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An end to end automated pipeline for brain structure segmentation in multiple sclerosis patients

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Background: The automatic brain structure segmentation methods available in the literature are not designed to segment images of Multiple Sclerosis (MS) patients. The demyelinating lesions characteristic of this disease affect their segmentation result, causing a performance oscillation.
Aims: To propose and evaluate a fully automated pipeline designed to segment 133 brain structures in magnetic resonance images (MRI) of MS patients with lesions. The proposed method is based on a well-known multi-atlas strategy.
Methods: Given a T1-w and a FLAIR image of the patient, the proposed pipeline includes the following steps: pre-processing (inhomogeneity correction and intensity normalization), lesion segmentation (Roura et al., 2015), atlas selection, masked registration, and the final label fusion to provide the brain structures segmentation. The label fusion strategy used in our pipeline is the m-NLSS (González-Villà et al., 2018), which was adapted to deal with MS lesions from the original NLSS method (Huo et al., 2017). To evaluate the robustness of the proposed approach, we compared the performance of the pipeline on the international MSSEG 2016 database in three different scenarios: i) using the whole automated pipeline including the lesion segmentation, ii) using the pipeline where lesion masks were manually annotated, and iii) using the pipeline where manually annotated lesions masks were filled according before brain structure segmentation.
Results: From the experiments done, we observed that with the proposed automated pipeline, no significant structure volume differences were found with respect to the use of manual lesion masks. In contrast, significant volume differences appeared on the cerebrospinal fluid ($1.13\% \pm 1.93$, $p < 0.05$) and the cerebral white matter ($0.13\% \pm 0.14$, $p < 0.05$) when comparing the segmentation results with those obtained when filling the lesions. We also noticed that when false positives were found by the automatic lesion segmentation, the use of lesion filling could be self-defeating causing brain structure misclassification in those areas.
Conclusions: The proposed pipeline allows to eliminate the manual delineation of MS lesion masks and the lesion filling pre-processing step, providing more accurate segmentation results and making them more robust since they are not relying on the quality of the filling method and the lesion masks used.
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