***MRI morphometry in Alzheimer’s disease***

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OSI-1

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MRI based evaluation of brain atrophy is regarded as a valid method to stage the disease and to assess progression in Alzheimer’s disease (AD). Over the last decade software packages such as FreeSurfer provide measurements of cortical and subcortical gray matter features based on MRI data. Moreover a recent advance in MRI analysis, automatic segmentation hippocampal subfields has made it possible to automatically measure hippocampal subfields and adjacent cortical subregions. For longitudinal morphometry to assess progression of brain atrophy using structural MRI, popular methods include boundary shift integral (BSI), tensor-based morphometry, and FreeSurfer-longitudinal. BSI uses linear registration to align the baseline and repeat images and then track the shift of the brain boundary location and has been shown to provide accurate measurements of brain atrophy that are sensitive biomarkers of disease progression. However these software tools have not become routinely used either, since the execution time of the volumetric workflow required long time. At present, voxel based morphometry (VBM) is easily applicable to the routine clinical procedure with a short execution time. The importance of the VBM approach is that it is not biased to one particular structure and is able to assess anatomical differences throughout the brain. Stand-alone VBM software running on Windows, Voxel-based specific regional analysis system for AD, has been widely used in the clinical diagnosis of AD in Japan. On the other hand, graph theoretical analysis offers a diverse range of quantitative measures for characterizing the topology of structural network for the whole brain without a priori hypothesis. AD patients showed altered small-world architecture in the structural cortical networks, implying a less optimal topological organization in AD.

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Figure: Group differences in voxel-based morphometry and regional network topology between early AD and normal control groups. Decreased betweenness centrality is observed at cingulate cortex in AD group.

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***ViBrism DB Platform***

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We introduce renewed ViBrism DB (http://vibrism.neuroinf.jp/) as a platform of NIJC activity, aiming at an increase of information about brain architecture based on molecular distribution of many genes on the three dimensional (3D) anatomical context. Comprehensive gene expression densities in the mouse brain were measured with microtomy-based technology, which we invented, Transcriptome Tomography1, and mapped on the 3D MRI space compatible to the INCF mouse standard brain coordinate (WHS)2. Now 172,023 maps of overall gene expression in the four developmental stages to the adult after the birth are searchable by gene IDs, and the results are shown as 2D/3D maps on the MRI images. Also, the measured densities at each stage are usable directly for gene-by-gene correlation analysis of co-expression using Pearson correlation coefficient as a similarity measure3, and then co-expression search results can be browsed as network tables and graphs associated with the 2D maps. These frameworks enable to comprehensively assess expression patterns underlying brain structures and functions. ViBrism DB is a unique database for anatomy/function association based on gene expression.
References:
1. Okamura-Oho, Y. et al. PLoS One 7, e45373 (2012).
2. Johnson, G. A. et al. Neuroimage 53, 365–72 (2010).
3. Okamura-Oho, Y. et al. Sci. Rep. 4, 6969 (2014).
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Figure: Integrated analysis of expression maps and co-expression networks in the ViBrism DB
A) Top page: select experimental stages and search genes of interest by gene ID or by expression similarity (SET search). B) In the SET search, set the threshold of r and see a co-expression table. Then, 1) click the “network view” button to show a co-expression network graph with 2D maps (blue arrow) or 2) check boxes and click the “open 3D view” button to see 3D gene expression maps (green circle). Map files (vcat format) and network tables (CSV/ GML format) are downloadable (orange circles). C) an example view of 3D anatomical maps and a network view of co-expressed genes.

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