

# Unobtrusive Integration of Data Management with fMRI Analysis

Xenia Hertenberg, Andrew Poliakov, PhD, James F. Brinkley, MD, PhD

Structural Informatics Group, Departments of Biological Structure and Medical Education and Biomedical Informatics,  
Computer Science and Engineering  
University of Washington, Seattle WA 98195



## Summary

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.

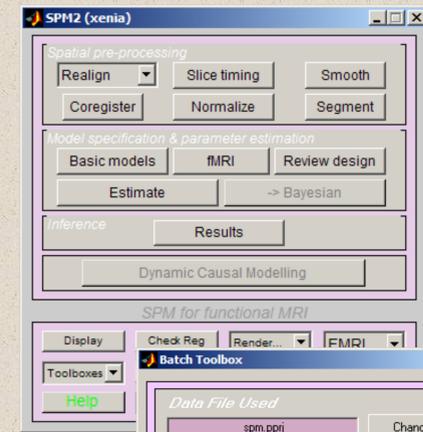
## Background

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 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 - a widely used fMRI statistical processing package - to automate metadata input into the experimental lab book while providing easy batch script creation.

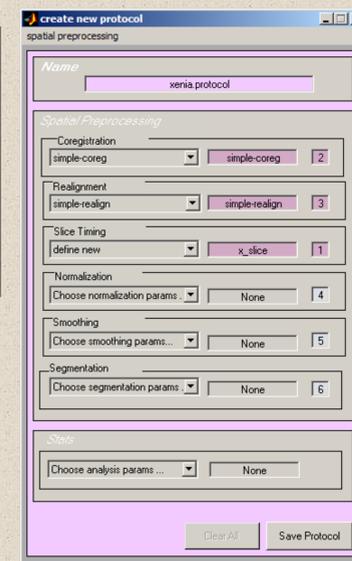
## Working with x\_batch

X\_batch is designed as a plugin ( '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 (Protégé) for the experiment lab book also be installed. Both 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.



## SPM toolbox:

- Default ontology loads automatically
- View/delete/run previously defined processing sequences (protocols)
- Create new processing sequences

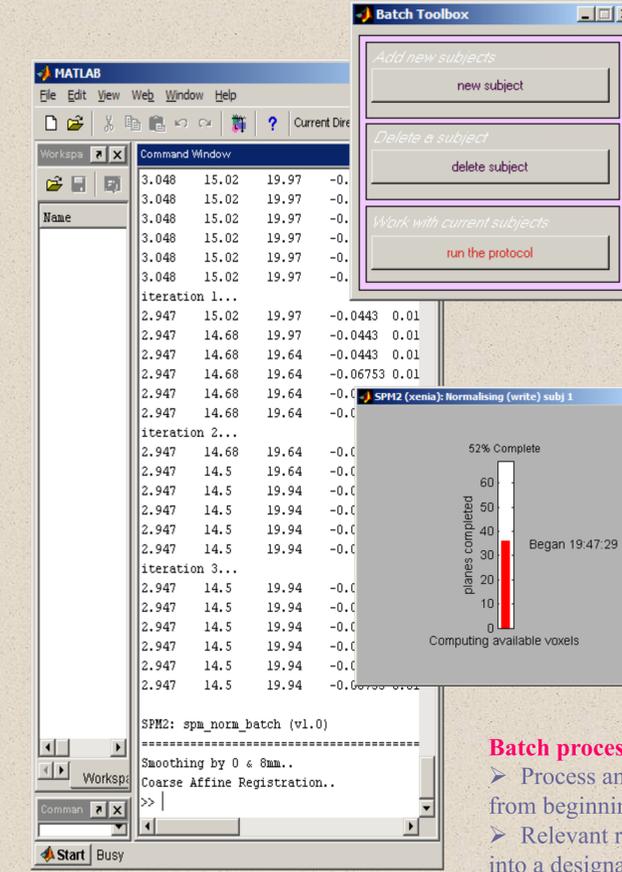


## Batch 'script' creation:

- No programming necessary
- Protocols consist of processing stages, each stage defined by its parameter set
- Use previously created parameter sets, define new ones, or use a combination
- Specify order of processing
- All parameters saved into the ontology

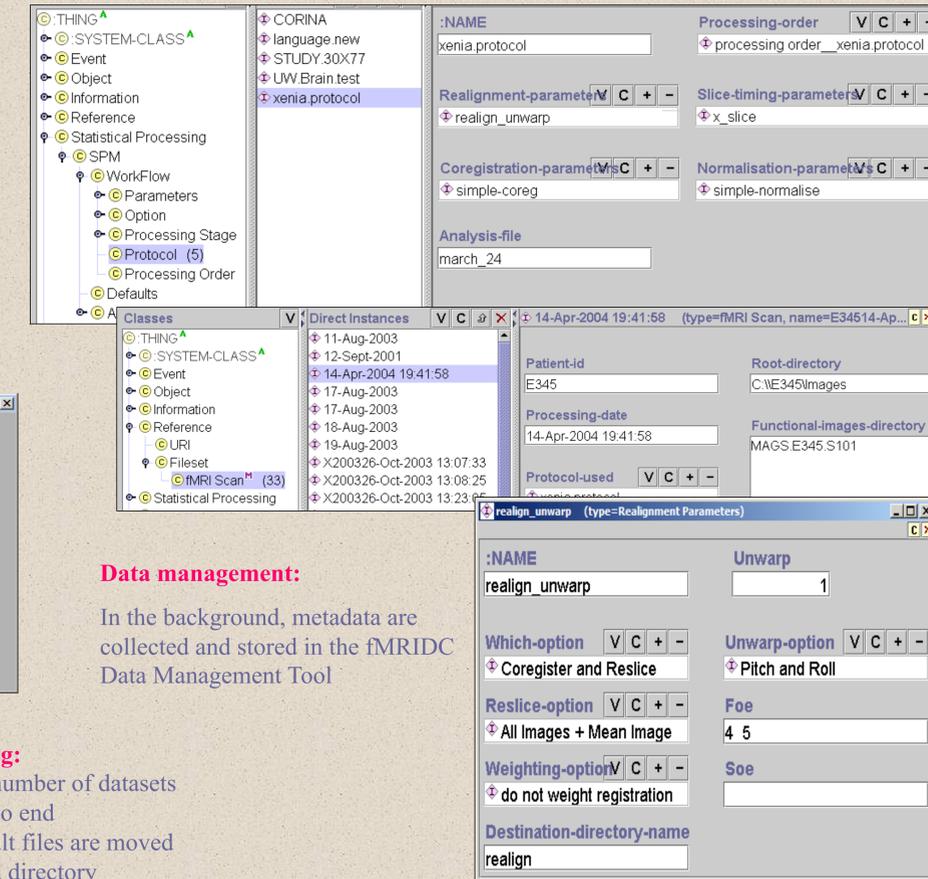
The batch toolbox presents the user with an easy to follow input driven interface. The researcher can define and store processing protocols and later run these protocols as SPM batch processes.

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.



## Batch processing:

- Process any number of datasets from beginning to end
- Relevant result files are moved into a designated directory



## Data management:

In the background, metadata are collected and stored in the fMRIDC Data Management Tool

## Acknowledgements

This work was funded by Human Brain Project grant RO1 MH/DC02310.

## Further information

SPM website: <http://www.fil.ion.ucl.ac.uk/spm/>  
fMRIDC website: <http://www.fMRIDC.org>  
Protégé website: <http://protege.stanford.edu>  
X\_batch webpage: <http://x-batch.sourceforge.net>

