MULTIMODAL IMAGING BRAIN CONNECTIVITY ANALYSIS TOOLBOX

Luis Miguel Lacerda[1,2], André Santos Ribeiro[2,3], Nuno Andre da Silva[2,4], Rafael Neto Henriques[2,5], and Hugo Alexandre Ferreira[2]

[1]Centre for Neuroimaging Sciences, Institute of Psychiatry, King's College London, London, Denmark Hill, United Kingdom, [2]Institute of Biophysics and Biomedical Engineering, Faculty of Sciences of the University of Lisbon, Lisbon, Portugal, [3]2Centre for Neuropsychopharmacology, Division of Brain Sciences, Department of Medicine, Imperial College London, London, London, United Kingdom, [4]Forschungszentrum Jülich GmbH, Institute of Neuroscience and Medicine - 4, Jülich, Germany, [5]Cognition and Brain Science Unit, Medical Research Council, Cambridge, United Kingdom

TARGET AUDIENCE- Neuroimaging researchers and clinicians interested in brain connectivity and/or in multimodal/hybrid MR-PET imaging.

PURPOSE – In recent years, connectivity analyses of multimodal neuroimaging data have increased our understanding of the organization of large-scale structural and functional brain networks [1,2].This information plays an important role in the comprehension of the effect of several diseases, e.g. Alzheimer's Disease or Parkinson's Disease, in the human brain structure and networks. However, the analysis of such multimodal data (e.g. MRI and PET) is time consuming and it is often performed in a non-automatic manner. Multimodal Imaging Brain Connectivity Analysis (MIBCA) toolbox is a fully automated all-in-one connectivity analyses toolbox that offers pre-processing, connectivity and graph theoretical analyses of multimodal images such as T1-weighted structural MRI (sMRI), diffusion MRI (dMRI), functional MRI (fMRI), and PET. In this work we aim to help establishing the backbone for a solid multimodal neuroimaging analysis approach that extracts relevant information from different techniques and present some applications of the tool. Moreover, MIBCA also provides different visualisation tools for a better comprehension of the complex information generated with the toolbox.

METHODS – MIBCA was developed in MATLAB environment and pipelines different neuroimaging procedures and softwares. MIBCA's framework can be identified in Figure 1 and represents the procedure for one subject, which is naturally extended in the tool to multiple tasks that run in parallel. The first steps involve pre-processing whichever kind of data is going to be analysed as protocols are fully adapted to all techniques currently used in the clinical setting. Particularly, each subject's structural image is corrected for intensity normalization and registered to an atlas for further extraction of specific metrics, dMRI data are motion and eddy current corrected; fMRI undergoes motion correction, Gaussian smoothing, intensity normalization and temporal filtering; and PET images are also smoothed with a customized kernel. All images undergo non-brain removal .The second step of the framework consists in extracting different metrics from the aforementioned image modalities, which have already been pre-processed. Cortical thickness (CT), surface area (SA) and gray matter volume (GMV) measures (obtained from sMRI) are computed for each region calling Freesurfer functions [3]. Tractography data is obtained via Diffusion toolkit software [4] and fed into an in-house built algorithm to calculate the number of fibres between pairs of ROIs. The same algorithm is used to isolate resting-state fMRI and PET timeseries for specific ROIs. All metrics can then be used to generate connectivity matrices. CT, SA and GMV matrices, which depict ratios for each pair of regions, can be calculated. Structural connectivity matrices (s-CM) are obtained by computing the number of tracts between each ROI pairs. Functional connectivity matrices (resting state-fMRI and PET) are calculated by the partial correlation algorithm applied to pairs of regions. Additionally, effective connectivity matrix (e-CM) can also be calculated by applying Granger causality to fMRI data. Combined matrices, such as structural+functional or structural+effective, can also be computed depending on the scientific/clinical hypothesis to be tested. Finally, matrices can be further evaluated using the node degree, cluster coefficient, characteristic path length and small-worldness indexes derived from the Network Theory [5]. Connectivity and network metrics can then be presented in the textual form or in the form of matrices, connectogram or 3D graphs.
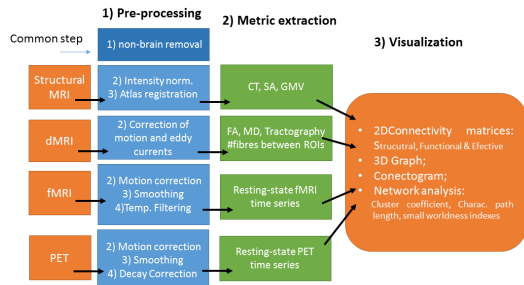

Figure1. MIBCA's framework is identified and divided into three steps: pre-processing, metrics evaluation and visualization
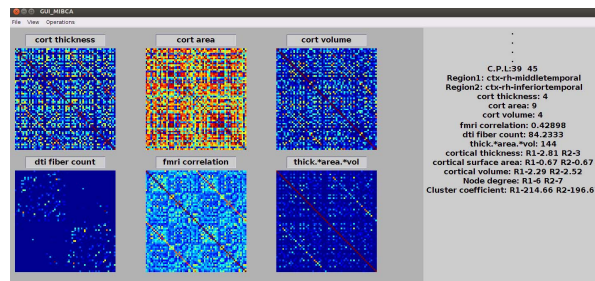

Figure2. MIBCA generates several connectivity matrices based on the hypothesis that is being tested.

RESULTS AND DISCUSSION – The MIBCA toolbox was developed and tested with multimodal data (sMRI, dMRI, fMRI and PET) obtained for 9 subjects from ICBM database. Figure 2 shows several connectivity matrices obtained for the 9 subject group. Figure 3 depicts the connectogram and the 3D graph visualization which includes textual data from several imaging and network metrics. Known aspects of brain connectivity were confirmed and it was shown that the approach has the potential to provide new insights into the relation between brain structure and function via the combination of multiple connectivity matrices and network metrics.

CONCLUSION - We have introduced a flexible and automatic multimodal approach for the analysis of brain connectivity that can integrate information from different image modalities. While bridging the gap between the high numbers of packages and tools widely available over the neuroimaging community, including pre-processing, connectivity and graph theoretical analyses in one toolbox, MIBCA also offers different visualization tools to a better understanding of the human brain. This is also a request from the neuroimaging community where the number of multi-modal systems available worldwide (e.g. MR-PET) increased considerably in the last two years.

REFERENCES – [1] Van den Heuvel et al, HBM.2009, 30(10), 3127–41; [2]ICBM database. (2013.) [3]. Fischl, B. Neuroimage (2012)., 62(2): 774-781.; [4]. Wang, R. (2007). Diffusion Toolkit and Trackvis; [5]. Rubinov, M. et al NeuroImage. (2010), 52(3), 1059–1069.
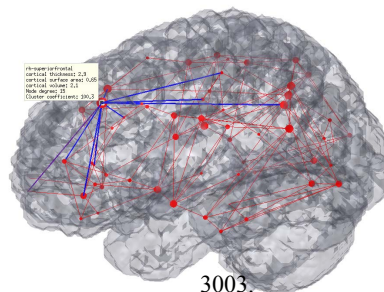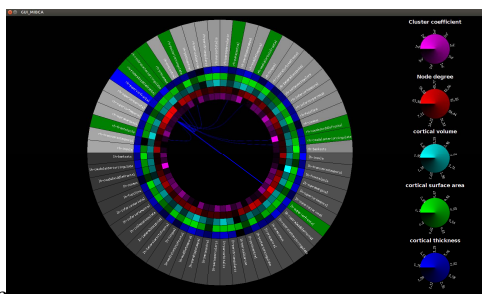
Figure3. Illustration of the 3D graph visualization tool. A brain mask is overlayed with nodes of interest. For the chosen node relevant information is presented as well as the connected regions. A conectogram is also shown.