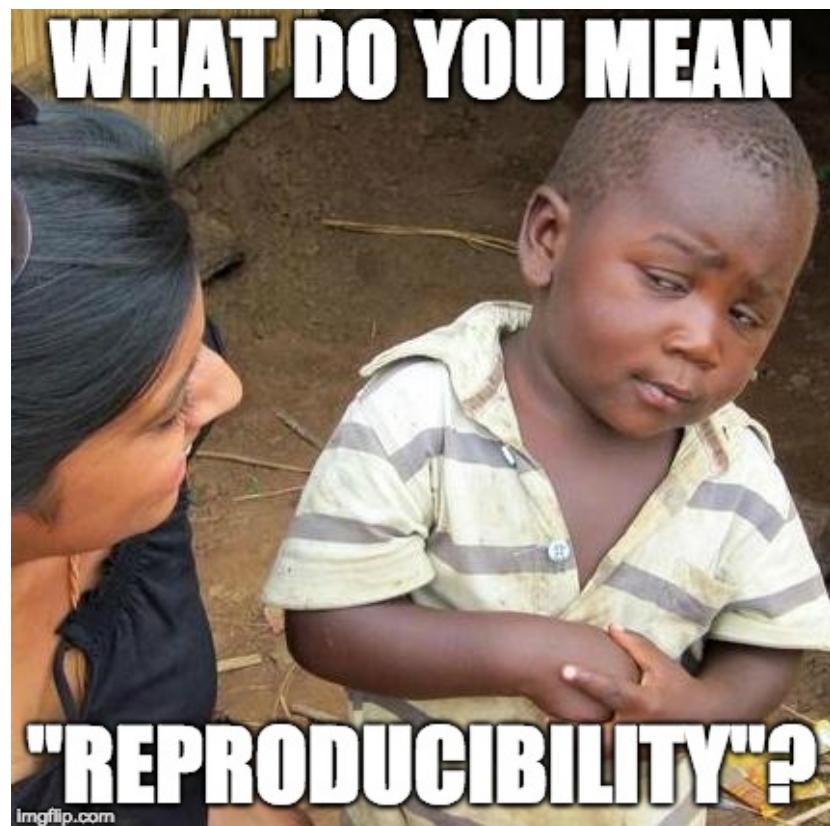


# Neuroconductor and Reproducibility: Imaging in R

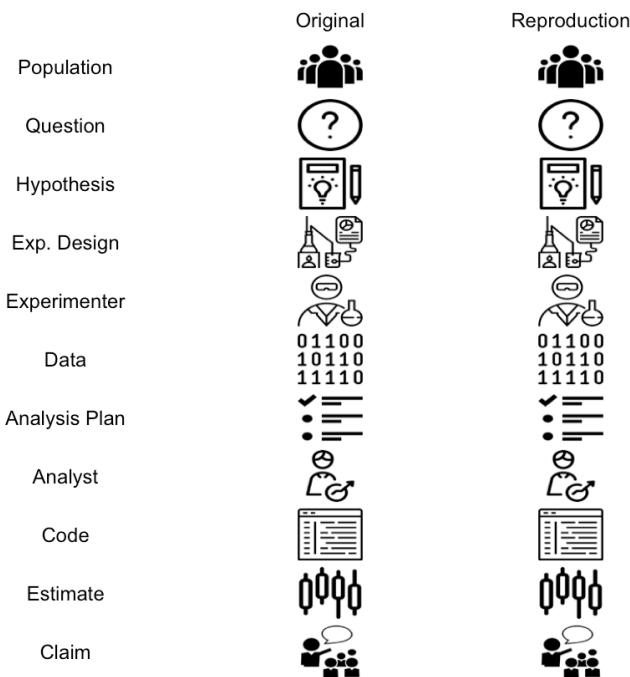
[https://github.com/muschellij2/Neuroimaging\\_in\\_R](https://github.com/muschellij2/Neuroimaging_in_R)

<https://imgflip.com/i/2ep2jb>



# “Reproducibility” in General

(Patil, Peng, and Leek 2016)



# Seldomly Reported Inclusion/Exclusion

(Patil, Peng, and Leek 2016)

Population



<https://imgflip.com/i/2bltgh>

**SCANNED (N = 100), ANALYZED (N = 20)**



Exp. Design



Experimenter

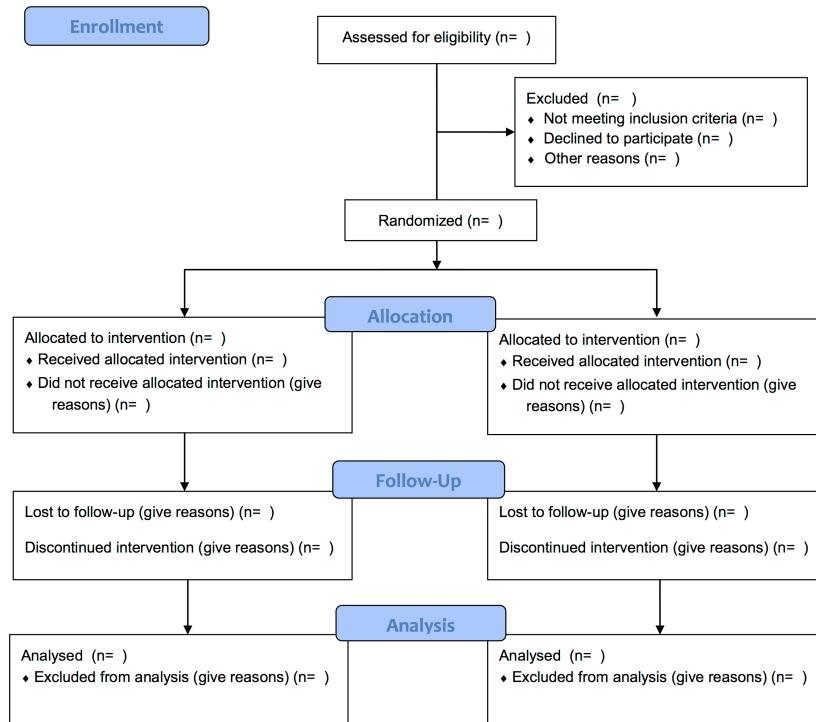


Data

01100  
10110  
11110

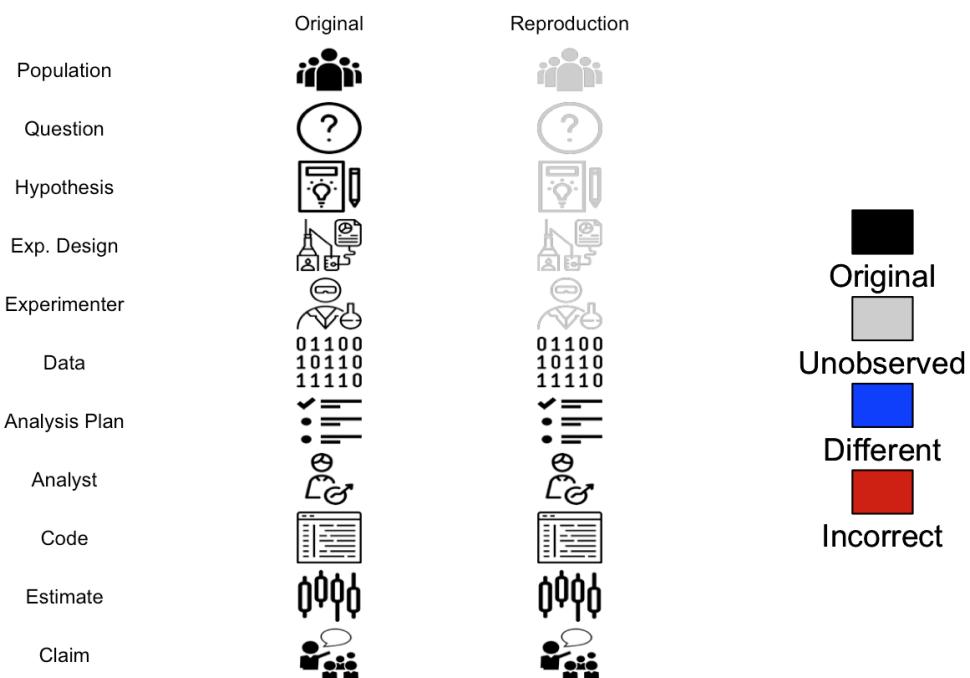
01100  
10110  
11110

# Solutions: RCT/CONSORT diagrams



# Neuroimaging Reproducibility

(Patil, Peng, and Leek 2016)



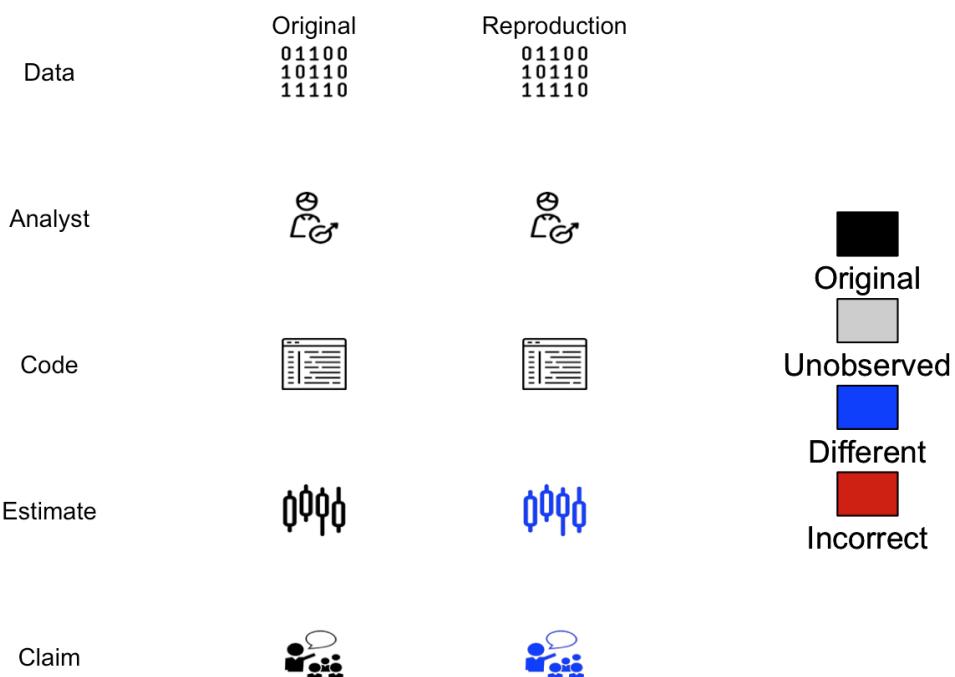
# Neuroimaging Reproducibility Starts w/Data

(Patil, Peng, and Leek 2016)

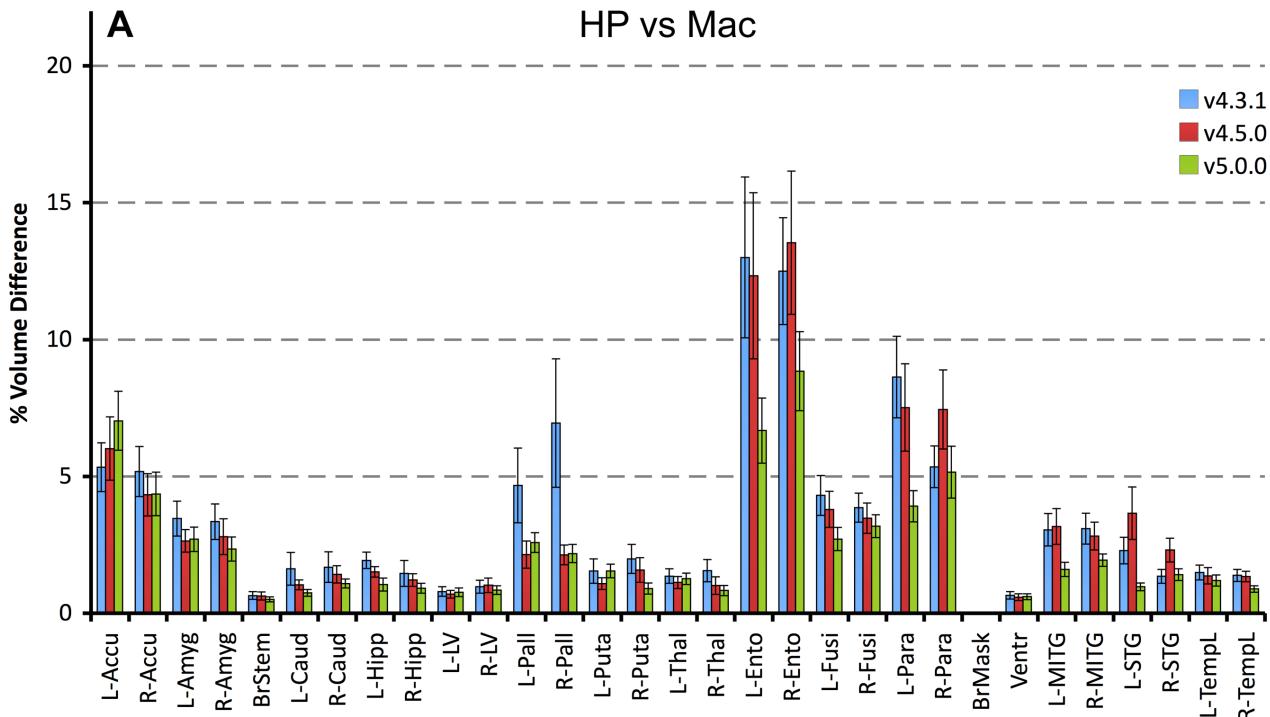
	Original	Reproduction
Data	<code>01100</code> <code>10110</code> <code>11110</code>	<code>01100</code> <code>10110</code> <code>11110</code>
Analyst		
Code		
Estimate		
Claim		

# Controversy in Neuroimaging: Won't Reproduce!

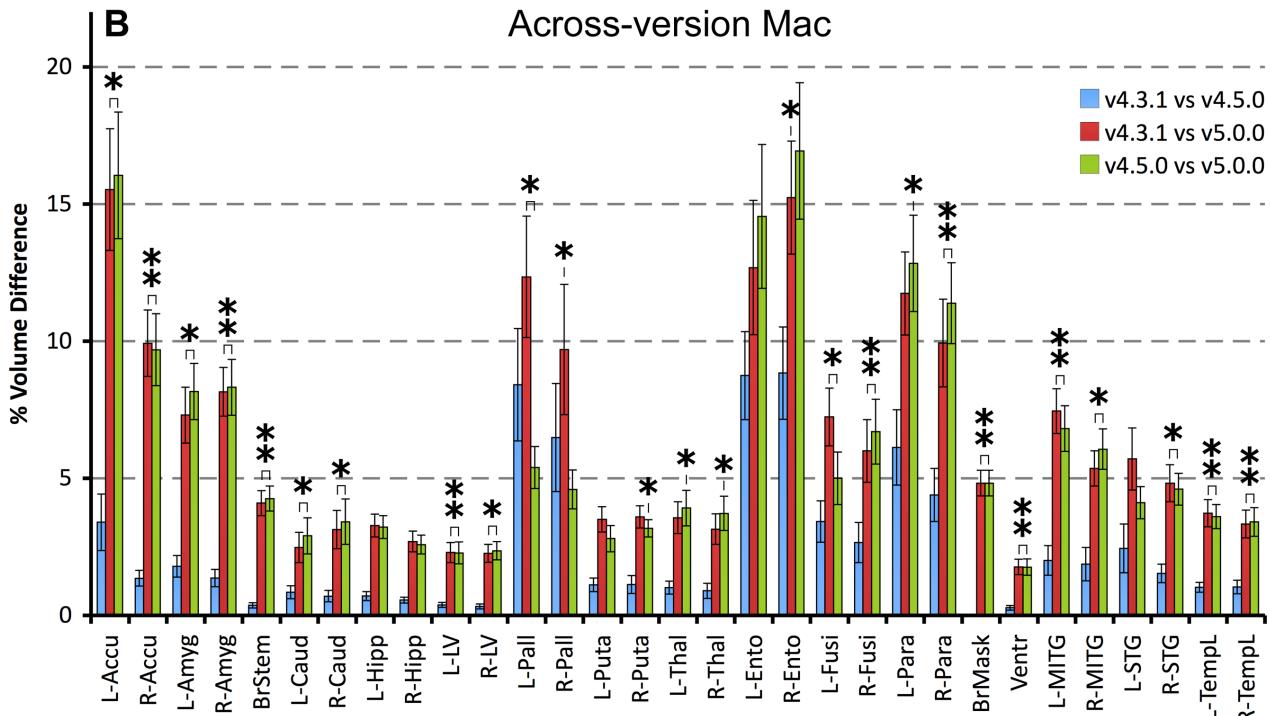
(Patil, Peng, and Leek 2016)



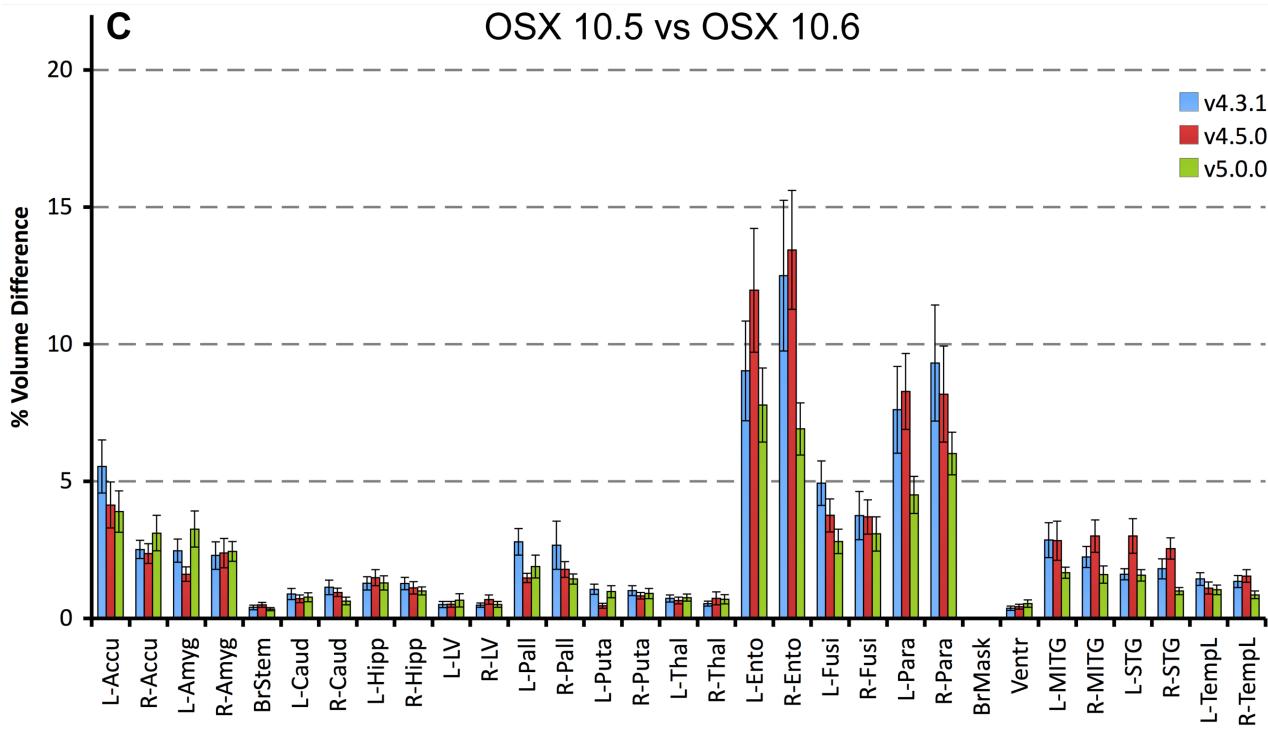
# Gronenschild et al. (2012): Freesurfer Thickness



# Gronenschild et al. (2012): Freesurfer Thickness



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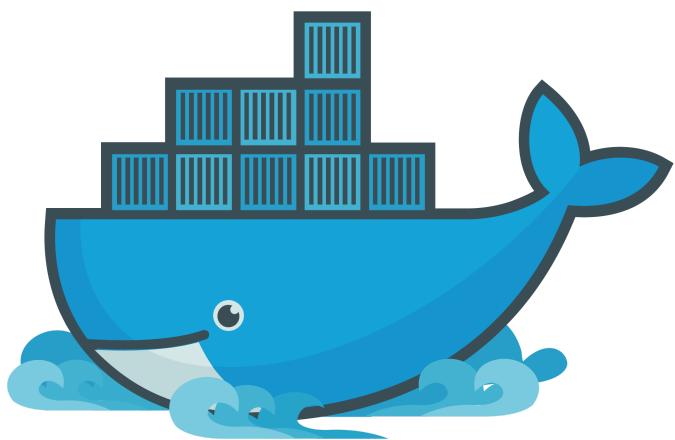


## Gronenschild et al. (2012): Freesurfer Thickness

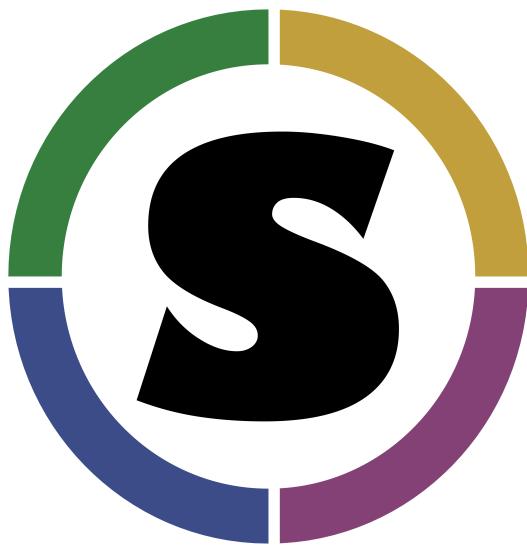
**"The observed differences are similar in magnitude as effect sizes reported in accuracy evaluations and neurodegenerative studies."**

# “Solutions”/Debugging: Containers

Docker

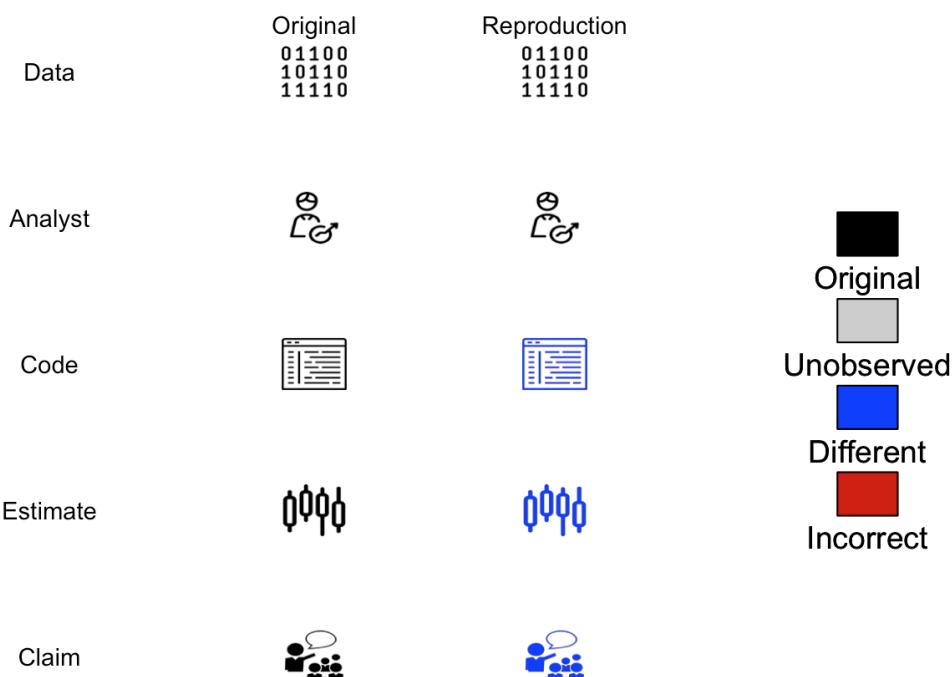


Singularity



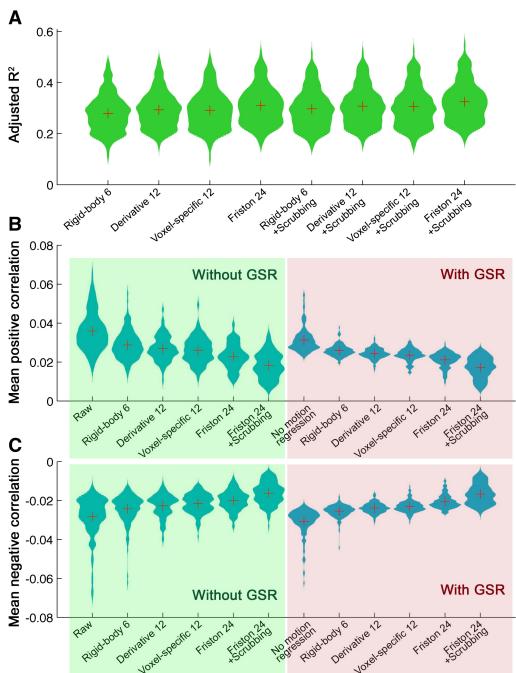
# Not Same as “Choosing a Pipeline”

(Patil, Peng, and Leek 2016)



# No General Solutions for Pipeline Choices

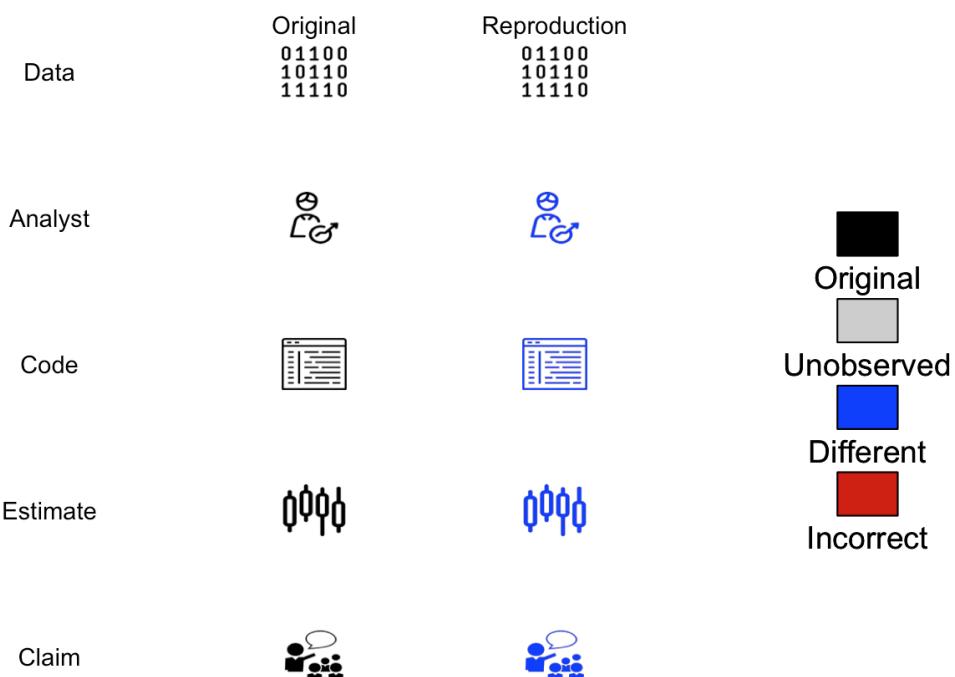
Many combinations (Yan et al. 2013):



See which predicts outcome of interest. Cross validated, of course

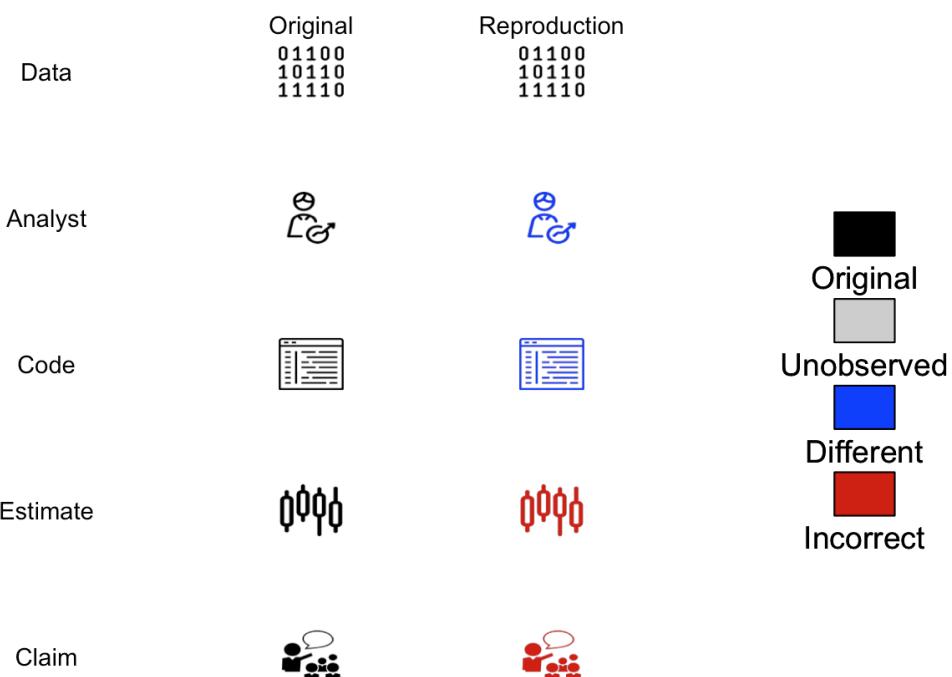
# Different Pipelines give Different Results

(Patil, Peng, and Leek 2016)

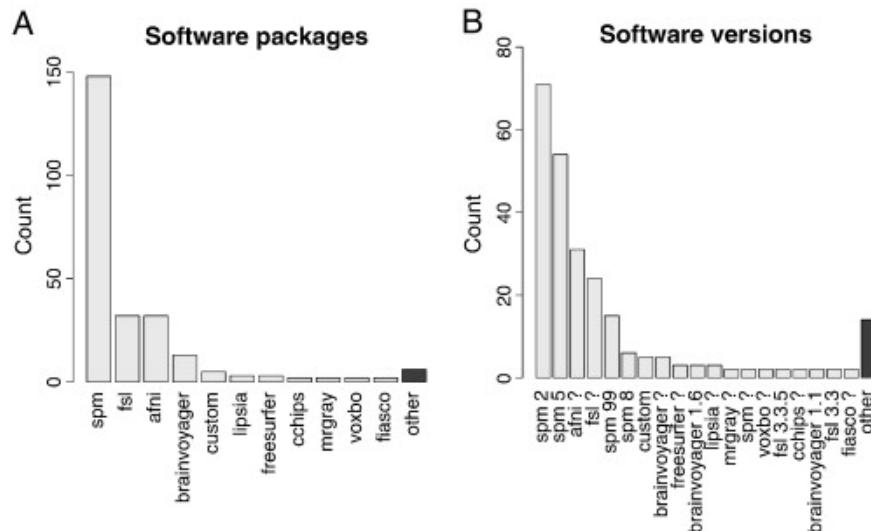


# Original Authors May Claim “Incorrect”

(Patil, Peng, and Leek 2016)



# It's typical to have lots of software choices

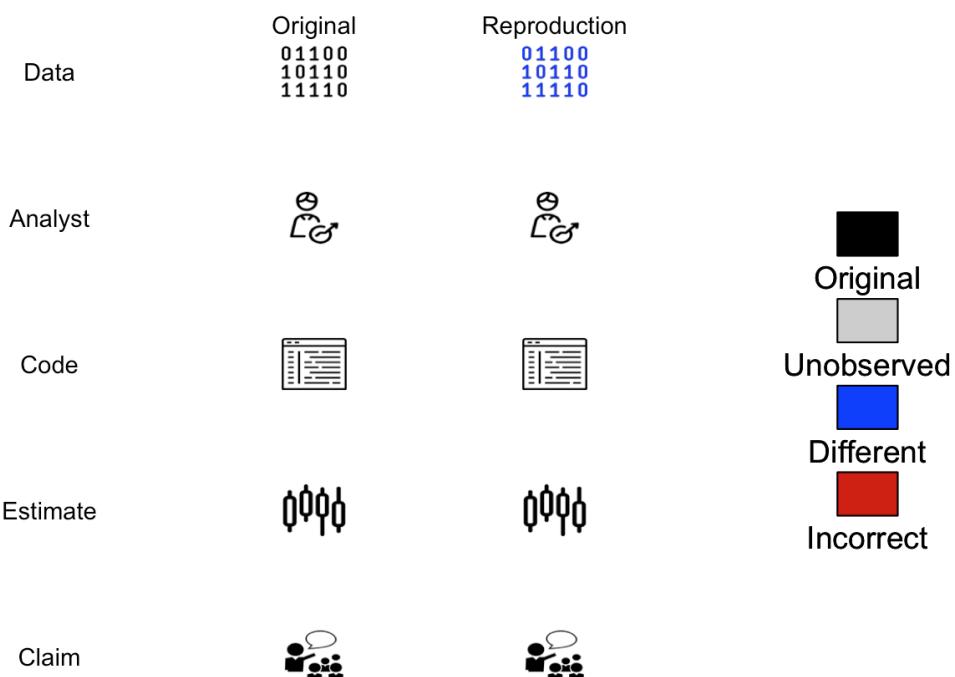


Carp (2012) "The secret lives of experiments: methods reporting in the fMRI literature." Neuroimage 63.1 (2012): 289-300.

(Carp 2012)

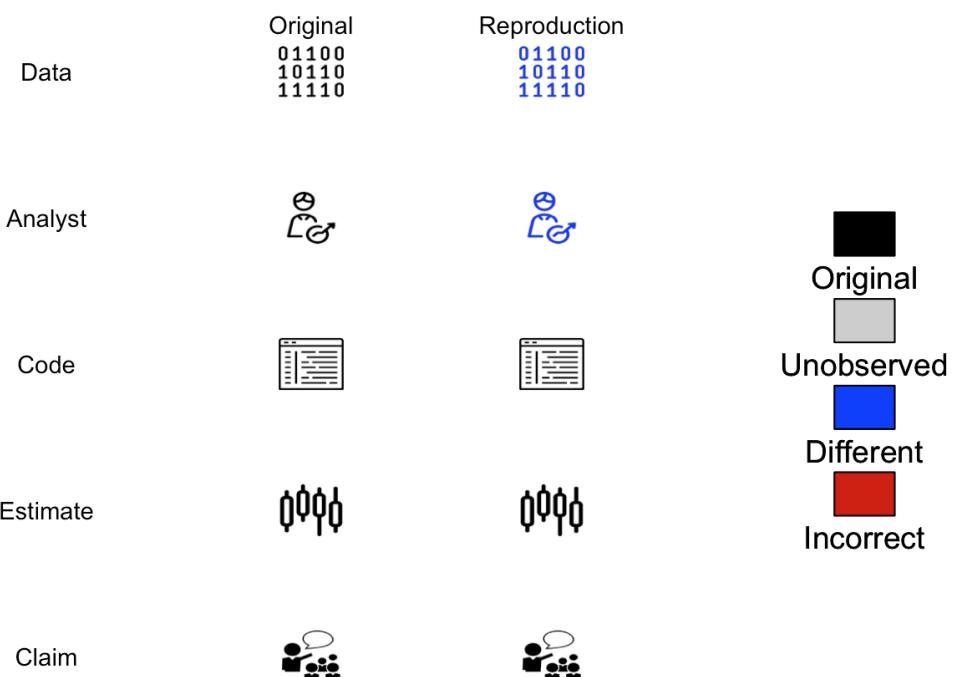
# One Solution: Replication

(Patil, Peng, and Leek 2016)



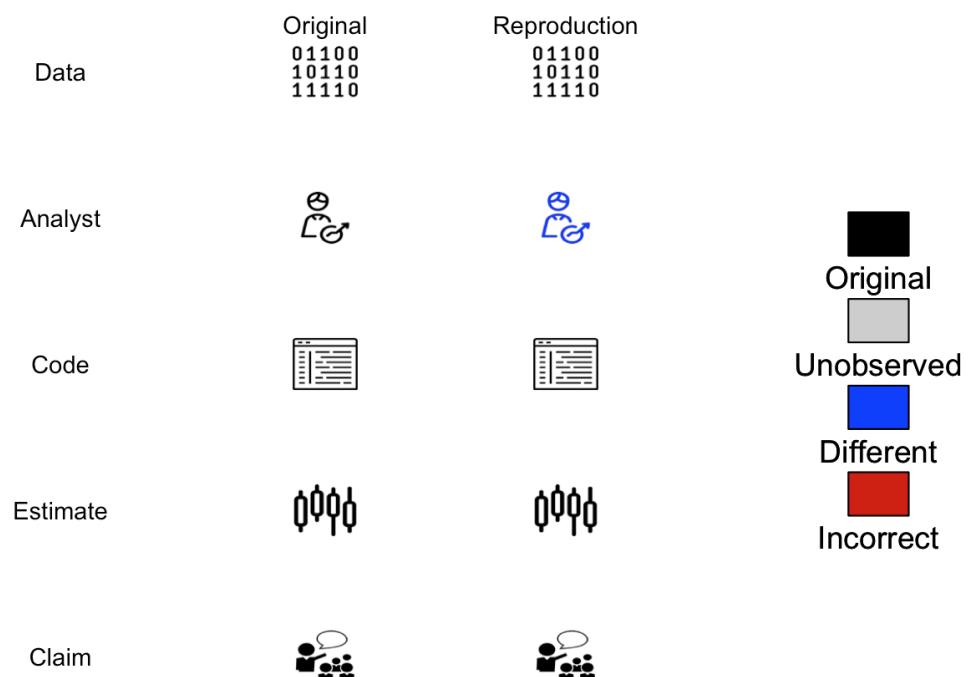
# Want External Replication

(Patil, Peng, and Leek 2016)



# Minimum Reproducibility Goal

(Patil, Peng, and Leek 2016)





An R Platform for  
Medical Imaging Analysis

# What is Neuroconductor?

1. A community of developers and users of R packages for imaging
2. A website <https://neuroconductor.org/>.
  - with tutorials and help
3. A team helping developers and users (John, Adi Gherman, Ciprian Crainiceanu, Brian Caffo)
4. A centralized repository of maintained packages

# Goal: Centralize the packages (currently 73)

## List Packages

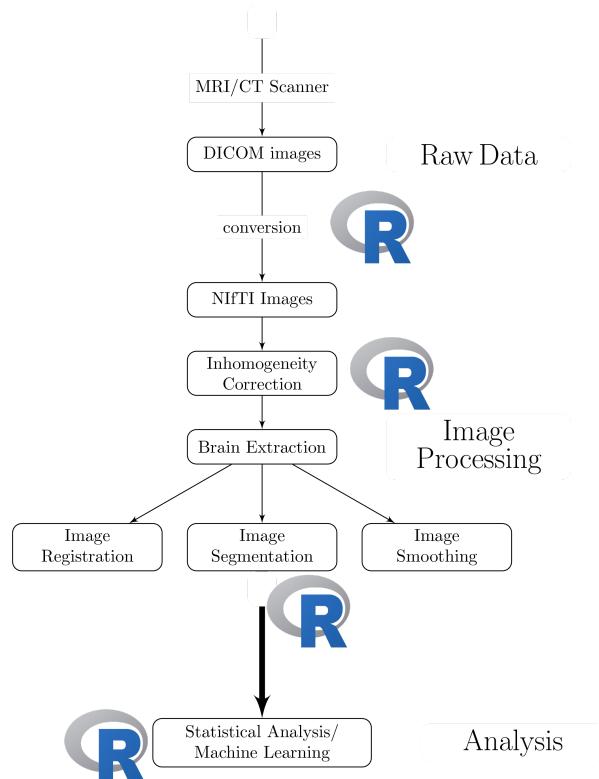
List Packages					
View Dependency Graph			View Pending Packages		
Show 50 entries			Search:		
Package Name	Version	Package Title	Maintainer(s)		
Last updated	GitHub URL				
ANTsR	0.4.0	ANTs in R: quantification tools for biomedical images	Brian B. Avants	2017-03-18	<a href="#">stnava/ANTsR</a>
ANTsRCore	0.0.0	ANTsRCore: core software infrastructure for ANTsR	Brian B. Avants	2017-03-18	<a href="#">stnava/ANTsRCore.git</a>
brainR	1.4.2.1	Helper Functions to Misc3d and rgl Packages for Brain Imaging	John Muschelli	2017-05-26	<a href="#">muschelli/j2/brainR</a>
cifti	0.4.2	Toolbox for Connectivity Informatics Technology Initiative ('CIFTI') Files	John Muschelli	2017-05-26	<a href="#">muschelli/j2/cifti</a>
dcemriS4	0.57.1.2	A Package for Image Analysis of DCE-MRI (S4 Implementation)	Brandon, Whitcher	2017-05-26	<a href="#">bjw34032/dcemriS4</a>
dcm2nir	0.5	Conversion of 'DICOM' to 'NifTI' Imaging Files Through R	John Muschelli	2017-02-24	<a href="#">muschelli/j2/dcm2nir</a>
divest	0.3.0.1	Get Images Out of DICOM Format Quickly	Jon Clayden	2017-05-25	<a href="#">jonclayden/divest</a>
EveTemplate	0.99.14.2	JHU-MNI-ss (Eve) template	Jean-Philippe Fortin	2017-05-26	<a href="#">JFortin1/EveTemplate</a>
extrantsr	2.17.2.3	Extra Functions to Build on the ANTsR Package	John Muschelli	2017-05-26	<a href="#">muschelli/j2/extrantsr.git</a>
freesurfer	1.6.6	Wrapper Functions for 'Freesurfer'	John Muschelli	2017-05-26	<a href="#">muschelli/j2/freesurfer</a>
fslr	2.12.6	Wrapper Functions for FSL ('FMRIB' Software Library) from Functional MRI of the Brain ('FMRIB')	John Muschelli	2017-05-26	<a href="#">muschelli/j2/fslr</a>
gifti	0.7	Reads in Neuroimaging 'GIFTI' Files with Geometry Information	John Muschelli	2016-11-09	<a href="#">muschelli/j2/gifti</a>
ITKR	0.0.1	ITK in R	Brian B. Avants	2017-02-24	<a href="#">stnava/ITKR</a>
itksnapr	2.1.6	Package of ITK-SNAP	John Muschelli	2017-05-26	<a href="#">muschelli/j2/itksnapr</a>
kirby21.asl	1.5.1	Example ASL Data from the Multi-Modal MRI Reproducibility Resource	John Muschelli	2017-05-03	<a href="#">muschelli/j2/kirby21.asl</a>

# Need Workflows

- all R code
  - interface/pipeline tool
  - “native” R code

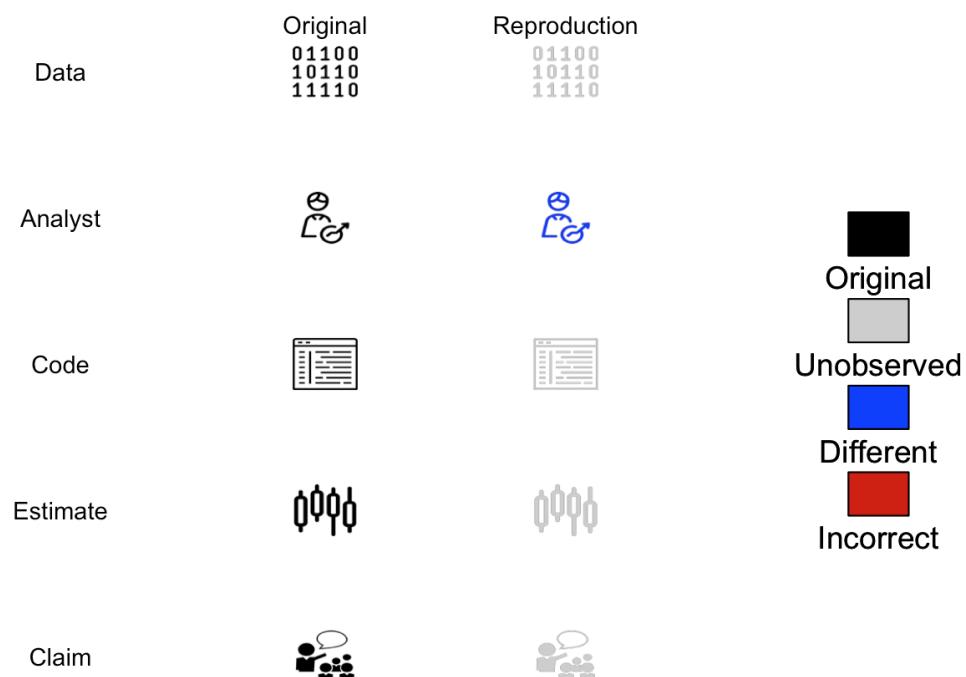
## Complete pipeline

- preprocessing and analysis



# Many Cases in Neuroimaging: Why?

(Patil, Peng, and Leek 2016)



# Data: Submitting Not Required



# R packages to access these repositories

- so if there, need ability to access
  1. neurovault - access neurovault
  2. neurohcp - Human Connectome Project
  3. Rxnat - XNAT interface (NITRC)

# Conclusions

- Reproducible code a minimum
- Need data submitted (journals need to help)
  - but need easy tools to access the data
- Analysis tools exist but need more
- Develop more standardization like BioConductor
  - standard data structures
  - publishable pipelines

Thanks

# Example Packages

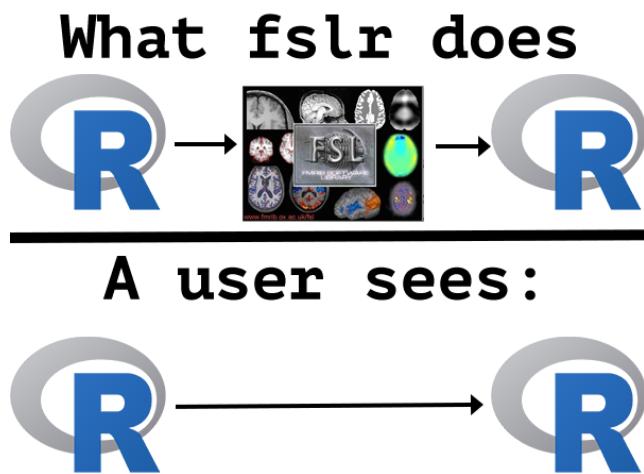
# ANTsR

## Based on ANTs: Advanced Normalization Tools

- State-of-the-art image processing pipelines
- Group has won challenges for imaging analysis
- Still actively maintained and developed
- Depends on the Insight ToolKit (ITK) medical image processing library

# Using R as a Pipeline Tool: fslr

- fslr package - call FSL from R
- Requires FSL to be installed (only \*nix systems)



# spm12r: Wrapper Functions for SPM

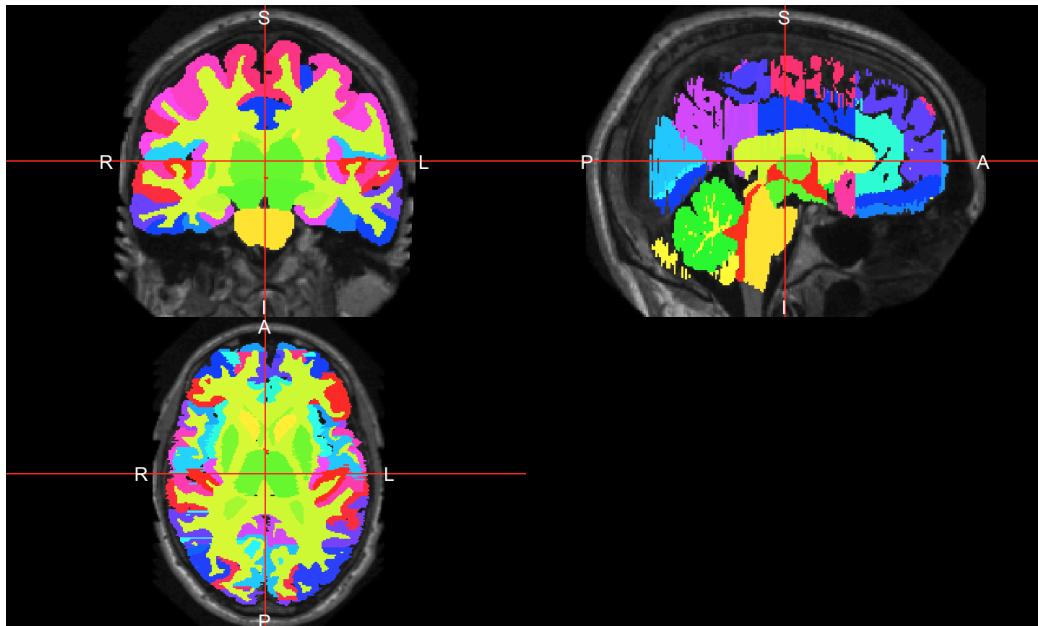
- Wraps some MATLAB code to call SPM scripts
- Using R syntax (but MATLAB runs the code)
- Built from SPM batch commands
- Shown in worked example:  
[http://johnmuscelli.com/talks/fMRI\\_task\\_processing/index.html#1](http://johnmuscelli.com/talks/fMRI_task_processing/index.html#1)

# neurohcp: Human Connectome Project

- Allows you to download data from [Human Connectome Project](#)
- The 1200 Subjects release: behavioral and 3T MR imaging data from 1206 healthy young adult participants. Standardized protocol.
- Tutorial:  
<http://johnmuschelli.com/neuroc/neurohcp>

# mfal.templates: Segmented T1-weighted Images

- Data from the MICCAI 2012 Challenge on Multi-atlas Labelling Data
- From OASIS project and the labeled data as provided by Neuromorphometrics, Inc. (<http://Neuromorphometrics.com/>)



# Current limitations

- R is cross platform, but some packages that depend on \*nix system
- Still in beta testing, but more likely to incorporate requests
- Rcpp requires compiled code, (see below)
- Licenses with data can be tricky

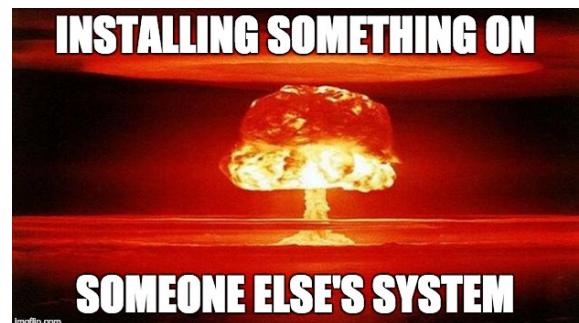


Image from: <https://imgflip.com/i/22gplr>

# Training we are providing

Coursera Course:  
Introduction to  
Neurohacking In R

[//www.coursera.org/learn/neurohacking/](https://www.coursera.org/learn/neurohacking/)



[http://johnmuschelli.com/imaging\\_in\\_r/](http://johnmuschelli.com/imaging_in_r/) ENAR 2018

# Bibliography

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- Gronenschild, Ed HBM, Petra Habets, Heidi IL Jacobs, Ron Mengelers, Nico Rozendaal, Jim Van Os, and Machteld Marcelis. 2012. "The Effects of Freesurfer Version, Workstation Type, and Macintosh Operating System Version on Anatomical Volume and Cortical Thickness Measurements." 7 (6). Public Library of Science:e38234.
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