Increased efficiency of MRI brain segmentation: An interactive manual, automated, and scripted approach.

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ABSTRACT

At the recent ISMRM meeting in Seattle, Dr. Elias Zerhouni predicted growth for the use of quantitation in medical imaging. It may seem obvious that quantitative information should be extracted from MRI brain images, but this currently isn't being done in clinical cases because there are difficult issues to overcome, not just technical, but also political and regulatory. Computer aided detection (CAD) of structural brain changes promises to alleviate some of the barriers to the clinical application of quantitative measurements and this will allow new ways to diagnose, measure treatment response and guide interventions.

We believe that for CAD to be successfully used on magnetic resonance brain scans, it not only needs to rely on automation for efficiency, but it also requires manual interaction and oversight. We present the results of a study involving 40 T1-weighted human MRI brain scans that demonstrates an increase in the efficiency of extracting quantitative measurements. The method begins with automated pre-processing to remove intensity inhomogeneities from the raw scans and then proceeds with interactive automation to generate outlines around specific neuroanatomical regions of interest. The outlines are finally converted into morphometric results (volumetric and/or shape metrics) but only after manual over-reads assure correctness and accuracy. Open source software, "NVM" provides the manual interface to automated analyses and "SegMentor" scripts glue all aspects of the data pipeline together while also assuring accuracy and accountability. We compare the results against purely manual and purely automated outputs and conclude with a discussion of the benefits of interactive automation.

INTRODUCTION

Radiologists visually interpret medical images to help diagnose and treat diseases, but this is generally qualitative. The future growth of quantitation in medical imaging – obtaining numerical metrics of disease state and progression – will help with diagnoses and also provide evidence to document the response to treatment.

Quantitative information from MRI not used clinically for many reasons. A manual analysis can be prohibitively expensive in time and cost, and no completely automated method of MRI brain segmentation has been proven to have sufficient sensitivity, specificity and repeatability. Moreover, a quantitative method must adhere to complicated and detailed neuroanatomical measurement protocols, and individual measurements must then be validated against a large clinical database.

Beyond these technical and medical issues, a quantitative approach has not been adopted because of turf battles (who is going to do it), accountability (who is responsible for the results), and finances (who's going to pay for it). There are also large costs associated with clinical trials necessary to push research methods through regulatory agencies.

Despite these facts, Computer Aided Detection has become well established in areas such as mammography (which received FDA-approved in 1998), lung cancer [1], pap smears [2], and is beginning to be used for detecting polyps in CT colonography [3]. CAD systems generally operate by performing image segmentation, followed by feature extraction, and then application of various rules for discriminant classification. CAD is usually used as a second-reader. It assists users by drawing attention to regions of interest that may require further review. In mammography, the computer catches calcifications better than most radiologists, but for the moment, radiologists have resisted the idea of allowing the computer the first look. CAD helps to alleviate the image overload that has come with high resolution imagery. It can improve radiologic interpretation by making lesions easier to detect and classify and can sometimes help identify lesions at an earlier stage. It aids in quality assurance in situations that foster high interobserver and intraobserver variation such as tedious tasks and tasks involving multiple image features.

In this poster, we highlight the need for both automated processing and manual interaction and oversight for quantitation in medical imaging, and we believe that only the combination will allow CAD to grow in use as predicted.

METHODS

Automated pre-processing: Removing intensity inhomogeneities

A sequence of operations is used to locate the white matter in the scan and to remove slowly changing variations in the MRI signal (i.e. intensity inhomogeneity or "bias field"). These operations involve histograms, morphological operations, and fuzzy ad-hoc rules for identifying intensity peaks. The original scan is smoothed and shrunken in 3D using a large Gaussian-shaped filter and the average intensity is divided out. The inhomogeneity is estimated by tri-cubic interpolation of the result. A fraction of this is removed by dividing the original scan by the inhomogeneity estimate.

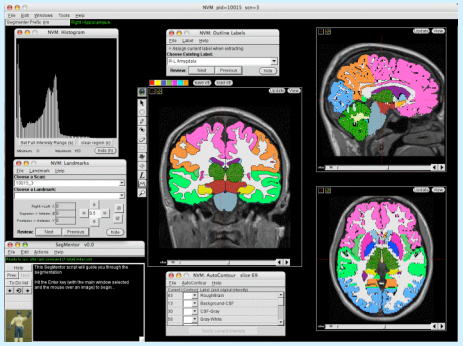

Figure1. NVM, the manual interface

Interactive automation: NVM

Structural MRI scans are segmented using open source software, "NVM" (freely available from Neuromorphometrics, Inc. at http://neuromorphometrics.org:8080/nvm/).

Images are loaded by running NVM and providing a description of their location, byte size, column, row, and slice dimensions and resolutions, along with other parameters. The scan is then displayed in three orthogonal views and a pallet of tools is used to adjust the display and segment the desired neuroanatomical regions of interest. Scans are positionally normalized to help decrease measurement variability across multiple subjects by designating landmarks and saving the re-sliced volume as a new scan. Three dimensional cropping is applied to make efficient use of display space.

Outlines around regions are created using isointensity contours along with manual drawing and erasing. Intensities used to define isointensity contours are chosen by clicking on a location in the image or by taking a histogram over a specific region and clicking on the histogram. Contours are then dynamically adjusted using the mouse. Manual editing is used to clean up and join multiple contours. Contours are then "extracted" as outlines. These outlines are assigned labels and saved for each slice where the desired regions appear. Outlines can be toggled on and off and filled in with colors to facilitate review of their precise boundary location and proper label assignment. Color filling is done in two ways: with a different color for each structure or else just in red and green to check the left-right assignment.

After segmentation is completed in this way, a menu option causes NVM to write out a comma separated value (.csv) spreadsheet file that contains voxel counts from all saved outline files. When loaded into Excel, volumes are calculated in this spreadsheet by 1) multiplying the number of voxels enclosed in the outlines by their volume and 2) adding half of the volume of the voxels located on the outline itself. To make segmentation easier, NVM displays each slice image at twice the original in-plane size so the row and column voxel dimensions in the spreadsheet are half of their original values.

"SegMentor" is a feature of NVM that explicitly defines and embeds measurement methods into the tool by providing on-line, context-sensitive instructions and definitions, and also by assisting in making the measurements. SegMentor records, plays, and allows viewing and editing of scripts that provide information to the user and also control the rest of the program. Using SegMentor scripts helps ensure that the technician adheres to the segmentation protocol. It also saves time by automating segmentation as much as possible except for difficult steps that need to be done using the operator's experience and anatomical knowledge.

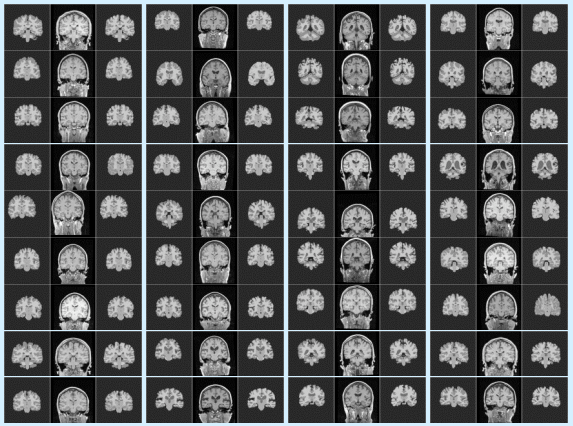

Figure2. Initial segmentation and auto-corrected

Corrections

Because the results of the manually guided segmentations using NVM can depend heavily on the inhomogeneity correction, some parts of the gray-white boundaries did not seem to adequately delineate the actual gray-white boundary. Therefore, additional corrections were performed on all scans. The final result was done in two ways, manually and automatically but using the previous segmentations as a starting point.

Manual corrections involved checking white matter boundaries on each slice. Contour lines were created by an experienced technician to delineate more inclusive white matter borders by "eye" and with the help of adjusting the brightness and contrast. To ensure better accuracy, the scan was viewed in both the axial and sagittal views with and without color-filled labels.

Automated corrections began with the assumption that the brain exterior and subcortical structure boundaries were correct and were to be left as is. The intensity inhomogeneity was then estimated and removed from the raw MRI signal by using the previous assignments of gray and white labels to voxels along with the average intensity values for those voxels as determined when initially removing the intensity inhomogeneity. This produced an "idealized" MRI intensity scan that was then subtracted from the raw MRI scan. This difference was then shrunken and smoothed to produce a more accurate estimate of the intensity inhomogeneity. This was then subtracted out and the corrected MRI volume was re-classified.

RESULTS

An example of an initial result is shown in Figure 2. This shows the initial segmentation along with the manually and automatically corrected segmentations. Figure 3 shows the raw automatically generated corrections. A detailed analysis of these results is on-going.

References

[1] Radiology 2002; 225(P): 476.

[2] Diagnostic Cytopathology 1998; 18(4): 307-311.

[3] IEEE Trans Med Imaging. 2004 Jun;23(6):661-75.

Conflict of Interest: Both authors are employees of Neuromorphometrics, Inc.

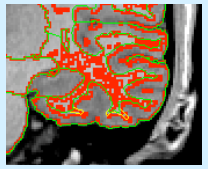

Fig 3 Auto vs. manual