Data analysis for Neuroimaging - PSYG4043 / C84DAN

Overview

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What's the plan?

- 1. Acquire some [functional] MRI data in a simple, but real experiment
- 2. Analyze the data with two commonly used software packages spm (matlab) and fsl
- 3. Learn a bit about UNIX, organising data and code: version control, in particular git and github
- 4. Use different tools to inspect and visualise data
- 5. [optional] anatomical, diffusion weighted +/- multi-echo data (T2*)

Learning objectives

- 1. Build a better understanding of principles (and practice of) magnetic resonance imaging
- 2. Learn about state of the art analysis tools for (f)MRI
- 3. Appreciate usefulness of scripting, unix, version control for reproducibility / transparency of work
- 4. Discover matlab, toolboxes for data visualisation

Timeline

| Unit | Topic |
|------|---|
| 1 ★ | Introduction, Administrivia, computers, |
| 2 | Data acquisition (scanning on 3T at SPMIC) |
| 3 | Inspecting & analysing data in SPM |
| 4 | FSL + Version control (git and github.com) |
| 5 | Images in Matlab , display, analyze |
| 6 | Timeseries signals in Matlab |
| 7 | wrapup + Reading/writing text, CSV, data files Matlab |

What's the assignment?

A short, written report

Summarise the experimental setup, analysis methodology and results. Need to have clearly written abstract (250w), methods, results and discussions (and **figures**).

Aim: Get you thinking about journal-style writing, rather than essays. Plus: presenting your own data, identifying key points, a story/pitch.

When to work on this? 👷

Start as soon as we have the data

- explore your analysis ideas
- talk to us about questions you could address
- think about plots + data visualisations you'd like to make

Submission details 🦠 듣





Currently w/ Student Services, date to-be-confirmed

- turn-it-in submission on moodle page
- deadline: end of March (the week after last class of this module - check moodle page for details)

What's the assignment (2) iii 📈 📉







- 250w abstract
- plus a main document (max 1500w)
- references / citations as for standard written work
- max 5 figures¹ illustrating
 - details of the experimental setup
 - analysis methodology
 - results

¹figures can have sub-panels or subplots

For next time (lab 2)

- sign up for 1 of 3 groups (max 7 people) moodle
- complete visitor screening form
- we also need a volunteer (~40 min in scanner)

Setting up computers, logins

Let's check log-ins and make sure we can find:

- Terminal
- Matlab & set up paths for SPM

Note

Each user (at a particular machine) needs to make sure that Terminal/shell is set up correctly – if you move machines between labs (or want to do things elsewhere, repeat the above step!)

Set up colors in terminal

```
alias ls='ls -G'

# or append to bash_profile
echo "alias ls='ls -G'" >> ~/.bash_profile
```

```
bash-3.2$ ls
mgl nottingham startup.m
mrTools spm12
bash-3.2$ ls -G
mgl mrTools nottingham spm12 startup.m
bash-3.2$
```

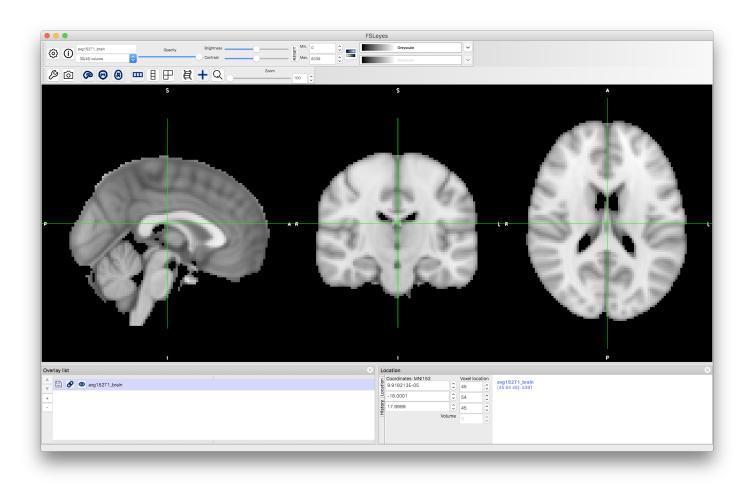


Has setup worked? fsl

Look at some existing anatomies with fsleyes

```
which fsl # see anything?
fsleyes & # File -> Add Standard -> Pick 1st or 2nd
```

do you see



SPM/FSL analysis

- get data from sessions S001 to S004 into a common folder data
- make folders, copy files by "drag & drop"
- point & click version (like some of you have already done)
- digging into the details of how this is implemented
- inspecting analysis output, intermediate files, ...

```
cd ~/data/S001/ # for example
# run SPM analysis in matlab (JJ)
# run FSL analysis (DS)
```

Some UNIX

- only basics needed for running fsl
- lots of functionality is available through point-and-click
- but command line is helpful for organising data!
- more complex analysis, e.g. freesurfer, require some working knowledge

```
# navigate file system
# cd, ls, pwd, which, ...

# some powerful commands for organising your data
# cp, rm, touch, mkdir, rmdir

# some stuff to show of how powerful
# grep, "lists", "wildcards (*, ., ?)"
# "regular expressions"
```

Version control git

- 30min lecture on principles of version control (git)
- start using your (free) github.com id by working on a simple project
- make your first modifications to a local copy of code and get it into a repo.

```
mkdir test && cd test # what does this do?
git init
# [[ create, edit a file, say my_first.md ]]
git add my_first.md # add it to "staging area"
git commit # enter commit message
# - OR -
git commit -m 'adds first version of file'
git log
```

Version control (v2.0) 🧐

Everyone should sign up for a free github account, so we can work together on this from session 4 onwards:

https://github.com/join

- it's free and useful
- we'll want to play with this in lab #4
- once you have an username (pick one that I will recognise!),
 go to our github classroom at

https://classroom.github.com/a/7ZwbkqLl

matlab - reading images (1)

 we'll learn/revisirt how to read imaging data into matlab (nifti files)

```
% > R2017b
data = niftiread('file_from_scanner.nii');
```

matlab - reading images (2)

revisit indexing of arrays, "slicing", etc.

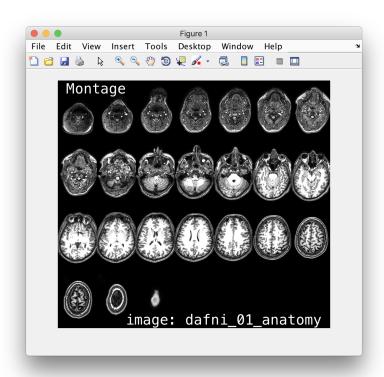
```
data(12, 24, :, 1) % what is this?
data(:, 24, 24, 1) % ... and this?
data(34, 44, 12, :) % ... or that?
```

• we built a returnSlice() function, to complete imageviewer:

```
% function signature
s = returnSlice(array, sliceNum, orientation);
```

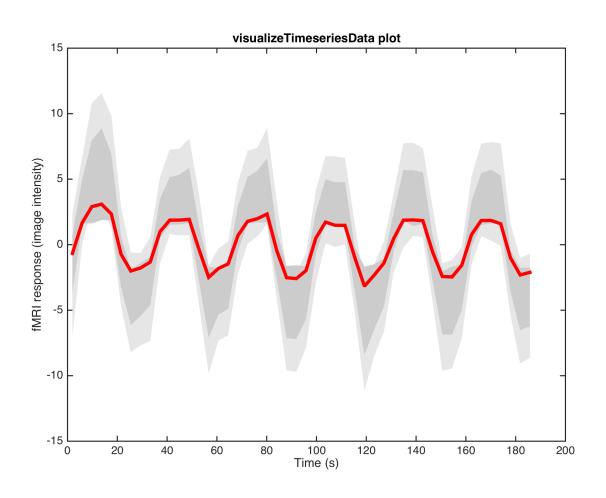
some more coding along these lines

makeMontage('dafni_01_anatomy.nii', 25)



function [] = makeMontage(fname, nSamples)
%makeMontage - make a montage from 3d/4d image

matlab - timeseries and subplots



Using toolboxes to visualise data (JJ)

- glass brains
- SPMs, cluster maps on anatomical images.
- cut-aways, ...

Wrap-up (Lab 7)

- recap what have we covered in the last 7 weeks?
- where to go to from here (unleash your inner coding
- try to approach each new problem, project where you find lots of repetition (analysis, writing, coding, ...):
 - there must be a better way!
 - what's the smallest unit that gets repeated all the time?
 - o can luse bash/unix, matlab or another tool to automate?
- just try things out you'll learn tons in the process

For next time

- make sure you complete screening form (and/or get in touch with any concerns)
- to volunteer for a scan, send me an e-mail: denis.schluppeck@nottingham.ac.uk
- next week: see you at SPMIC for your timeslot if you don't know where on campus, google SPMIC ... first hit is imaging centre w/ directions

Random technical stuff

Some notes of manipulating text files in the shell (using awk) and (viz timing files, etc.)

Notes - text hacking in shell

Small awk program for adding a counter n and time t and turn one column txt file into csv file:

```
awk 'NF {print NR-1 ", " (NR-1)*1.5 ", " $1}' \
    timecourse.txt > timecourse.csv
```

• with a headerline (matlab's csvread() doesn't like!)

Solution in matlab?

Turn timecourse.txt (column of y-values), into timecourse.csv:

- where first column is a counter that goes from 1...n,
- the second column is t (in s), which goes up from
 0..1.5s.. and
- the third column is the y values

What about something else?

• Excel? R? Another cool idea that's worth having in your set of tools?