Generation of a minimal set of templates in MR neuroimages

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Magnetic Resonance Imaging (MRI) has been used in numerous *in vivo* anatomical studies of the brain [1] especially for the hippocampus, and plays an important role in the diagnosis of temporal lobe epilepsy, or degenerative diseases such as Alzheimer's dementia, and in the evaluation of their course [2]. Studying and quantifying local anatomical differences or changes in a population, in a sense of characterizing anatomical differences between subjects, is a very challenging and danatomical reference images (templates) are then becoming of vital importance.

In general, MR images are not based on a common standard grey level scale, so robust standardization is to be applied. Thus we built up a robust method for standardizing the intensity scale of brain Magnetic Resonance (MR) images. This way similar tissues have similar intensities, even across images coming from different sources [3]. Then an 'exhaustive' extraction of the hippocampal region is performed, starting from a fixed hippocampal box (HBo), considering various MRI datasets [5]. Data were obtained from the Alzheimer's Disease Neuroimaging Initiative (ADNI) database (adni.loni.ucla.edu). At the beginning, the early extractions exhaust the set of the HBs which are very similar to the defined HBo. Then, the procedure continues extracting HBs which are progressively different from the first ones, but diversity creeps into the growing HB database very slowly, thanks to the relevant size of the population of the available MR images. Thus, the orientation and position of the essential geometrical features of the searched region are preserved during the whole process of HB extraction. After the extraction, the HBs are clusterized, in order to choose the most representative images in a large population.

In order to give an estimation of the '*minimum*' number of templates, we propose a metric based on the geometrical position of the boxes (D parameter in Fig. 1) . For each MR_i image, we take the corresponding HB_j^x extracted by the 'exhaustive' procedure and HB_j^k extracted by the 'normal' one, i.e. by using k templates, provided by clusterization
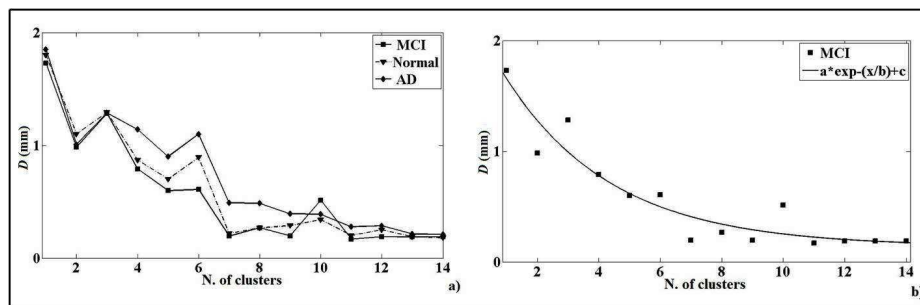

Figure 1. a) The pattern of the D parameter versus the number k of clusters, for datasets of images belonging to patients with homogeneous clinical conditions (Alzheimer's Disease); b) fitting curve on the D parameter for a dataset of images belonging to Mild Cognitive Impairment (MCI) patients.

D(k) (Fig. 1) has a downward trend, therefore we could estimate a '*minimum*' *k* value where this function becomes stable and low enough, as a good compromise for describing population variability.

We assess that this '*minimum*' number of templates is largely independent on the clusterization method and on the number of the MR images, if statistically consistent with respect to the clinical conditions of the patients. From the above, the best strategy, to be used when non-homogeneous populations are considered, strictly depends on the features and characteristics we want to emphasize better.

We stress that the templates not as the mean images of a dataset, but as a group of the most representative ones, and the number of templates able to describe the population is lower for patients with homogeneous clinical conditions than with mixed degrees of neuropathology (e.g. Alzheimer's Disease).

The selected template set can be used for the extraction/evaluation of that region on various and different MRI datasets [3, 4].

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