



Welcome

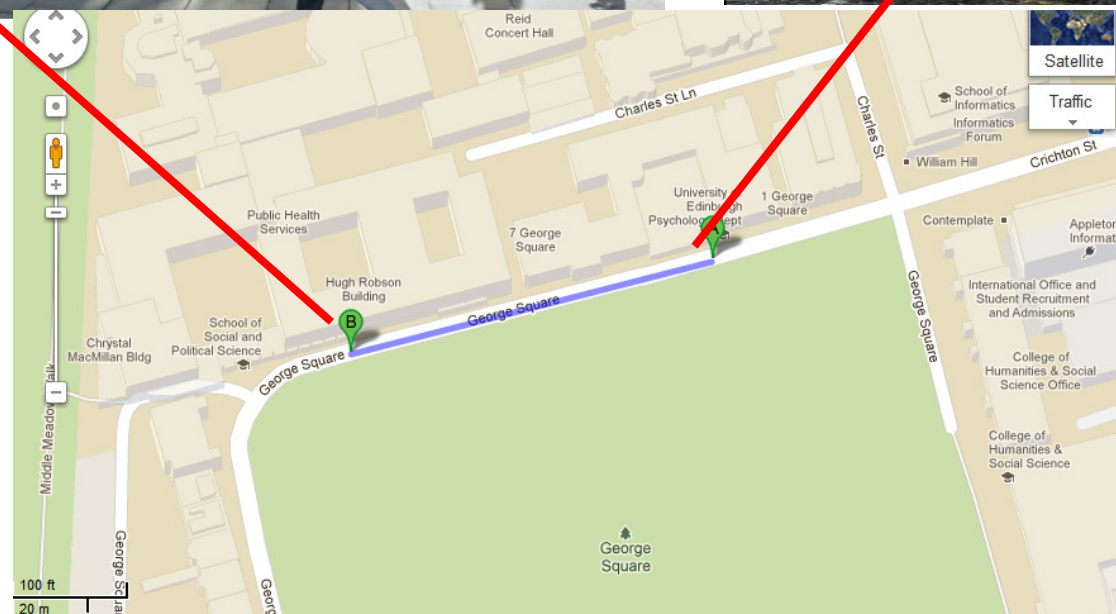
Edinburgh SPM course
Beginner session



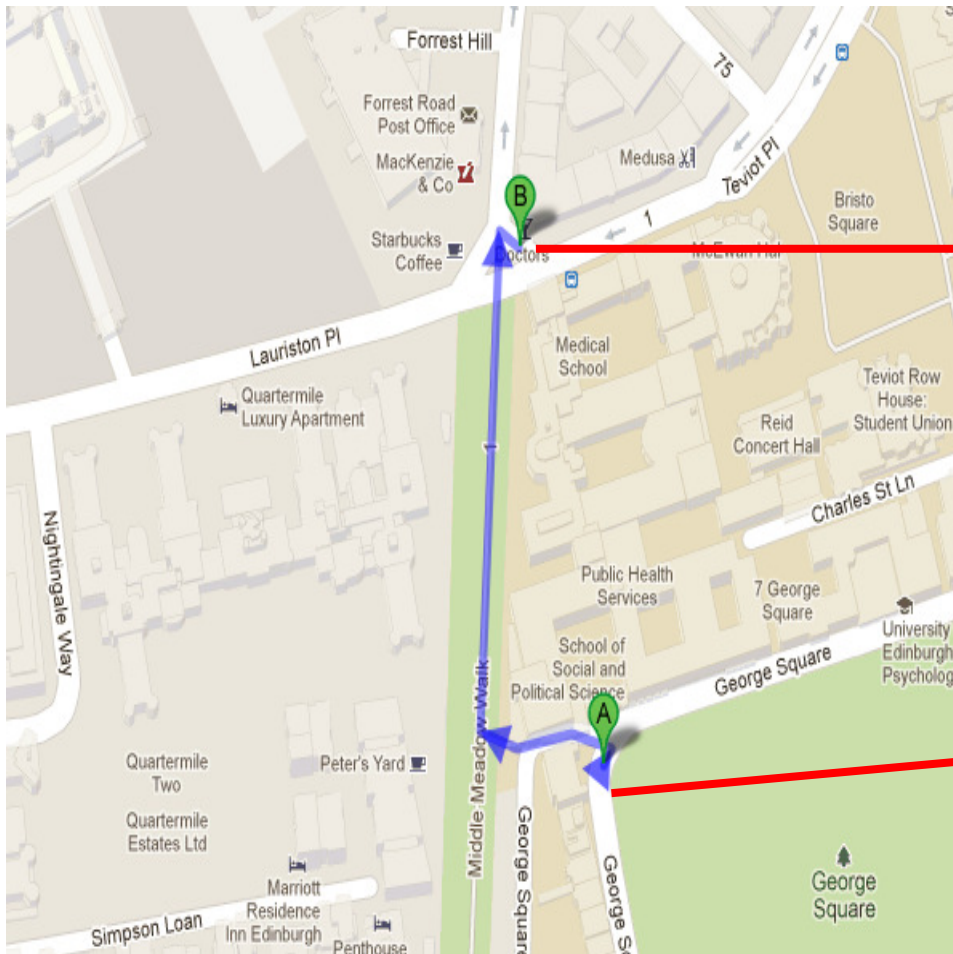
Program

- Today: data pre-processing (prepare the data before the stats)
- Tomorrow: stats, the massive univariate approach
- Afternoon hands-on: we use the SPM data set that is freely available, so you can try it at home

Where



Where



Who

- John Ashburner: Professor of Imaging Science at UCL – SPM developer: generative models for brain image registration and tissue segmentation
- Alexa Morcom (Lecturer, UoE) Cyril Pernet (Academic Fellow, UoE) – simple SPM users like you, except we've done it for > 12 years (25 years of experience combined)

A word on fMRI analyses

Beginner course:

functional segregation

- fMRI can be used for studying both, *functional segregation* and *functional integration*.
- Functional localization corresponds to localize in the brain a function. This was the approach advocated by the phrenologists and long discarded.
- ‘Traditional’ mass-univariate fMRI analyses allow investigating functional segregation, that is the specialization of brain regions for some aspect(s) of a function.

Advanced users:

functional integration

- fMRI can be used for studying both, *functional segregation* and *functional integration*
- Functional integration is the study of connected processes.
- Methods for functional integration can be broadly divided into functional connectivity (~ finding statistical patterns) and effective connectivity (~ model how regions interacts).

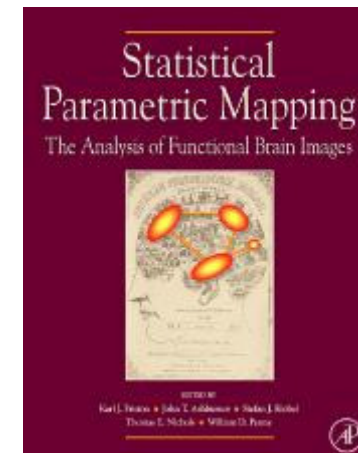
SPM: the software

<http://www.fil.ion.ucl.ac.uk/spm/>

Overview

- The SPM software package has been designed for the **analysis of brain imaging data sequences**. The sequences can be a series of images from different cohorts, or time-series from the same subject. The current release is designed for the analysis of fMRI, PET, SPECT, EEG and MEG.

The bible *Statistical Parametric Mapping: The Analysis of Functional Brain Images* (2007)



Overview

- SPM website

Software, data, literature

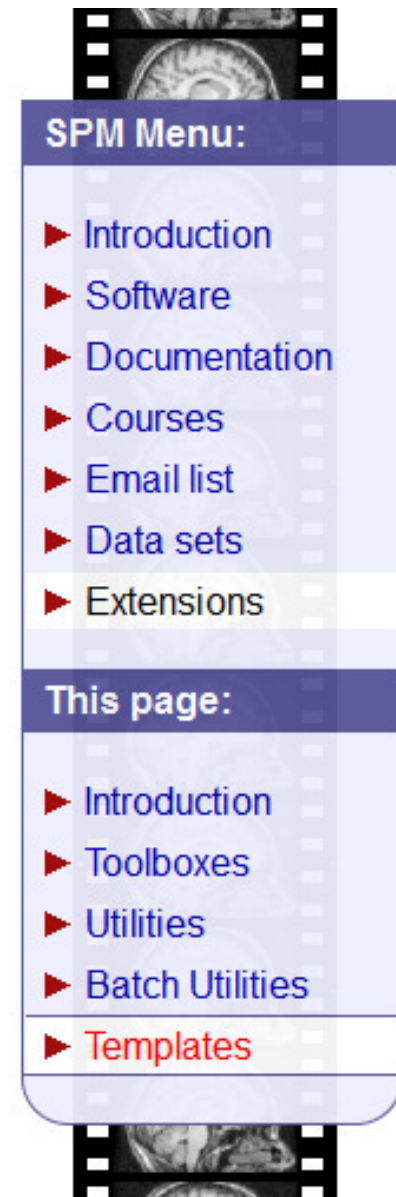
Email list for support

Extensions – likely to have something for you

Counted 61 plug-in for SPM8 !

+ old ones which can certainly be

Re-used with a bit of work

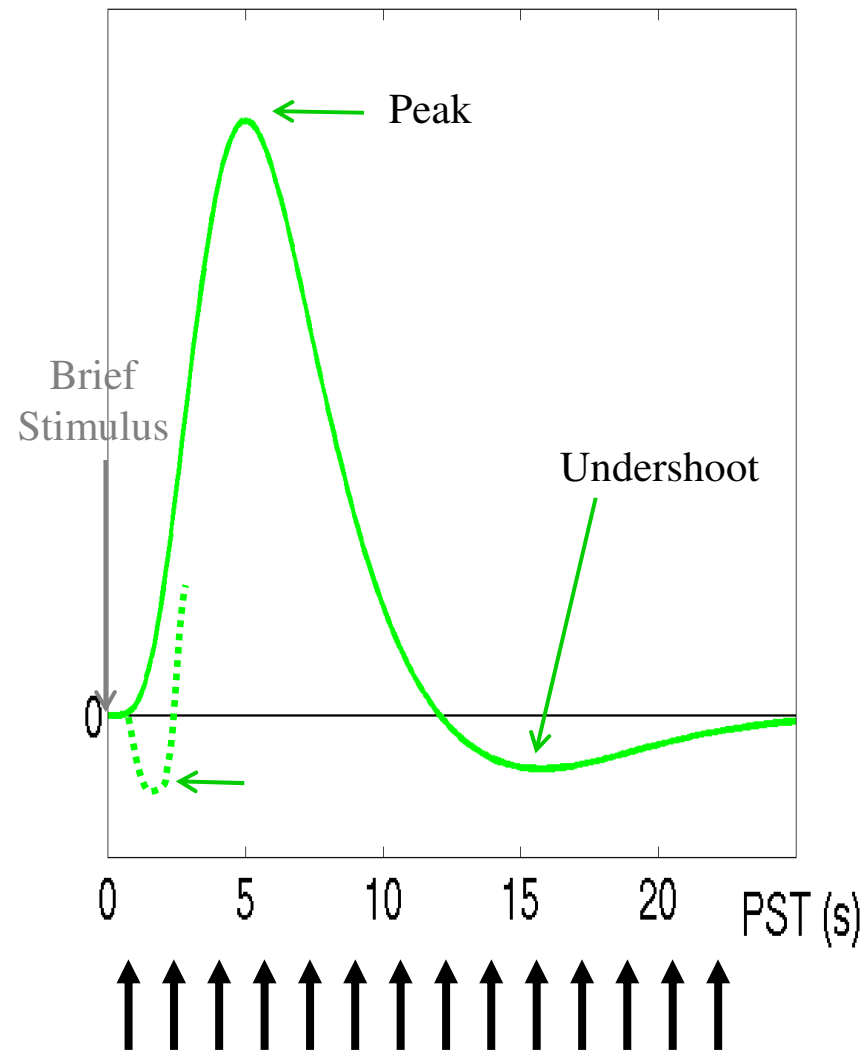


Before data processing

- **What are we measuring already?**
- PET studies using $\text{H}_2\text{O}_{15}^*$ and FDG^* have shown that the regional cerebral blood flow (rCBF) and the regional cerebral metabolic rate (rCMR) increase during activation phases (neuronal stimulation). However, rCBF and rCMR are not completely coupled. During activations, the rCMRO_2 increase of 5% but the rCBF increase of 29% (Fox & Raichle, 1986).
- This hyper-perfusion (McIntyre, et al. 2003) is the basis of the BOLD contrast. At rest, the oxygen level is around 95% in the arterial system and around 60-80% in the venous system (Bandettini, 1999). During activation, the oxygen level increases up to 90% in the venous system.

Before data processing

- The BOLD signal increases about 2 sec after the neural activity, it then reaches a plateau at about 5 – 8 sec. It will plateau if the neural activity continues. Once the neural activity stops, the signal returns to baseline 8 to 11 sec later. Finally, a transient change referred to as the undershoot can be observed.



We need fast multiple acquisitions
= time series of 3D volumes

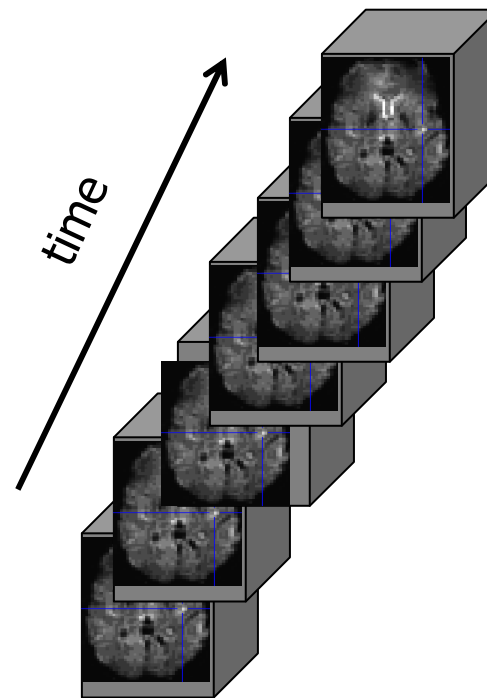
Before data processing

- Keys to good experiment and good data
- Understanding the steps involved in the analysis allows knowing what is going to make bad data
→ allows acquiring data in the best conditions
- Understanding the statistical analysis and issues related to it allows designing good experiments.

Data have been acquired, what's next?

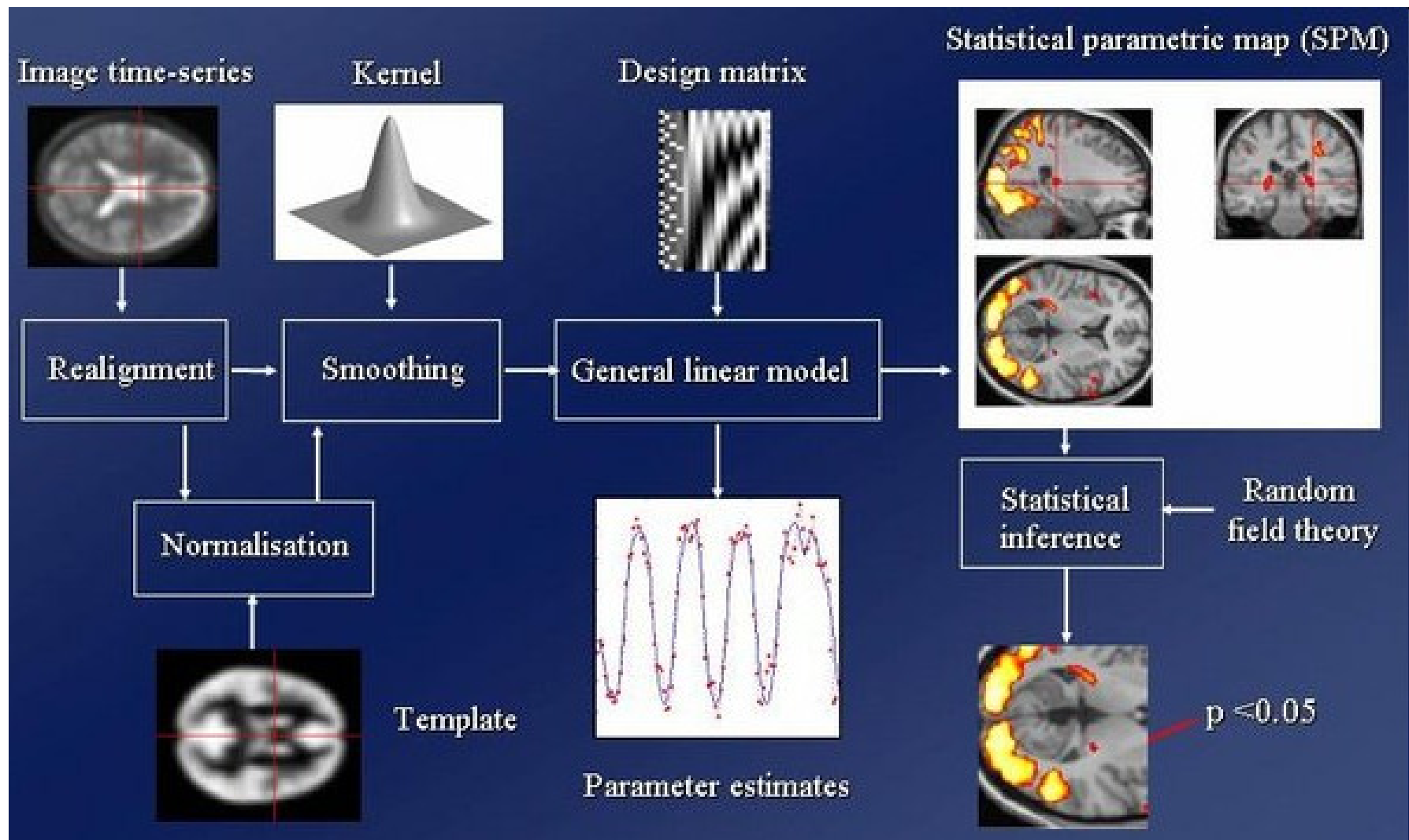


"OK, Mrs. Dunn. We'll slide you in there, scan your brain, and see if we can find out why you've been having these spells of claustrophobia."



No matter the design, multiple volumes (made from multiple slices) have been acquired in time. Before getting results out, we need to make sure the signal from each voxel contains the right temporal and spatial information.

Data processing



Slice Timing Correction

- Most of the time, fMRI data are acquired using multiple 2D imaging like single shot EPI.
- Since fMRI statistics are about analyzing the time course of the BOLD signal, exact timing with regard to the stimulus presentation is crucial.

Motion artefacts

- Subjects will always move in the scanner: swallowing for instance lead to motion along the x axis or some movements may be related to the tasks performed.
- Motion will results in a mismatch of the location of subsequent images in the time-series. Since the sensitivity of the statistical analysis is determined by the amount of residual noise in the image series, mismatch of the location will add to this noise and reduce the sensitivity.
- This type of motion problem corresponds to wholesale movements (*bulk-motion*) and is well corrected by realignment algorithms.

Normalization

- Inter-subject averaging
 - extrapolate findings to the population as a whole
 - increase activation signal above that obtained from single subject
 - increase number of possible degrees of freedom allowed in statistical model
- Enable reporting of activations as co-ordinates within a known standard space
 - e.g. the **MNI space**

Smoothing

- Increase signal to noise by removing high-frequency information (small-scale changes in the image)
- Inter-subject averaging as spatial normalization cannot perfectly align all structures
- Increase validity of statistics when using random field theory.