Clinical MRI Based Volumetry: The Cerebral Ventricles

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1 Introduction

Cerebral ventricular volume is an important factor in quantifying various neurological diseases and in neurosurgical therapy monitoring. We describe a method to efficiently segment and visualize the intracerebral fluid spaces based on MRI and to reproducibly quantify their volumes. At present, no system is available for routine clinical use which is (1) *fast* (less than 10 min for image analysis), (2) *flexible* (robust for normal and pathological anatomy), and (3) *reproducible* (less than 5 % relative variation).

2 Methods

The method presented combines acquisition of thin slices, fast 3D marker-based segmentation, and automatic histogram analysis. T1-weighted anatomic data is acquired on a 1.5 T Siemens Magnetom Vision (Figure 1): MPRAGE, TR 9.7 ms, TE 4.0 ms, flip angle 20 deg, sagittal, FOV 256 mm, matrix 256×256, 160 slices, slice thickness 1.0 mm, acquisition time approx. 8 min. The segmentation algorithm is based on a fast watershed transformation as described in [1]. Additionally, five different marker types are used for ventricle labeling (R, L, 3, and 4) and region exclusion, thereby imposing watersheds at respective borders. The watershed transformation takes approx. 1 sec on a standard PC for a typical region of interest (1 million voxels). It automatically tracks the ventricular boundaries in 3D, taking the marker positions into account. In a standard case, 10 markers suffice to define the ventricular anatomy accurately. The complete segmentation procedure, including user interactions, takes an average of 2 min for all slices.

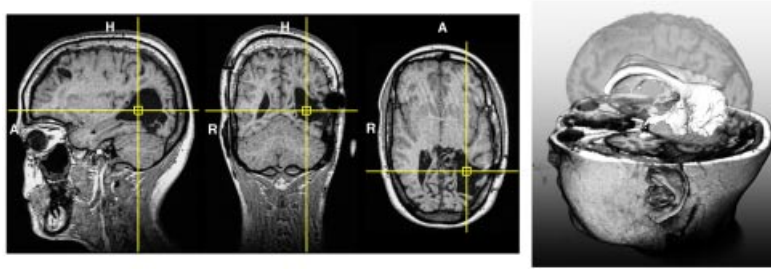

Fig. 1. Patient (F, 29 yrs), postoperative data. **left.** Original data. **right.** Ventricular segmentation result fused with segmented brain and original data. Total ventricular volume: 54.6±0.6 ml.

W. Niessen and M. Viergever (Eds.): MICCAI 2001, LNCS 2208, pp. 1291-1292, 2001.

Table 1. Evaluation of total reproducibility on a healthy volunteer (M, 38 yrs) who underwent five separate MRI scans with 30 min rest between acquisitions (V_1–V_5). Volumes in ml.

	V_1	V_2	V_3	V_4	V_5	mean ± SD	SD/mean	V_6†
right	17.96	17.83	17.73	18.01	17.83	17.87 ± 0.11	0.63 %	17.84
left	14.37	14.26	14.06	14.37	14.23	14.26 ± 0.13	0.88 %	14.59‡
3rd	2.22	1.99	2.07	2.17	2.00	2.09 ± 0.10	4.80 %	2.01
4th	2.64	2.75	2.60	2.74	2.78	2.70 ± 0.08	2.82 %	2.84
total	37.16	36.95	36.42	37.25	36.98	36.95 ± 0.32	0.87 %	37.33
lateral	32.33	32.12	31.79	32.39	32.12	32.15 ± 0.24	0.74 %	32.48

† acquired 2 months later ‡ significantly enlarged left ventricle

A model based histogram analysis robustly accounts for image noise, non-uniformity, and partial volume effects. The volumes of each of the four segmented ventricles are computed automatically from corresponding over-inclusive regional image histograms. Assuming symmetric, equally distributed partial voluming, we introduce a set of mixed Gaussians to extend the trimodal normal distribution model. Least squared error minimization is used to fit the model. The expected volumetric uncertainties are calculated individually, based on image quality.

3 Results and Discussion

We thoroughly evaluated inter- and intraobserver variance as well as reproducibility for the complete system. Mean values and standard deviations have been recorded. The variance between raters for lateral ventricular volumes is less than 0.5 %. With independently repeated acquisitions on patients and healthy volunteers, reproducibility has been excellent, with relative deviations less than 1 % (Table 1). Larger variations are observed for 3rd and 4th ventricles due to small object sizes and the frequently imprecise delineations in MRI. Repeated acquisitions on a ventricle shaped paraffin phantom yielded a relative standard deviation of 0.4 % for the total volume (Mean ± SD: 60.89 ± 0.22 ml).

We present a new semiautomatic approach which speeds up image analysis while improving reproducibility and accuracy compared to manual or semiautomatic slice-based evaluation [2]. User-induced errors are minimized by placing markers inside the objects instead of tracing object borders interactively. The 3D segmentation procedure is equally applicable to normal and pathological anatomy (Figure 1), since it does not require an anatomical model. Furthermore, contralateral differences are directly quantified.

Accurate measurements are achieved on commonly available high-resolution T1-weighted MR images. Image fusion and higher dimensional histogram analysis were avoided. Combining short interaction times, applicability to pathological anatomy, and high reproducibility, the presented method meets the requirements posed by imaging and workflow conditions in a clinical setting.

References

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