A dynamic MRI brain atlas

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Synopsis

We describe a dynamic brain atlas that uses the capabilities of computational grids to customize a brain atlas on the fly to a study subject. The atlas can be generated from a sub-set of 180 reference brains closest in age and gender to the study subject. The dynamic atlas can be used to assist in interpretation of volume MR images of the brain for clinical or research purposes.

Introduction

Computational grids have the potential to transform medical imaging by coupling large volumes of data to sophisticated computing resources, using secure and flexible protocols. Brain atlases are widely used in neuro-imaging, and many such atlases have been made available on the web. We describe how the grid can dramatically extend the capabilities of such imaging atlases, by making it possible to customize them to an individual patient on the fly.

Method

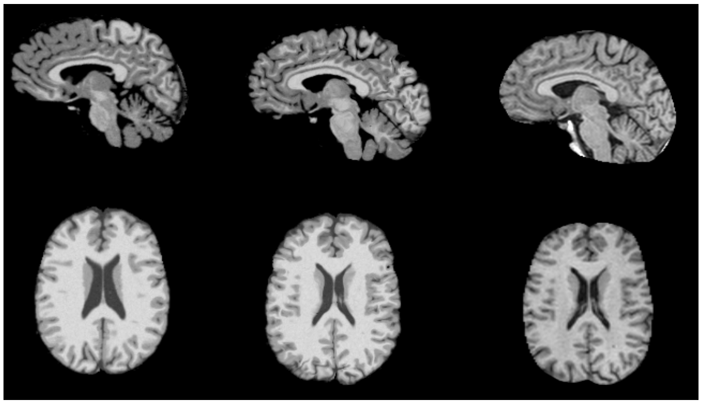
The reference subject data comprised 180 whole brain magnetic resonance (MR) images of normal controls and patients with non-space-occupying brain lesions. All images were rf spoiled T1 weighted gradient echo volume acquisitions interpolated to approximately 1mm cubic voxels. Each reference subject brain was automatically segmented into grey matter, white matter, and CSF using a statistical classifier implemented as part of the publicly available FSL package (www.fmrib.ox.ac.uk/fsl), running on a 16 CPU alpha server with 16Gbytes of RAM. Anatomical structures were automatically delineated from the reference subjects by registering the Montreal Brainweb image (segmented into structures) to each reference subject in turn using a non-rigid registration algorithm based on manipulating a uniform array of B-spline control points (separation 2.4mm) while optimizing normalized mutual information[1]. The calculated deformation field was used to warp the segmented tissue labels and delineated structure boundaries to each of the 180 reference images, automatically segmenting and labeling each dataset to the accuracy of the registration algorithm. The non-rigid registration took 2 hours per dataset, and on a condor cluster of sixteen 1.4GHz Athlon PCs running linux, could process all 180 datasets in 24 hours.

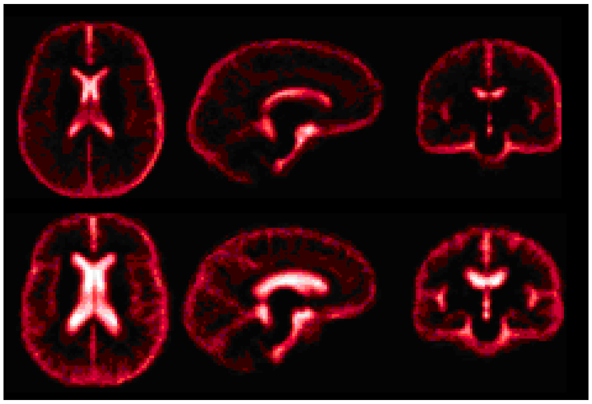
The dynamic aspect of the system is the ability to generate an atlas specific to a particular *study subject* (patient or research subject) in near real-time, rather than making use of a pre-computed atlas that may not be appropriate. The user:

- loads a *study subject* of interest onto their local computer
- queries the network database to identify *reference subjects* that are close to the study subject in age, gender etc.
- specifies the number of computers from the remote condor cluster they wish to use.
- launches the analysis using globus protocols.The study subject is then transferred to the remote condor cluster. Each of the selected reference subjects is then registered to the study subject using an affine registration algorithm running on the condor cluster, and the resulting transformation is used to transform all the segmented tissue maps and delineated structures into the coordinate frame of the study subject and generate an atlas that comprises an average image of the tissue types and structure boundaries that can be used to assist in interpretation or subsequent analysis of the study subject. The results are securely transferred back to the local computer. On our cluster of 16 linux PCs, an atlas of up to 16 subjects could be generated in about 3 minutes, half of which was due to globus and condor overheads.

Results

The left figure illustrates the pre-processing, showing the Brainweb image (left), a reference subject brain (right) and the reference subject warped to Brainweb (center). The right figure shows example dynamic atlases: Probabilistic CSF volumes customized for subjects aged 30 (top) and 70 (bottom).





Conclusions

We have implemented a network application using computational grid protocols that allows the user to dynamically generate brain atlases customized to a selected study subject. It provides a network interface that can be used to launch processing that creates new data, rather than just retrieving stored data. One of the characteristics of our network application and of grid applications in general is that they are scaleable, and we plan to extend this demonstrator to much larger distributed collections of images and massive distributed computing facilities within a multicentre collaboration. As the grid protocols evolve, it should make it increasingly easy to build and use large scale network applications of this type.

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[1] • Rueckert D, et al. *Non-rigid Registration using Free-Form Deformations: Application to Breast MR Images* IEEE Trans. Medical Imaging 18(8): 712-721 1999