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# Pre-Processing

## SPM

#### Realignment (Estimate and Reslice)

Estimate – estimating the amount each volume is out of alignment with a reference volume

Reslice – these estimates will be used to nudge each of the volumes into alignment with the reference volume

Reference volume – set in field “Num Passes”, allows specification whether the volumes will be aligned to the mean of all the volumes or the first volume

?How to create field maps

#### Slice Timing Correction

We assume all slices of same image is taken at the same time (it is not). Can also address same problems later when model fitting using a temporal derivative in the statistical model.

#### Coregistration

Warping/normalising (standardising) individual brain regions onto template.

Affine transformations – motion correction transformations plus zooms and shears.

Registration – the alignment of the functional image to the anatomical image after warping the anatomical image

#### Segmentation

Categorising voxels into 6 tissue types based on MATLAB’s 6 priors

#### Normalisation

Using segmentation to normalise image

#### Smoothing

Replace signal at each voxel with weighted average of voxel’s neighbours

## By Jayson

Specifically, the data has been 'cleaned', but not smoothed yet. We may want to smooth later (6mm fwhm, this can be done in nilearn)

Steps:

SPACE space-MNI152NLin6Asym – *fMRIPrep: spatial normalisation to the MNI152NLin6Asym standard space*

ICA\_AROMA True – *ICA-AROMA: head-motions related movement artefacts removed*

Remove first 1 volumes (non-steady-state) and replace with first steady-state volume – *fMRIPrep: unstable signals are replaced with the first steady-state volume*

Set regions outside mask to zero – *fMRIPrep: zeroes out all voxel values that fall outside a defined brain mask*

detrend False – *Linear trending not applied*

remove\_confounds True – *Confounds below removed*

bandpass 0.01-0.15 – *Band pass filtering done here (lower = drift, higher = noise)*

add\_orig\_mean\_img False - *After confound regression and filtering, do not re-add the original mean image back to the data. Some workflows subtract the mean during processing and then restore it afterward. Setting this to False leaves the mean-removed (demeaned) data as-is.*

smooth False – *spatial smoothing not applied*

fwhm 0 – *as above (Full-width at half-maximum (FWHM) of smoothing kernel = 0 m)*

save\_confounds False – *confounds not saved, good for space saving, bad for reproducibility*

CONFOUND\_LIST ['csf', 'white\_matter', 'rot\_x', 'rot\_x\_power2', 'rot\_x\_derivative1', 'rot\_x\_derivative1\_power2', 'rot\_y', 'rot\_y\_power2', 'rot\_y\_derivative1', 'rot\_y\_derivative1\_power2', 'rot\_z', 'rot\_z\_power2', 'rot\_z\_derivative1', 'rot\_z\_derivative1\_power2', 'trans\_x', 'trans\_x\_power2', 'trans\_x\_derivative1', 'trans\_x\_derivative1\_power2', 'trans\_y', 'trans\_y\_power2', 'trans\_y\_derivative1', 'trans\_y\_derivative1\_power2', 'trans\_z', 'trans\_z\_power2', 'trans\_z\_derivative1', 'trans\_z\_derivative1\_power2', 'physio1', 'physio2', 'physio3', 'physio4', 'physio5', 'physio6', 'physio7', 'physio8', 'physio9', 'physio10', 'physio11', 'physio12', 'physio13', 'physio14', 'physio15', 'physio16', 'physio17', 'physio18']

*This is the list of confound regressors to use during the denoising step.*

*Examples of confounds included:*

*Anatomical noise:*

*'csf', 'white\_matter' – Mean signals from cerebrospinal fluid and white matter (often reflect non-neural noise).*

*Motion parameters:*

*'rot\_x', 'trans\_y', etc. – Rotational and translational motion estimates from realignment.*

*Their derivatives (\_derivative1) and squared terms (\_power2) are included to better model motion artifacts.*

*Physiological regressors:*

*'physio1' through 'physio18' – Principal components of physiological noise (likely extracted via aCompCor or similar).*

*Why it matters:*

*This detailed set of regressors aims to comprehensively capture various sources of non-neural variability to improve the signal quality.*

## Parcellation

|  |  |
| --- | --- |
| Choice | Explanation |
| Using the Yeo 17 thick atlas\* | Yeo is good for studying large scale brain networks to explore subnetwork dynamics of connectivity for whole network level analysis with fewer comparisons during naturalistic paradigms. It is a functional network based on resting network connectivity. |
| standardize='zscore\_sample', #"zscore\_sample", #Z scores the voxels to make mean = 0 | Interested in the changes to signal rather than actual value of the signals themselves. |
| memory="nilearn\_cache", |  |
| verbose=5, |  |
| #Temporal filter settings  high\_pass=0.01, # High pass frequency in Hz (slower)  low\_pass=0.15, # Low pass frequency in Hz (faster)  t\_r=0.8 # Repetition time in seconds | Hz = # cycle per second. Low frequencies (<0.1Hz) ~ slow neural related frequencies. High frequencies (>0.1) ~ physiological noise. (Davey et al., 2013)  *>0.01Hz:* Scanner drift accounts for signals < 0.01Hz. (Bianciardi et al., 2009)  *<0.1Hz:* Functional connectivity in the auditory, visual, and sensorimotor cortices is characterized predominantly by frequencies slower than those in the cardiac (0.6 – 1.2 Hz) and respiratory cycles (0.1 – 0.5 Hz). In functionally connected regions, these low frequencies are characterized by a high degree of temporal coherence. (Cordes et al., 2001) |
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|  |  |

### \*Atlas Choice

# HMM Mar

## FormatHmmmarInputs

Options.\_\_\_\_\_

|  |  |  |  |
| --- | --- | --- | --- |
| Setting | Set | Definition | Explanation |
| K | 6 | Number of hidden states | Can specify upper range, and model will fit with least number with no empty states. Calculate “free energy” for each state number, choose least number of states with lowest free energy. |
| Id\_mixture | 1 | if false, the model will be a mixture of distributions instead of an HMM, ignoring the temporal structure of the data (default to false). | Want HMM rather than mix of distributions |
| order | 1 | Maximum order of the MAR model; if zero, an HMM with Gaussian observations is trained (mandatory, with no default).  The order is how many past time points go into the MAR model. | 1 as per Saurabh, any larger and it becomes “time delayed embedding”  e.g. as fMRI has a slower sampling rate compared to EEG, the order for a MAR fMRI model is recommended to be 1. As EEG has a higher sampling rate compared to fMRI (greater Hz), order needs to be higher for a better fit model (but higher orders risk fitting noise into model). |
| Zeromean | 0 | if 1, the mean of the time series will not be used to drive the states (default to 1 if order is higher than 0, and 0 otherwise). | will default to 1 as order is >=1 |
| covtype | full | choice of the covariance matrix of the noise; "full" to have a full covariance matrix for each state (with off-diagonal elements different from zero), "sharedfull" to have one full covariance matrix for all states, "diag" to have a diagonal full covariance matrix for each state, and "shareddiag" to have one diagonal covariance matrix for all states (default to "full"). | Covariance matrix – matrix describing variability and co-variability of ROIs for each hidden state. Diag is variability of the ROI, offdiag is covariance of different ROIs (if positive high, regions cofluctuate together)  Full – unique covariance for every state, more memory, takes longer, estimation more unstable  Diag – most narrow  Bryan advises: first step – full, if not converge – shared full |
| standardise | 0 | whether or not to standardise each subject/trial such that each channel has mean equal to zero and standard deviation equal to one (default 1). | Standardised in pre-parcellation |
| standardise\_pc | X | whether or not to standardise each subject/trial such that each principal component (if PCA has been applied by setting options.pca) has mean equal to zero and standard deviation equal to one (default 0). | NA |
| verbose | 1 | Verbose outputs | Want text explanation as much as possible |
| Fs | 1/0.8 | Sampling frequency Fs is 1/0.8 (frequency is how many pictures per sec) |  |
| DirichletDiag | X | Makes states more sticky. Value of the diagonal of the prior of the transition probability matrix; the higher, the more persistent the states will be (default to 10). Note that this value is relative; the prior competes with the data, in such a way that if we have very long time series, DirichletDiag will have an irrelevant effect unless is set to a very big value. | A prior distribution placed over the diagonal of the transition probability matrix. Default to 10. (?the count of those states normalised).   * Hold out dataset to estimate parameters * Or try other algorithms to determine underlying set of states directly (HMM adjacent but not HMM) |
| cyc | 300 | maximum number of variational inference cycles. The algorithm with stop earlier if tol is reached. (Default to 1000). | Saurabh recommends: 300, should do as many as possible. |
| initrep | 10 | number of repetitions of the initialisation algorithm, out of which the best will be used as a starting point for the variational inference (default to 5). | Saurabh recommends: 10 |
| initcyc | 10 | maximum number of optimisation cycles in the initialisation algorithm, per repetition (default is 25). | Saurabh recommends: 10 |
| pca | X | Dimensionality reduction form initial number to number specified | NA |
| timelag | X | the lapse between lags; for example, timelag==2 skips one sample for each sample that is taken, time\_lag=3 skips 2, etc (default to 1). | NA |
| exptimelag | X | base for the exponential spacing of regressor samples. Samples are spaced by round(exptimelags^n) with n=0,1,2, never going further in the past than indicated by order. To check which past samples will be used, use the function formorders(); for finding out which value of exptimelag is needed to cover until certain frequency using a given number of lags, use higherorder(). If a value for exptimelag higher than 1 is specified, then timelag is ignored. | NA |
| orderoffset | X | offset to set the starting lag. For example, assuming order==4 and timelag==1, we will use lags (Ahman and Shah, 2004) for orderoffset=0, or lags (Ahman and Shah, 2004) for orderoffset==2. This parameter becomes particularly useful in situations of strong autocorrelations, as for example in MEG (default to 0). | NA |
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## AnalyseResults

### Transition Probabilities

The function getTransProbs(hmm) returns the transition probabilities from any state to any other state, without considering the persistence probabilities (i.e. the probability to remain in the same state). The transition probability matrix including the persistence probabilities is contained in hmm.P.

### Fractional Occupancy

using getFractionalOccupancy(Gamma,T,dim). This can refer to either (i) how much time the HMM spends on each state at each time point on average (across trials), or (ii) how much time each subject/trial/session spends in each state (i.e. the average state probability across time, per session or subject). The former, useful for task, is computed when dim=1; the latter, useful to investigate differences in occupancies between subjects, is computed when dim=2.

Very similar to Gamma or a soft state time course.

Fractional Occupancy where dim = 1 is identical to Gamma for one subject pipeline.

|  |  |  |  |
| --- | --- | --- | --- |
| Setting | Set | Definition | Explanation |
| dim | 1 | 1 = how much time the HMM spends on each state at each time point on average (across trials). Useful for task.  2 = how much time each subject/trial/session spends in each state (i.e. the average state probability across time, per session or subject). Useful for differences in occupancies between subjects. | Currently only one subject, so 1 and 2 should give same output, will need to revisit when running whole dataset through, might be 2 |

### Viterbi Path

i.e. hard state time course

AHMAN, E. & SHAH, I. 2004. Unsafe abortion: global and regional estimates of the incidence of unsafe abortion and associated mortality in 2000. *Geneva: World Health Organization***,** 13-7.

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CORDES, D., HAUGHTON, V. M., ARFANAKIS, K., CAREW, J. D., TURSKI, P. A., MORITZ, C. H., QUIGLEY, M. A. & MEYERAND, M. E. 2001. Frequencies contributing to functional connectivity in the cerebral cortex in "resting-state" data. *AJNR Am J Neuroradiol,* 22**,** 1326-33.

DAVEY, C. E., GRAYDEN, D. B., EGAN, G. F. & JOHNSTON, L. A. 2013. Filtering induces correlation in fMRI resting state data. *NeuroImage,* 64**,** 728-740.