

MATLAB TUTORIAL

The Basics of SPM

Independent Study in Psychology
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SPM Overview



Statistical Parametric Mapping (SPM)

- SPM refers to the construction and assessment of spatially extended statistical processes used to test hypotheses about functional imaging data from fMRI, PET, SPECT, EEG and MEG
- Analyses can be implemented using the Graphical user interface (GUI), the MATLAB command line (for writing scripts), or the batch input system (for repetitive analyses; sample batch scripts can be found in `history_subject1.m`)

SPM Models

- For statistical analysis, SPM uses:
 - General Linear Model (GLM)
 - Random Field Theory (RFT)
 - Bayesian Source Reconstruction
 - Dynamic Causal Modelling (DCM)



SPM for EEG



EEG Overview

1. Conversion
2. Epoching
3. Filtering
4. Baseline Correction
5. Artefact Detection and Rejection
6. Downsampling
7. Rereferencing
8. Grand Mean
9. Merge
10. Averaging
11. Sensor Space Analysis
12. 3D Source Reconstruction

Conversion

- The “fileio” toolbox is used in converting data from its native machine-dependent format to a MATLABbased, common SPM format
 - The *.mat file contains the data structure D
 - The *.dat file is the M/EEG data



Epoching

(spm_eeg_epochs)

- Epoching cuts out chunks of continuous data and saves them as “single trials” based on either their location in the time-series or on their event label
 - The trial starts at some user-specified pre-stimulus time (at least 100 ms before the stimulus onset) and ends at some post-stimulus time
 - Segment length (ms) = $2000/\text{frequency (Hz)}$
 - The data will be baseline-corrected (the mean of the pre-stimulus time is subtracted from the whole trial)
 - The default prefix is ‘e’

Filtering

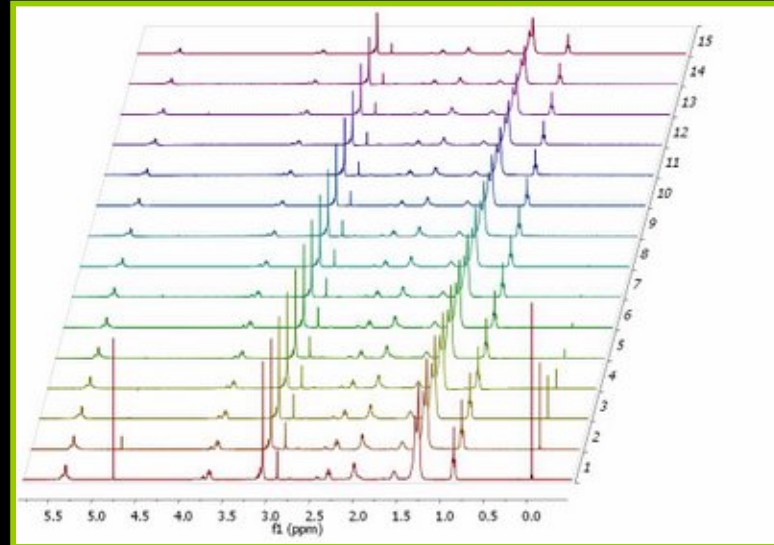
(spm_eeg_filter)

- Filtering removes particular frequencies (in Hz) from the data while retaining other frequencies
 - SPM will automatically use the Butterworth-filter
 - Types of filters:
 - **Lowpass filter** (attenuates higher frequencies)
 - **Highpass filter** (attenuates lower frequencies)
 - **Bandpass filter** (attenuates both higher and lower frequencies)
 - **Notch filter** (attenuates a narrow frequency band)
 - The default prefix is 'f'

Baseline Correction

(spm_eeg_bc)

- Baseline correction subtracts the baseline from channel data
 - The default prefix is 'b'



Artefact Detection and Rejection

(spm_eeg_artefact)

- Artefact detection and rejection identifies and removes physiological and extraphysiological activity that is unrelated to the neuronal signals of interest (i.e., eye blinks and muscle activity)
 - Algorithms include thresholding of the data, thresholding of the difference between adjacent samples (to detect jumps), thresholding peak-to-peak amplitude, and detection of flat segments
 - The default prefix is 'a'

Downsampling

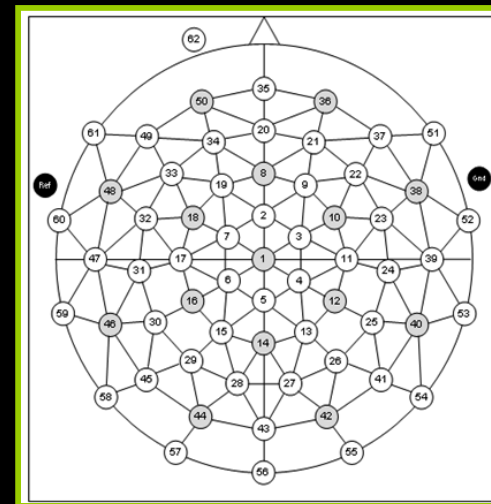
(spm_eeg_downsample)

- Downsampling allows you to choose a new and smaller sampling rate (Hz) in order to reduce unnecessarily large data files
 - **Nyquist Theory** stipulates that the minimum digital sampling frequency must be at least 2.5 times the maximum frequency in the analogue signal
 - The default prefix is 'd'

Rereferencing

(spm_eeg_montage)

- Re-referencing estimates a true, non-arbitrary zero value to which voltage measurements will later be compared with
 - SPM allows referencing to the **average over channels**, to single channels, or to any linear combination of channels
 - The default prefix is 'M'



Grand Mean

(spm_eeg_grandmean)

- The grand mean serves as the average of evoked responses over multiple subjects or multiple EEG files
 - Averaged weighting (based on the number of trials in each file) is suitable for averaging across sessions within a subject whereas unweighted averaging is suitable for averaging across subjects
 - The default prefix is 'g'

Merge

(spm_eeg_merge)

- Merging serves to concatenate multiple sessions for a single subject
 - The function will check whether there are at least two files and whether all data are consistent with each other
 - The simplest way to merge files is by keeping all condition labels the same; in other cases, it might be helpful to rename the conditions like “condition A” to something like “condition A, session 1”
 - The default prefix is ‘c’

Averaging

(spm_eeg_average)

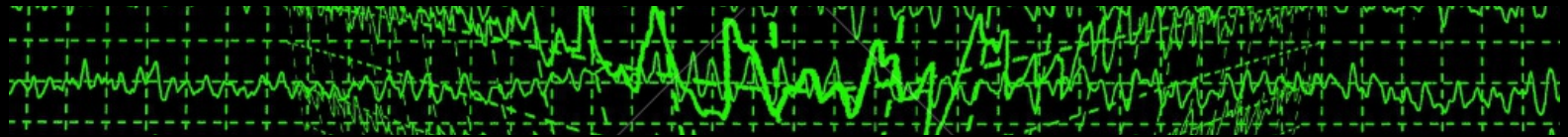
- Averaging combines all the trials into a single waveform in order to extract an evoked response potential (ERP)
 - The averaging method assumes that the ERP ‘signal’ is identical across trials and that the EEG noise is random
 - Robust averaging weights samples in each trial from 0 to 1 based on how artefactual they are and considers these weights when averaging
 - The default prefix is ‘m’

Sensor Space Analysis

- Sensor space analysis (second-level analysis) serves to make inferences about the population from which subjects are drawn using NIfTI formatted image files
 - **Data in the time domain** can be analyzed by averaging over a time window or by using an explicit mask
 - **Time-frequency data** must be reduced from a 4D format (space(X,Y), time, frequency) to either a 3D image (space(X,Y), time) or a 2D image (time, frequency)
 - **Smoothing** is necessary to accommodate spatial/temporal variability between subjects and make the images better conform to the assumptions of random field theory

Statistical Analyses

Please skip to slide 44, titled “Factorial Design Specification”, for information on first-level and second-level ERP analyses.



The statistical processes behind both EEG and fMRI analysis are incredibly similar and are best presented together.

3D Source Reconstruction

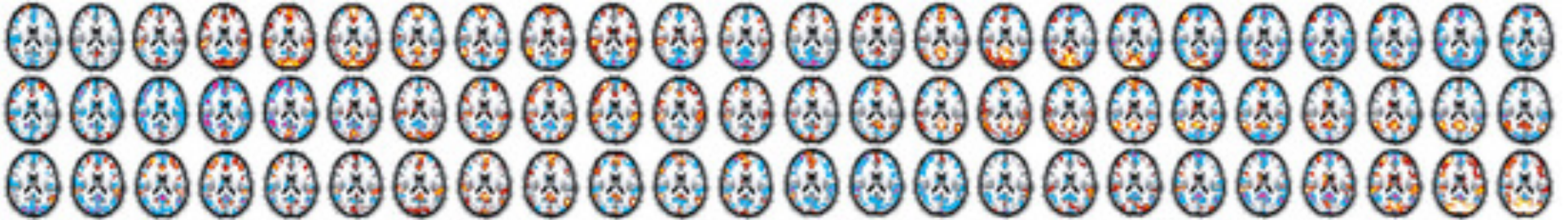
3D source reconstruction results in a spatial projection of sensor data into (3D) brain space and considers brain activity as comprising a very large number of dipole sources spread over the cortical sheet, with fixed locations and orientations

1. **Source space modeling** derives a mesh from either an subject's structural scan or the MNI template
2. **Data co-registration** links the coordinate system in which sensor positions are originally represented to the MNI coordinates (fiducials)
3. **Forward computation** determines the effect that each of the dipoles on the cortical mesh would have on the sensors (the default matrix name is SPMgainmatrix.mat; the default model name is _EEG_BEM.mat)
4. **Inverse reconstruction** localizes either the evoked response, the evoked power or the induced power; the results can be viewed by pressing "Render"
5. **Writing the results as 3D NiftI images** allows for a 2nd level analysis of between subject level effects in fMRI

Displaying Data with SPM/EEG Review

- SPM M/EEG Review, which can be called under “Display” → M/EEG, provides the user with basic visualization (data and source reconstruction) and reviewing tools
 - Main tabs: **EEG** displays EEG type data; **MEG** displays MEG type data; **Other** displays any other type of data (e.g., HEOG, VEOG, etc.); **info** displays basic information about the data file (“channels”, “trials” and “inv”); **Source** displays source reconstructions
 - For continuous (non-epoched) data, only “standard” mode is enabled; for time-frequency data, only “scalp” mode is enabled

SPM for fMRI



fMRI Overview

1. Slice Timing
2. Realign
3. Realign and Unwarp
4. Coregister
5. Segment
6. Normalise
7. Smooth

Slice Timing

- The staggered ordering of slice acquisition used in echo-planar scanning results in staggered ordering
- The “shifter” filter convolves the signal to produce a phase shift in the data such that all slices correspond to the same point in time
- The default prefix is ‘a’

Slice Timing

Necessary Components

- **Data** (subjects or sessions)
 - Session (images to slice-time correct)
- **Number of slices**
- **TR** (repetition time; seconds)
- **TA** (acquisition time; $TR - (TR/nslices)$ seconds)
- **Slice order**
 - **Ascending** (first slice = bottom): $[1:1:nslices]$
 - **Descending** (first slice = top): $[nslices:-1:1]$
 - **Interleaved (middle-top)**: for $k = 1:nslices$, $round((nslices - k)/2 + (rem((nslices - k), 2) * (nslices - 1)/2) + 1, end)$
 - **Interleaved (bottom-up)**: $[1:2:nslices \ 2:2:nslices]$
 - **Interleaved (top-down)**: $[nslices:-2:1, nslices-1:-2:1]$
- **Reference slice**

Realign

- Within-subject registration of the image time series aims to remove movement artefact
 - Estimate (realigns a time-series of images acquired from the same subject using a least squares approach and a 5 parameter spatial transformation; the default prefix is 'rp')
 - Reslice (reslices a series of registered images such that they match the first image selected voxel-for-voxel; the default prefix is 'r')
 - Estimate and Reslice

Realign

Necessary Components

- **Data** (new sessions for this subject)
 - **Session** (scans for this session)
 - **Images** (scans to reslice)
- **Estimation options** (quality; separation; smoothing/FWHM; num passes; interpolation; wrapping; weighting)
- **Reslice options** (resliced images; interpolation; wrapping; masking)

Realign and Unwarp

- Within-subject registration of the image time series aims to remove movement artefact; unwarping of the time series then formulates the inverse problem (“derivative fields” are formed given the observed variance and known/estimated movements) in order to further reduce variance
 - In order to achieve minimal distortion, use fast gradients, low fields (i.e., $< 3T$), low resolution (64x64) and SENSE/SMASH
 - The default prefix is ‘u’

Realign and Unwarp

Necessary Components

- **Data** (sessions to unwarp)
 - **Session** (similar session data added to a realign+unwarp branch)
 - **Images** or **Phase map**
- **Estimation options** (quality; separation; smoothing/FWHM; num passes; interpolation; wrapping; weighting)
- **Unwarp estimation options** (basis functions; regularisation; reg. factor; Jacobian deformations; first-order effects; second-order effects; smoothing for unwarp/FWHM; number of iterations; Taylor expansion point)
- **Unwarp reslicing options** (resliced images; interpolation; wrapping; masking)

Coregister

- Coregistration employs a rigid-body transformation (in 3D) with three translations and three rotations about the different axes in order to align a reference and source image
 - Coregistration can be performed by estimating the transformation, reslicing images according to some rigid-body transformations, or estimating and applying rigid-body transformations
 - The default prefix is 'r'

Coregister

Necessary Components

- **Reference image** (template image)
 - **Source image** (image that is jiggled to match the reference)
 - **Other images** (images that need to remain in alignment with the source image)
 - **Estimation options** (objective function; separation; tolerances; histogram smoothing)
 - Use Normalised Mutual Information for inter-modal registration; use Normalised Cross Correlation for within modality
- **Image defining space** (reference image)
 - **Images to reslice** (images resliced to the same dimensions, voxel sizes, etc. as the space defining image)
 - **Reslice options** (interpolation; wrapping; masking)

Segment

- Segmentation alternates among classification, bias correction and registration to determine the probability of different tissue classes being found at each location in an image
 - This routine produces:
 - Spatial normalisation parameters (*_seg_sn.mat files)
 - Tissue class images (grey matter = c1*; white matter = c2*; cerebro-spinal fluid = c3*)
 - Spatially normalised images - both with (mwc*) and without (wc*) modulation (Modulation removes volumetric differences caused by spatial normalisation)

Segment

Necessary Components

- **Data** (scan for each subject)
 - **Output files** (spatial normalisation parameters; images of tissue classes; bias corrected images)
- **Custom** (tissue probability maps; Gaussians per class; affine regularisation; warping regularisation)
- **Warp frequency cutoff** (cutoff of DCT bases)
- **Bias regularisation** (estimation and correction of smooth, spatially varying artifacts)
- **Bias FWHM** (FWHM of Gaussian smoothness of bias)
- **Sampling distance** (distance between sampled points when estimating the model parameters)
- **Masking image** (sets voxels to zero which need to be sampled from outside the original images)

Normalise

- Least squares registration aims to normalise MRI, PET, or SPECT images into a standard space defined by some similarly contrasted ideal model or template image(s)
 - Affine regularisation first searches for a solution that maximizes registration between two brains
 - Estimating nonlinear deformations then defines the deformations by a linear combination of three dimensional discrete cosine transform (DCT) basis functions
 - The default image prefix is 'w', and the parameters are saved in the *_sn.mat file

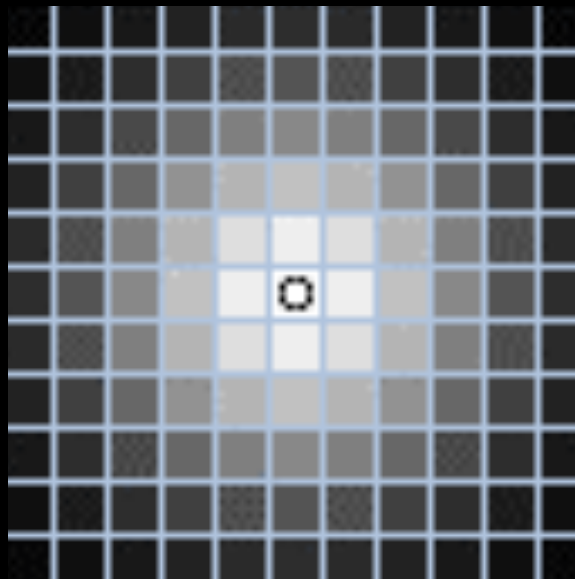
Normalise

Necessary Components

- **Normalise: Estimate** (computes the warp that best registers a source image to match a template)
 - **Data** (session; source image; source weighting image)
 - **Estimation options** (template image; template weighting image; source image smoothing; template image smoothing; affine regularisation; nonlinear frequency cutoff; nonlinear iterations; nonlinear regularisation)
- **Normalise: Write** (allows previously estimated warps to be applied to a series of images)
 - **Data** (subject; parameter file; images to write)
 - **Writing options** (preserve; bounding box; voxel sizes; interpolation; wrapping)
- **Normalise: Estimate and Write** (computes the warp that best registers a source image to match a template and also allows the contents of the image files to be applied to a series of images)

Smooth

- Smoothing (or convolving) image volumes involves the application of a Gaussian kernel to suppress noise and effects due to functional differences in anatomy
 - The default prefix is 's'

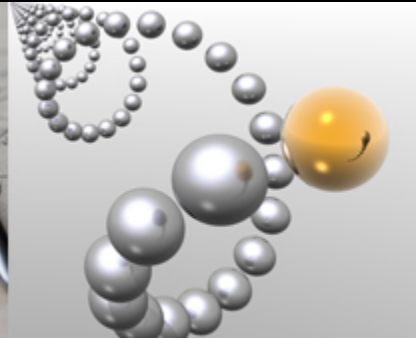


Smooth

Necessary Components

- **Images to smooth**
- **FWHM** (full-width at half maximum of the Gaussian smoothing kernel; mm)
- **Data type** (data-type of output images)
- **Implicit masking** (mask implied by a particular voxel value)

SPM for Statistical Analysis



Statistical Analysis Overview

1. fMRI Model Specification
 - GLM design matrix
 - fMRI data files
 - Filtering
2. fMRI Model Estimation
 - Classical approach
 - Bayesian approach
3. Factorial Design Specification
 - Statistical Parametric Maps (SPMs)
 - Posterior Probability Maps (PPMs)

fMRI Model Specification

- The design matrix defines the experimental design and the nature of hypothesis testing to be implemented (one row per scan; one column per effect/explanatory variable)
 - Responses can be either event-related (stochastic or deterministic) or epoch-related
 - A two-level approach is used to analyze data from multiple subjects: within-subject analyses serve as case studies (“first level” model); “Random-Effects (RFX) analyses” allow inferences to be made about the population from which subjects were drawn (“second level” model)

fMRI Model Specification

Necessary Components

- **Timing parameters** (units for design; interscan interval; microtime resolution; microtime onset)
- **Subject/session** (scans; conditions/multiple conditions; regressors/multiple regressors; high-pass filter)
- **Factorial design** (automatically generates contrasts for the within- and between-subject main effects and interactions)
- **Basis functions** (models the hemodynamic response)
- **Model interactions** (generalized convolution of inputs, U , with basis set, bf)

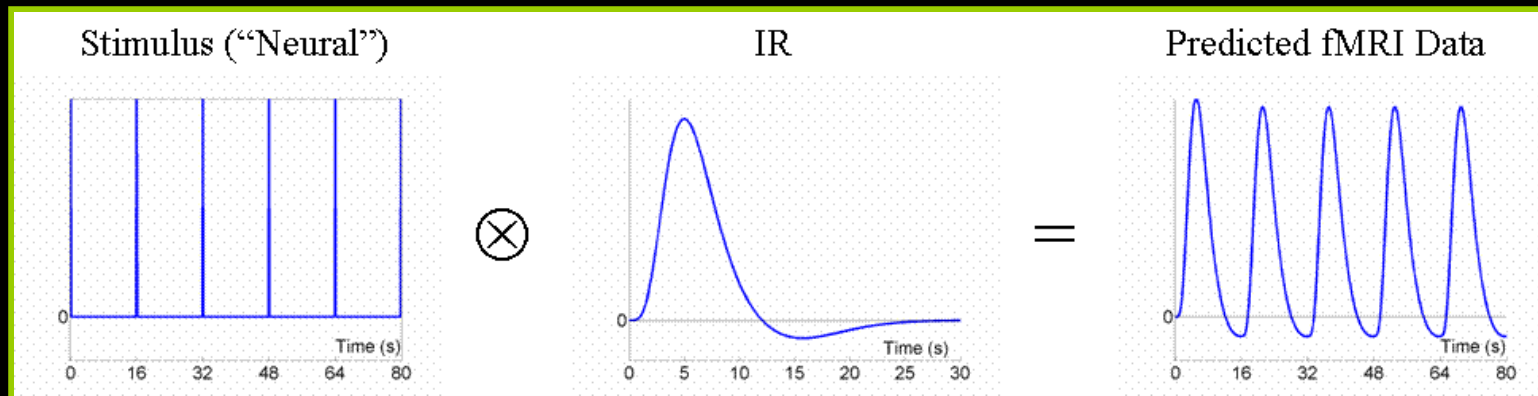
fMRI Model Specification

Necessary Components

- **Directory** (where the SPM.mat file containing the specified design matrix will be written)
- **Global normalisation** ('None' or 'Scaling')
- **Explicit mask** (image for explicitly masking the analysis)
- **Serial correlations** (aliased biorhythms and unmodelled neuronal activity can be accounted for using an autoregressive AR(1) model during Classical (ReML) parameter estimation)
- **Reviewing your design** (ensures that experimental variance has not been removed by high-pass filtering)

fMRI Model Estimation

Model parameters can be estimated using classical (ReML - Restricted Maximum Likelihood) or Bayesian algorithms



fMRI Model Estimation

Necessary Components

- **Select SPM.mat** (output directory for the results of analyses)
- **Method** (Classical estimation of first or second level models; Bayesian estimation of first level models; Bayesian estimation of second level models)
- **Output files** (files are written to the output directory following estimation)
 - SPM.mat file containing specification of the design and estimated model parameters
 - **Classical 1st-level** (beta_000k.img; ResMS.img; mask.img; RPV.img; con_000i.img or ess_000i.img)
 - **Bayesian 1st-level** (Cbeta_000k.img; Sdbeta_000k.img; Sess1_SDerror.img; mask.img; Sess1_AR_000p.img; con_000i.img and con_sd_000i.img)
- **Model comparison** (compare GLMs based on different basis sets using the Bayesian model evidence)

Factorial Design Specification

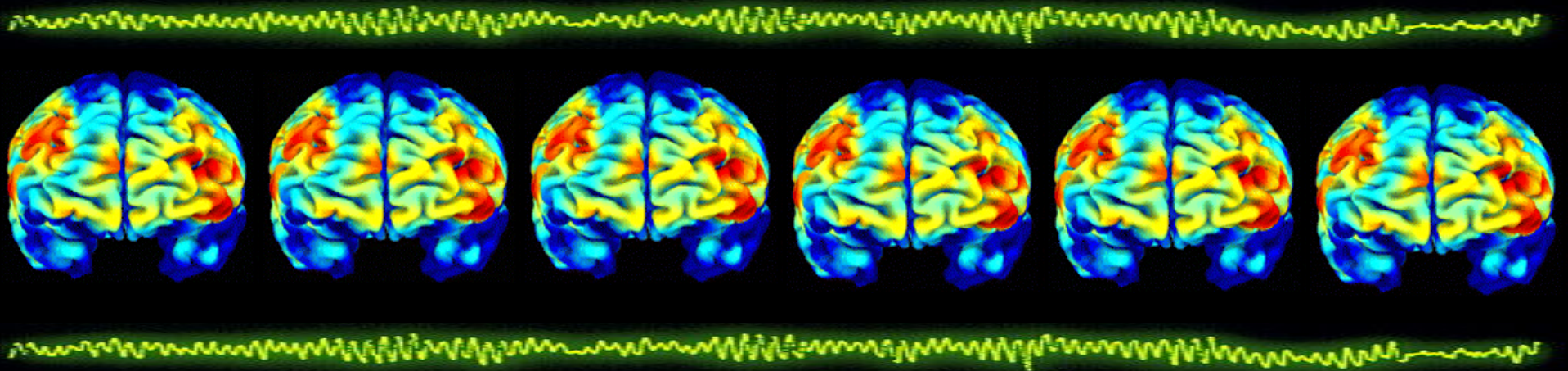
- With this interface, first level models can be used to produce appropriate summary data, which can then be used as raw data for a second-level analysis
- Various data and parameters need to be supplied to specify the design:
 - Image files
 - Indicators of the corresponding condition/subject/group
 - Any covariates, nuisance variables, or design matrix partitions
 - Type of global normalisation
 - Grand mean scaling options
 - Thresholds and masks defining the image volume to analyze

Factorial Design Specification

Necessary Components

- **Directory** (where the SPM.mat file containing the specified design matrix will be written)
- **Design** (one-sample t-test; two-sample t-test; paired t-test; multiple regression; one-way ANOVA; one-way ANOVA - within subject; full factorial; flexible factorial)
- **Covariates** (allows for the specification of covariates and nuisance variables)
- **Masking** (threshold masking; implicit mask; explicit mask)

**Now That You Understand
the Logic Behind EEG and
fMRI Analysis Using SPM...**



**...Apply this Knowledge to
Analyze a Real EEG and
fMRI Data Set!**