ACURRY OF BMAS HIPPOCAMPUS SEGMANTATION USING THE HARMONIZED HIPPOCAMPAL PROTOCOL

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INTRODUCTION

• Hippocampal volume (HCV) measured with MRI has been widely used as a key biomarker for both improving subject selection and monitoring treatment efficacy in Alzheimer’s Disease (AD) studies. However various hippocampal protocols exist in the literature, each including a different set of subfields and sub-structures, potentially leading to confusion and additional complexity for direct comparison and consistency in reporting study results.

• The main goal of the Hippocampal Protocol (www.hippocampal-protocol.net/) was to harmonize the multiple existing hippocampal protocols in order to define a standard protocol. Once that protocol was defined, expert tracers manually outlined hippocampal regions on samples of ADNI cases. 100 expert hippocampus segmentations were made available as of January 2014. 35 more cases are expected to be released shortly [1].

• The purpose of this work was to evaluate the accuracy of the BioClinica Multi-Atlas Segmentation (BMAS) algorithm which had been previously validated using independent and in-house ADNI-based atlases [2-4] - with respect to the newly released hippocampal structures as defined by the Harmonized Hippocampal Protocol.

METHODS

Population

• The Harmonized Hippocampal Protocol was based on 100 subjects from the ADNI-1 database. This cohort included 37 AD, 34 Mild Cognitive Impairment (MCI) and 29 Normal Controls (NC) subjects. Demographic data are reported in Table 1. AD, MCI and NC groups were matched for age, gender, and education level.

• All subjects underwent MRI examinations composed of a high-resolution 3DT1 imaging protocol, using MP-RAGE (Siemens), 3D TFE (Philips) and 3D Fast SPGR (General Electric) pulse sequences.

• Images were re-oriented along the AC-PC line for the purpose of the Harmonized Protocol.

• Images were manually contoured by expert tracers according to the Harmonized Hippocampal protocol.

The whole set of objects was used as atlases for the BioClinica Multi-Atlas Segmentation algorithm (BMAS) [4].

• Hippocampal segmentations were automatically computed with the BMAS algorithm using a “leave-one out” fashion to evaluate the accuracy of the proposed segmentation method with respect to this new standard.

Image analysis

Pre-processing

• All atlases were registered to a common atlas space using an optimized affine and non-linear registration.

Multi-atlas segmentation

• For a given subject among the 100 available cases, the 3DT1 sequence was non-linearly registered to the common atlas space.

• Rectangular ROIs were automatically extracted around each hippocampus. All of the subsequent image processing was performed over those ROIs for improved segmentation accuracy.

• The resulting segmentation results were fused using the BMAS algorithm in a “leave-one out” fashion to generate a volumetric segmentation of the hippocampus.

• The resulting segmentation was subsequently refined by expert tracers identified with high accuracy.

• The resulting segmentation results were fused using the BMAS algorithm in a “leave-one out” fashion to generate a volumetric segmentation of the hippocampus. Images were re-constructed with joint Label Fusion, Wang et al. in Parallel Analysis and Multi-Intelligence. March 2013

Statistical analysis

• Segmentation accuracy was assessed using the Dice similarity index, signed and unsigned relative volume error (RVE) with the provided hippocampal segmentation as a reference.

• Pearson correlation was also calculated, between computed and reference HCV values.

RESULTS & CONCLUSIONS

• As detailed in Table 2, accuracy of the proposed BMAS segmentation method was assessed with respect to the newly introduced harmonized hippocampal volumes (right + left) were RVE=4.5% ± 3.3 and signed RVE=2.8% ± 4.8. Harmonized BMAS hippocampus segmentation results were highly correlated to the newly introduced harmonized hippocampal segmentation (r=0.96 with p<0.001).

• Similar ability for subject group separation was observed for the reference and Harmonized BMAS hippocampus segmentations (see Table 2).

• This work demonstrated that BMAS could be successfully implemented using the Harmonized Protocol atlases and provided sufficient accuracy. It is noteworthy that manual and automated segmentations lead to similar group dissociation ability on this small sample of ADNI1 subjects.

REFERENCES


Figure 1. Overview of the general workflow of the Harmonized BMAS algorithm

Table 1. Subject demographics

- Alzheimer’s Association International Conference (AAIC) • July 12 – 17, 2014 • Copenhagen, Denmark