Prediction of Vascular Dementia brain in distinct frequency bandwidths with whole-brain functional connectivity patterns

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Introduction: Vascular Dementia (VaD), also called multi-infarct dementia (MID), is one of the most common types of dementia, second only to Alzheimer's disease. It is typically characterized by the sudden onset and "stepwise" progression of symptoms that include forgetfulness, difficulty with speech and/or language, and balance. Due to its high incidence, VaD gets great attention by society. However, we know little about the neuron ensemble behind. Recently, multivariate pattern analysis (MVPA) methods, such as Support Vector Machines (SVM), have been explored in neuroimaging with the aim of categorical predictive classification of individual functional brain scans (e.g. Control vs Patient) [1]. Here we use SVM method to predict the VaD brain states from the BOLD-based functional brain scans according to the whole-brain functional networks, and compare the detection efficiency at different frequency bandwidths, slow-5 (0.01~0.27 Hz), slow-4 (0.027~0.073 Hz), and whole band (0.01~0.073 Hz) [2, 3].

Methods: Twenty patients and 19 healthy volunteers were recruited. All participants were scanned on a Siemens Avanto 1.5T MR scanner. Functional images were acquired along the AC-PC line with the GE-EPI sequence (TR/TE/FA = 2000ms / 39ms / 90°, slice thickness/gap =4mm/1mm, data matrix = 64×64, FOV = 240mm×240mm, 30 slices, 180 time points). The steps of data preprocessing include slices timing, realignment, normalization, and removing linear trends. We performed three band-pass filters, slow-5 (0.01~0.27 Hz), slow-4 (0.027~0.073 Hz), and whole band (0.01~0.073 Hz), on the functional datasets. Then we removed spurious variances (six motion parameters; signals of global mean, white matter, and CSF). For each of the bandwidths, we extracted the time series of 90 brain regions according to AAL atlas, calculated Pearson's correlation coefficients between any pair of brain regions, and constructed whole brain functional networks. For each subject, the whole-brain connectivity matrix contains 4005 independent elements. We took all of whole-brain functional connectivity matrices as the raw data (Fig.1) and transformed the matrix elements to the z-score values. We performed RFE (recursive feature elimination) based SVM classifier for feature selection [4]. The classification was carried out with the LIBSVM. The leave-one-out-cross-validation (LOOCV) was used to test the accuracy convergence. Finally, we obtained the pattern on which the prediction accuracy getting convergence.

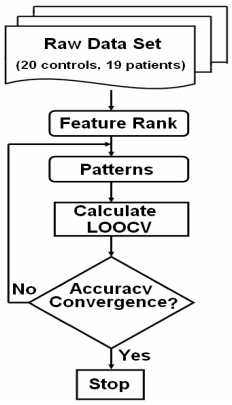

Fig.1 Flow chart of classification functional brain scans with MVPA LOOCV: leave-one-out-cross-validation

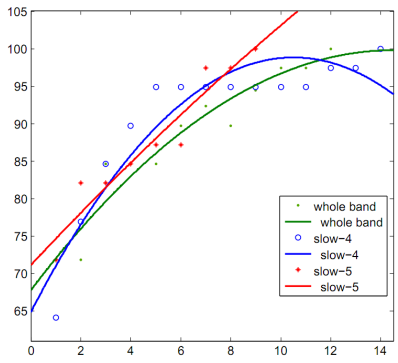

Fig.3 Prediction accuracy rate changing in the patterns of 3 different frequency bandwidths. (slow-5: 0.01~0.27 Hz; slow-4: 0.027~0.073 Hz; whole band: 0.01~0.073 Hz)

Results: Analysis indicates that we can predict VaD brains from normal control group within each of 3 frequency bandwidths with the RFE-based SVM method. Fig. 2 shows the patterns derived from the whole-brain connectivity, with which the prediction accuracy rate turned convergence (the accuracy rate is 100%). Fig.3 shows the prediction accuracy rate changing before convergence within 3 frequency bandwidths. It indicated that the detection efficiency at different frequency bandwidths was obviously different.

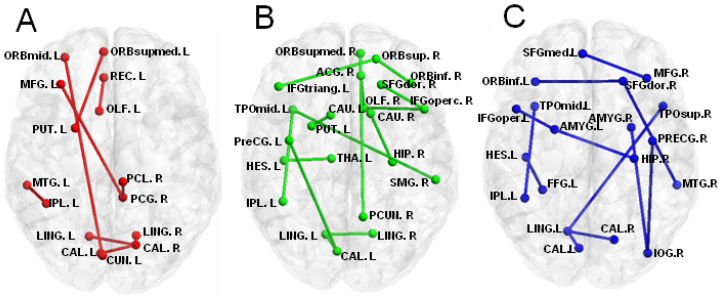

Fig.2 The patterns on which the prediction accuracy turned convergence for three different frequency bandwidths (A: for slow-5; B: for slow-4; C: for the whole band).

Discussion: Our findings suggest that functional brain scans and whole-brain functional connectivity contain adequate information about neurobiological changes in VaD patients to allow predictions of brain states from normal control group. The whole brain functional connectivity on different bandwidths showed different efficiency for detecting VaD patients, but the efficiency related to the slow-5 was more prominent. The results contribute to the understanding of VaD and may facilitate discovery of biomarkers for the diagnosis and clinical management of individual VaD patient.

References: [1] Craddock, R.C. et al. MRM. 2009. 62(6): 1619-28. [2] Buzsaki, G. et al. Science. 2004. 304(5679): 1926-9. [3] Han, Y., et al. NeuroImage. 2011. 55(1): 287-295. [4] Guyon, I. et al. Machine Learning. 2002. 46(1-3): 389-422.