

# **Data analysis for Neuroimaging - PSYG4043**

## **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, **incl. safety**
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 ( <b>scanning on 3T at SPMIC</b> )
3	Inspecting & analysing data in <b>SPM</b>
4	<b>FSL</b> + Version control ( <code>git</code> and <code>github.com</code> )
5	Images in <b>Matlab</b> , display, analyze
6	Timeseries signals in <b>Matlab</b>
7	<b>wrapup</b> + Reading/writing text, CSV, data files <b>Matlab</b>

## ! 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 (~30 min in scanner) // **different screening + consent form**

# MRI safety



**Dieser Magnet 3,0T ist IMMER AKTIV**

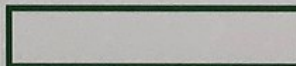
Gebrauch des Systems und Zugang zum Untersuchungsraum NUR für  
MR-authorized Personal



NUR geprüfte und genehmigte Geräte im Untersuchungsraum zulässig



Während der Messung: HF-Felder und Geräuschentwicklung



# Visitor screening form



University of  
Nottingham  
Sir Peter Mansfield Imaging Centre

**Sir Peter Mansfield  
Imaging Centre**

## Visitor Safety Screening Questionnaire

MR scanning uses strong magnetic fields, for your own safety and the safety of others, it is **very important** that you do not go into the magnet halls with any metal in or on your body or clothing.

NAME	DATE
ORGANIZATION OR ADDRESS	
REASON FOR VISIT	

Please answer the following questions carefully and ask if anything is not clear. All information is held in the strictest confidence.

1. Do you have any implants in your body?  
e.g. replacement joints, drug pumps Y/N
2. Do you have aneurysm clips?  
(clips put around blood vessels during surgery) Y/N

# Safety Questions (1)

1. Do you have any implants in your body?

e.g. replacement joints, drug pumps

2. Do you have aneurysm clips?

(clips put around blood vessels during surgery)

3. Do you have a pacemaker or artificial heart valve?

(These stop working near MR Scanners)

4. Have you ever had any surgery? Please give brief details\*

(\*We do not need to know about uncomplicated caesarean delivery, vasectomy or termination of pregnancy)



5. Do you have any foreign bodies in your body (e.g. shrapnel)?
6. Do you wear a hearing aid or cochlear implant?
7. Will you remove all metal including coins, body-piercing jewellery, false-teeth, hearing aids etc before entering the magnet hall? (lockers available by the changing rooms)

# Volunteers

For those wanting to go into the scanner: a few more detailed questions and

- contact of GP (why? discuss)
- information sheet
- consent form (ethics!)
- tattoo form (if applicable)

# Setting up computers, logins

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

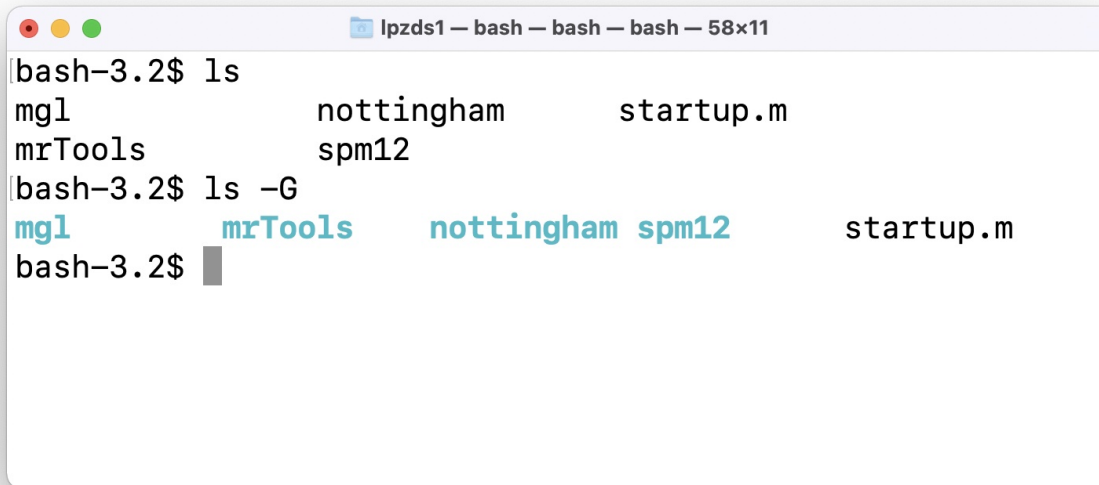
- Terminal
- Matlab & set up paths for SPM

## 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 --color=auto"  
# or append to .zshrc  
echo "alias ls='ls --color=auto' " >> ~/.zshrc
```



A terminal window titled "lpzds1 — bash — bash — bash — 58x11" showing the following commands and output:

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

in Terminal ✓

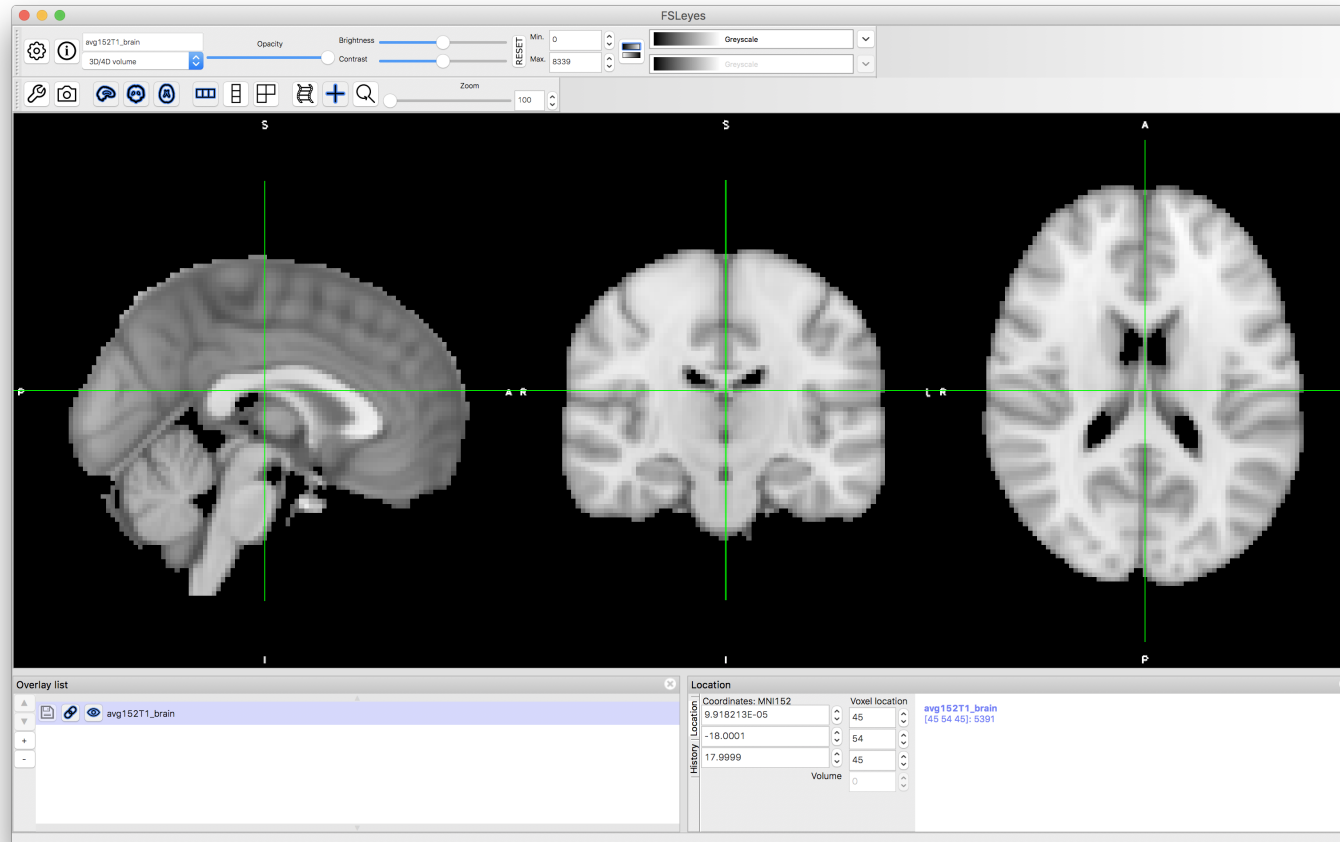
Has setup worked? `fsl`

Look at some existing anatomies with `fsleyes` ✓

```
which fsl # see anything?
```

```
fsleyes & # File -> Add Standard -> Pick 1st or 2nd
```

do you see



**JJ**

**Assignment, etc.**



# 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

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)

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

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figures can have sub-panels or subplots

# 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 `fs1`
- 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 ... details to follow

## matlab - reading images (1)

- we'll learn/revisit 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.

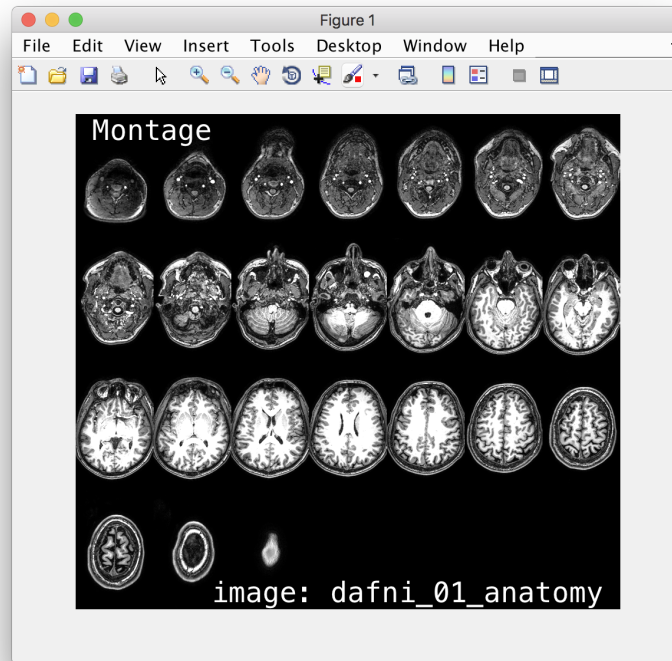
```
data(12, 24, :, 1) % what is this?  
data(:, 24, 24, 1) % ... and this?  
data(34, 44, 12, :) % ... or that?
```

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

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

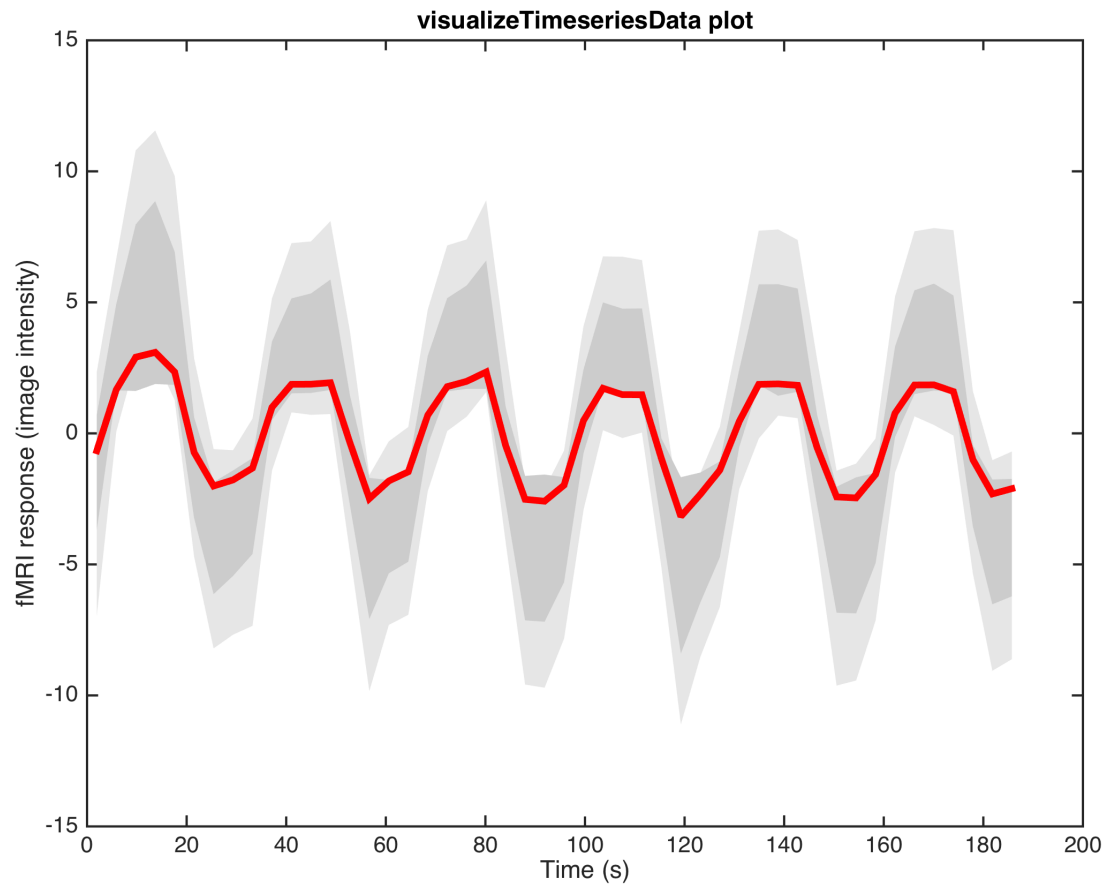
- some more coding along these lines

```
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?
  - can I use `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](mailto: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!)

```
awk 'BEGIN {print "n, t, response"}  
NF      {print NR-1 ", " (NR-1)*1.5 ", " $1}' \  
timecourse.txt > timecourse.csv
```



## 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?