Unobtrusive Integration of Data Management with fMRI Analysis

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We describe a plugin for SPM, a popular fMRI statistical processing package, which interfaces to the Dartmouth Experiment lab book, an ontology-based tool to help researchers manage metadata and maintain it in a uniform format. The SPM plugin permits the creation of batch processing scripts that automatically populate the lab book, thereby hiding the details of data management while permitting researchers to continue using an analysis tool with which they are familiar.

An important goal of the neuroscience community is widespread sharing of functional brain imaging data, both the images themselves and the associated metadata. The Dartmouth fMRI Data Center (fMRIDC, http://www.fMRIDC.org) provides a global repository for storing images, and is developing an extensible ontology of fMRI metadata to serve as a template for organizing and relating metadata from diverse labs. However, the data for the experiment lab book must currently be entered by hand, thereby decreasing the likelihood that a researcher will go to the extra trouble of using it.

This project builds upon fMRIDC work by integrating the experiment lab book with SPM (http://www.fil.ion.ucl.ac.uk/spm/) - a widely used fMRI statistical processing package - to automate metadata input into the experimental lab book while providing easy batch script creation.

The integration is accomplished by designing a plug-in ('toolbox') for the latest release of SPM. Like SPM itself, the toolbox is implemented in MatLAB. It is platform independent and easy to install, although it requires that the software necessary for the experiment lab book (Protégé, http://protege.stanford.edu) also be installed. (Both
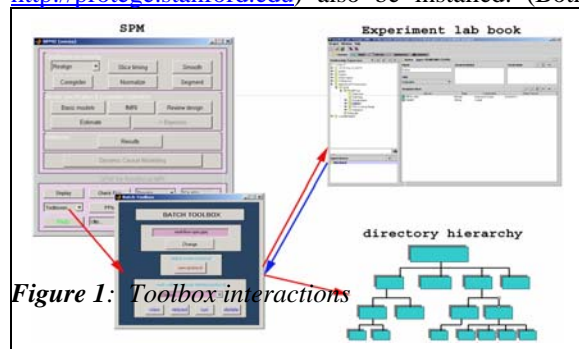

Figure 1: *Toolbox interactions*

SPM and Protégé are available free of charge). After being invoked from the main SPM interface, the toolbox interacts with the experiment lab book and the file system to read and write metadata into the ontology slots and to create the directory hierarchy (Figure 1).

The batch toolbox presents the user with an

Figure 2: *Defining a new protocol*

easy to follow input-driven interface. The researcher can define and store processing protocols (Figure 2) and later run these protocols as SPM batch processes (Figur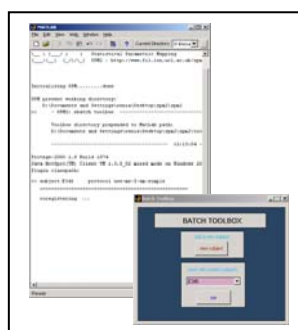e 3). When the toolbox is used for batch processing, it automatically saves the associated metadata into the experiment lab book and organizes processed images into an appropriate directory hierarchy. Thus, the toolbox eliminates the necessity for manual input of the statistical processing metadata in the lab book. Additionally, it allows the user to effortlessly define batch processing sequences via a familiar interface without using any programming or scripting language.

Figure 3: *Running a batch script from the toolbox*

This project is part of an effort to automate as much data input into the experiment lab book as possible, thus encouraging its use in neuroimaging laboratories, and leading to more widespread sharing of images and metadata.