



Resting state fMRI and ICA

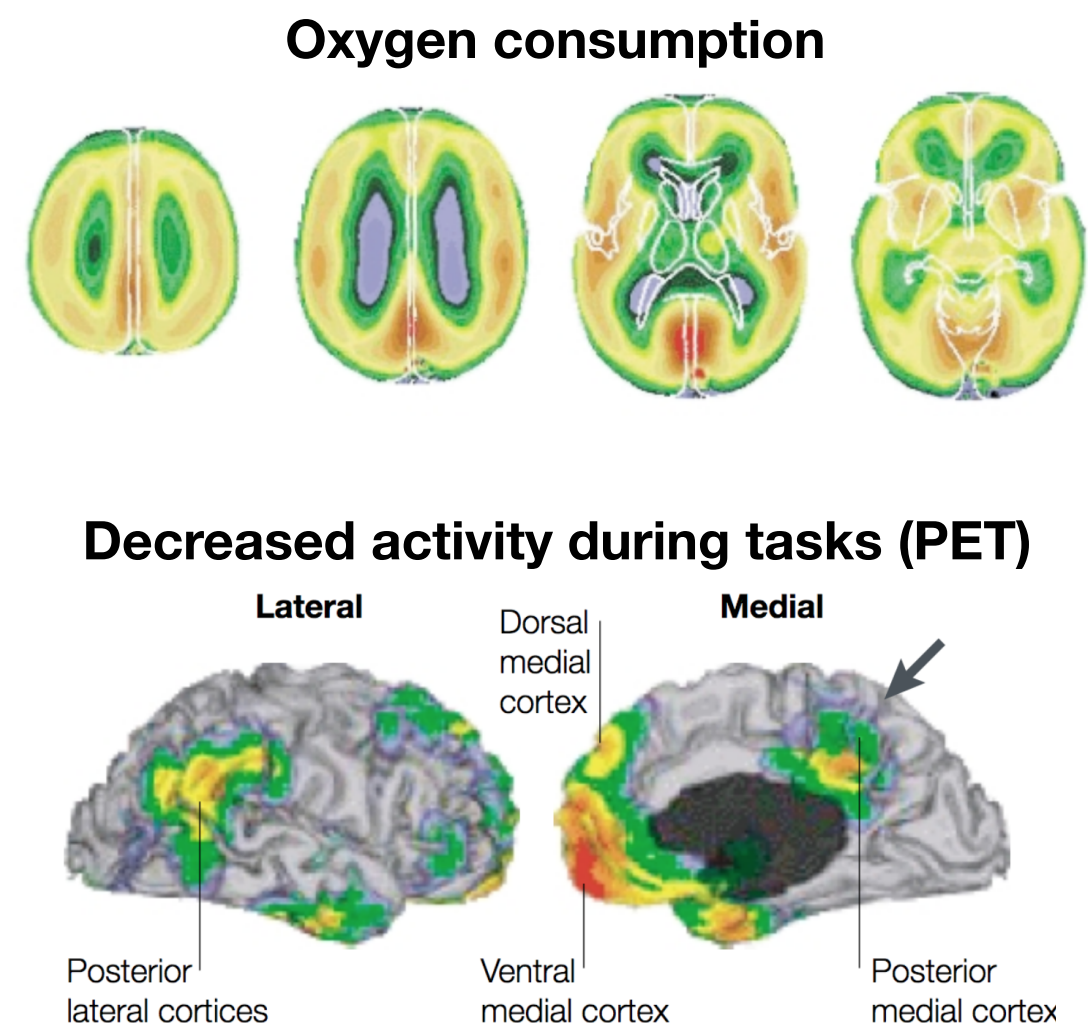
- Introduction to resting state
- Independent Component Analysis
- Single-subject ICA
- Multi-subject ICA
- Dual regression



Energy consumption in the brain

- Brain $< 2\%$ body weight but consumes $\sim 20\%$ of total energy
- estimated 60-80% of this energy used to support communication between cells
- task-evoked activity accounts for $\sim 1\%$

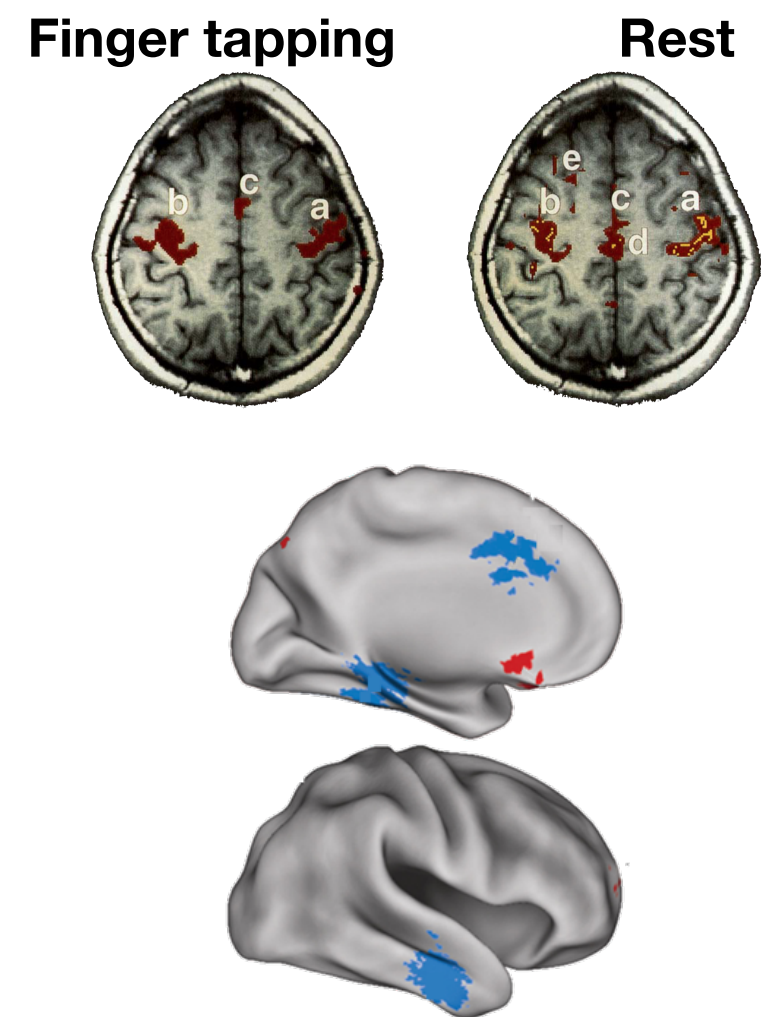
Raichle et al (2001), Gusnard et al (2001)





Why study the brain at rest?

- Localisation versus connectivity
- Understand the inherent functional organisation of the brain
- Clinical/ cognitive biomarker
- Pragmatic benefits: can be done in any population, with relatively little setup and expertise required



Biswal et al (1995), Sheline et al (2010)



Principles of resting state analysis

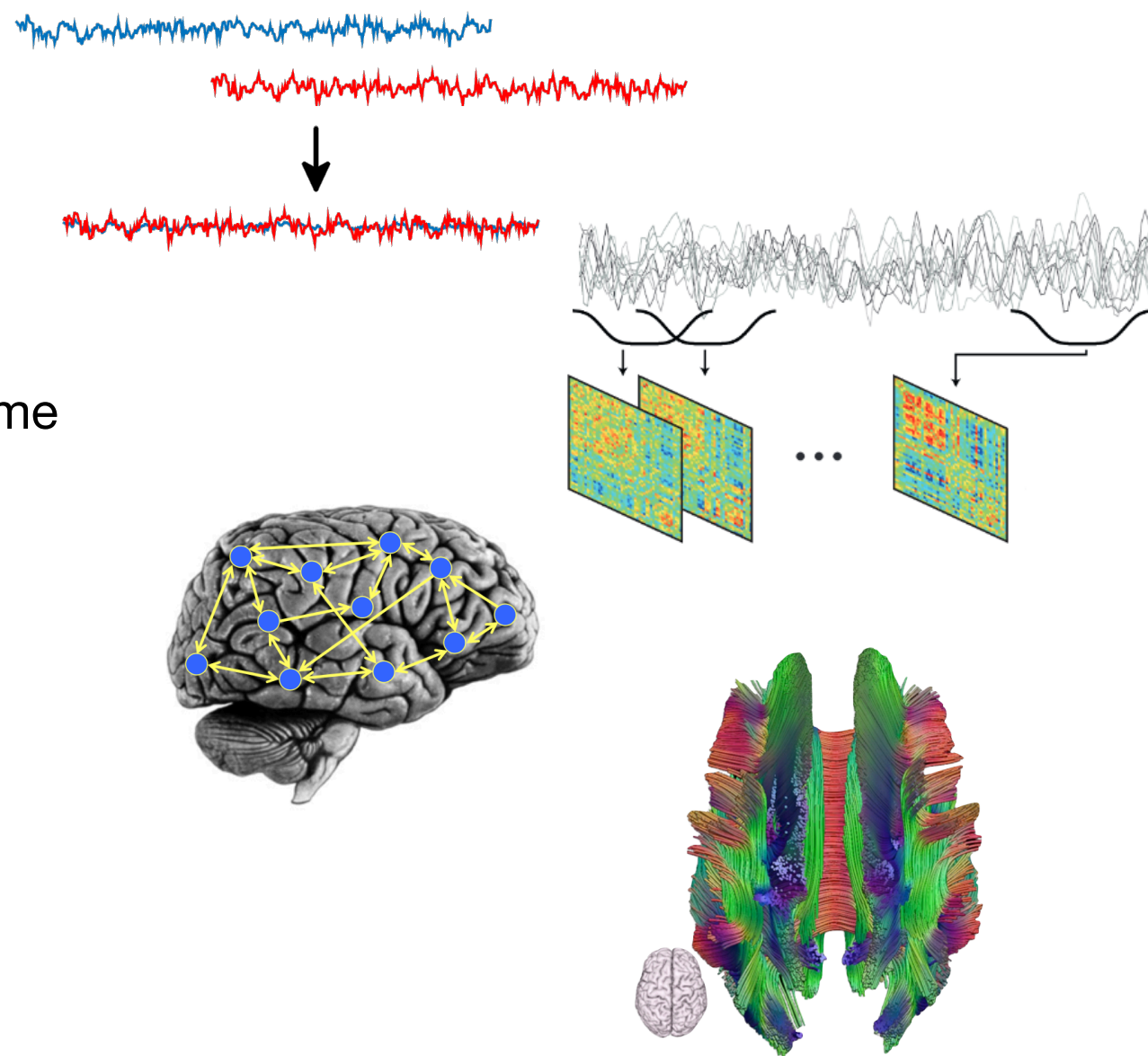
- Many different methods available for analysis
- All have one assumption in common:
- i.e. definition of functional connectivity is based on a statistical dependency between timeseries
- Differences between methods lie in the way these similarities are estimated and/or represented

If two brain regions show similarities in their BOLD timeseries, they are functionally connected



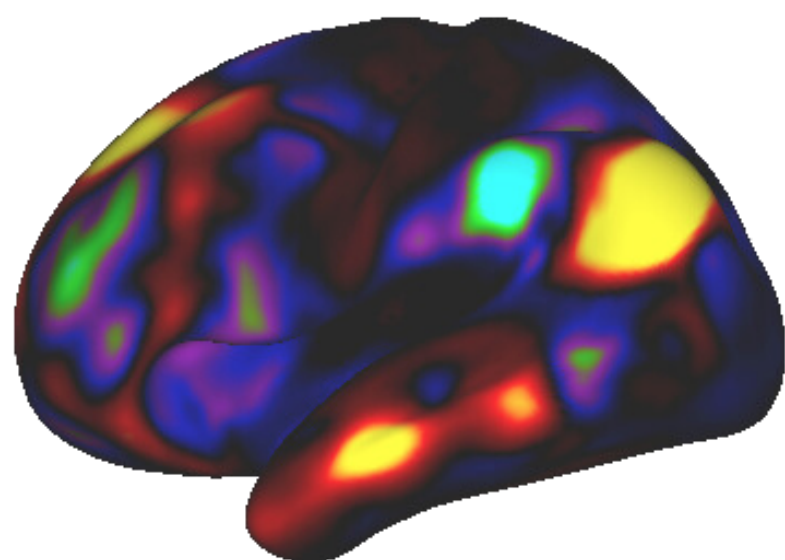
Types of connectivity

- Functional connectivity
 - Statistical dependency
- Dynamic connectivity
 - Changes in functional connectivity over time
- Effective connectivity
 - Directional influence
- Anatomical (structural) connectivity
 - Presence of a white matter tract

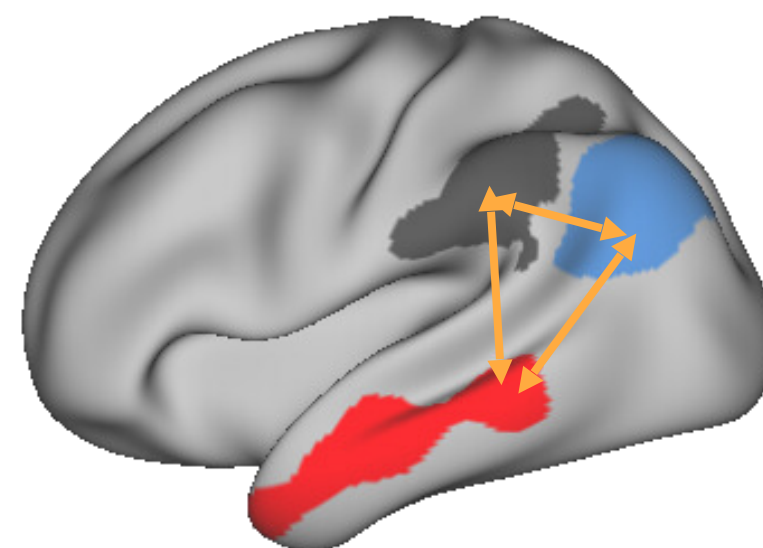




Overview of resting state methods



Voxel-based methods



Node-based methods



Overview of resting state methods

Voxel-based methods

- Seed-based correlation analysis
 - SCA
- Independent component analysis
 - ICA

Node-based methods

- Network modelling analysis
 - FSLnets
- Graph theory analysis
 - Such as degree, hub, path length



Overview of resting state methods

Voxel-based methods

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Resting state methods

ICA

- Multivariate voxel-based approach
- Finds interesting structure in the data
- Exploratory “model-free” method
- Spatial approach

Network modelling

- Node-based approach (first need to parcellate the brain into functional regions)
- Map connections between specific brain regions (connectomics)
- Temporal approach



Model-based (GLM) analysis

A diagram illustrating the General Linear Model (GLM) equation. It features three vertical wavy lines representing time-series data. The first line on the left is the measured time-series. An equals sign follows, then a second vertical wavy line representing the design matrix. This is followed by the Greek letter beta with a subscript '1' (β_1), a plus sign, and a third vertical wavy line representing the noise term.

- model each measured time-series as a linear combination of signal and noise
- If the design matrix does not capture every signal, we typically get wrong inferences!



Data Analysis

Confirmatory

- “How well does my model fit to the data?”

Problem \Rightarrow Data \Rightarrow

Model \Rightarrow Analysis

\Rightarrow Results

- results depend on the model

Exploratory

- “Is there anything interesting in the data?”

Problem \Rightarrow Data \Rightarrow

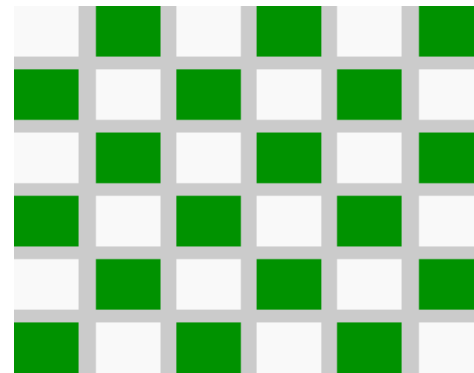
Analysis \Rightarrow Model

\Rightarrow Results

- can give unexpected results

FMRI inferential path

Experiment



Physiology

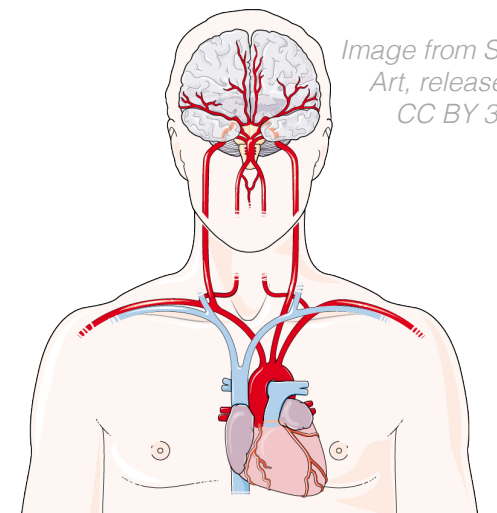


Image from Servier Medical Art, released under the CC BY 3.0 license

MR Physics

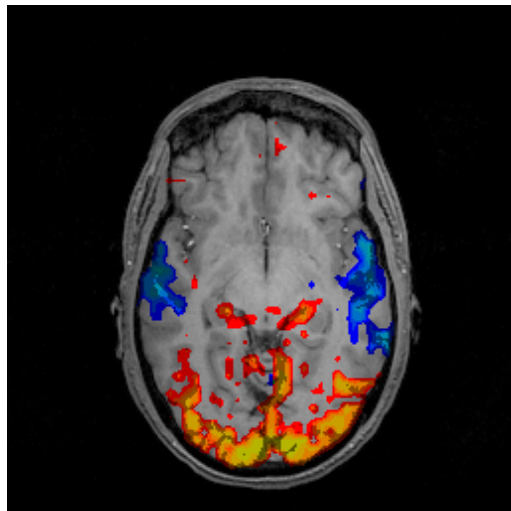


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Analysis



Interpretation
of final results





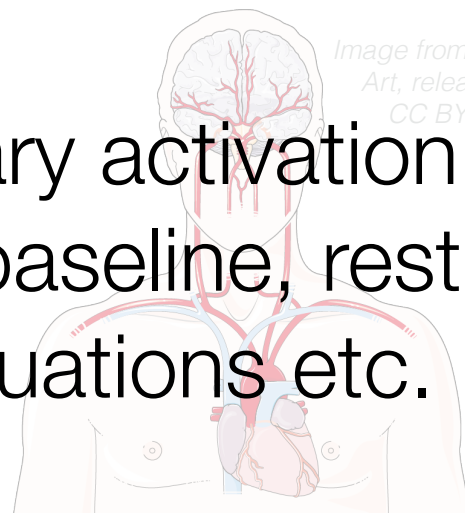
Variability in fMRI

Experiment



suboptimal event timing,
inefficient design, etc.

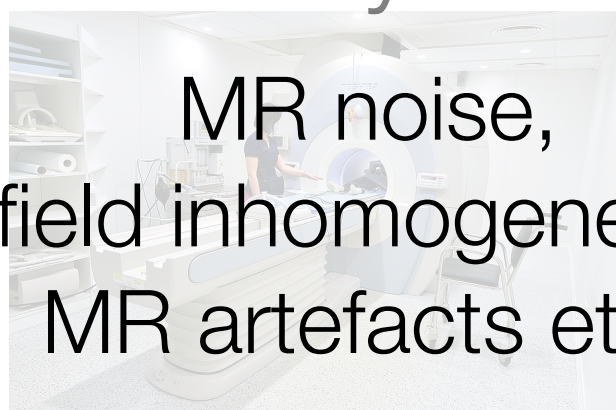
Physiology



secondary activation, ill-
defined baseline, resting-
fluctuations etc.

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MR Physics



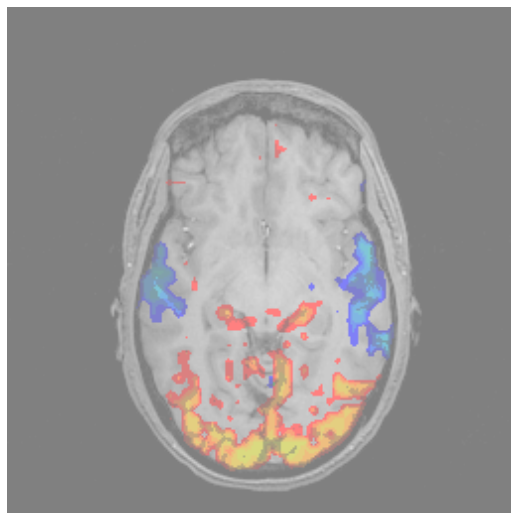
MR noise,
field inhomogeneity,
MR artefacts etc.

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Analysis

filtering & sampling artefacts, design
misspecification, stats &
thresholding issues etc.

Interpretation
of final results





Model-free?



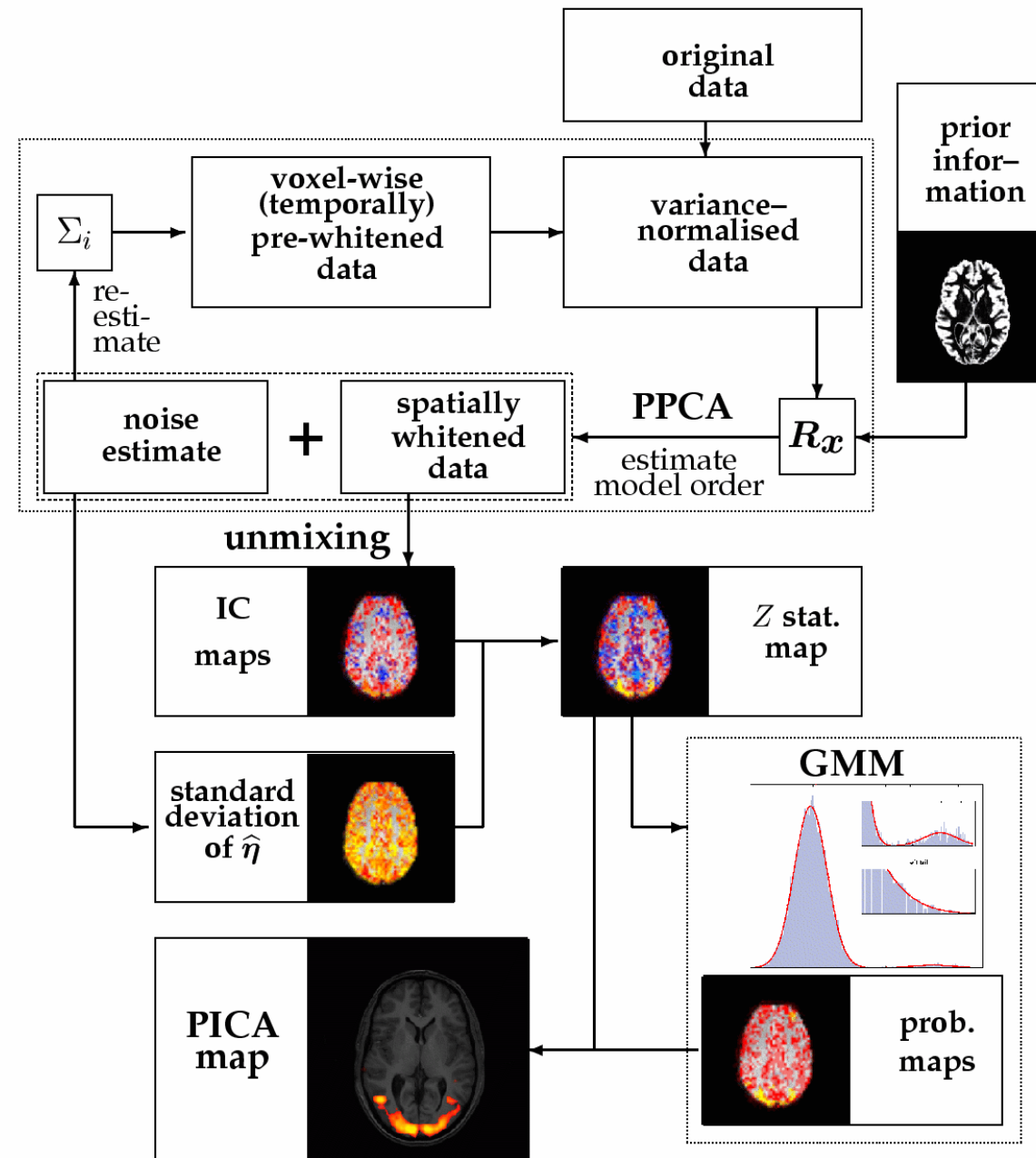
There is no explicit time-series model
of assumed 'activity'



Model-free?



$$Y^i = S^i A^i + E^i, \quad \text{where} \quad E_{.j}^i \sim \mathcal{N}(0, \sigma_Y^2 I)$$



There is an underlying mathematical (generative) model

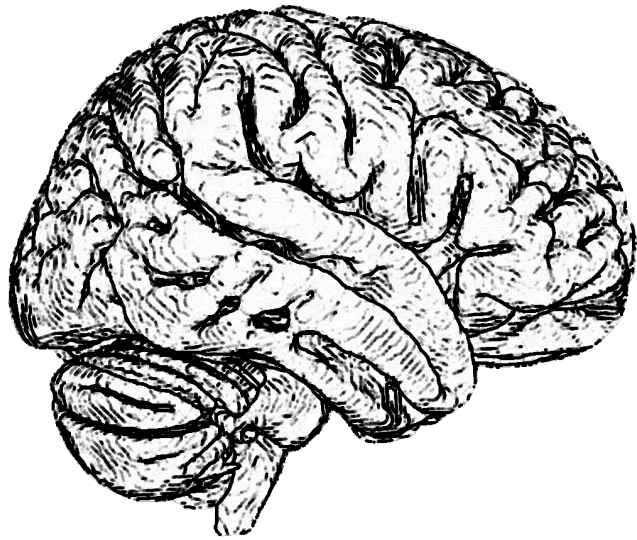


Decomposition techniques

- try to ‘explain’ / represent the data
 - by calculating quantities that summarise the data
 - by extracting underlying ‘hidden’ features that are ‘interesting’
- differ in what is considered ‘interesting’
 - are localised in time and/or space (Clustering)
 - explain observed data variance (PCA, FDA, FA)
 - are maximally independent (ICA)

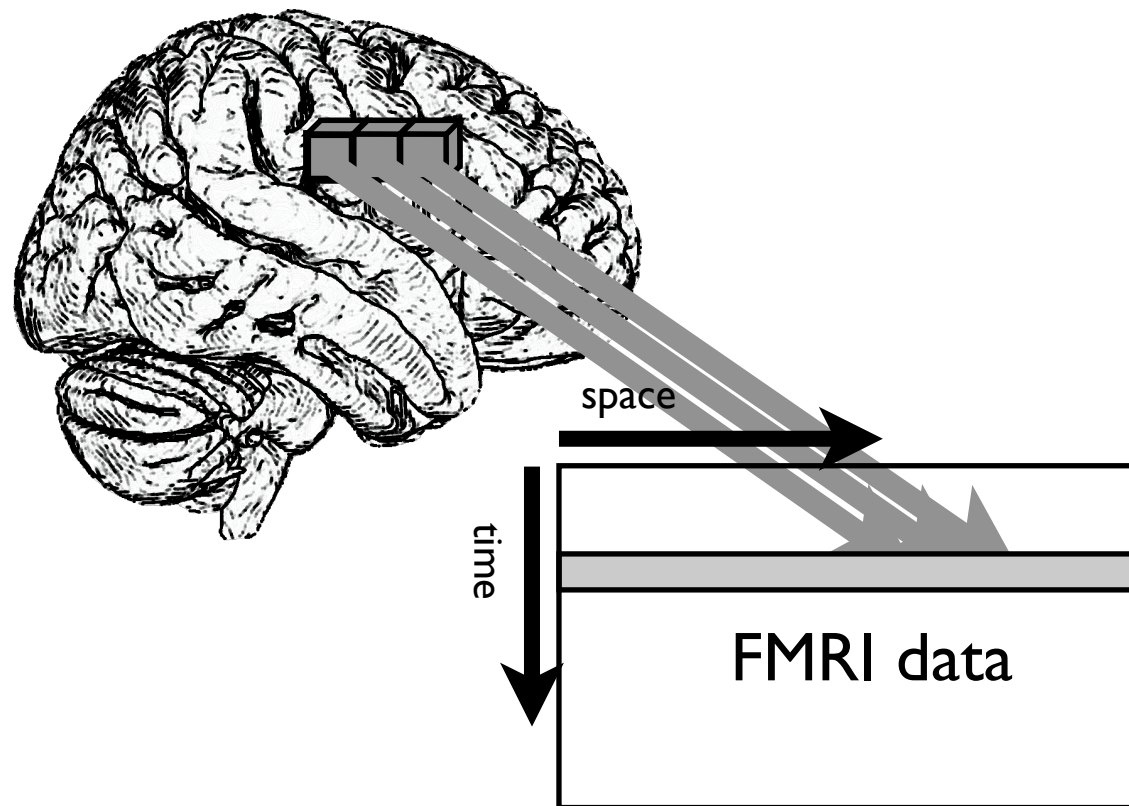
Melodic

multivariate linear decomposition:



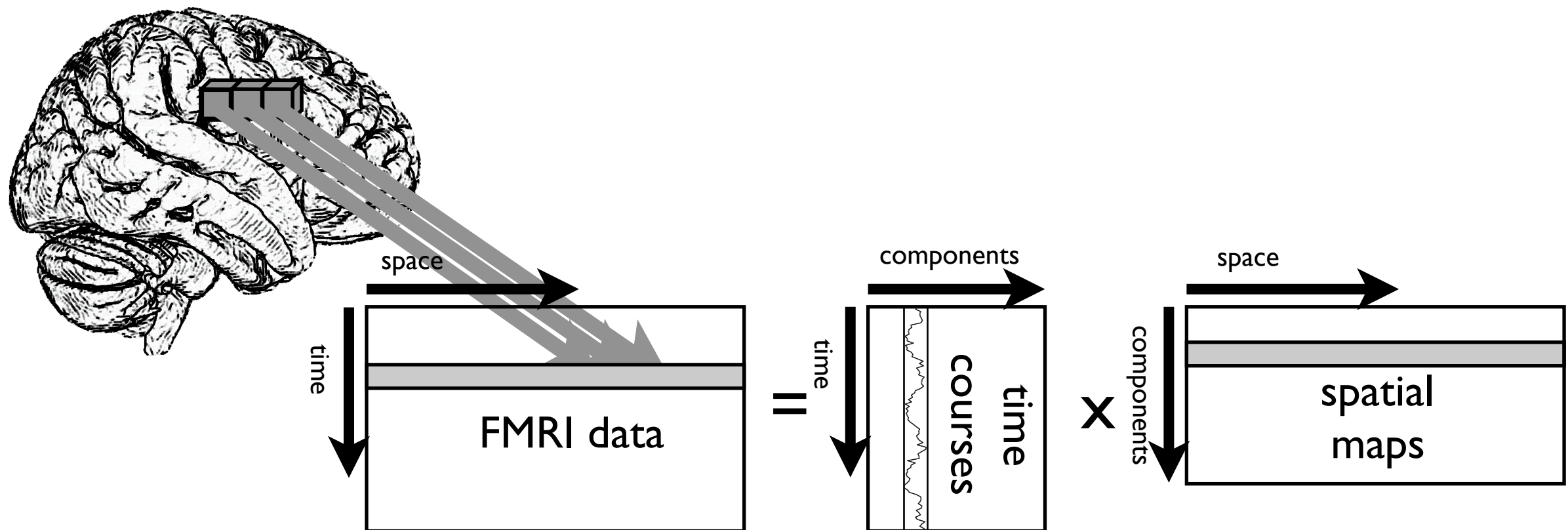
Melodic

multivariate linear decomposition:



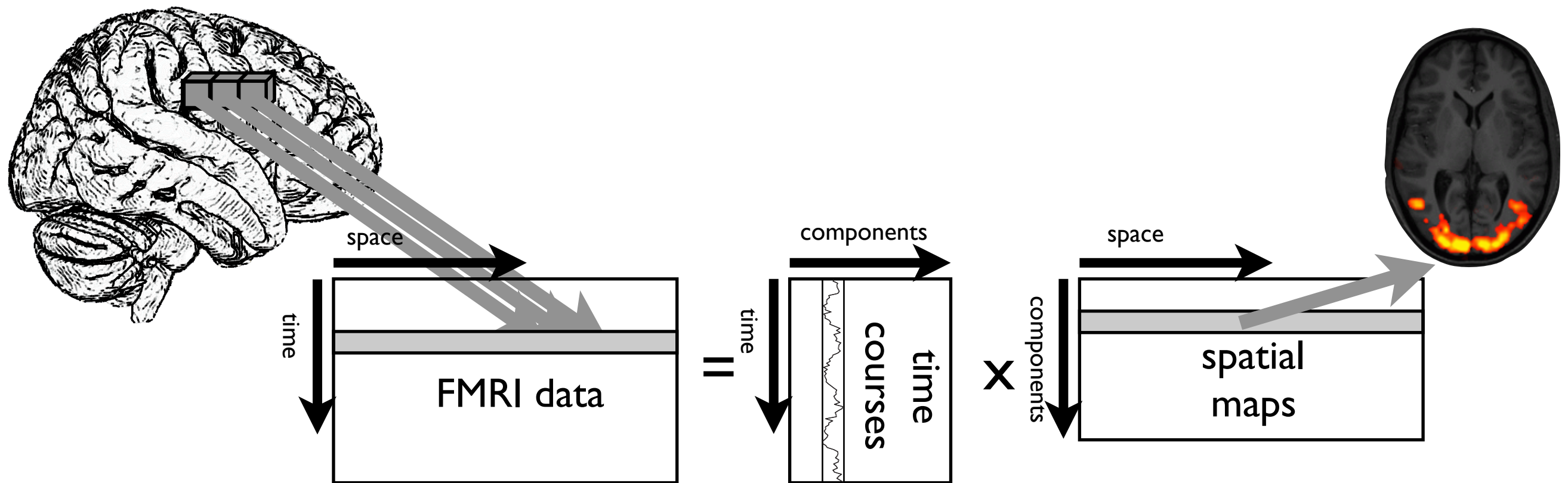
Melodic

multivariate linear decomposition:



Melodic

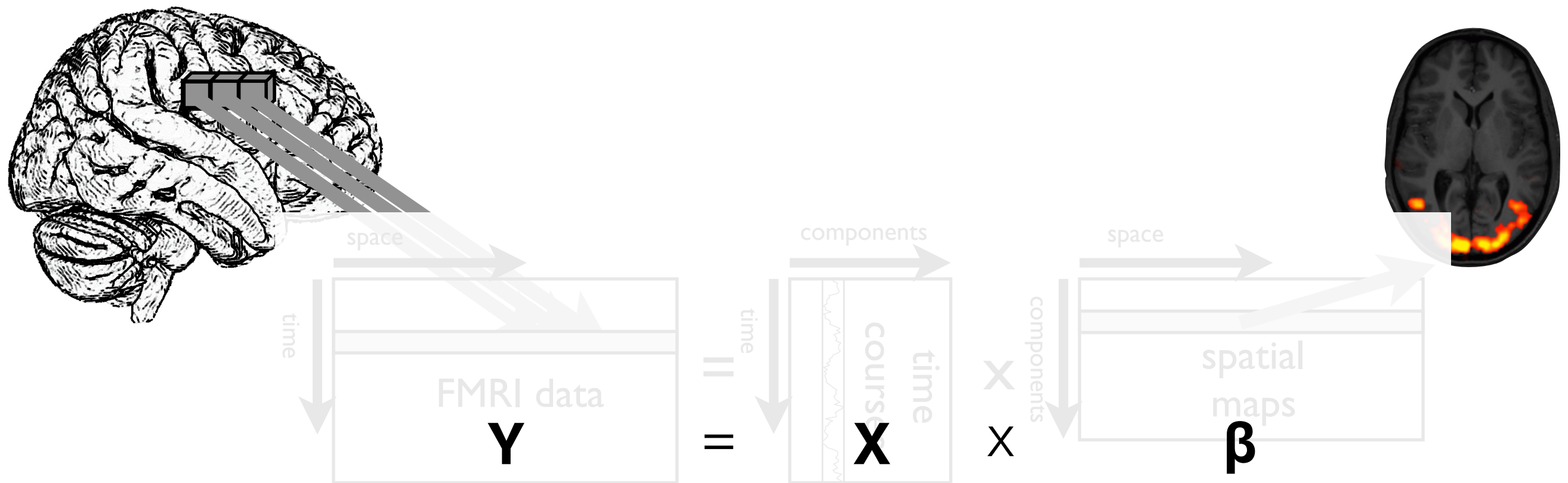
multivariate linear decomposition:



Data is represented as a 2D matrix and decomposed into components

Melodic

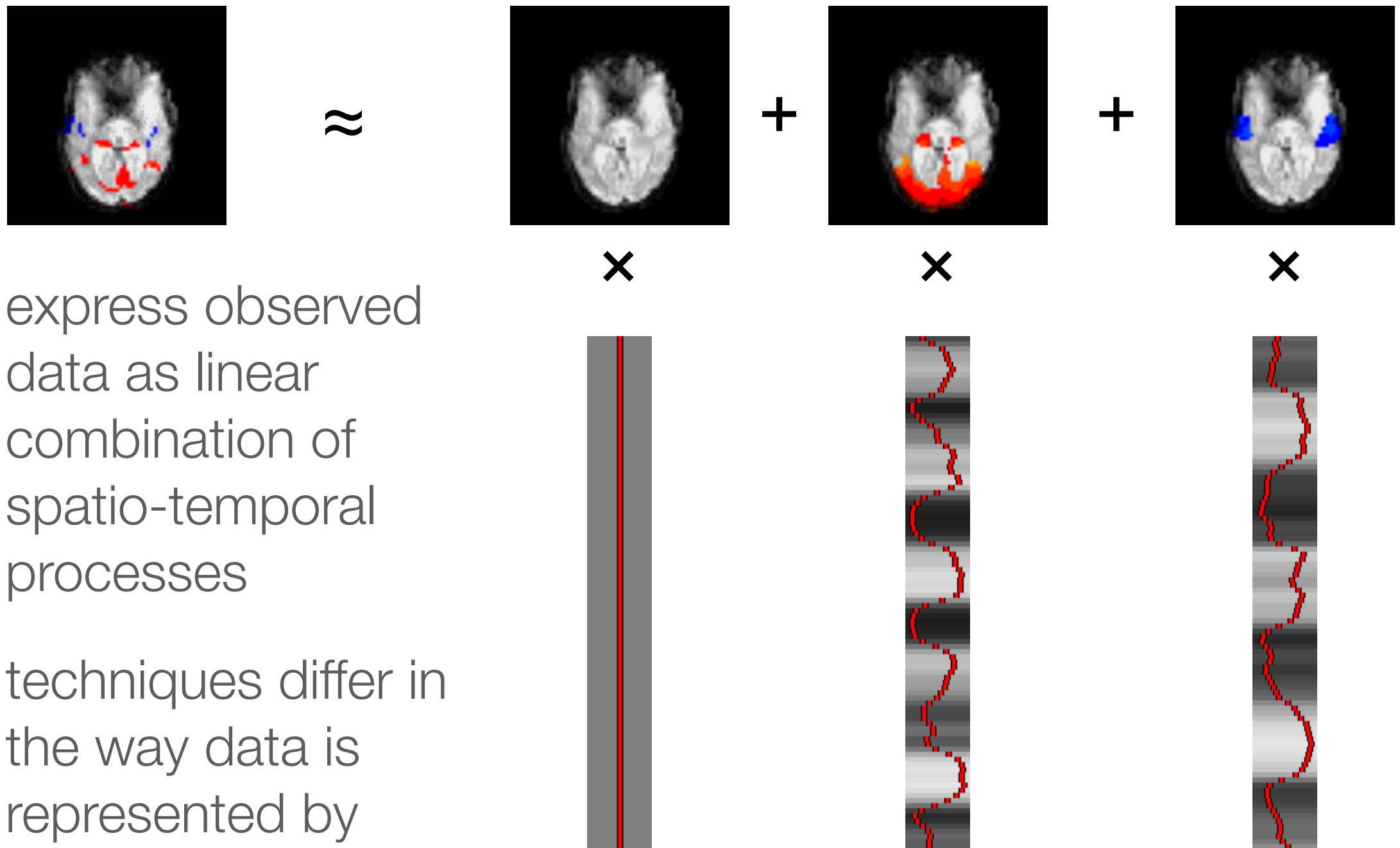
multivariate linear decomposition:



Data is represented as a 2D matrix and decomposed into components



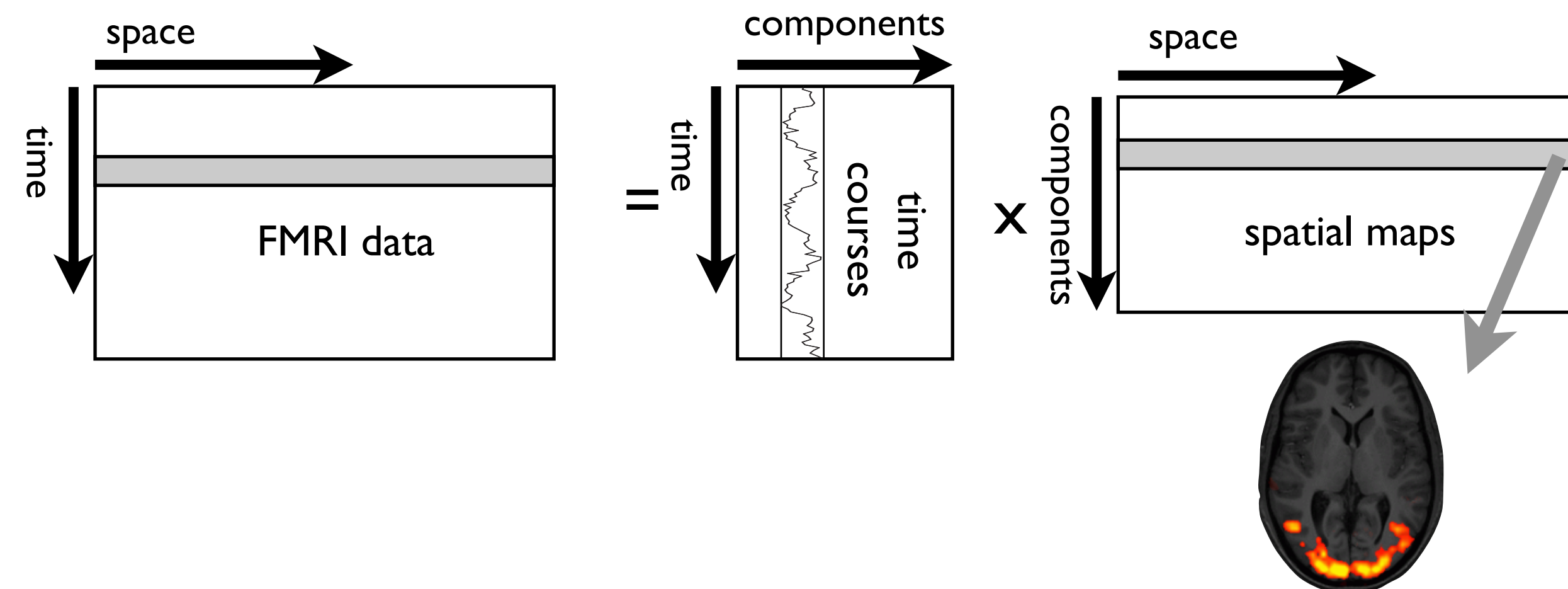
What are components?



- express observed data as linear combination of spatio-temporal processes
- techniques differ in the way data is represented by components



Spatial ICA for FMRI



- data is decomposed into a set of **spatially independent** maps and a set of time-courses





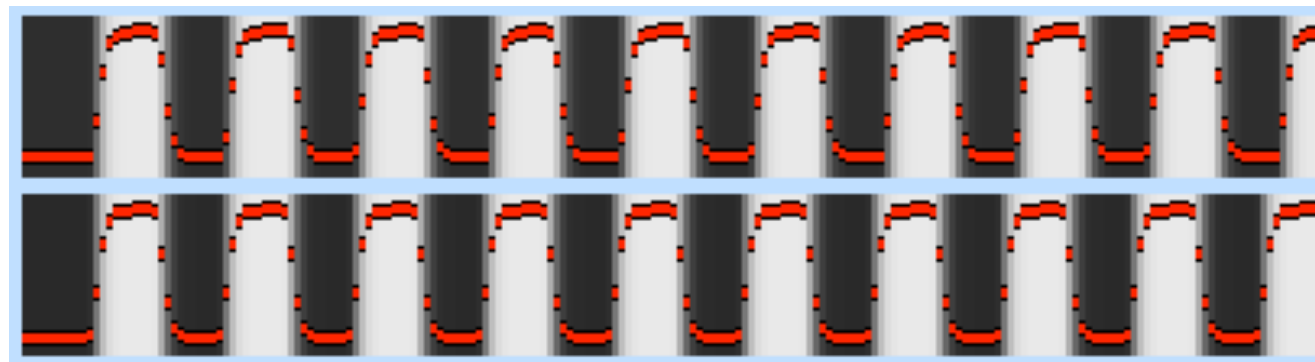
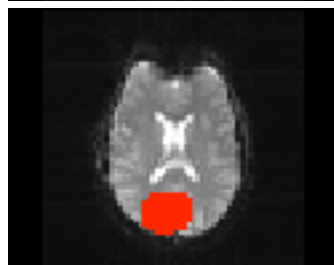
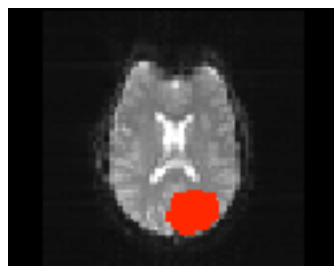
Independence



PCA vs. ICA ?

Simulated
Data

(2 components, slightly
different timecourses)

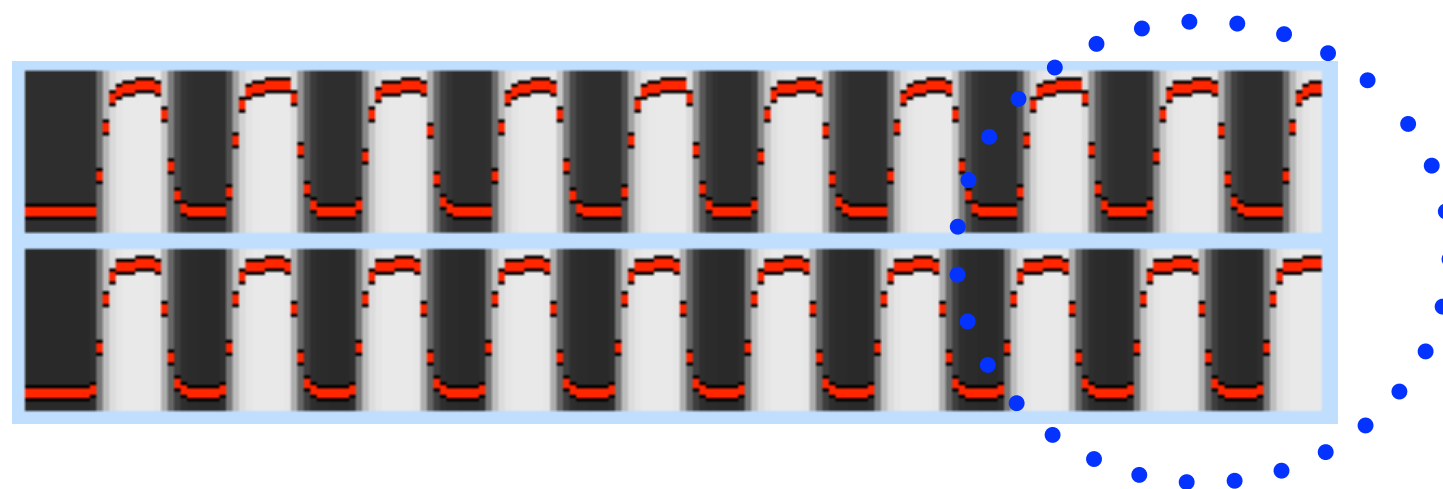
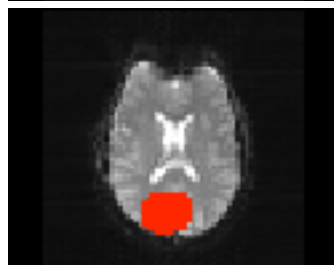
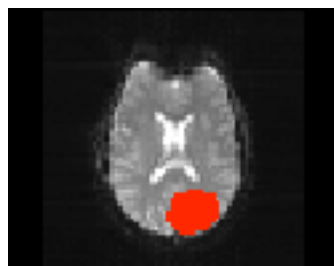




PCA vs. ICA ?

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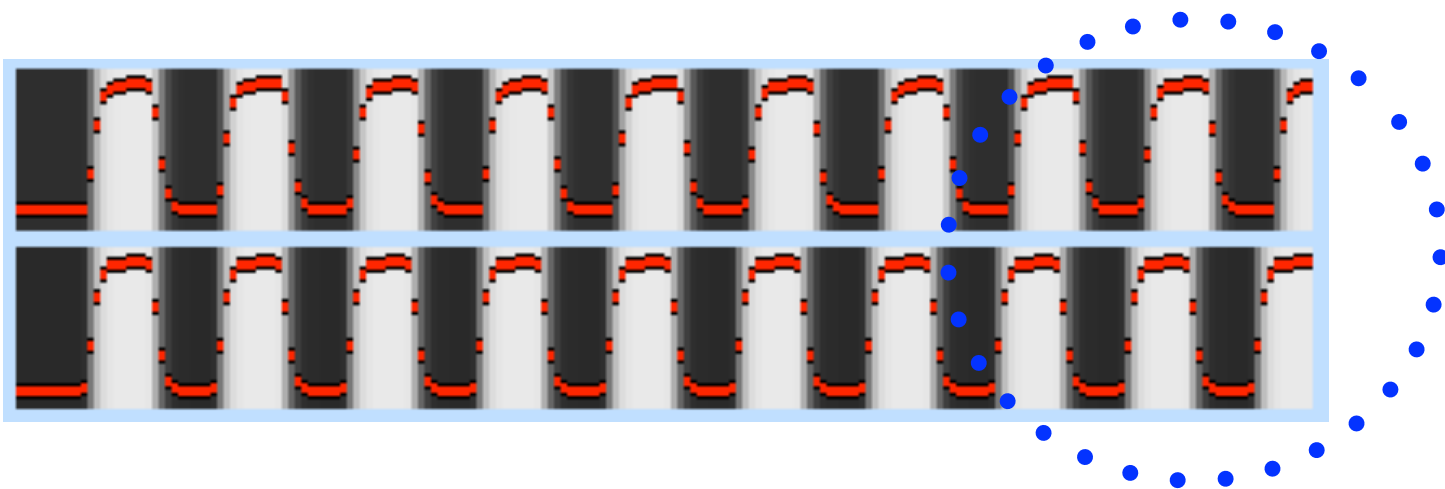
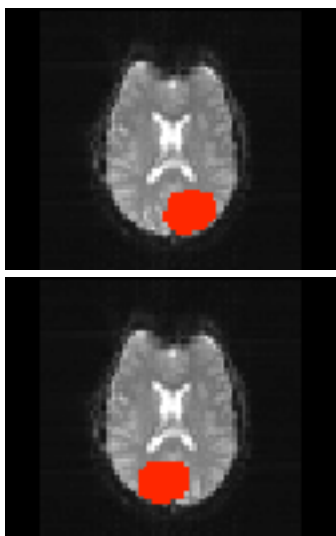




PCA vs. ICA ?

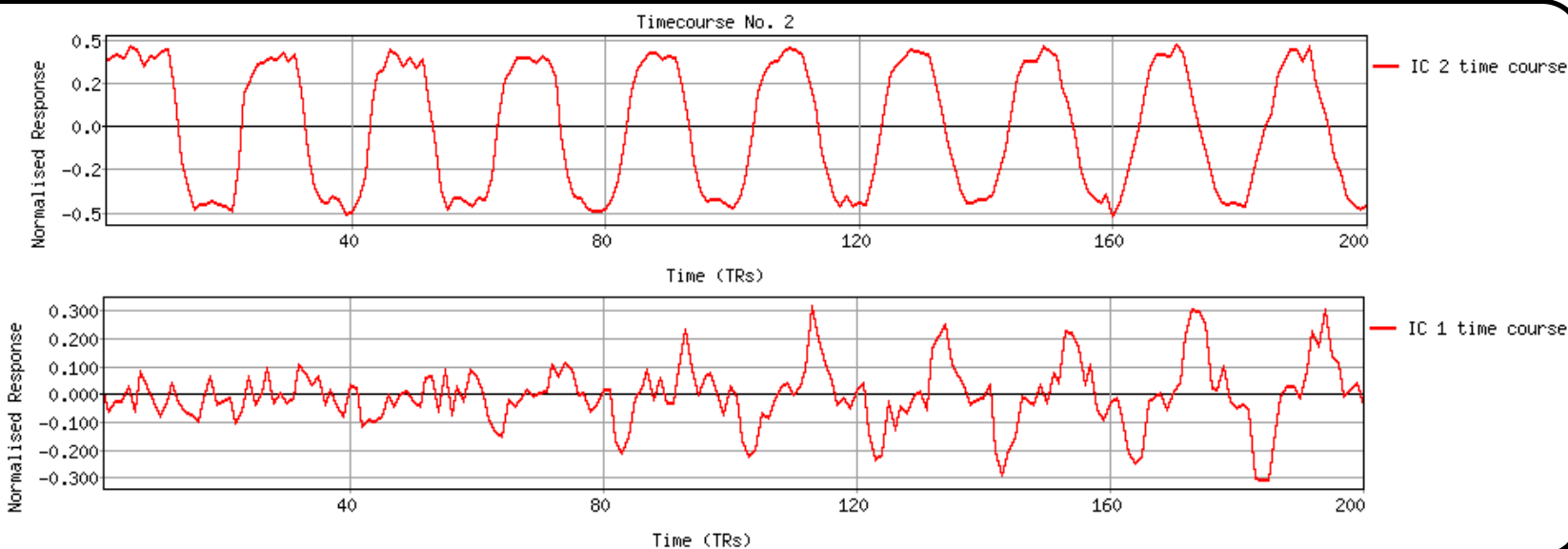
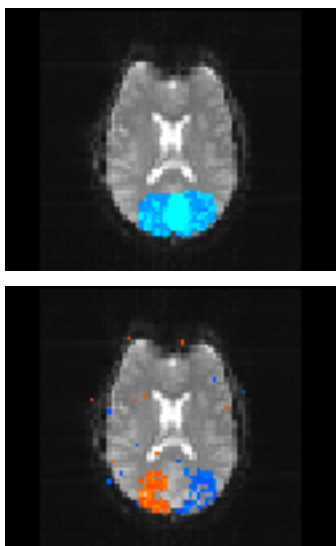
Simulated Data

(2 components, slightly different timecourses)



PCA

- Timecourses orthogonal
- Spatial maps and timecourses “wrong”

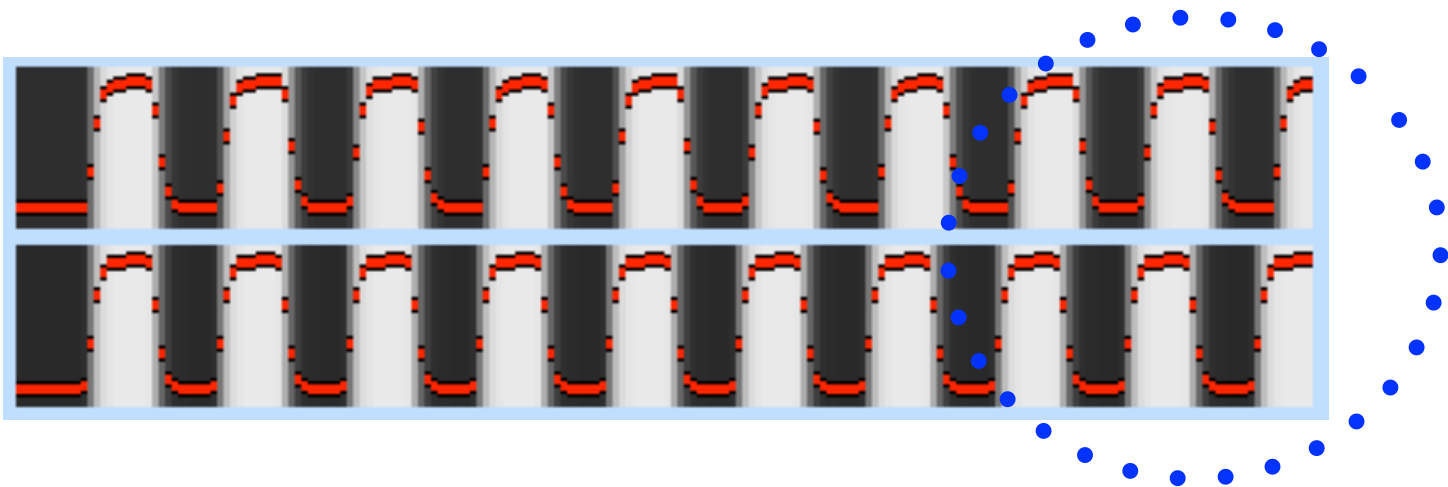
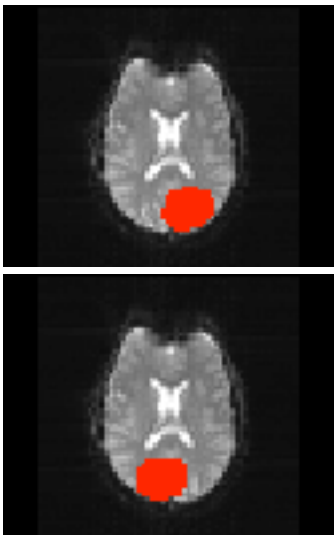




PCA vs. ICA ?

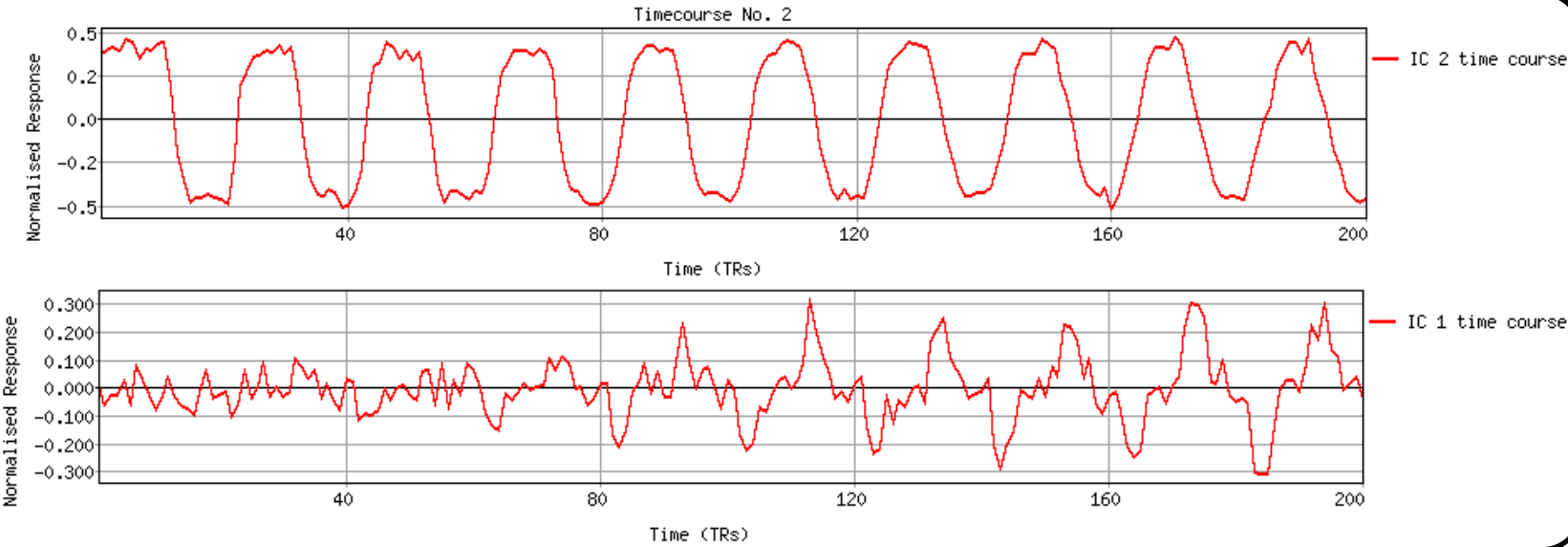
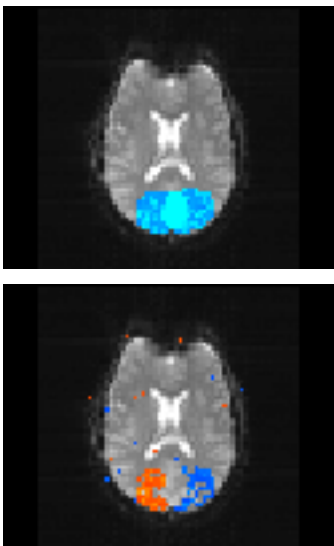
Simulated Data

(2 components, slightly different timecourses)



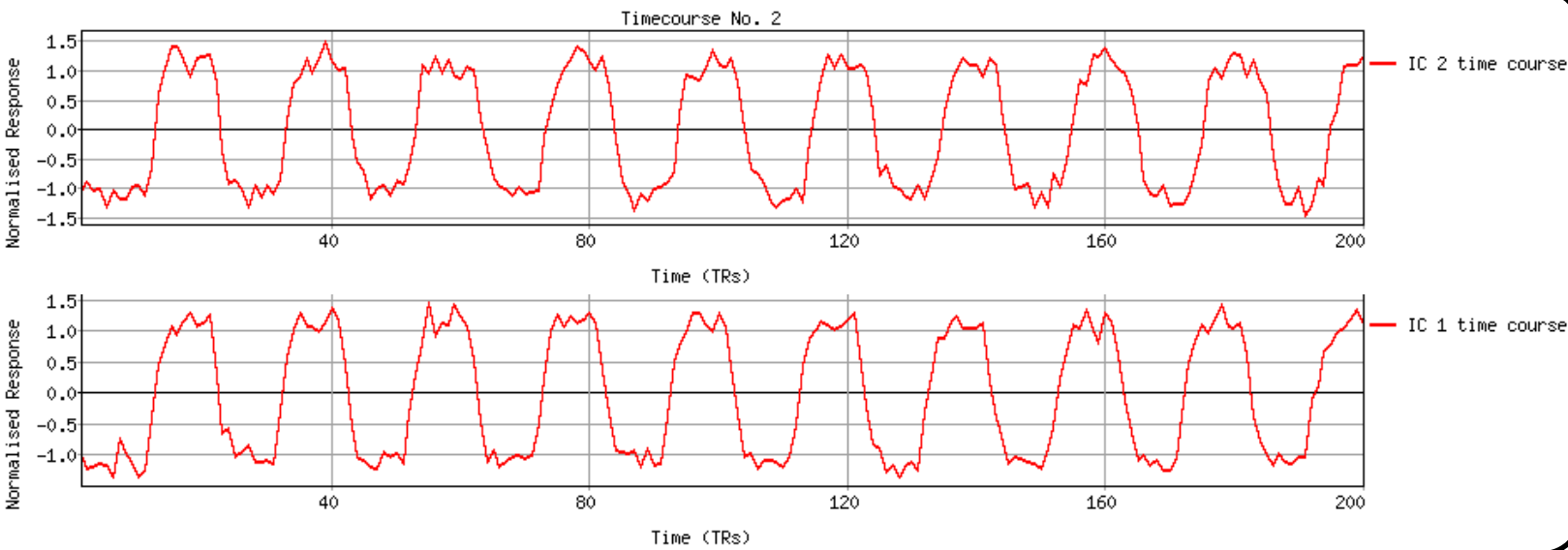
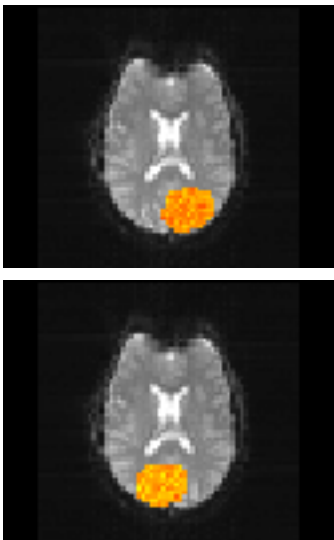
PCA

- Timecourses orthogonal
- Spatial maps and timecourses “wrong”



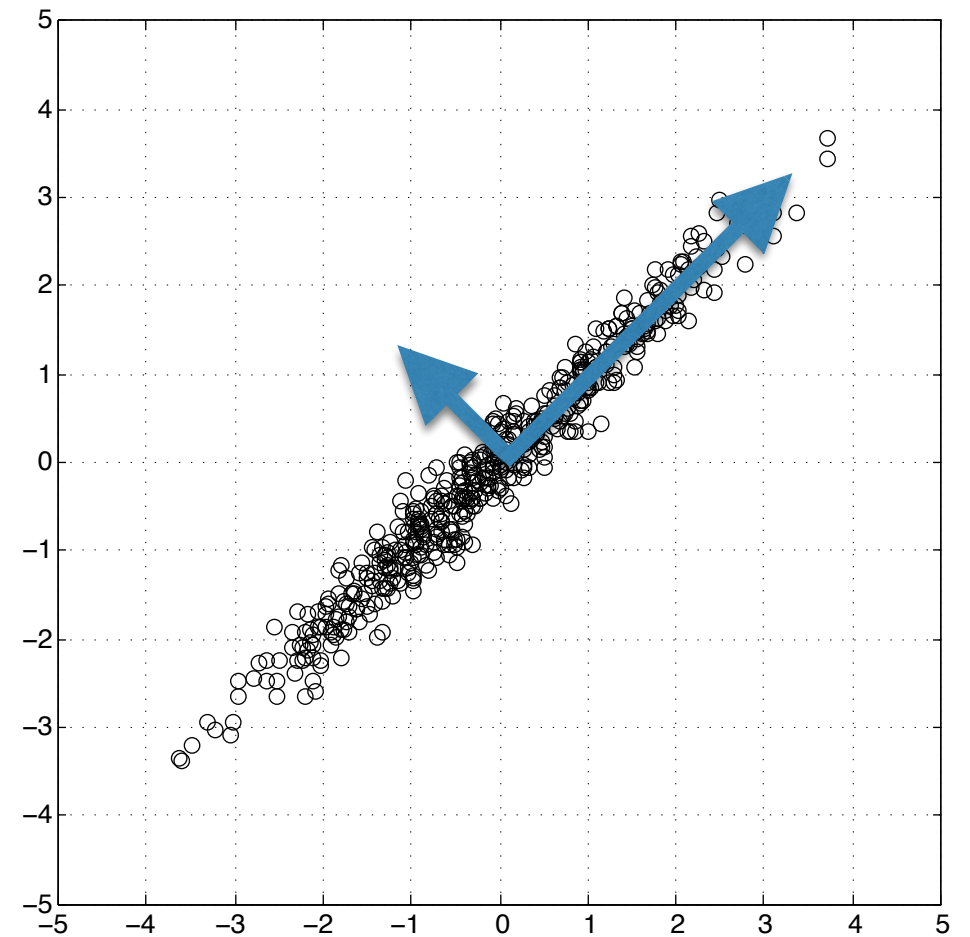
ICA

- Timecourses non-co-linear
- Spatial maps and timecourses “right”



PCA vs. ICA

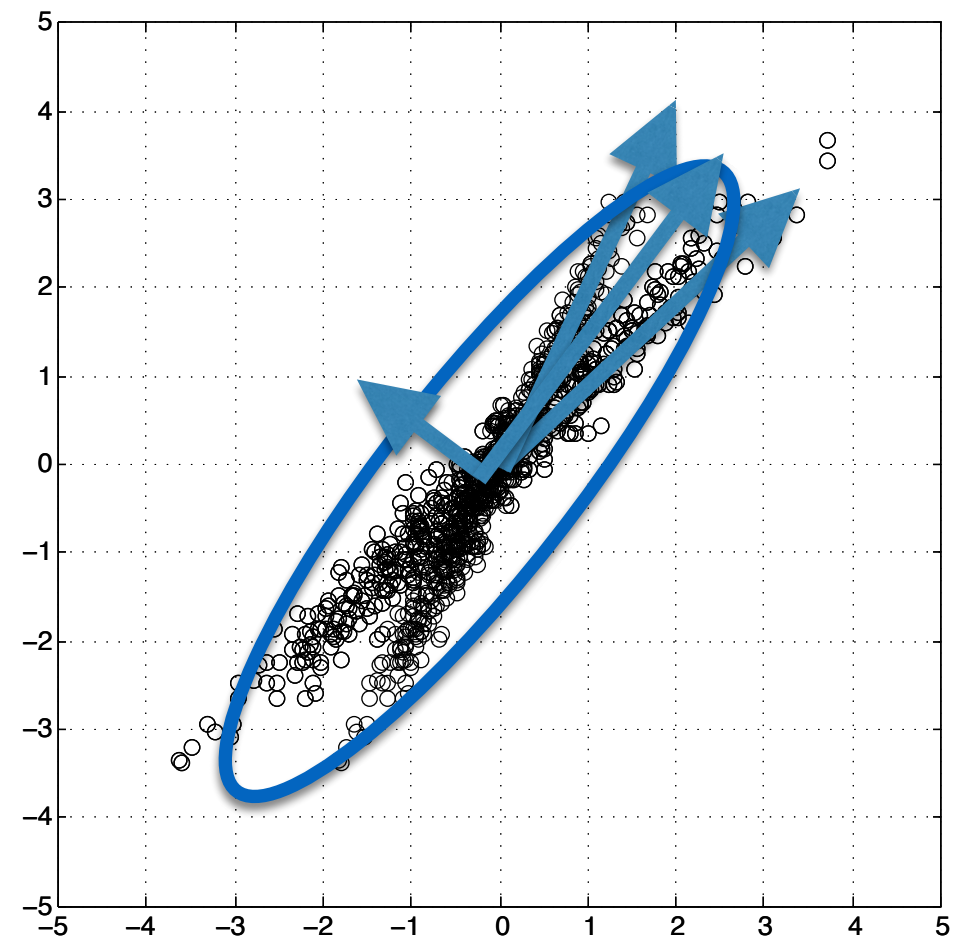
- PCA finds projections of maximum amount of variance in Gaussian data (uses 2nd order statistics only)



Gaussian data

PCA vs. ICA

- PCA finds projections of maximum amount of variance in Gaussian data (uses 2nd order statistics only)
- Independent Component Analysis (ICA) finds projections of maximal independence in non-Gaussian data (using higher-order statistics)

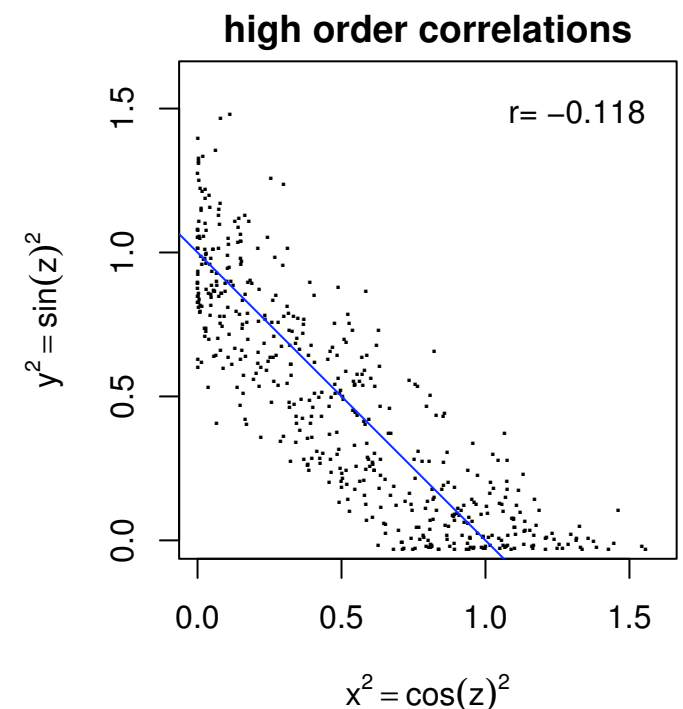
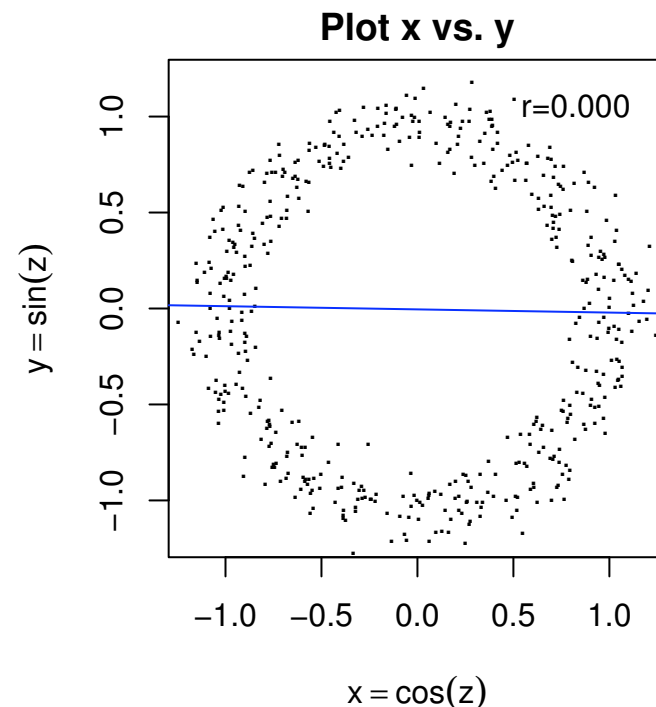


non-Gaussian
data

Correlation vs. independence

- de-correlated signals can still be dependent
- higher-order statistics (beyond mean and variance) can reveal these dependencies

 Stone et al. 2002





Non-Gaussianity



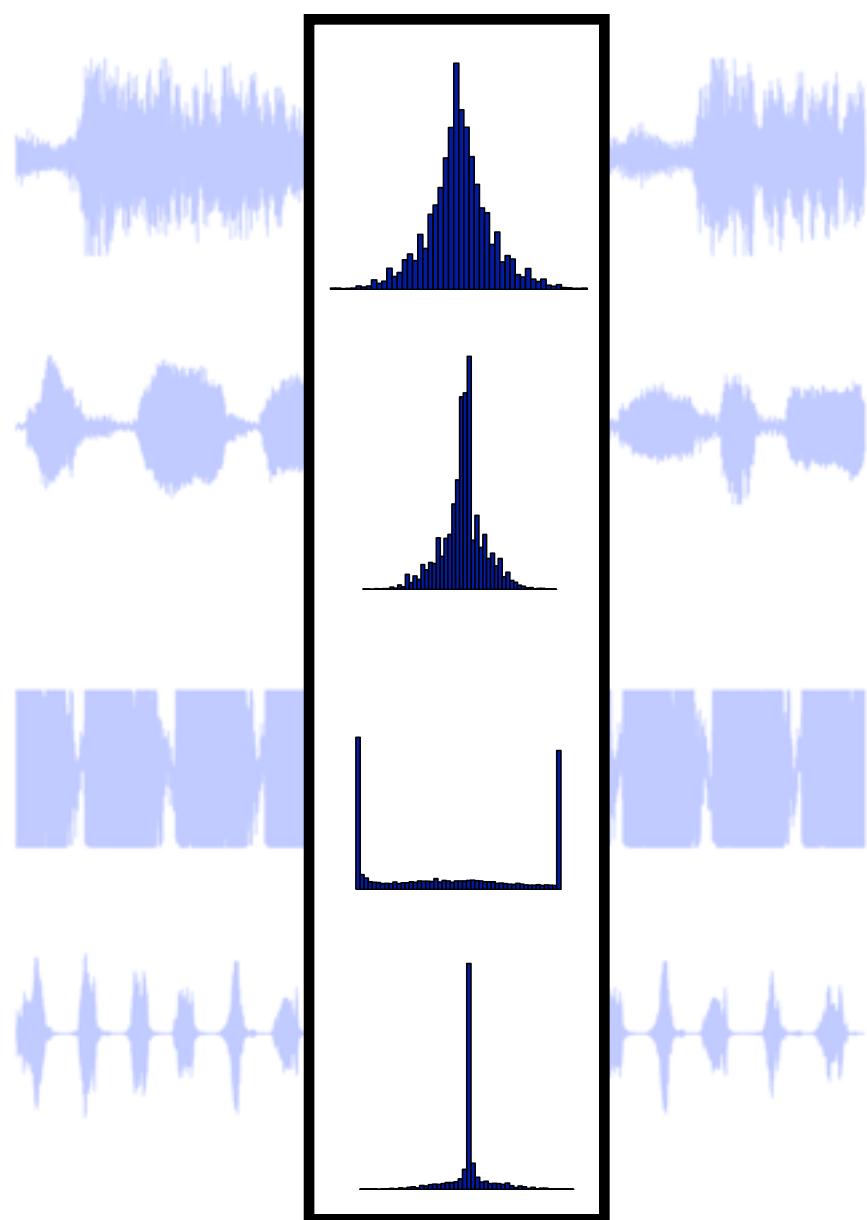
sources



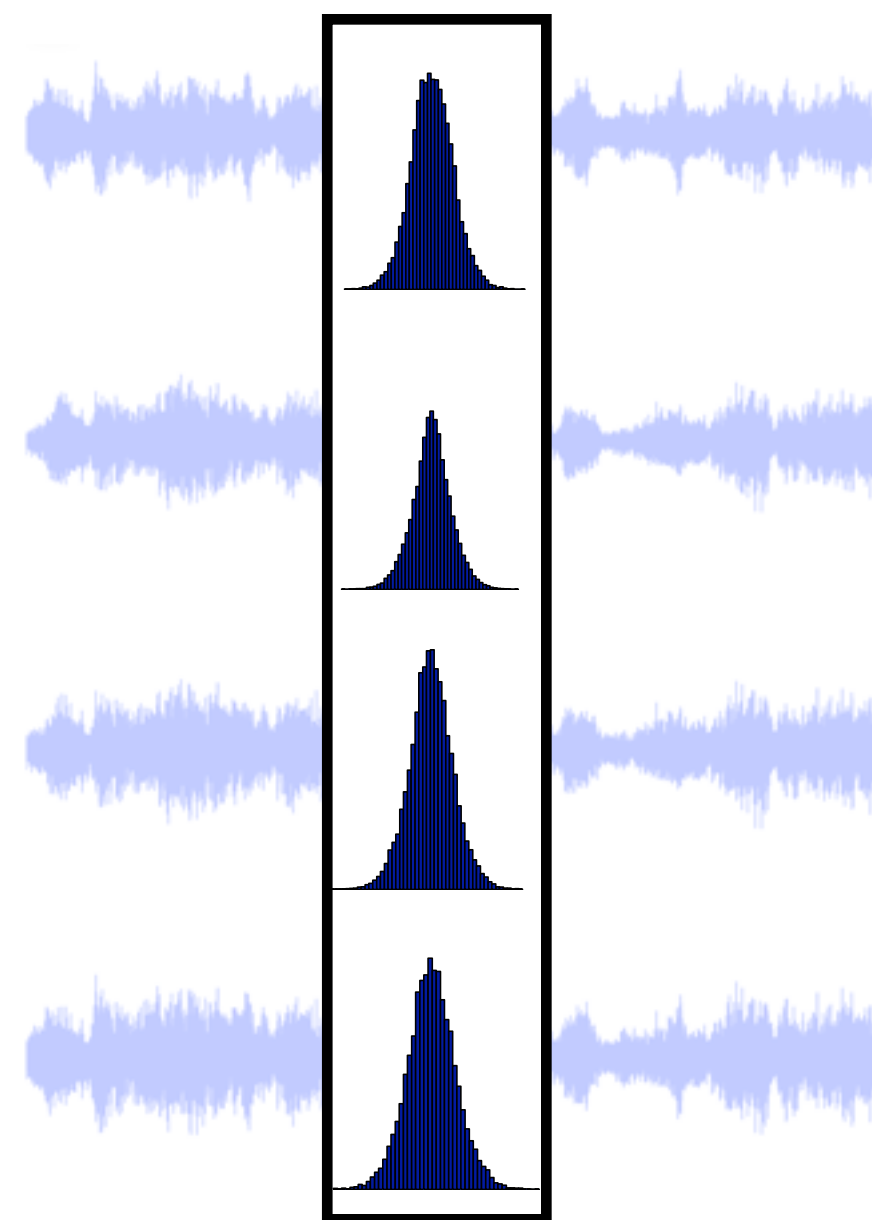
mixtures



Non-Gaussianity



non-Gaussian



Gaussian



ICA estimation

- **Random** mixing results in **more** Gaussian-shaped PDFs (Central Limit Theorem)
- conversely:

if mixing matrix produces **less** Gaussian-shaped PDFs this is unlikely to be a random result

➡ measure non-Gaussianity
- can use **neg-entropy** as a measure of non-Gaussianity





ICA estimation

- need to find an **unmixing matrix** such that the dependency between estimated sources is minimised
- need (i) a **contrast (objective/cost) function** to drive the unmixing which measures statistical independence and (ii) an **optimisation technique**:
- kurtosis or cumulants & gradient descent (**Jade**)
- maximum entropy & gradient descent (**Infomax**)
- neg-entropy & fixed point iteration (**FastICA**)



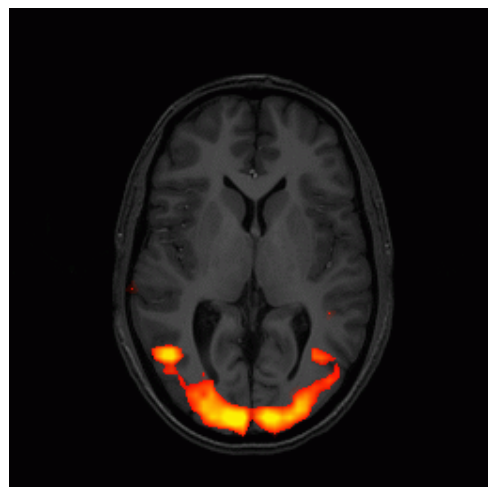
Overfitting & thresholding



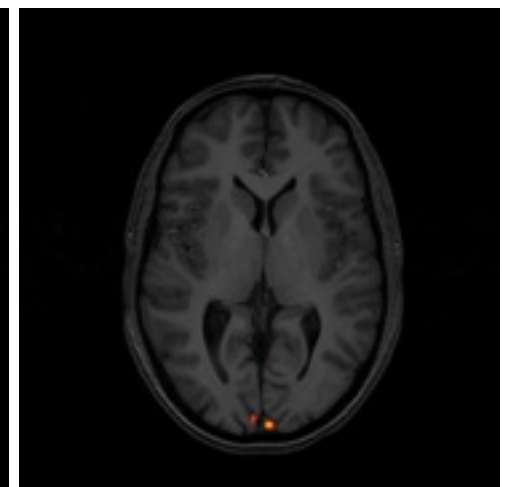
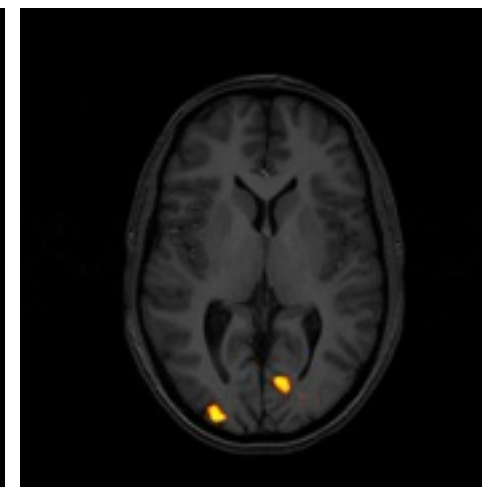
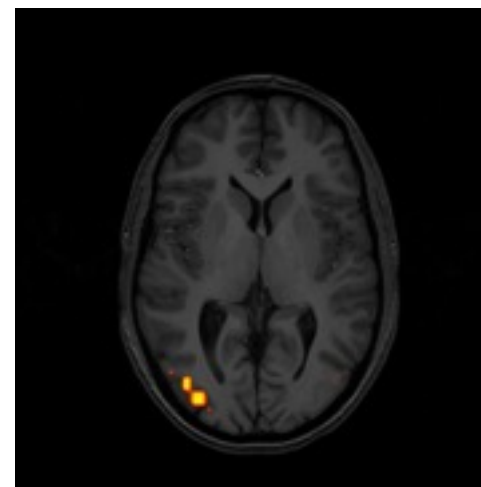
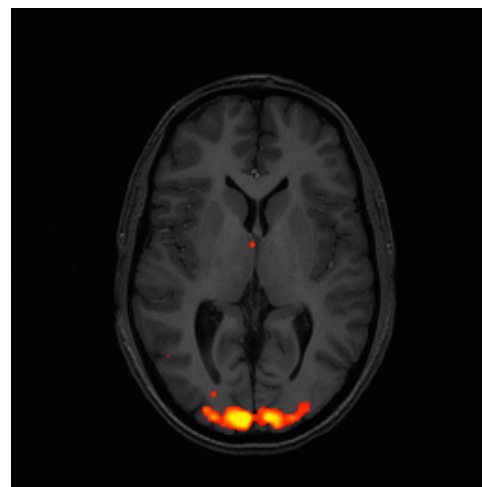
The 'overfitting' problem

fitting a noise-free model to noisy observations:

- no control over signal vs. noise (non-interpretable results)
- statistical significance testing not possible



GLM analysis

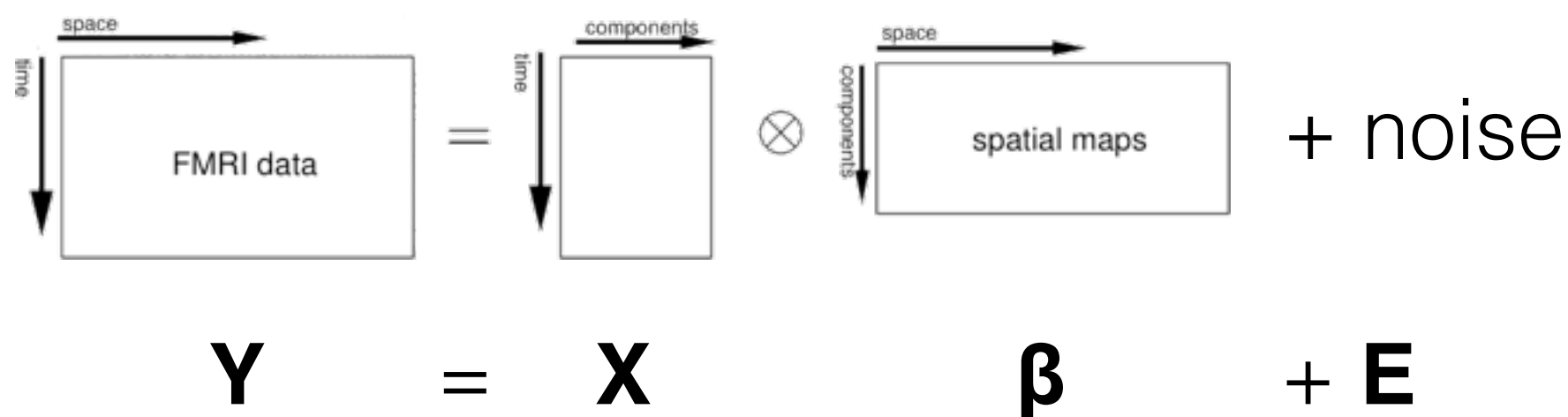


standard ICA (unconstrained)



Probabilistic ICA model

statistical “latent variables” model: we observe linear mixtures of hidden sources in the presence of Gaussian noise



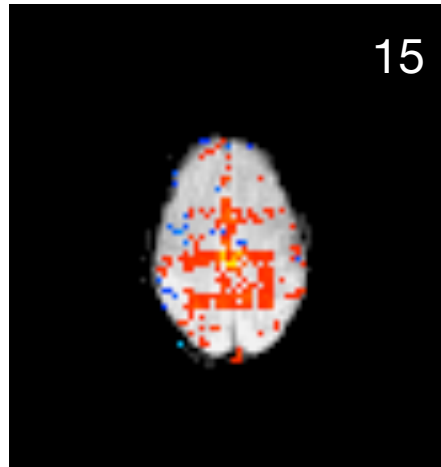
Issues:

- Model Order Selection: how many components?
- Inference: how to threshold ICs?

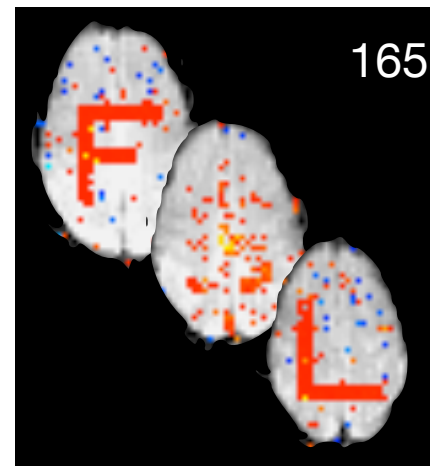


Model Order Selection

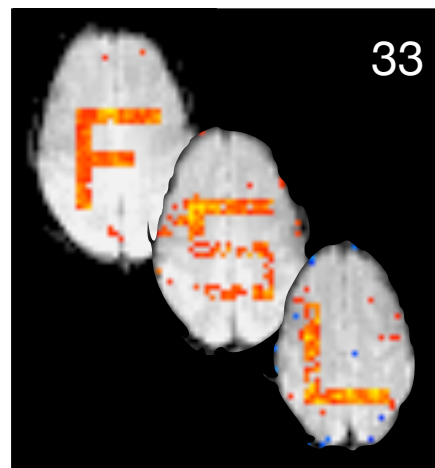
‘How many components’?



under-fitting: the amount of explained data variance is insufficient to obtain good estimates of the signals



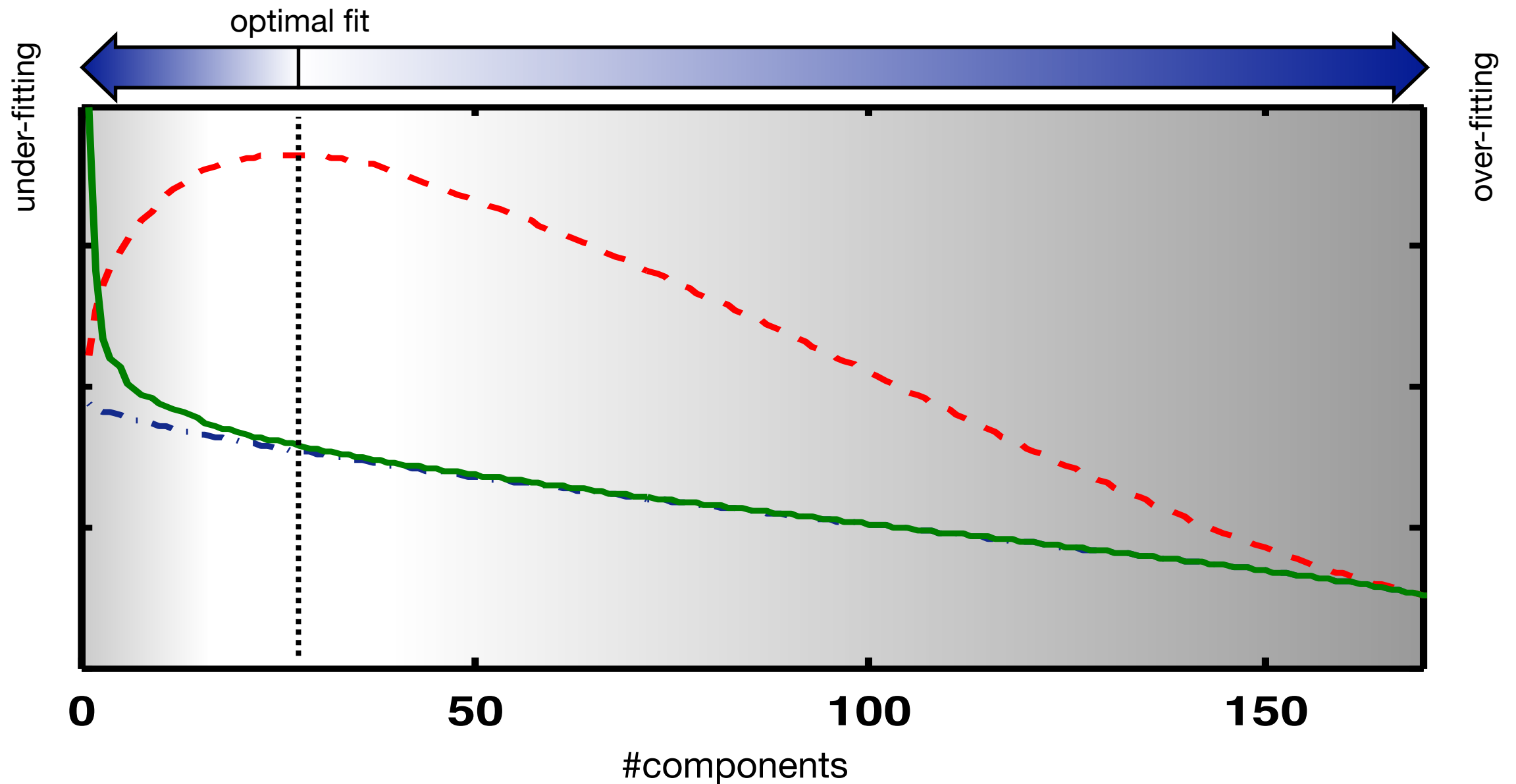
over-fitting: the inclusion of too many components leads to fragmentation of signal across multiple component maps, reducing the ability to identify the signals of interest



optimal fitting: the amount of explained data variance is sufficient to obtain good estimates of the signals while preventing further splits into spurious components



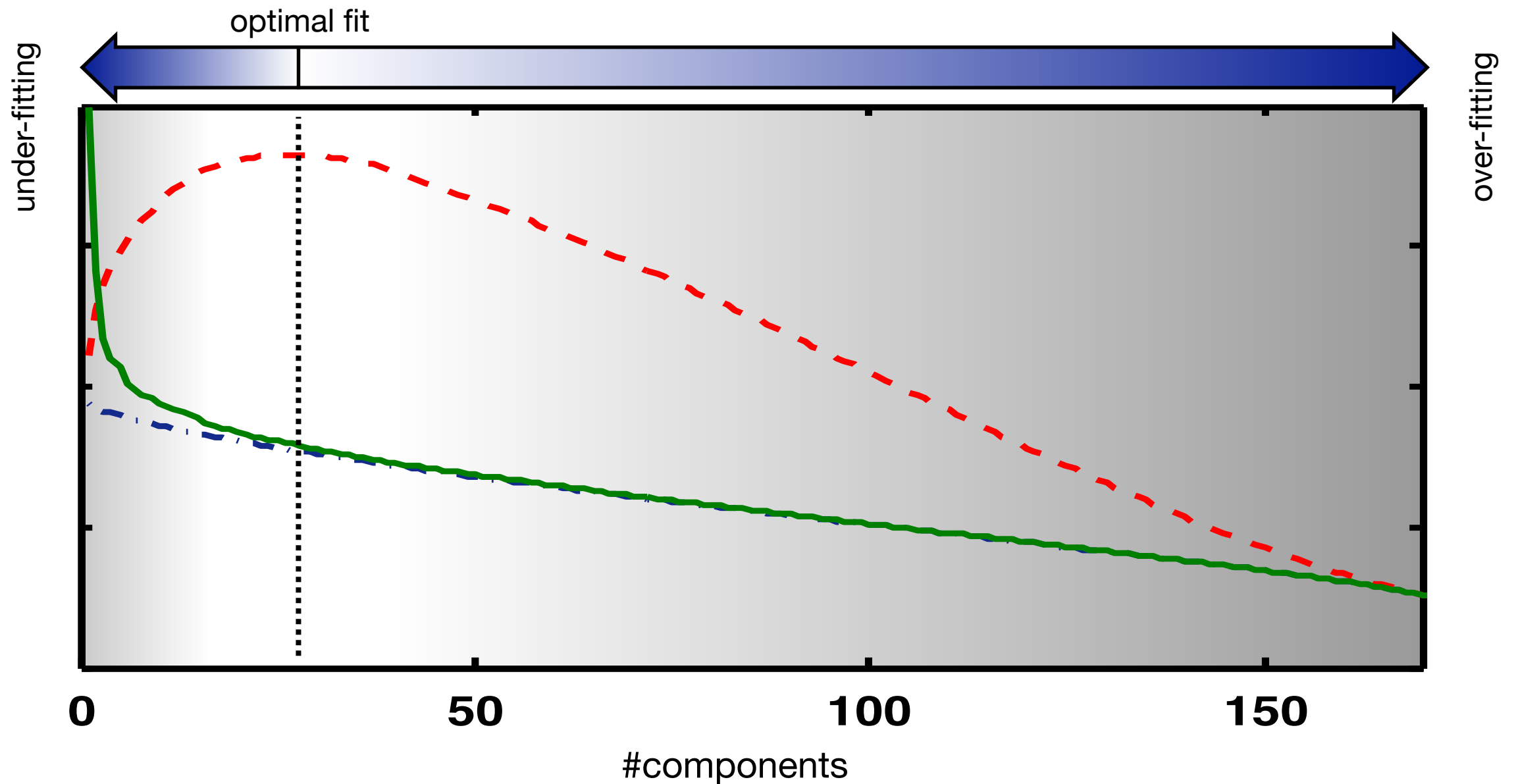
Model Order Selection



- observed Eigenspectrum of the data covariance matrix
- - - Laplace approximation of the posterior probability of the model order
- . - theoretical Eigenspectrum from Gaussian noise



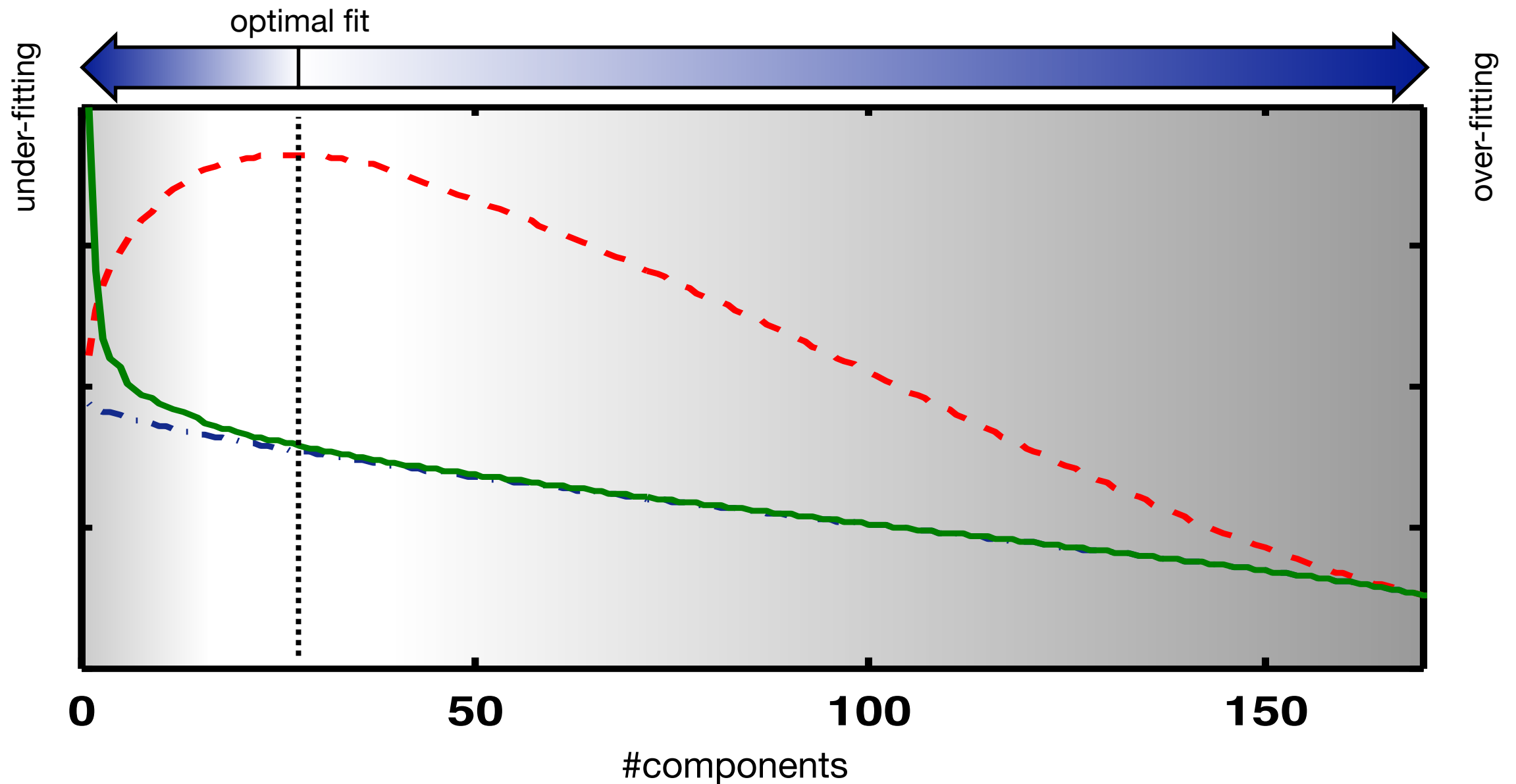
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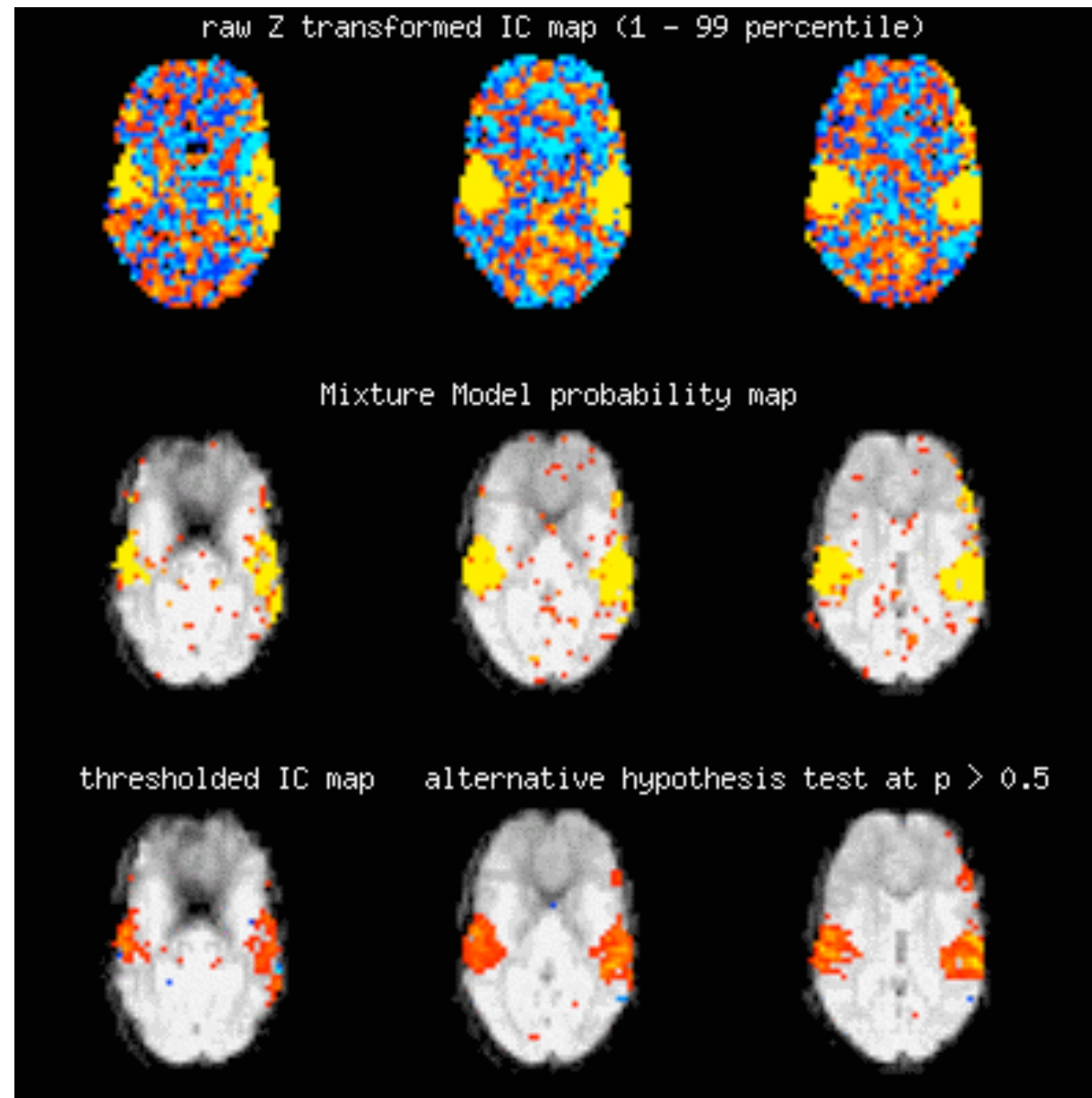


Model Order Selection



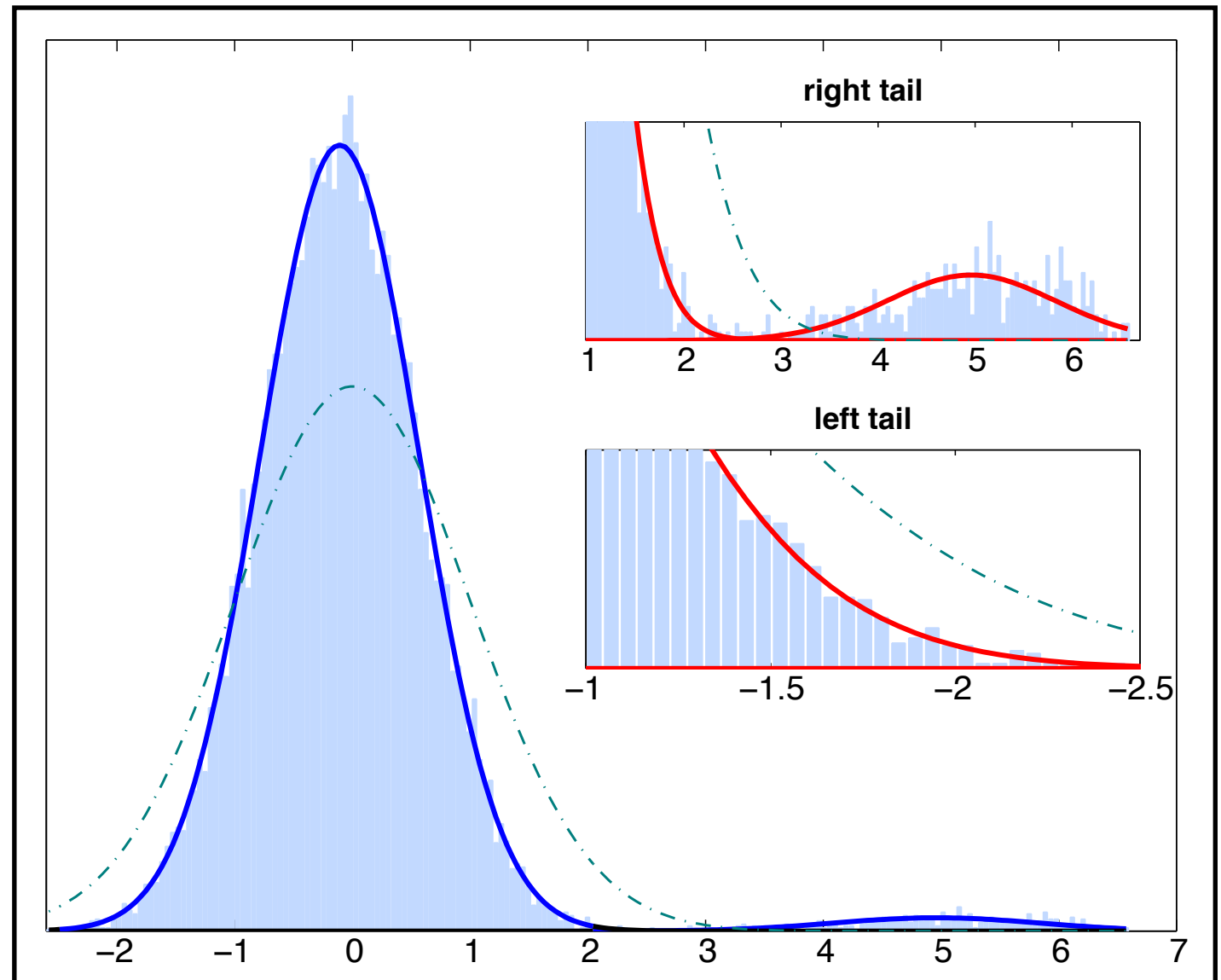
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Thresholding

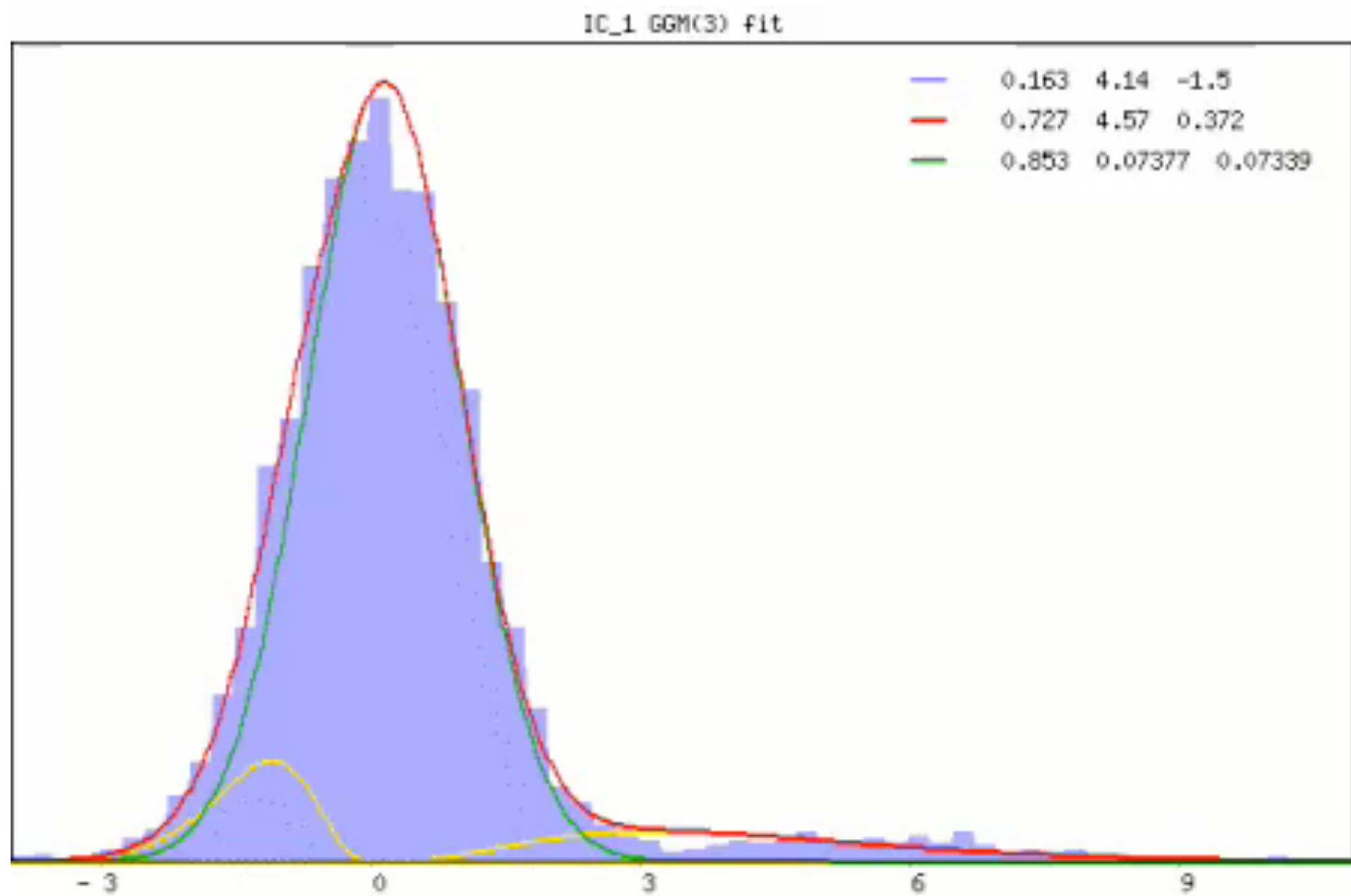


Thresholding

- classical null-hypothesis testing is invalid
- data is assumed to be a linear combination of signals and noise
- the distribution of the estimated spatial maps is a mixture distribution!



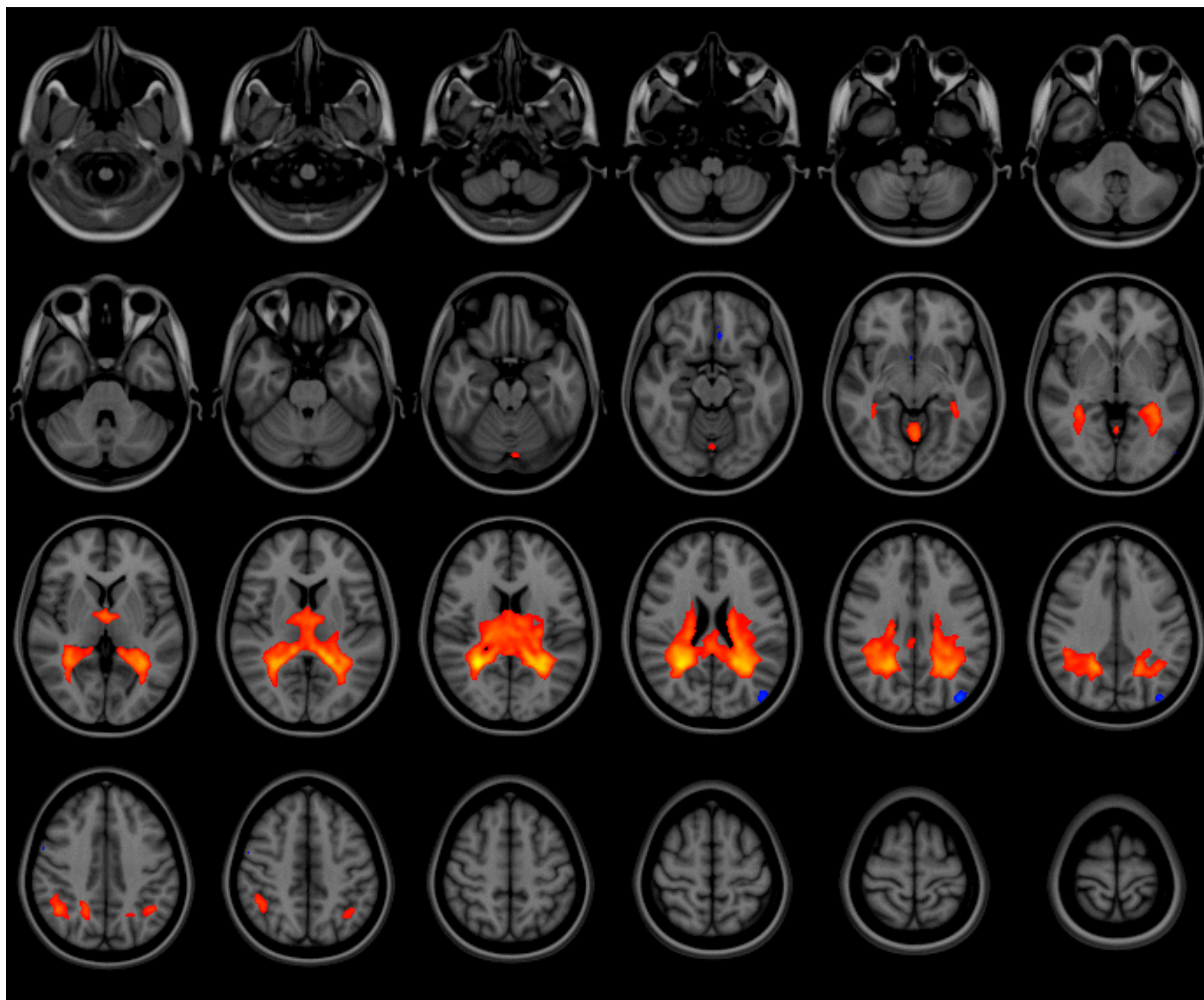
Alternative Hypothesis Test



- use Gaussian/Gamma mixture model fitted to the histogram of intensity values (using EM)



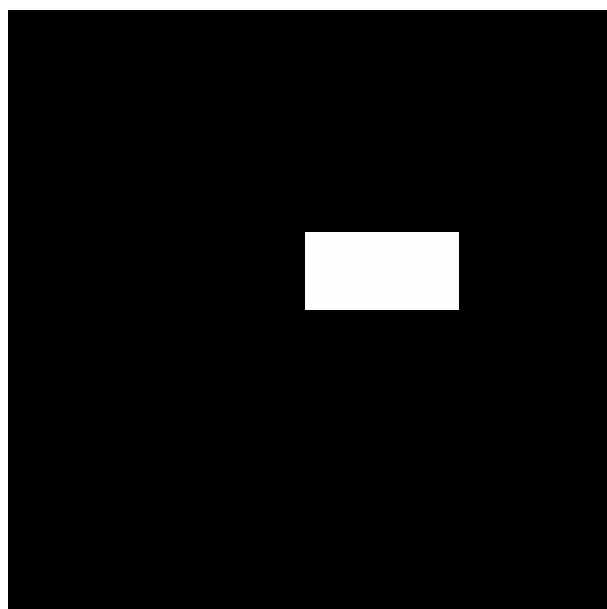
What about overlap?





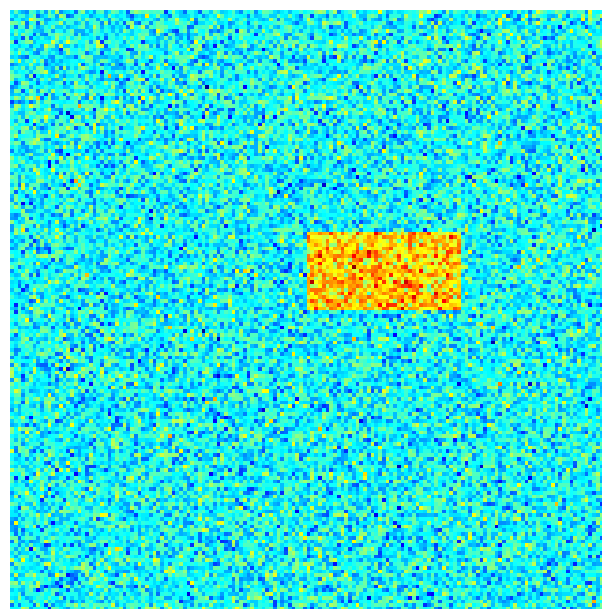
What about overlap?

Sources



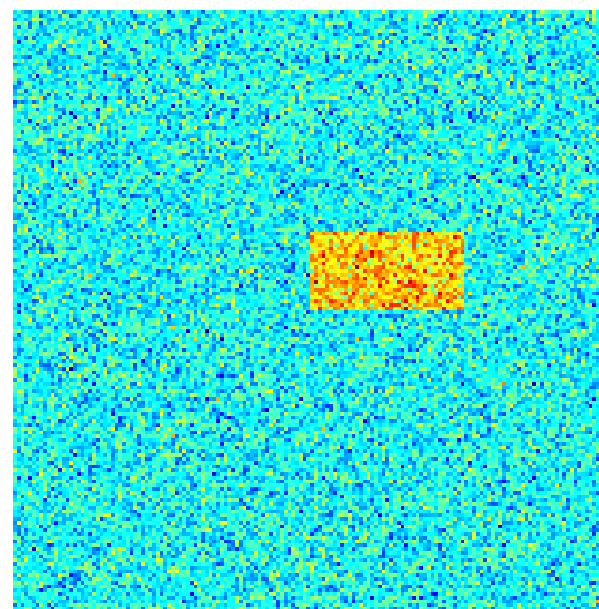
$\rho = 0.5$

Sources +
noise



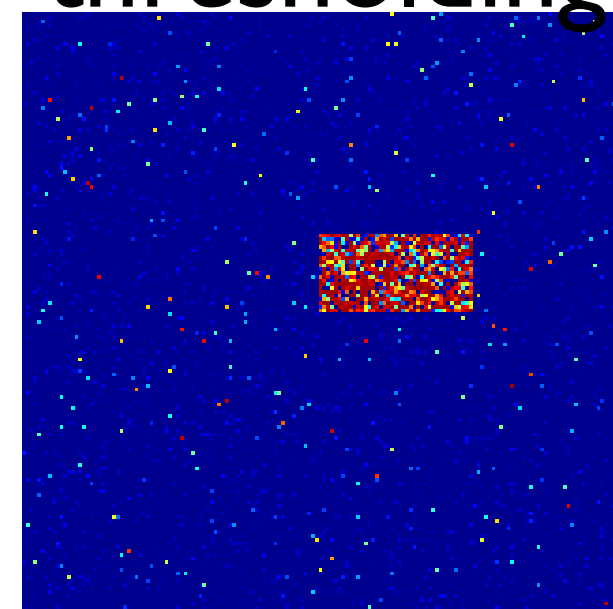
$\rho < 0.1$

ICA
solution

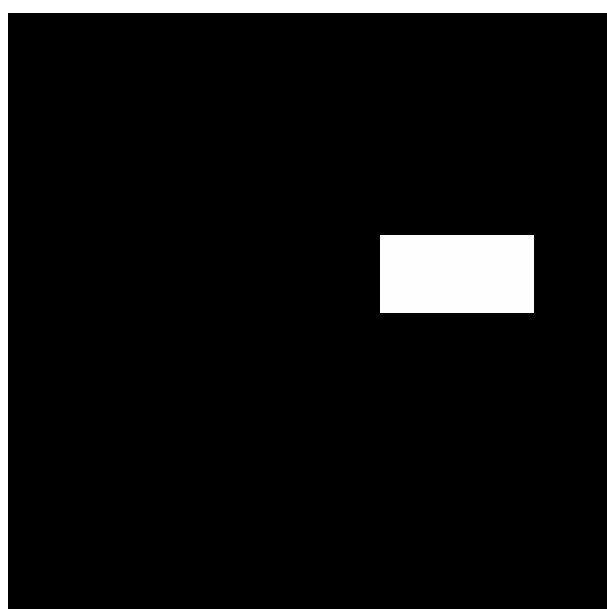


$\rho = 0$

after
thresholding



$\rho \approx 0.5$





Resting state fMRI and ICA

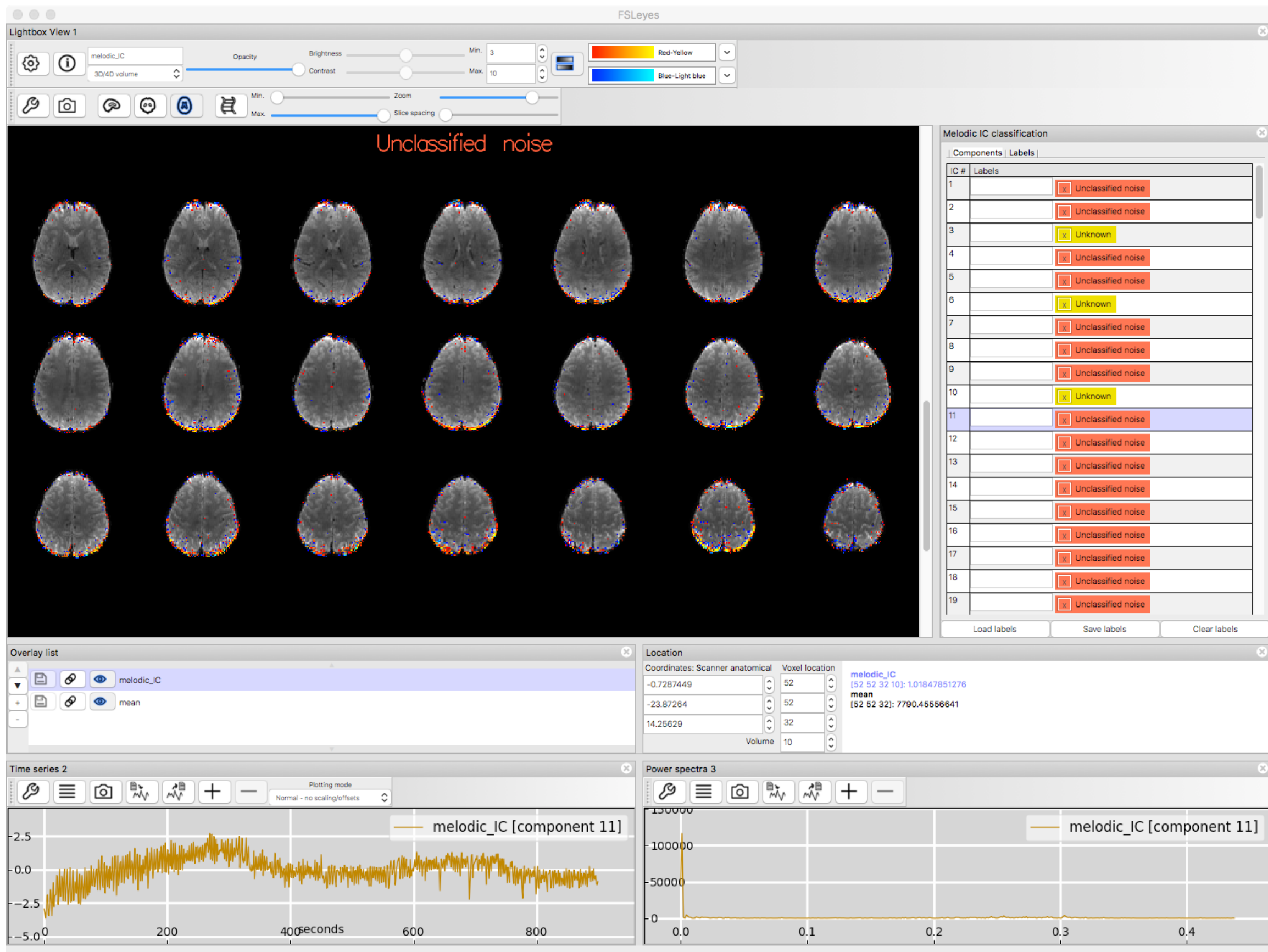
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Artefact detection

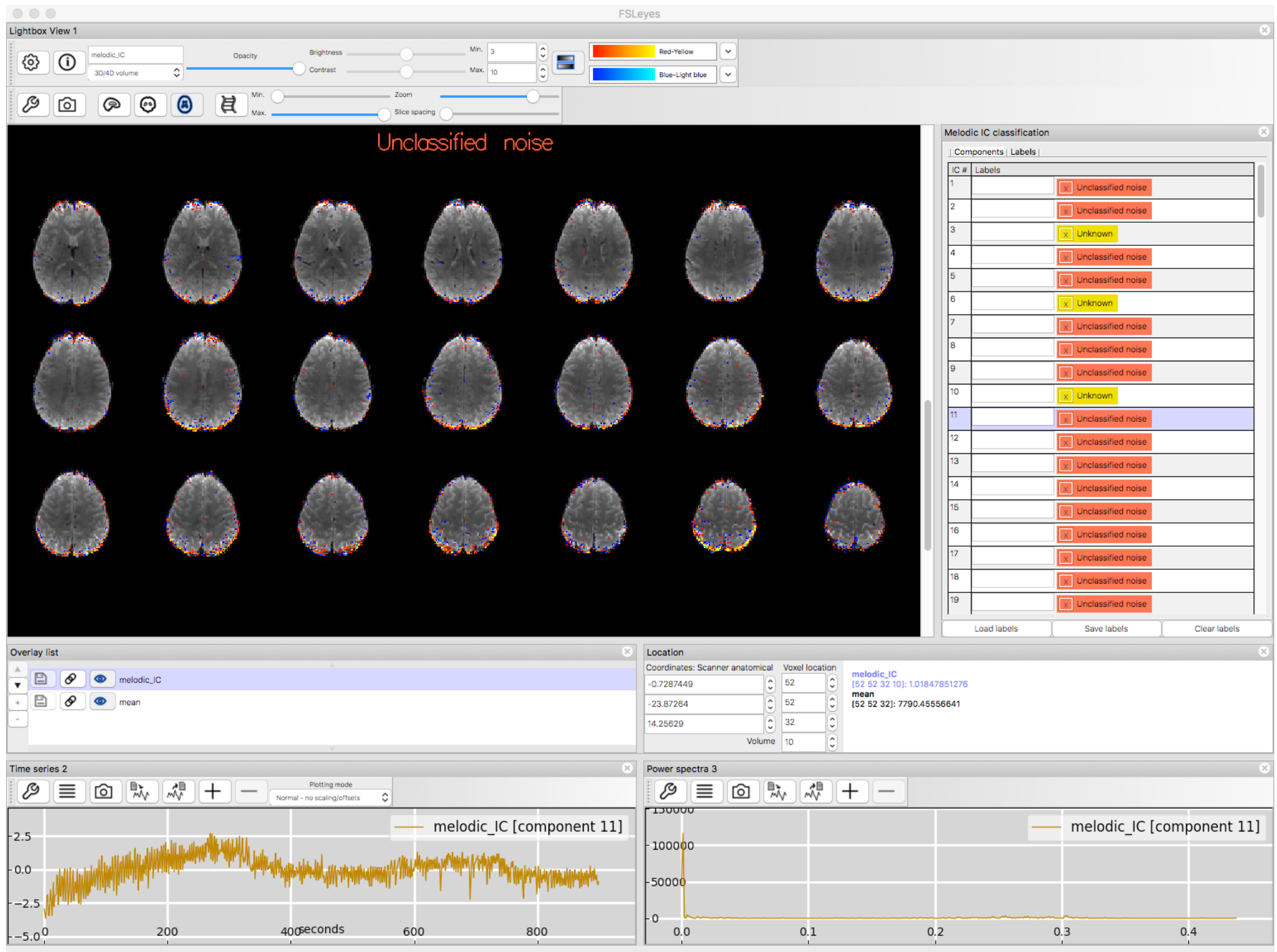
- FMRI data contain a variety of source processes
- Artifactual sources typically have unknown spatial and temporal extent and cannot easily be modelled accurately
- Exploratory techniques do not require a priori knowledge of time-courses and spatial maps

FSLeyes Melodic Mode



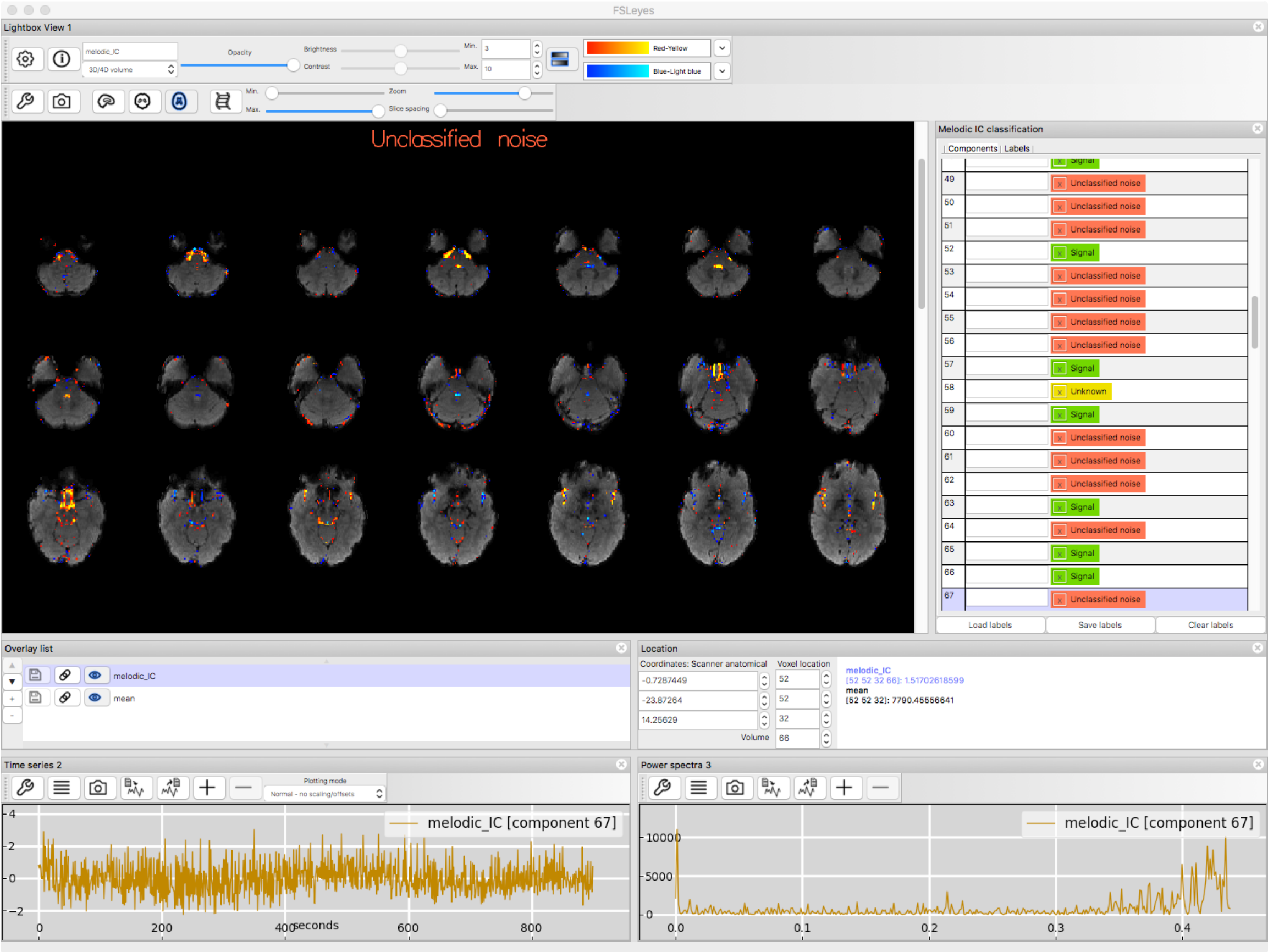


motion



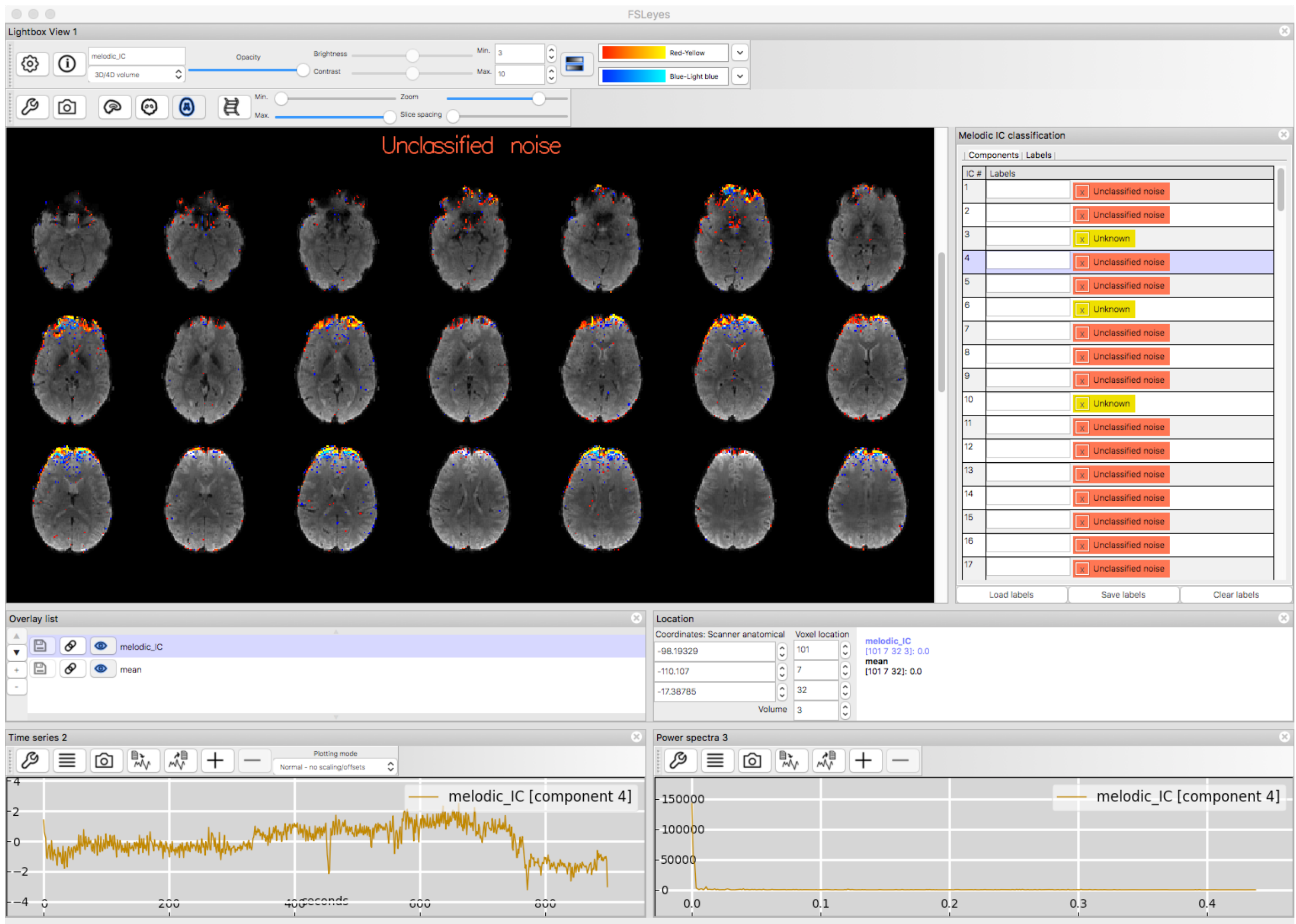


cardiac



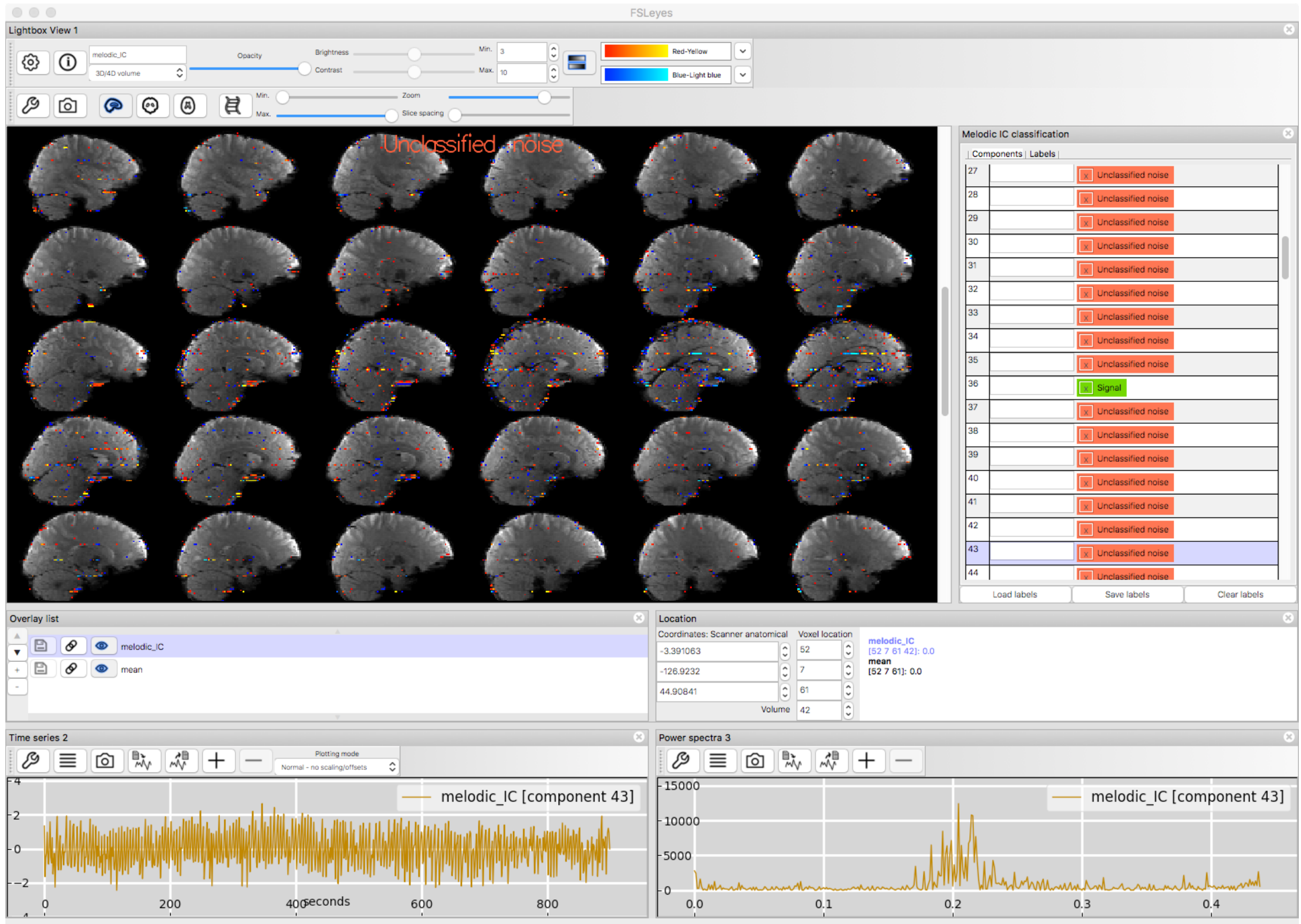


susceptibility motion



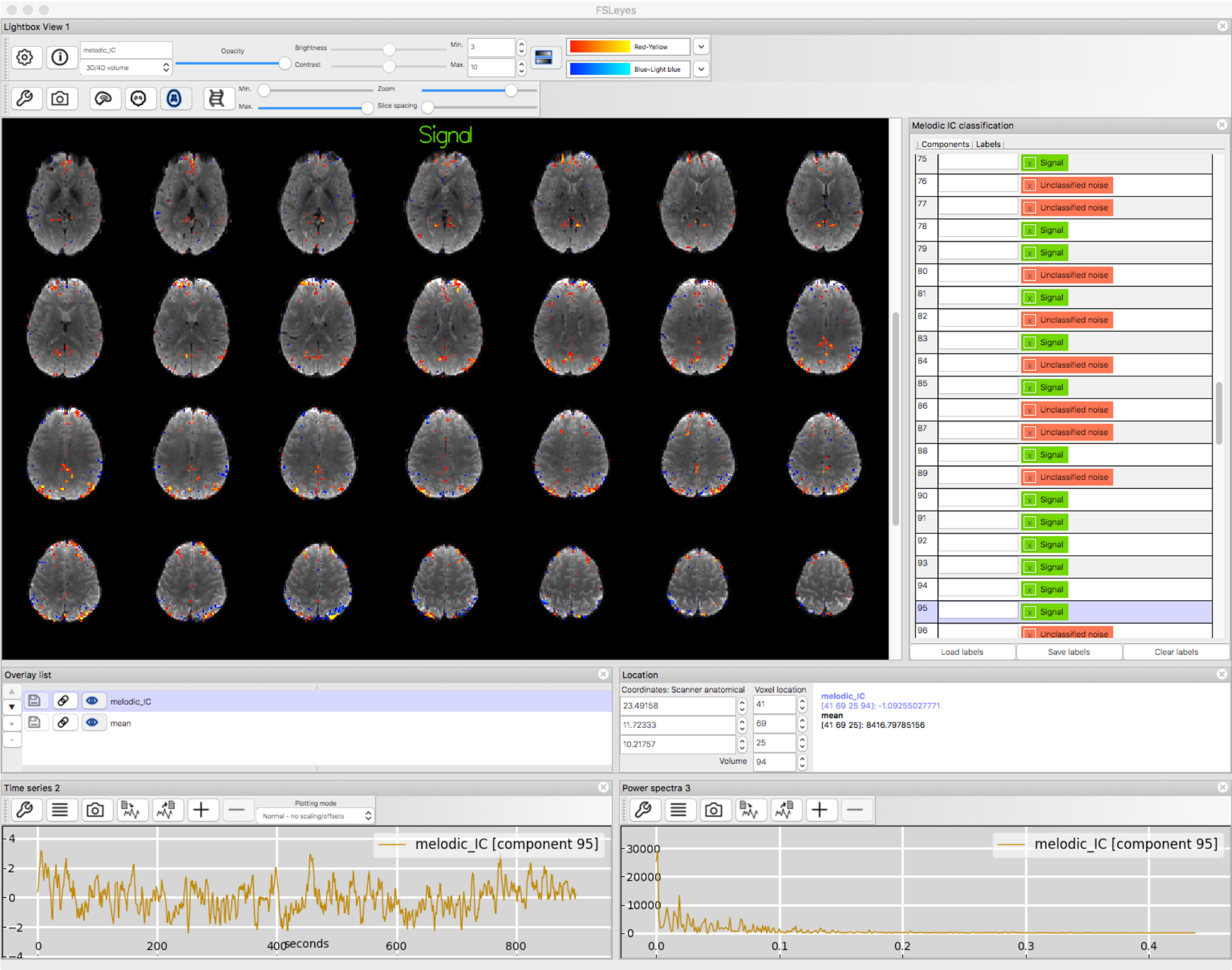


multiband

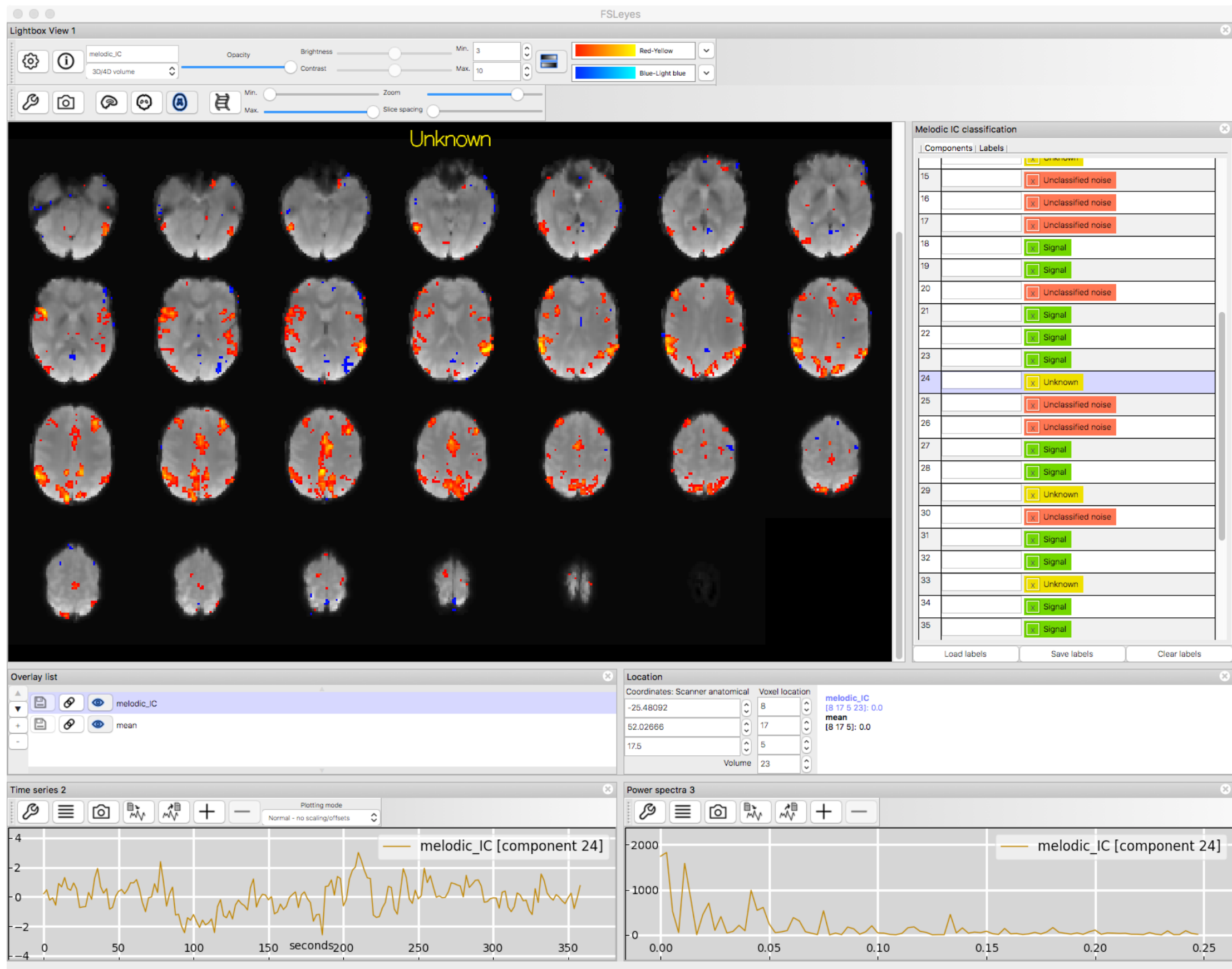




signal

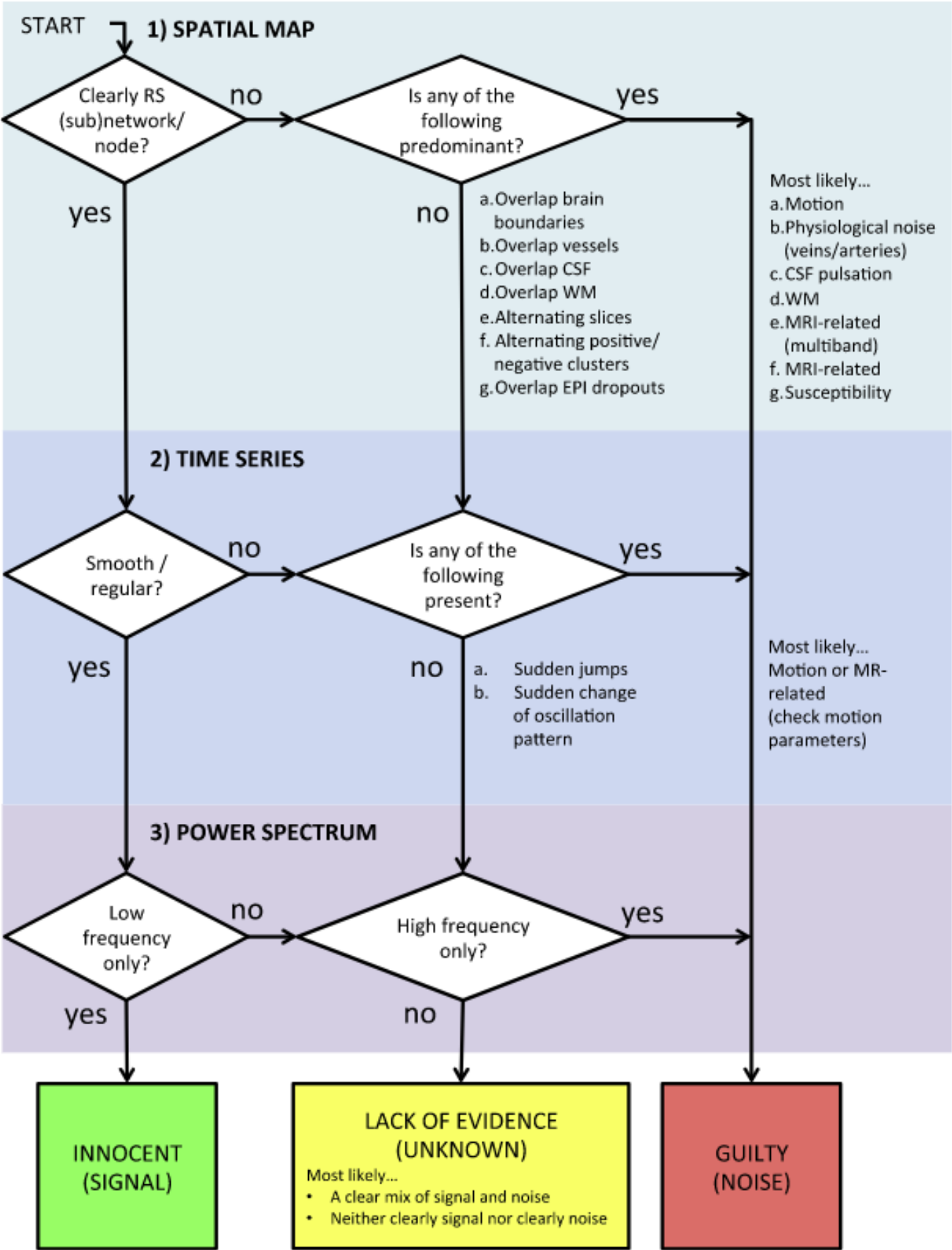


effects of scan parameters





manual classification

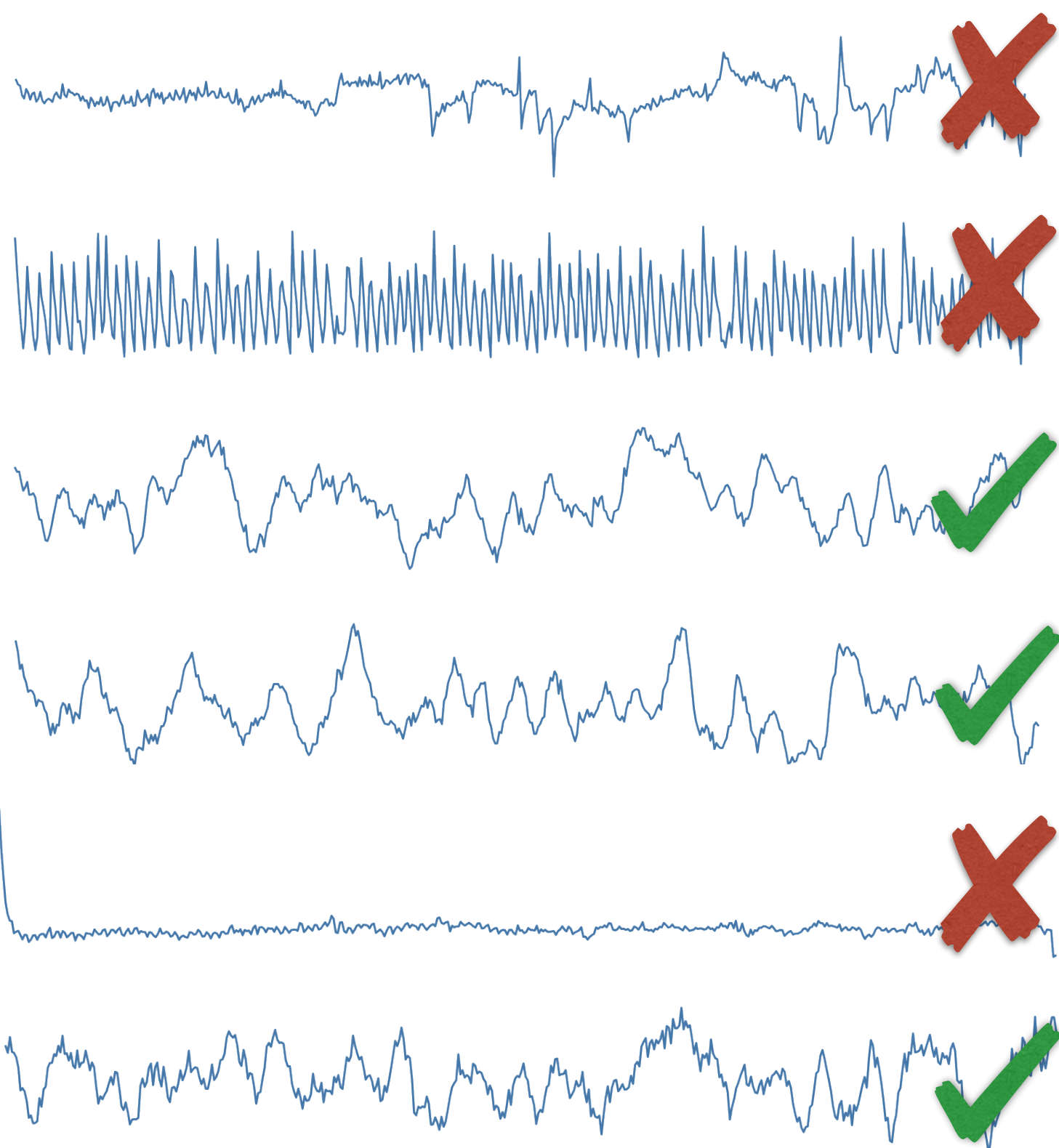
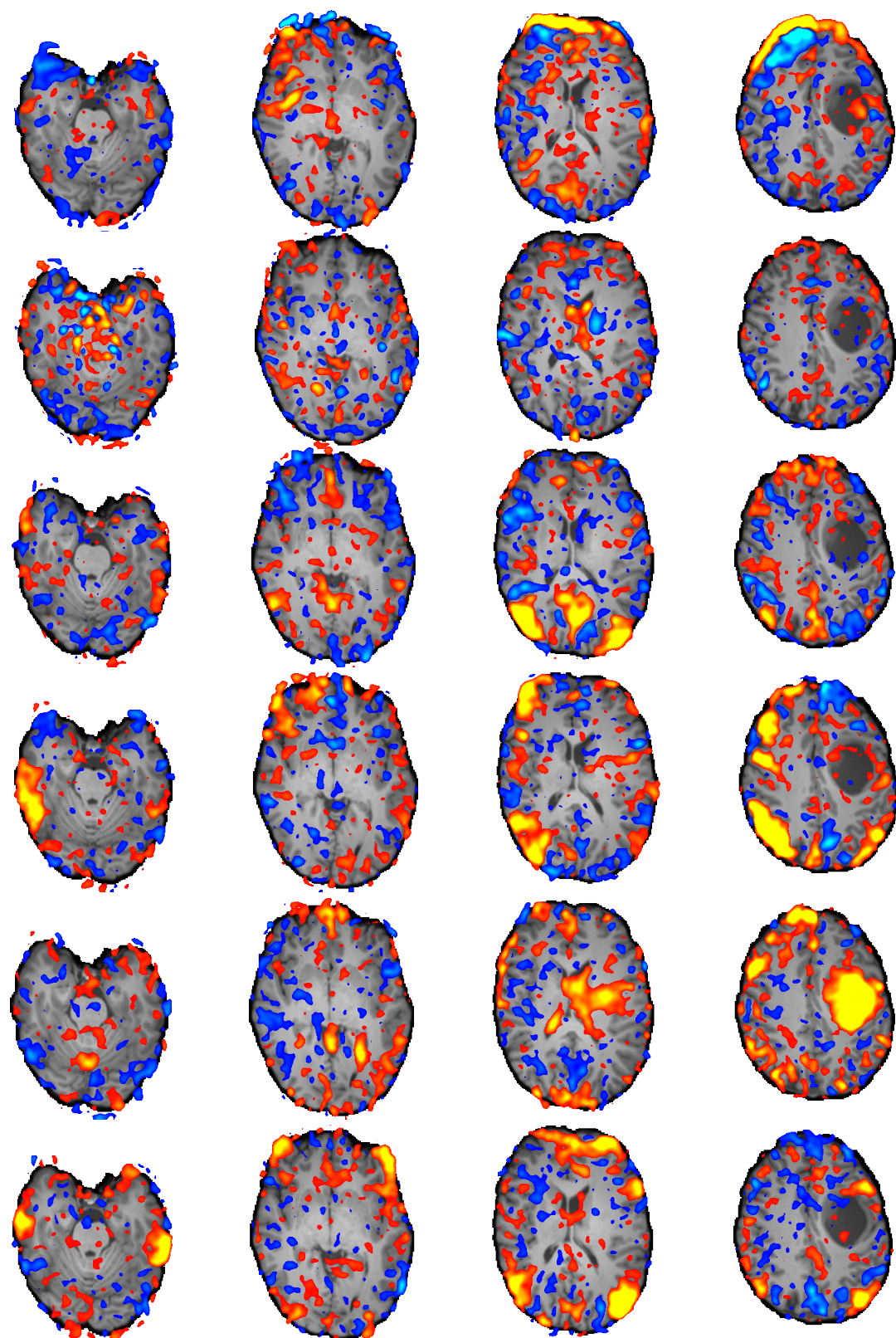


Griffanti et al (2016).

<https://doi.org/10.1016/j.neuroimage.2016.12.036>

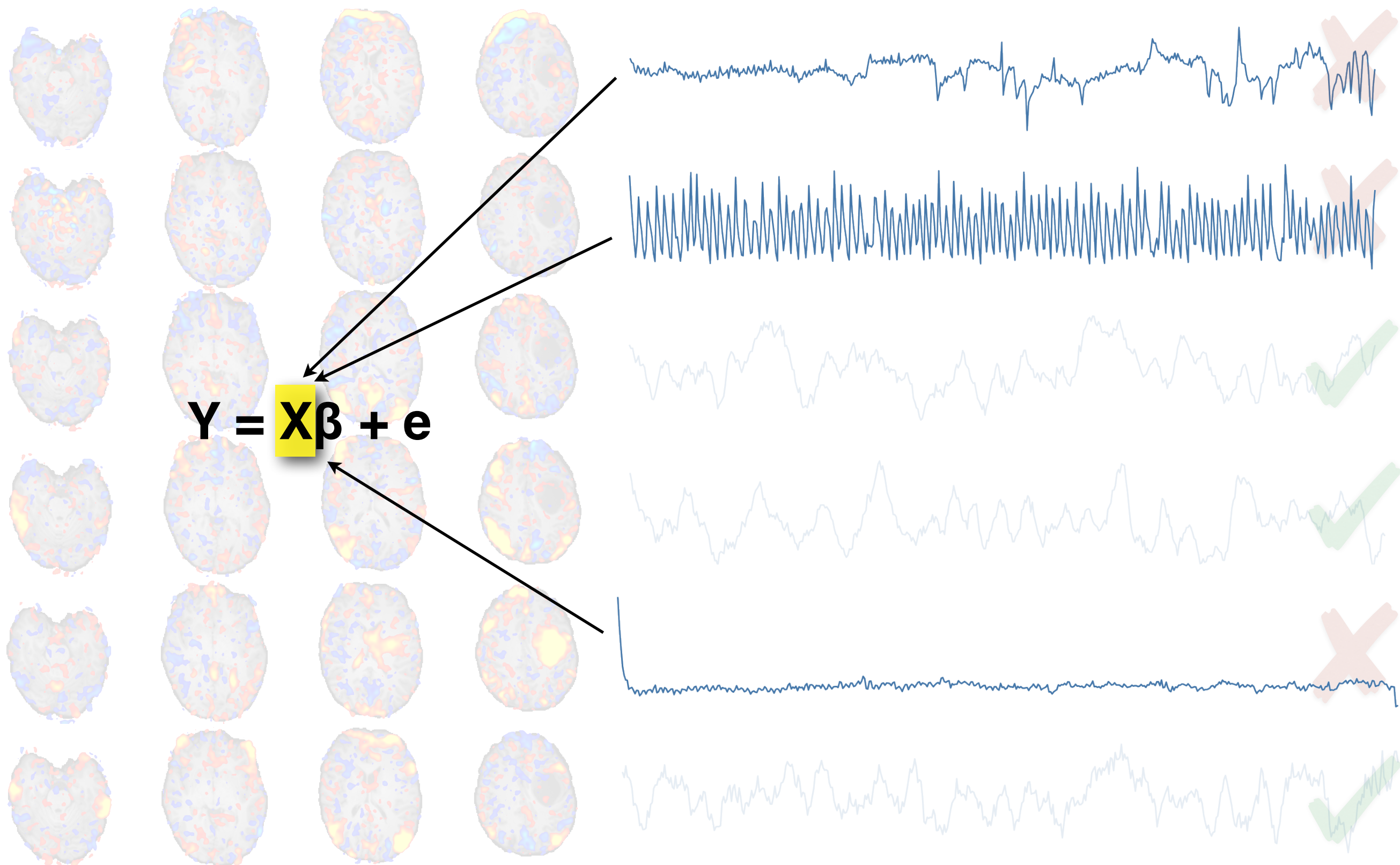


ICA-based denoising



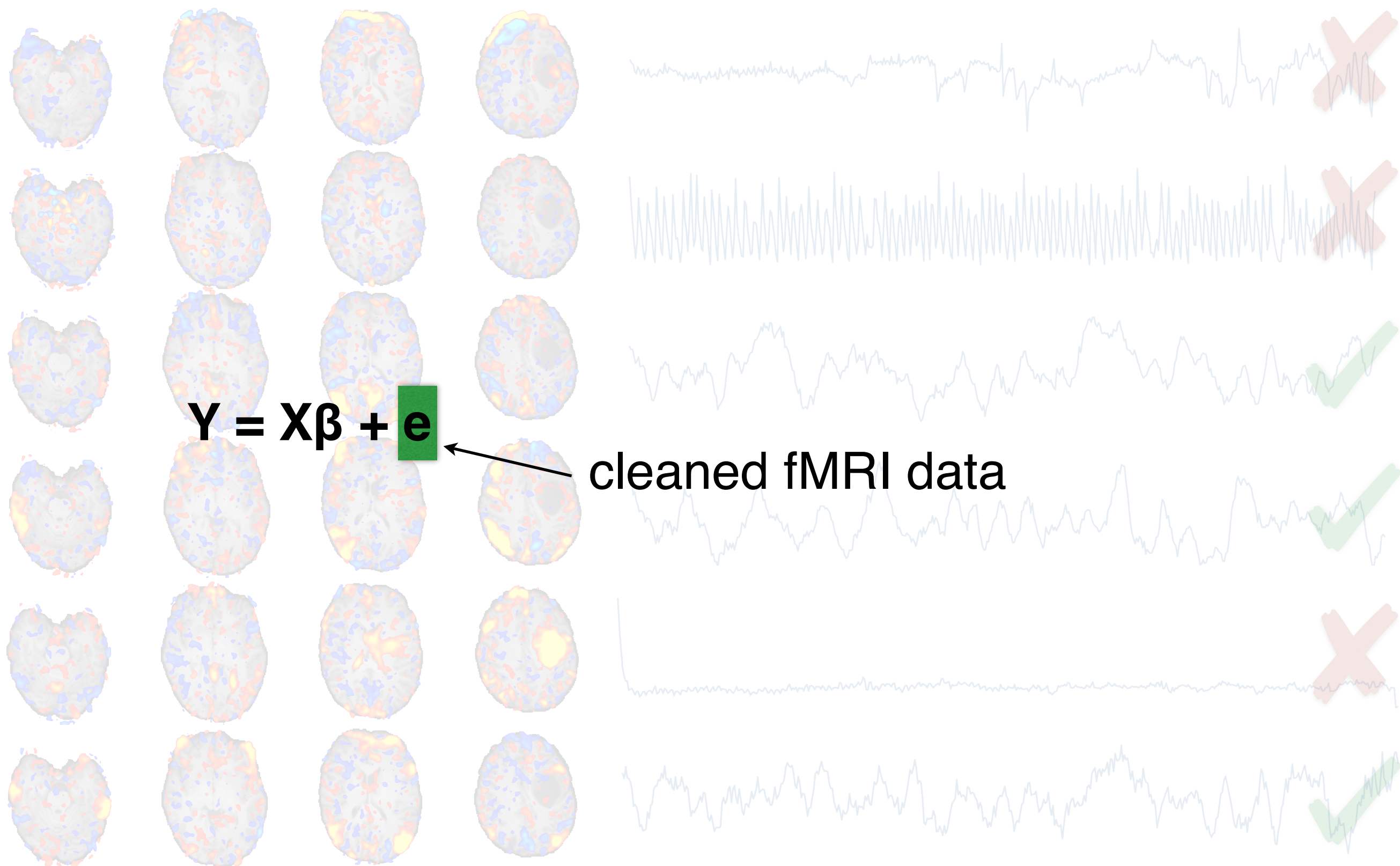


ICA-based denoising



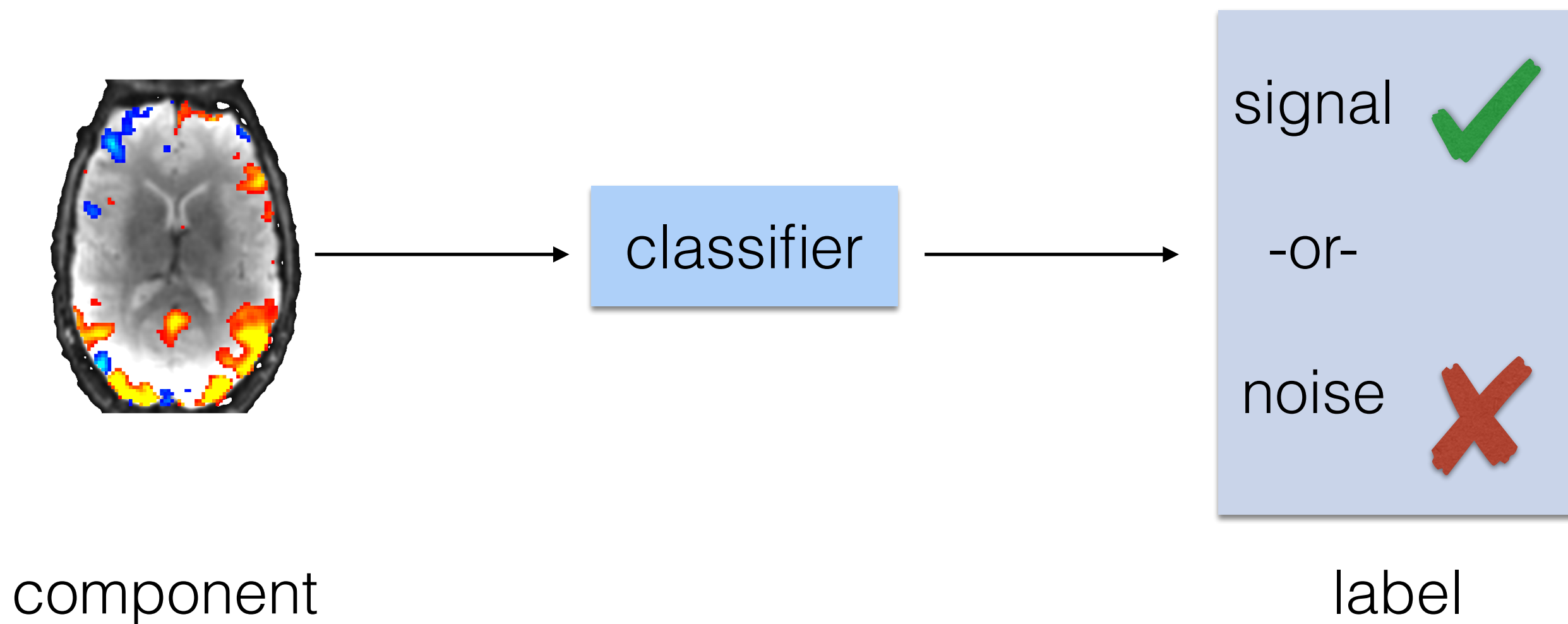


ICA-based denoising





semi-automatic classification





semi-automatic classification

- FIX (fsl.fmrib.ox.ac.uk/fsl/fslwiki/FIX)
 - Classifier with many features
 - Requires manually labelled training data
 - 99% accuracy on high-quality data



semi-automatic classification

- FIX (fsl.fmrib.ox.ac.uk/fsl/fslwiki/FIX)
 - Classifier with many features
 - Requires manually labelled training data
 - 99% accuracy on high-quality data
- ICA-AROMA (github.com/rhr-pruim/ICA-AROMA)
 - Simple classifier with only 4 features
 - No training data required
 - Mainly designed for motion artefacts



Resting state fMRI and ICA

- Introduction to resting state
- Independent Component Analysis
- **Single-subject ICA**
- Multi-subject ICA
- Dual regression



Resting state fMRI and ICA

- Introduction to resting state
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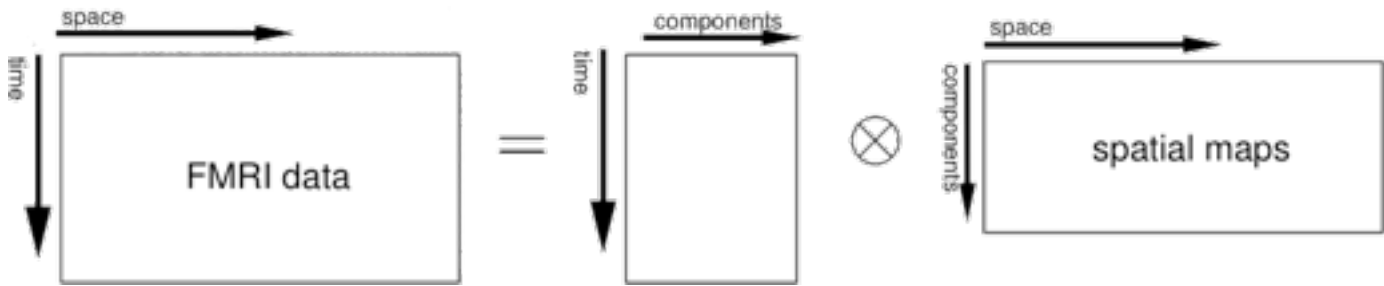
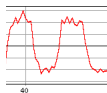
Different ICA models

Single-Session ICA

each ICA component comprises:



spatial map & timecourse



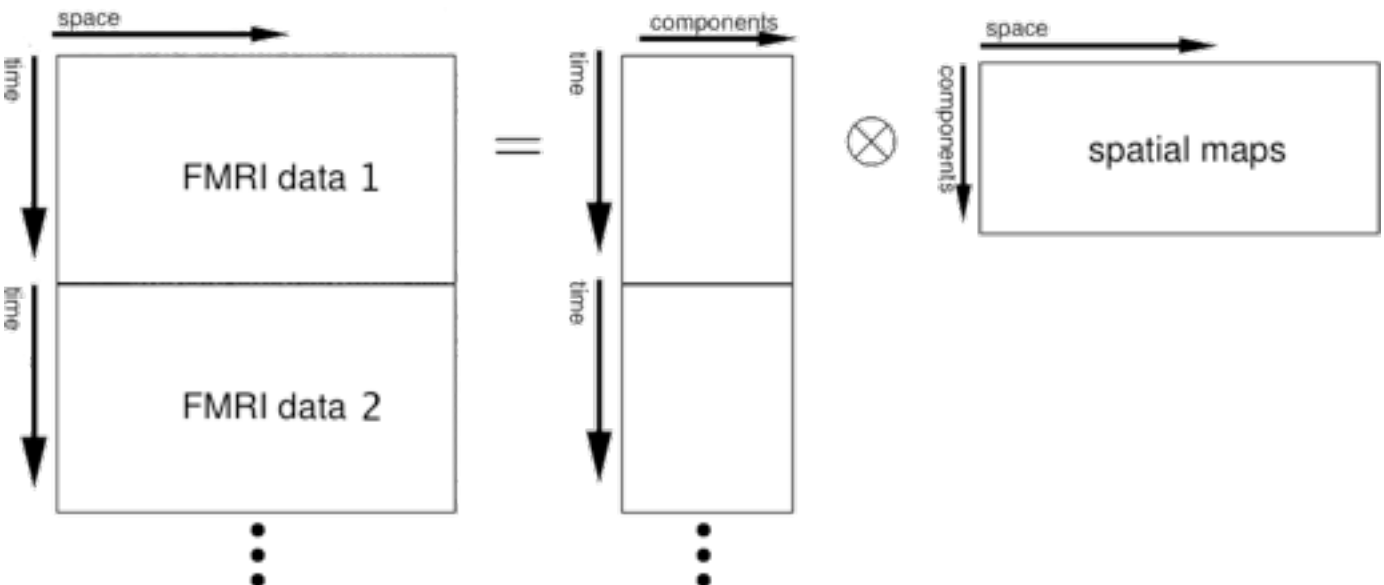
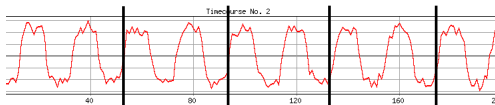
Multi-Session or Multi-Subject ICA: Concatenation approach

each ICA component comprises:



spatial map & timecourse

(that can be split up into subject-specific chunks)

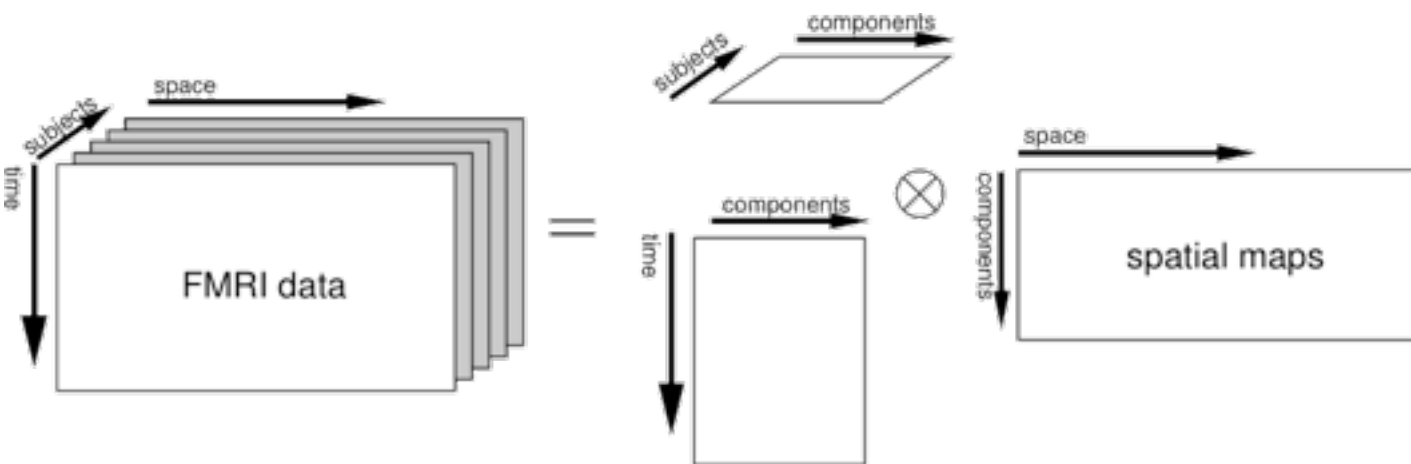
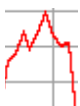
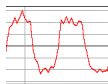


Multi-Session or Multi-Subject ICA: Tensor-ICA approach

each ICA component comprises:



spatial map, session-long-timecourse
& subject-strength plot

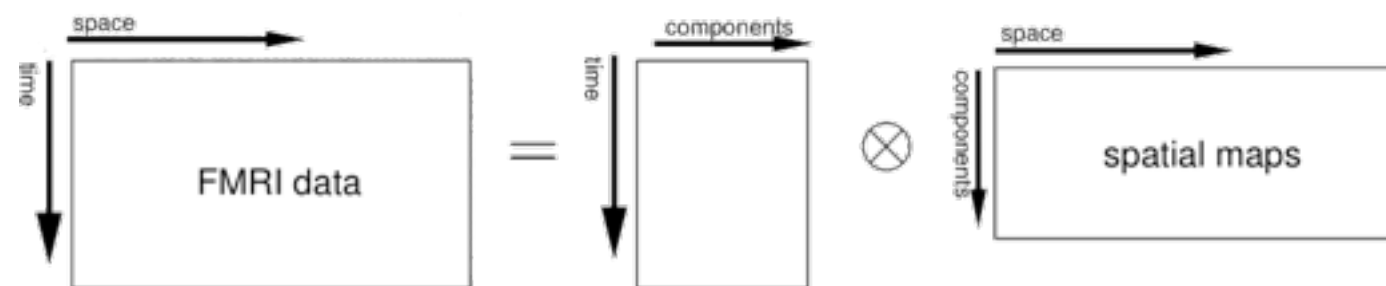




Different ICA models

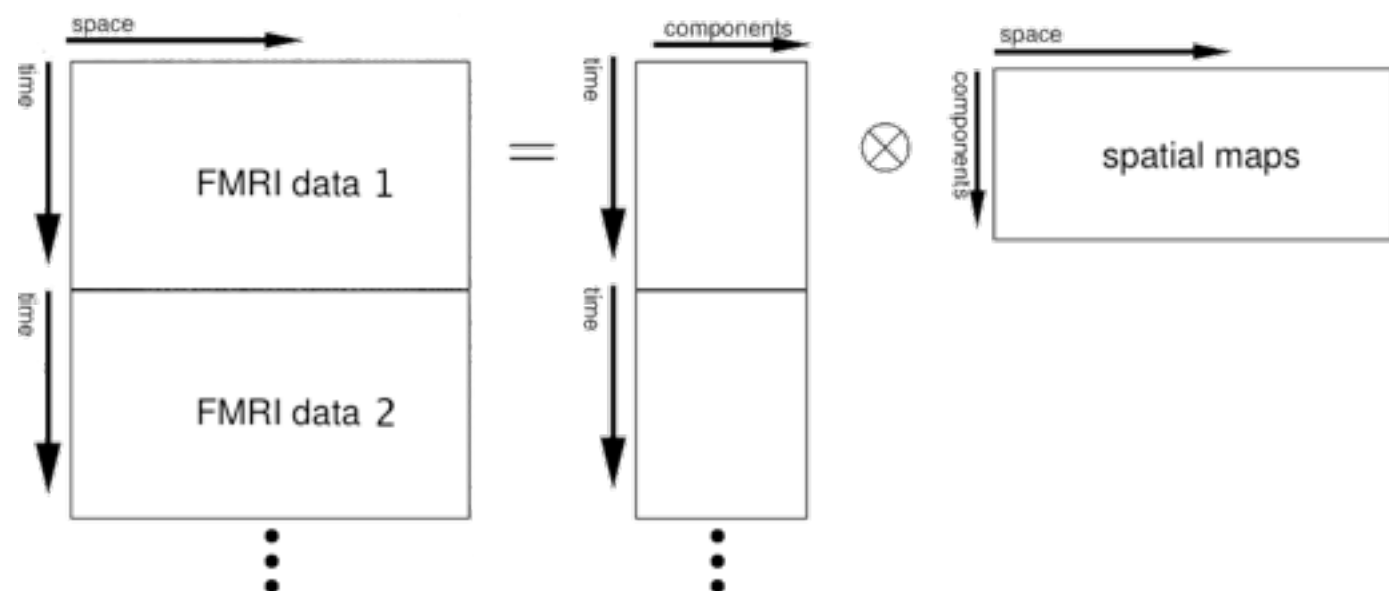
Single-Session ICA

each ICA component comprises:
spatial map & timecourse



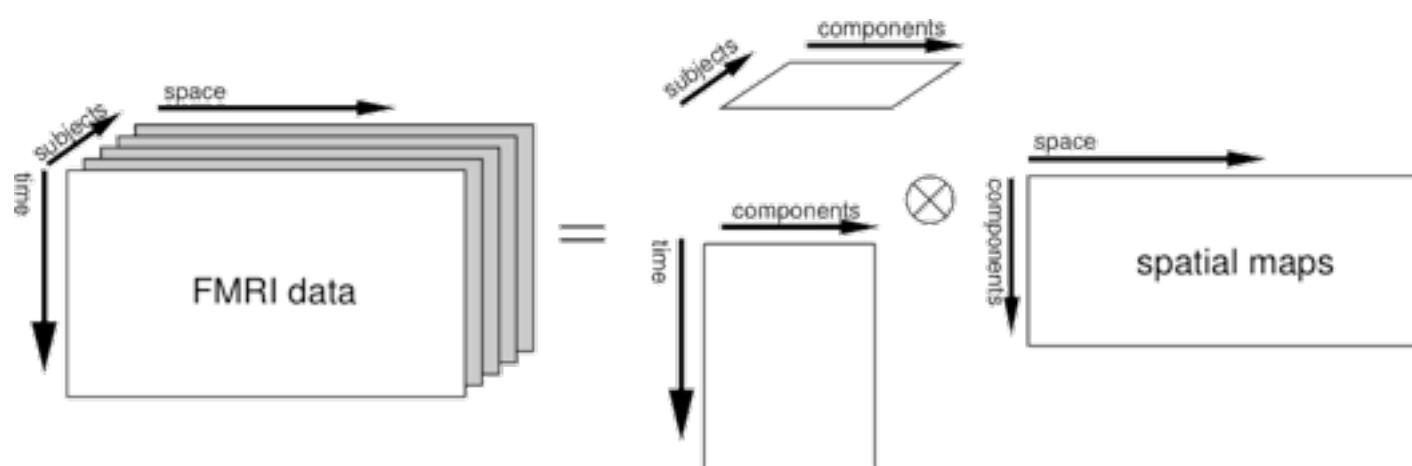
Multi-Session or Multi-Subject ICA: Concatenation approach

good when:
each subject has **DIFFERENT** timeseries
e.g. resting-state FMRI



Multi-Session or Multi-Subject ICA: Tensor-ICA approach

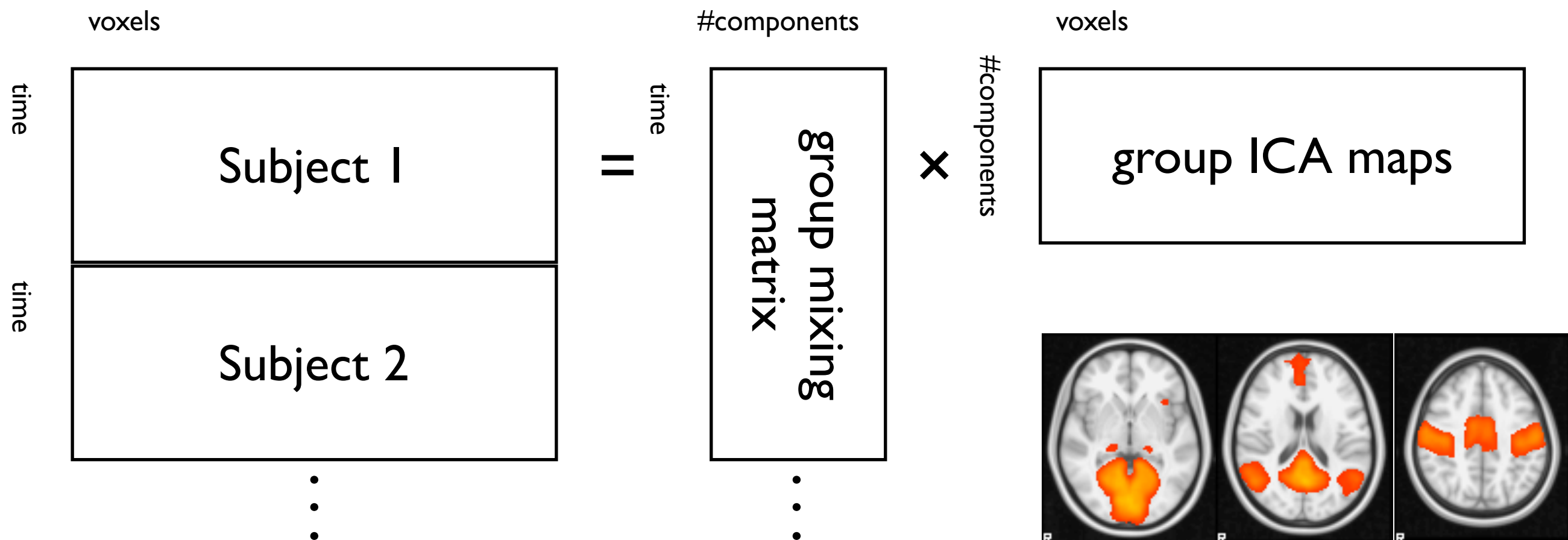
good when:
each subject has **SAME** timeseries
e.g. activation FMRI





Concatenated ICA

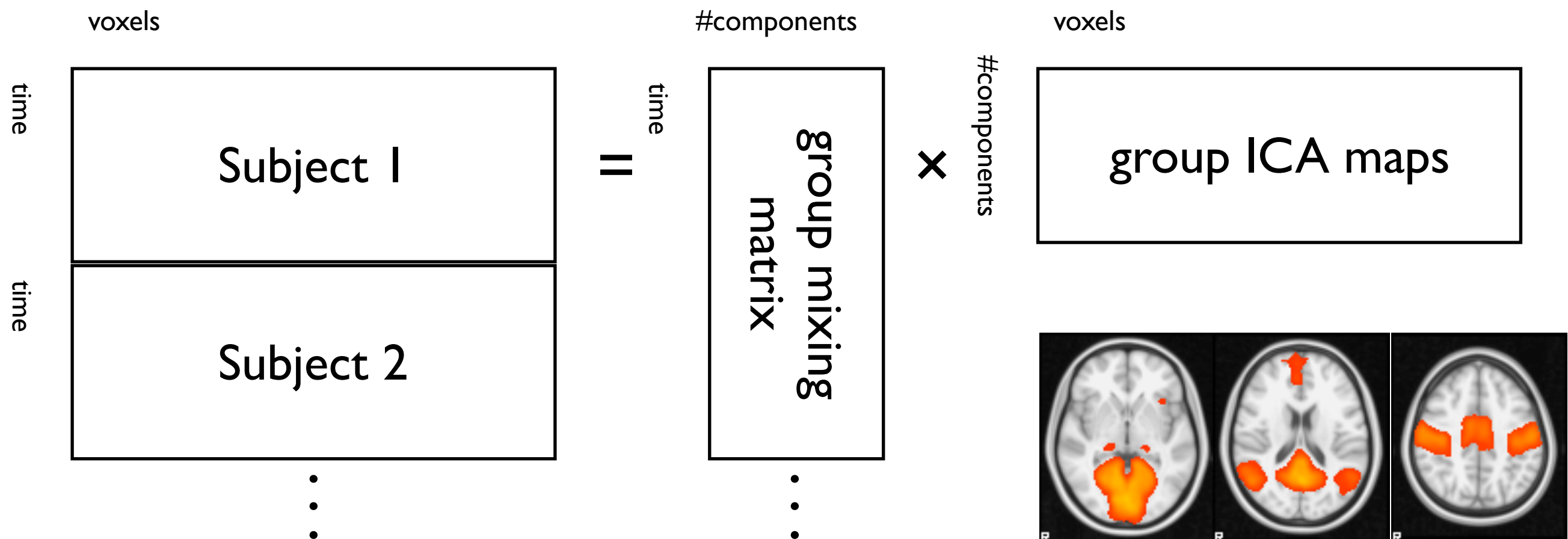
- Concatenate all subjects' data temporally
- Then run ICA
- More appropriate than tensor ICA (for RSNs)





Concatenated ICA

- Data sets must be registered to a common space (anatomical alignment)
- Memory optimisation trick (called MIGP) means that time courses are not interpretable





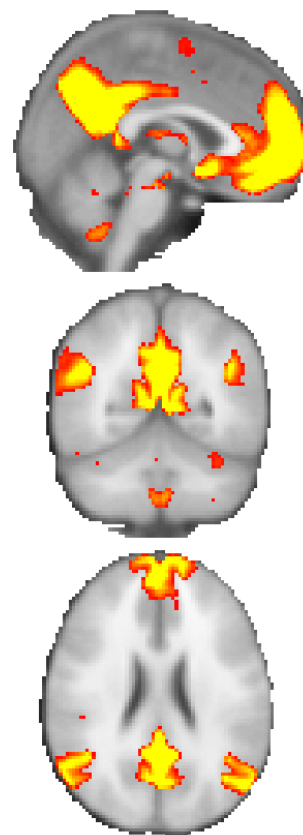
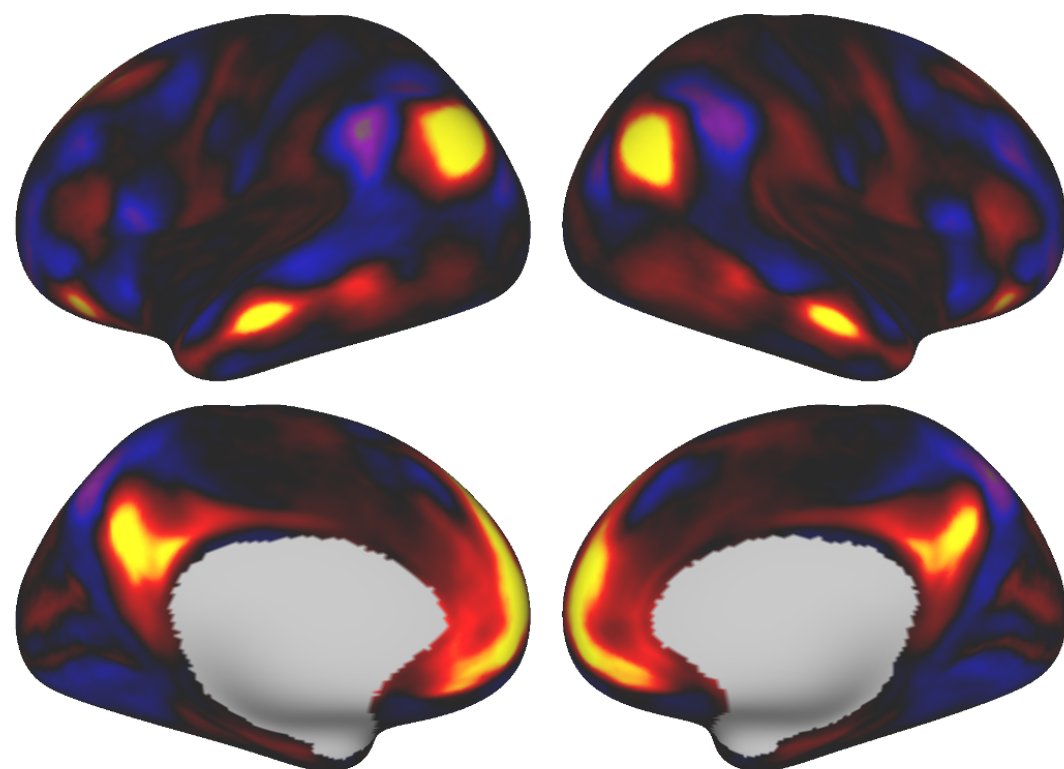
Resting state multi-subject ICA

- Why not just run ICA on each subject separately?
 - Correspondence problem (eg RSNs across subjects)
 - Different splittings sometimes caused by small changes in the data (naughty ICA!)
- Instead - start with a “group-average” ICA
 - But then need to relate group maps back to the individual subjects

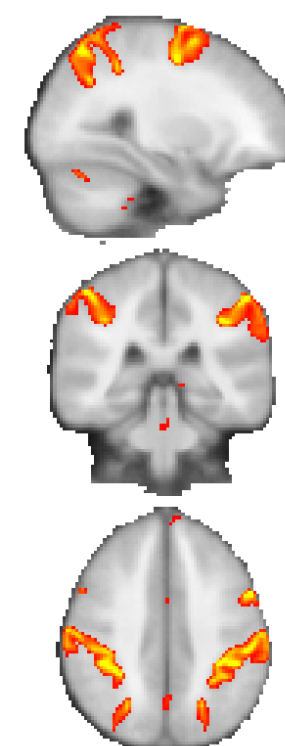
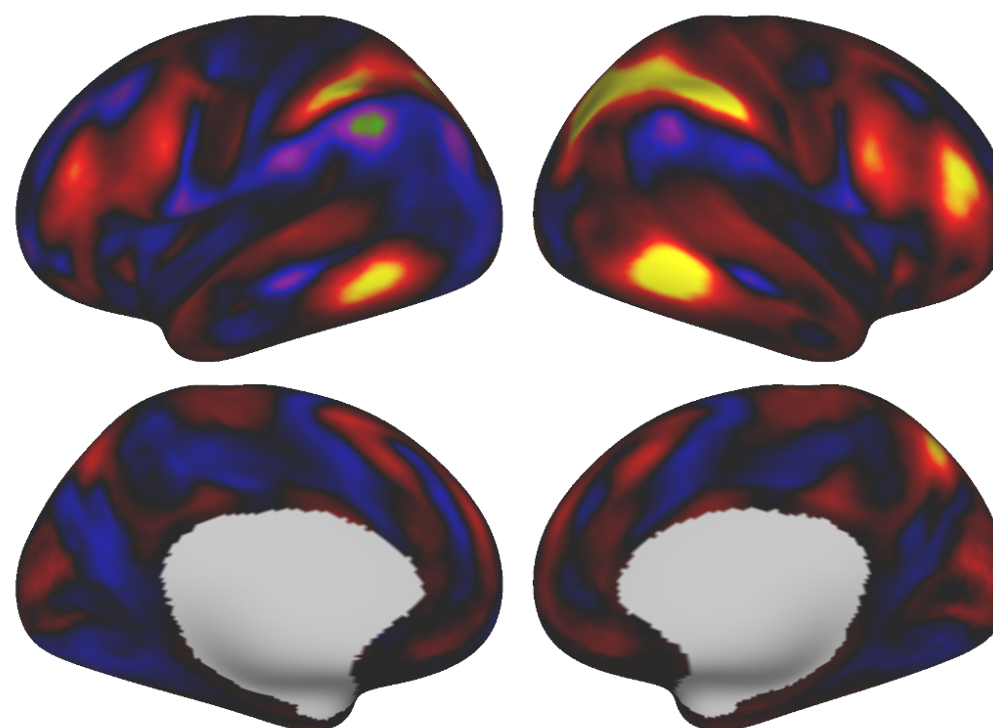


Resting state networks

Default Mode Network



Dorsal Attention Network





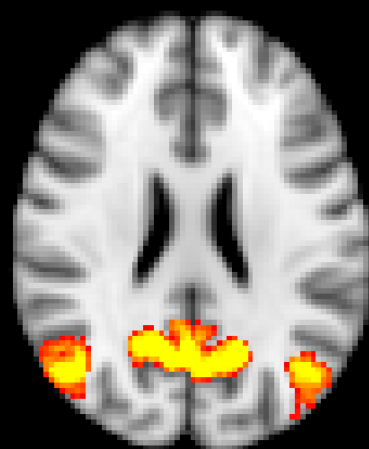
Resting state fMRI and ICA

- Introduction to resting state
- Independent Component Analysis
- Single-subject ICA
- Multi-subject ICA
- Dual regression

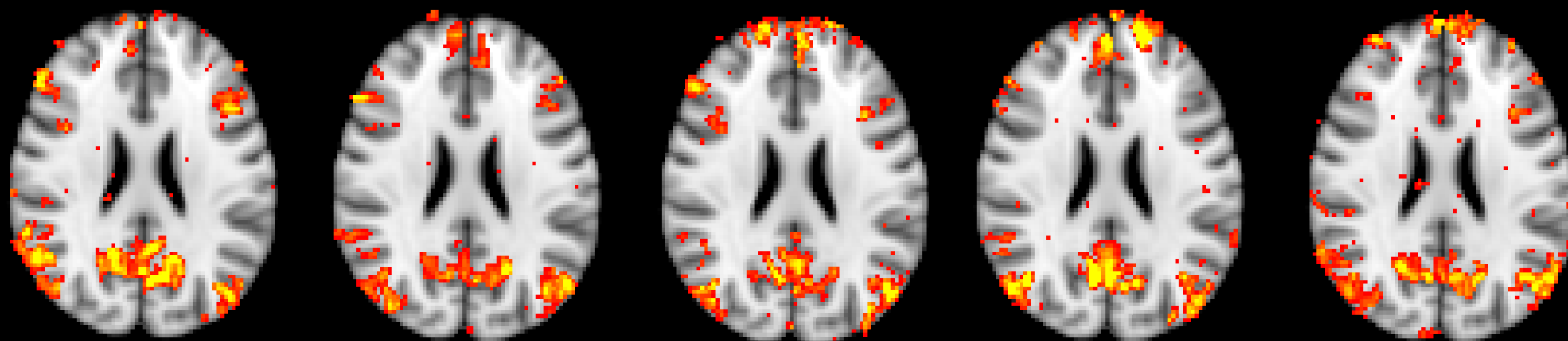


Resting state multi-subject ICA

Group ICA map



Example subject maps derived from dual regression

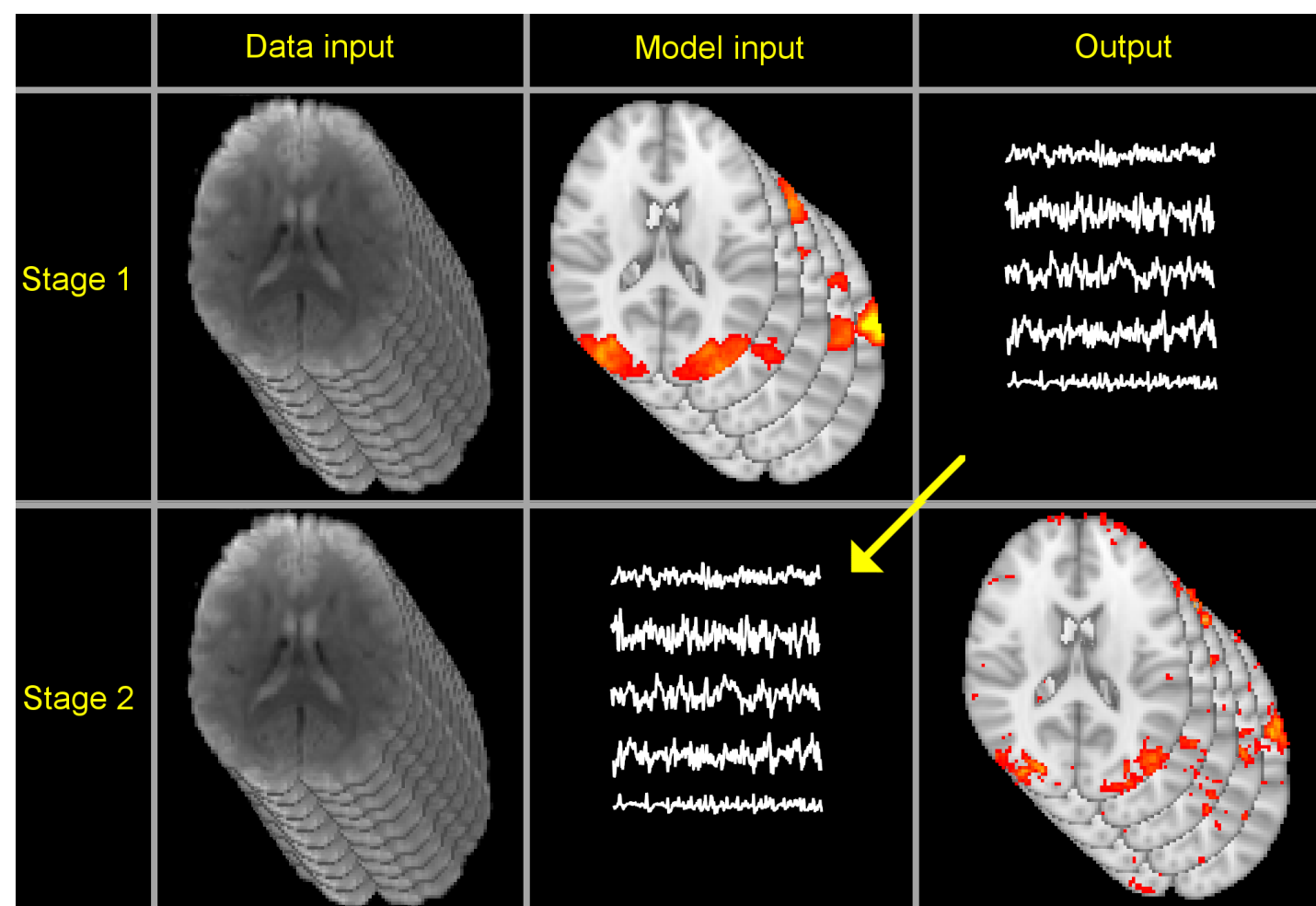




Dual Regression

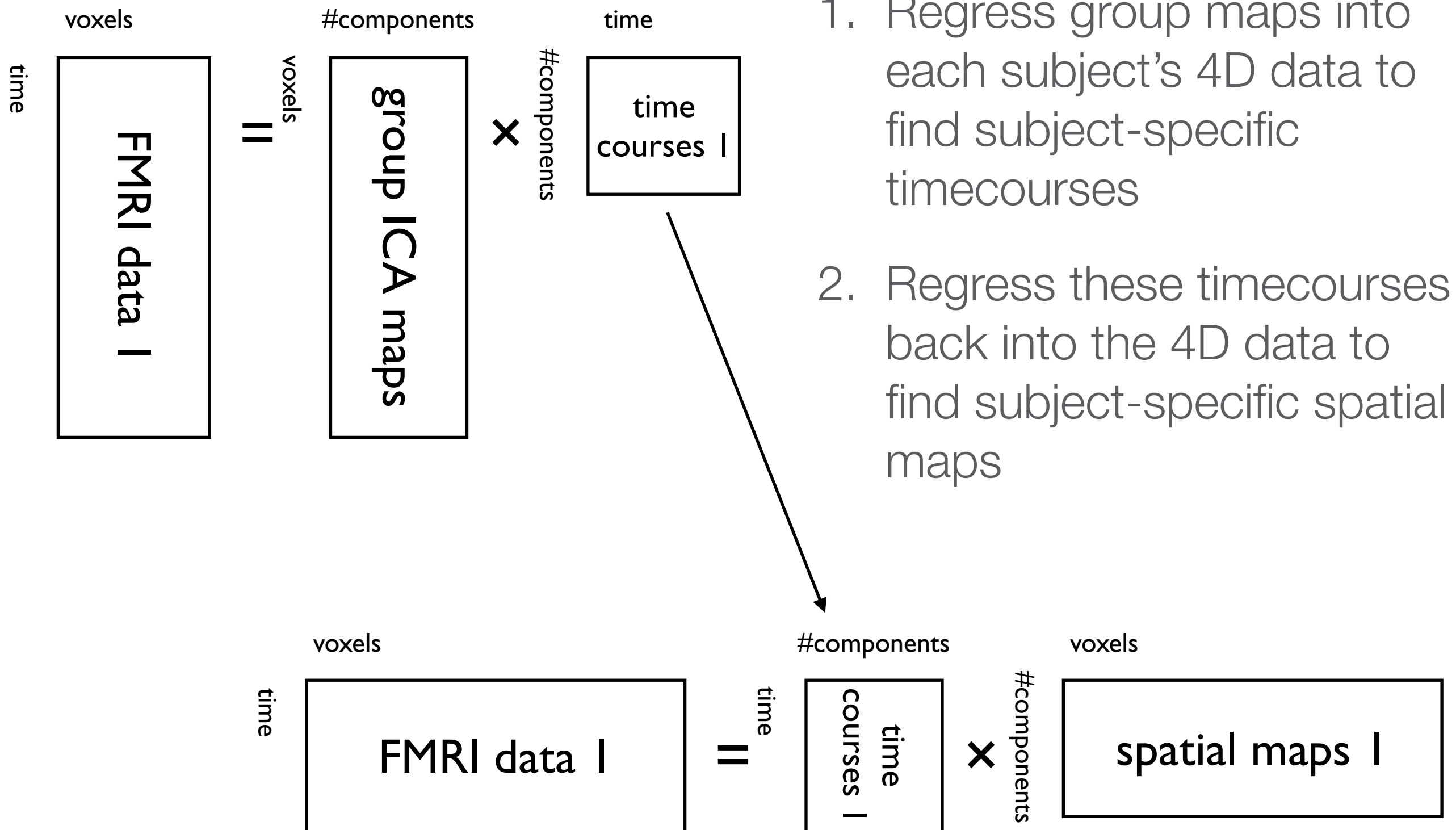
Two steps that both involve multiple regression:

1. Extract subject timeseries
2. Extract subject maps





Dual Regression



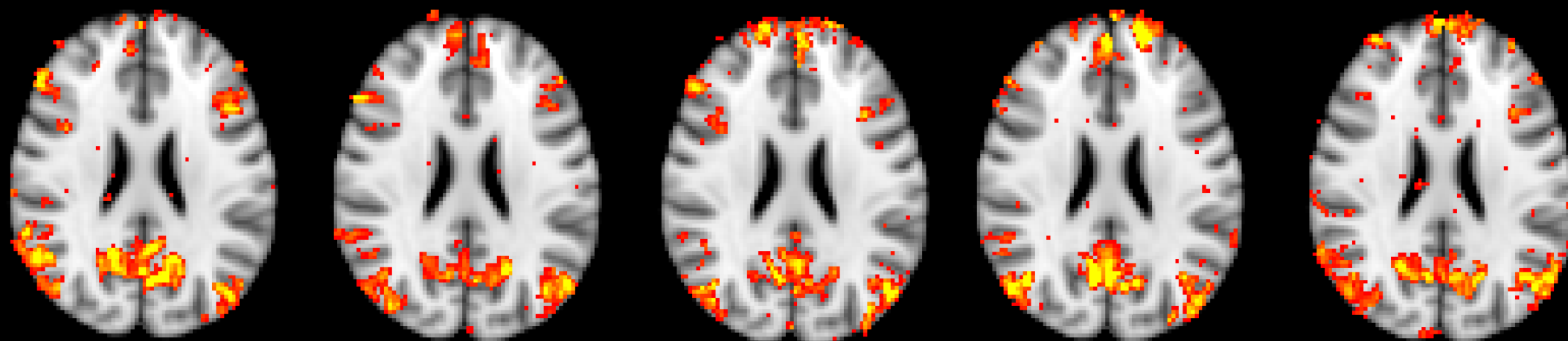



Dual Regression

Group ICA map



Example subject maps derived from dual regression





Running dual_regression

```
beckmann — bash — bash — 142x23
[islay:~] dual_regression.sh

dual_regression v0.5 (beta)

***NOTE*** ORDER OF COMMAND-LINE ARGUMENTS IS DIFFERENT FROM PREVIOUS VERSION

Usage: dual_regression <group_IC_maps> <des_norm> <design.mat> <design.con> <n_perm> <output_directory> <input1> <input2> <input3> .....
e.g.  dual_regression groupICA.gica/groupmelodic.ica/melodic_IC 1 design.mat design.con 500 grot `cat groupICA.gica/.filelist`

<group_IC_maps_4D>      4D image containing spatial IC maps (melodic_IC) from the whole-group ICA analysis
<des_norm>              0 or 1 (1 is recommended). Whether to variance-normalise the timecourses used as the stage-2 regressors
<design.mat>            Design matrix for final cross-subject modelling with randomise
<design.con>            Design contrasts for final cross-subject modelling with randomise
<n_perm>                Number of permutations for randomise; set to 1 for just raw tstat output, set to 0 to not run randomise at all.
<output_directory>     This directory will be created to hold all output and logfiles
<input1> <input2> ...   List all subjects' preprocessed, standard-space 4D datasets

<design.mat> <design.con> can be replaced with just
-1                      for group-mean (one-group t-test) modelling.
If you need to add other randomise option then just edit the line after "EDIT HERE" below

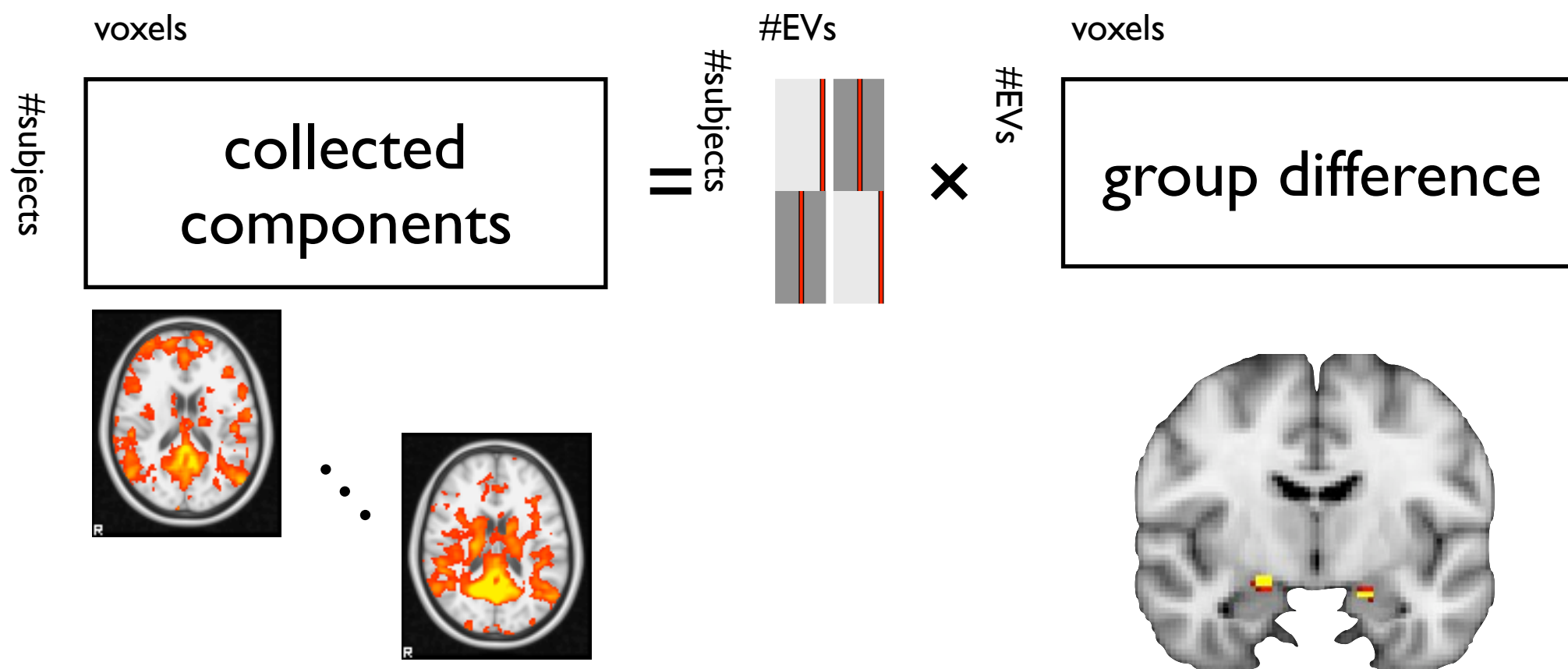
[islay:~] █
```

- FSL command line tool, combining:
 - DR to create subject-wise estimates (stage 1 + stage 2)
 - Group comparison using randomise (stage 3)



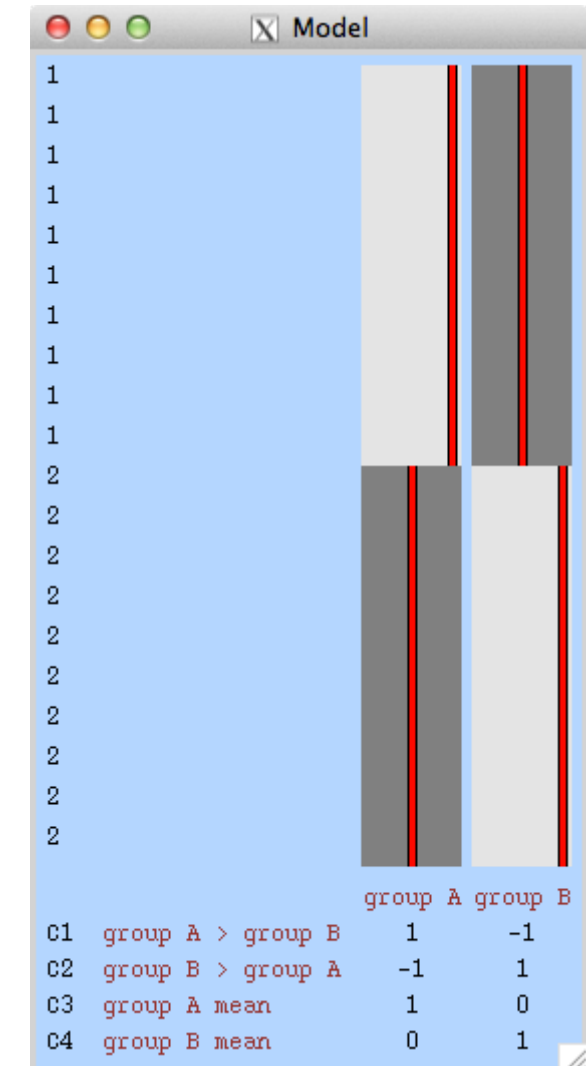
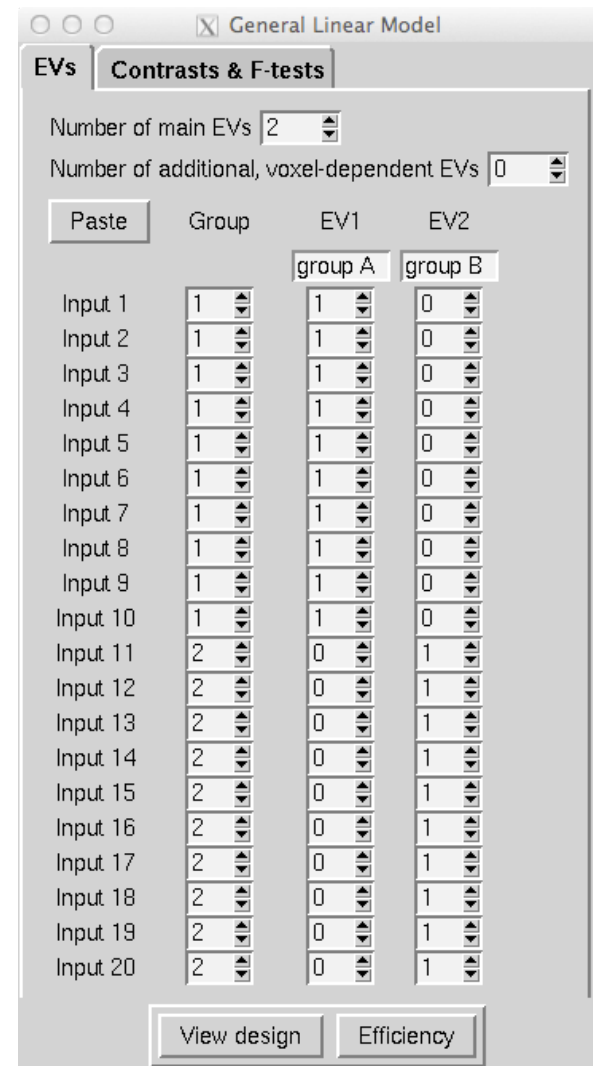
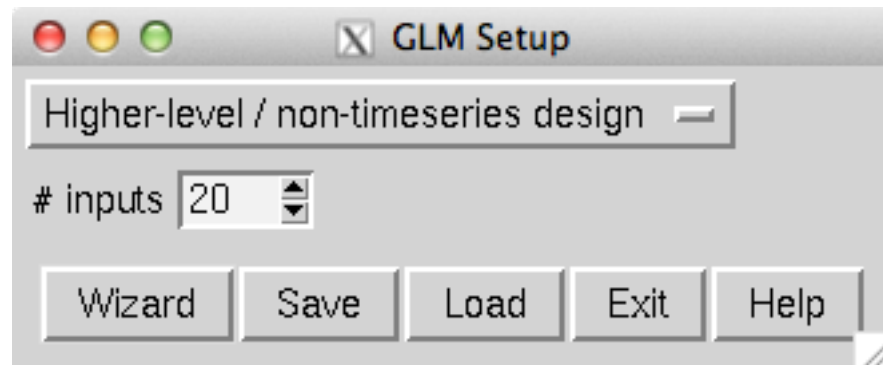
Group comparison

- Collect maps and perform voxel-wise test (e.g. randomisation test on GLM)



- Can now do voxelwise testing across subjects, separately for each original group ICA map
- Can choose to look at strength-and-shape differences

Group analysis on maps

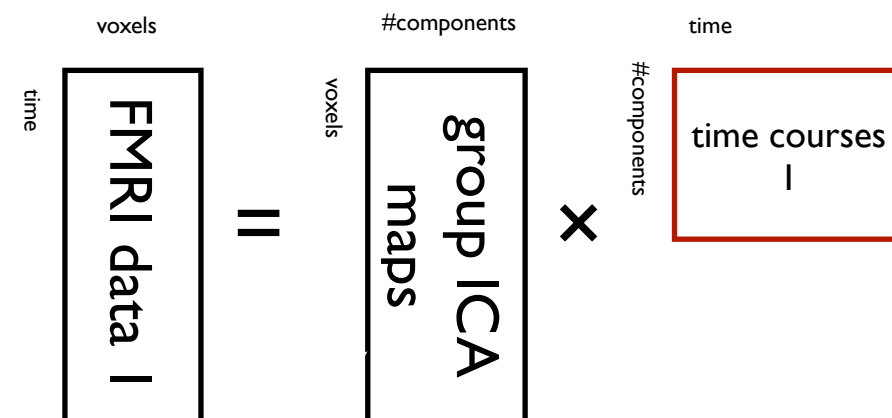


- can use the Glm tool (Glm_gui on mac) to create GLM design and contrast matrices



Dual regression outputs

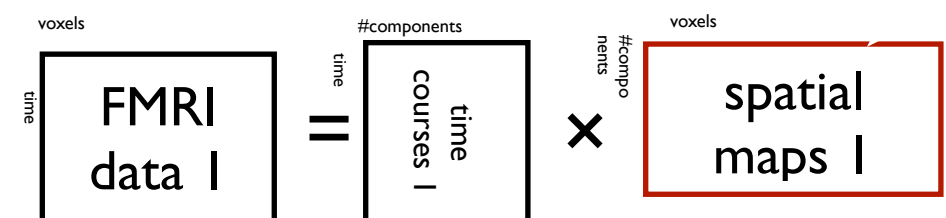
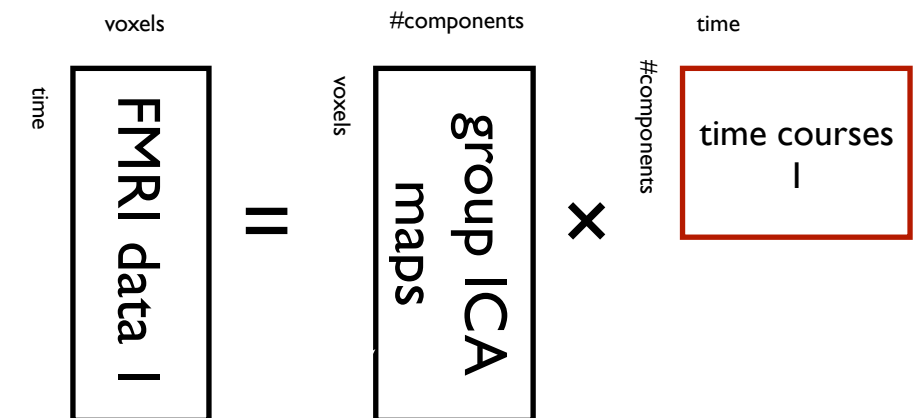
- `dr_stage1_subject[#SUB].txt` - the timeseries outputs of stage 1 of the dual-regression.





Dual regression outputs

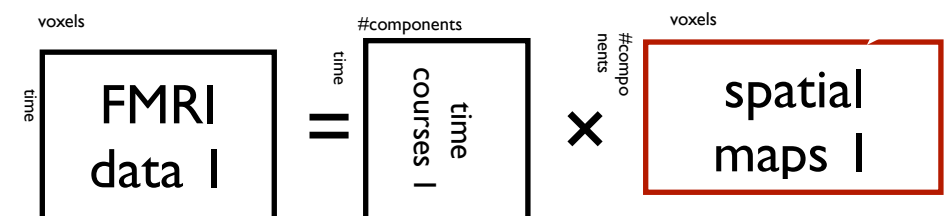
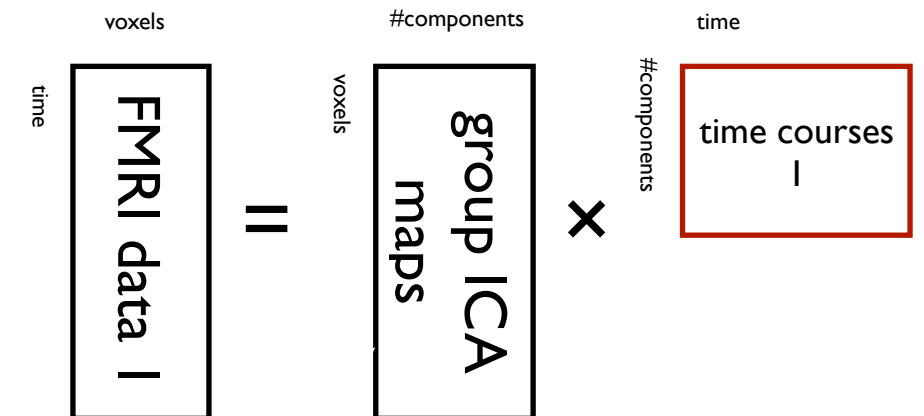
- `dr_stage1_subject[#SUB].txt` - the timeseries outputs of stage 1 of the dual-regression.
- `dr_stage2_subject[#SUB].nii.gz` - the spatial maps outputs of stage 2 of the dual-regression.





Dual regression outputs

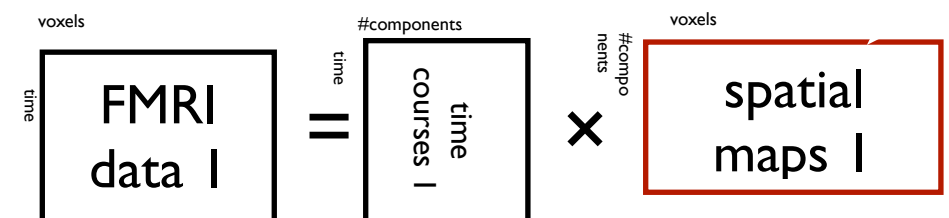
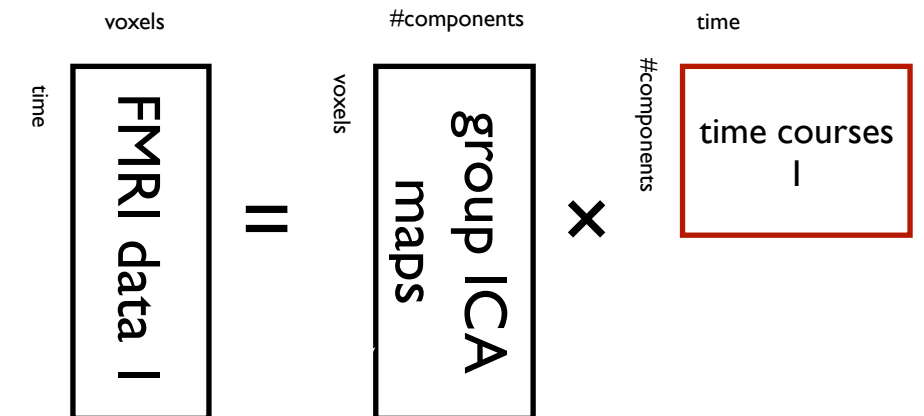
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- `dr_stage2_subject[#SUB].nii.gz` - the spatial maps outputs of stage 2 of the dual-regression.
- `dr_stage2_ic[#ICA].nii.gz` - the re-organised parameter estimate images





Dual regression outputs

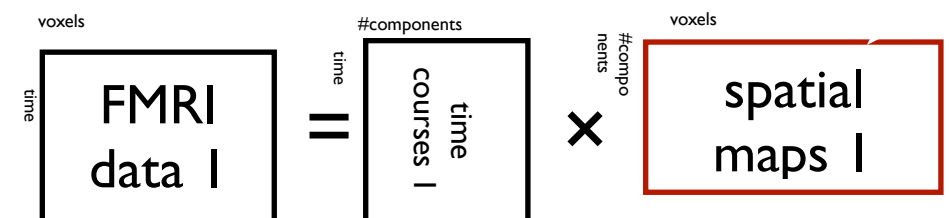
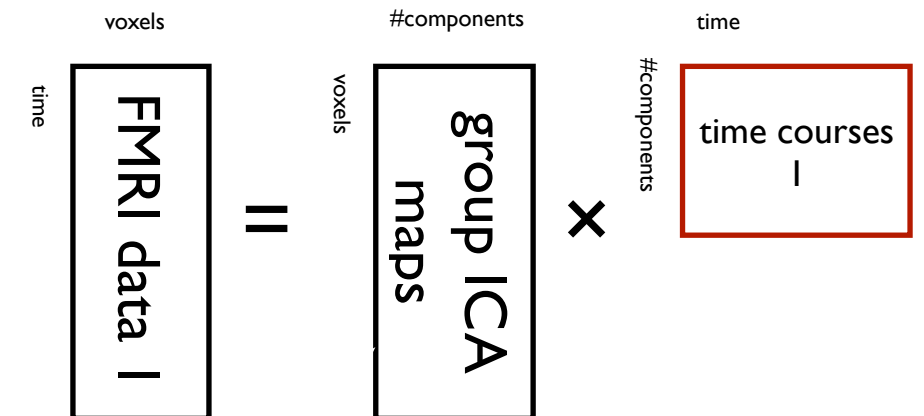
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- `dr_stage2_subject[#SUB].nii.gz` - the spatial maps outputs of stage 2 of the dual-regression.
- `dr_stage2_ic[#ICA].nii.gz` - the re-organised parameter estimate images
- `dr_stage3_ic[#ICA]_tstat[#CON].nii.gz` - the output from randomise





Dual regression outputs

- `dr_stage1_subject[#SUB].txt` - the timeseries outputs of stage 1 of the dual-regression.
- `dr_stage2_subject[#SUB].nii.gz` - the spatial maps outputs of stage 2 of the dual-regression.
- `dr_stage2_ic[#ICA].nii.gz` - the re-organised parameter estimate images
- `dr_stage3_ic[#ICA]_tstat[#CON].nii.gz` - the output from randomise

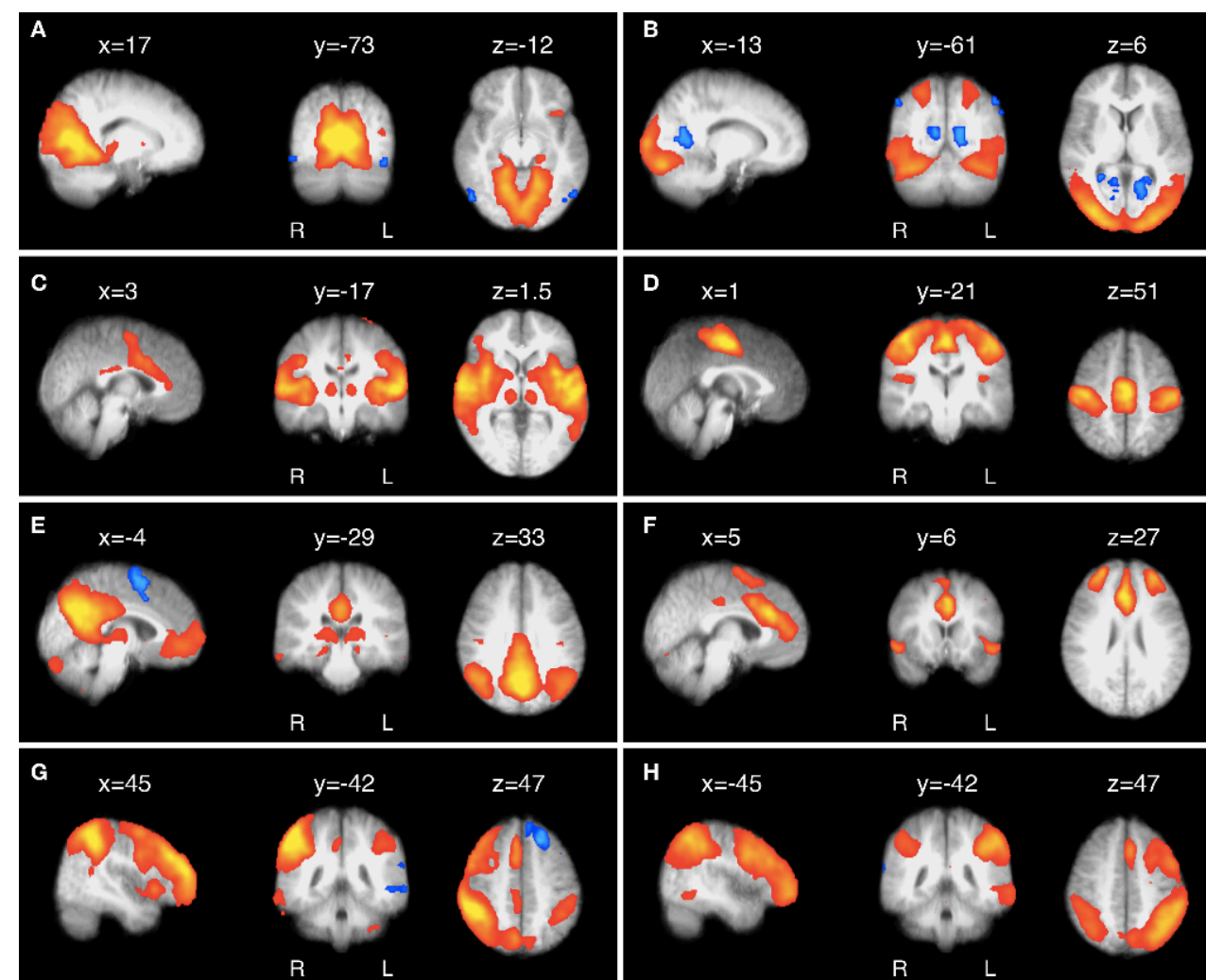


(corrected for multiple comparisons across voxels
but not across #components!!)



Group template maps

- Generate from the data using ICA
- use all data to get unbiased templates



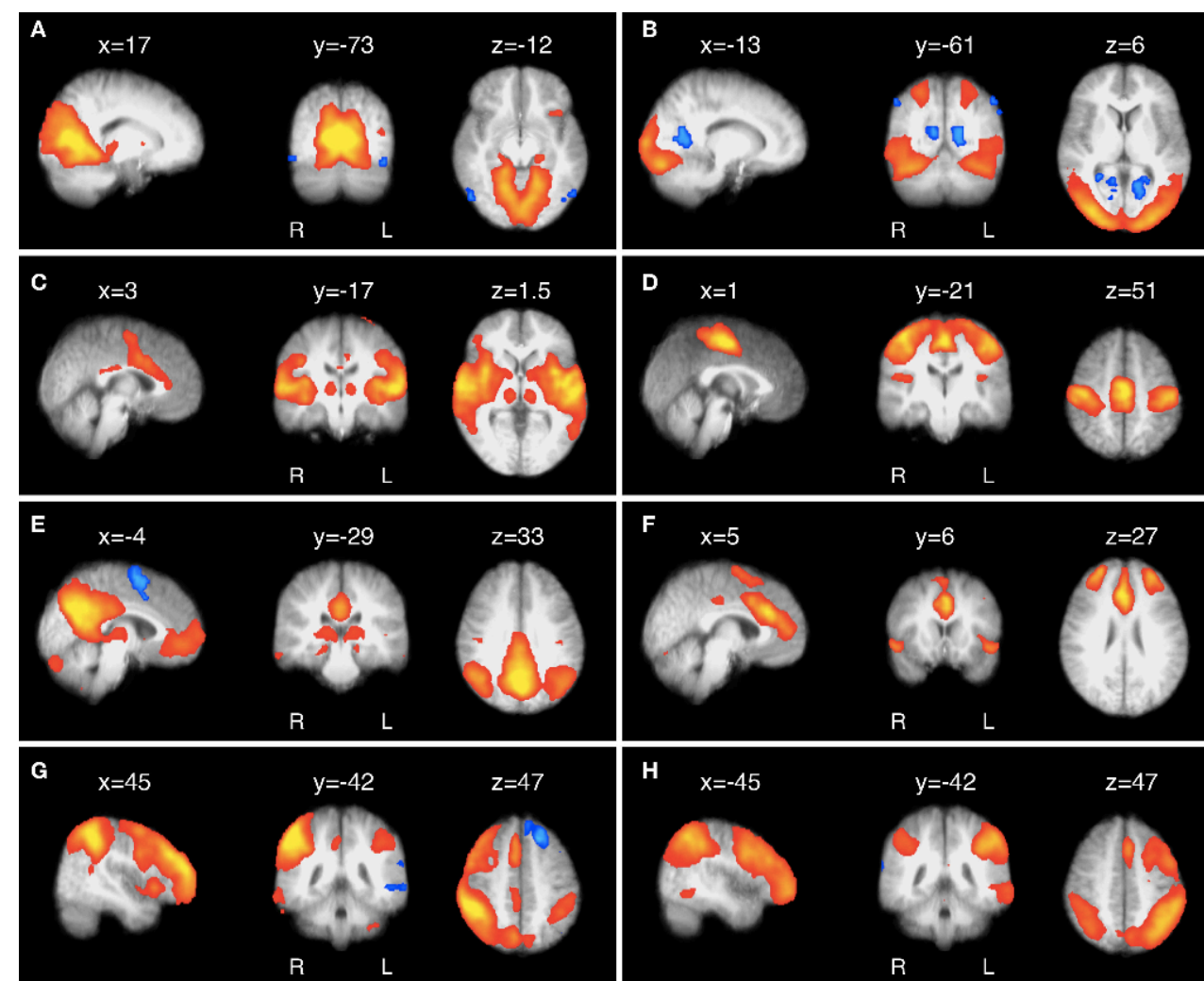
template RSNs

<https://www.fmrib.ox.ac.uk/datasets/royalsoc8/>



Group template maps

- Generate from the data using ICA
 - use all data to get unbiased templates
 - use independent control group
 - will model signals and artefacts



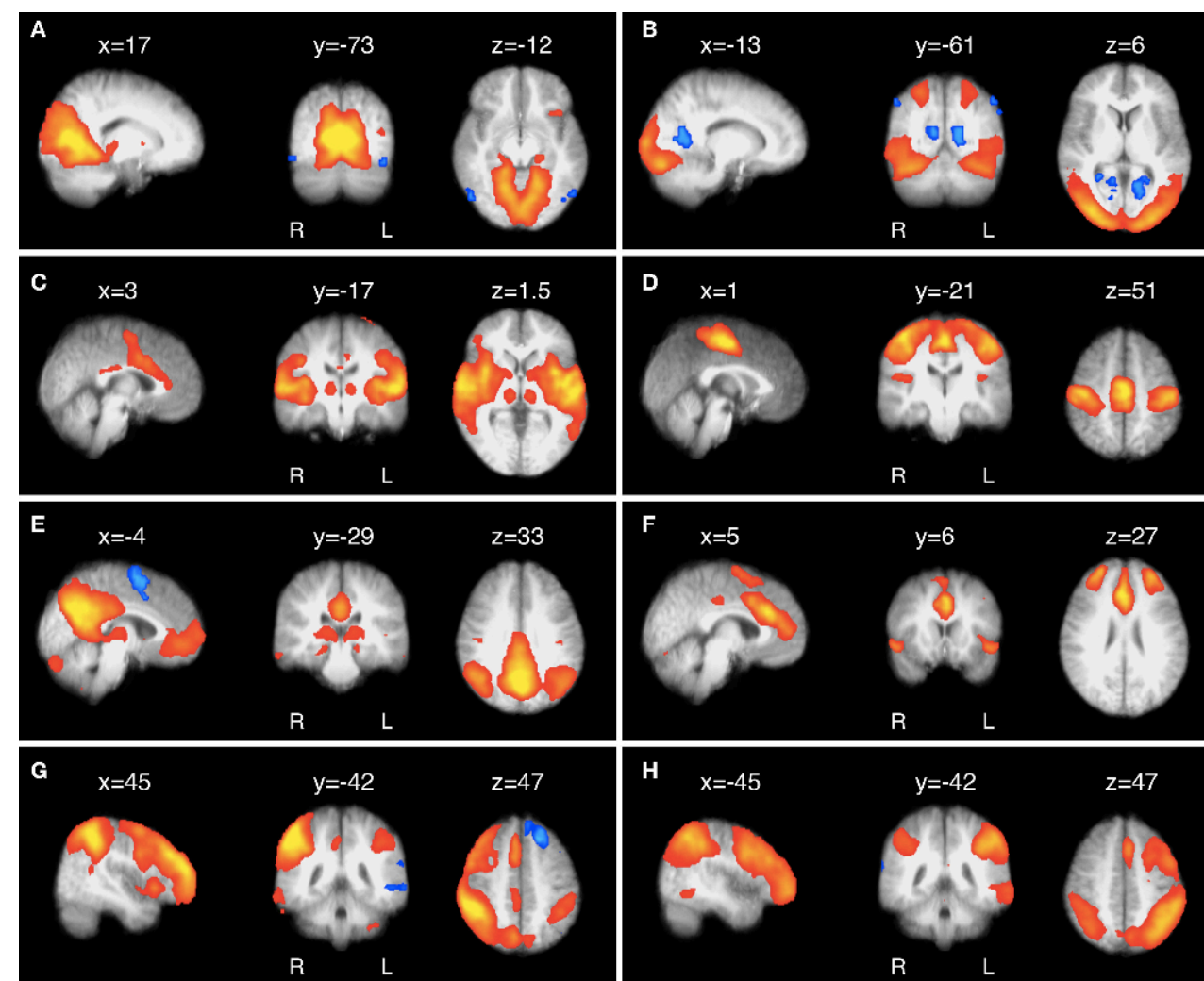
template RSNs

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Group template maps

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- Dual regression



Resting state fMRI and ICA

Available from:

- [Oxford University Press](#)
- [Amazon](#)

