

Signal, Noise and Preprocessing*

Zurich SPM Course 2015

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Generous slide support:

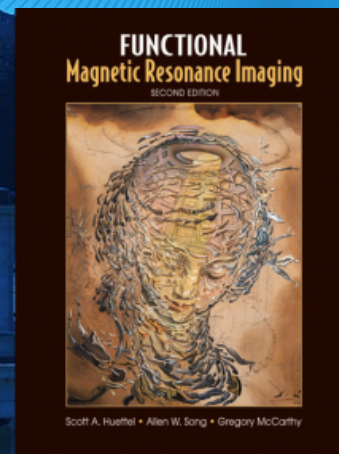
Guillaume Flandin

Ged Ridgway

Klaas Enno Stephan

John Ashburner

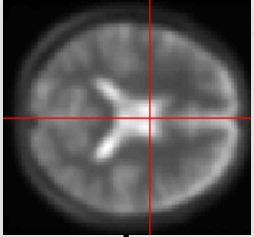
*Huettel et al.



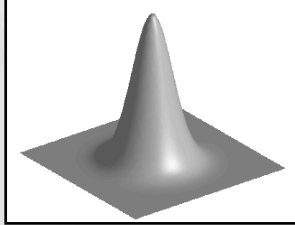
Overview of SPM for fMRI

Preprocessing

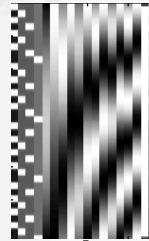
Image time-series



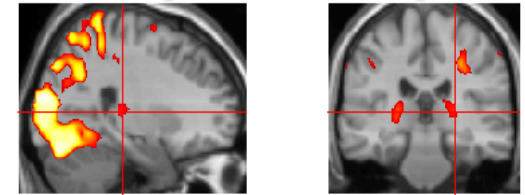
Kernel



Design matrix



Statistical parametric map (SPM)



Realignment

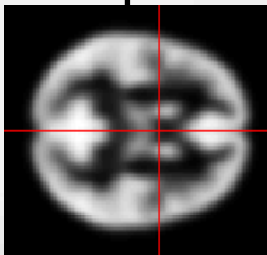
Smoothing

General linear model

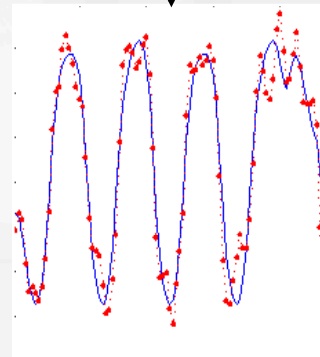
Statistical
inference

Random
field theory

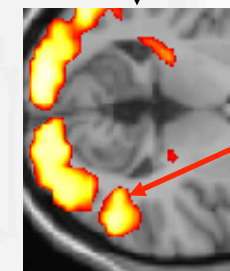
Normalisation



Template

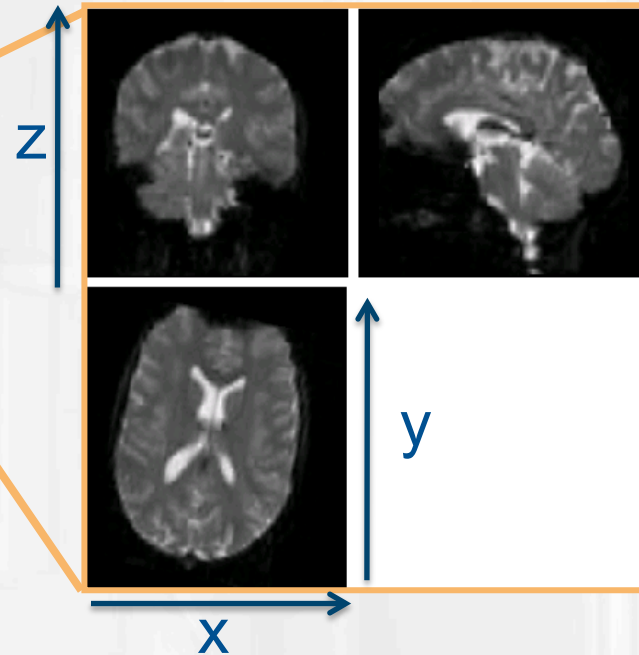
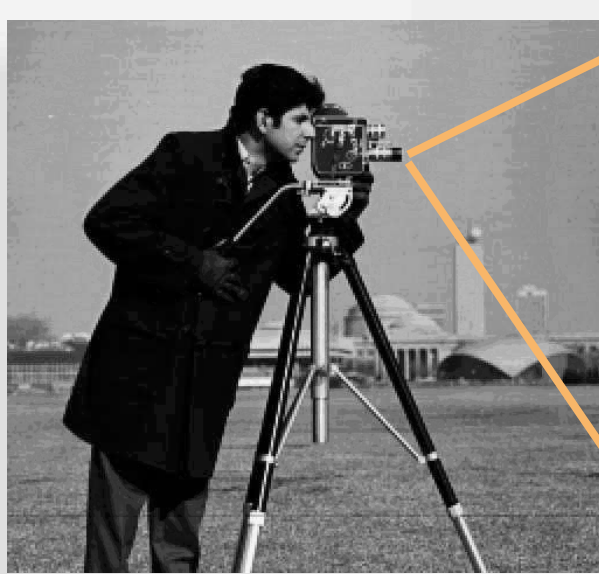


Parameter estimates



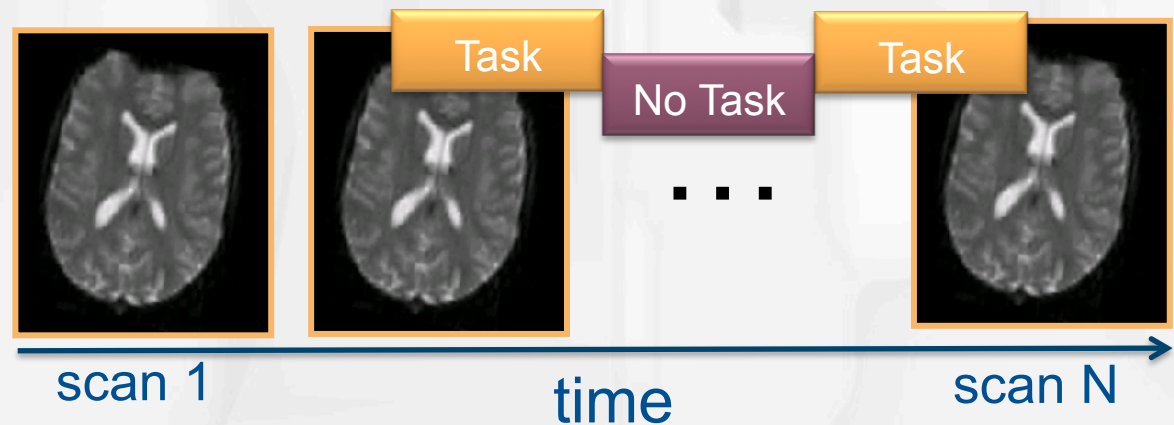
$p < 0.05$

fMRI = Acquiring Movies



- ...of three-dimensional Blood Oxygen-Level Dependent (BOLD) contrast images
- typically echo-planar images (EPI)

- Run/Session: Time Series of Images

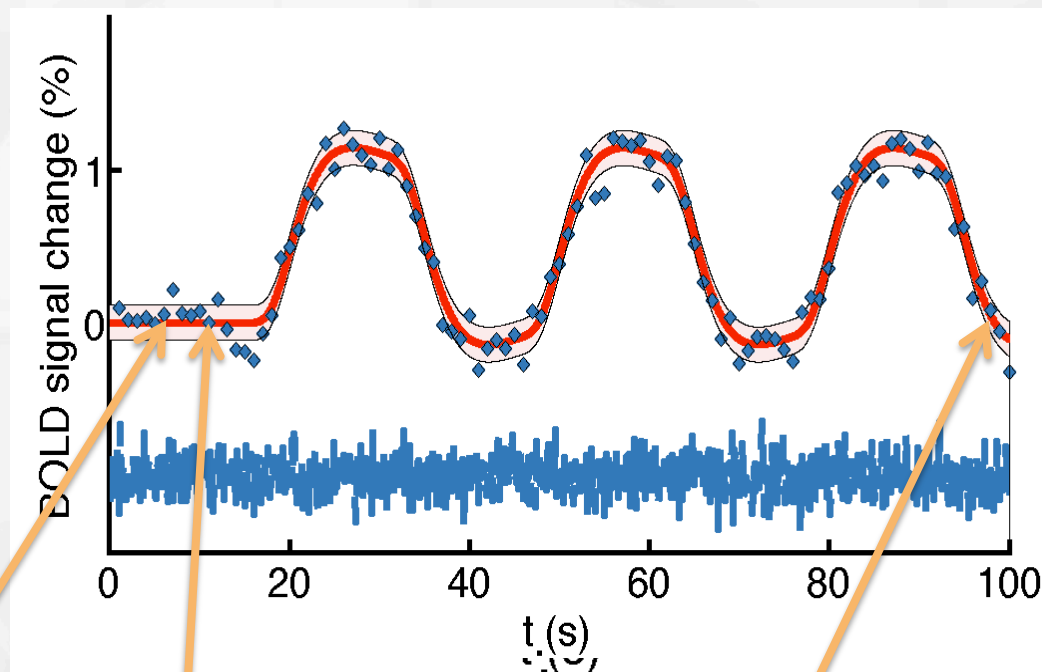


fMRI = Acquiring Movies

- The Localized Time-series is the Fundamental Information Unit of fMRI

Signal: Fluctuation through Blood oxygen level dependent (BOLD) contrast

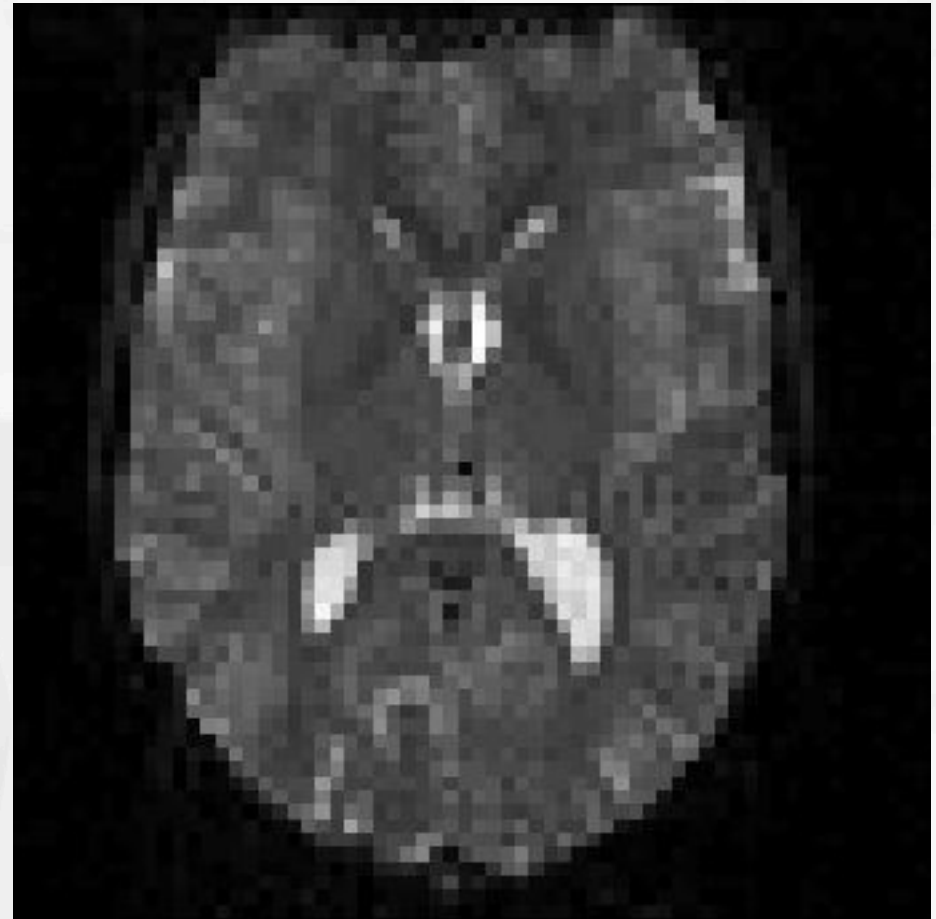
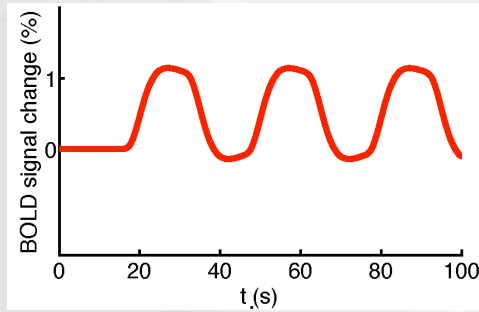
Noise: All other fluctuations



- Run/Session: Time Series of Images

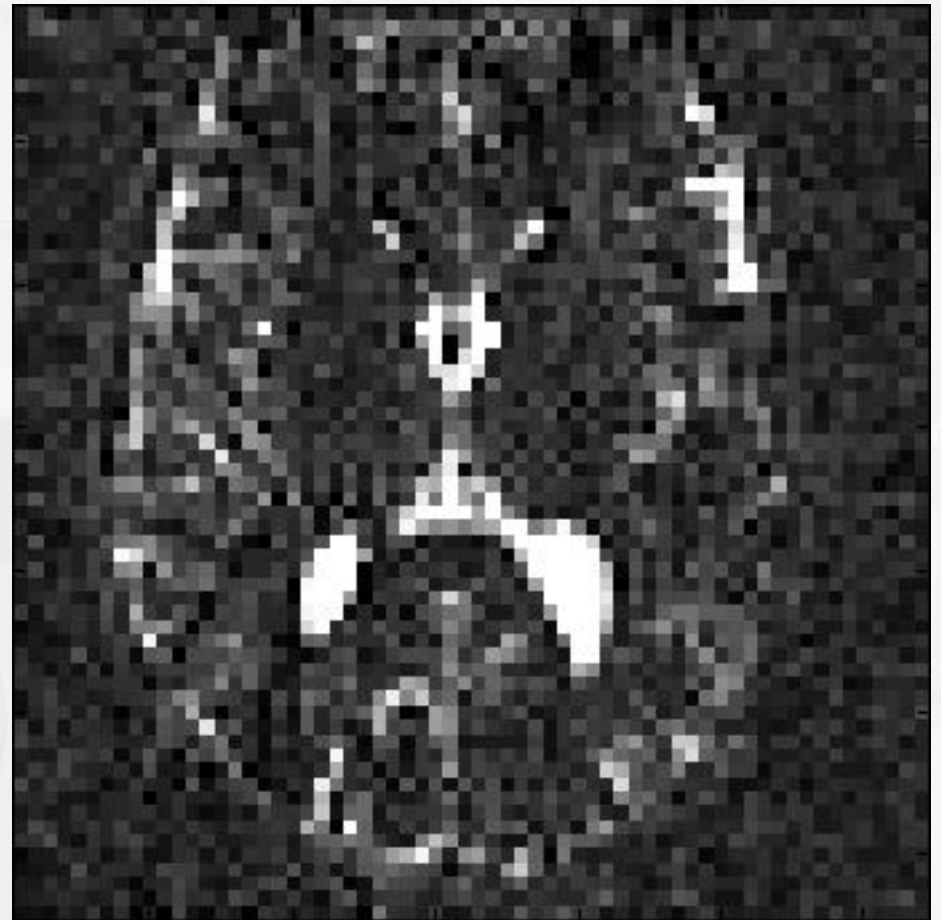


fMRI Movie: An example



fMRI Movie: Subtracting the Mean

- interest in fluctuations only



Introducing the Dataset (MoAE)

- Mother of All Experiments: Auditory Stimulation
 - TR 7 seconds
 - 6 TR rest
 - 6 TR binaural stimulation (1 bi-syllabic word per second)
- Chapter 28 of SPM manual

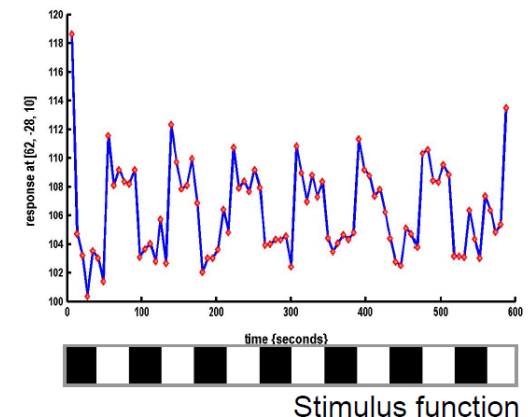
A very simple fMRI experiment

One session

Passive word
listening
versus rest

7 cycles of
rest and listening

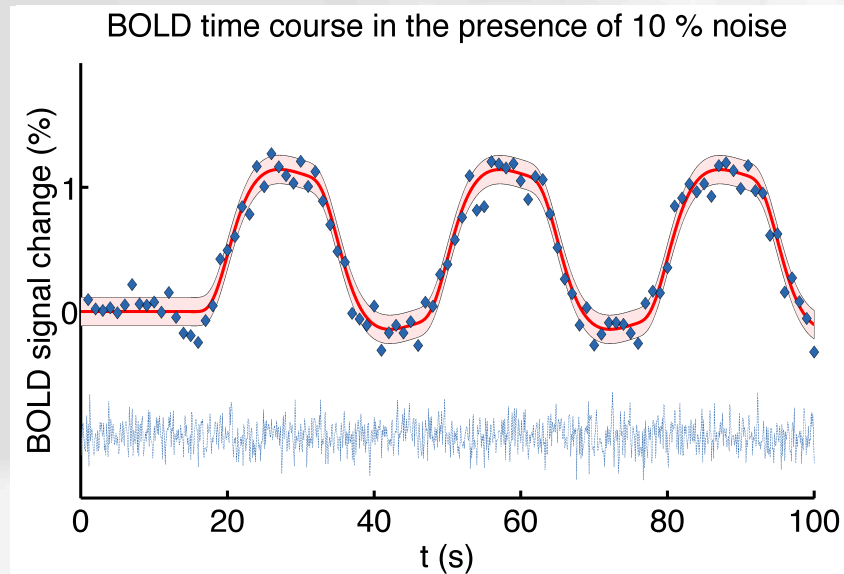
Blocks of 6 scans
with 7 sec TR



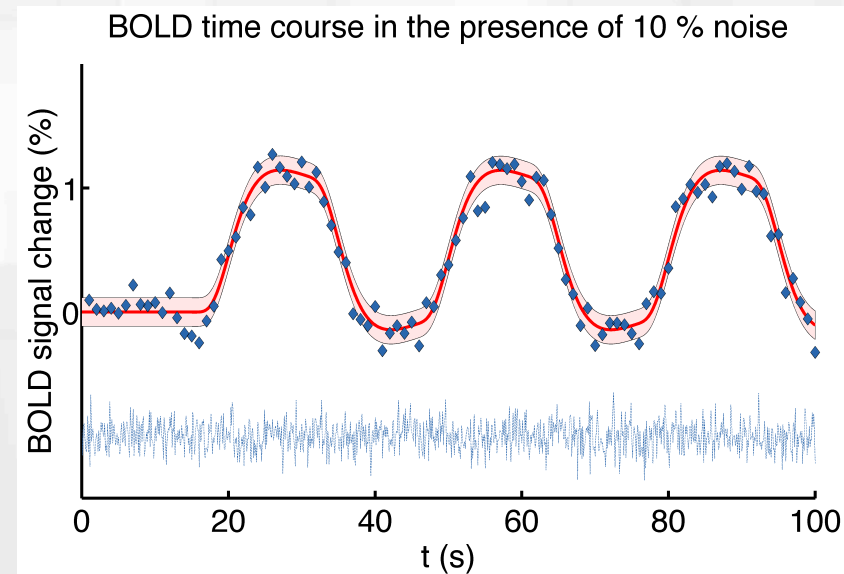
Question: Is there a change in the BOLD response between listening and rest?

The Goal of Preprocessing

Before

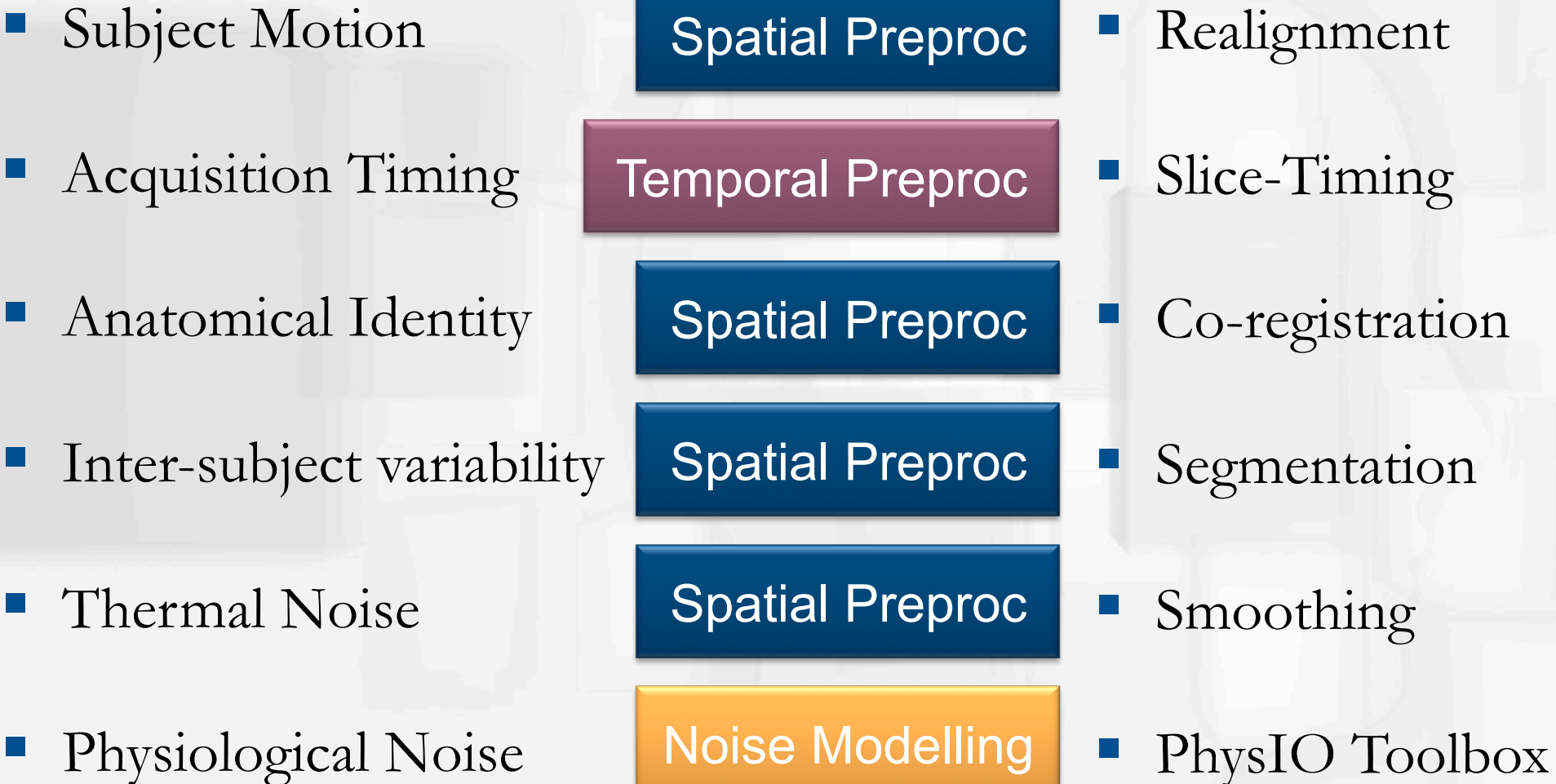


After

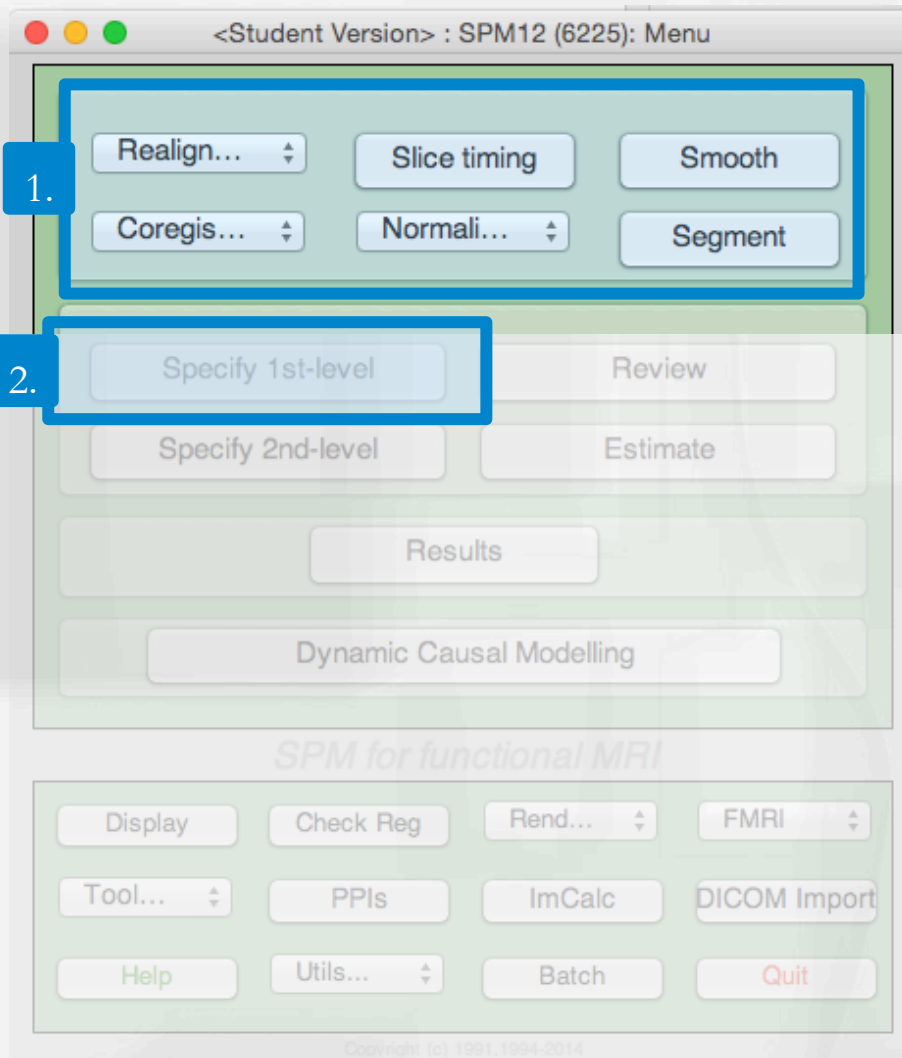


Preprocessing

Sources of Noise in fMRI



The SPM Graphical User Interface (GUI)



■ Preprocessing

- Realignment
- Slice-Timing Correction
- Co-registration
- Unified Segmentation & Normalisation
- Smoothing...

■ Noise Modelling

- Physiological Confound Regressors

Sources of Noise in fMRI

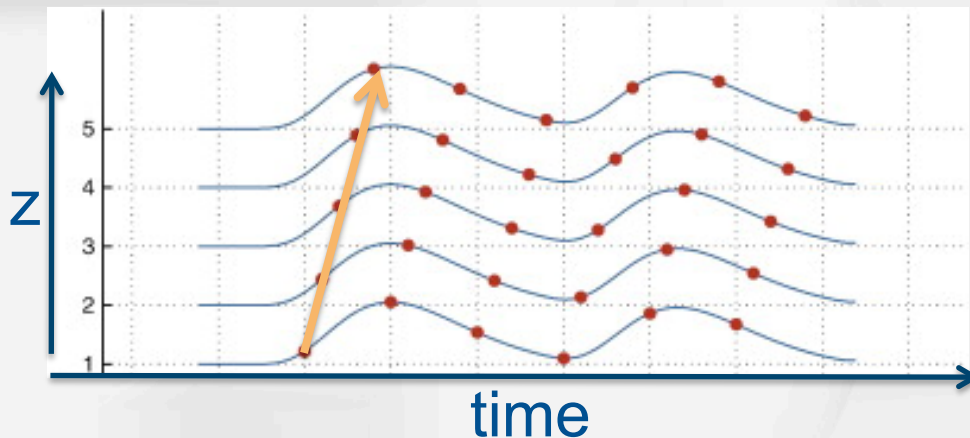
- Subject Motion
 - Acquisition Timing
 - Anatomical Identity
 - Inter-subject variability
 - Thermal Noise
 - Physiological Noise
- Temporal Preproc
- Realignment
 - Slice-Timing
 - Co-registration
 - Segmentation
 - Smoothing
 - PhysIO Toolbox

Slice-timing correction (STC)

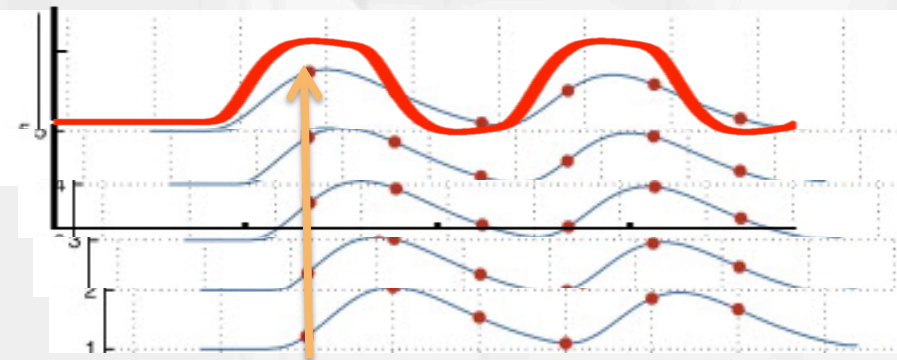


- Slices of 1 scan volume are not acquired simultaneously (60 ms per slice)
- Creates shifts of up to 1 volume repetition time (TR), i.e. several seconds
- Reduces sensitivity for time-locked effects (smaller correlation)

True 2D Acquisition

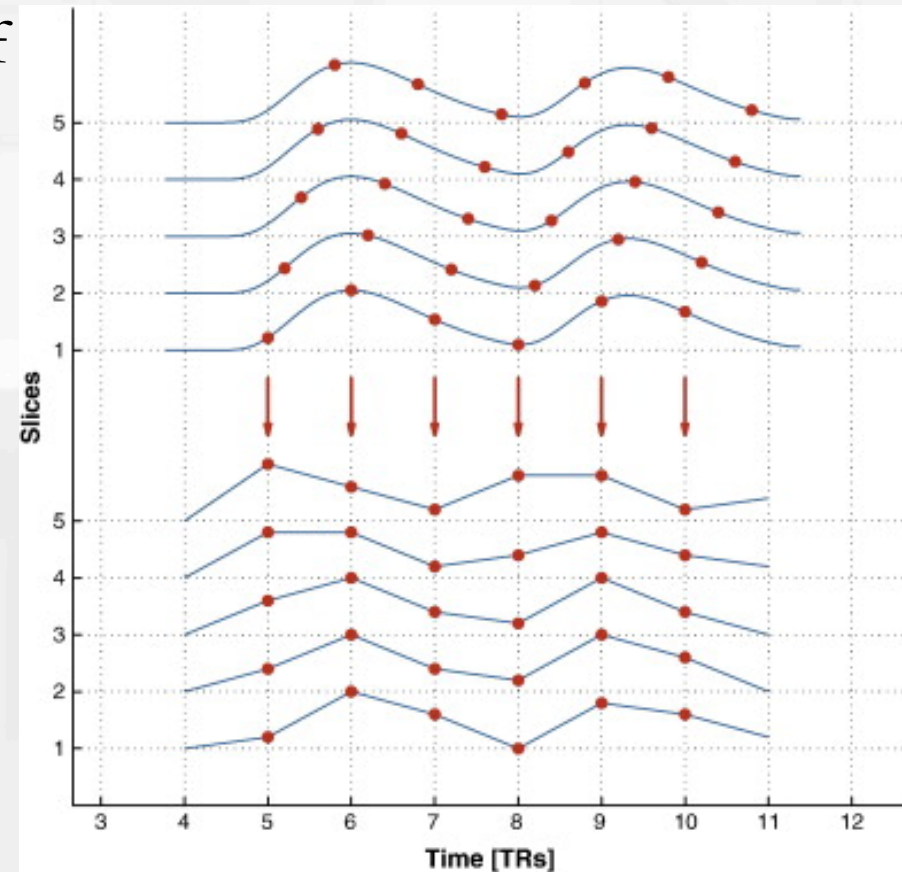


Same-Timepoint Assumption



Slice-timing correction (STC)

- Slice-timing correction: All voxel time series are aligned to acquisition time of 1 slice (e.g. centre slice)
- Missing data is interpolated via sinc-interpolation (band-limited signal)
- Before or after realignment?
 - before: dominant through-slice motion
 - after: dominant within-slice motion
- At all?
 - block design: for long TR (3s+) & short blocks (10s) improves estimates $> 5\%$
 - event-related: for normal TRs (2s+) improves estimates $> 5\%$



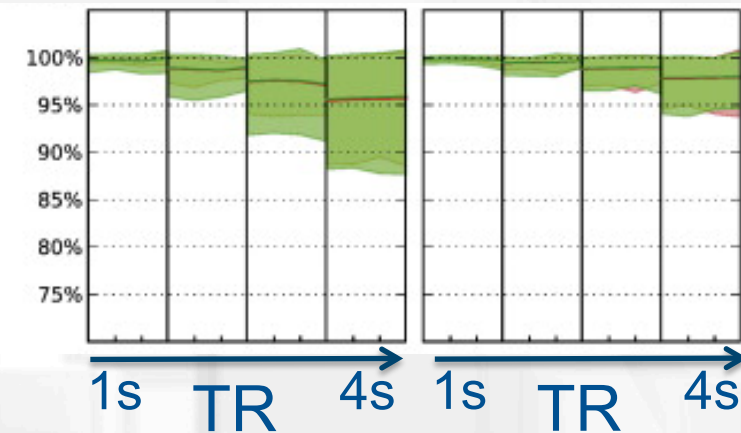
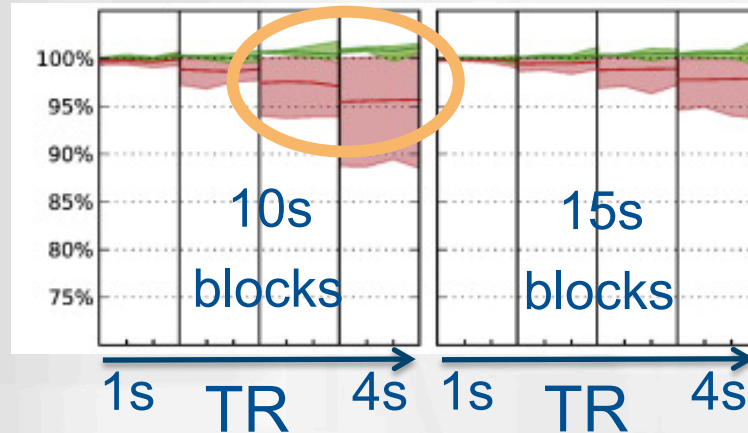
Sladky et al, NeuroImage 2011

Slice-timing correction (STC): Simulation

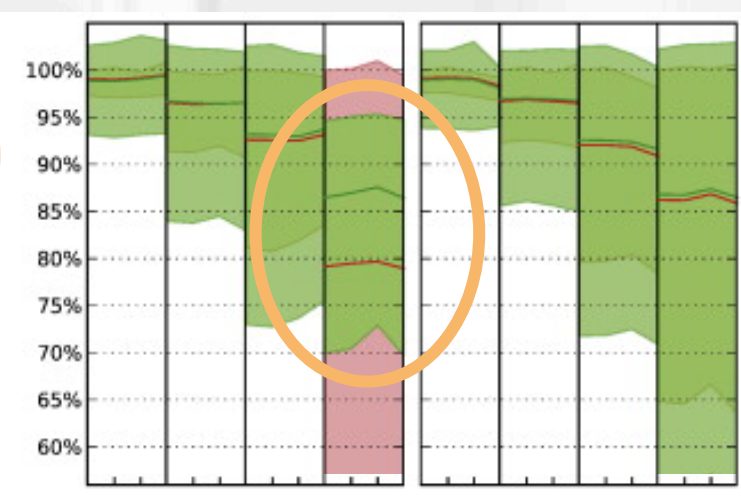
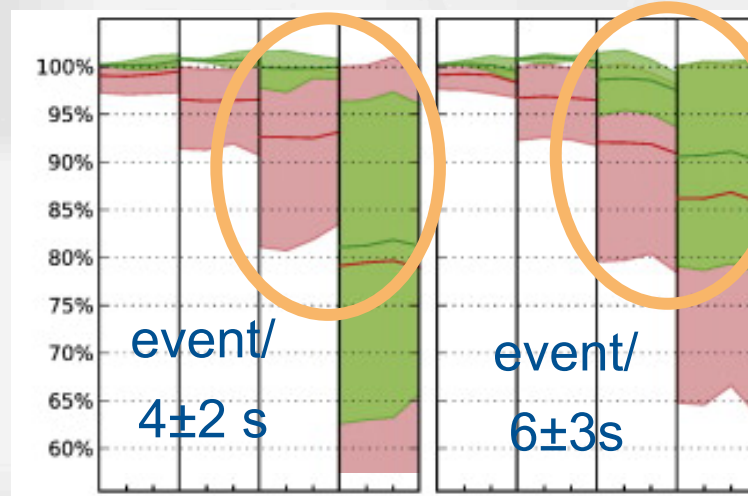
Slice-timing
Correction

Temporal-Derivative
Modelling

Block
Stimulation

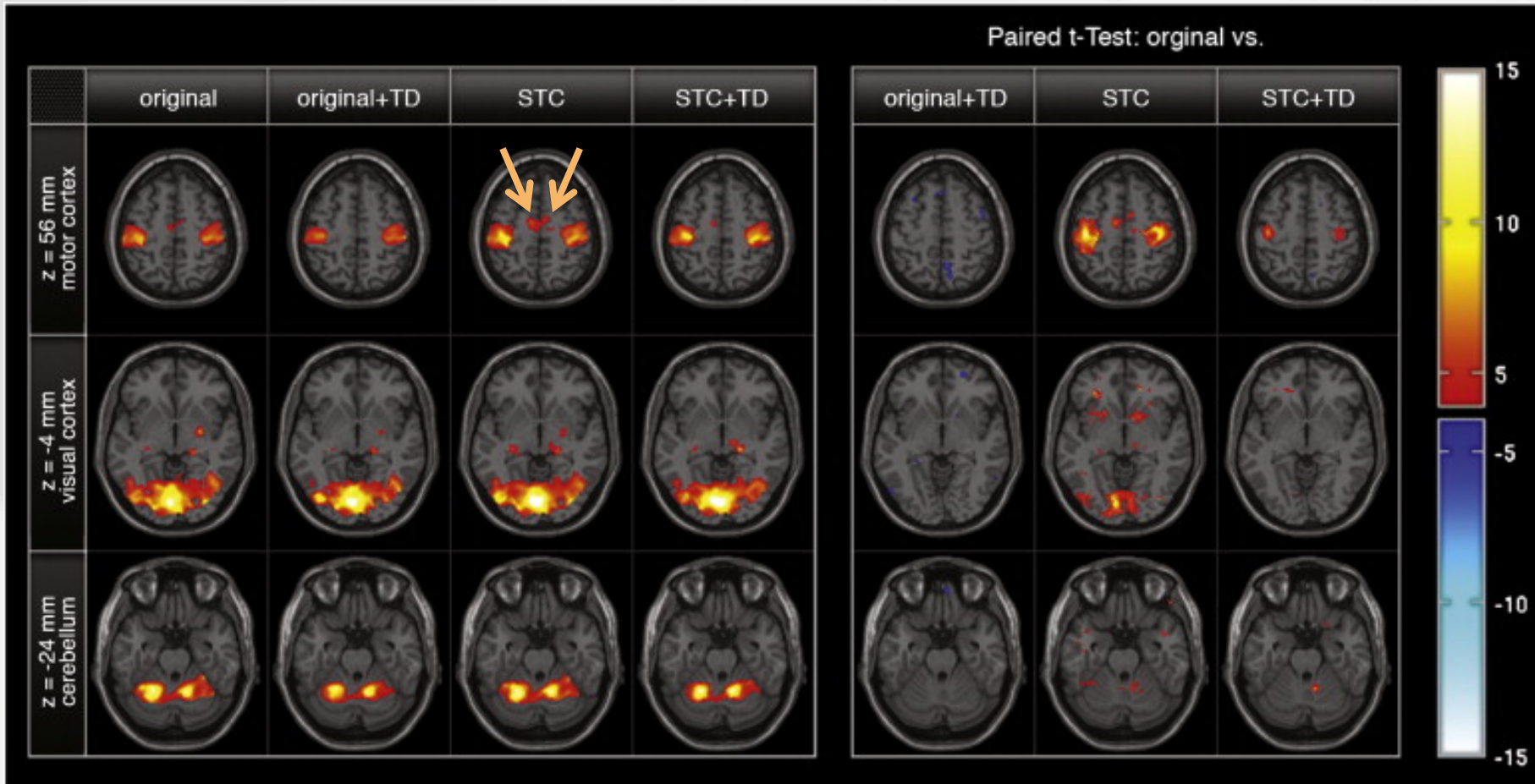


Event-Related
Stimulation



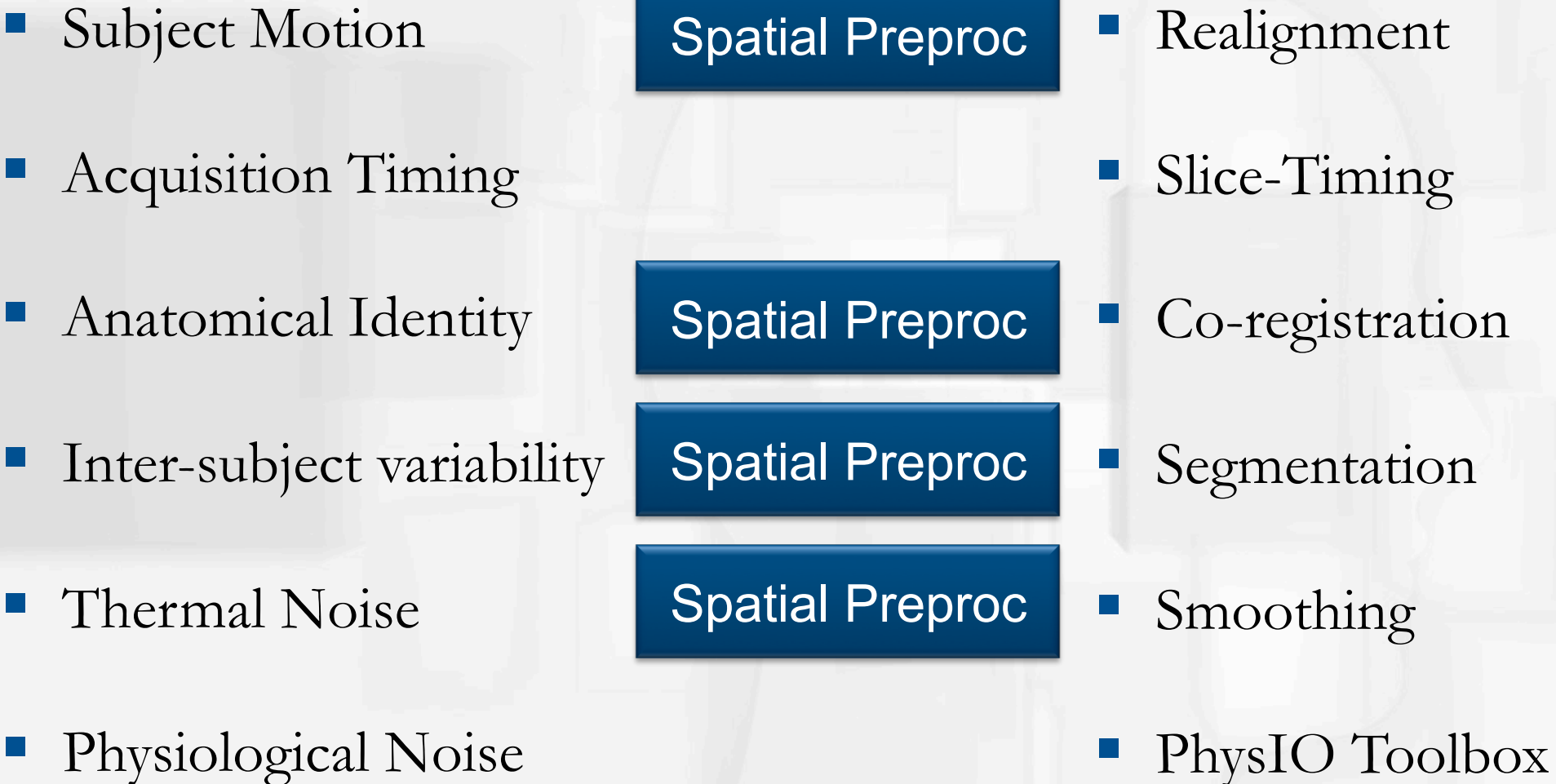
Sladky et al, NeuroImage 2011

Slice-timing correction (STC): Experiment



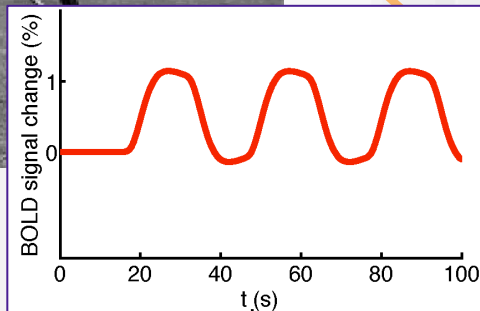
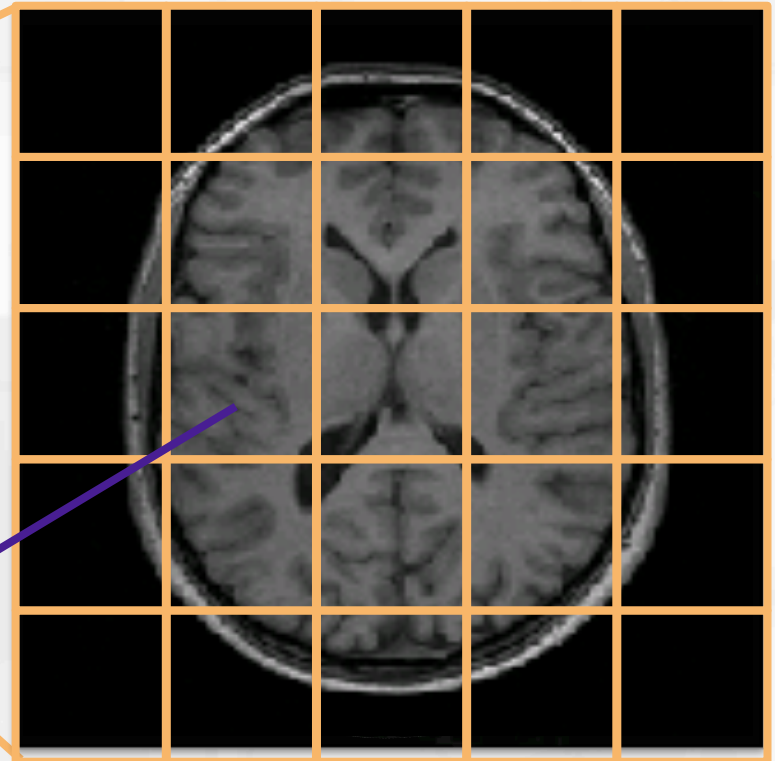
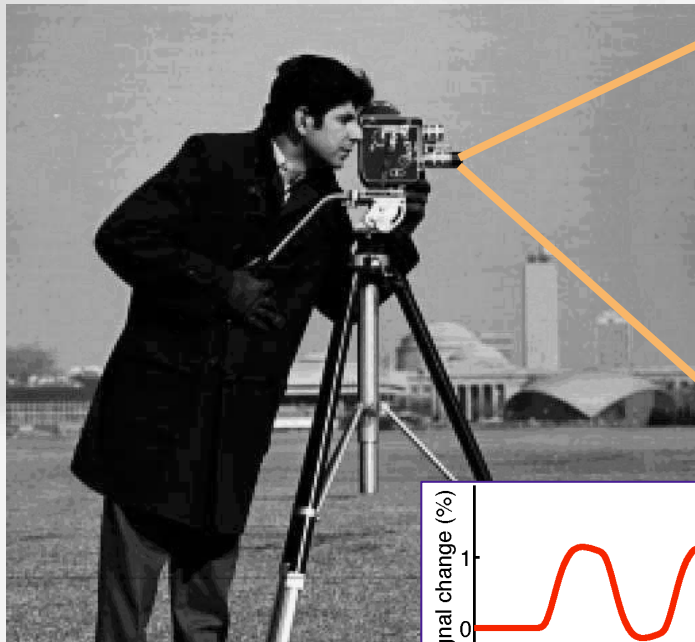
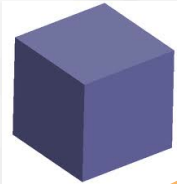
Sladky et al, NeuroImage 2011

Sources of Noise in fMRI

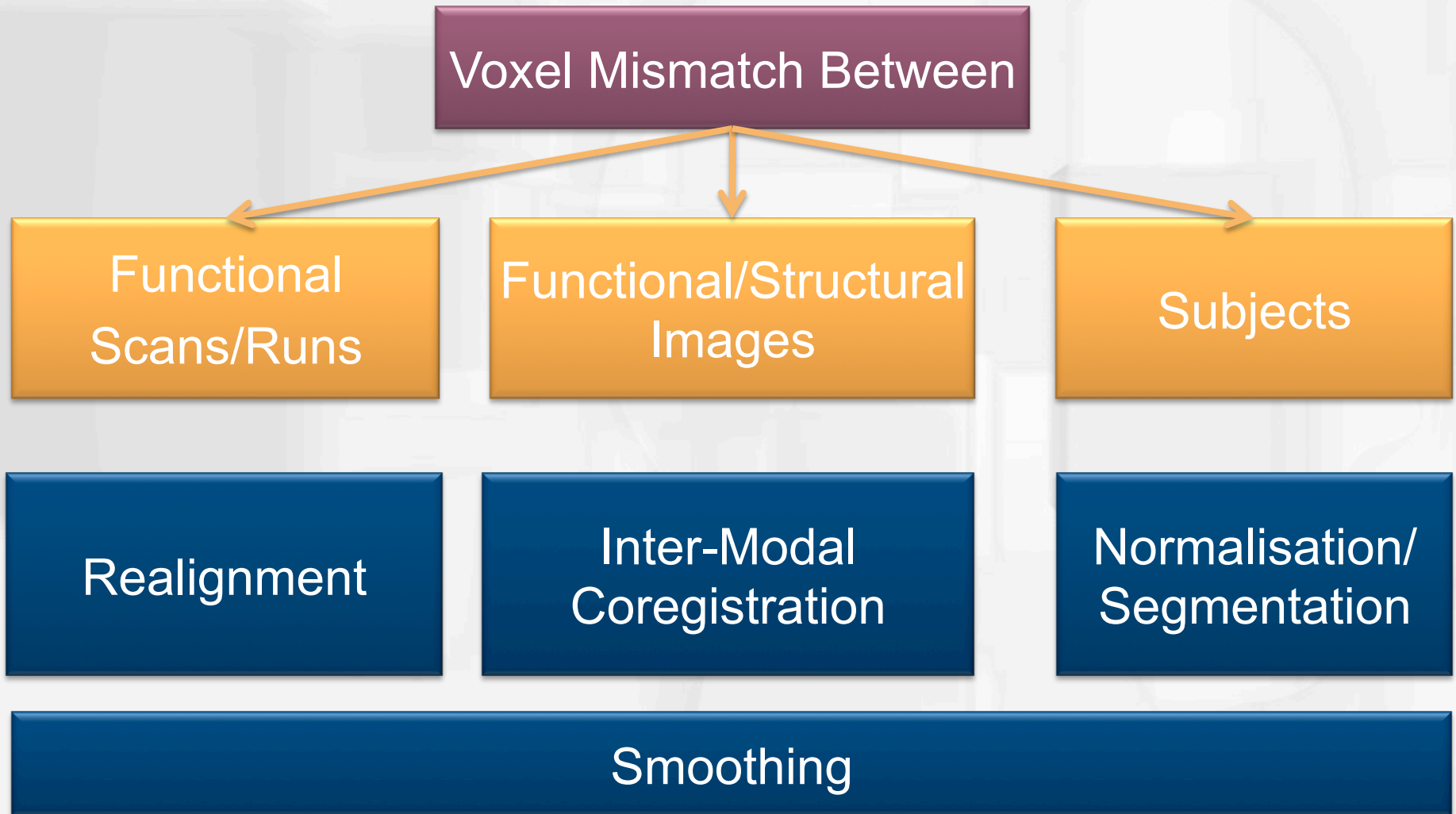


Finite Resolution and Voxel Identity

- voxel = volume element (3D pixel)



Spatial Preprocessing = Correcting Voxel Mismatches



Spatial Preprocessing

REALIGN

COREG

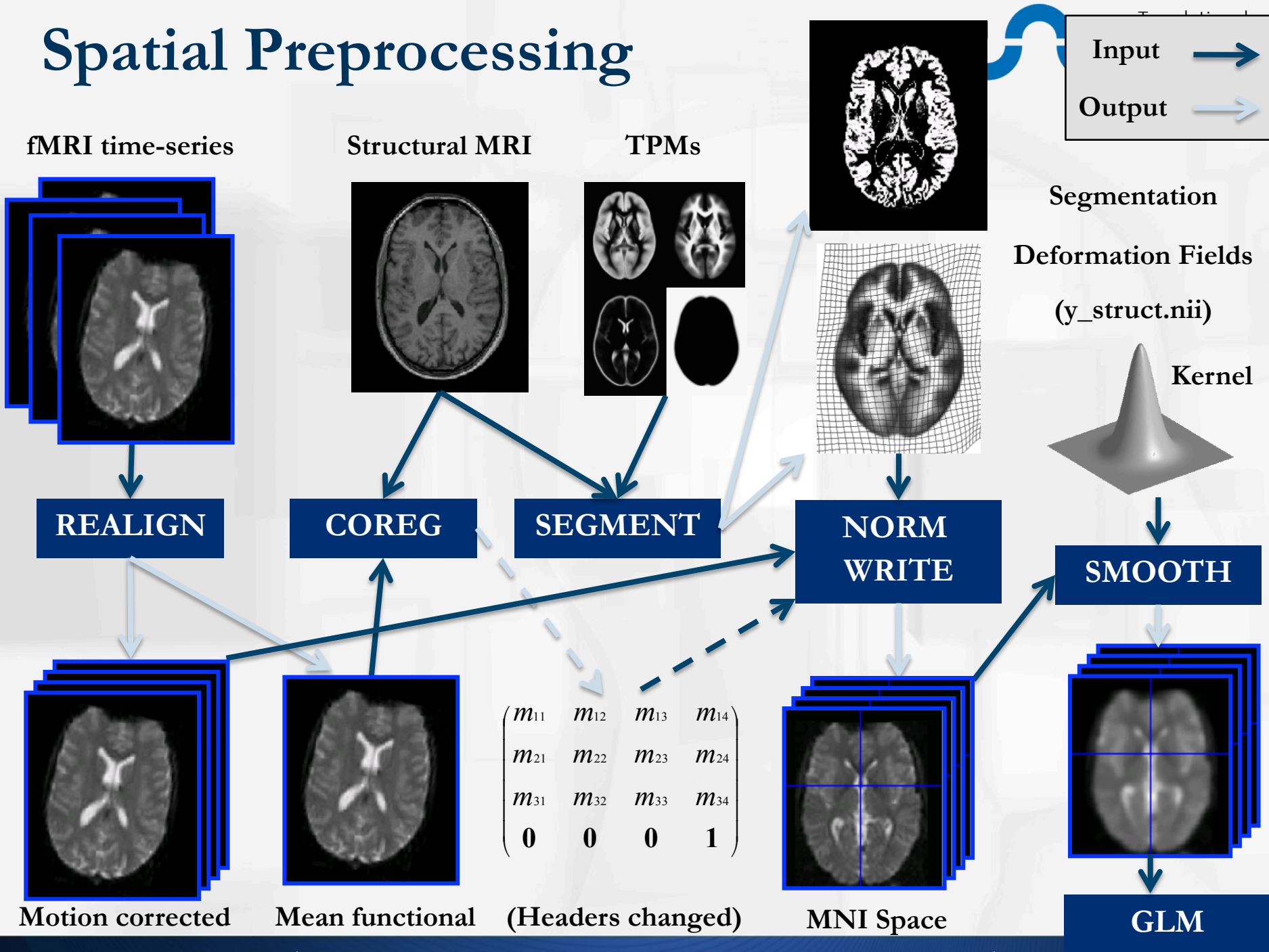
SEGMENT

**NORM
WRITE**

SMOOTH

GLM

Spatial Preprocessing

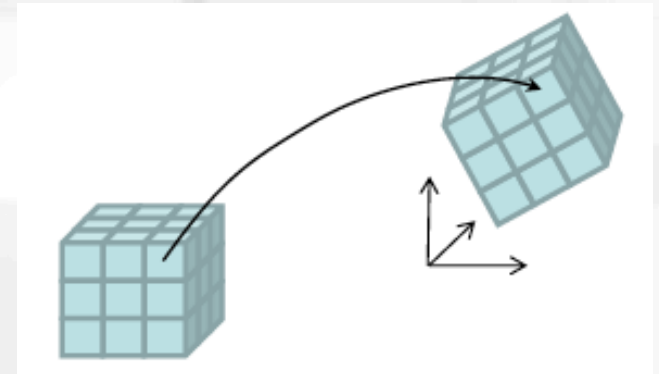


General Remarks on Image Registration

- Realignment, Co-Registration and Normalisation (via Unified Segmentation) are all *image registration methods*
- Goal: Manipulate one set of images to arrive in same coordinate system as a reference image
- Key ingredients for image registration
 - A. Voxel-to-world mapping
 - B. Transformation
 - C. Similarity Measure
 - D. Optimisation
 - E. Interpolation

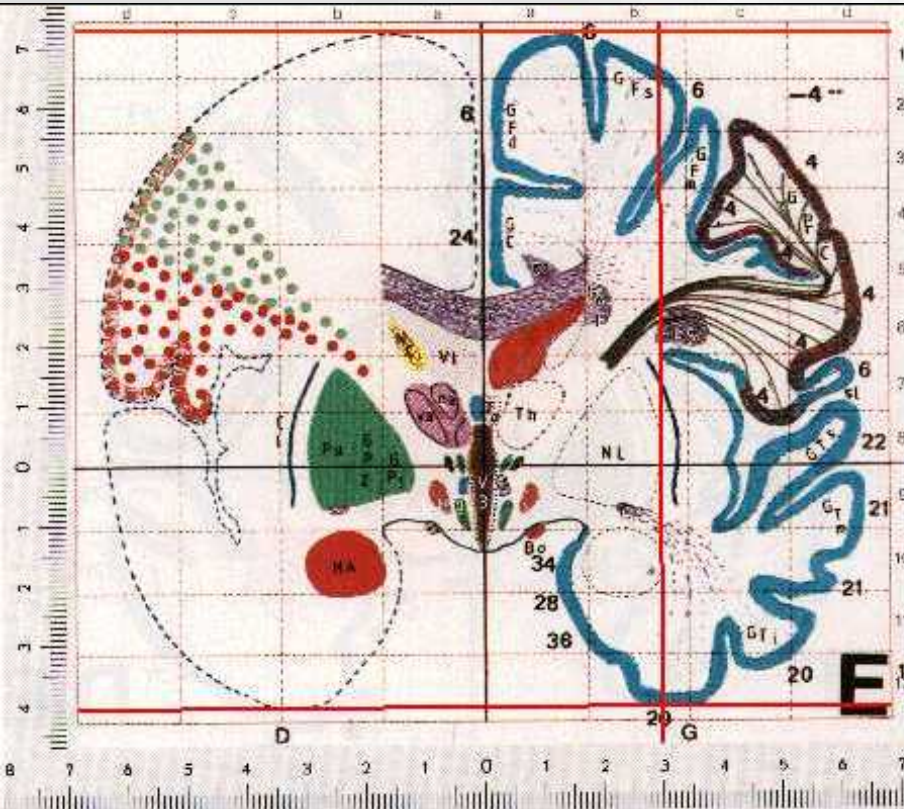
A. Voxel-to-World Mapping

- 3D images are made up of voxels.
- Voxel intensities are stored on disk as lists of numbers.
- Meta-information about the data:
 - image dimensions
 - conversion from list to 3D array
 - “voxel-to-world mapping”
 - Spatial transformation that maps
 - from: data coordinates (voxel column i , row j , slice k)
 - to: a real-world position (x, y, z mm) in a coordinate system e.g.:
 - Scanner coordinates
 - T&T/MNI coordinates

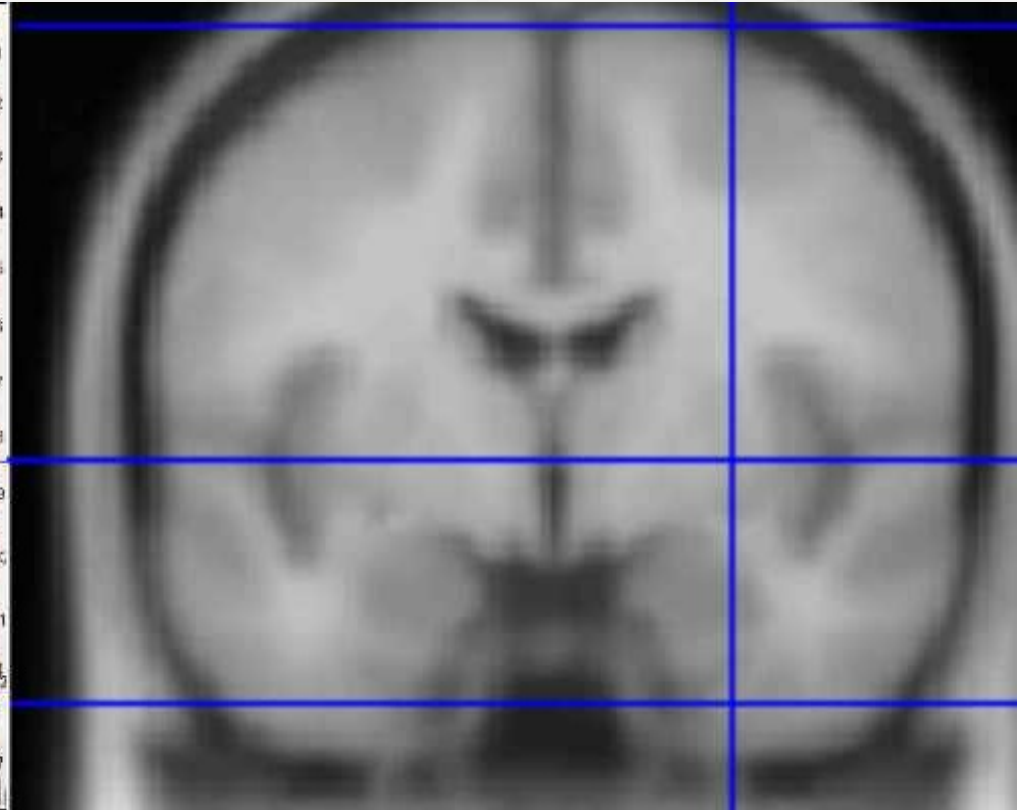


A. Voxel-to-World: Standard Spaces

The Talairach Atlas



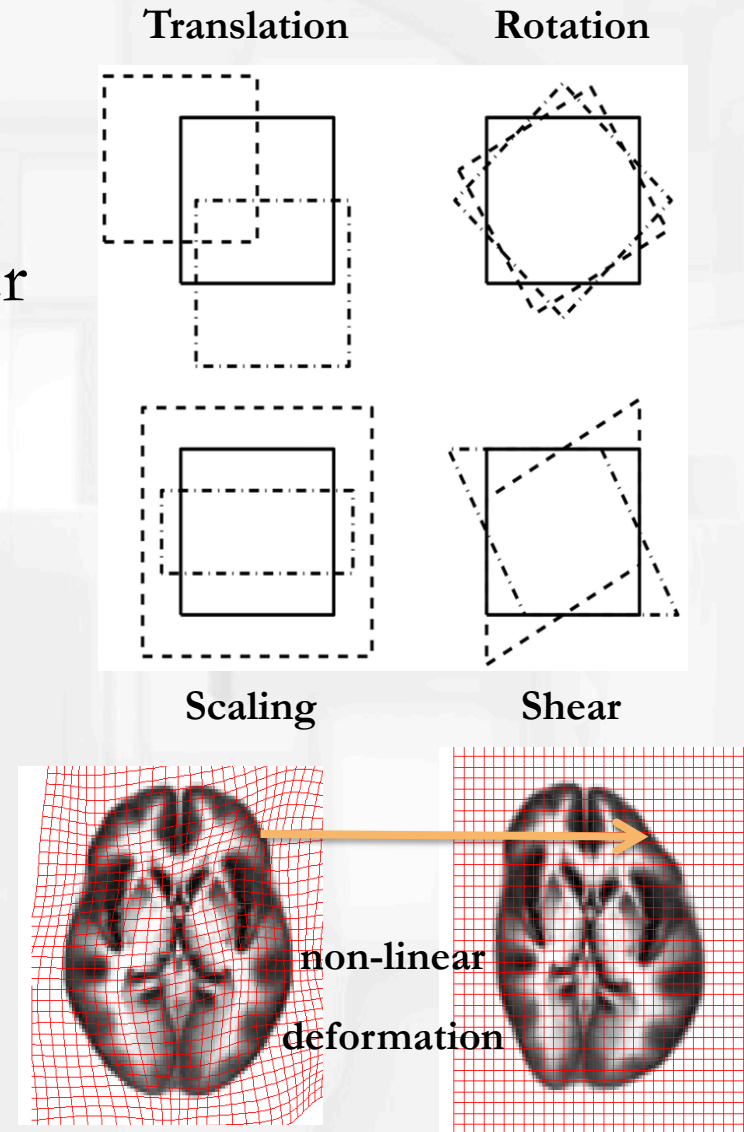
The MNI/ICBM AVG152 Template



The MNI template follows the convention of T&T, but doesn't match the particular brain
Recommended reading: <http://imaging.mrc-cbu.cam.ac.uk/imaging/MniTalairach>

B. Transformations

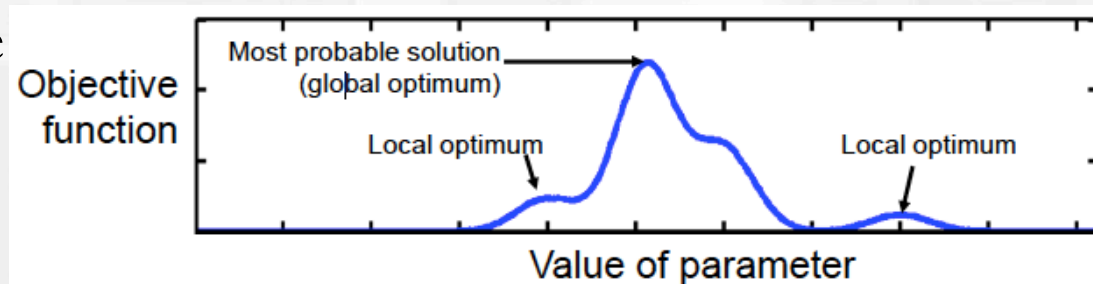
- Transformations describe the mapping of all image voxels from one coordinate system into another
- Types of transformations
 - rigid body = translation + rotation
 - affine = rigid body + scaling + shear
 - non-linear = any mapping
 - (x,y,z) to new values (x',y',z')
 - described by deformation fields



C. Similarity Measures & D. Optimisation

- Similarity measure summarizes resemblance of (transformed) image and reference into 1 number

- mean-squared difference
- correlation-coefficient
- mutual information



- Automatic image registration uses an optimisation algorithm to maximise/minimise an “objective function”
 - Similarity measure is part of objective function
 - Algorithm searches for transformation that maximises similarity of transformed image to reference
 - Also includes constraints on allowed transformations (priors)

Spatial Preprocessing & Image Registration Contents

B. Allowed Transformations

Rigid-Body

REALIGN

Affine

COREG

Non-linear

SEGMENT

**NORM
WRITE**

C. Similarity Measure

Mean-squared
Difference

Mutual
Information

Tissue Class
Probability

D. Optimisation

Exact Linearized
Solution

Conjugate Direction
Line Search

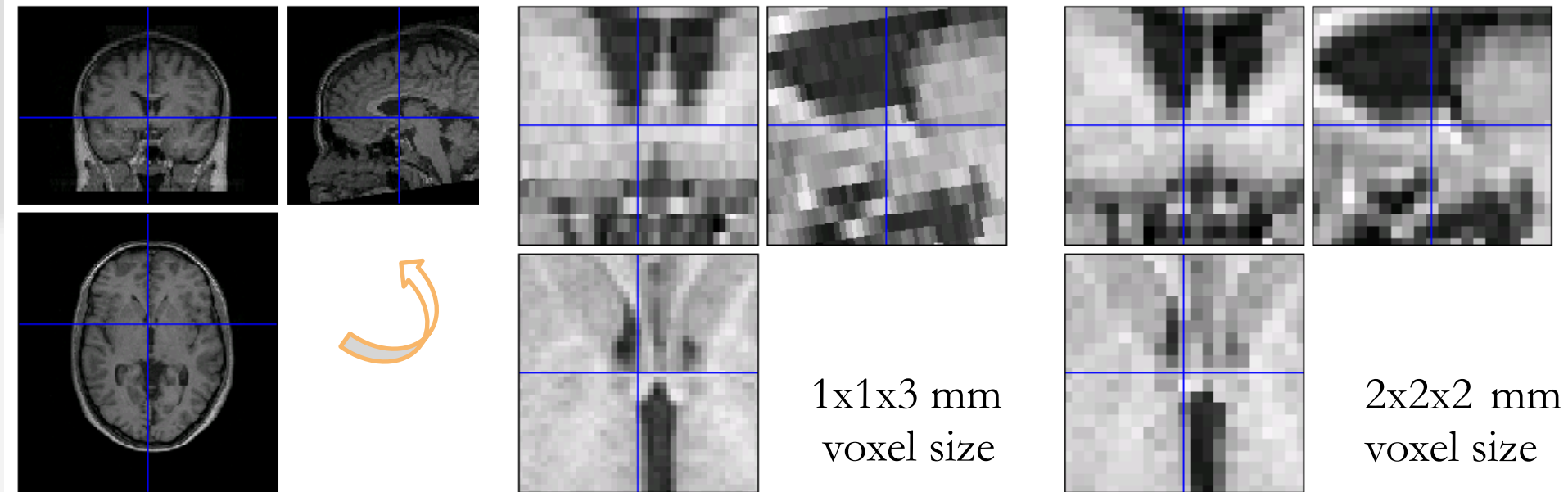
Iterated Conditional Modes
(EM/Levenberg-Marquardt)

E. Reslicing/Interpolation

- Finally, images have to be saved as voxel intensity list on disk again
- After applying transformation parameters, data is re-sampled onto same grid of voxels as reference image

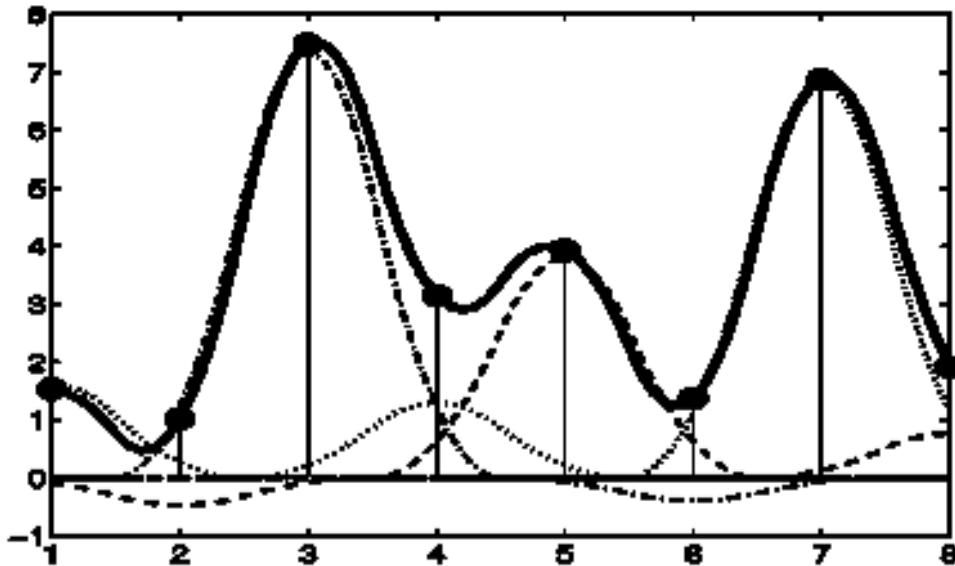
Reoriented

Resliced

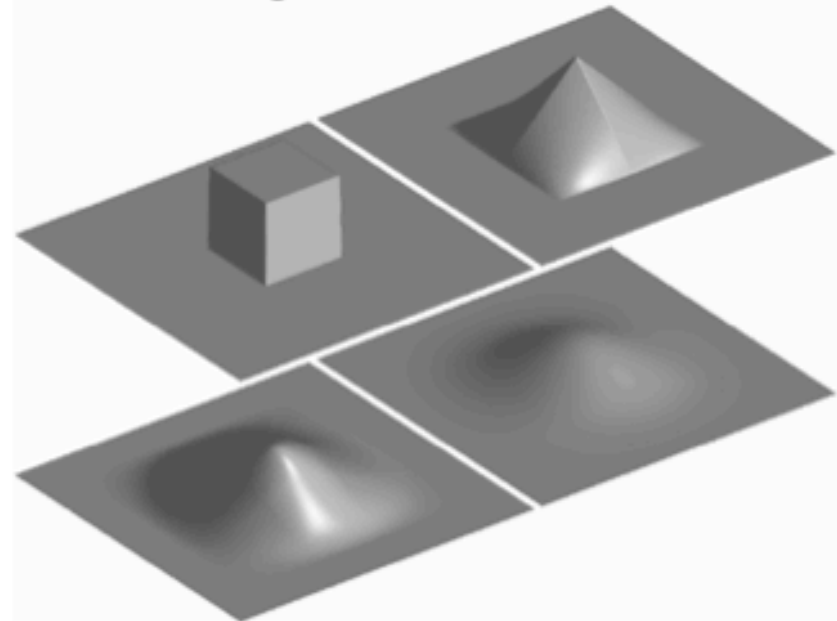


E. B-spline Interpolation

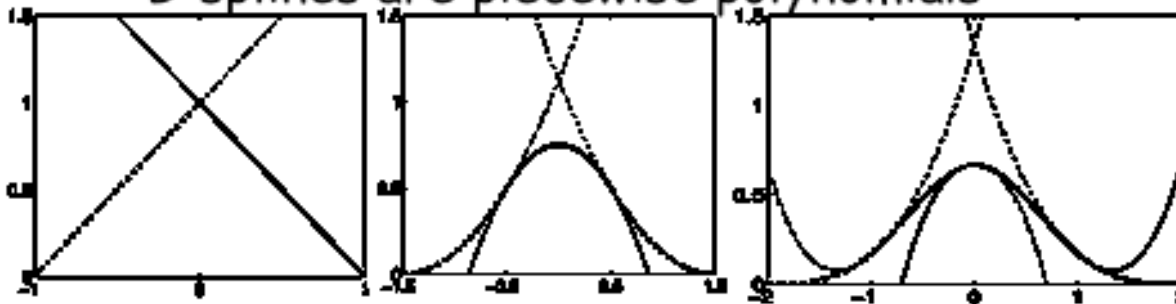
A continuous function is represented by a linear combination of basis functions



2D B-spline basis functions of degrees 0, 1, 2 and 3

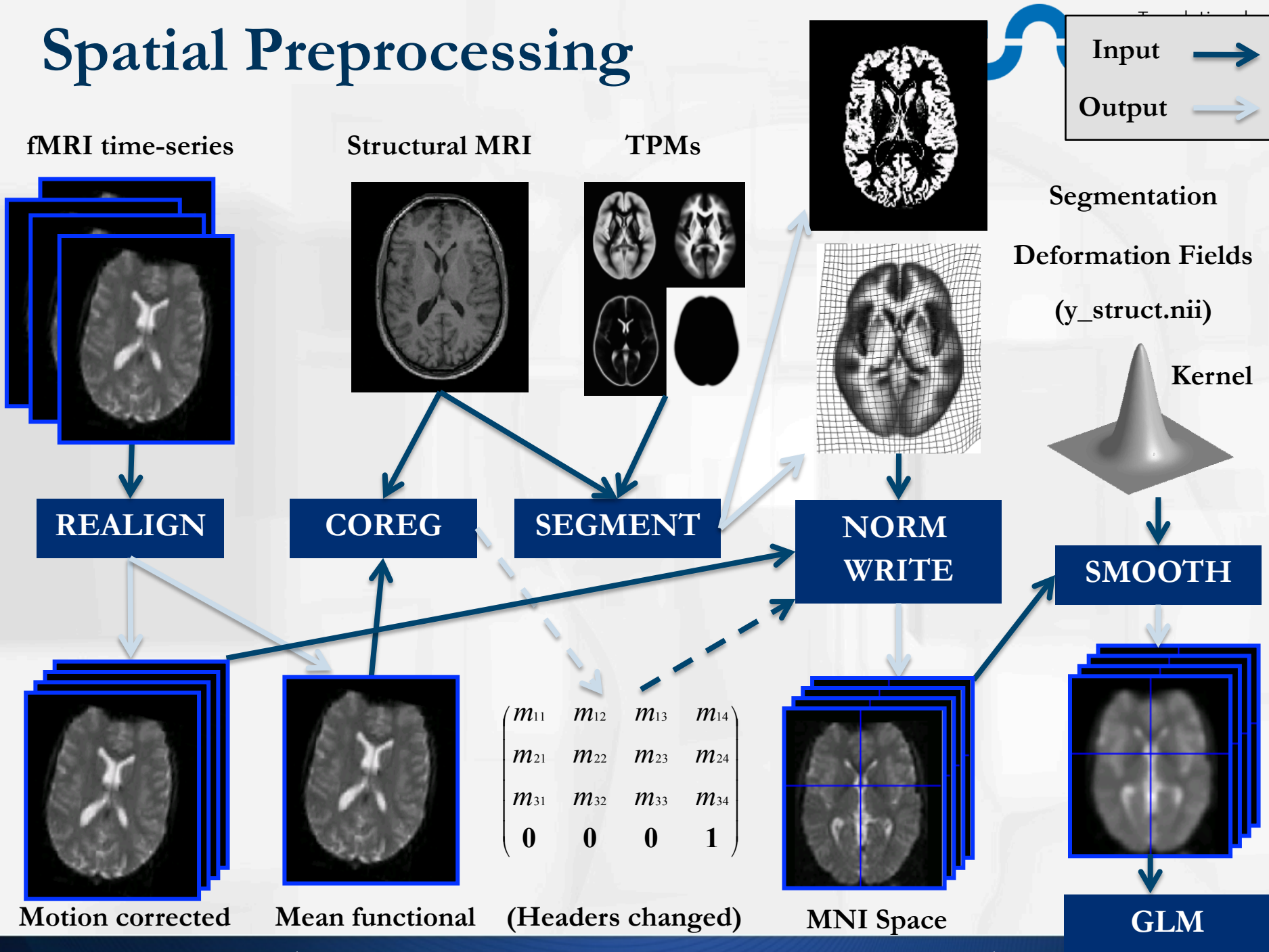


B-splines are piecewise polynomials



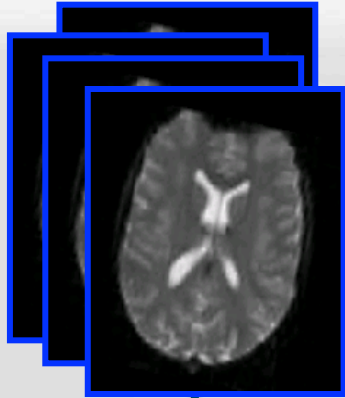
Nearest neighbour and trilinear interpolation are the same as B-spline interpolation with degrees 0 and 1.

Spatial Preprocessing

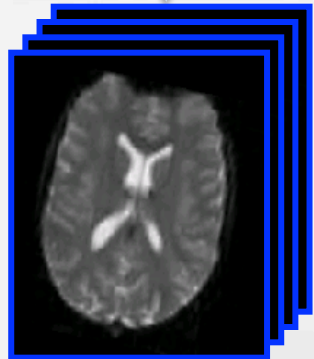


Realignment

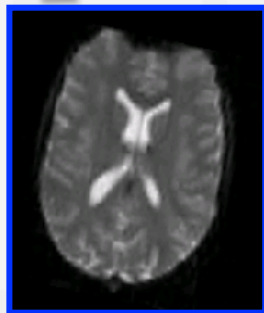
fMRI time-series



REALIGN



Motion corrected



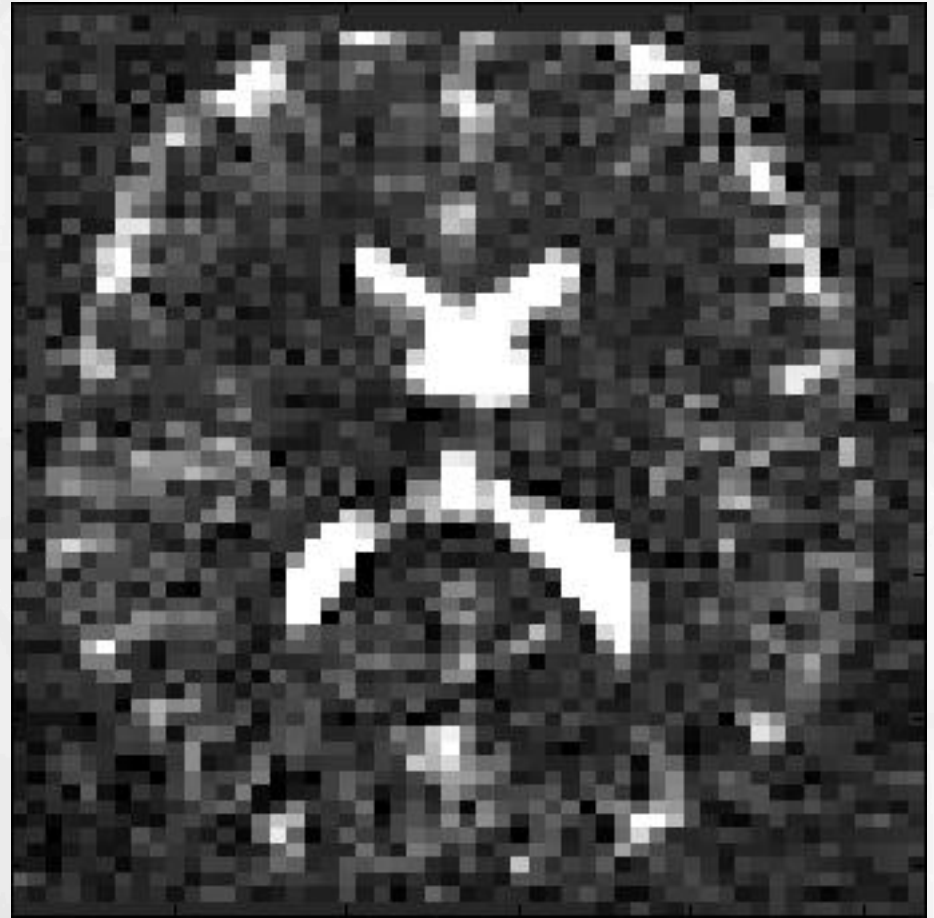
Mean functional

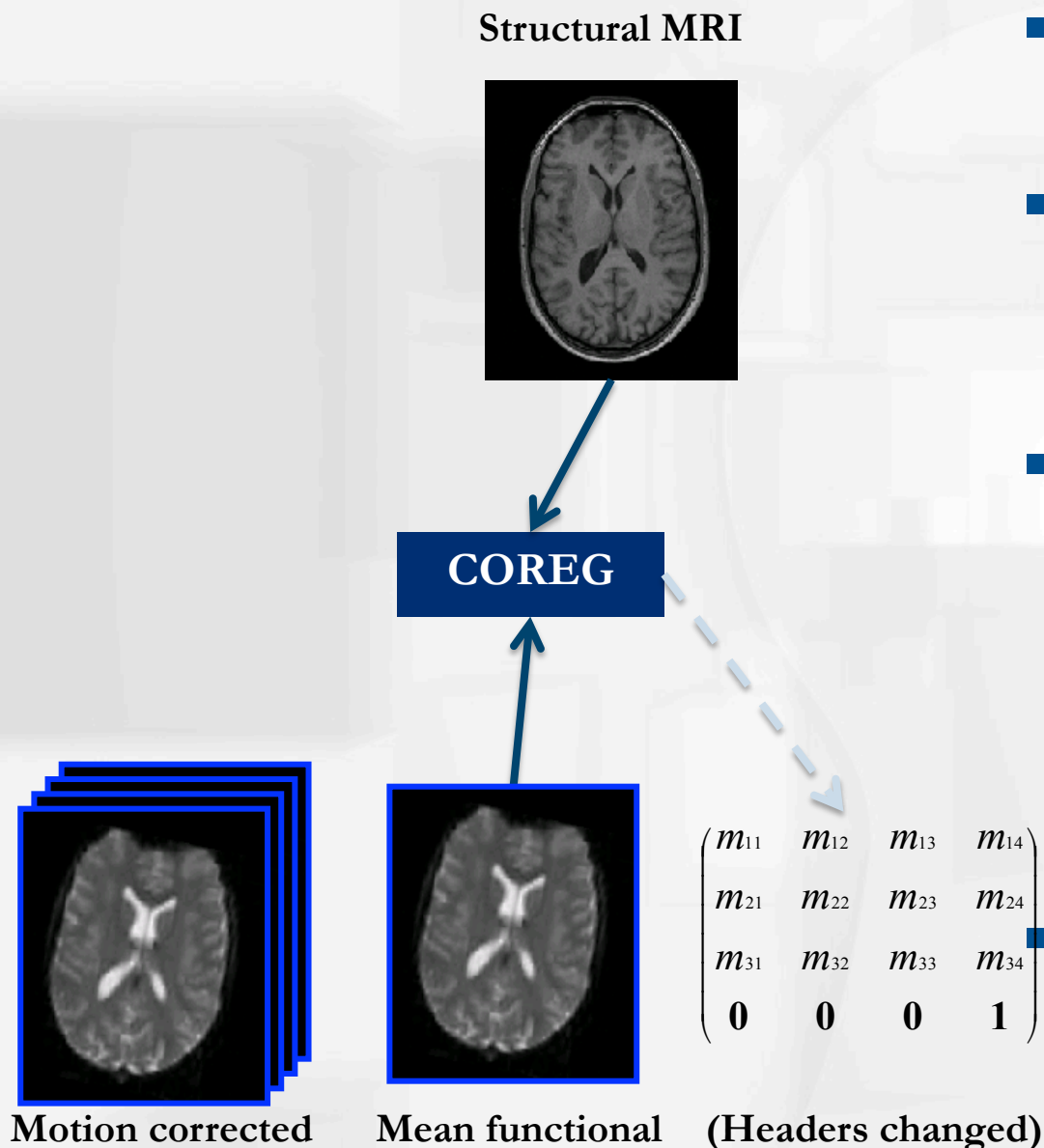
- Aligns all volumes of all runs spatially
- Rigid-body transformation: three translations, three rotations
- Objective function: mean squared error of corresponding voxel intensities
- Voxel correspondence via Interpolation

Realignment Output: Parameters



fMRI Run after Realignment

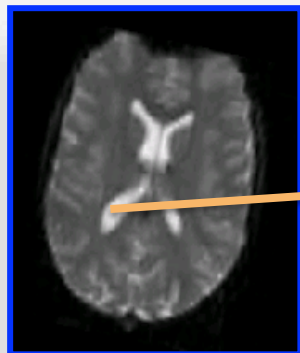




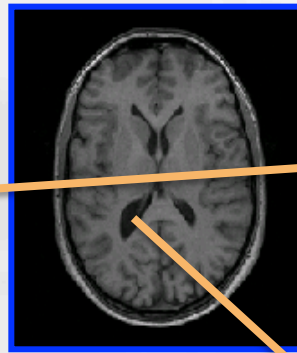
- Aligns structural image to mean functional image
- Affine transformation: translations, rotations, scaling, shearing
- Objective function: mutual information, since contrast different
 - Optimisation via Powell's method: conjugate directions, line search along parameters

Typically only transformation matrix (“header”) changed (no reslicing)

Co-Registration: Output

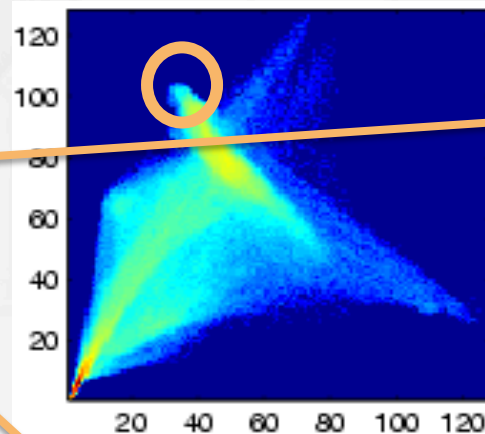


Mean functional

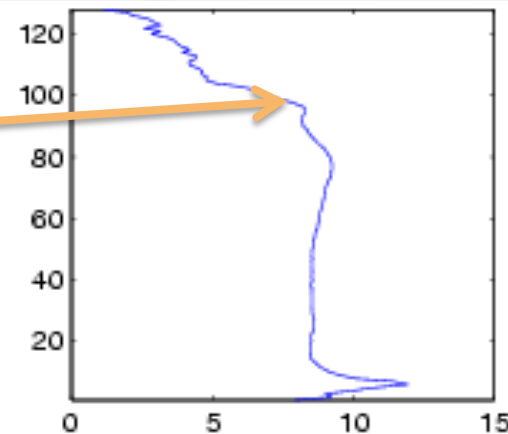


Anatomical MRI

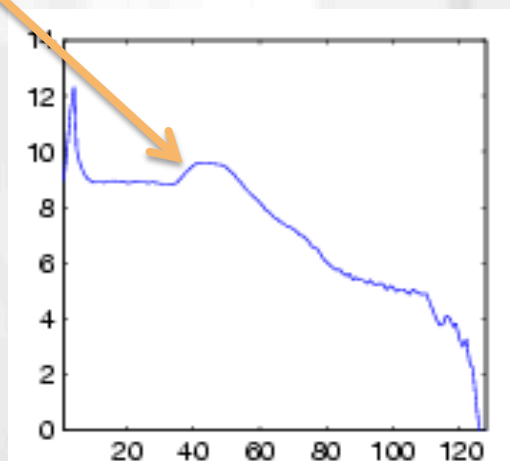
Joint Histogram



Marginal Histogram



- Joint and marginal Histogram
 - Quantify how well one image predicts the other
 - how much shared information
 - Joint probability distribution estimated from joint histogram



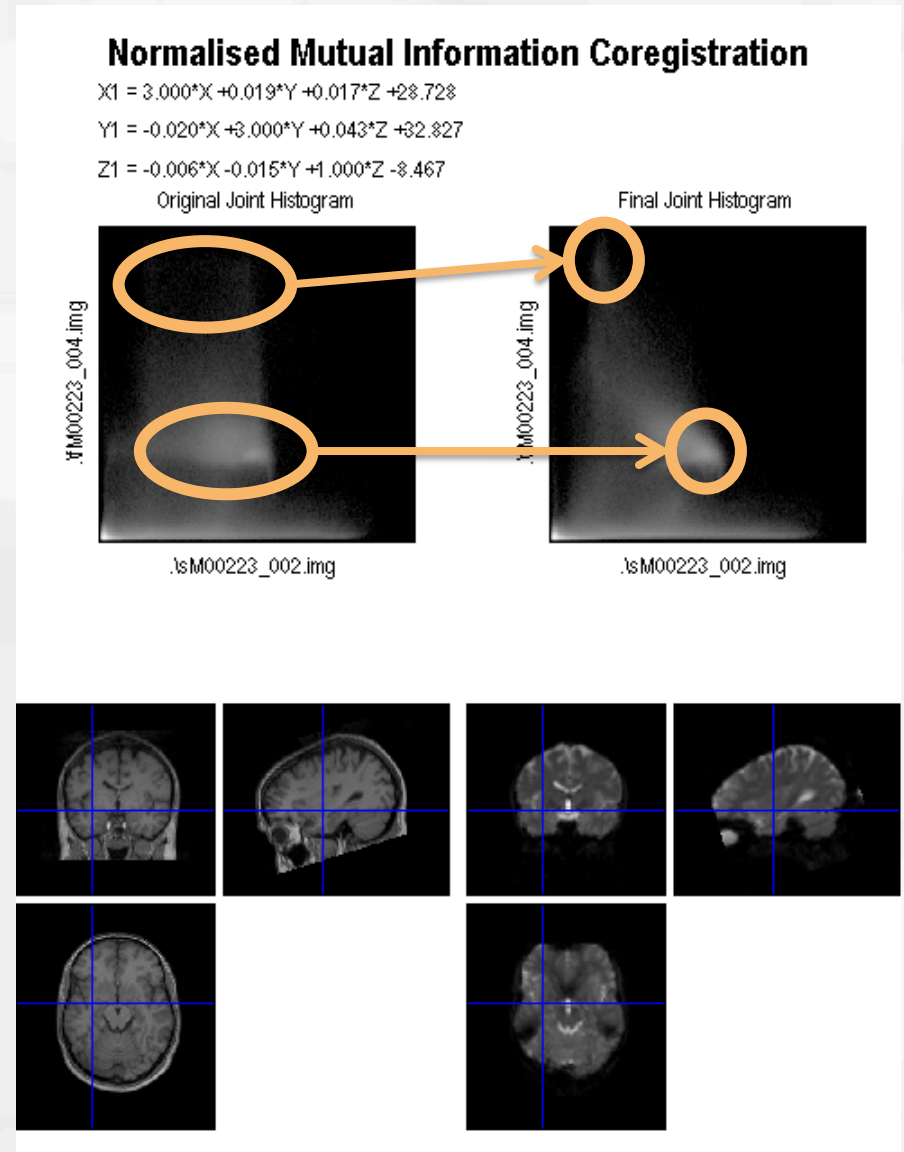
intensity bins
structural

intensity bins
functional

Joint Histogram:
 $h(i_f, i_s)$

Count of voxels who
have intensity i_f in
functional and i_s in
structural image

- Voxels of same tissue identity should have same intensity in an MR-contrast
- In a second MR contrast, this intensity might be different, but still the same among all voxels of the same tissue type
- Therefore, aligned voxels in 2 images induce crisp peaks in joint histogram



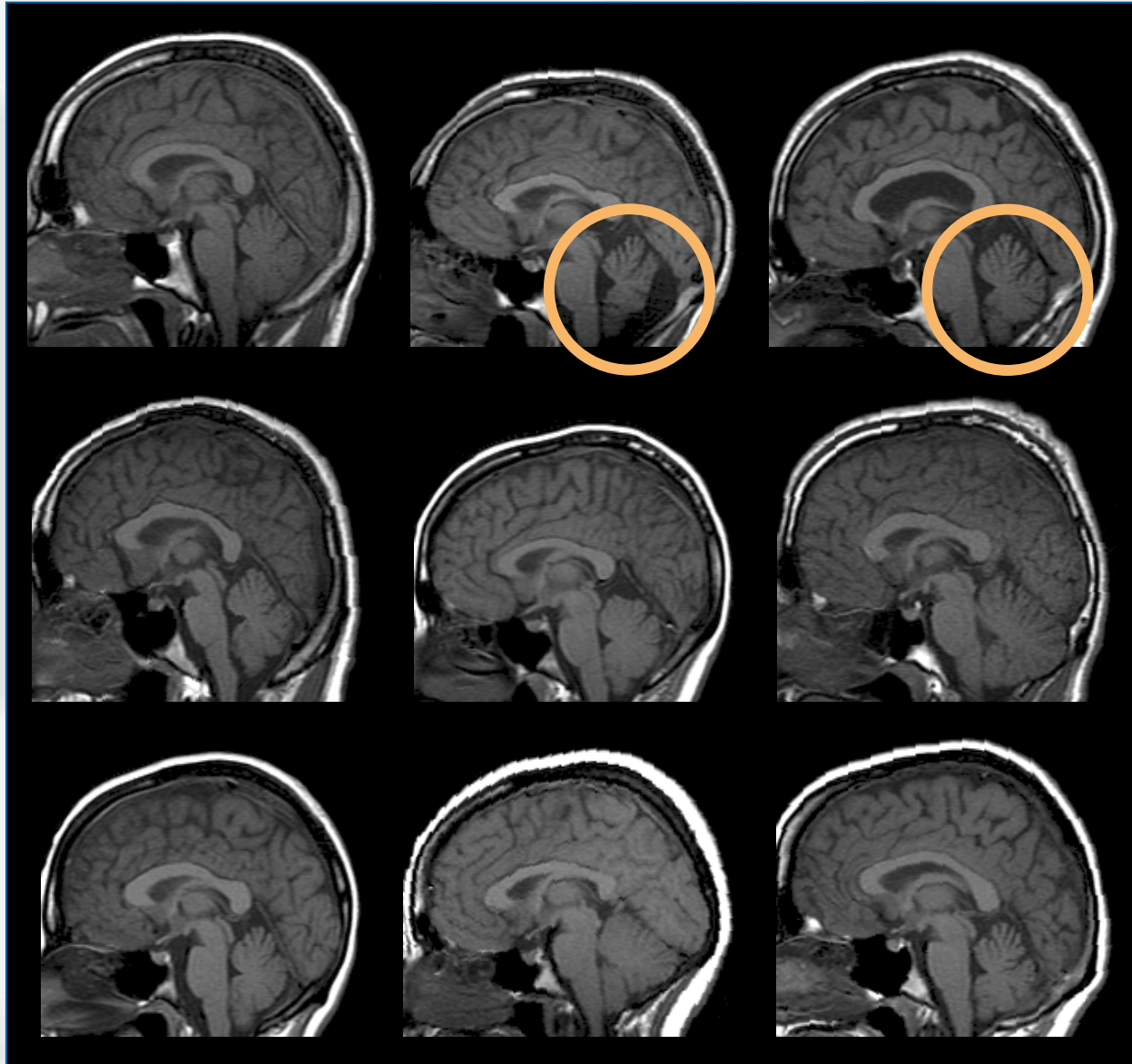
Sources of Noise in fMRI

- Subject Motion
- Acquisition Timing
- Anatomical Identity
- Inter-subject variability
- Thermal Noise
- Physiological Noise

Spatial Preproc

- Realignment
- Slice-Timing
- Co-registration
- Segmentation
- Smoothing
- PhysIO Toolbox

Inter-subject Variability

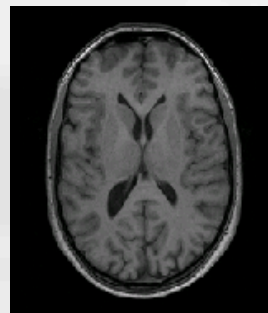


- Reasons

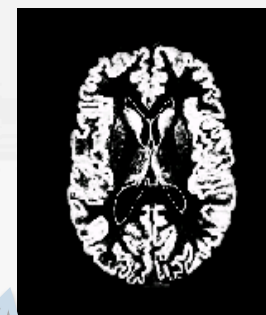
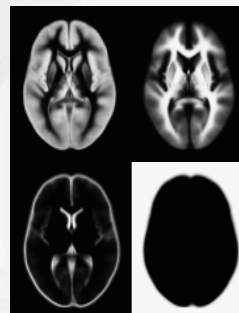
- Inter-Subject Averaging
 - Increase sensitivity with more subjects (fixed-effects)
 - Generalise findings to population as a whole (mixed-effects)
- Ensure Comparability between studies (alignment to standard space)
 - Talairach and Tournoux (T&T) convention using the Montreal Neurological Institute (MNI) space
 - Templates from 152/305 subjects

Unified Segmentation

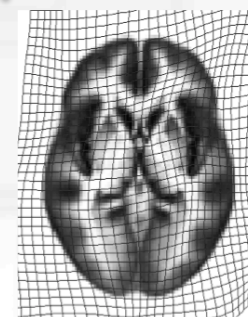
Structural MRI



TPMs



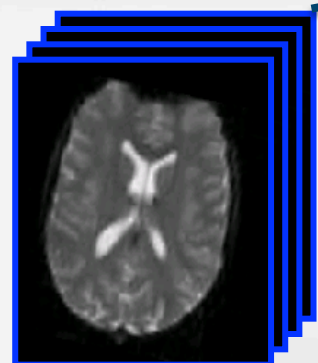
Segmentation



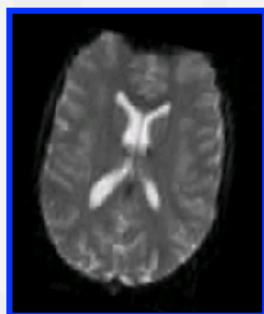
Deformation Fields
(y_struct.nii)

SEGMENT

**NORM
WRITE**



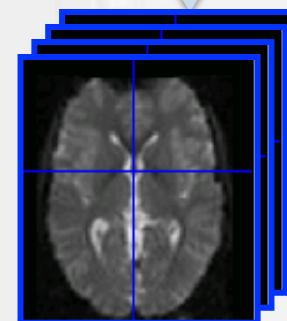
Motion corrected



Mean functional

$$\begin{pmatrix} m_{11} & m_{12} & m_{13} & m_{14} \\ m_{21} & m_{22} & m_{23} & m_{24} \\ m_{31} & m_{32} & m_{33} & m_{34} \\ 0 & 0 & 0 & 1 \end{pmatrix}$$

(Headers changed)



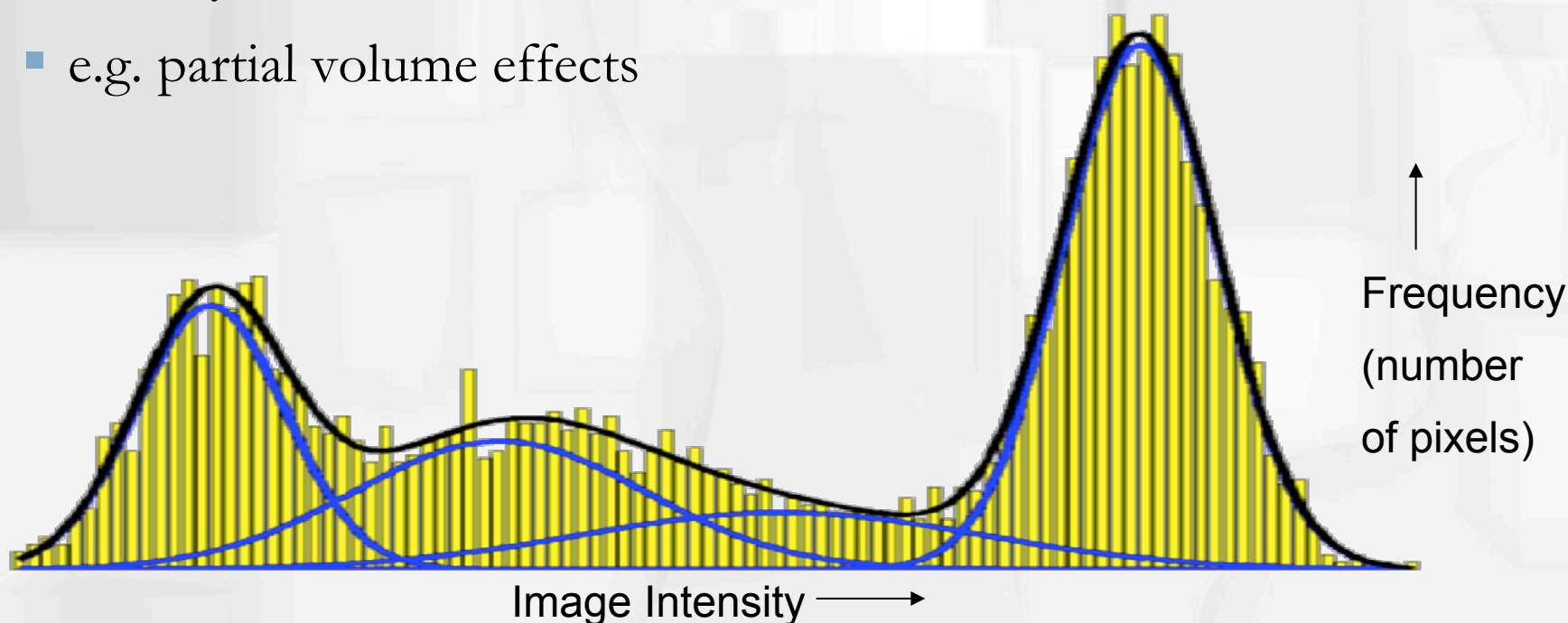
MNI Space

Normalisation via Unified Segmentation

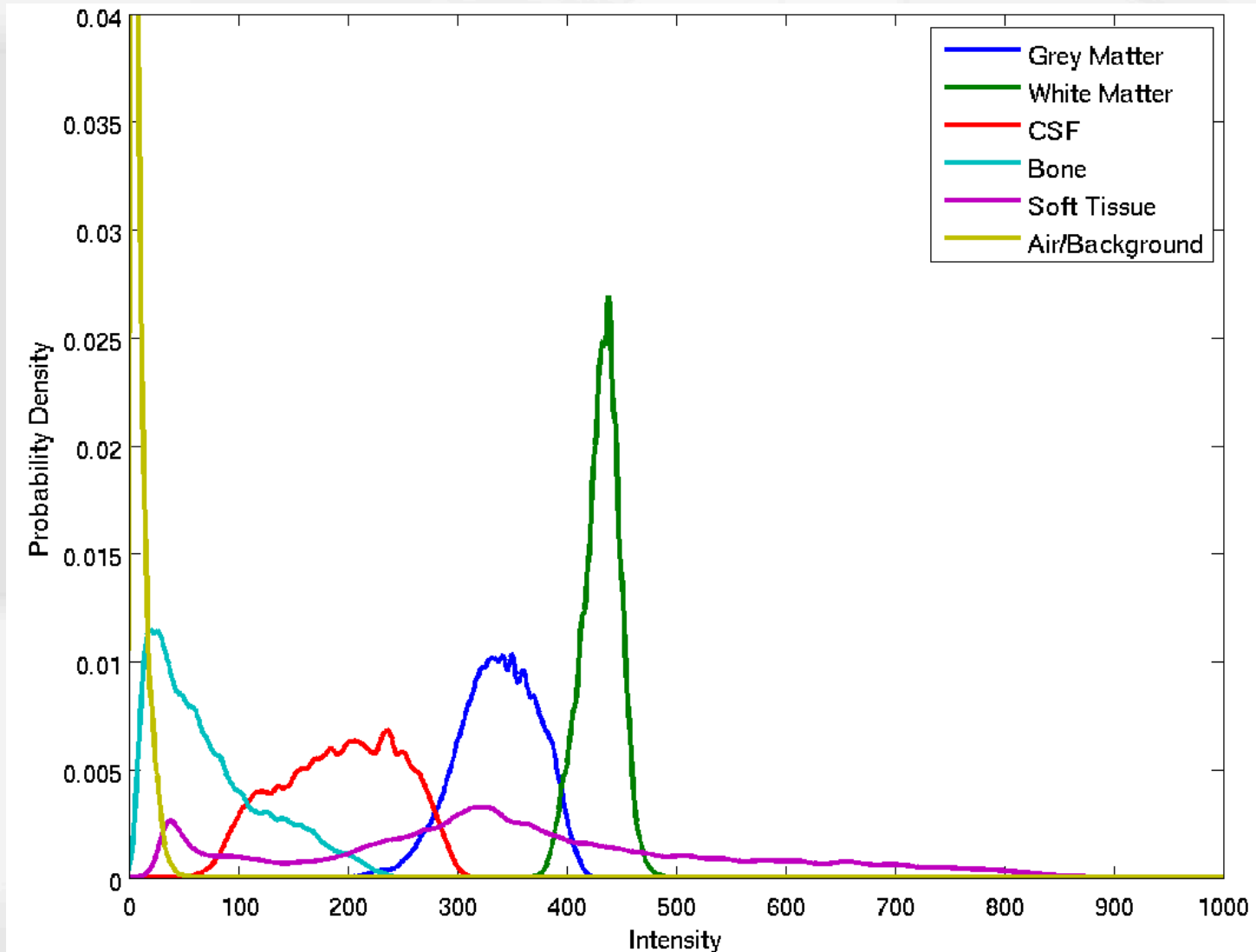
- MRI imperfections: No simple similarity measure, a lot of possible transformations...
 - Noise, artefacts, partial volume effects
 - Intensity inhomogeneity (bias field)
 - Geometric/Contrast differences between sequences
- **Normalisation** of segmented tissues is more robust and precise than of original image
- Tissue **segmentation** benefits from spatially aligned tissue probability maps (of prior segmentation data)
- This *circularity* motivates simultaneous segmentation and normalisation in a unified model

- SPM12 implements a generative model of voxel intensity from tissue class probabilities
 - Principled Bayesian probabilistic formulation
 - Segmentation by inverting a Gaussian mixture model
- Deformations of prior tissue probability maps (TPMs, priors) are also part of the model
 - The inverse of the transformation that aligns the TPMs can be used to normalise the original image
 - Non-linear deformations are constrained by regularisation factors
- Bias correction is included within the model

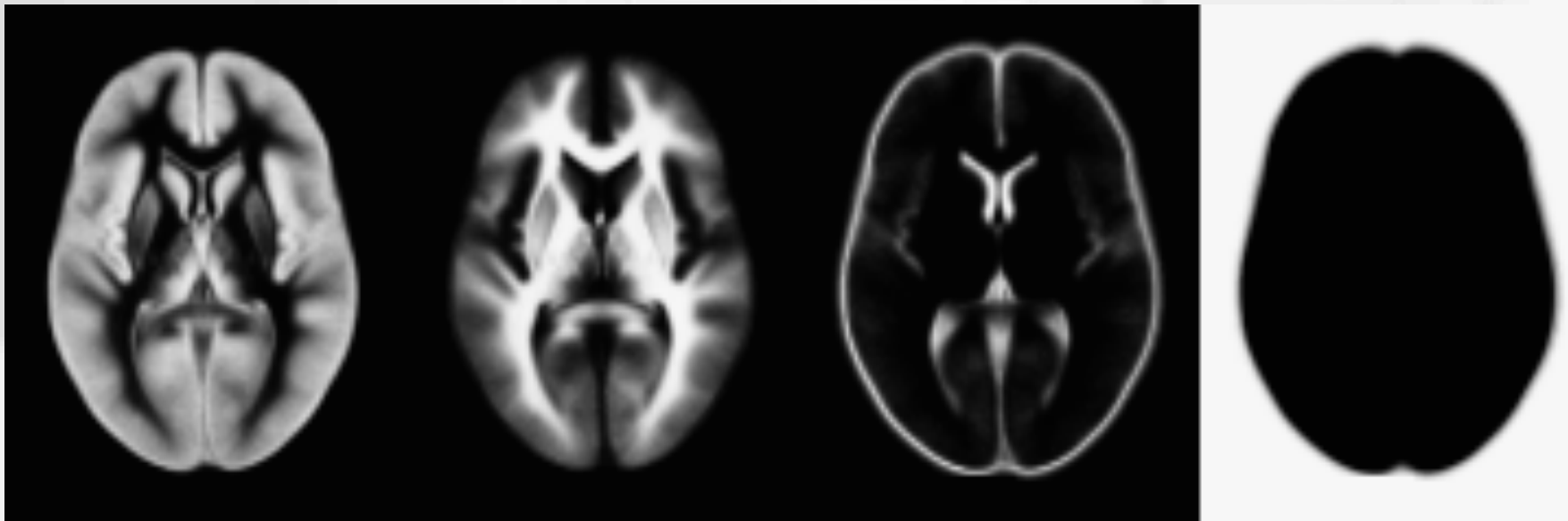
- Classification is based on a Mixture of Gaussians model, which represents the intensity probability density by a number of Gaussian distributions.
- Multiple Gaussians per tissue class allow non-Gaussian intensity distributions to be modelled
 - e.g. partial volume effects



Tissue intensity distributions (T1-weighted MRI)



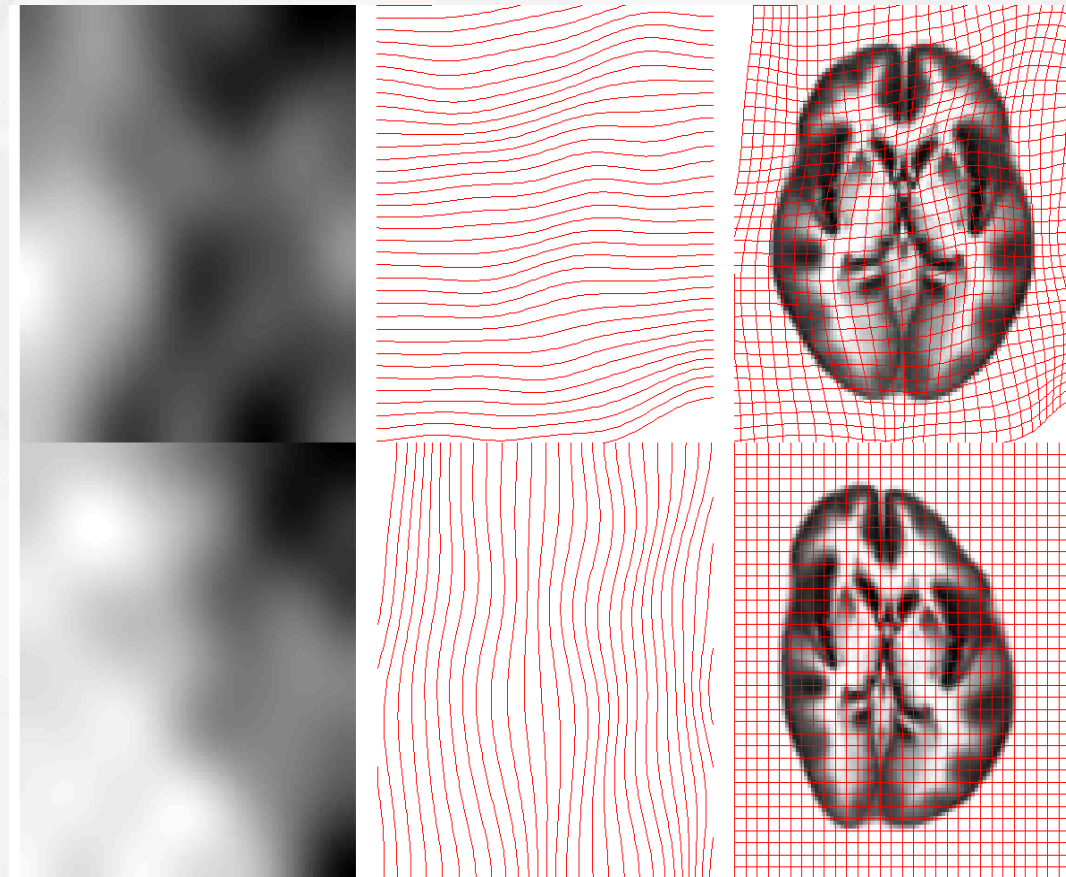
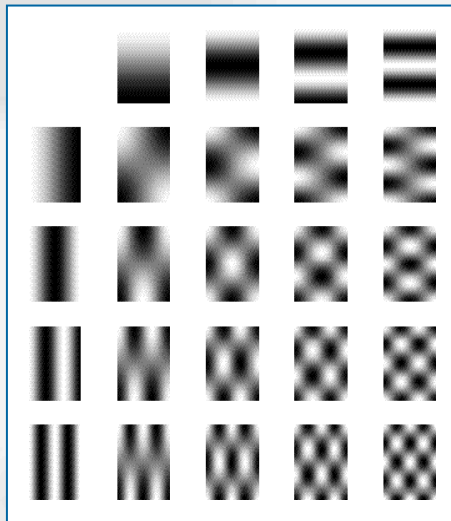
- Tissue probability maps (TPMs) are used as the prior, instead of the proportion of voxels in each class



ICBM Tissue Probabilistic Atlases. These tissue probability maps were kindly provided by the **International Consortium for Brain Mapping**

Deforming the Tissue Probability Maps

- Tissue probability maps images are warped to match the subject
- The inverse transform warps to the TPMs

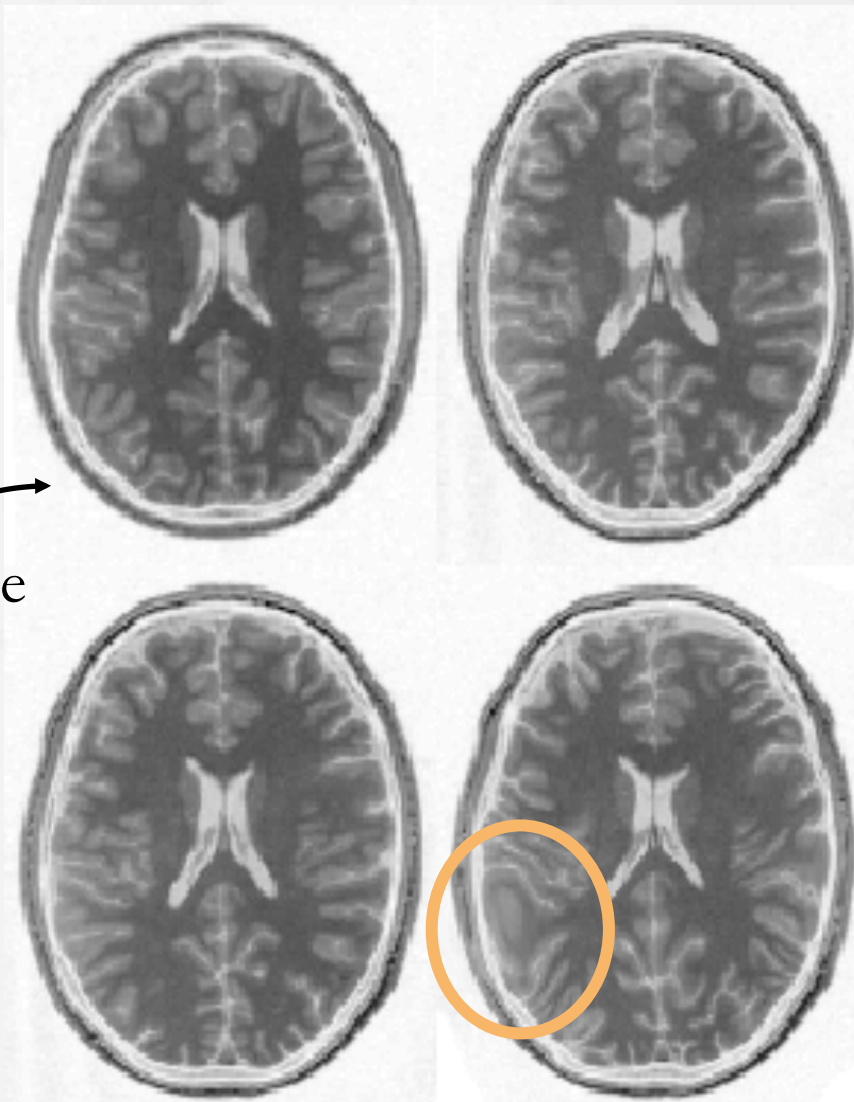


Why regularisation? – Overfitting

- Regularisation constrains deformations to realistic range (implemented as priors)

Non-linear
registration
using
regularisation
(error = 302.7)

Template
image

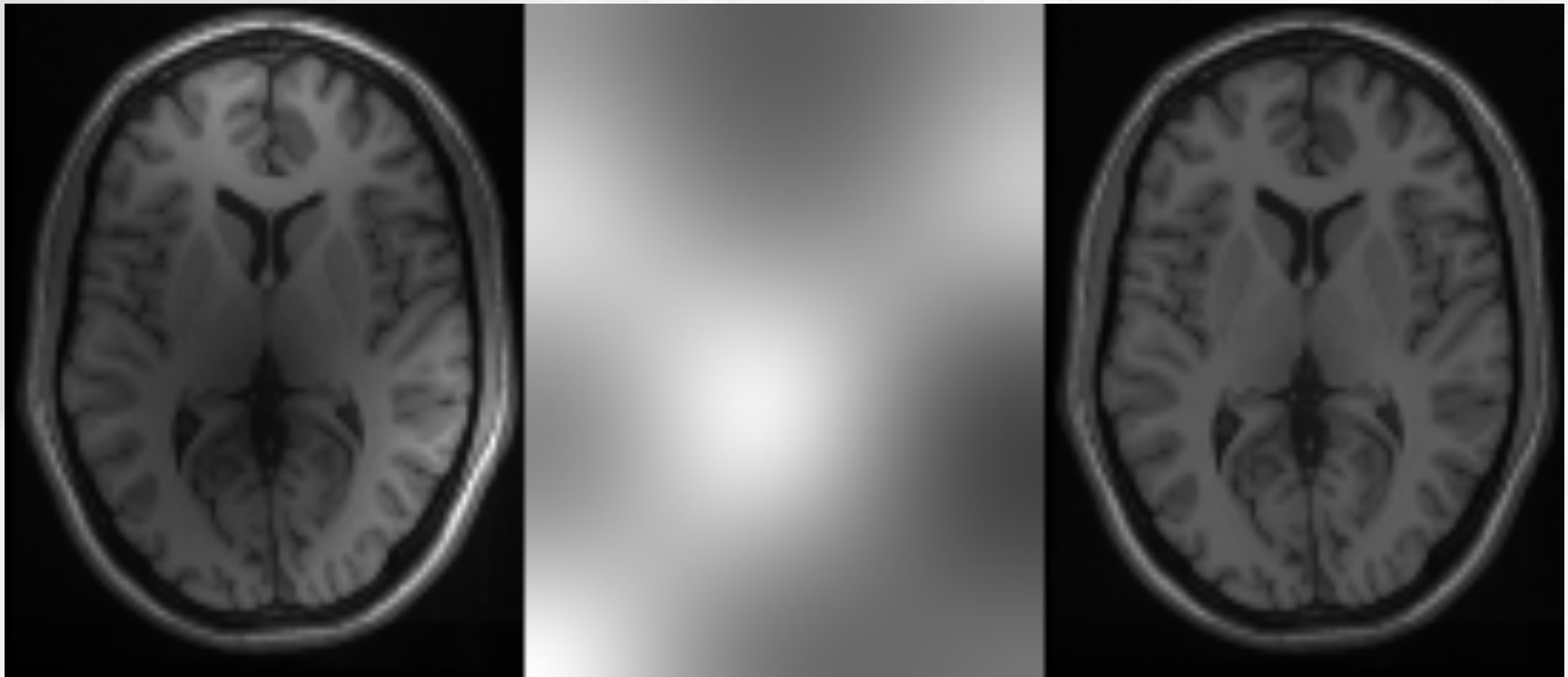
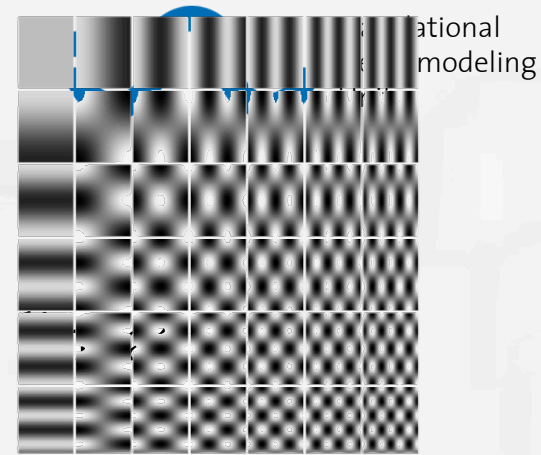


Affine
registration
(error =
472.1)

Non-linear
registration
without
regularisation
(error =
287.3)

Modelling inhomogeneity

- A multiplicative bias field is modelled as a combination of basis functions.

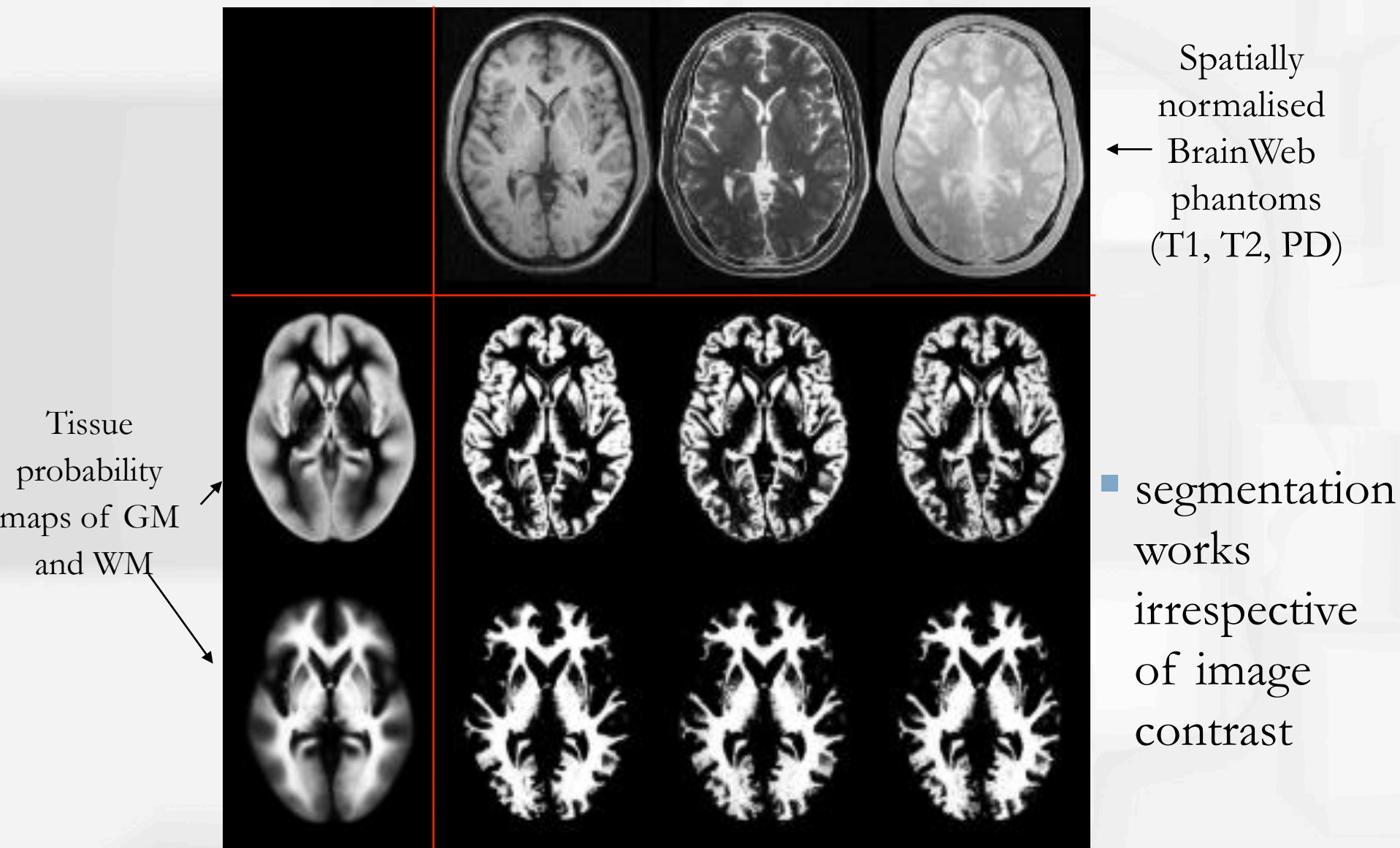


Corrupted image

Bias Field

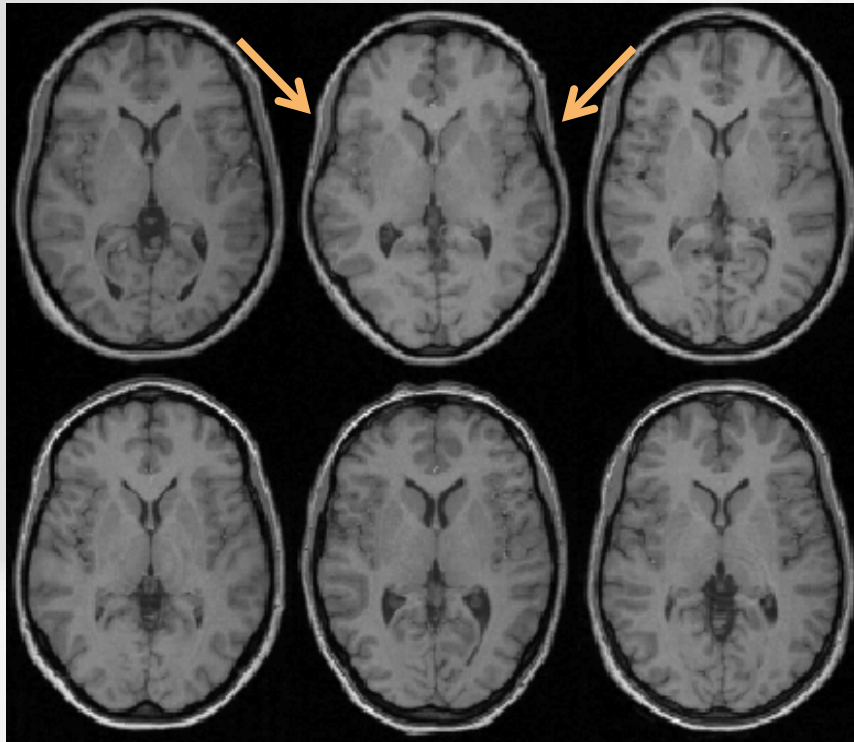
Corrected image

Segmentation results

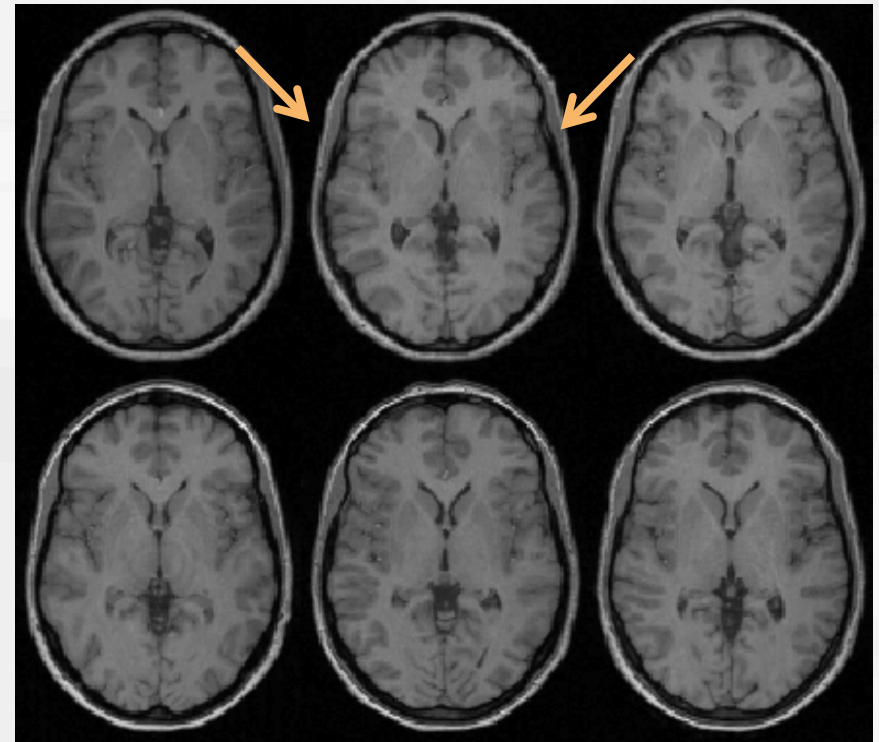


Cocosco, Kollokian, Kwan & Evans. "BrainWeb: Online Interface to a 3D MRI Simulated Brain Database". NeuroImage 5(4):S425 (1997)

Benefits of Unified Segmentation



Affine registration



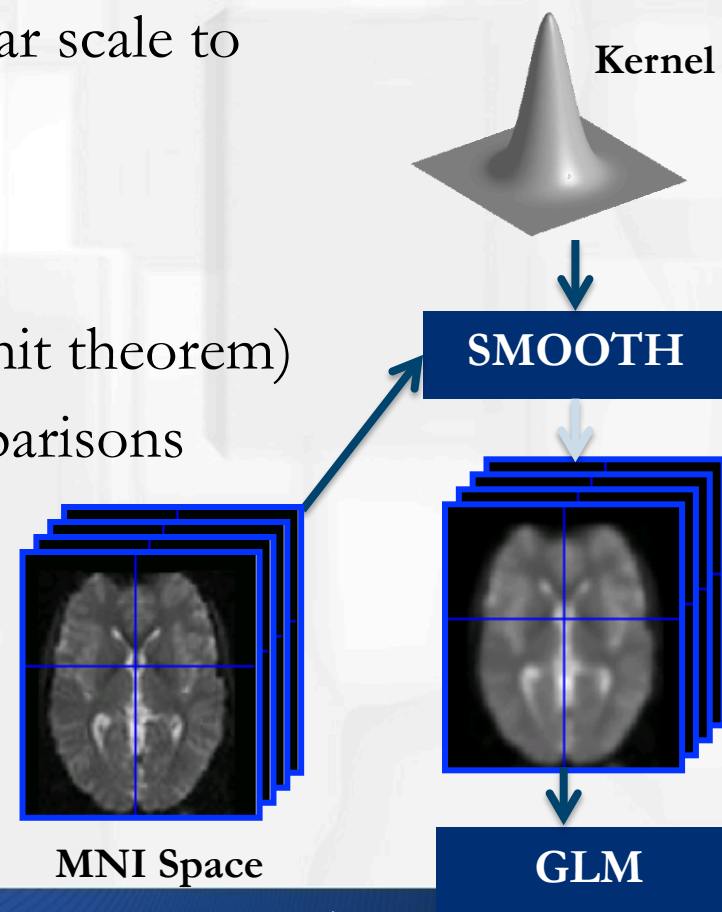
Non-linear registration

Spatial normalisation – Limitations

- Seek to match functionally homologous regions, but...
 - Challenging high-dimensional optimisation
 - many local optima
 - Different cortices **can** have different folding patterns
 - No exact match between structure and function
 - Interesting recent paper Amiez et al. (2013), PMID:23365257
- Compromise
 - Correct relatively large-scale variability
 - Smooth over finer-scale residual differences

Smoothing – Why blurring the data?

- Intra-subject signal quality
 - Suppresses thermal noise (averaging)
 - Increases sensitivity to effects of similar scale to kernel (matched filter theorem)
- Single-subject statistical analysis
 - Makes data more Gaussian (central limit theorem)
 - Reduces the number of multiple comparisons
- Second-level statistical analysis
 - Improves spatial overlap by blurring anatomical differences

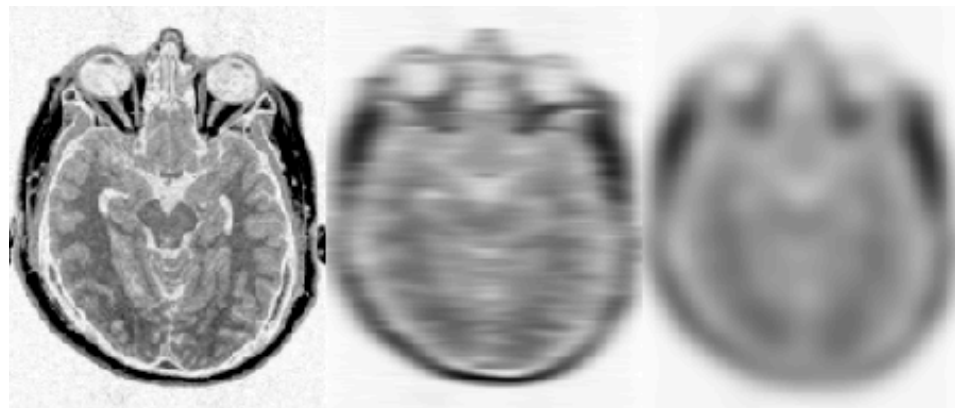
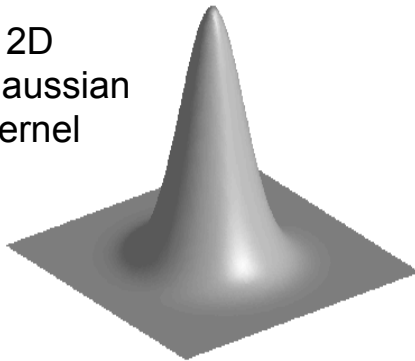


Smoothing –

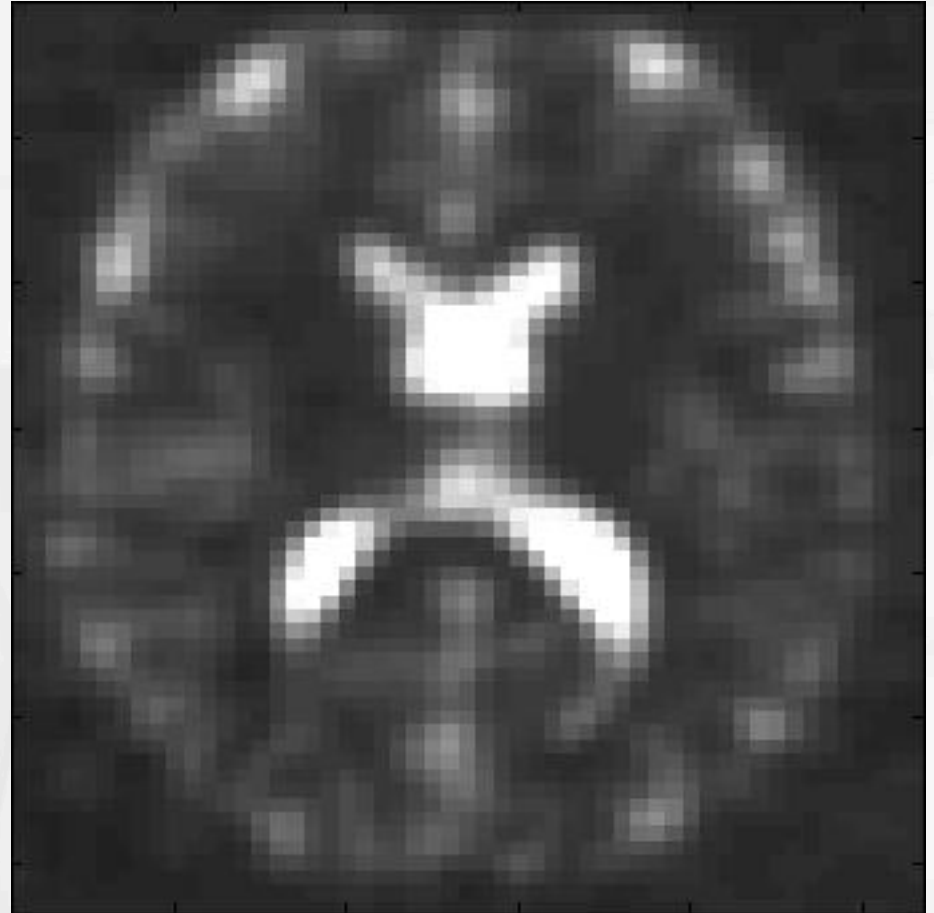
How is it implemented?

- Convolution with a 3D Gaussian kernel, of specified full-width at half-maximum (FWHM) in mm
 - mathematically equivalent to slice-timing operation or reslicing, but different kernels there (Sinc, b-spline)
- Gaussian kernel is separable, and we can smooth 2D data with 2 separate 1D convolutions

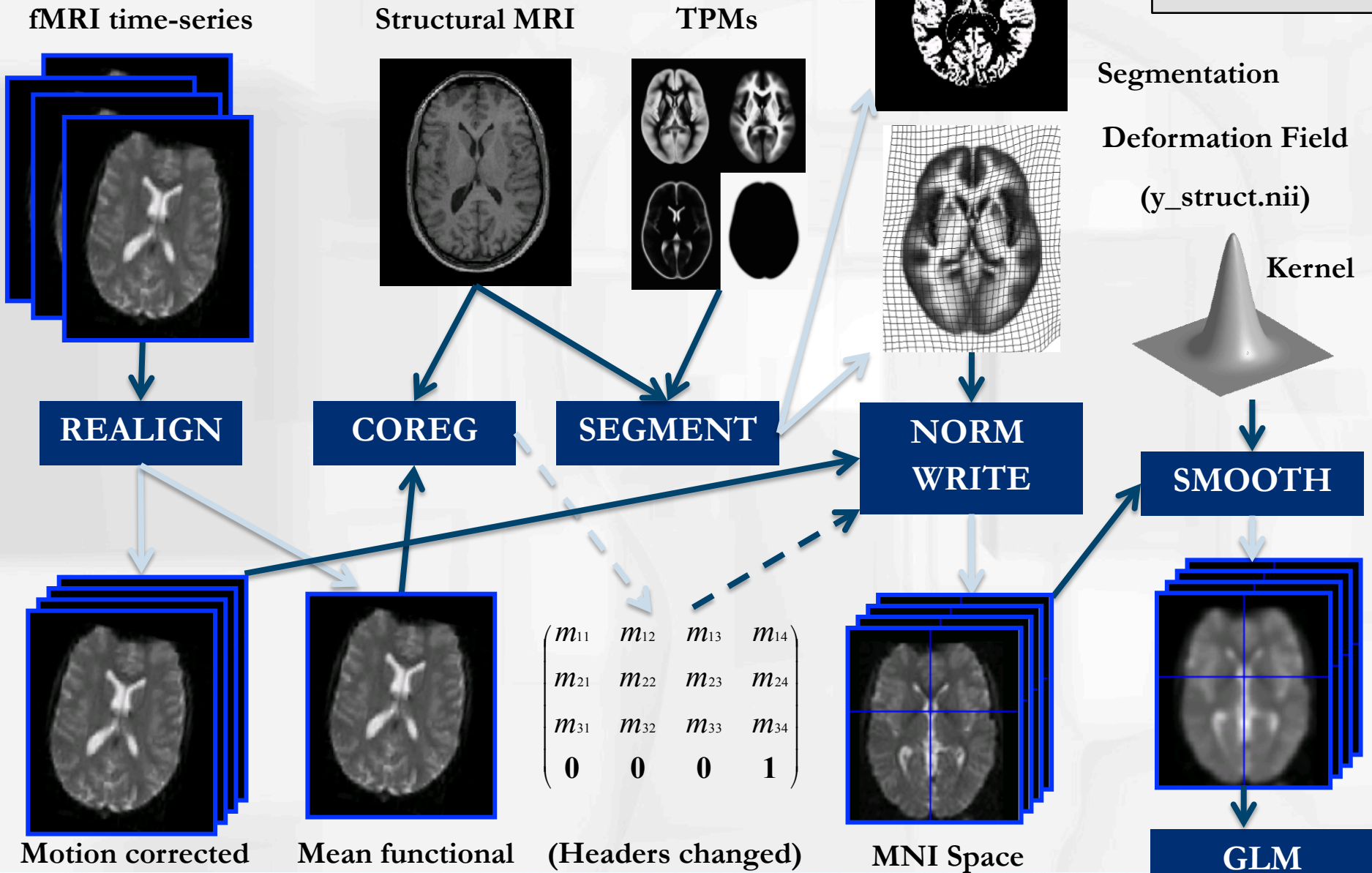
A 2D
Gaussian
Kernel



fMRI Run after Smoothing



Spatial Preprocessing



Sources of Noise in fMRI

- Subject Motion
- Acquisition Timing
- Anatomical Identity
- Inter-subject variability
- Thermal Noise
- Physiological Noise
- Realignment
- Slice-Timing
- Co-registration
- Segmentation
- Smoothing
- PhysIO Toolbox

Noise Modelling

The Problem: Physiological Noise

- 
- A blue line starts from a single point at the top center and branches out into two arrows pointing downwards and outwards to the left and right, indicating a split or two different categories.
- Cardiac effects
 - Respiratory effects

The Problem: Physiological Noise



■ Cardiac effects

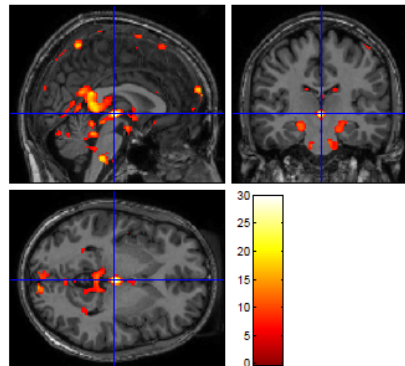
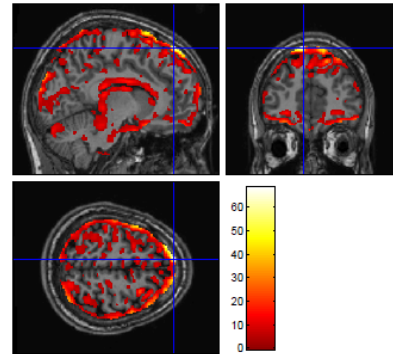
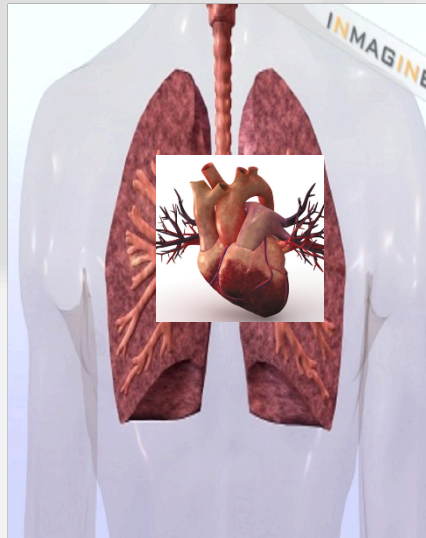
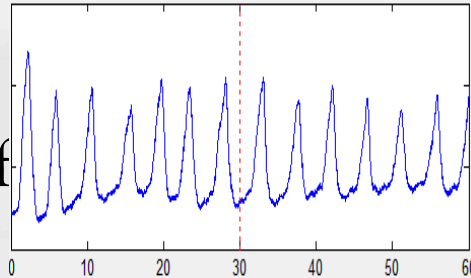
- Systole:
 - Blood pumped into brain, vessel volume increases: pulsatile vessels
 - CSF pushed down: pulsatile CSF
- Diastole:
 - Vessel volume decreases
 - CSF flows back into “void” brain volume

A Cardiac Cycle in the Brain



The Problem: Physiological Noise

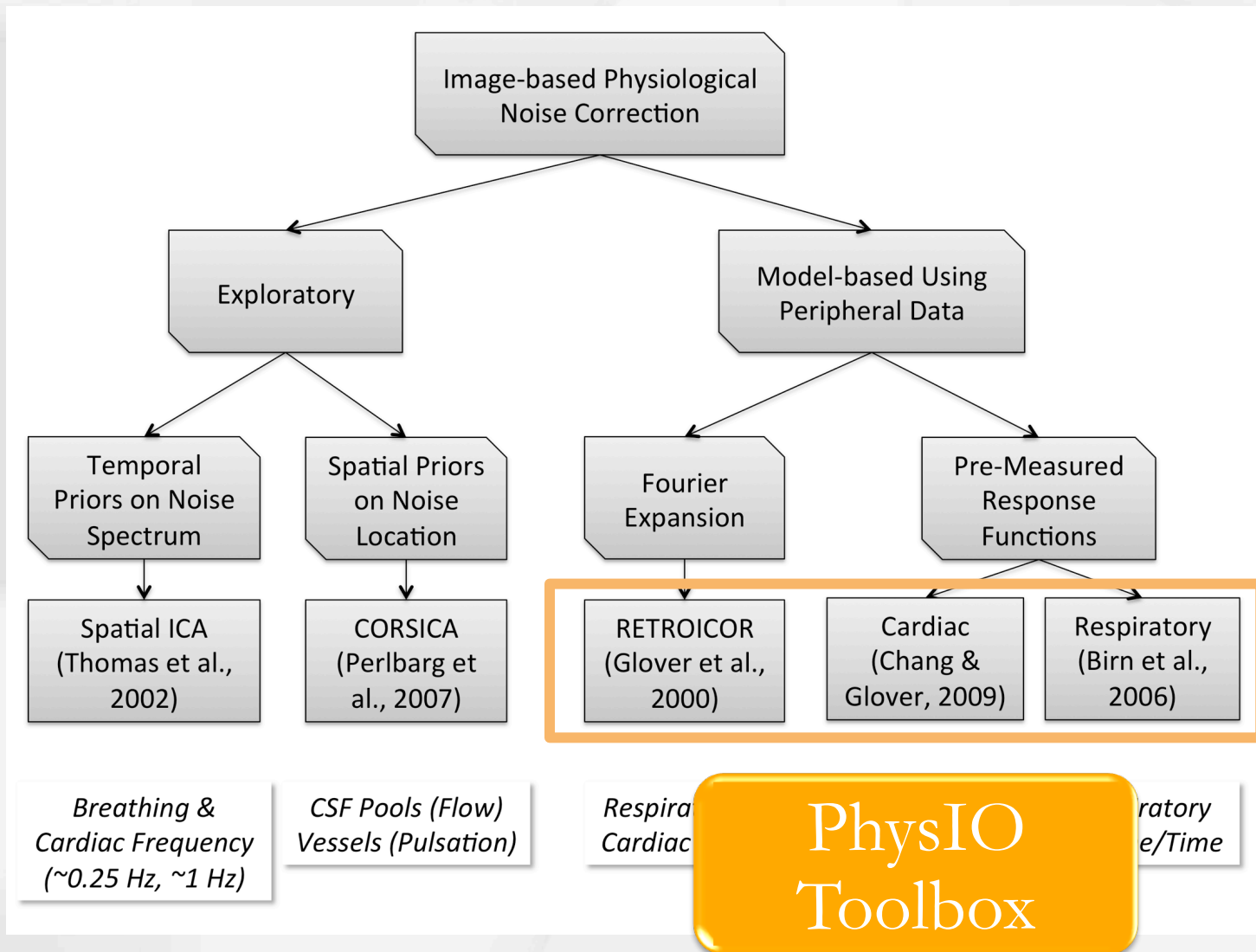
■ Cardiac effects



■ Respiratory effects

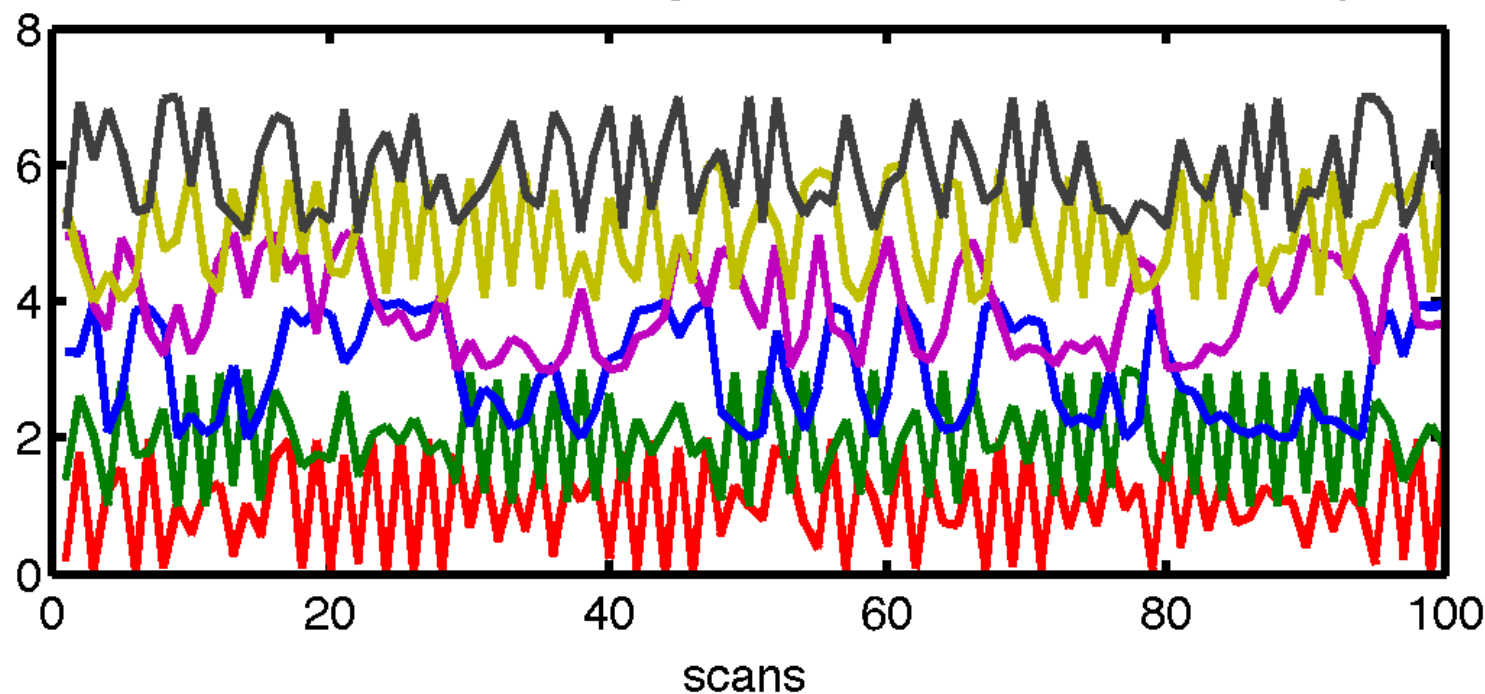
- Chest (& head) moves with respiratory cycle
- Changes in lung volume change encoding magnetic field for MR
 - Geometric distortion/scaling
- Respiratory-sinus arrhythmia
 - Heart beats faster during inhalation

The Solution: Image-based Physiological Noise Correction



The Solution: Physiological Noise Correction

, RETROICOR cardiac regressors, vertical shift for visibility



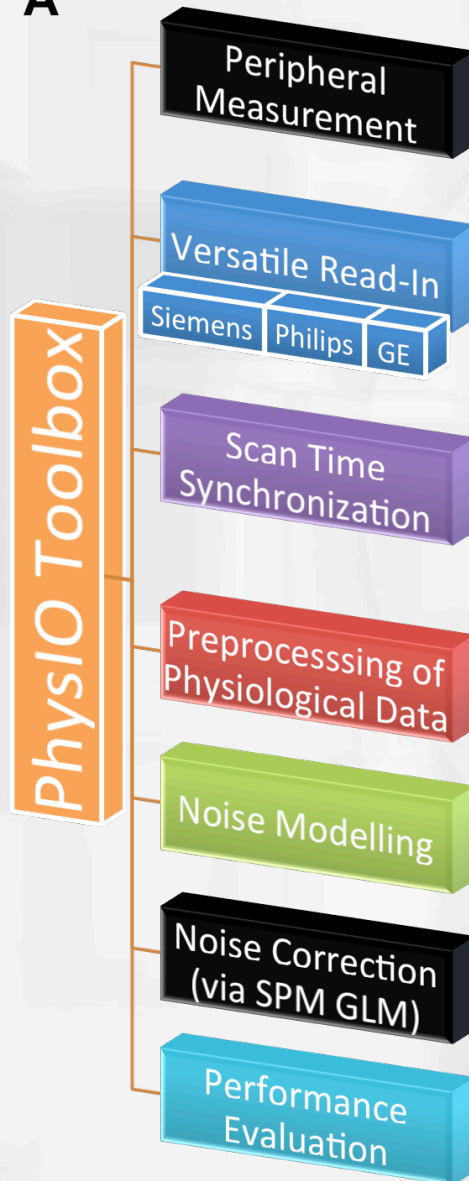
ECG, PPU → Cardiac cycle
Breathing belt → Respiratory cycle
Capnograph → CO₂ concentration

Confound
regressors

SPM Batch Editor Interface



A



B

Module List

Realign: Estimate & Res
TAPAS PhysIO Toolbox
fMRI model specification

Current Module: TAPAS PhysIO Toolbox

Help on: TAPAS PhysIO Toolbox

save_dir

log_files Philips

.vendor <-X

.log_cardiac <-X

.log_respiration <-X

.log_scan_timing <-X

sampling_interval 0

relative_start_acquisition 0

sqpar (Sequence timing parameters)

.Nslices <-X

.NslicesPerBeat 0

.TR <-X

.Ndummies <-X

.Nscans <-X

.onset_slice <-X

.time_slice_to_slice 0

.Nprep 0

thresh (Thresholding parameters for de-noising and timing)

.Scan/Physlog Time Synchronization

.nominal

.cardiac ECG

.modality

.Initial Detection of Heartbeats

.load_from_logfile

.Post-hoc Selection of Cardiac Pulses

.Off

model

.type ... (RETRO)

.order

.cardiac 3

.respiratory 4

.cardiac X respiratory 1

.orthogonalise none

.input_other_multiple_regressors

.output_multiple_regressors ... errors.txt

verbose

.level 2

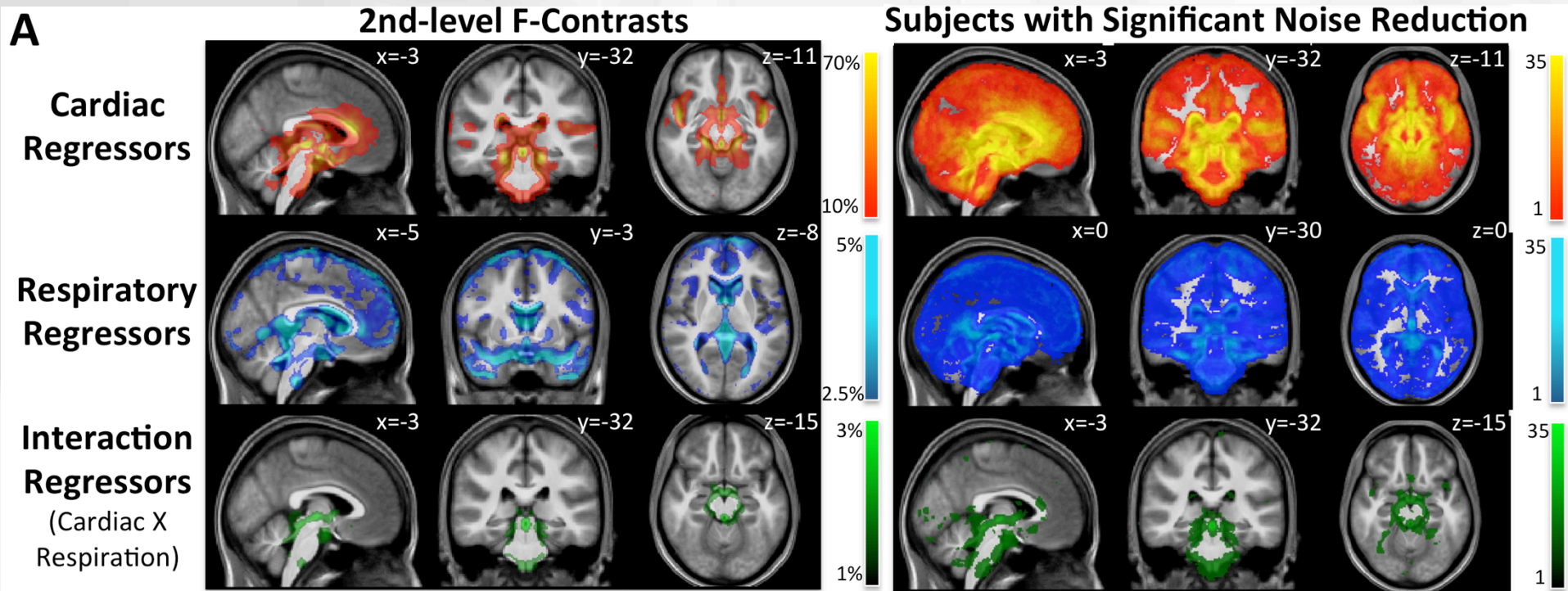
.fig_output_file

.use_tabs false

tapas_physio_report_contrasts()

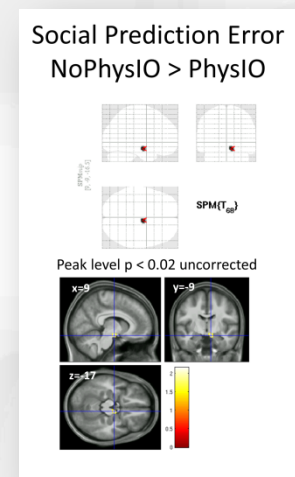
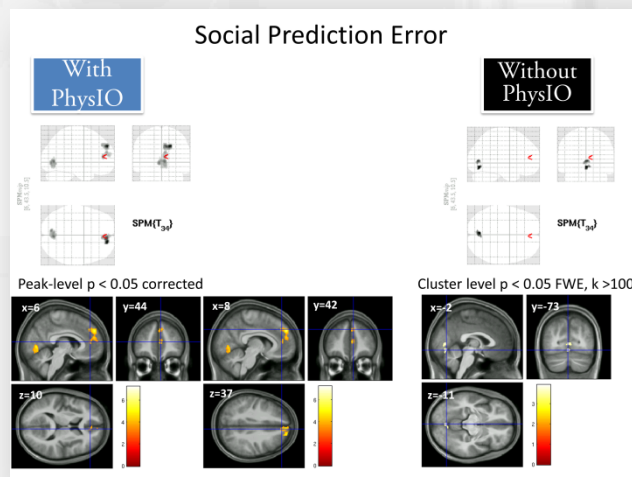
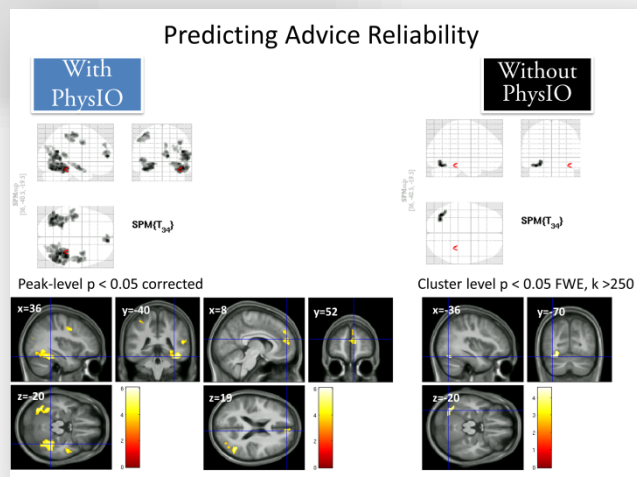
When? – PhysIO experience

- Andreea Diaconescu (TNU): Social Learning Experiment, “Inferring on the Intentions of Others”



Diaconescu, et al., 2014. PLoS Comput Biol 10

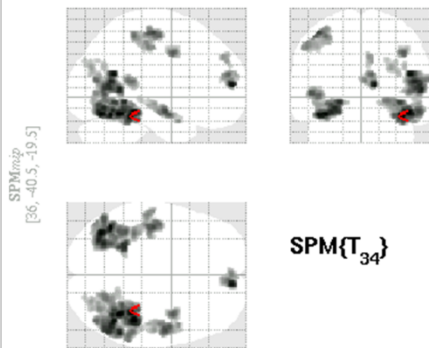
- Andreea Diaconescu (TNU): Social Learning
 - Higher sensitivity for group effects (N=35)
 - Prediction of advice reliability: dmPFC, bilateral FFA
 - Prediction error: dmPFC
 - Less false/ambiguous positives:
 - Brainstem (Substantia Nigra)



When? – PhysIO experience

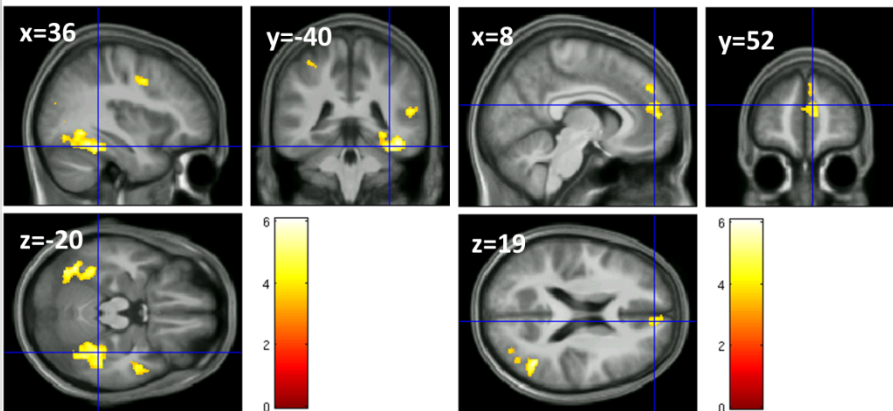
Predicting Advice Reliability

With
PhysIO

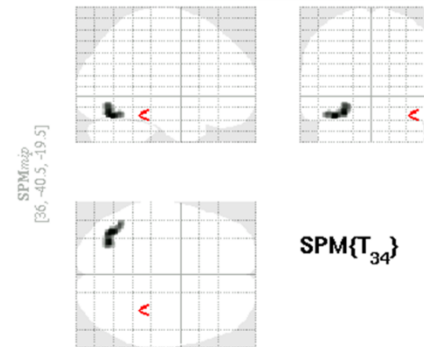


$SPM\{T_{34}\}$

Peak-level $p < 0.05$ corrected

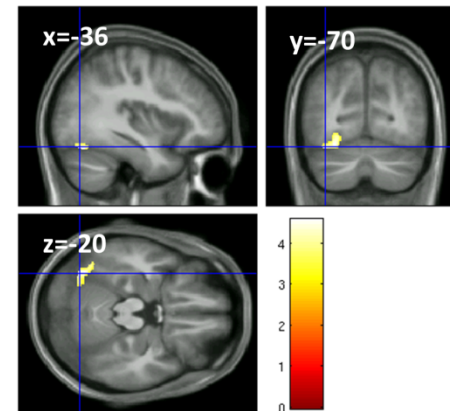


Without
PhysIO

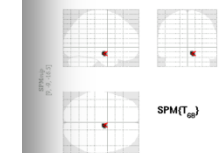


$SPM\{T_{34}\}$

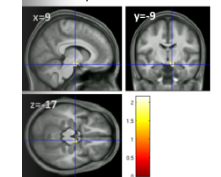
Cluster level $p < 0.05$ FWE, $k > 250$



Special Prediction Error
NoPhysIO > PhysIO



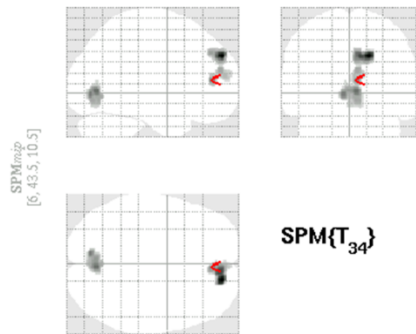
Peak level $p < 0.02$ uncorrected



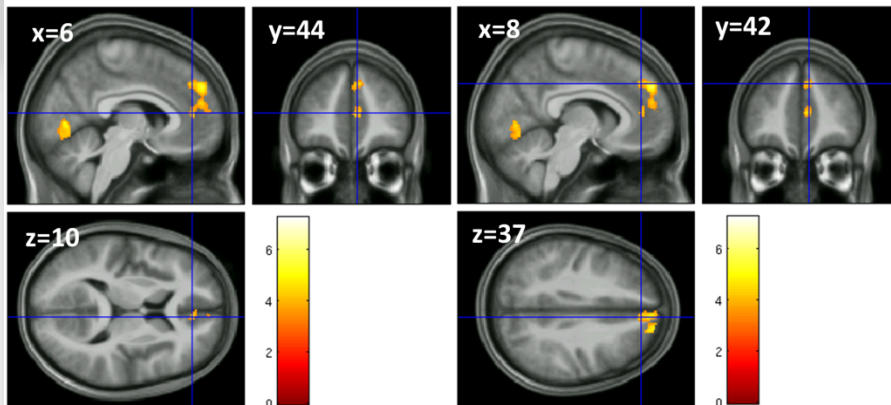
When? – PhysIO experience

Social Prediction Error

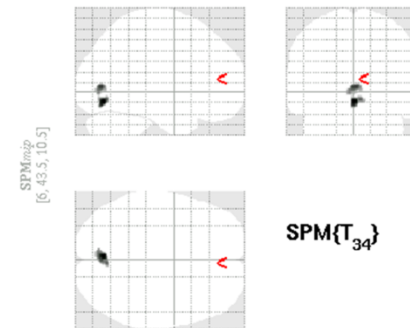
With
PhysIO



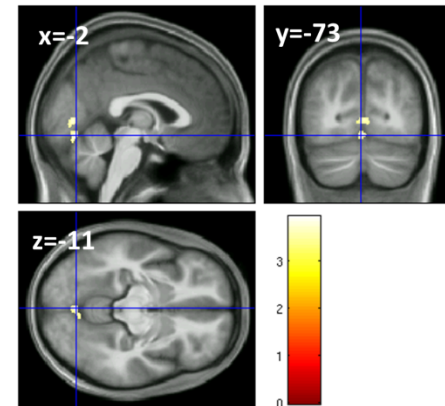
Peak-level $p < 0.05$ corrected



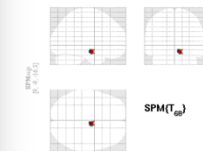
Without
PhysIO



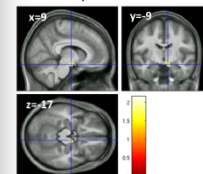
Cluster level $p < 0.05$ FWE, $k > 100$



Social Prediction Error
NoPhysIO > PhysIO



Peak level $p < 0.02$ uncorrected



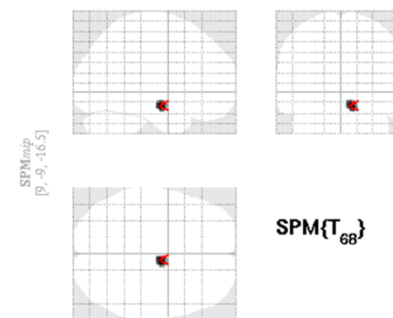
When? – PhysIO experience



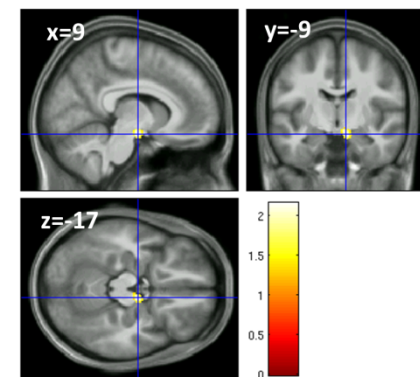
■ Andreea Diaconescu (TNU): Social Learning

- Higher sensitivity for group effects (N=30)
 - Prediction of advice reliability: dmPFC, bilaterally
 - Prediction error: dmPFC
- Less false/ambiguous positives:
 - Brainstem (Substantia Nigra)

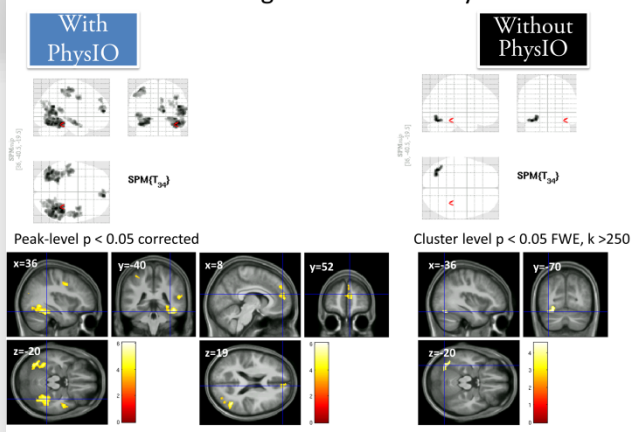
Social Prediction Error
NoPhysIO > PhysIO



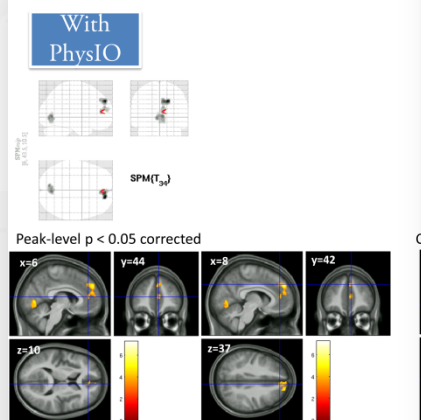
Peak level $p < 0.02$ uncorrected



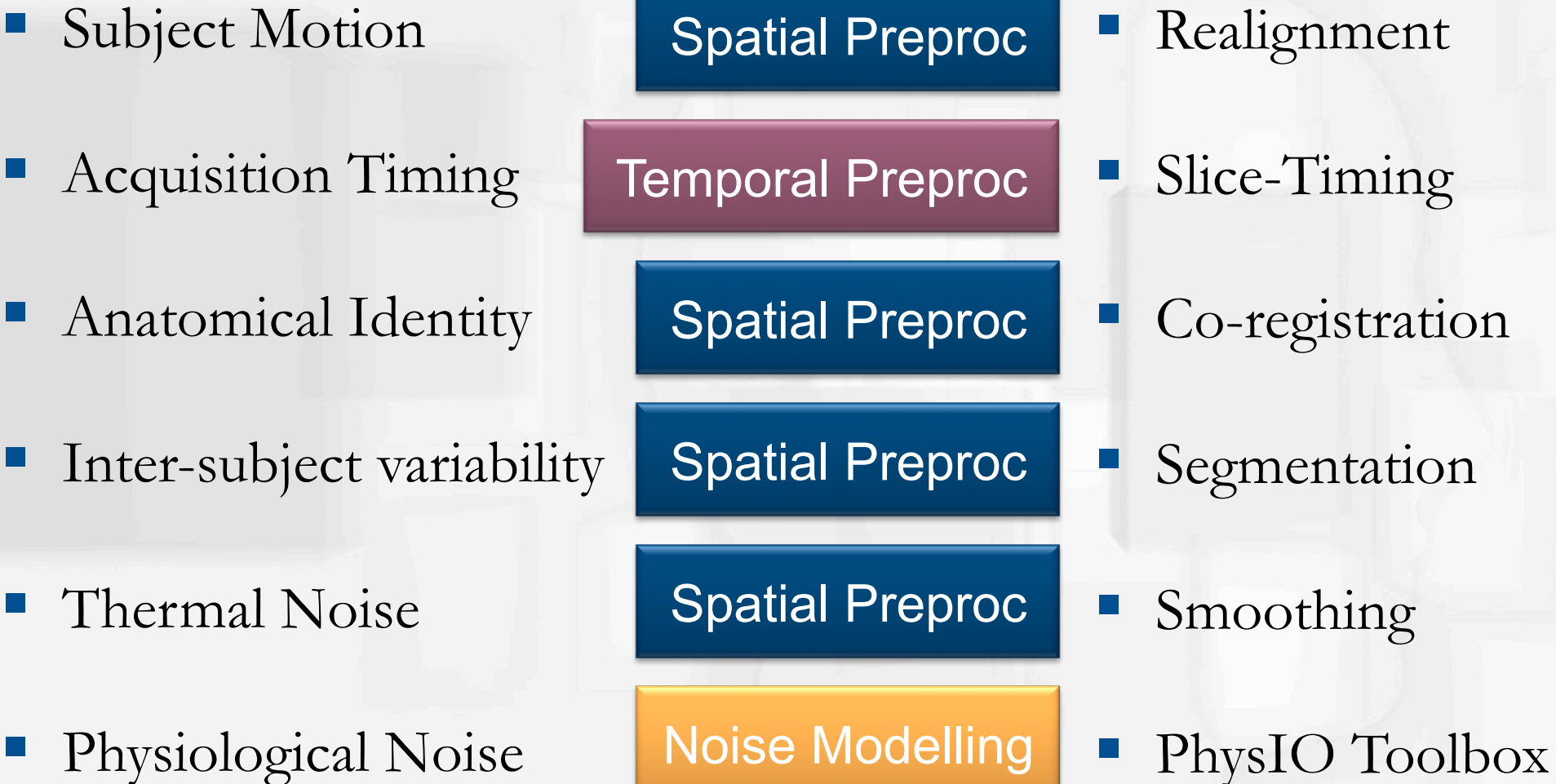
Predicting Advice Reliability



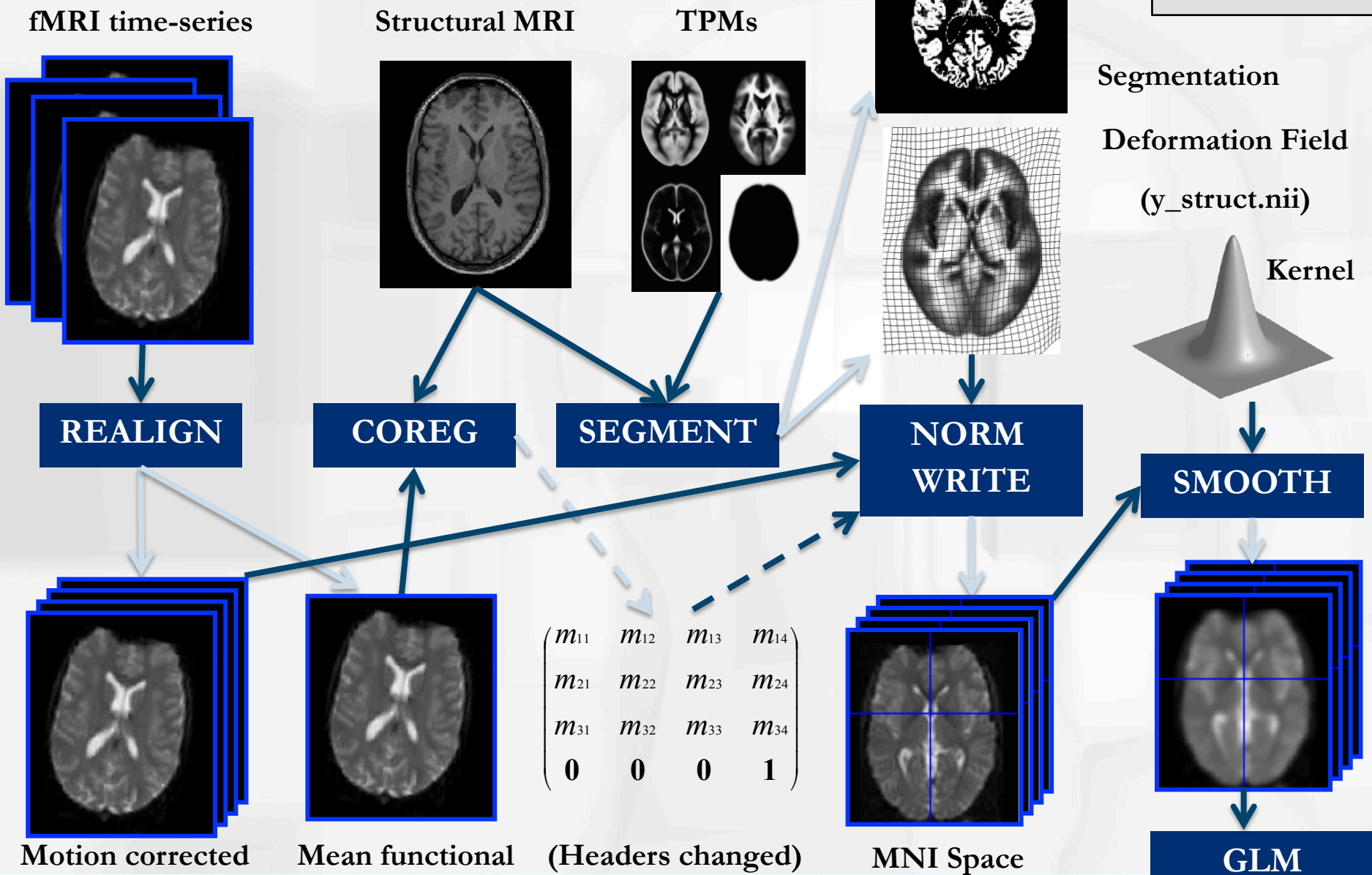
Social Prediction Error



Sources of Noise in fMRI



Spatial Preprocessing



Thank you...

- ...and:
 - TNU Zurich,
in particular: Klaas
 - MR-technology Group IBT,
in particular: Klaas
 - Everyone I borrowed slides
from 😊

