Adaptive Template Moderated Brain Tumor Segmentation in MRI

M. Kaus, S.K. Warfield, F.A. Jolesz and R. Kikinis

Surgical Planning Laboratory
Department of Radiology, Brigham & Women's Hospital
Harvard Medical School,
75 Francis Street, Boston, MA 02115, USA
Email: kaus,warfield,jolesz,kikinis@bwh.harvard.edu

Abstract. This paper describes a new method for the automated segmentation of MRI images of brain tumors. The algorithm is an iterative, hierarchical approach that integrates a statistical classification scheme and anatomical knowledge from an aligned digital atlas. For validation, the method was applied to 10 tumor cases in different locations in the brain including meningiomas and astrocytomas (grade 1–3). The brain and tumor segmentation results were compared to manual segmentations carried out by 4 independent medical experts. It is demonstrated that the algorithm produces results of comparable accuracy to those of the manual segmentations in a shorter time.

Keywords: Image Registration, Magnetic Resonance, Brain Tumor, Template based Segmentation

1 Introduction

Many applications of computer assisted neuro-surgery and -radiology rely on previously segmented medical images. However, this task often requires labor intensive and time consuming manual interaction. The goal was to develop a method for the automated segmentation of brain and tumor.

When considering the design of a tumor segmentation method, a large number of tumor types which vary greatly in size, shape, location, tissue composition and homogeneity has to be accounted for. Clinical image analysis reports large inter- and intra-patient variations and considerable overlap in grey value distribution both among different tumor histologies and with normal tissue, indicating that segmentation methods based on image information alone may be insufficient for successful differentiation between normal and tumor tissues [8].

Consequently, preliminary work on tumor segmentation using general segmentation methods that rely on the image information alone like thresholding and morphological operators [7], neural networks [16] or statistical classification methods [2] work well in some cases but may not differentiate between active tumor, associated pathology and normal tissue.

Template based segmentation methods solve the segmentation problem by aligning a digital atlas of a normal brain to the individual [3, 9, 12]. The anatomical knowledge represented in the atlas then may serve as a lookup map. However, these methods rely on the correctness of the alignment, and, by definition, normal digital brain atlases don't include pathologic structures, which poses a problem if used for the segmentation of pathology.

This paper describes a template based segmentation technique for the segmentation of meningiomas and grade 1-3 astrocytomas. The method is a hierarchical, iterative approach that uses anatomical knowledge to moderate a multi-spectral classification scheme.

2 Methods

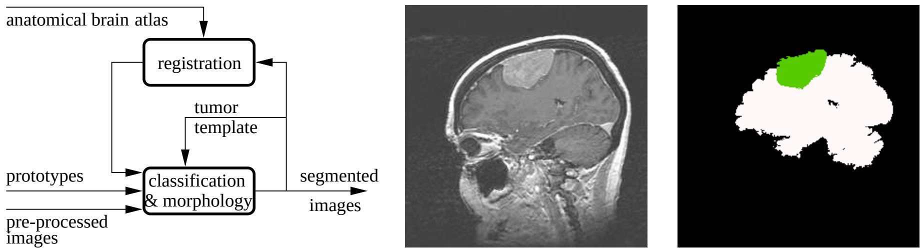
Image database Development and validation of the algorithms are based on an MRI database of appr. 100 manually segmented tumor patients. Each dataset consisted of an SPGR volume ($256 \times 256 \times 124$, $1 \times 1 \times 1.5$ mm), and pre- and post-contrast T1 and T2 weighted volumes ($256 \times 256 \times 30$, $1 \times 1 \times 5$ mm) obtained with a GE 1.5 T MR imaging device [10].

Preprocessing Before the actual segmentation process, mis-registration due to patient movement was minimized with a linear registration algorithm based on the maximization of mutual information [15]. For noise reduction, edge preserving anisotropic diffusion filtering was applied [6].

Combining statistical classification with anatomical knowledge. For supervised multi-spectral statistical classification the k-Nearest-Neighbor (kNN) rule was applied, which has shown to be the most accurate and robust statistical classifier for application to MRI [1, 5].

Overlapping intensity distributions of different tissue classes result in voxel mis-classification. To resolve such ambiguities, a pre-segmented anatomical atlas can be used as a template to interact with the classification process. Since the atlas usually differs significantly from the individual to be segmented, some kind of spatial alignment is required. However, the registration produces some error so the atlas cannot be used directly for segmentation. Thus, the template's influence on the segmentation should reflect some amount of uncertainty. This is achieved by presenting the atlas information as additional feature channels to the classifier, one for each anatomical structure[13]. The classification is spatially constrained if both the prototype and the voxel of unknown class are located in different anatomical structures suggested by the atlas. The certainty of anatomical localization is modeled by generating distance maps for each structure.

Registration. The goal of the registration is to achieve alignment between the anatomical brain atlas and the patient. Alignment is computed in two steps: First, a linear registration based on segmented data accounts for the global translation and rotation [14]. The remaining mis-alignment is considered local and non-linear. This step is based on a fast multi-resolution optical-flow algorithm using a sum-of-squared-difference similarity measure on labeled data [4].



(a) (b) (c)

Fig. 1. Tumor segmentation algorithm scheme (a), original SPGR image (b) and automated segmentation result (c).

Local refinement of classified structures. Artifacts from the previous classification (small holes and unrelated structures connected with thin lines) were eliminated automatically with an erosion to remove thin connections, followed by a seeded region growing to fill small holes and remove non-connected pixels, and a dilation to recover the previously eroded boundaries [11].

Tumor Segmentation. Figure 1(a) presents a schematic overview of the tumor segmentation algorithm. The pre-processed image data and anatomic templates enter a closed loop of segmentation (classification and local refinement) and registration. Hierarchically, the method proceeds starting with skin-neck-bone, icc, ventricles and finally tumor. For the purpose of elastic matching the pathology is labeled as normal brain.

3 Results

The algorithm was validated on 10 tumor cases including meningiomas and grade 1-3 astrocytomas of compact shape in different locations of the brain. For quantitative analysis of the algorithm, we compared the brain and tumor from the 3D automatic segmentation to a randomly selected 2D slice within the tumor region that was segmented by 4 independent medical experts. A standard segmentation was defined as the area of overlapping voxels identified in at least 3 out of 4 manual segmentations. The variation in the expert's opinion is denoted as the disagreement (D), the area where less than 3 experts agreed.

To measure agreement and disagreement between automated and standard segmentations, we compared the volumes of brain and tumor respectively from the automatic method (V_a) to the volume from the standard segmentation (V_s). The voxels in V_a and V_s are the true positives, the voxels in V_a and not in V_s the false positives and the voxels in V_s and not in V_a the false negatives. All measures are given with respect to the standard volume V_s.

High true positive (TP) ratios for automatic segmentation (brain: 94–99%, tumor: 91–97%) and low false positive (FP) (brain: 2–14%, tumor: 2–9%) and false negative (FN) (brain: 0.1–6%, tumor: 4–10%) ratios express good comparability to the expert's standard. The expert's disagreement ratio (brain: 0.1–6%, tumor:14–22%) were in the range of or higher than the automated segmentation's error ratios FP and FN. The false positives are partially due to the expert's variation and in part due to the oversegmentation of the algorithm in the area of the lateral sulcus with abundant vessels and the tentorium cerebelli. Some of the extrinsic tumor cases (meningiomas) were underestimated by our method due to an underestimation of the brain. This may be accounted for by adapting the weight of the spatial constraint to the location of the tumor.

The overall computation time for a typical tumor case on an 8-processor Sun ES 5000 amounted to appr. 75 minutes including appr. 5-10 minutes operator time for training of the classifier. Complete manual segmentation time has been reported to be in the range of 180 minutes [10], which implies that the automatic method achieves a 95% reduction of operator time.

4 Discussion and Conclusion

We have developed a new automated anatomy atlas moderated statistical classification scheme for the segmentation of MRI of meningiomas and grade 1–3 astrocytomas.

The comparison between the new method and manual segmentations obtained from medical experts demonstrate comparable quality and significant reduction of operator time. Our algorithm may fail in cases where the intensity value distribution of the tumor is highly inhomogeneous and shows large spectral overlap with spatially close brain tissue. In such a case the initial tumor estimate may impose an incorrect spatial constraint on the classification process that may not be resolved in subsequent iterations. However, this can easily be corrected by extending the manual interaction.

Several issues remain uninvestigated. We are currently in the process of extending our model for more complex tumors such as the glioblastoma multiforme. This involves the improvement of the elastic matching technique to explicitly deal with the pathologic structures and the investigation of the use of additional feature channels for discrimination between the various tumor tissue classes.

Acknowledgments

This work was supported in part by a grant from the Deutscher Akademischer Austauschdienst (DAAD), a Postdoctoral Fellowship from the National Multiple Sclerosis Society (SW), NIH grants RO1 CA 46627-08, PO1 CA67165-01A1, PO1 AG04953-14, NSF grant BES 9631710 and Darpa grant F41624-96-2-0001. The authors thank Drs. A. Chabrerie, E. Chatzidakis, A. Nabavi and F. Ozlen, Brigham & Women's Hospital, for their help with the manual segmentations.

References

1. L.P. Clarke, R.P. Velthuizen, S. Phuphanich, J.D. Schellenberg, J.A. Arrington and M. Silbinger: MRI: Stability of Three Supervised Segmentation Techniques. Magnetic Resonance Imaging, 11(1):95–106, 1993.
2. L.P. Clarke, R.P. Velthuizen, M.A. Camacho, J.J. Heine, M. Vaidyanathan, L.O. Hall, R.W. Thatcher, and M.L. Silbinger: MRI Segmentation: Methods and Applications. Magnetic Resonance Imaging, 13(3):343–368, 1995.
3. D.L. Collins, T.M. Peters, W. Dai and A.C. Evans: Model based Segmentation of Individual Brain Structures from MRI Data. SPIE Proceedings of the 1st International Conference on Visualization in Biomedical Computing, 1808:10–23, 1992.
4. J. Dengler and M. Schmidt: The Dynamic Pyramid - A Model for Motion Analysis with Controlled Continuity. International Journal of Pattern Recognition and Artificial Intelligence, 2(2): 275–286, 1987.
5. R.O. Duda and P.E Hart, Pattern Classification and Scene Analysis. John Wiley and Sons, 1973.
6. G. Gerig, R. Kikinis, O. Kübler and F.A. Jolesz: Nonlinear Anisotropic Filtering of MRI Data. IEEE Transactions on Medical Imaging, 11(2):221–232, 1992.
7. P. Gibbs, D.L. Buckley, S.J. Blackband and A. Horsman: Tumour Volume Determination from MR Images by Morphological Segmentation. Physics in Medicine and Biology, 41:2437–2446, 1996.
8. M. Just and M. Thelen: Tissue Characterization with T1, T2 and Proton Density Values: Results in 160 Patients with Brain Tumors. Radiology, 169:779–785, 1988.
9. M. Kamber, R. Shinghal, D.L. Collins, G.S. Francis and A.C. Evans: Model-Based 3-D Segmentation of Multiple Sclerosis Lesions in Magnetic Resonance Brain Images. IEEE Transactions on Magnetic Resonance Imaging, 14(3):442–453, 1995.
10. S. Nakajima, H. Atsumi and R. Kikinis: Use of Cortical Surface Vessel Registration for Image-guided Neurosurgery. Neurosurgery, 40:1201–1210, 1997.
11. J. Serra: Image Analysis and Mathematical Morphology. Academic Press, 1982.
12. S.K. Warfield, J. Dengler, J. Zaers, C.R.G. Guttmann, W.M. Wells, G.J. Ettinger, J. Hiller and R. Kikinis: Automatic Identification of Grey Matter Structures from MRI to Improve the Segmentation of White Matter Lesions. Journal of Image Guided Surgery, 1(6):326–338, 1995.
13. S.K. Warfield, M. Kaus, F.A. Jolesz and R. Kikinis: Adaptive Template Moderated Spatially Varying Statistical Classification. Proceedings of the International Conference on Medical Image Computing and Computer-Assisted Intervention, Springer Verlag, 1496:431–438, 1998.
14. S.K. Warfield, F.A. Jolesz and R. Kikinis: A High Performance Computing Approach to the Registration of Medical Image Data. Parallel Computing, 24: 1345–1368, 1998.
15. W.H. Wells, P. Viola, H. Atsumi, S. Nakajima and R. Kikinis: Multi-Modal Volume Registration by Maximization of Mutual Information. Medical Image Analysis, 1(1): 35–51, 1996.
16. Y. Zhu, H. Yan: Computerized Tumor Boundary Detection using a Hopfield Neural Network. IEEE Transactions on Medical Imaging, 16(1):55–67, 1997.