NeuroImage **11**, Number 5, 2000, Part 2 of 2 Parts IDEAL®

METHODS - ACQUISITION

Automated Segmentation of MS Lesions in MR

Koen Van Leemput*, Frederik Maes*, Fernando Bello†, Dirk Vandermeulen*, Alan Colchester†, Paul Suetens*

**Medical Image Computing, Radiology-ESAT, K.U. Leuven, Belgium*

†Neurosciences Medical Image Analysis Group, University of Kent at Canterbury, UK

Objective

Quantitative analysis of MR images is becoming increasingly important in assessing the progression of multiple sclerosis (MS) and in monitoring the effect of a drug therapy. In clinical trials, manual analysis of the MR images by human experts is prohibitively time-consuming because of the large amounts of data typically involved. The inter- and intra-observer variability associated with manual delineations, and the unclear decision making process when multi-spectral MR data are presented to a human expert, further complicate matters. The goal of our work is to develop a fast, fully-automated method for MS lesion segmentation that analysis multi-spectral MR data in an objective and reproducible way.

Materials and Methods

The method we propose builds on recent previous work for fully automated classification of MR images of normal brains [1]. The MR signal is modeled as a realization of a random process whereby each voxel is drawn independently from one out of K tissue classes. The intensity probability distribution of each of the tissue classes is modeled as a normal distribution, and the smoothly varying intensity inhomogeneity that is often present in MR images, is modeled as a 4-th order polynomial. Assessing the Maximum Likelihood model parameters results in an iterative algorithm that interleaves classification of the image voxels, estimation of the normal distribution parameters, and correction for the intensity inhomogeneity. The method is initialized with a digital brain atlas that is distributed with the SPM99b package.

Based on the observation that MS lesions are not included in the model, we exploit the idea that therefore, such lesions could be detected as model outliers. We robustize the model parameter estimation for the presence of such outliers based on the concept of robust M-estimators [2]. More specifically, a voxel weight is introduced that reflects the belief that a voxel is actually coming from the mixture model. The higher the mahalanobis distance to each of the normal distributions, the higher the probability for an outlier, and the smaller the weight on the model parameter estimation. Upon convergence of the thus robustized iterative algorithm, MS lesions are discerned from other model outliers, such as partial volume voxels, based on intensity- and contextual constraints.

We have implemented the method in Matlab code, on top of the SPM99b software environment. Rigid co-registration of multi-spectral MR data, as well as affine registration to the digital brain atlas, is performed with a method based on maximization of Mutual Information [3].

Results

We compared the automated lesion classifications with manual expert delineations on 2 consecutive scans of each of 10 MS patients, drawn from a set of time series consisting of approximately 12 serial scans of 20 MS patients [4]. Each scan contained low-resolution T1-, T2-, and PD-weighted images (24 axial 256x256 slices, voxel dimensions 0.9mmx0.9mmx5.5mm). The expert segmentations were performed on the T2-weighted images only, while the automated method worked on the full 3-channel data. We compared the total lesion load (TLL) of both methods, measured as the total volume of detected MS lesions, with a linear regression analysis. As can be seen from figure 1, the slope is close to unity, and the intercept is approximately zero. The correlation coefficient is high: 0.98.

Conclusions

We have developed a technique for segmenting MS lesions from multi-spectral MR images. Since the method is fully automated, it yields objective and reproducible results. The segmentations of the automated method were compared with the lesions delineated by human experts, showing a significant total lesion load correlation.

References

[1] K. Van Leemput, F. Maes, D. Vandermeulen & P. Suetens. *IEEE Trans. Med. Imag., vol. 18, pp. 885-896, Oct. 1999*

[2] P.J. Huber. *Robust Statistics, J. Wiley & Sons*

[3] F. Maes, A. Collignon, D. Vandermeulen, G. Marchal, & P. Suetens. *IEEE Trans. Med. Imag., vol. 16, pp. 187-198, Apr. 1997*

[4] BIOMORPH: *EC-funded BIOMED-2 program*