Human Brain Mapping 2009

Print

Abstract Number: 2340 Last Modified: January 14 2009 Submitted By: Fernando Perez

NIPY: an open library and development framework for FMRI data analysis

M Brett¹, J Taylor², C Burns¹, K J Millman¹, F Perez¹, A Roche³, B Thirion⁴, M D'Esposito¹

¹Helen Wills Neuroscience Institute, University of California, Berkeley, CA, United States/²Dept. of Statistics, Stanford University, Palo Alto, CA, United States/³Neurospin, Commissariat à l'Energie Atomique, Gif-sur-Yvette, France/⁴Parietal team, INRIA, Saclay, France

Introduction: The NeuroImaging in Python project (NIPY: http://neuroimaging.scipy.org), developed with NIH funding (grant No. 5R01MH081909-02), is a modular package for FMRI data analysis and development that can be used both as a standalone tool or as a component library. Although several current analysis packages provide high quality algorithms (e.g. SPM, AFNI, FSL), the need exists for a highly scriptable environment that allows concise and flexible specification of job structure, exploration of algorithmic approaches, transparent parallel execution, and integration of algorithms across packages.

NIPY uses the Python programming language, the leading open-source language for high-level scientific computing. High-quality libraries allow Python to cover a range of areas for which Matlab is typically used. However, as a general language, Python has many advantages over Matlab in terms of maintainability, extensibility and scalability.

Methods: We use modern software development practices that improve software quality. Scientific computing projects often overlook these issues, resulting in suboptimal outcomes regarding reproducibility of results, usability of the tools and sustainability of the development effort. Some of these practices are:

- * Testing: extensive automated testing helps maintain the software's functionality during development. We use a testing framework that allows for fine grained and comprehensive test coverage of the software (Nose: http://somethingaboutorange.com/mrl/projects/nose).
- * Documentation: we document NIPY as part of its development, providing both automatically generated library references and end-user manuals with equations and graphics, both in HTML and print-quality PDF formats (Sphinx: http://sphinx.pocoo.org).
- * Collaborative development: we use a distributed version control system and the Launchpad site (http://launchpad.net) for code hosting and bug tracking. This enables parallel development by several groups while tracking the history and integrity of NIPY.

Results: We will show how to produce a standard univariate FMRI analysis, including a complete and scriptable pipeline with time series diagnostics, within and between subject registration, multi-subject statistics and visualization. This will illustrate the NIPY architecture in a context familiar to neuroimaging researchers. We will describe the available statistics functionality, which includes fixed effects as well as some random and mixed effects modeling, the specification of designs in terms of functions and factors, and tools for setting thresholds based on random field theory. We will show how to use high-level interfaces for parallelizing aspects of the analysis (being open source, NIPY imposes no licensing limits on how many processors can be used).

Finally, we will explain the NIPY architecture and how its components can be used both for implementing standard analysis protocols common in current tools and for developing new ones. This can be done by using NIPY's tools in a separate project, as illustrated by how BrainVisa (http://brainvisa.info) calls NIPY routines as part of its computational engine.

Conclusions: We have built an open library for FMRI data analysis development, with a focus on extensibility, reproducibility and openness. Our development process is fully open and we invite interested researchers to participate by using the system and adding their own contributions.