SIIM 2016 Scientific Session
Posters & Demonstrations
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Automated Volumetric Report with Normative Ranges: A Ruby Based Tool Integrated with FSL

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Background

Among others effects, some brain diseases affect the integrity of some brain tissues and structures. One effect of these changes is the volume loss of some brain structures, therefore, by calculating the volume of the main brain structures and comparing them with the distribution of these volumes on a group of healthy subjects could be a good strategy for characterize markers associated to the atrophy or hypertrophy of these brain structures in some diseases.

Volumetric measurement of segmented brain structures allows to get quantitative information that cannot be inferred from visual inspection.

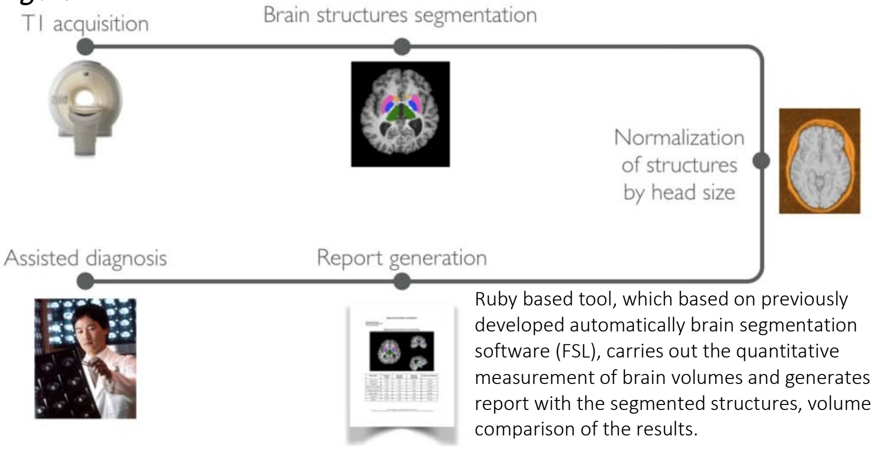
Brain volumetry could be carried out manually by an experienced radiologist (gold-standard), however due the required time for this job, this is not an efficient alternative. On the other hand, by carrying out the automatically brain volumetry assisted by a specialized software, it is possible to have comparable results to the obtained with the manual approach. However, it requires knowledges in imaging processing software and inversion of time in data preparation, preprocessing and analysis of the results.

Currently there are some commercial software packages (e.g. NeuroQuant), which provide the functionality of automatically brain volume estimation and report generation (Farid N et al 2012), but for to our knowledge, there is not an open source tool that allows the generation of a volumetric report based on statistical analysis of a group of healthy subjects.

Evaluation

We proposed a Ruby based tool, which based on previously developed automatically brain segmentation software (FSL), carries out the quantitative measurement of brain volumes. By using a T1 MRI series, the tool generates a report with the segmented structures, volumes and comparison of the results (Figure 1). This process does not depend of the user and therefore it is possible to integrated it in the quantitative radiology of clinical practice (Brewer 2009).

Figure 1



Ruby based tool, which based on previously developed automatically brain segmentation software (FSL), carries out the quantitative measurement of brain volumes and generates a report with the segmented structures, volumes and comparison of the results.

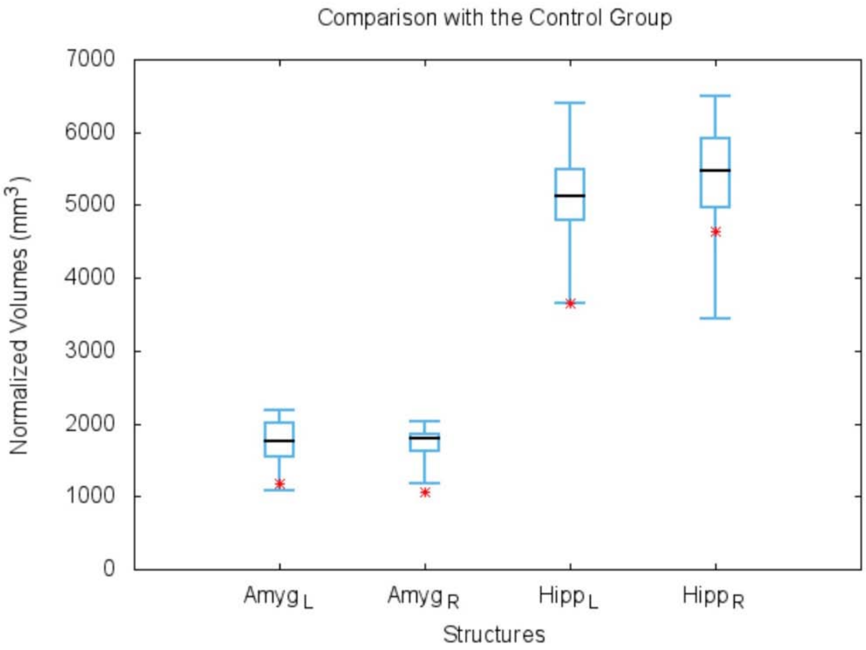
We used the neuroimaging processing library (FSL), which has been validated in multiple studies, showing a good correlation (ICC > 0.7) between automatic and manual segmentation (Nugent et al 2012). We used FIRST for segmenting subcortical structures and SENAX for Brain tissue volume. The manually generated labels are parameterized as surface meshes and then modeled as a point distribution. FIRST uses a Bayesian probabilistic approach. The shape and appearance models in FIRST are constructed from a library of manually segmented images. The manually generated labels are parameterized as surface meshes and then modeled as a point distribution. Using the learned models, FIRST searches through shape deformations that are linear combinations of the modes of variation to find the most probable shape instance given the observed intensities from the input image (Patenaude et al 2012). Sienax estimates total brain tissue volume, from a single image, normalised for skull size. It calls a series of FSL programs: It first strips non-brain tissue, and then uses the brain and skull images to estimate the scaling between the subject's image and standard space. It then runs tissue segmentation to estimate the volume of brain tissue, and multiplies this by the estimated scaling factor, to reduce head-size-related variability between subjects (Smith et al 2004). This procedure was performed for all control subjects without neurodegenerative or psychiatric conditions, we used the database Oasis, available in http://www.oasis-brains.org.

The tool presented in this work automatically analyzes T1 MRI, providing precise measurements of brain structures and comparing them with normal measures adjusted for age and gender. It provides valuable information that could improve the report made by the radiologist.

DICOM images are uploaded through a web platform and an email address is provided to receive the final report. This automatic tool, segments and measures the volume of the hippocampus, amygdala, putamen, caudate nucleus, nucleus accumbens, the globus pallidus and thalamus of each hemisphere, additionally it also calculates the volumes of the ventricles, cerebral cortex, gray and white matter as well as the total brain volume.

After that, all measures (age and gender adjusted) are compared with values of processed images from a database of healthy subjects and graphs are generated. Patient information is obtained from DICOM metadata. Finally, a personalized report in PDF format for each patient is generated, this report contains images segmentations of all structures, measured quantitative values, the asymmetry index for each subcortical structure, percentile charts comparing values of the patient and healthy subjects (Figure 2) as well as a short analysis with the relevant information.

Figure 2



Amygdale and Hippcampal volume are compared with the control group. Candlestick graph indicates a normative percentile which was statistically and clinically significant with the 5%, 25%, 50%, 75% and 95% percentile.

We report our institutional experience with the use of this tool as a support for medical diagnosis, due to its ease of use, it can be used in a large number of patients and detect small volumetric changes reducing the number of false negatives studies. The healthy subjects database continues increasing constantly with images acquired at the institution in several research projects with the aim to increase the statistical power of the comparisons.

Discussion

This tool has been tested in more than 30 MR studies (1.5T y 3T), including pathologies like epilepsy, brain tumors, cortical dysplasias; neurodegenerative diseases like Alzheimer disease and Parkinson and neuropsychiatric diseases like schizophrenia and bipolar disorder. This software has been used as a support diagnosis tool, helping the Radiologists to check brain structures which could being atrophied, generating a more objective and accurate report. However, it is important to keep in mind that the accuracy of the segmentation depends on factors like image quality and voxel size, therefore, it is necessary to check segmentation results and validate them by checking the image, to assure that the brain volume changes are effects of the disease and not an image quality effect.

Additionally, referring physicians have given a positive feedback about the addition of this information in the radiology report, due to the easy of interpretation of this changes by a quantitative measure, allowing to localize on the images the structures affected by these changes.

Conclusion

We present a fully automated tool to measure and report volumes of brain structures, adjusted for age and sex. These developments are crucial to provide medical specialists a framework in which they could assess the degree of regional atrophy in brain structures of a patient. This tool can be easily applied in clinical practice.

Reference

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Keywords

Quantitative Radiology, Neuroimaging, Brain Atrophy, Structured Report