COMPUTER METHODS AND PROGRAMS IN BIOMEDICINE 95 (2009) 146–157

journal homepage: www.intl.elsevierhealth.com/journals/cmpb

STAMPS: Software Tool for Automated MRI Post-processing on a supercomputer

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ARTICLE INFO

Article history:
Received 19 November 2008
Received in revised form
13 February 2009
Accepted 15 February 2009

Keywords:
Nonlinear image registration
PBS
Cluster
Supercomputer
MRI
Image processing

ABSTRACT

This paper describes a Software Tool for Automated MRI Post-processing (STAMP) of multiple types of brain MRIs on a workstation and for parallel processing on a supercomputer (STAMPS). This software tool enables the automation of nonlinear registration for a large image set and for multiple MR image types. The tool uses standard brain MRI post-processing tools (such as SPM, FSL, and HAMMER) for multiple MR image types in a pipeline fashion. It also contains novel MRI post-processing features. The STAMP image outputs can be used to perform brain analysis using Statistical Parametric Mapping (SPM) or single-/multi-image modality brain analysis using Support Vector Machines (SVMs). Since STAMPS is PBS-based, the supercomputer may be a multi-node computer cluster or one of the latest multi-core computers.

1. Introduction

Magnetic resonance imaging (MRI) has evolved as a superior tool to non-invasively study and monitor neurodegenerative diseases in vivo; which is critical for developing therapies treating these diseases. This fact has led to the creation of large-scale, multi-center, neuroimaging initiatives such as the Alzheimer's Disease Neuroimaging Initiative (ADNI) [1] and the Open Access Series of Imaging Studies (OASIS) [2]. ADNI is a 5-year study of 200 elderly controls, 400 subjects with mild cognitive impairment, and 200 with Alzheimer's disease. OASIS contains over 400 MRIs of subjects age 18–96, some of which have mild cognitive impairment. Extraction of useful information in a timely manner from such large image sets demands computing resources and organized patient database management. Many MRI post-processing tools (e.g. SPM [3], FSL [4], freesurfer [5], HAMMER [6,7], ITK [8]) are available for this purpose, but not all are designed

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doi:10.1016/j.cmpb.2009.02.006

for supercomputers[2] that drastically reduce processing time for large image sets. Also the listed tools do not perform all of the post-processing on all MRI types we discuss herein. Therefore, it is desirable to combine key functions of these tools into one image processing "pipeline" such that specific processing results are produced that are otherwise unattainable.

We present a software tool for automated post-processing of multiple types of brain MRIs on a workstation (STAMP) or on a supercomputer (STAMPS). The tool is designed to manage multiple types of image data using a few key attributes (e.g. patient ID, age) which a user can control in a central intuitive GUI independent of their values in image files.[3] The tool then processes these images in a pipeline, using linear registration and segmentation tools in FSL and SPM5/VBM5 [9,10], or nonlinear registration tools in HAMMER. The MR image types that can currently be processed by the STAMP pipeline are T_2 and T_2^*maps, T_1- and T_2-weighted images, and all types of DTI images. Support for other image types may be added as needed. For some image types (e.g. T_2, T_2^* maps, and DTI images), custom STAMP tools were developed using ITK for nonlinear registration (HAMMER) and ROI statistical analysis. These registered images may be used to perform voxel-based statistical analysis or to perform "machine learning" experiments (e.g. with Support Vector Machines (SVMs) [11]) which are capable of analyzing image types individually or jointly for biomarker discovery and validation.

Since the nonlinear registration task motivated STAMP, here we provide an introduction of this task and the rationale for using it. Due to intra- and inter-person anatomic variations, nonlinear registration of brain MRIs, as opposed to linear (affine) registration, is considered essential for morphological analysis. We use the HAMMER method [6] for several reasons. First, the HAMMER tool [6,7] is a freely available nonlinear brain registration method designed for high accuracy in anatomical correspondence. In this method, which is a hierarchical (coarse-to-fine) matching algorithm, the objective function (in the optimization algorithm) is successively approximated by lower-dimensional smooth functions constructed to have significantly fewer local minima. The method constructs them based on selecting driving anatomical features, represented as distinct "attribute" vectors, for the "matching". The aim is to highly reduce ambiguity in finding correspondence. Second, HAMMER registered our data well and it was stable and reasonably fast as a rigorous nonlinear registration method (i.e. approximately 2 h per image). The third column of Fig. 6 illustrates how well HAMMER was able to squeeze oversized ventricles (shown in the second column) into the atlas used for registration.[4] Third, the HAMMER software generates a tissue (e.g. gray matter) density map named "RAVENS" map [12–15], with interesting properties for our image analyses. For example, by adjusting the density of a tissue whenever nonlinear registration expands or contracts the brain geometry, the RAVENS map preserves the total amount of tissue in any defined region, which sets it apart from density maps of other methods. Furthermore, a validation [12] supported that SPM voxel-based statistical analysis can be performed on these maps. The RAVENS maps can also be analyzed with machine-learning methods.

Section 2 describes the MRI post-processing. Section 3 describes the system architecture, including samples of program usage. The paper concludes with Section 4, which discusses system requirements and program availability.

2. MRI post-processing

2.1. *Overview*

Fig. 1 shows the current input image types for STAMP. These image types (T_1- and T_2-weighted image, T_2 map, T_2^* map, DTI image) are each spatially in their own distinct "subject space", but here it suffices to identify them with a shared "S" tag (i.e. "subject space") as shown. STAMP outputs many image types. Among these, we first define some key ones below, and use Fig. 1 to group them spatially for clarity:

(1) An image spatially normalized by deformable nonlinear registration using the HAMMER tool into an atlas space, i.e. the "Hammer space" ("H"), identified as, e.g. $I_{T_1,\mathrm{H}}$ and $I_{T_2,\mathrm{H}}$.
(2) An image created by segmentation into numerous brain regions defined by an atlas, aka labeling. The labeling generates, e.g. $I_{T_1,\mathrm{S}}$ from $I_{T_1,\mathrm{S}}$.
(3) RAVENS map for each of GM ($I_{\mathrm{RAVENS\_GM,R}}$), WM ($I_{\mathrm{RAVENS\_WM,R}}$), ventricles (V) ($I_{\mathrm{RAVENS\_V,R}}$).[5]

The "A1" tag in Fig. 1 indicates some output images are spatially in a standard atlas space we identify as "Atlas1", distinct from the atlas defined earlier for HAMMER use. By aligning all of its input image types into this standard A1 space (using rigid-body and affine transforms prior to HAMMER) STAMP ensures that the HAMMER registration will put all input image types into the same space. Note that the HAMMER tool supports the HAMMER registration of 8-bit unsigned integer images but not other datatypes such as 16-bit integer or 32-bit floating point (such as our T_2 map, T_2^* map, and DTI images), but STAMP does, which is a novel contribution. The HAMMER tool generates a deformation vector field file during the registration of an image and contains a program that can apply this file to identically deform (i.e. spatially normalize) a second image. We have developed an improved version of this program, based on ITK [8], for STAMP that supports signed and unsigned 8-, 16-, and 32-bit images and 32- and 64-bit floating point images.

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[2] In this paper "supercomputer" means a multi-node computer cluster using PBS or one of the latest multi-core computers using PBS.

[3] The data management is based on uniquely identifying images, their types, and their relations (Section 3.3).

[4] The subject used in the figures is a 79-year-old male ALS subject chosen as a "worst-case scenario" registration example.

[5] While RAVENS images are created by the HAMMER tool they are not in the H space, as the HAMMER tool uses a different nonlinear registration when creating RAVENS, hence our "R" tag to identify the "RAVENS space".