Grey-Level Morphology Based Segmentation of T1-MRI of the Human Cortex

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Abstract. In this paper an algorithm for fully automatic segmentation of the cortex from T1-weighted transversal, coronal or sagittal MRI data is presented. A histogram-based method is used to find accurate threshold values. Four initial masks are generated, containing background, brain tissue, 3D grey-level eroded brain tissue and 3D grey-level dilated surrounding fat. Information from previous slices are used to avoid leaking from non-brain tissue.

1 Overview of the Method

A histogram-based method is used to select the threshold intervals. The different kinds of tissues that are found are brain matter (white and grey matter), dark tissue types (fluids, bone, background) and bright tissue types (fat). The thresholding is performed on kernel density estimates (continuous histogram (KDE)). From this KDE the four greatest maxima of the second derivative are chosen and sorted. The interval from the lowest to the second maximum correspond to CSF and bone, and below the first threshold is air. Grey matter is approximately the second to third threshold and white matter is the third to fourth threshold. Surrounding tissues (and sometimes some internal structures in the brain) are above the fourth threshold. The histogram from the start slice has been used.

Two additional volumes are calculated. The original volume , called **OrgImage**, is grey-level-eroded using a $3 \times 3 \times 3$ structure element; this new volume is given the descriptive name **MinImage**. The original volume is also grey-level-dilated using a $3 \times 3 \times 3$ structure element; called **MaxImage**. These images are used to eliminate false connectivities to surrounding tissues. In the grey-level eroded volume the background is below the second max found from the second derivate of the continuous histogram. In the grey-level dilated volume the surrounding tissue is above the third max.

In the transaxial case a slice in the middle of a brain is selected as the start slice, see Fig. 1a). Objects large enough are decided to be brain tissue. The segmented slice is used as a mask on following slices. In the sagittal case, two slices are determined, one in the left and one in the right hemisphere, see

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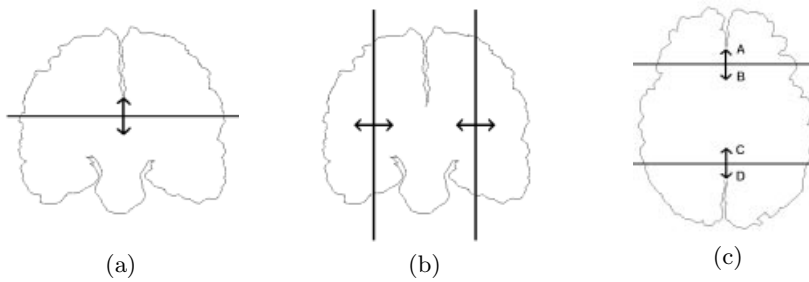

Fig. 1. How the algorithm advances on: a) A transaxial volume. b) A sagittal volume. c) A coronal volume.

Fig. 1b). As in the transaxial case, the information from previously segmented slices is used. In the coronal case, two starting positions are selected, see Fig. 1c). Here the same algorithm that is used to determine the start slices in the two other algorithms is used for all slices from position B to C in conjunction with propagating information from previous slices. For the slices from position A and position D, outwards, the same criterias that were used in the sagittal case are used. The information from previously segmented slices are also used.

2 Results

The segmentation algorithm generates reproducible results and has been visually evaluated on 30 patient data sets in transaxial, sagittal and coronal cases. A frequent problem is when cranial nerves that link brain tissues to non-brain tissue cause bridges that the binary morphology doesn't break. When involving both grey-level dilations and erosions these bridges are almost always broken. Another problem is that the algorithm does not handle volumes that are severely shaded very well. The main reason for this is our using the mid-slice only as a base for the automatic thresholding. This can be compensated for and more slices can be used in the thresholding. The method is improved from earlier work [2], [1].

References

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