Evaluation of three automated methods of identifying the hippocampus on T1 weighted images

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Target Audience: Researchers who are interested in automatic segmentation of hippocampus on brain MR images.

Purpose: The hippocampus is a frequently studied anatomical structure, implicated in a range of neuropsychiatric and neurodegenerative disorders. Until recently, the most common method of identifying this complex structure was manual tracing on an anatomic image. As neuroimaging has grown in popularity and scope, the time and effort involved in tracing individual hippocampi has become prohibitive. Popular automated methods of identification, such as FMRIB Software Library (FSL/first) [1] and FreeSurfer (FS) [2], are adequate but often show greater variance in size and can create systematic distortions in shape [5].

In this study, we compare the two most popular and full automated methods of identifying hippocampus from T1 weighted whole-brain images (T1W), FSL/first and FreeSurfer, to a third candidate, a template registration method developed by our group based on Advanced Normalizaiton Tools and symmetric image normalization method(ANTS/SyN) [3][4].

Methods: Six healthy controls (1 male, mean age 49.5 ± 5.24) were scanned under an IRB-approved protocol on a 3 tesla Siemens whole body Tim-Trio scanner (Erlangen, Germany). T1W images were acquired using a 3D MPRAGE sequence with the following scan parameters, FOV=256x256, voxel size=1x1x1.2mm and reconstructed matrix size=256x256x120, TE/TR/TI=1.75/1900/900ms. In each subject, bilateral hippocampi were identified manually by a trained expert, and automatically using FSL/first, FS and ANTS. In FSL/first, T1W images were input to routine run_first_all with auto option. In FS, the dicom files of T1W were input to routine recon-all. For the ANTS analysis, T1W data as described above were acquired for one additional healthy control (male, age 32) and hippocampal ROIs were drawn manually by the same expert as above. T1W images and ROIs from the additional subject were used as the ANTS template. We developed two approaches to propagate the ROIs from the template to target subjects, both using SyN as transformation model and cross-correlation as similarity measure. In the first case to which was referred as ANTS forward (ANTSf), the template image was aligned to the target subjects' images, and the resulting transformation was applied to the template hippocampal ROIs to obtain ROIs in the targets. In the second case to which was referred as ANTS inverse (ANTSi), the target images were registered to the template image. Utilizing the invertible feature of SyN, we applied the inverse transformation on the ROIs on the template to obtain the ROIs in the target space.
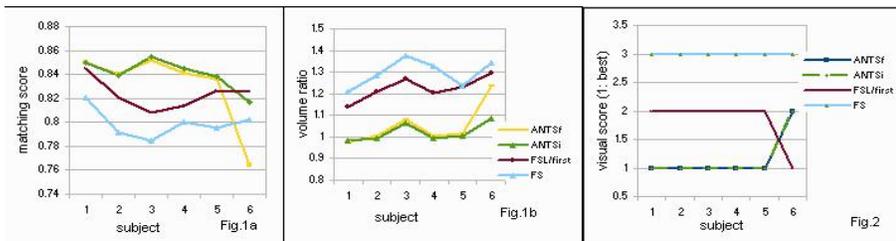
Using the manually traced ROIs as the "gold standard," a matching score (Dice's coefficient) and volume ratio were calculated for each of the four methods. The volumes of right and left hippocampal volumes were calculated and compared to the manually-drawn ROIs. All automatic ROIs were visually inspected and rated by the expert.

Fig.3
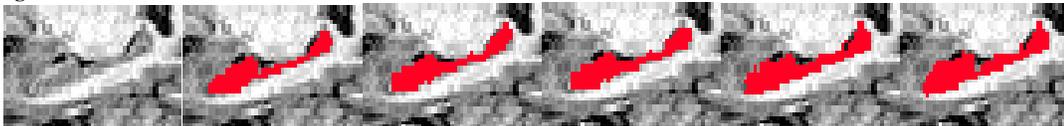
Results: As seen in Fig.1a, 1b and Fig.2, the ANTS method has higher matching score (matching score ranges from 0 to 1; 1 means perfect matching), better volume ratio (volume ratio ranges from 0 to +∞; 1 means the same volume), and best visual inspection rating , comparing with other methods for 5 out 6 subjects. The ANTSi is also shown to be better than ANTSf, which provides another evidence of the unsymmetrical nature of template-target and target-template registration. Fig.3 shows an example of sagittal view of hippocampus on T1W and manual traced ROI, and ROIs identified with ANTSf, ANTSi, FSL/first and FS in the order from left to right.

Discussion: After quantative matching analysis and qualitative visual inspection, we conclude that the ANTS method produced ROIs that are closest to the hand traced hippocampal.   The ANTS method requires selection of a template ROI, and this template can affect the resulting ROIs. Our future work includes template selection and refinement, potentially adding shape information to increase accuracy, and applying the ANTS method to disease populations.

References
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