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# Multi-template approaches for segmenting the hippocampus: the case of the SACHA software

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## Introduction:

The hippocampus has been shown to play a crucial role in memory and learning. Its volumetry is a well-established biomarker of Alzheimer's Disease (AD) and hippocampal sclerosis in temporal lobe epilepsy (TLE). Manual segmentation being time consuming and suffering from low reproducibility, robust automatic segmentation from routine T1 images is of high interest for studying large datasets. We previously proposed such an approach (SACHA, Chupin et al, 2007, 2009), based on competitive region deformation constrained by both anatomical landmarks and a single probabilistic template of 16 young healthy subjects registered using SPM5. The atlas being introduced as a soft constraint, robust results have been obtained in large series of patients with various pathologies. In recent years, multi-template approaches have proven to be a powerful mean to increase segmentation robustness (Barnes et al, 2008) (Aljabar et al, 2009) (Heckemann et al 2006), more specifically for subjects with very large atrophy or atypical shapes (such as malrotations (Bernasconi et al, 2005) (Kim et al, 2012)). We propose here to evaluate the introduction of multiple-template constraints in SACHA.

## Methods:

The template library was built from the 16 young healthy subjects (S1-S16), eight patients with probable AD (AD1-AD8) and a mixed group of eight controls (C1-C8), eight patients with TLE with hippocampal sclerosis (HS) (HS1-HS8) and seven patients with TLE but no HS (TLE1-TLE7) (Chupin et al 2007, 2009). The template library embeds T1 images and corresponding manual hippocampus and amygdala segmentations registered in MNI space with the *new segment* module of SPM8 (<http://www.fil.ion.ucl.ac.uk/spm>).

The segmentation of a new subject is done as follows. The *new segment* and *deformation* modules of SPM8 are first applied to correct the T1 image for intensity non uniformity and register it to MNI space.

The normalized cross correlation between the new image and each library T1 image is then computed in a region-of-interest automatically derived around the hippocampus and the amygdala. This similarity measure allows selecting the N closest library subjects that will be used to create the subject-specific probabilistic atlas. This atlas is then deformed back to the subject's space and used as in Chupin et al (2009) to both obtain seeds and constrain the segmentation process.

## **Results:**

Segmentation performance was evaluated on the library dataset, with a leave-one-out procedure. Segmentation performance was compared for multi-template (MT-SACHA) and original SACHA (S1S16-based atlas). An estimate of the performance of the multi template strategy without SACHA was obtained by thresholding the subject-specific atlas above 0.5 probability value. Dice similarity index and relative volume error with respect to manual segmentation were computed. Dice values are shown in Figure 1. Median Dice values were increased by 2 percentage points when using MT-SACHA compared to original SACHA. The improvement of the SACHA refinement step is still obvious, with a gain of 8 percentage points with respect to the thresholded subject specific atlas. The relative volume error did not change (median: -6% and dispersion: -3 to 10%). Figure 2 displays an example for one of the most difficult cases. N was studied for {8, 12, 16, 20} but its influence on the subject specific atlas proved small (mean Dice for the thresholded atlas about 78%). Total computation time for one subject was less than 15 min.

## **Conclusions:**

We proposed to evaluate the usefulness of the multi template strategy within the SACHA software. Average performance was slightly improved and variability was decreased, whereas the refinement step still proved crucial. The template library still has to be enlarged to embed more cases with strongly atypical hippocampal shape or position (e.g. malrotations), and further evaluation will then be required to fully evaluate the improvement in robustness for new atypical cases.

## **Categories**

Primary Category : Segmentation and Parcellation

Secondary Category : AD and Other Dementias

## **Keywords:**

Segmentation

Other : Hippocampus, Multi-template

## Figures

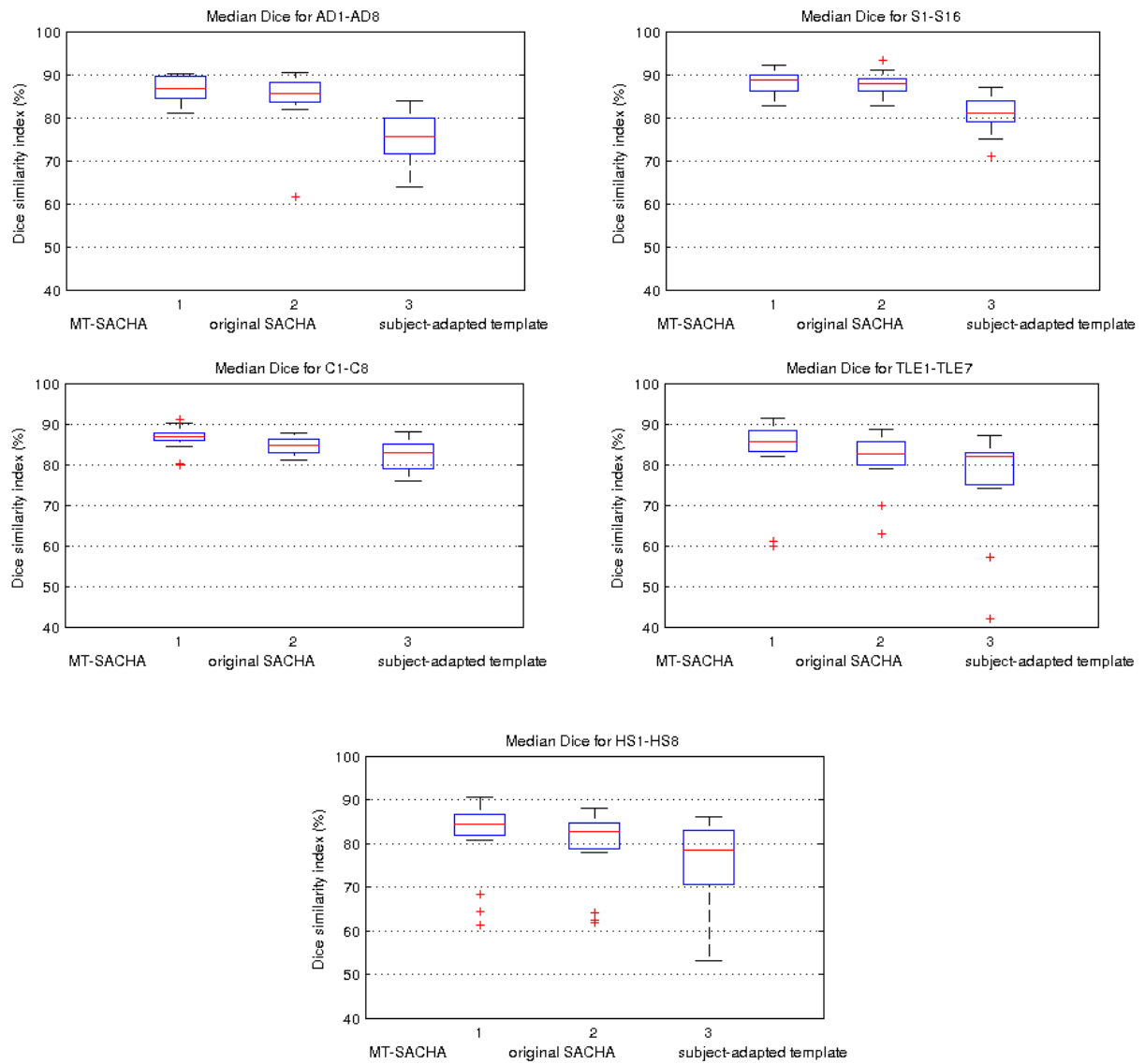


Figure 1: Dice values for each datasets with N=16.

On each box, the central mark (red) is the median. The edges of the box are the 25th and 75th percentiles. The whiskers extend to the most extreme datapoints the algorithm considers to be not outliers. The outliers are plotted individually (red cross).

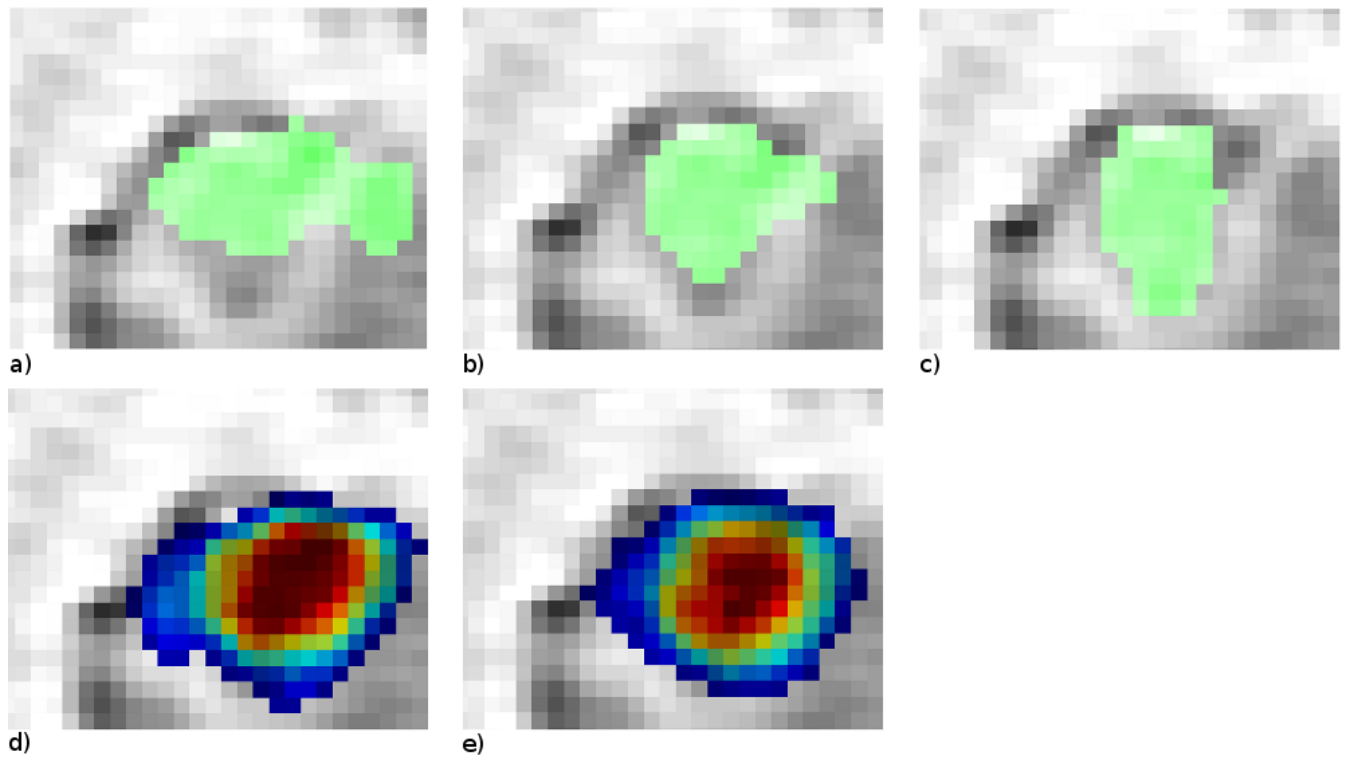


Figure 2: Example of the hippocampus segmentation with the left hemisphere of a HS patient (N=16). MT-SACHA yields a mean Dice of 68,2% compared to original SACHA (62,4%).

- a) Segmentation with original SACHA
- b) Segmentation with MT-SACHA
- c) Manual segmentation
- d) S1S16-based atlas
- e) Subject-specific atlas

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