SUBCORTICAL BRAIN SEGMENTATION OF TWO-DIMENSIONAL T1W DATA SETS WITH *FIRST*

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Introduction

Deep grey matter (DGM) structures of the brain are thought to play a pivotal role in functional cerebral pathways including pathways mediating motor control. Multiple sclerosis has an impact on DGM perfusion [1] and iron deposition [2] already at early stages of the disease and DGM atrophy occurs throughout the disease. Reliable subcortical segmentation can be performed using the FSL tool FIRST (FMRIB's Integrated Registration and Segmentation Tool) [3] applying Bayesian shape models on three dimensional T1w MRI data sets. In this work, we investigated the feasibility of FIRST segmentation of interpolated 2D T1w data sets by comparing the results with the respective segmentation of 3D data.

Subjects and Methods

30 patients (20 women, 10 men) who underwent routine MRI at our institution were included in this study. 25 patients had multiple sclerosis (17w/8m) and five patients had other neurological diseases. The mean age of the patients was 46.3 years (range 26y-72y). The MR scans were performed on either one of the following three 1.5T scanners (all Siemens Medical, Germany): 19 patients on Magnetom Symphony, 7 patients on Magnetom Espree and 4 on Magnetom Avanto. The scanning protocol included two pre-contrast T1-weighted scans: an isotropic 3D MPRAGE sequence (TR/TI/TE/α=2.7s/950ms/5ms/8°) and a 2D T1w-SE sequence with (TR/TE=552ms/17ms) for Avanto and Espree and slightly different parameters (TR/TE=450ms/10ms) for the Symphony. In the MPRAGE sequence, 192 sagittal slices with a spatial resolution of 1x1x1 mm^3 were acquired, in the T1w-SE, 40 slices parallel to the inferior borders of the corpus callosum were scanned in interleaved order (spatial resolution 0.9x0.9x3 mm^3).

In a first pre-processing step, the 2D data were sinc-interpolated to an isotropic resolution of 1x1x1 mm^3 with FLIRT [3] (also part of FSL). Then, both interpolated 2D data and 3D data were processed using the run_first_all routine of FIRST v5.0. In the first part of this routine, the patient's data are co-registered onto the 1 mm T1w MNI152 template by FLIRT in a two-step approach. The first step is an affine registration of the whole head onto the template, whereas in the second step the registration is refined to the subcortical structures. The inverse transformation of this two-step registration is then applied to FIRST's subcortical model to bring it to the native space of the original data. The subsequent segmentation of the subcortical structures is then performed in the native space (for details [3]). By default, the FIRST routine also segments brain stem and forth ventricle. As these structures were only partially covered by the 2D data sets, we excluded them from the segmentation. Additionally amygdala and hippocampus, which are not consistently considered as DGM structures by different authors, are segmented by default. We included these two structures in the statistical analysis, but not in the calculation of the whole DGM volume.

The processed data sets were visually inspected at two stages of the FLIRT routine: First, the results of the two-step registration of the head were checked. If either the brain outline or the subcortical structures were not well aligned to the MNI template, the respective data sets were discarded. Next, the subcortical segmentation was evaluated for inaccuracies. In the statistical comparison, only patients whose 2D and 3D data sets passed both visual quality control steps were included. The statistical analysis was carried out using IBM SPSS Statistics 21. We tested the performance of the interpolated 2D data segmentation and as compared to that of the 3D data segmentation by calculating correlations between the volumes of the subcortical structures. More specifically, intra-class correlation coefficients (ICC) were calculated to describe to what degree the results of the two methods differed. We used a two-way mixed model for single measures ICC (3,1) for each subcortical structure and calculated the values for consistency and absolute agreement.

Results

A correctly segmented 2D data set is shown in Fig. 1. On visual inspection of the registration results, the data of five patients had to be discarded (two from the Symphony, two from the Avanto, and one from the Espree scanner). In these cases, both the registration of the 3D and the 2D data failed. None of the remaining 25 patients showed major inaccuracies of the subcortical segmentation and these data sets were included in the statistical analysis. The results of the correlation analysis are shown in Table 1. There was strong agreement between total DGM volumes as determined by FIRST using the interpolated 2D versus 3D data sets both for consistency and absolute value. For the substructures, we found strong or moderate agreement for the larger subcortical structures as caudate, thalamus, and putamen, and fair agreement for the smaller structures pallidum and nucleus accumbens. Moderate agreement was found for the hippocampus and poor agreement for the amygdala.

Discussion

In this work, we were able to demonstrate that subcortical segmentation of interpolated 2D data with FIRST is feasible and that the results at least for the total volume of the DGM and the larger subcortical structures agree well with those of 3D data. The crucial step for correct segmentation seems to be the two-step FLIRT co-registration. We found no major segmentation errors when the registration was correct. The co-registration failures might be caused by pathologically enlarged ventricle volumes, as severe brain atrophy was observed in the respective cases. This might be a limitation of the FIRST routine for the data analysis of patients with a high degree of brain atrophy in longitudinal studies with a long follow-up duration.
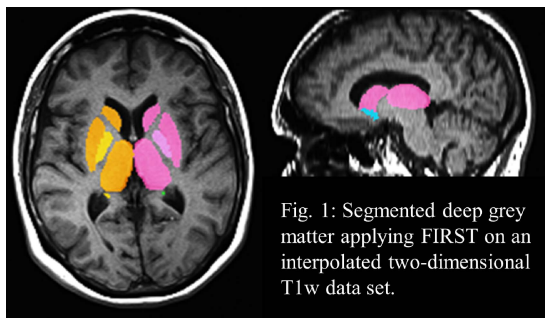

Fig. 1: Segmented deep grey matter applying FIRST on an interpolated two-dimensional T1w data set.

Structure	Intra-Class Correlation Coefficient ICC (Consistency)	Intra-Class Correlation Coefficient ICC (Absolute Value)	Pearsons Correlation Coefficient R
Caudatus	0.783	0.550	0.852
Pallidum	0.505	0.482	0.604
Putamen	0.582	0.553	0.612
Thalamus	0.707	0.661	0.753
Accumbens	0.505	0.368	0.537
total DGM	0.759	0.748	0.818
Hippocampus	0.688	0.631	0.698
Amgydala	0.208	0.207	0.215
red: strong agreement			
bold: moderate agreement			

Tab. 1: Intra-class Correlation Coefficients (ICC) between 3D data sets and interpolated 2D data sets (N=21) for different subcortical structures. ICC was also calculated for the total deep grey matter (DGM) volume including bilateral caudate nucleus, pallidum, putamen, thalamus and nucleus accumbens. Pearson's correlation coefficients are shown for comparison.

References

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