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

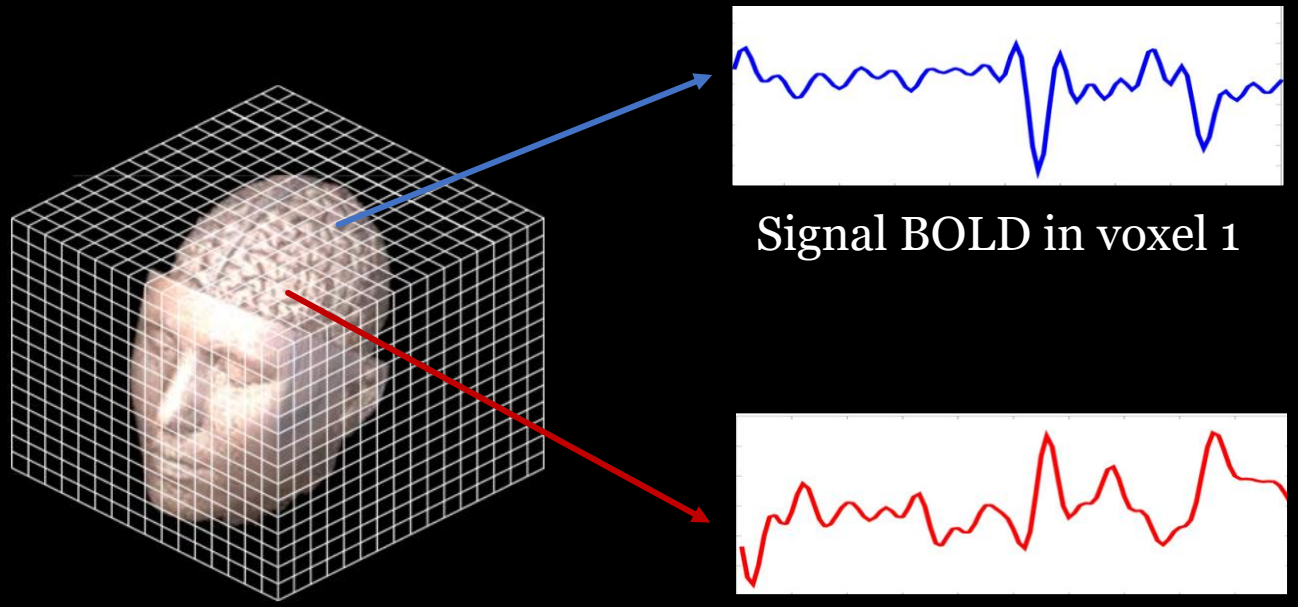
- The H2H project is carried out by a CNIC research group that aims to unravel the relationship between cardiovascular and neurocognitive diseases.
- The pipelines must be able to obtain correlation matrices to determine functional connectivity and the degree of correlation between brain regions.
- In 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.

Index of the presentation

- Introduction
- Preprocessing
- Processing
- Practical case
- Conclusions
- Future lines

Introduction

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



Magnetic Resonance Image

Signal BOLD in voxel 1

Signal BOLD in voxel 2

Synchronization in the activation of voxels.

Functional connectivity

Preprocessing

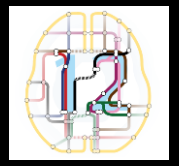
Why fMRI preprocessing is necessary ?

- 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

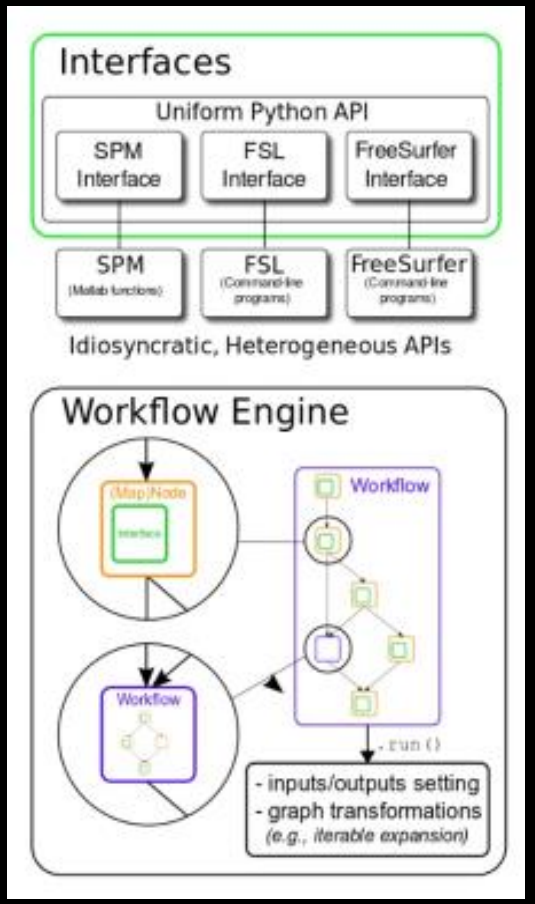


- Open source
  - FSL
  - AFNI
  - ANTs
  - FreeSurfer

How to merge their functions? → 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.



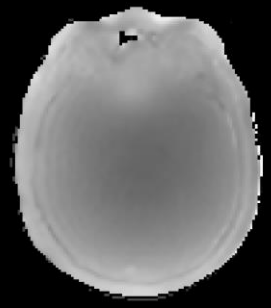
Nipype Library

Data Organization

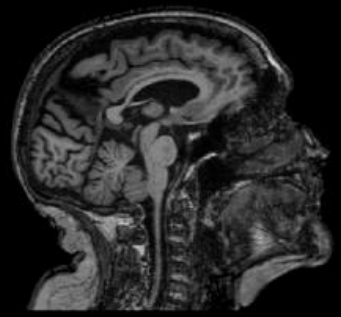
- Create the folder in which the results obtained for each subject will be stored and where the input images necessary for the operation of the pipeline will be stored.

- Input Images required by the pipeline:

BO_I

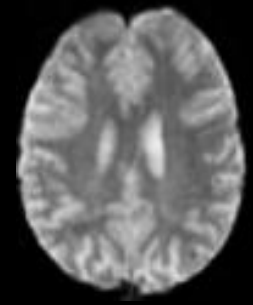


BO_II



T1

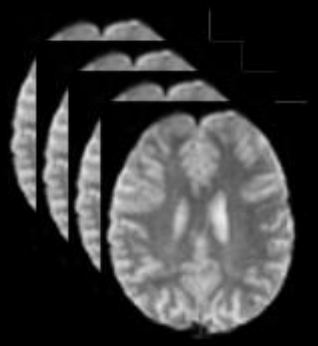
Template



Resting

Preprocessing

R – fMRI



Motion Correction

Field Map Obtention

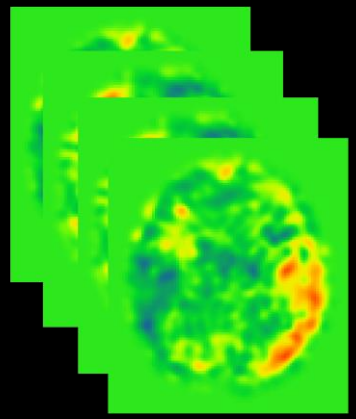
Epi Register

Spatial Normalization

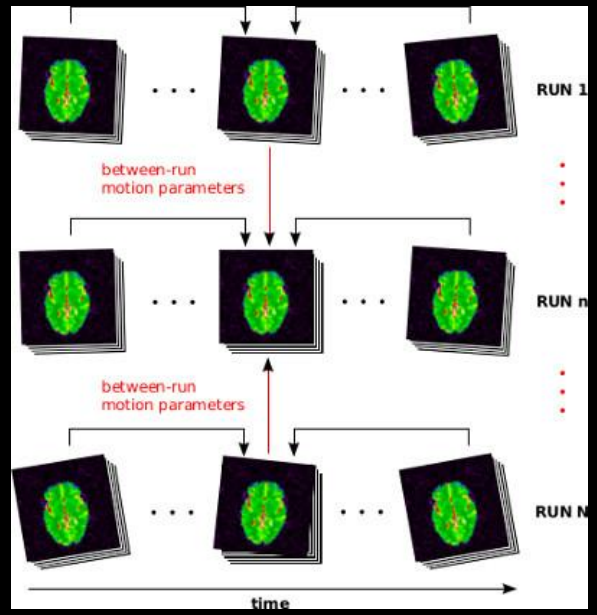
Filters

GLM

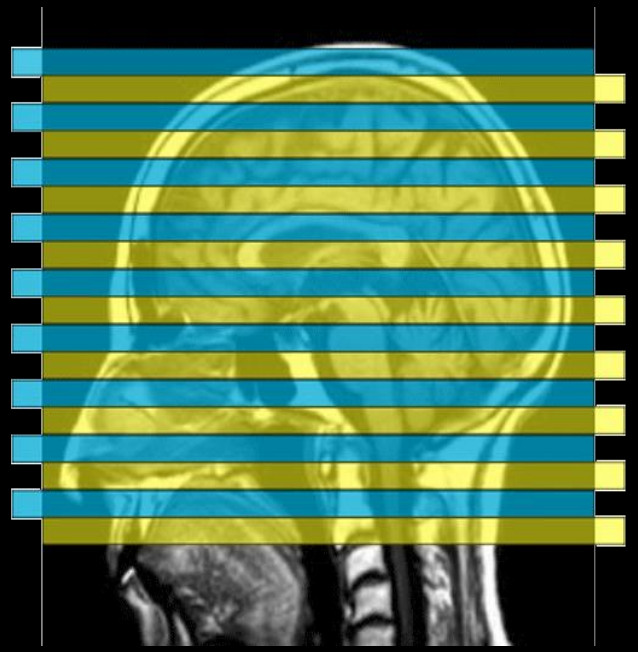
Output GLM



Motion correction



SpaceTimeRealigner



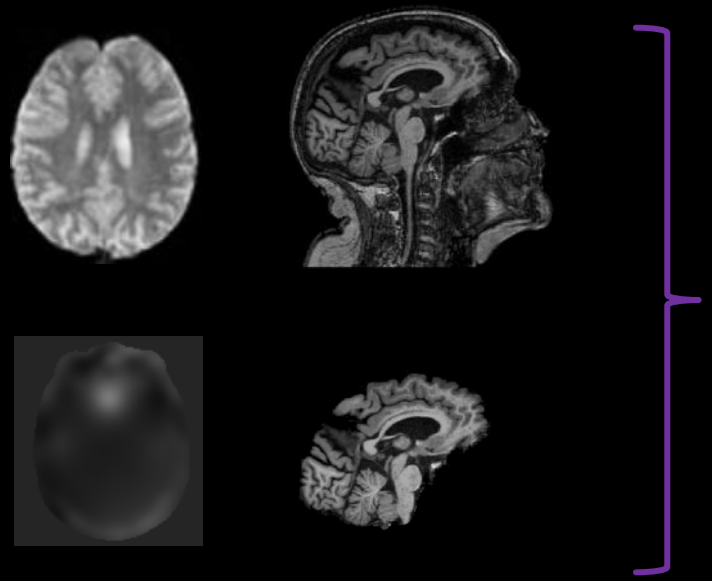
Field Map

Original EPI image

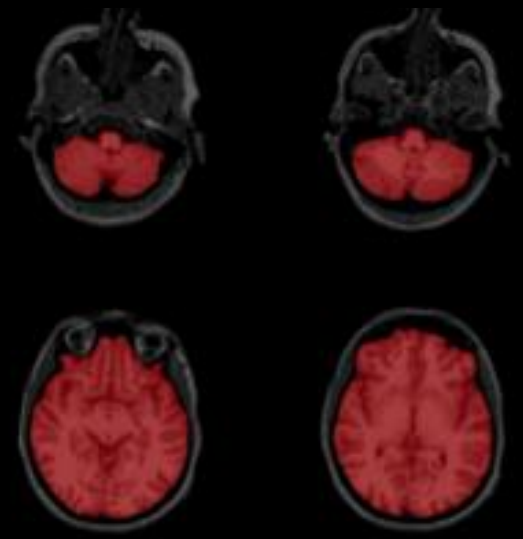
Field Map

EPI image corrected

Epi Register



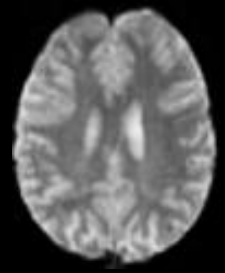
EPI Register



Native Space

T1 Space

Spatial Normalization



Native Space

EPI to T1

T1 Space

ANTs

Concatenate both transformation matrices

Apply

Image obtained MNI Space

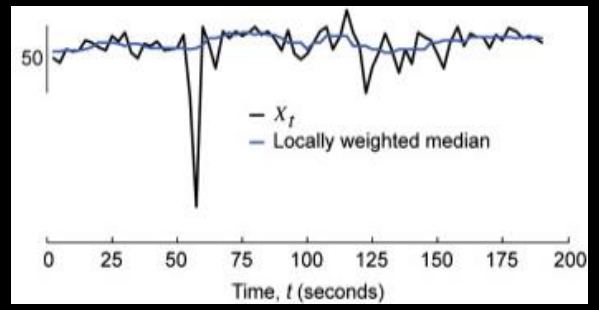
T1 Space

T1 to MNI

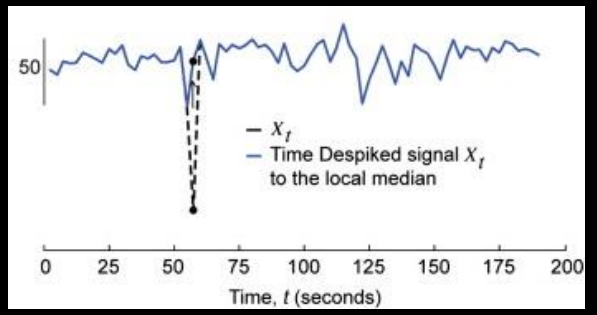
Template - MNI Space

Filters

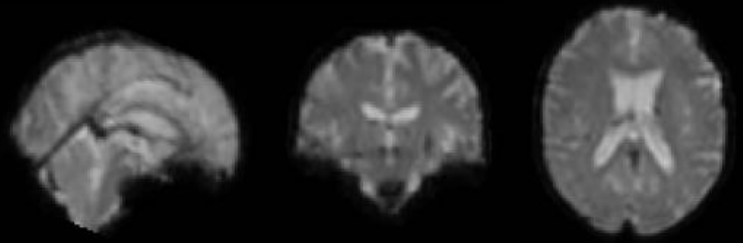
Original signal



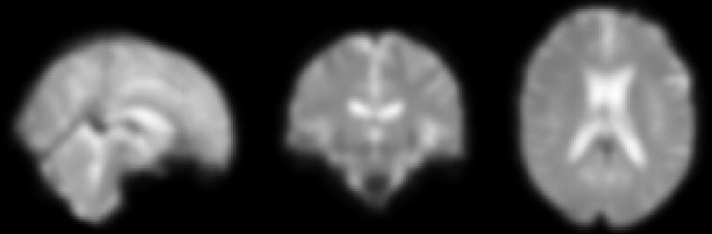
Despiked signal



Original image



Smoothing



General Linear Model

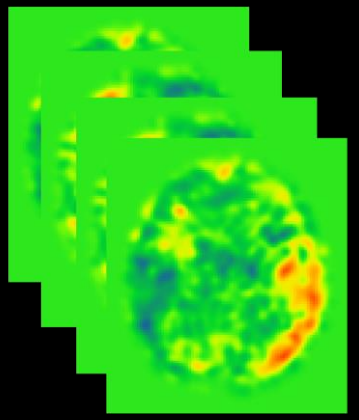
Y response in each voxel is modeled as a linear combination of predictors, stored in the columns of a design matrix X times β. Then, to eliminate the variability of these components, the residues from this model are assigned as the new voxel time series.

$$\begin{pmatrix} Y_1 \\ Y_j \\ Y_J \end{pmatrix} = \begin{pmatrix} X_{11} \dots X_{1l} \dots X_{1L} \\ X_{j1} \dots X_{1l} \dots X_{1L} \\ X_{11} \dots X_{1l} \dots X_{1L} \end{pmatrix} \begin{pmatrix} \beta_1 \\ \beta_j \\ \beta_J \end{pmatrix} + \begin{pmatrix} \varepsilon_1 \\ \varepsilon_j \\ \varepsilon_J \end{pmatrix}$$

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

Observed data | Design Matrix | Parameters | Residuals/Error

Output GLM

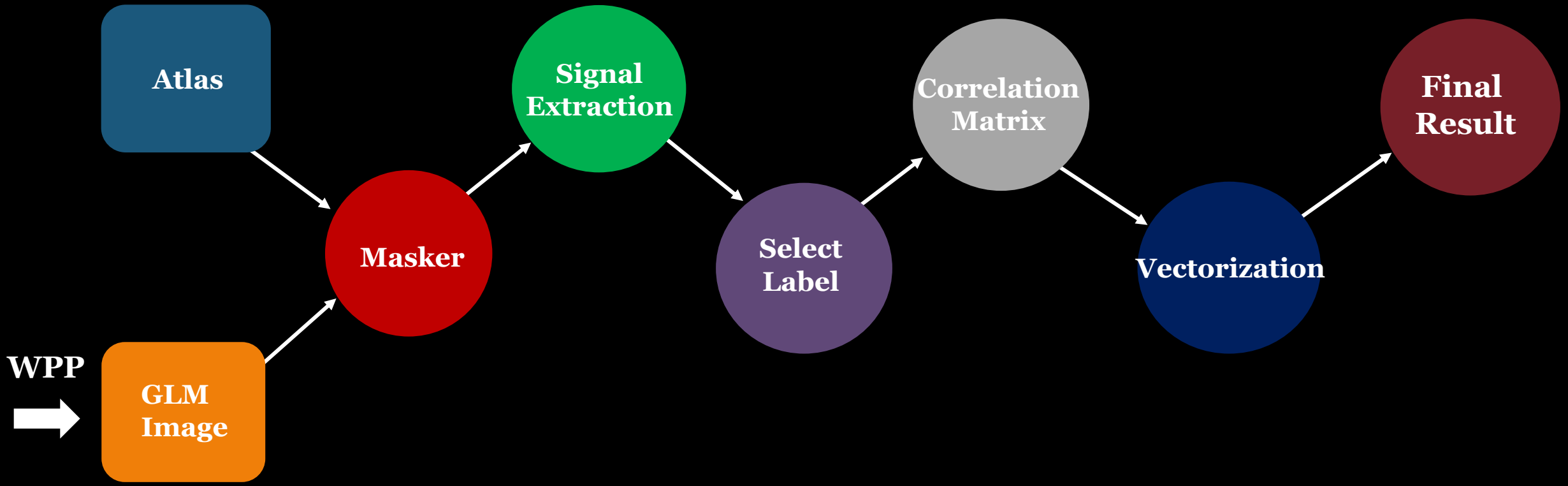


Processing

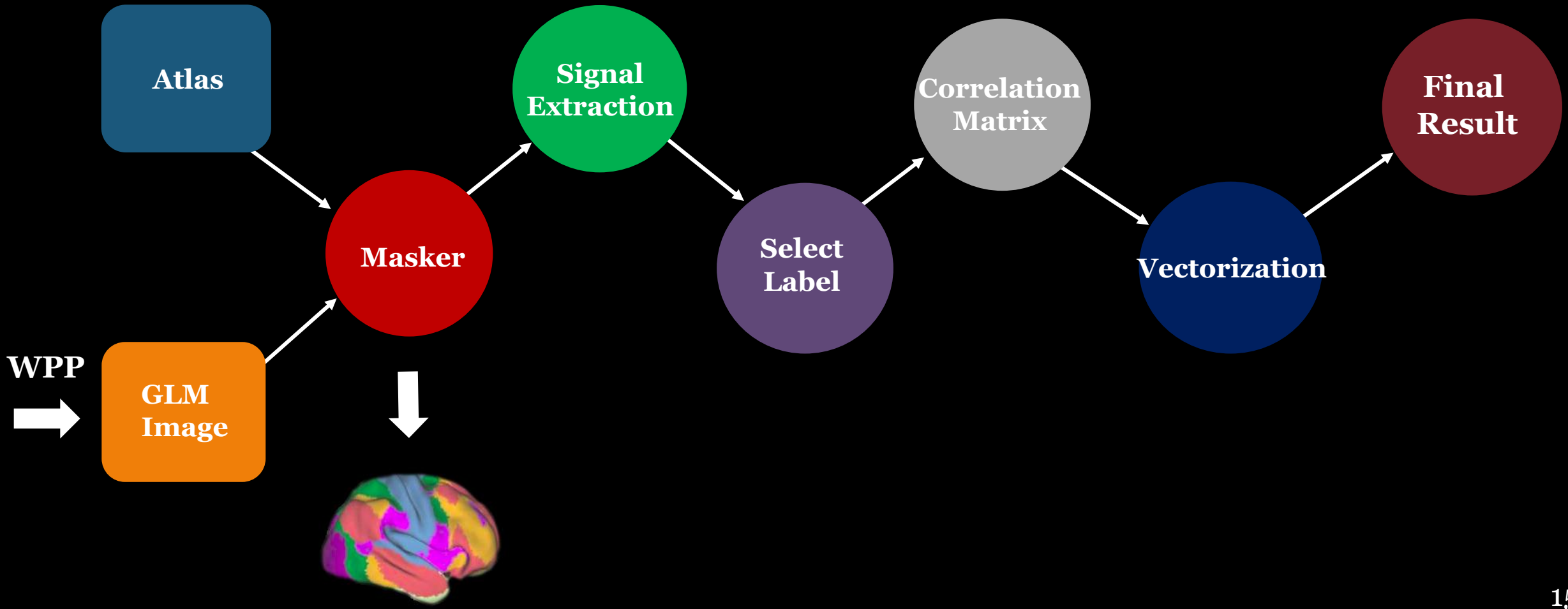
Why fMRI processing is necessary ?

- 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.

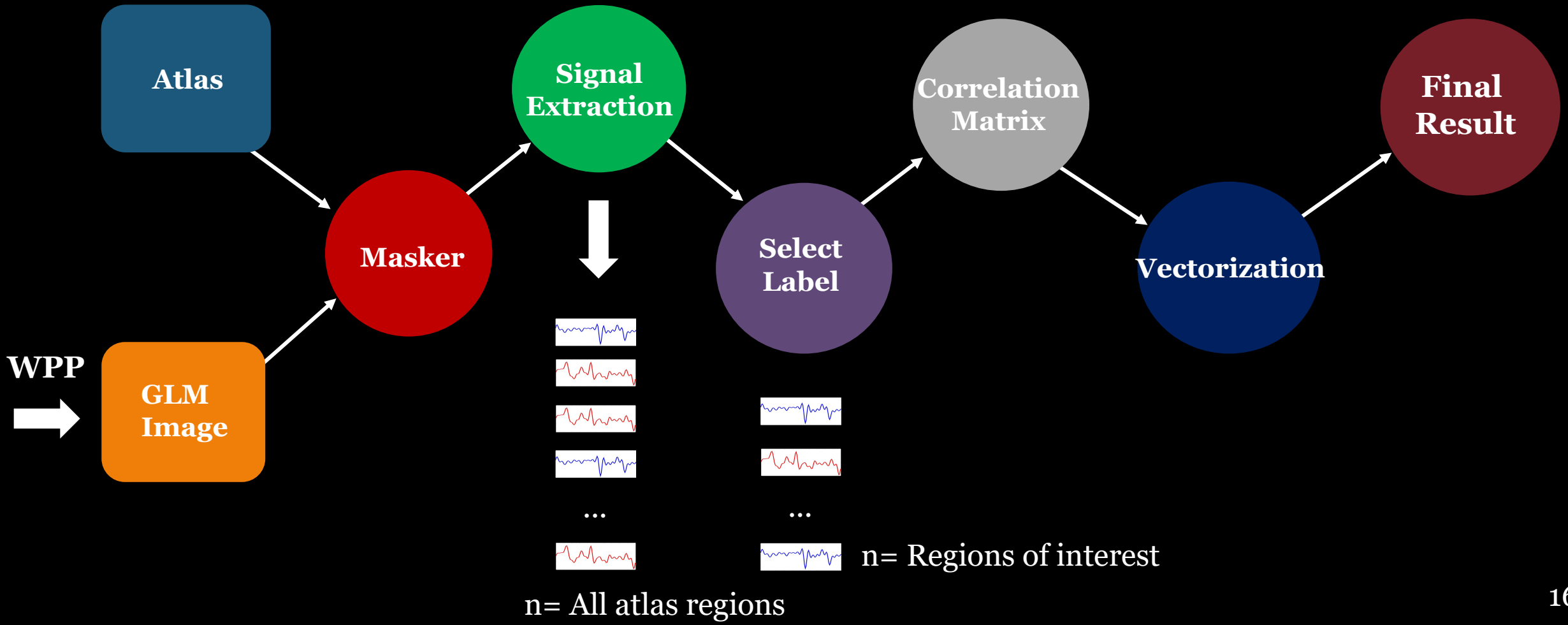
Workflow for processing



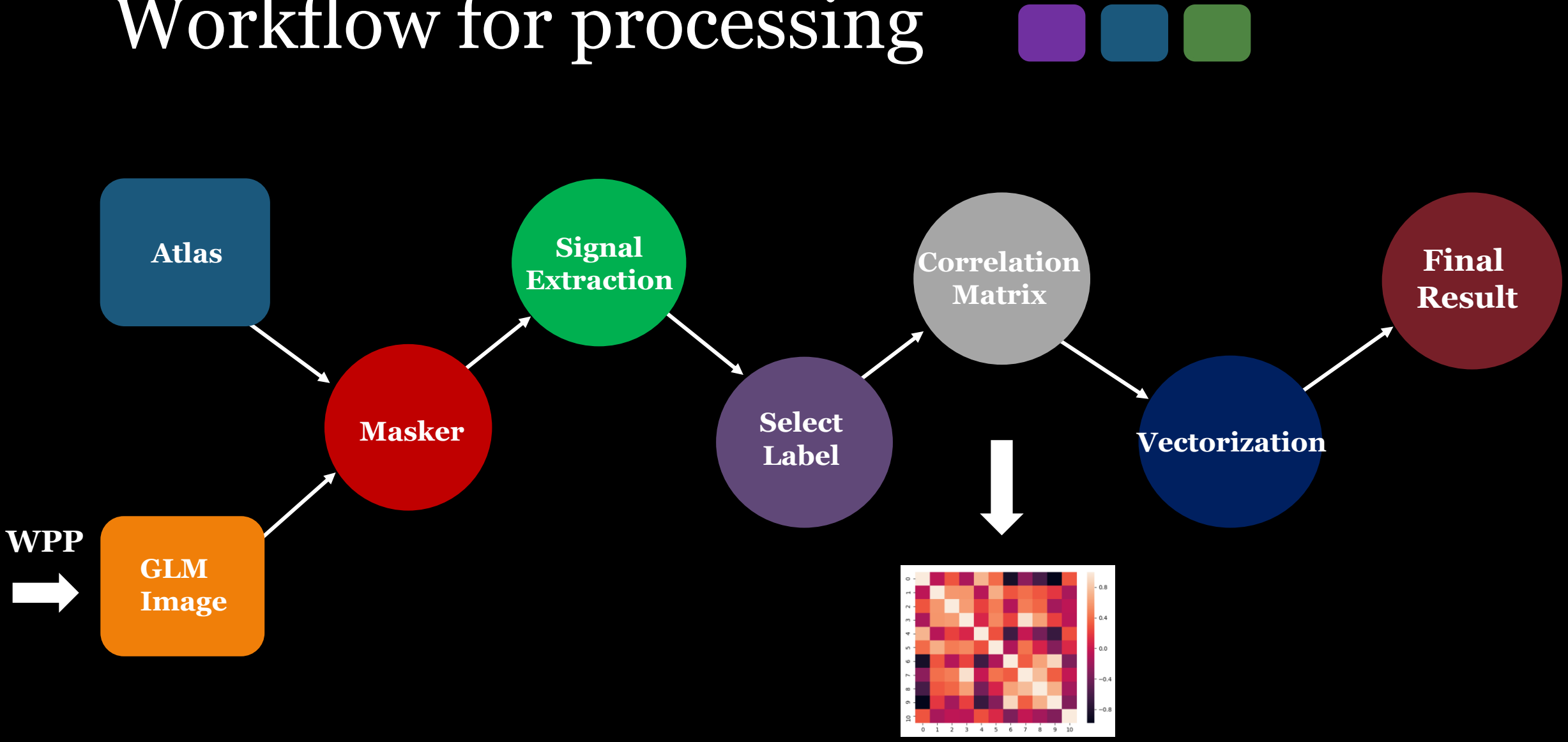
Workflow for processing



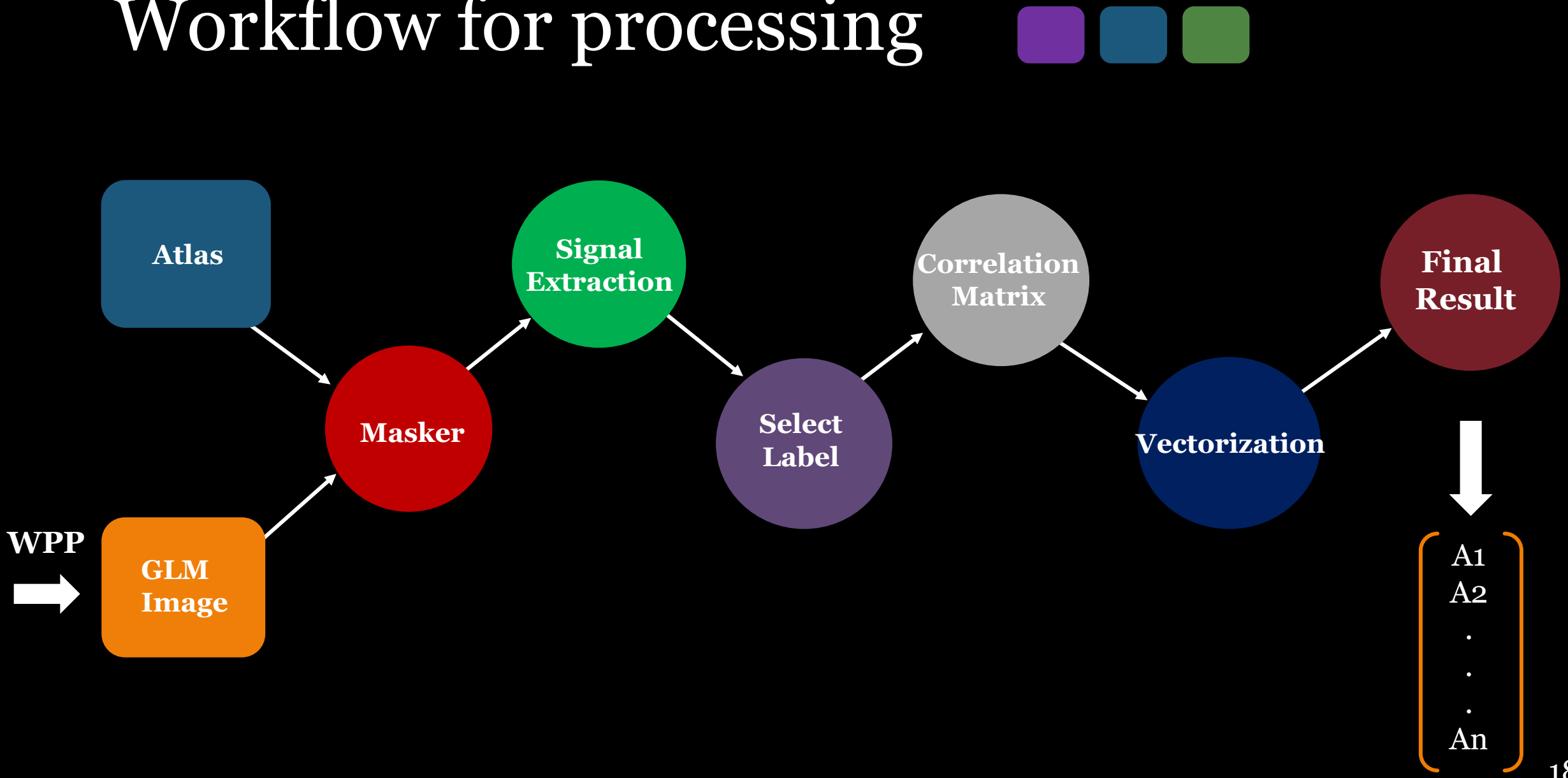
Workflow for processing



Workflow for processing



Workflow for processing



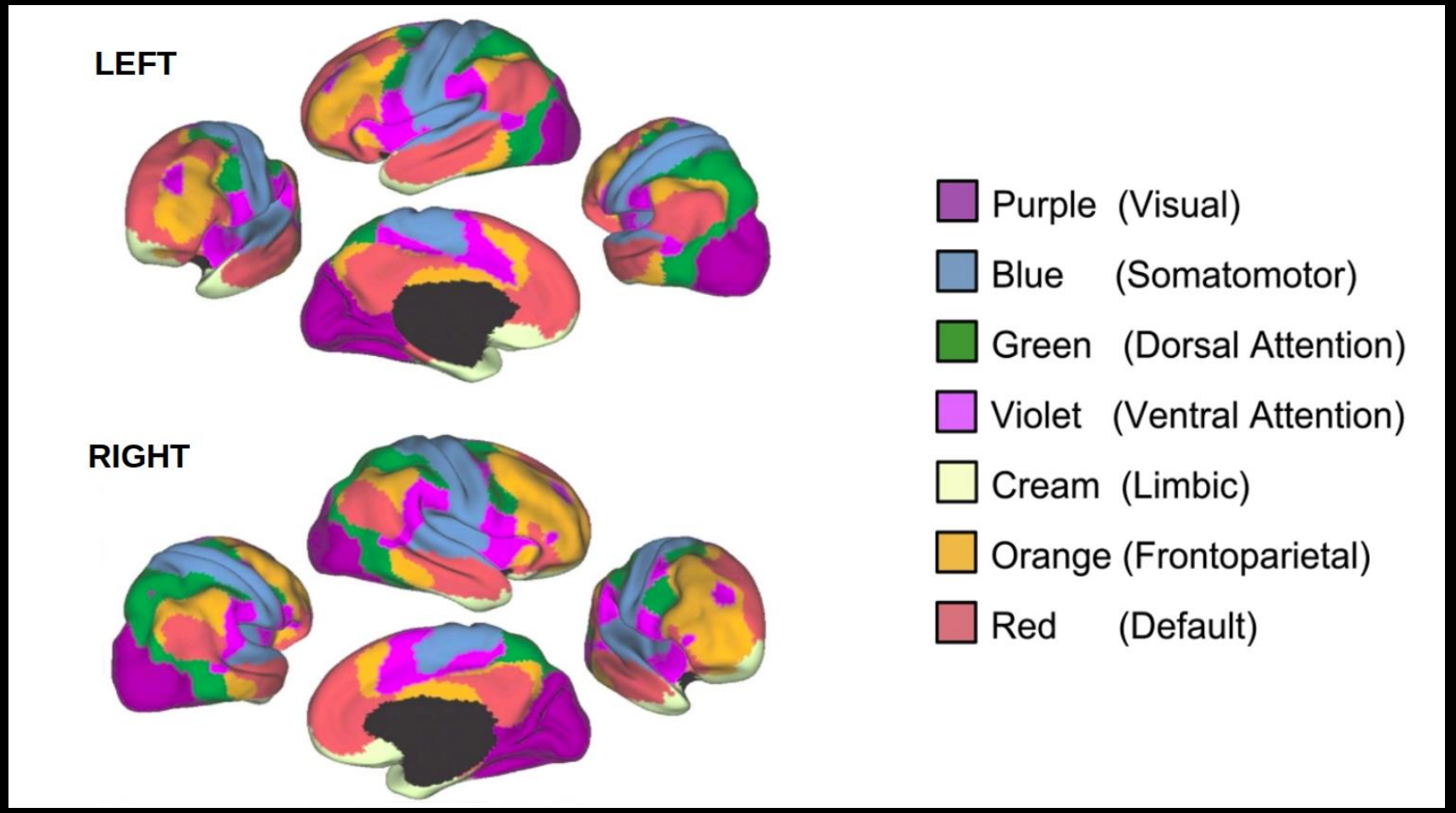
Practical Case

- 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.

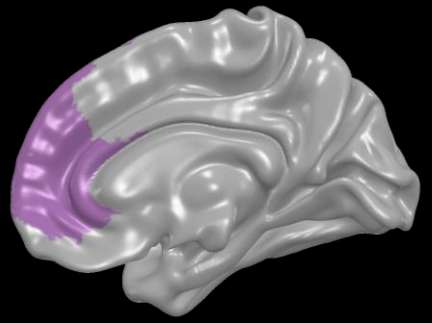
Default Mode Network

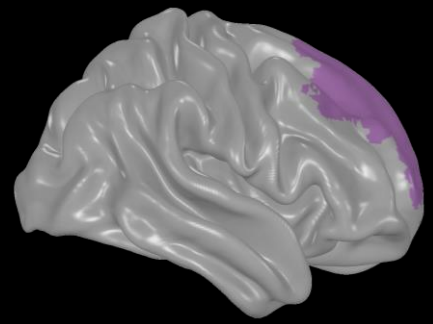


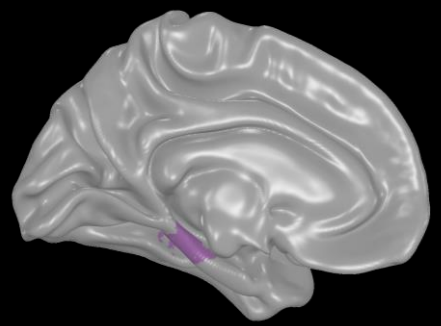
Reference: Network Cortical Parcellation (Thomas Yeo et al., 2011)

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.







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.