Neuroanatomical priors improve image-based cortical thickness computation: ROI-DiReCT

Abstract

Cortical thickness measures derived from structural MRI demonstrate reproducible associations with IQ, aging and disease and may be a valuable biomarker for intervention studies. Thickness of the cortical mantle also varies predictably with neuroanatomical regions as shown by von Economo in 1927. Recent research demonstrates that training segmentation data is able to automatically partition the cortex into major neuroanatomical divisions. The correlation of neuroanatomical region and cortical thickness implies that cortical labeling may improve cortical thickness quantification by introducing additional prior information. We thus propose a new solution, ROI-DiReCT, to image-based cortical thickness estimation (ICTE) that leverages recent advances in multi-template labeling, distributed computing and reproducible research to both extend and validate prior work. We use an open-source image processing toolkit and public data to test the hypothesis that additional priors introduced through cortical parcellation can be used in a divide-and-conquer strategy to improve the accuracy and speed of ICTE. For instance, the expected range of cortical thickness in post-central gyrus differs from that of inferior temporal gyrus and, via ROI-DiReCT, this information may be included in the thickness estimation. We use the semi-manually labeled NIREP data to contrast whole-brain ICTE with those

gained by ROI-DiReCT with respect to known patterns of cortical thickness values as provided by von Economo and others. We also use multi-template labeling, based on NIREP, to automatically label the T1 images from the multi-modality reproducibility dataset. This allows us to compare the reproducibility of our whole-brain and ROI-DiReCT ICTE. ROI-DiReCT provides more stable and neuroanatomically plausible results.

Keywords:

Introduction

in pumed, look at cortical thickness parcellation

Materials and Methods

Subjects

The resting state fMRI data presented here was collected from six hospitals in China which paticipated in the Brainnetome Project for Schizophrenia. The six hospitals are Patients and controls are matched as much as possible for age, sex, handedness, and race distributions with each site. Peking University Sixth Hospital (PKUH6); Beijing Huilongguan Hospital (HLG); Xijing Hospital (XJ); Henan Mental Hospital (HM); Renmin Hospital of Wuhan University (RWU); and Zhumadian Psychiatric Hospital (ZMD). Henan Mental Hospital provided two distinct MRI scanners: Siemens (HMS) and General Electric (HMG), for a total of eight scanning centers. The study at each center was approved by the local ethical review board. All the participants provided written informed consent.

All patients had a diagnosis of schizophrenia confirmed by trained psychiatrists using the Structured Clinical Interview for DSM-IV-TR Axis I Disorders (SCID-I/P). (First et al., 2002b). Exclusion criteria were a current neurologic disorder, a history of serious medical illness, substance dependence, pregnancy, electroconvulsive therapy within the last six months, or a diagnosis of any other Axis I disorder. The Positive and Negative Syndrome Scale (PANSS) (Kay et al., 1989) was used to assess positive, negative, and general psychopathology symptoms in the patients. The healthy controls,

who had no current axis I psychiatric disorders, were recruited from the local community near each center through advertisements. None of the HCs had any personal history of psychotic illness and no family history of psychosis in their first, second, or third degree relatives. All the participants were Han Chinese in origin, right-handed, and had no contraindications to MRI scanning. After extensive quality checking of the brain imaging data, 662 patients and 613 HCs were included in the analysis.

Data acquisition and preprocessing

Two types of 3 T MRI scanners (four Siemens, three General Electric) were used at the participating centers. To ensure equivalent data acquisition protocol and high quality imaging data, the scanning parameters of the functional scans at each of the six centers were set up by an experienced researcher before data acquisition. An echo planar imaging sequence was used to obtain the functional images, the parameters were as follows: 30 axial slices, TR = 2000 ms, TE = 30 ms, matrix = 64 64, flip angle = 90, FOV = 240*240 mm 2, slice thickness = 4 mm, gap = 0.4 mm. A total of 250 brain volumes were collected, resulting in a total scan time of 500 s.The MRI scan sequences and parameters for each center are listed in eTable 1. To be noticed, the time point number of the images from ZMD is 180 and is different from the 240 of the other sites. We did not exclude this site since we are eager to keep as much data and sites as possible, to support the validation of the muli-site analysis.

The iamges were preprocessed with a based in-house software: Brainnetome Toolkit which utilized Statistical Parametric Mapping SPM8 (http://www.fil.ion.ucl.ac.uk/s
The pipeline includes the following steps: The first ten images were deleted

for the signal equilibration. The remaining iamges were conducted for slice acquisition correction and head motion correction. The fMRI data which had less than 3.0 mm of head motion and 3.0 of angular rotation were included. Moreover, the mean framewise displacement (FD) was computed by averaging FDi from every time point for each subject. There were no differences for the mean FD between groups (t = 0.413, p = 0.682) (Table 1). Then the fMRI images were normalized to the standard Montreal Neurological Institute (MNI) template provided by SPM and resample to the 3-mm isotropic voxels. Artefacts due to changes in global, ventricle and white matter signals, residual motion were removed using voxel-wise regression. A temporal filter (0.01 Hz ¡ f ¡ 0.08 Hz) were used to reduce the low-frequency drift and physiological high frequency respiratory and cardiac noise. Finally, the data was smoothed with an isotropic Gaussian kernel of 6 mm full-width at half-maximum.

For a single label,

$$E(\phi(\mathbf{x},1)) = \int_0^1 \|\mathbf{v}(\mathbf{x},t)\|^2 dt + \|P_w(\mathbf{x}) - P_{wg}(\mathbf{x})\|^2 \tag{1}$$

$$\sum_{n=1}^{N} E_n(\phi_n(\mathbf{x},1)) \tag{2}$$

Discussion

Conclusions

Acknowledgments

References