

# A Toolbox on Analysis of Functional Connectivity in BOLD fMRI

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## Objectives

To create a Functional Connectivity (FC) toolbox with a graphical user interface (GUI) which computes connectivity for 'n' Regions of Interest (ROIs) given as in input. The project aims full analysis including statistics and efficient data handling.

## Introduction

To measure the difference in interaction between the different regions of the brain among the groups of population, the FC analysis becomes important. Hence, it necessitates the development of easy to use and highly optimized FC tools. There have been many tools in the past such as CONN [1], C-PAC [2], REST etc which perform seed to whole brain FC with the support of parallel computing but none of them deals with analyzing groups of Regions of Interest (ROIs) nor perform collective False Discovery Rate (FDR) for all ROIs. So, in order to automate this analysis parallelly and making this process faster, we come up with a highly optimized FC toolbox with an end-to-end graphical user interface (GUI) which computes connectivity for 'n' ROIs as given in input file.

We employ Nipype [3] methods for running the preprocessing and correlation workflow parallelly and later use python multiprocessing library to parallelize the FDR correction. Keeping the target audience to be neuroscientists and non-computer engineers, who require such tools for saving their time and handling and interpreting the large amount of the data in a better manner, we also perform the statistical analysis (including t-test on combinations of groups, collective and separate ROI FDR correction, Fisher transformation).

## Methods

We output the R-dimensional (where R is number of ROIs) t-value map file, correlation difference file, p-value and q-value (adjusted p-values) map files in log format. The pipeline involves asking the user to fill the inputs in the GUI, validating the inputs, preprocessing the files, finding the correlations for ROI mean to whole brain [4], statistical analysis and then doing FDR correction.

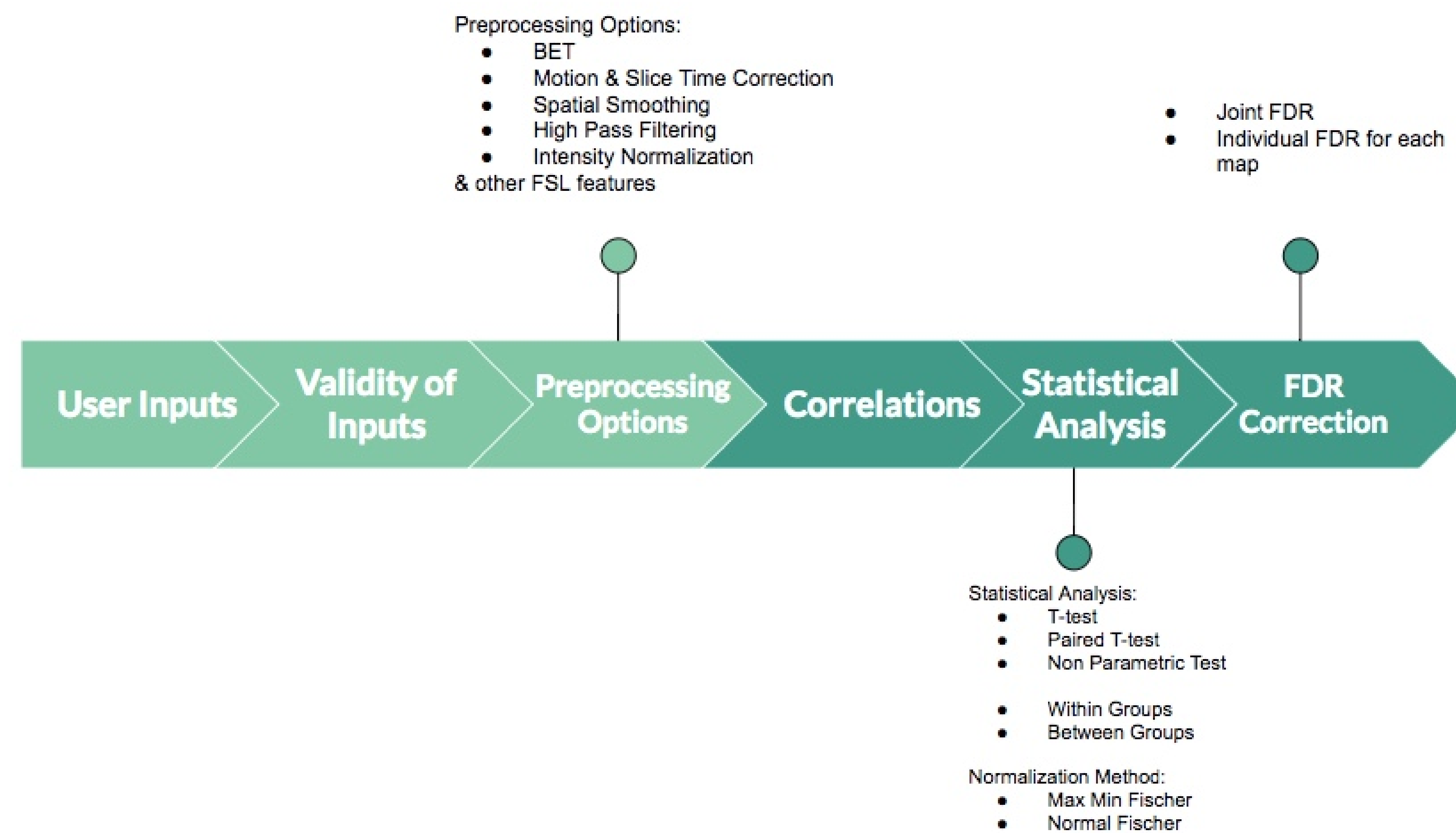


Figure 1: Pipeline for Functional Connectivity Analysis along with the options

## Important Result

The toolkit speeds up the preprocessing by a factor of 5 and parallelized the jobs to a great extent.

## Results

On a 3.5 GHz Intel Xeon processor with 8 cores, the complete preprocessing of subjects in 3mm (including registration) took 2.4 minutes per subject as compared to FSL which took approximately 13 minutes per subject. Computing correlations for 274 seed regions took 5.8 seconds per subject with the whole analysis on 158 subjects (79 per group) completing in 6.85 hours. The toolkit was validated using NYU Cocaine resting state dataset with 27 subjects in cocaine group and 23 controls. We tested the difference in region-wise FC in addicted versus the normal subjects. For 274 ROIs, at false discovery rate (FDR) of 10%, we found increased connectivity of cerebellum with occipital regions. We also found precentral gyrus overconnected with frontal lobe and underconnected with cuneal region. The results were consistent with the ones obtained from the custom home grown code in our lab.

## Discussion

Since the design of the FC toolbar is modular, the FC engine can be improved by this technique. Being standalone, it can be used to increase the speed of the whole program, remove the redundant processes to a great extent and since it will be made open source, this tool will be very helpful for the neuroscience community.

## References

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