

# Quantification of the alteration in the Resting State Networks for measuring brain pathologies and diseases

Ibai Díez<sup>1,2</sup>, Asier Erramuzpe<sup>1,2</sup>, Sebastiano Stramaglia<sup>1,3,4</sup> and Jesus M Cortes<sup>1,2,4,\*</sup>

1. Computational Neuroimaging Lab. Biocruces Health Research Institute. Cruces University Hospital, Barakaldo, Spain

2. Quantitative Biomedicine Unit. Biocruces Health Research Institute. Cruces University Hospital, Barakaldo, Spain

3. Dipartimento di Fisica, Universit degli Studi di Bari and INFN, Bari, Italy

4. Ikerbasque, The Basque Foundation for Science. Bilbao, Spain

\*Correspondence to [jesus.cortesdiaz@osakidetza.net](mailto:jesus.cortesdiaz@osakidetza.net)

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*Abbreviations: RSN (Resting State Network); PICA (Probabilistic Independent Component Analysis); BOLD (Blood-Oxygen-Level-Dependent); fMRI (functional Magnetic Resonance Imaging); rs (resting state);*

## **Brief summary:**

Resting State Networks (RSNs) are the result from the coherence across brain regions in the high-amplitude ultra-slow (0.1 Hz) fluctuations in the Blood-Oxygen-Level-Dependent (BOLD) signal acquired with resting state functional magnetic resonance imaging (rs-fMRI) [1,2]. The RSNs are universal, meaning that, beyond individual brain differences, they emerge at rest in all healthy subjects. This universal behavior in healthy brains has pushed forward the strategy for quantification of the RSNs alterations in brain pathological conditions to find for new neuroimaging markers for both mental and cognitive disorders. Indeed, alterations in the RSNs have been found in patients with deficit of consciousness after brain traumatic injury [3-5], in Alzheimer disease [6] and schizophrenia [7,8]. Based on these results, it is expected that RSNs alterations occur as well for other brain disorders and diseases. This is the main motivation of this project, given an input rs-fMRI data of a specific patient, to develop new and efficient methods capable to quantify the precise amount of alteration (respect to control) for each of the resting networks.

## **Technical details:**

Since a signal processing point of view, the RSNs are corresponding with the different spatial components obtained by Independent Component Analysis (ICA) of the rs-fMRI time-series. Thus, given an input matrix of rs-fMRI with dimensions time points \* voxels number, after ICA we get two matrices, one with dimensions time points \* components number and other with dimensions components number \* voxels number. A big technical problem is the very large dimensionality in the rs-fMRI data (a whole-brain division of about  $10^5$ - $10^6$  voxels number); thus to apply ICA one needs first to reduce dimensionality via Principal Component Analysis (PCA) or alternative methods. In concrete, we are suggesting here to apply the Probabilistic Independent Component Analysis (PICA) method for rs-fMRI [9], plugged-into the popular neuroimaging software FSL [10].

In [2], they apply PICA to get 8 different components or RSNs, all having a corresponding cognitive function: the medial visual, the lateral visual, the auditory,

the sensory-motor, the default mode, the executive control, the dorsal visual right and the dorsal visual left. In this project, we will study these same 8 components.

The control rs-fMRI data will be obtained from the 1000 Functional Connectomes Project [11], in which there are available rs-fMRI data from healthy subjects. This will allow for the construction of spatial templates corresponding to the healthy RSNs [12], as well as to evaluate the dispersion of RSNs around the template RSNs in the population of healthy subjects, evaluated in terms of the distribution of the spatial correlation coefficient between the RSN of each healthy subject and the corresponding template.

At the second stage, we will make use of the database from Alzheimer Disease Neuroimaging Initiative (ADNI), in which there are available rs-fMRI data belonging to AD patients [12] at different disease stage (from very early to mild cognitive impairment to AD). For a quantification of the RSNs alteration in the brain pathology, we will calculate the spatial correlation between the RSNs in patients and the healthy RSNs templates, to eventually assess to what extent the RSNs alteration might be correlated with the behavioral index of the disease (eg., one of the clinical assessments provided by ADNI is the ADAS test score, quantifying the seriousness of the pathology at the cognitive level).

The expected output of the project is a software that, given the input data of the rs-fMRI of a specific patient [14], return a number indicating the alteration level for each of the different 8 components, ie., the spatial correlation between each RSN of that specific patient and its corresponding RSN template.

Finally, a possible extension of this project might be to construct a regression machine to predict the stage of the disease from the rs-fMRI input data, previously trained to make predictions based on the 8 values of the spatial correlations of RSNs.

#### **Required Experience:**

Courses on Biomedical Engineering at MSc Level.

#### **References:**

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- [10] <http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/MELODIC>
- [11] [http://www.nitrc.org/projects/fcon\\_1000/](http://www.nitrc.org/projects/fcon_1000/)
- [12] The precise method to obtain each of 8 different components is first to use the template obtained in [2] to then apply spatial regression to obtain each of these components. Once detected the desired component, we can compute the correlations between all the voxels time series and the chosen component to estimate how much each voxel is correlated with that component.
- [13] <http://adni.loni.usc.edu/data-samples/>
- [14] The student will get support from the Computational Neuroimaging Group in Biocruces for preprocessing the input data, including motion correction, slice-time correction, brain extraction, smoothing, intensity normalization, band pass filter, detrend, transformation between structural and functional information, regress out white matter/cerebrospinal fluid/global signal/head motion, transform fMRI into MNI space, etc.