

Showing your working:

A guide to reproducible neuroimaging analyses



 @kirstie_j

<https://GitHub.com/KirstieJane/ReproducibleResearch>
doi: <https://dx.doi.org/10.6084/m9.figshare.4244996>



- Postdoc in Brain Mapping Unit, Department of Psychiatry, University of Cambridge
- 2016/17 Mozilla Fellow for Science



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doi: <https://dx.doi.org/10.6084/m9.figshare.4244996>

Reproducible vs Replicable



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Code

Same

Different

Data

Same

Different



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Same

Different

Reproducible

Data

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Code

Same

Different

Reproducible

Robust

Data

Same

Different

Replicable



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Code

Data

Same

Different

Same

Reproducible

Replicable

Different

Robust

Generalisable



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Barriers to reproducible research



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Is not considered
for promotion

Requires
additional skills

Plead the 5th

Support
additional users

Takes time

Barriers to reproducible research

Held to higher
standards than
others

Publication bias
towards novel findings



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Start small



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Protocols.io



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doi: <https://dx.doi.org/10.6084/m9.figshare.4244996>



Your protocols x



Explore

View

Help



protocols.io > researchers > Kirstie Whitaker > protocols > UCHANGE structural neuroimaging pipeline protocols groups researchers jobs articles journal

+ New protocol

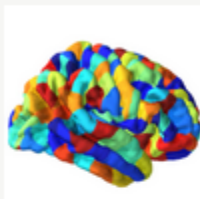
Viewing

✓ How to create a new protocol

v 2 ●

Personal

🌐 UCHANGE structural neuroimaging pipeline



UCHANGE structural neuroimaging pipeline [v1]



AUTHORS: KIRSTIE WHITAKER
BRAIN MAPPING UNIT, DEPARTMENT OF PSYCHIATRY, UNIVERSITY OF CAMBRIDGE

6 steps
0 private and 0 public forks
34 views

CONTACT:  KIRSTIE WHITAKER



Run



Publish

Edit



Steps

Before start

Comments

Metrics

Step 1
Check or complete software installation

Step 1
Check or complete software installation

You must have the following software libraries installed:

• **FreeSurfer** <https://surfer.nmr.mgh.harvard.edu>

Kirstie_J
research
14996



search protocols, groups and more

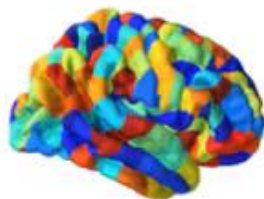


My protocols

Journal



save in journal



UCHANGE structural neuroimaging pipeline

13 steps

KIRSTIE WHITAKER, BRAIN MAPPING UNIT, DEPARTMENT OF PSYCHIATRY, UNIVERSITY OF CAMBRIDGE

CONTACT:  KIRSTIE WHITAKER

0/13

STEPS
COMPLETED

Step 1 Check or complete software installation You must have the following software libraries installed: Freesurfer: <https://s...> [read more](#)

Step 2 Set up your .bashrc file Open gedit and make sure your .bashrc file contains the following text:

Step 3 Set up directory structure You must have the appropriate input files in the displayed directory structure: Inside SUB_... [read more](#)

Step 4 Put the fsaverageSubP folder in the SUB_DATA directory The fsaverageSubP directory contains the 308 parcellation and nee... [read more](#)

Step 1

Check or complete software installation

You must have the following software libraries installed:

- **Freesurfer**: <https://surfer.nmr.mgh.harvard.edu/fswiki/DownloadAndInstall>
- **FSL**: <http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FslInstallation>
- **Anaconda**: <https://www.continuum.io/downloads>

From within **Anaconda** install the following python packages following the command below:

- [VTK](#)
- [Mayavi](#)
- [Nibabel](#)
- [pysurfer](#)

COMMAND (LINUX)

```
conda install vtk
```



Help



j
h
6

Coding your analyses



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Comments are your friend!



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```

1  #!/bin/bash
2
3  #=====
4  # Created by Kirstie Whitaker on 13th April 2016
5  #
6  # DESCRIPTION:
7  #   This code conducts a brain and head extraction of the PDw image to which
8  #   the quantitative multiparametric mapping (MPM) images have been aligned.
9  #   It then uses the head mask to set all voxels outside of the head to
10 #   zero for the quantitative MPM images and uses the brain mask to create
11 #   brain extracted versions of the MPM images (where all voxels outside of
12 #   the brain have been set to zero.
13 #
14 # USAGE:
15 #   NSPN_mpm_bet_mask.sh <pdw_file>
16 #
17 # INPUTS:
18 #   pdw_file : Proton density weighted file to which the MPM
19 #               quantitative maps are aligned.
20 #
21 # EXPECTS:
22 #   The following files should be in the same directory as the
23 #   input file:
24 #
25 #       R1.nii.gz      MT.nii.gz
26 #       R1s.nii.gz     A.nii.gz
27 #
28 # OUTPUTS:
29 #   All output are in the same directory as the input file.
30 #   A sub-directory called PDw_bet is created and contains all the
31 #   files created by FSL's bet command
32 #
33 #       R1_head.nii.gz   R1_brain.nii.gz

```

```

91
92 # Erode the brain mask by 3mm
93 if [[ ! -f ${mpm_dir}/PDw_brain_ero3.nii.gz ]]; then
94     fslmaths ${bet_dir}/PDw_brain.nii.gz -ero ${bet_dir}/PDw_brain_ero3.nii.gz
95 fi
96
97 #=====
98 # Now make the brain and head files for each of the
99 # calculated MPM files
100 #=====
101 echo -n " Applying masks"
102 for f_name in PDw ${calc_filename_list[@]}; do
103
104     # Don't run if it's already complete!
105     if [[ ! -f ${mpm_dir}/${f_name}_head.nii.gz ]]; then
106         echo -n " - ${f_name}"
107         fslmaths ${bet_dir}/PDw_brain_ero3.nii.gz \
108             -bin \
109             -mul ${mpm_dir}/${f_name}.nii.gz \
110             ${mpm_dir}/${f_name}_brain.nii.gz
111
112         fslmaths ${bet_dir}/PDw_brain_outskin_mask.nii.gz \
113             -bin \
114             -mul ${mpm_dir}/${f_name}.nii.gz \
115             ${mpm_dir}/${f_name}_head.nii.gz
116     fi
117 done # Close the mpm calculated file loop
118 echo ""
119
120 #=====
121 # ALL done!
122 #=====

```



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Aim for 40% comments in your code



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Share your comments with the original author



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(which is almost
always going to be
YOU!)



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Python vs R

(vs Matlab vs STATA etc...)



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R Studio

<https://www.rstudio.com>



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RStudio

File Edit Code View Plots Session Build Debug Tools Help

Go to file/function

Project: (None)

Environment History

Files Plots Packages Help Viewer

The R Language Find in Topic

Statistical Data Analysis

Manuals

Reference

Console

```
> mean(c(1,2,5))
[1] 2.666667
```

198 observations of 8 variables

	column1	column2	column3	column4	column5
1	training	1	right	leftresponse	incompati
2	training	2	right	rightresponse	compatibl
3	training	2	right	rightresponse	compatibl
4	training	0	left	leftresponse	compatibl
5	training	1	right	leftresponse	incompati
6	training	1	right	leftresponse	incompati
7	training	2	right	rightresponse	compatibl
8	block1	1	right	leftresponse	incompati
9	block1	2	right	rightresponse	compatibl

An Introduction to R
Writing R Extensions
R Data Import/Export

The R Language Definition
R Installation and Administration
R Internals

Packages
Search Engine & Keywords

RStudio

File Edit Code View Project Workspace Plots Tools Help

Go to file/function

Project: (None)

Workspace History

Data

diamonds 53940 obs. of 10 variables

Values

aveSize 0.7979

clarity character[8]

p ggplot[8]

Functions

format.plot(plot, size)

Files Plots Packages Help

Zoom Export Clear All

Diamond Pricing

Price

Carat

Clarity

- I1
- SI2
- SI1
- VS2
- VS1
- VVS2
- VVS1
- IF

Console

```
15:1 (Top Level) R Script
> library(ggplot2)
> source("plots/formatPlot.R")
> View(diamonds)
> summary(diamonds)
> summary(diamonds$price)
> aveSize <- round(mean(diamonds$carat), 4)
> clarity <- levels(diamonds$clarity)
> p <- qplot(carat, price,
+ data=diamonds, color=clarity,
+ xlab="Carat", ylab="Price",
+ main="Diamond Pricing")
> format.plot(p, size=24)
> |
```

Min. x: 0.000 Min. y: 0.000 Min. z: 0.000
1st Qu.: 4.710 1st Qu.: 4.720 1st Qu.: 2.910
Median: 5.700 Median: 5.710 Median: 3.530
Mean: 5.731 Mean: 5.735 Mean: 3.539
3rd Qu.: 6.540 3rd Qu.: 6.540 3rd Qu.: 4.040
Max.: 10.740 Max.: 58.900 Max.: 31.800

> summary(diamonds\$price)
Min. 1st Qu. Median Mean 3rd Qu. Max.
326 950 2401 3933 5324 18820



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OVERVIEW

TUTORIAL

ARTICLES

GALLERY

REFERENCE

DEPLOY

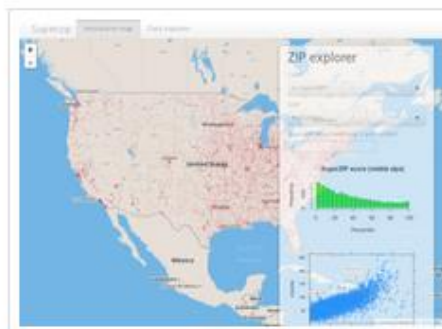
HELP

Gallery

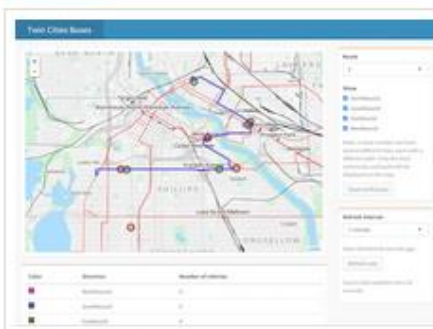
This gallery contains useful examples to learn from. Visit the [Shiny User Showcase](#) to see an inspiring set of sophisticated apps.

Interactive visualizations

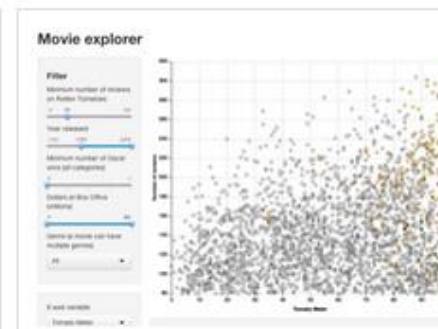
Shiny is designed for fully interactive visualization, using JavaScript libraries like [d3](#), [Leaflet](#), and [Google Charts](#).



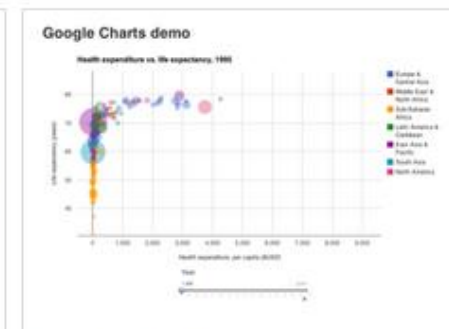
SuperZip example



Bus dashboard



Movie explorer



Google Charts



Shiny gallery

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doi: <https://dx.doi.org/10.6084/m9.figshare.4244996>

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Powered by Python**

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Matplotlib & Seaborn

<http://matplotlib.org>

<http://stanford.edu/~mwaskom/software/seaborn>

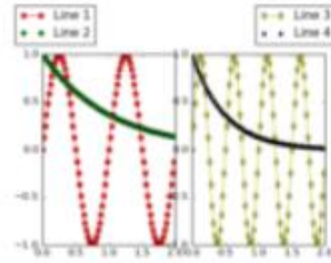


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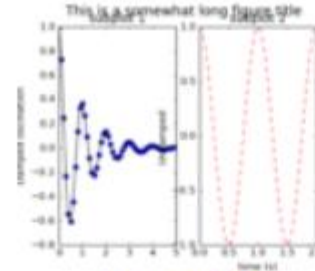
<https://GitHub.com/KirstieJane/ReproducibleResearch>
doi: <https://dx.doi.org/10.6084/m9.figshare.4244996>

Matplotlib gallery

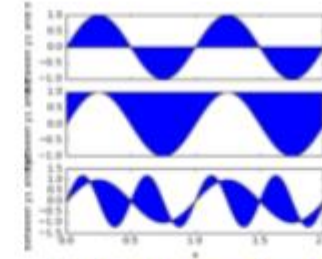
Click each
example to see
source code



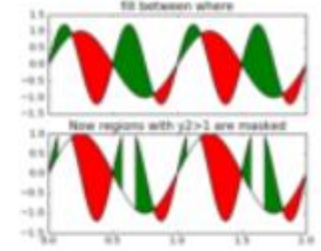
figlegend_demo



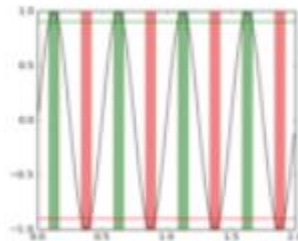
figure_title



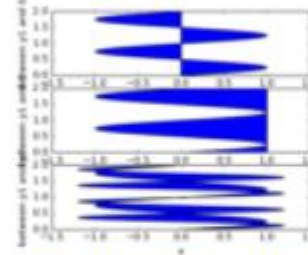
fill_between_demo



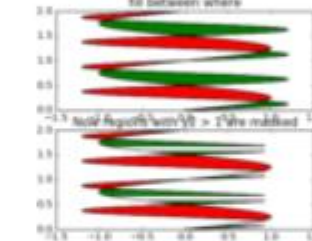
fill_between_demo



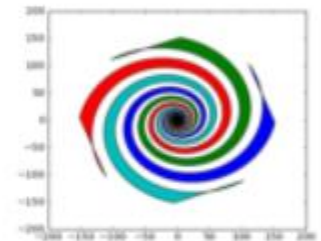
fill_between_demo



fill_betweenx_demo



fill_betweenx_demo



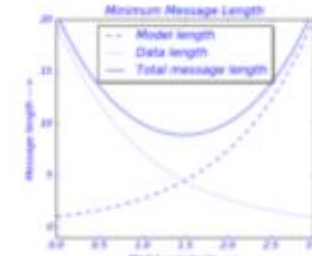
fill_spiral



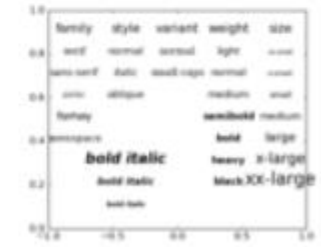
finance_demo



finance_work2



findobj_demo

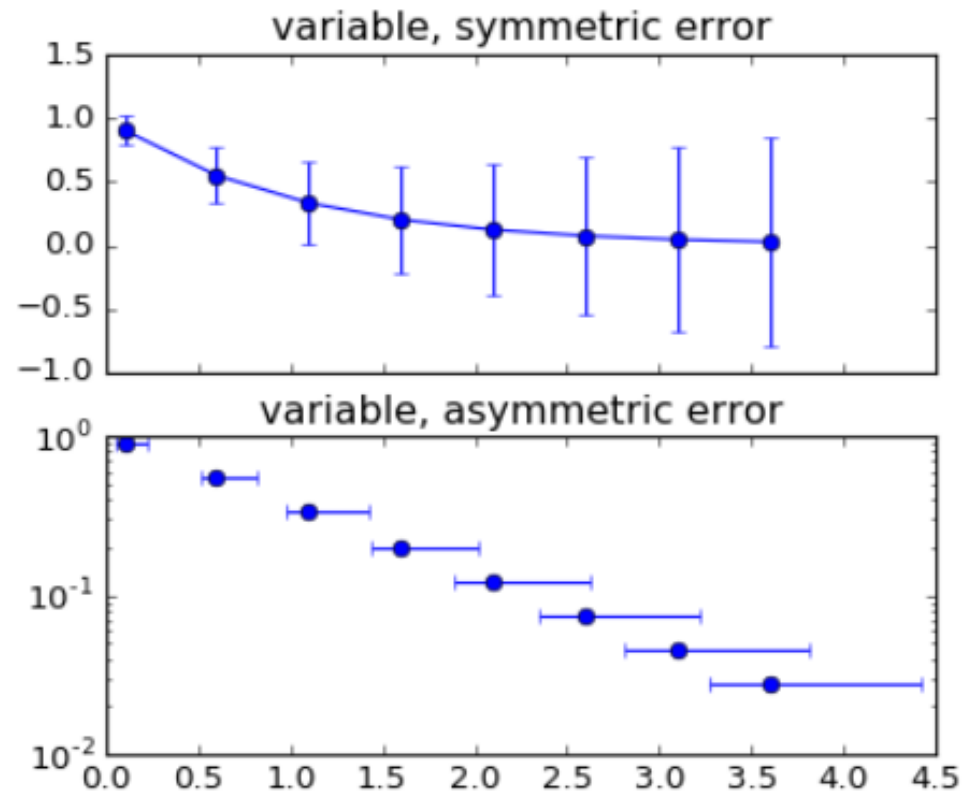


fonts_demo



statistics example code: errorbar_demo_features.py

(Source code, png, hires.png, pdf)



```
"""
Demo of errorbar function with different ways of specifying error bars.

Errors can be specified as a constant value (as shown in `errorbar_demo.py`),
or as demonstrated in this example, they can be specified by an  $N \times 1$  or  $2 \times N$ ,
where  $N$  is the number of data points.
```

```
 $N \times 1$ :
    Error varies for each point, but the error values are symmetric (i.e. the
    lower and upper values are equal).

 $2 \times N$ :
    Error varies for each point, and the lower and upper limits (in that order)
    are different (asymmetric case)
```

```
In addition, this example demonstrates how to use Log scale with errorbar.
```

```
"""
import numpy as np
import matplotlib.pyplot as plt

# example data
x = np.arange(0.1, 4, 0.5)
y = np.exp(-x)
# example error bar values that vary with x-position
error = 0.1 + 0.2 * x
# error bar values w/ different +/- errors
lower_error = 0.4 * error
upper_error = error
asymmetric_error = [lower_error, upper_error]

fig, (ax0, ax1) = plt.subplots(nrows=2, sharex=True)
ax0.errorbar(x, y, yerr=error, fmt='o')
ax0.set_title('variable, symmetric error')

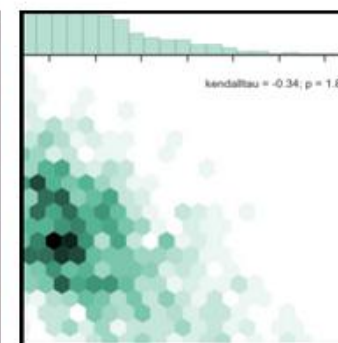
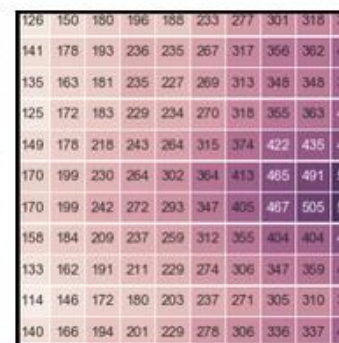
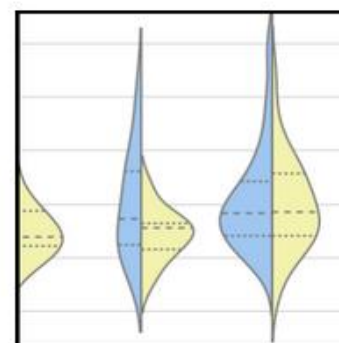
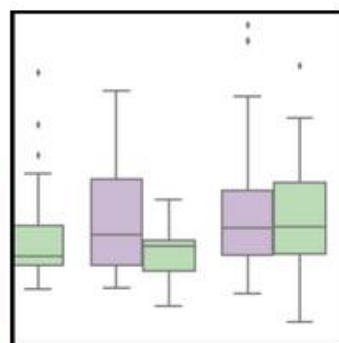
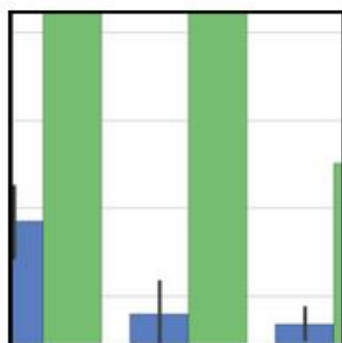
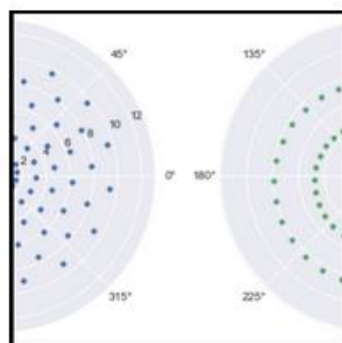
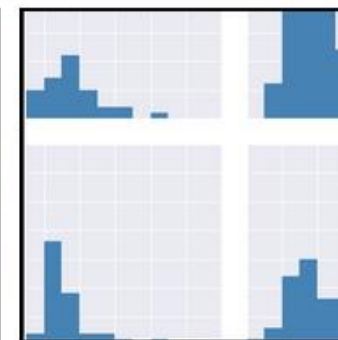
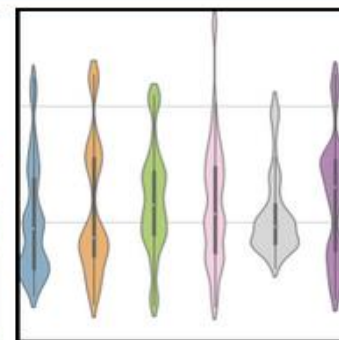
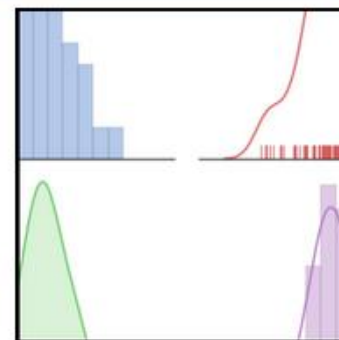
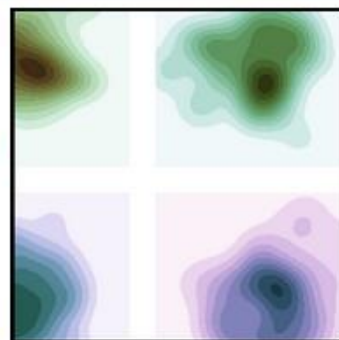
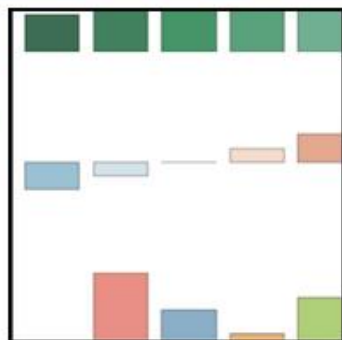
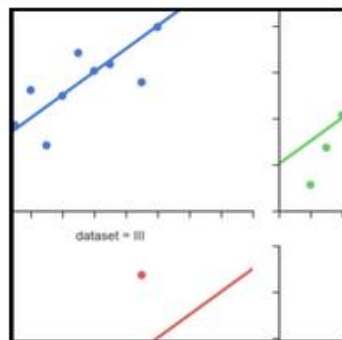
ax1.errorbar(x, y, xerr=asymmetric_error, fmt='o')
ax1.set_title('variable, asymmetric error')
ax1.set_yscale('log')
plt.show()
```



http://matplotlib.org/examples/statistics/errorbar_demo_features.html

<https://GitHub.com/KirstieJane/ReproducibleResearch>
doi: <https://dx.doi.org/10.6084/m9.figshare.4244996>

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[seaborn](#)[0.7.0](#)[API](#)[Tutorial](#)[Gallery](#)[Site ▾](#)[Page ▾](#)

Seaborn gallery

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<https://GitHub.com/KirstieJane/ReproducibleResearch>

doi: <https://dx.doi.org/10.6084/m9.figshare.4244996>

Jupyter Notebook



<http://jupyter.org>



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doi: <https://dx.doi.org/10.6084/m9.figshare.4244996>

SIGNAL PROCESSING WITH GW150914 OPEN DATA

Welcome! This ipython notebook (or associated python script GW150914_tutorial.py) will go through some typical signal processing tasks on strain time-series data associated with the LIGO GW150914 data release from the LIGO Open Science Center (LOSC):

- <https://losc.ligo.org/events/GW150914/>
- View the tutorial as a web page - https://losc.ligo.org/s/events/GW150914/GW150914_tutorial.html
- Download the tutorial as a python script - https://losc.ligo.org/s/events/GW150914/GW150914_tutorial.py
- Download the tutorial as iPython Notebook - https://losc.ligo.org/s/events/GW150914/GW150914_tutorial.ipynb

To begin, download the ipython notebook, readligo.py, and the data files listed below. You can then run the python script GW150914_tutorial.py. You will need the python packages:

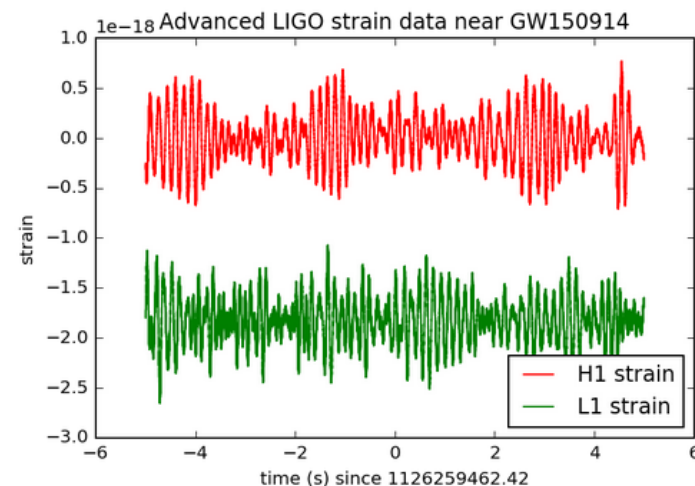
On Windows, or if you prefer, you can use a python development environment such as Anaconda (<https://www.anaconda.com/>) or Enthought Canopy (<https://www.enthought.com/products/canopy/>)

Questions, comments, suggestions, corrections, etc: email losc@ligo.org

v20160208b

```
In [6]: # plot +/- 5 seconds around the event:
tevent = 1126259462.422      # Mon Sep 14 09:50:45 GMT 2015
deltat = 5.                  # seconds around the event
# index into the strain time series for this time interval:
indxt = np.where((time_H1 >= tevent-deltat) & (time_H1 < tevent+deltat))

plt.figure()
plt.plot(time_H1[indxt]-tevent, strain_H1[indxt], 'r', label='H1 strain')
plt.plot(time_L1[indxt]-tevent, strain_L1[indxt], 'g', label='L1 strain')
plt.xlabel('time (s) since ' + str(tevent))
plt.ylabel('strain')
plt.legend(loc='lower right')
plt.title('Advanced LIGO strain data near GW150914')
plt.savefig('GW150914_strain.png')
```




Observation of Gravitational Waves from a Binary Black Hole Merger

B. P. Abbott *et al.**
(LIGO Scientific Collaboration and Virgo Collaboration)
(Received 21 January 2016; published 11 February 2016)



Situating the default-mode network along a principal gradient of macroscale cortical organization

Daniel S. Margulies^{a,1}, Satrajit S. Ghosh^{b,c}, Alexandros Goulas^d, Marcel Falkiewicz^a, Julia M. Huntenburg^{a,e}, Georg Langs^{f,g}, Gleb Bezgin^h, Simon B. Eickhoff^{i,j}, F. Xavier Castellanos^{k,l}, Michael Petrides^m, Elizabeth Jefferies^{n,o}, and Jonathan Smallwood^{n,o}

DOI: 10.1073/pnas.1608282113



[JUPYTER](#) [FAQ](#)

gradient_analysis

master

Name

NeuroanatomyAndConnectivity's repositories

gradient_data

01_create_human_connectome.ipynb

01_create_macaque_connectome.ipynb

02_embed_connectomes.ipynb

03_visualize_embeddings.ipynb

04_visualize_distance.ipynb

04_visualize_networks.ipynb

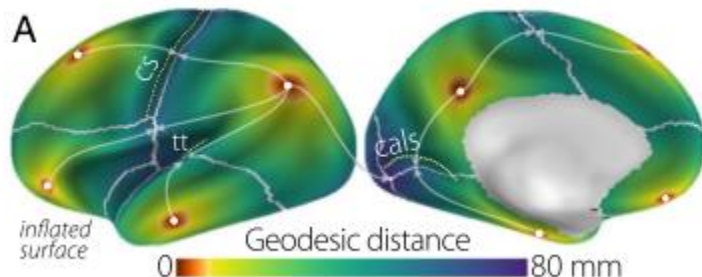
05_metaanalysis_brainmap.ipynb

05_metaanalysis_neurosynth.ipynb

06_supplementary_analysis_and_figures.ipynb

LICENSE

README.md





gradient_analysis / 04_visualize_distance.ipynb

In [1]: % matplotlib inline

```
import nibabel as nib
import nibabel.gifti
import nilearn
from nilearn import datasets, plotting
import pandas as pd
import numpy as np

import seaborn as sns
import matplotlib as mpl
import matplotlib.pyplot as plt
from matplotlib.colors import ListedColormap
mpl.rcParams['svg.fonttype'] = 'none'

import sys
sys.path.append('gradient_data/src/')
from viz import *

import surfdist as sd
from surfdist import viz, load, utils, surfdist
```

```
/Applications/miniconda3/envs/topography/lib/python2.7/site-packages/matplotlib/font_manager.py:273: UserWarning: Matplo
warnings.warn('Matplotlib is building the font cache using fc-list. This may take a moment.')
/Applications/miniconda3/envs/topography/lib/python2.7/site-packages/matplotlib/__init__.py:872: UserWarning: axes.color
warnings.warn(self.msg_depr % (key, alt_key))
```



In [2]: def imageCrop(filename):



Asking for help: StackOverflow & MWEs

<http://stackoverflow.com>



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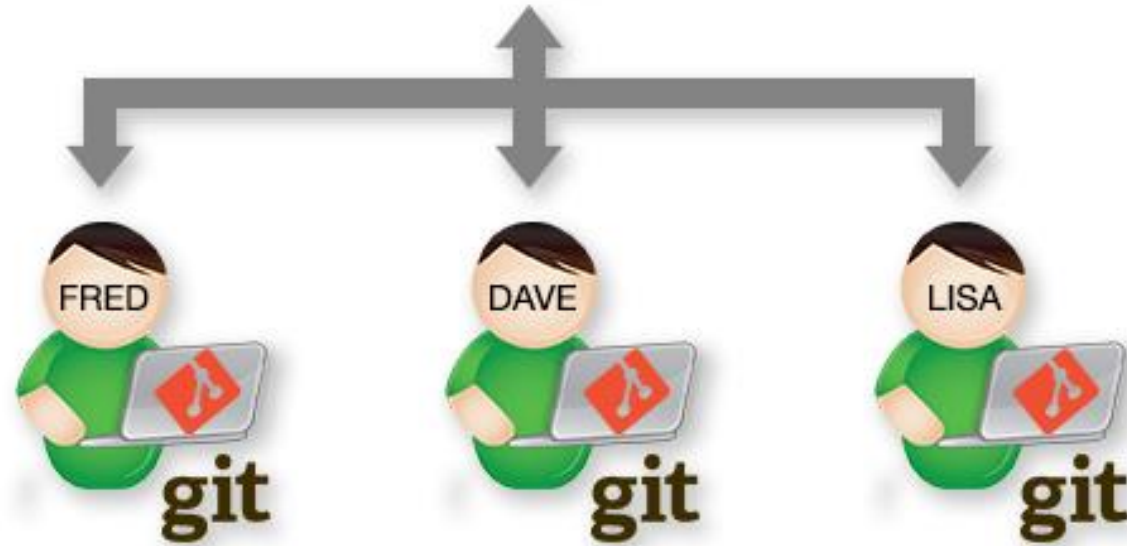
<https://GitHub.com/KirstieJane/ReproducibleResearch>
doi: <https://dx.doi.org/10.6084/m9.figshare.4244996>

Git vs GitHub



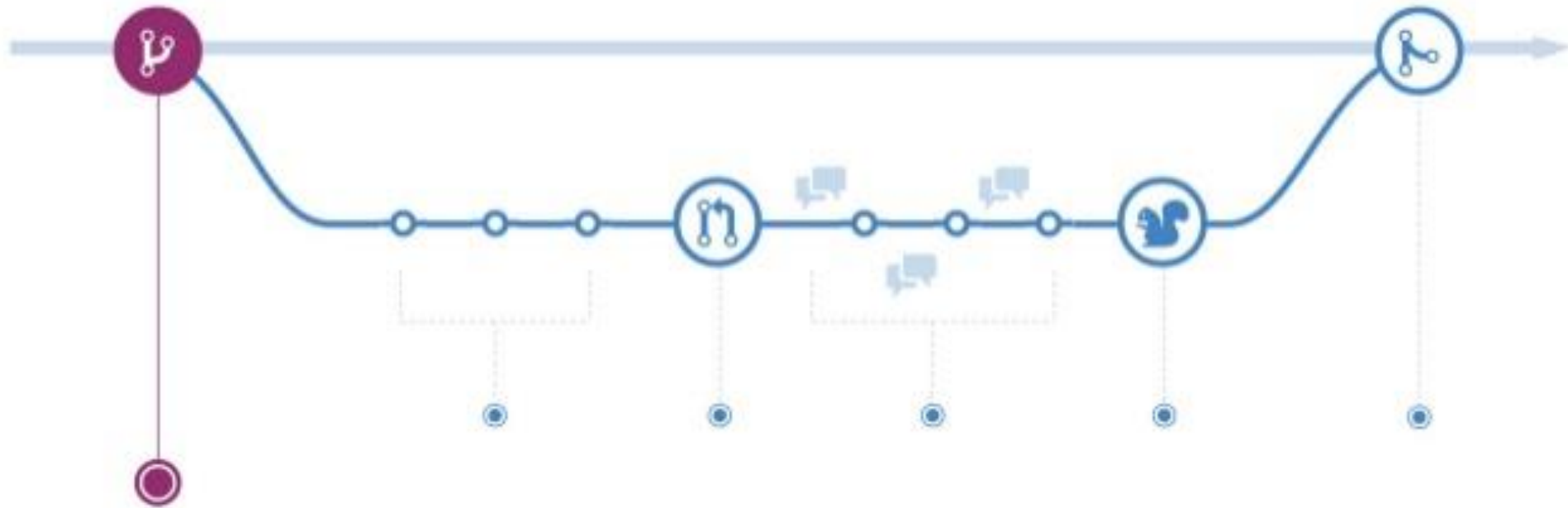
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doi: <https://dx.doi.org/10.6084/m9.figshare.4244996>
www.stemrolemodels.com
www.github.com/KirstieJane/STEMMRoleModels
@kirstie_j

GitHub Flow - Create a Branch

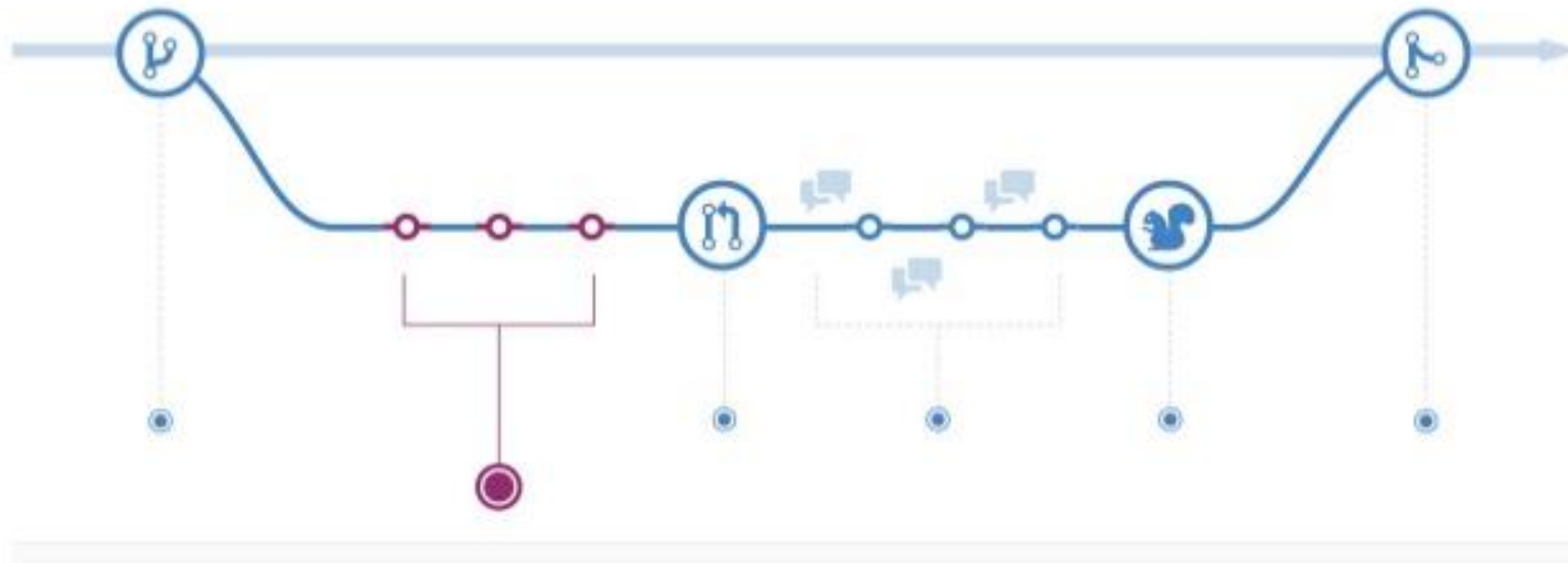


<http://www.slideshare.net/nishanbose/introduction-to-github-55872492/7>

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doi: <https://dx.doi.org/10.6084/m9.figshare.4244996>

GitHub Flow - Add Commits

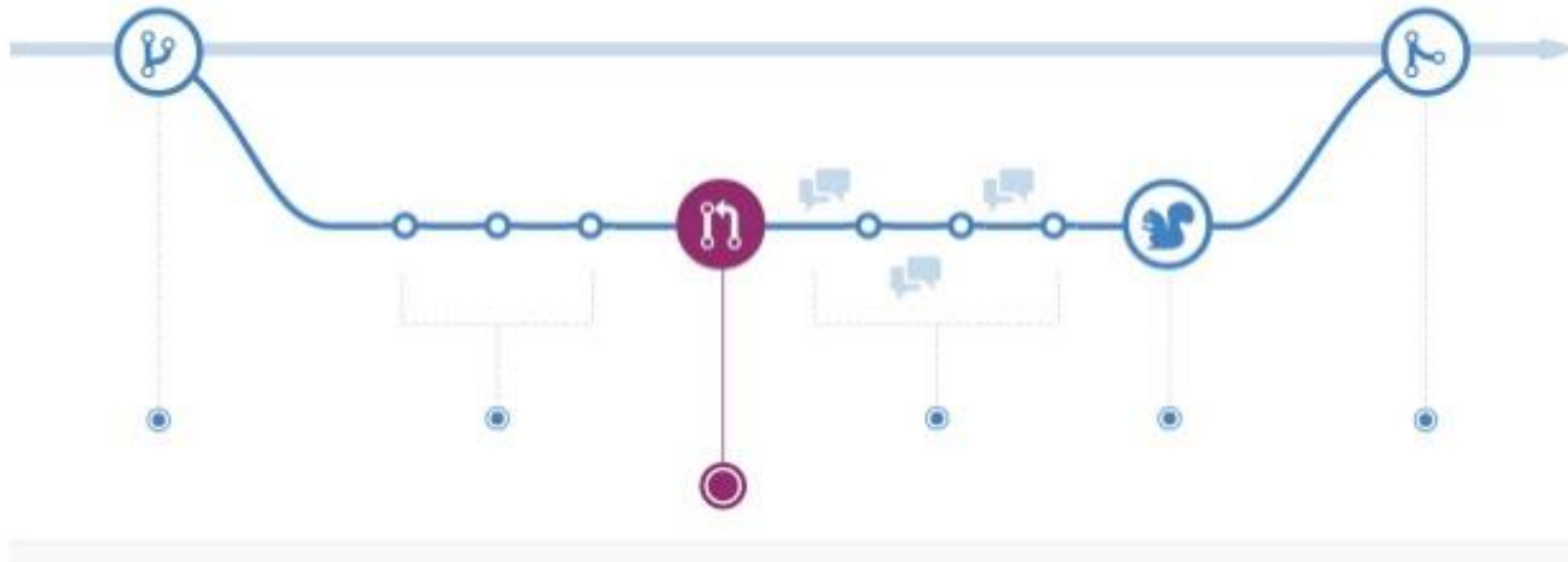


<http://www.slideshare.net/nishanbose/introduction-to-github-55872492/7>

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doi: <https://dx.doi.org/10.6084/m9.figshare.4244996>

GitHub Flow - Open a pull request

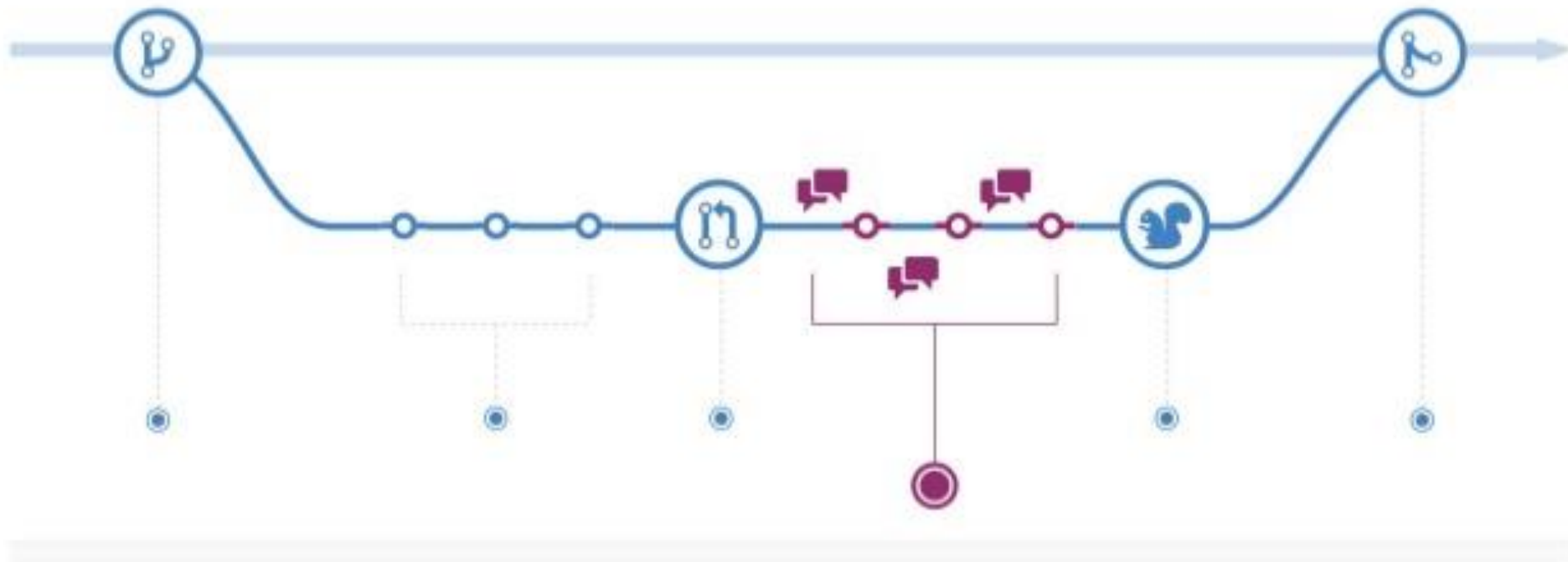


<http://www.slideshare.net/nishanbose/introduction-to-github-55872492/7>

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doi: <https://dx.doi.org/10.6084/m9.figshare.4244996>

GitHub Flow - Discuss and Review your code



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GitHub Flow - Deploy / Test



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GitHub Flow - Merge



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Repository

Clone

Pull request

Branch

Version control

Some jargon busting

Merge

Issues

Release

Commit

Fork

Markdown



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Submit your first pull request!

Inspired by: <https://yourfirstpr.github.io>



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doi: <https://dx.doi.org/10.6084/m9.figshare.4244996>

ReproducibleResearch

This repository supports [Kirstie's](#) presentation on tips and tricks for making your research reproducible.

The goal is to build a directory of useful links, and a jargon busting glossary.

Guide for contributors

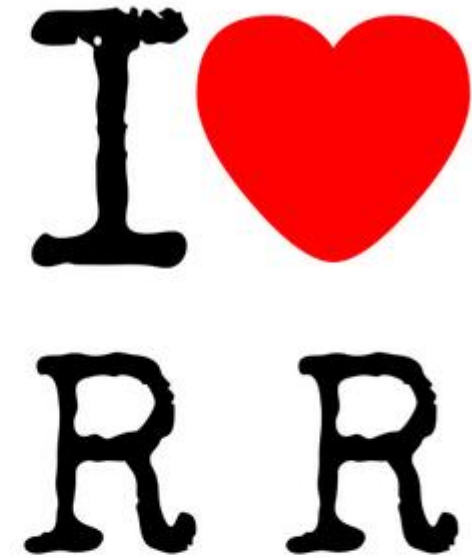
See our [guidelines](#) for how to contribute to the project.

Code of conduct

Everyone is welcome to join this project, particularly people who have not used GitHub before and are feeling unsure of how to begin!



Please follow our [code of conduct](#) in all your on and offline interactions.



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 [@kirstie_j](#)
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Create a glossary



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Branch: master ▾

ReproducibleResearch / Glossary.md

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KirstieJane Create Glossary.md

46fc2e6 a minute ago

1 contributor

14 lines (8 sloc) | 454 Bytes

Raw

Blame

History

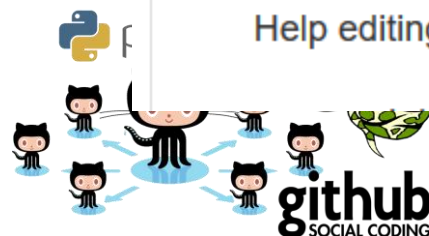


Jargon Busting

If you remember not knowing what a word means, there's probably someone else who could benefit from you defining it here!

Please be brief in your description, but do link to further information as appropriate.

Help editing markdown can be found [here](#) and [here](#).



🐦 @kirstie_j

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Share resources



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doi: <https://dx.doi.org/10.6084/m9.figshare.4244996>

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ReproducibleResearch / Resources.md

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KirstieJane Added link to free private repositories

1406a83 a minute ago

1 contributor

27 lines (14 sloc) | 2.16 KB

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Useful Resources

If you know of a useful resource that has helped you make your research reproducible, please add it here.

Help editing markdown can be found at this excellent [markdown cheatsheet](#)

Git & GitHub

- [Friendly GitHub Introduction](#): an afternoon workshop created originally by [Joey Lee](#) for the [Mozilla Science Lab](#) and further developed by [Kirstie Whitaker](#) and [Anne Pajon](#).
- [Get private GitHub repositories](#): a [paid GitHub account](#) allows you to have private repositories that only people you choose to make collaborators can see. If you're a member of an academic institution you can [request a discount](#) (to \$0) and therefore have free private repositories. The discount lasts for 2 years but you can request another at the end of that period no problem 🙌.



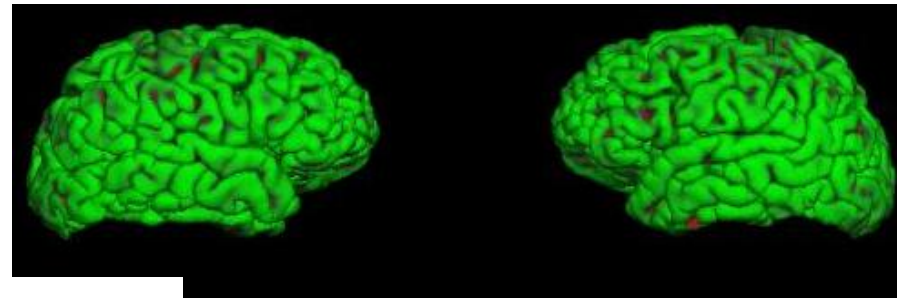
SOCIAL CODING

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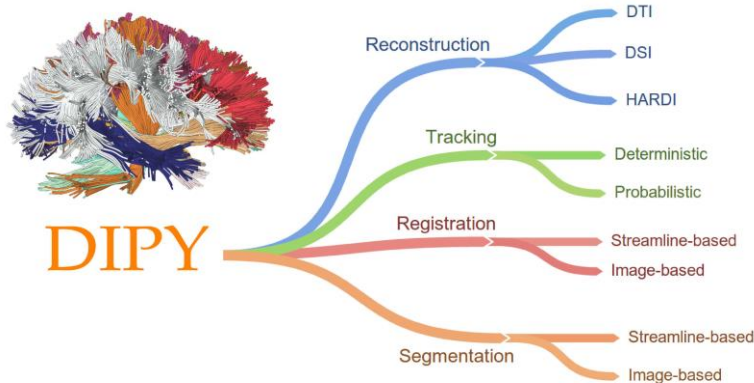


Nipype:
Neuroimaging in Python
Pipelines and Interfaces

SPM



MNE
MEG + EEG ANALYSIS & VISUALIZATION



FreeSurfer

**Automatic analysis (aa): efficient
neuroimaging workflows and parallel
processing using Matlab and XML**

Rhodri Cusack^{1*}, Alejandro Vicente-Grabovetsky², Daniel J. Mitchell³, Conor J. Wild¹, Tibor Auer³, Annika C. Linke¹ and Jonathan E. Peelle⁴

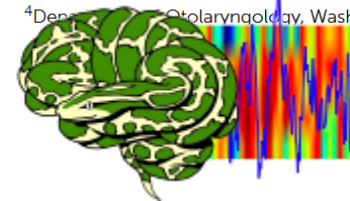
¹Brain and Mind Institute, Western University, London, ON, Canada

²Donders Institute for Brain, Cognition and Behaviour, Nijmegen, Netherlands

³MRC Cognition and Brain Sciences Unit, Cambridge, UK

⁴Department of Otolaryngology, Washington University in St. Louis, St. Louis, MO, USA

Nitime: time-series analysis
for neuroscience





Community

<https://www.mozillascience.org>

<http://software-carpentry.org>

<http://data-carpentry.org>

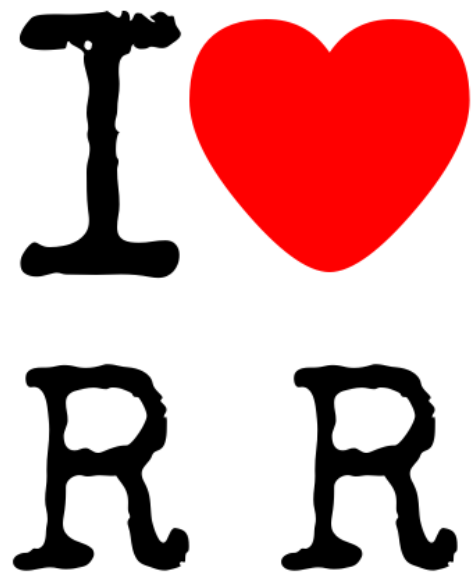
<https://www.coursera.org/specializations/jhu-data-science>

<https://www.coursera.org/learn/python/home/info>



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Thank you!



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