Swallowing
- Heartbeats
- Breathing
- Others



# Preprocessing



What software alternatives are possible to use?

- Commercial
  - BrainVoyager
  - SPM MATLAB
  - Others



- FSL
- AFNI
- ANTs
- FreeSurfer



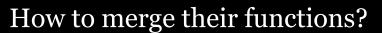












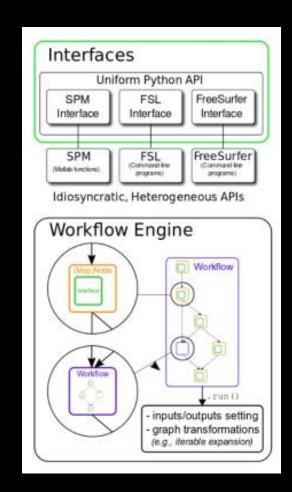


Python Nipype Library

### Python's Nipype Library



- It offers the opportunity to analyze images using a variety of different algorithms.
- Nipype allows to easily interact and combine tools from different neuroimaging software packages and facilitates interaction between these packages within a single workflow.
- Reduces the learning curve required to use different packages.
- Allows data to be processed faster by running it in parallel on many cores/machines.
- It is possible to organize the results in folders and delete any result that is not used avoiding storage problems.

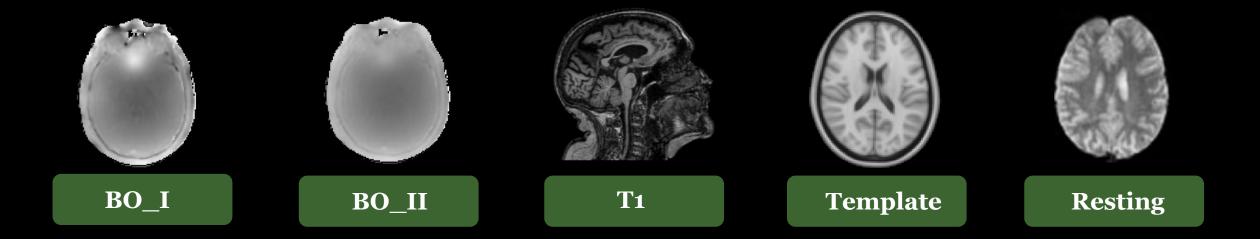


### Nipype Library



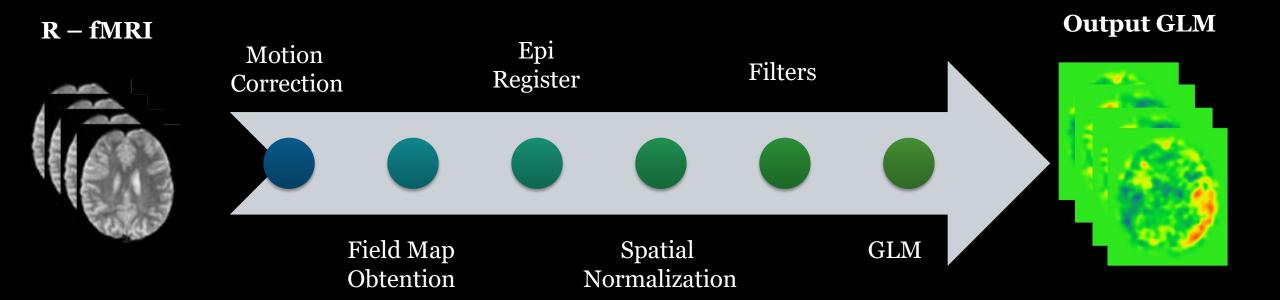
#### **Data Organization**

- Create the folder in which the results obtained for each subject will be stored and where the input images necessary for the operation of the pipeline will be stored.
- Input Images required by the pipeline:

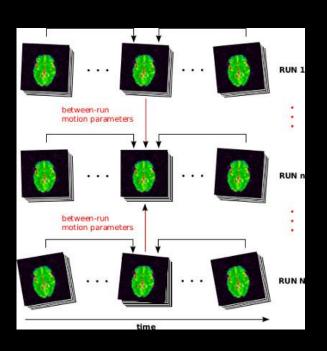


# Preprocessing





### Motion correction





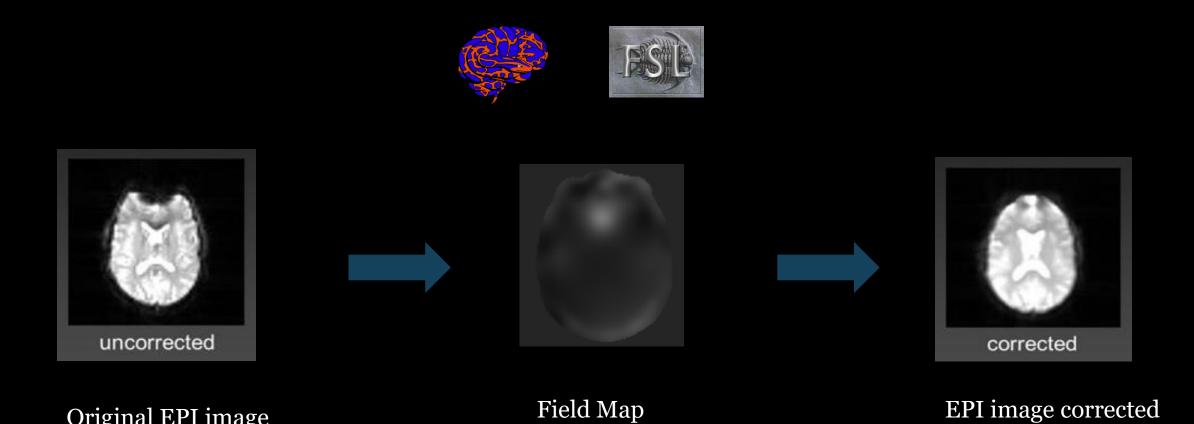


SpaceTimeRealigner

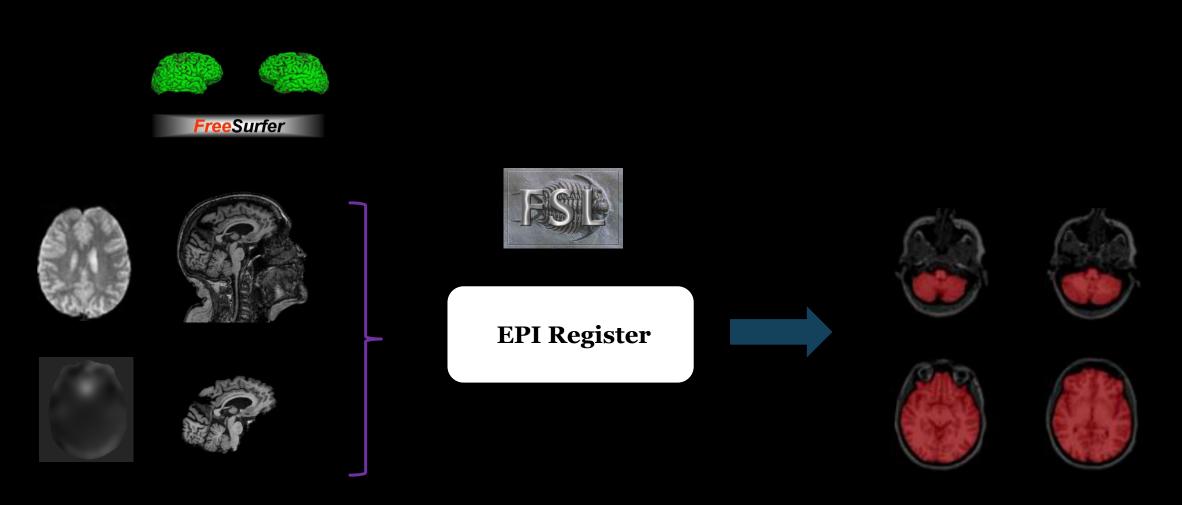


# Field Map

Original EPI image

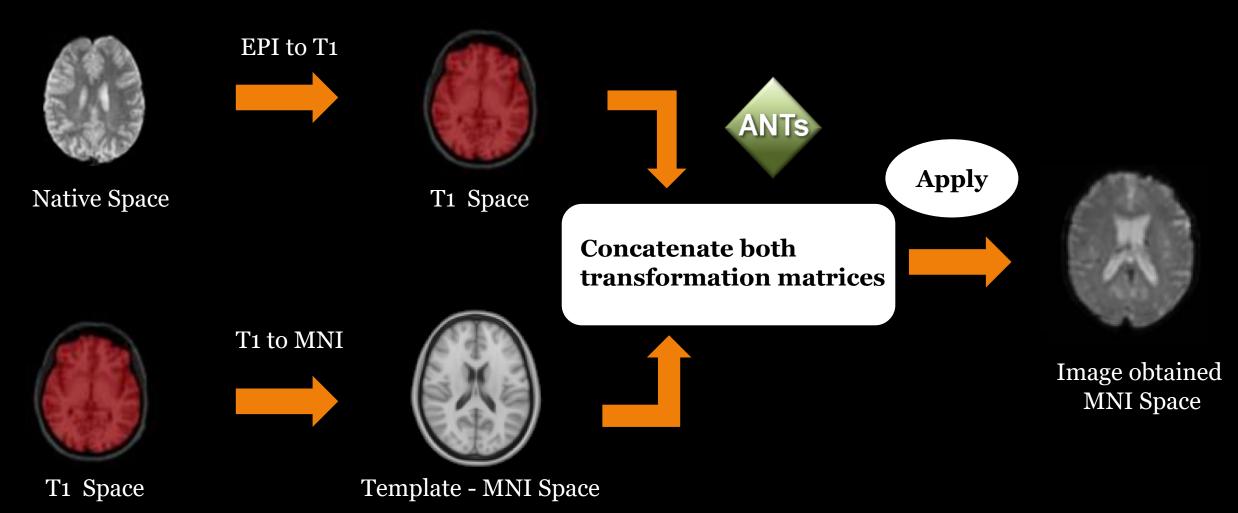


# Epi Register



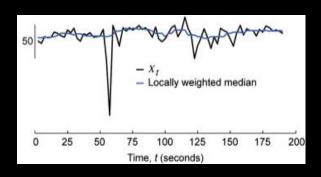
Native Space T1 Space

# Spatial Normalization



## Filters

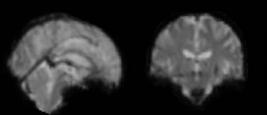
#### Original signal

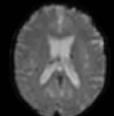






#### Original image

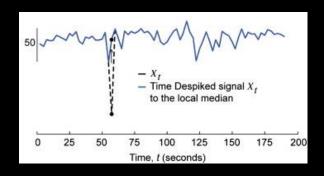




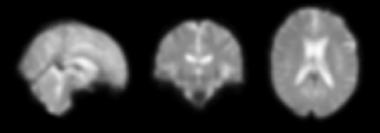




#### Despiked signal

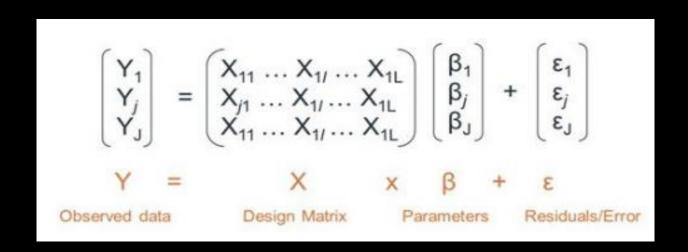


#### Smoothing

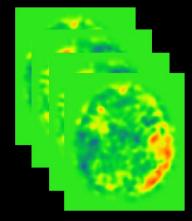


### General Linear Model

Y response in each voxel is modeled as a linear combination of predictors, stored in the columns of a design matrix X times  $\beta$ . Then, to eliminate the variability of these components, the residues from this model are assigned as the new voxel time series.



#### **Output GLM**



## Processing

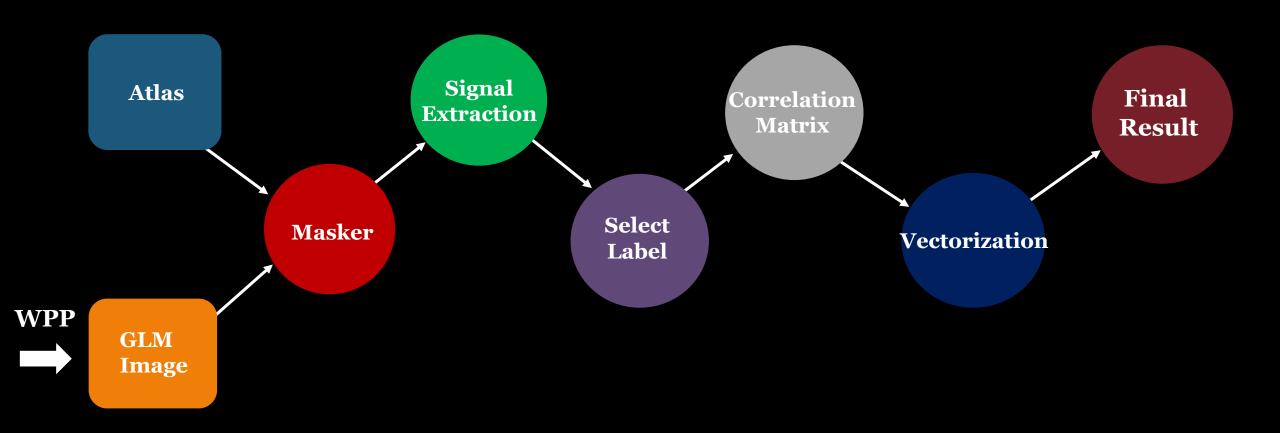


### Why fMRI processing is necessary?

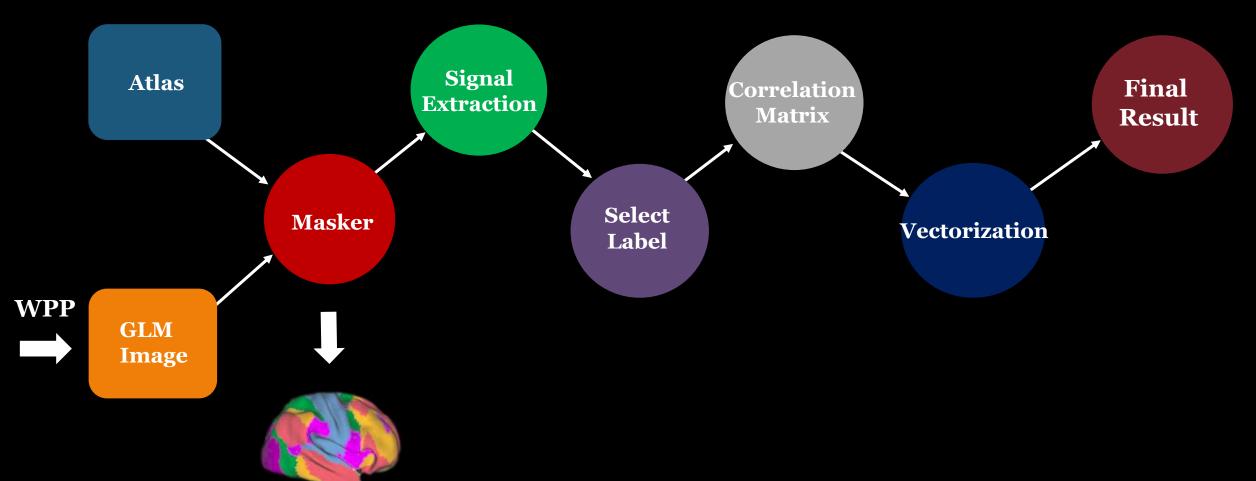
- It is not possible to obtain valuable information for analysis purposes in visual form.
- It is necessary to obtain correlation matrices in order to quantify the relationship between brain regions.
- The correlation matrix will allow a quantitative analysis of the degree of correlation for each region of interest.



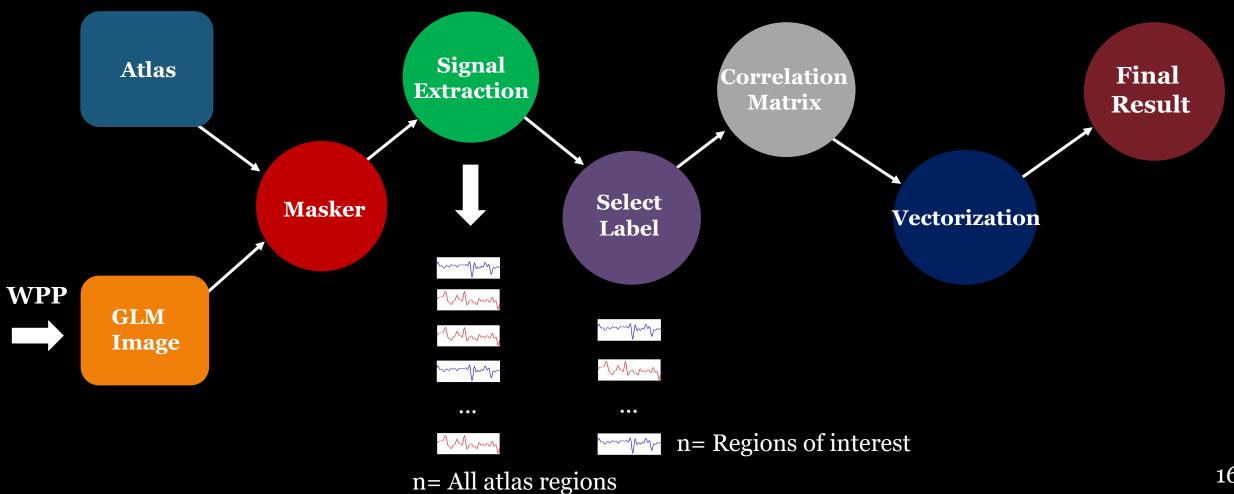




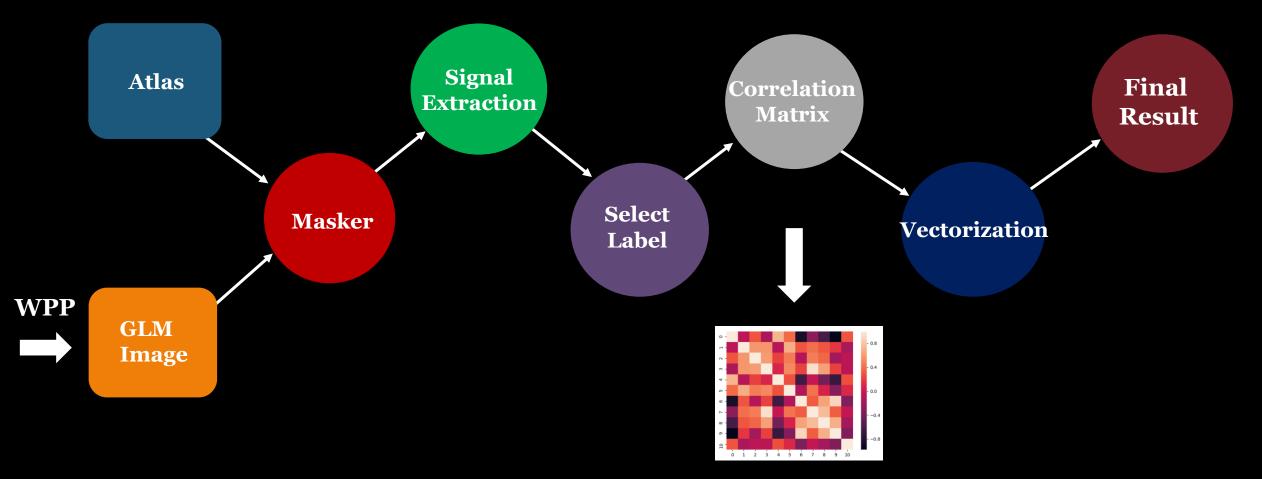




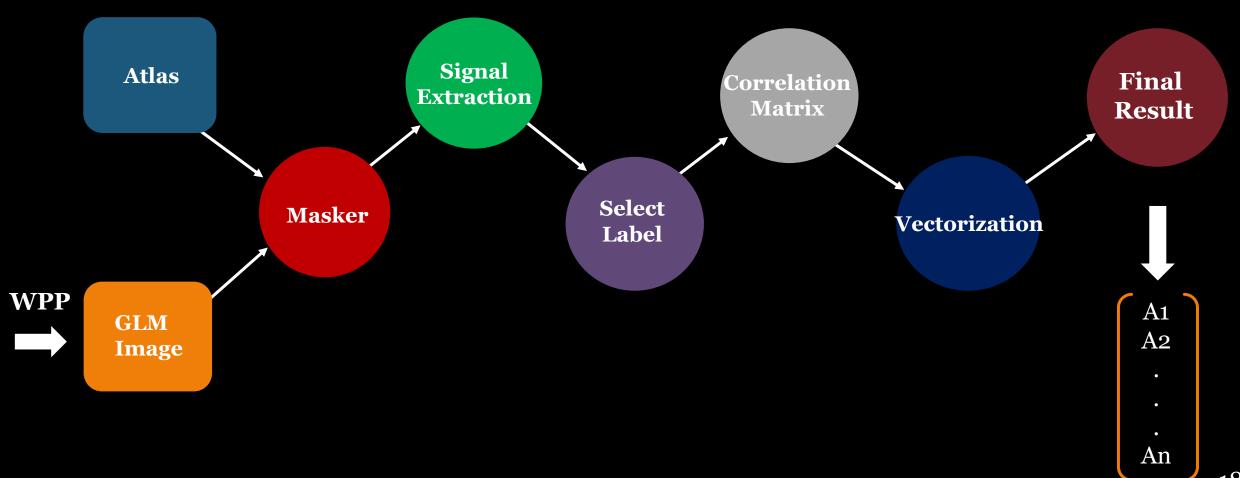












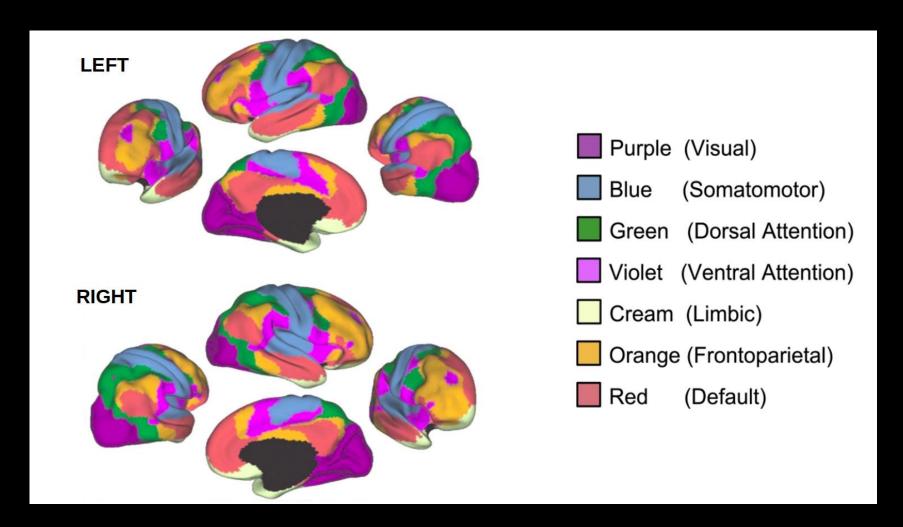
### Practical Case



- Two groups with 59 patients were analyzed. The first group is the control group (27 subjects) and the second group (32 patients) is composed of patients with mild cognitive impairment.
- The case of study is the analysis of the *Default Mode Network (DMN)*
- The DMN analysis will allows to evaluate if there are differences in the functional connectivity between both groups of patients analyzed.

### Default Mode Network

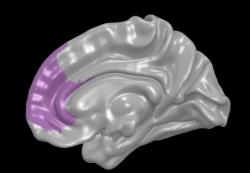


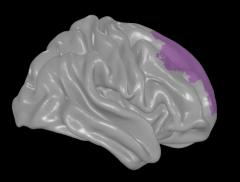


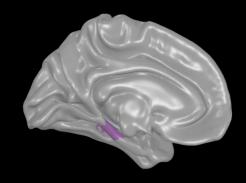
Reference: Network Cortical Parcellation (Thomas Yeo et al., 2011)

### Results

- It was found that there are differences in connectivity between the control group and the group with mild cognitive impairment.
- The difference is found between the left hippocampus and the right middle prefrontal cortex.
- The null hypothesis is rejected.
- There are less connectivity between regions in the group with mild cognitive impairment with respect to the control group.







## Practical Case



### Organization of tasks

	February	March	April	May	June
Research					
Field Map Obtention					
From EpiReg to GLM analysis					
Processing and Group Comparison					

# Practical Case



### **Economical Budget**

	Number	Costs	Total (€)
Image acquisition	59 subjects	400 € (per scan)	23.600 €
Personal	1 Person Per Month (PPM)	2500€	12.500 €
Other goods and services	-	-	1000 €
Direct costs	-	_	37.100 €
Indirect costs (21%)	-	-	7.791 €
Total costs	-	_	44.891 €

### Conclusions



- A preprocessing and processing pipeline capable of removing artifacts from the BOLD signal and obtaining correlation matrices using the individual strengths of open source fMRI software was implemented.
- The achieved pipeline can be executed in a standard PC or in a cluster of computers, in a single execution or simultaneously, being possible to analyze automatically as many patients as necessary.
- Its correct functioning was validated after the comparison of groups of patients, obtaining results that respond to the needs of the research project that motivated the realization of this project.