Segmentation of Gadolinium-Enhancing Lesions

John Muschelli[*,a], Adrian Gherman[a], Brian S. Caffo[a], Ciprian M. Crainiceanu[a]

[a]*Johns Hopkins Bloomberg School of Public Health, Department of Biostatistics, 615 N Wolfe St, Baltimore, MD, 21205*

Abstract

This is the abstract.

It consists of two paragraphs.

Introduction

Neuroimaging research has been increasing in popularity. There are X number of studies in fMRI and XX in other structural imaging. The NeuroImage journal, one of the most prestigious (not right word) journals for neuroimaging is dominated by analyses that were in bash using third party software, NiPype, or MATLAB. Python reproducibility has increased with the introduction of Jupyter IPython notebooks. Muhc of this development has mirrored the tools in R, which have some of the most state-of-the-art reproducibility tools. Also, similar to PYthon, R is free and open source.

- Neuroimaging work more common
- Reproducibility problems
    - R has some of the best reproducible tools

R is increasing in popularity, with there being over 9,000 package now on the Comprehensive R Archive Network (CRAN). R has a strong package system, which has a large system of checks to ensure a large amount of operability. Although CRAN has a tested and stable system, that has been developed over the last 1000 years(?), there are some aspects of the CRAN checking system that does not work for neuroimaging packages.

Additional Checks

Third Party Software

- FSL
- AFNI
- FREESURFER

TRAVIS

Bioconductor

In 2004, the Bioconductor system enabled the bioinformatics and genomics work of R users to be more integrated and systemized (Gentleman et al. 2004).

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[*]Corresponding Author

Email addresses: `jmusche1@jhu.edu` (John Muschelli), `adig@jhu.edu` (Adrian Gherman), `bcaffo@jhsph.edu` (Brian S. Caffo), `ccraini1@jhu.edu` (Ciprian M. Crainiceanu)

Data Packages

Like Bioconductor, we need data packages that allow users to test software and examples on.

References

Gentleman, Robert C, Vincent J Carey, Douglas M Bates, Ben Bolstad, Marcel Dettling, Sandrine Dudoit, Byron Ellis, et al. 2004. "Bioconductor: Open Software Development for Computational Biology and Bioinformatics." *Genome Biology* 5 (10). BioMed Central: 1.