Preprocessing of fMRI data (basic)

Practical session
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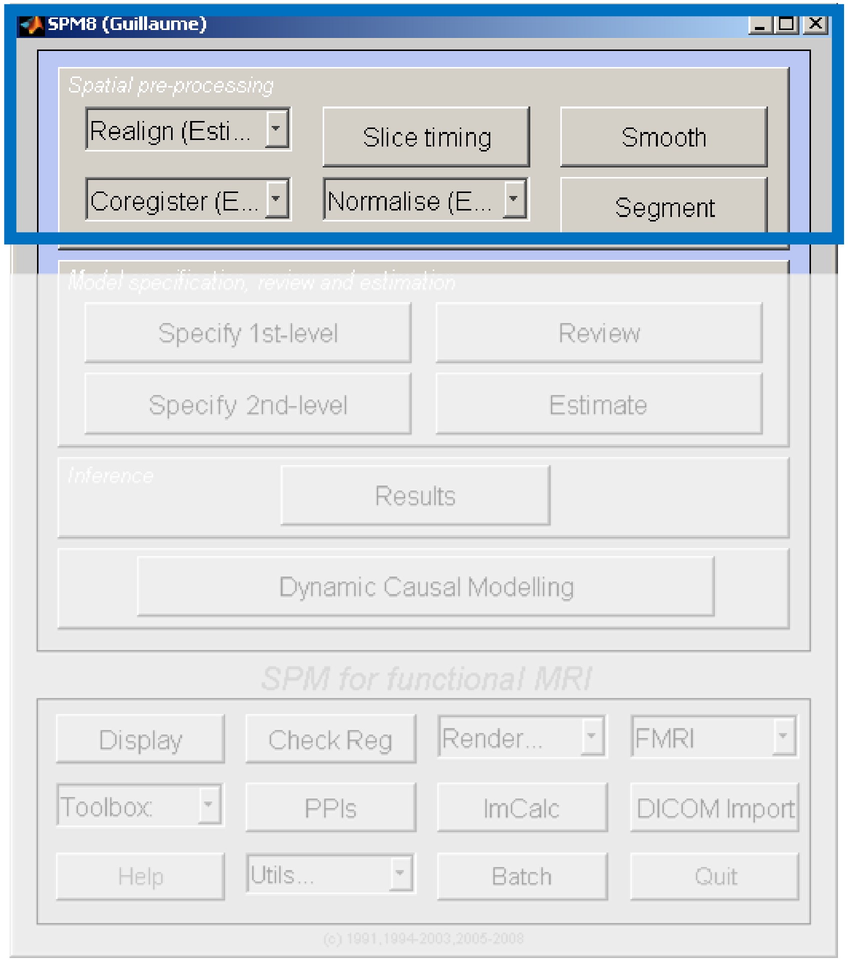
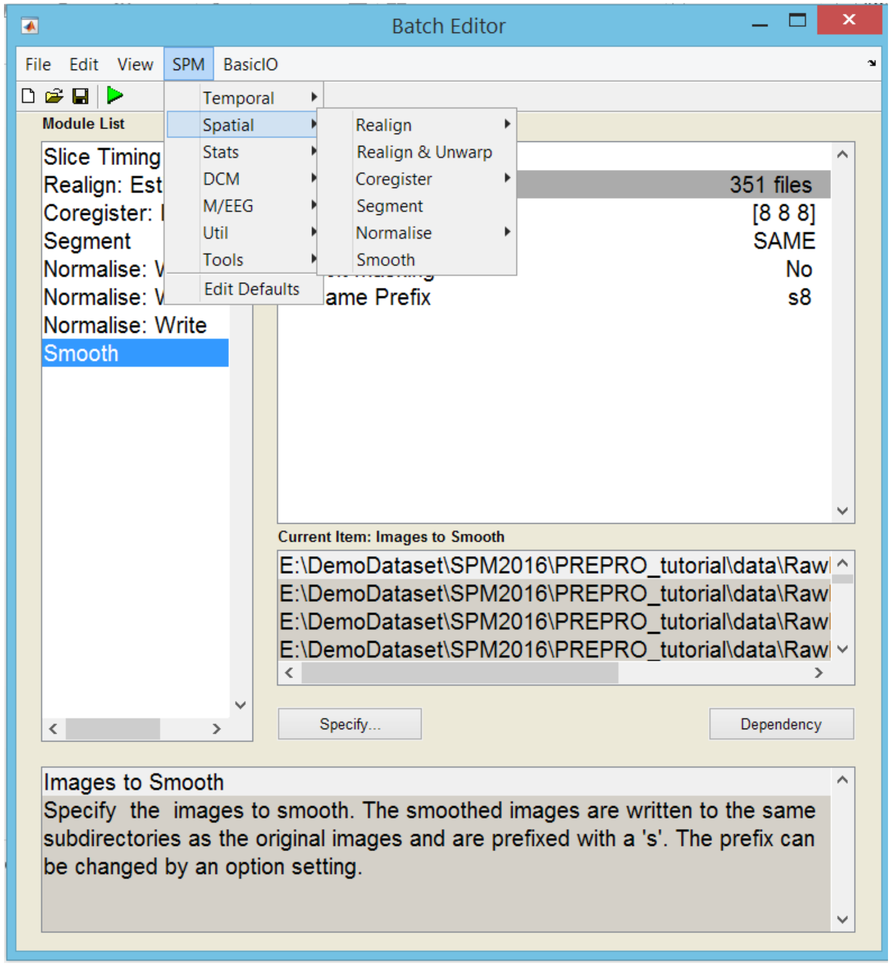
Translational Neuromodeling Unit

Goals of this session

- Go through a preprocessing pipeline in SPM.
- Learn how to check whether some basic steps worked.
- Some basic file operations in SPM.
- Save, load and modify batches
- How to make your own preprocessing script.
- Answers to "all" your questions.

Preprocessing tools on the SPM GUI and Batch Editor





Slice Timing
Realign: Est
Coregister: I
Segment
Normalise: V
Normalise: V
Normalise: Write
Smooth

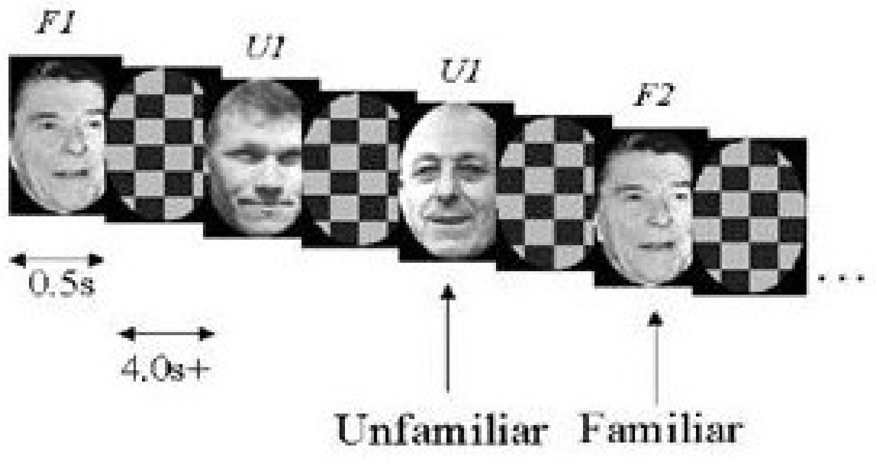
351 files
[8 8 8]
SAME
No
ame Prefix s8

Current Item: Images to Smooth

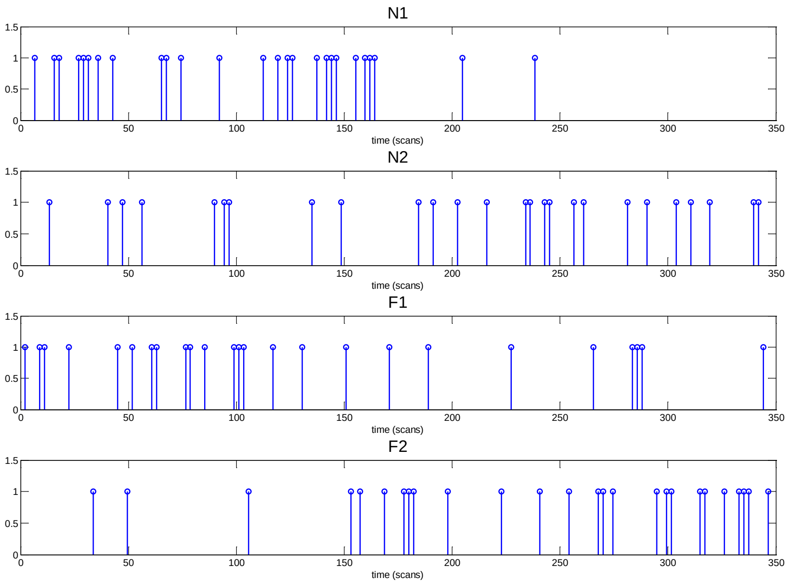
E:\DemoDataset\SPM2016\PREPRO_tutorial\data\Raw\
E:\DemoDataset\SPM2016\PREPRO_tutorial\data\Raw\
E:\DemoDataset\SPM2016\PREPRO_tutorial\data\Raw\
E:\DemoDataset\SPM2016\PREPRO_tutorial\data\Raw\

Images to Smooth
Specify the images to smooth. The smoothed images are written to the same subdirectories as the original images and are prefixed with a 's'. The prefix can be changed by an option setting.

The Dataset: Event-related fMRI



- Goal: Investigate Repetition Suppression
- How: Each face presented twice during the session, 26 famous and 26 non-famous faces
  - 2x2 factorial design
  - Factor Fam(iliarity): long-term memory,
    - Level: Famous or Unfamous
  - Factor Rep(itition)
    - Level: 1 or 2
  - Task: Button press to decide fame



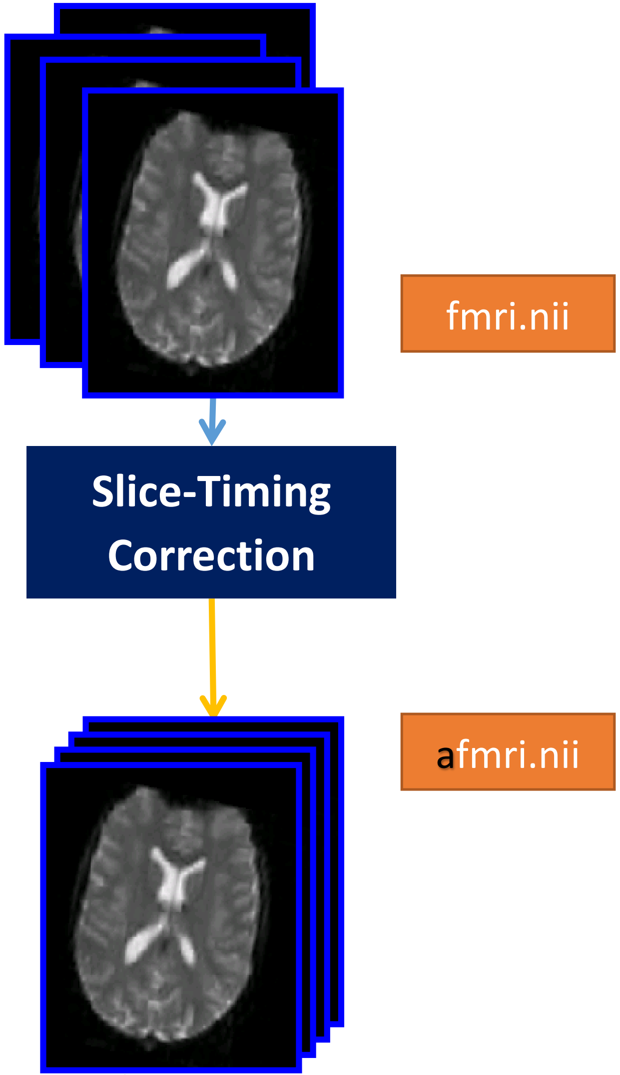
Stimulus Onsets

all_conditions.mat

R. Henson et al., Cereb Cortex 2002

Slice-Timing Correction (Temporal Preproc)

fMRI time-series



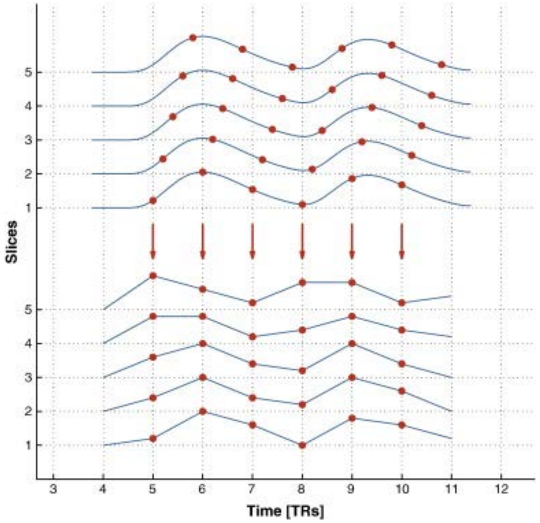
fmri.nii

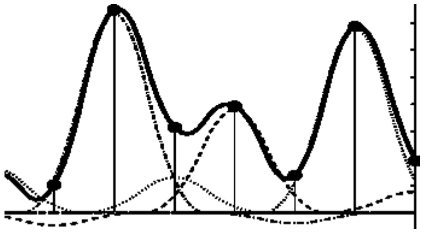
Slice-Timing Correction

afmri.nii

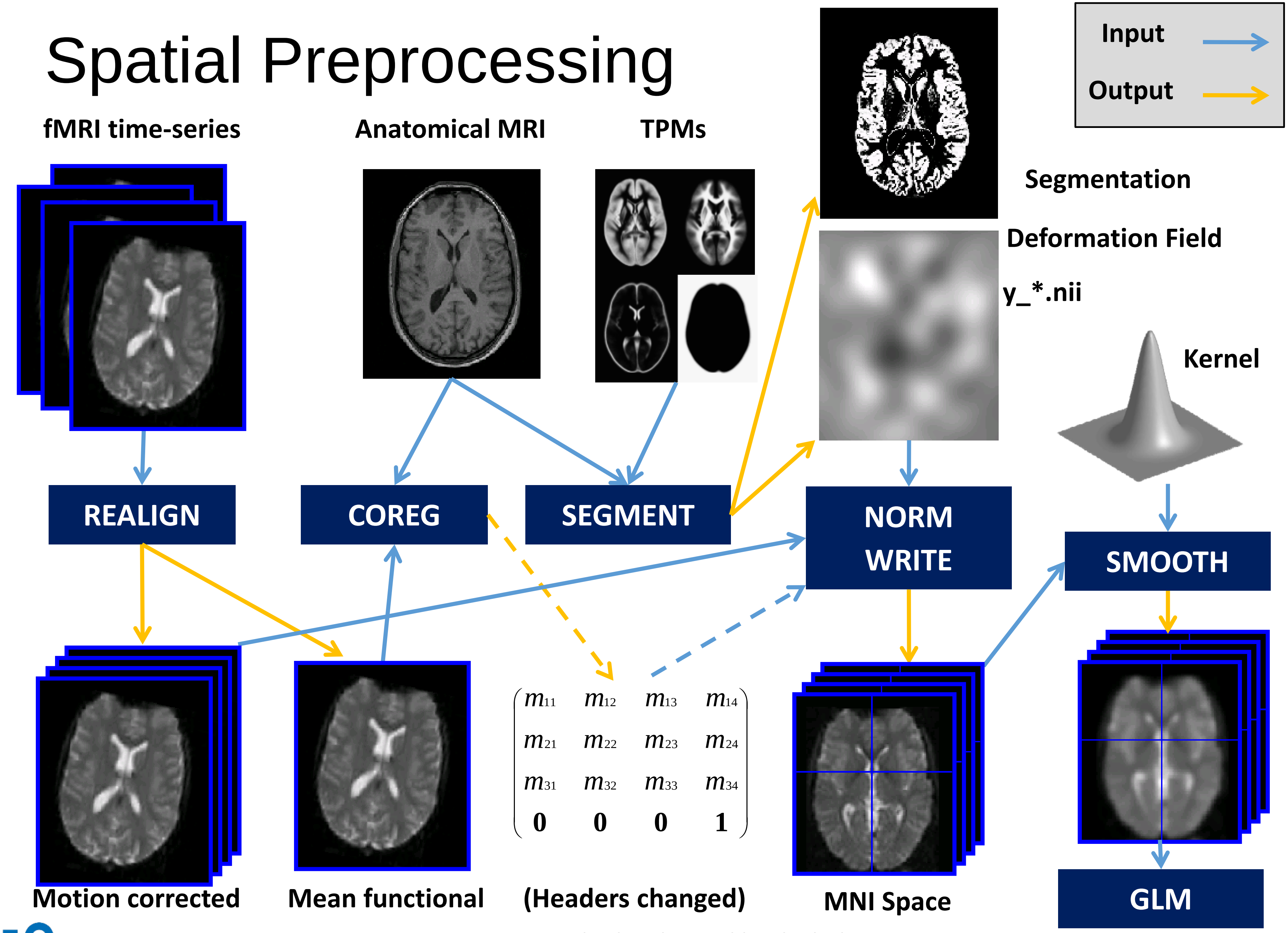
Slice-timing corrected images

- Goal: Correct for different acquisition time of each slice within an image volume
- How: All voxel time series are aligned to acquisition time of 1 slice via Sinc-interpolation of each voxel's time series





Spatial Preprocessing



Input

Output

fMRI time-series

Anatomical MRI

TPMs

Segmentation

Deformation Field

y_*.nii

Kernel

REALIGN

COREG

SEGMENT

NORM WRITE

SMOOTH

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

Motion corrected

Mean functional

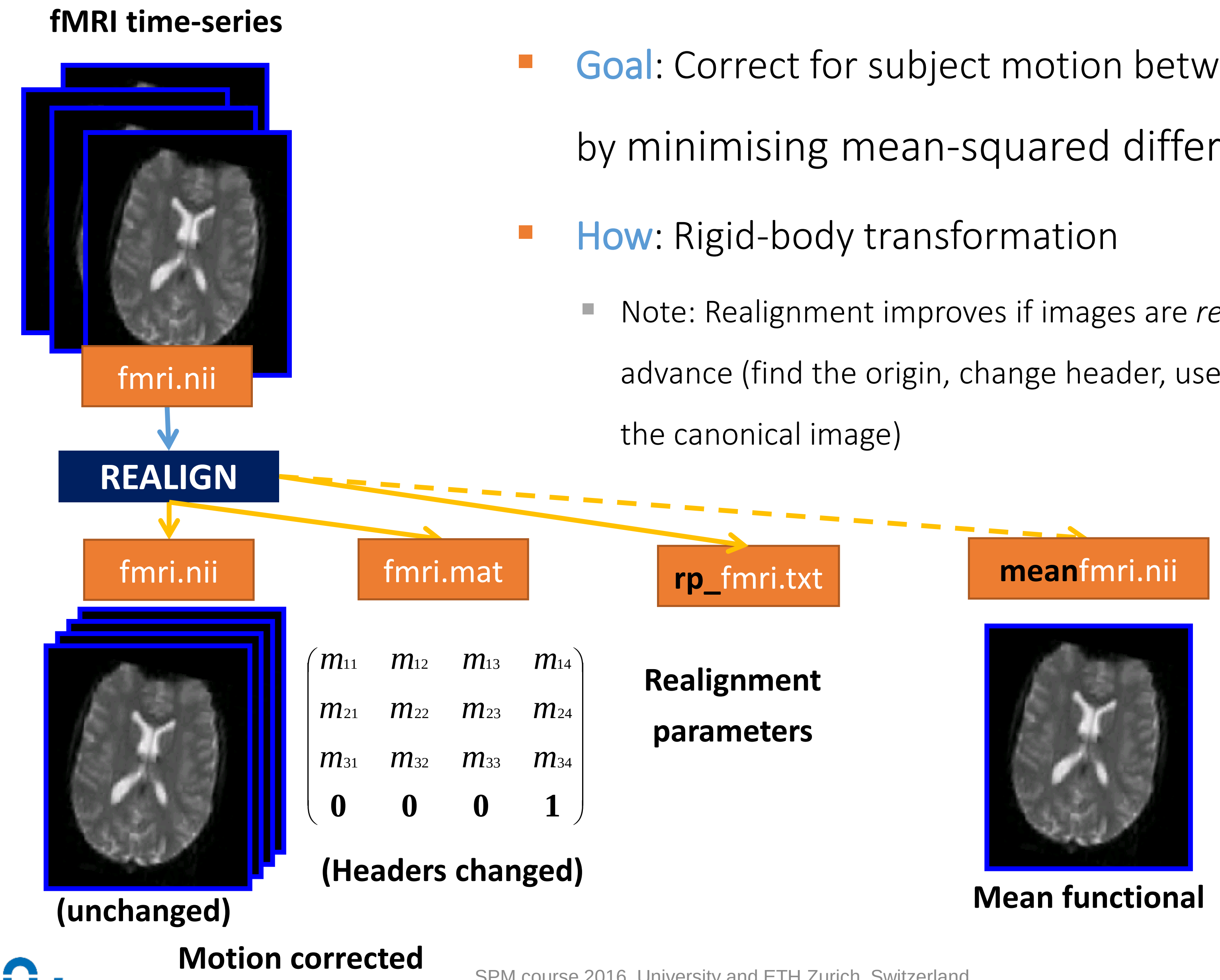
(Headers changed)

MNI Space

GLM

Realignment

- Goal: Correct for subject motion between volumes by minimising mean-squared difference
- How: Rigid-body transformation
  - Note: Realignment improves if images are *reoriented* in advance (find the origin, change header, use check reg with the canonical image)



fMRI time-series

fmri.nii

REALIGN

fmri.nii

fmri.mat

rp_fmri.txt

meanfmri.nii

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

Realignment parameters

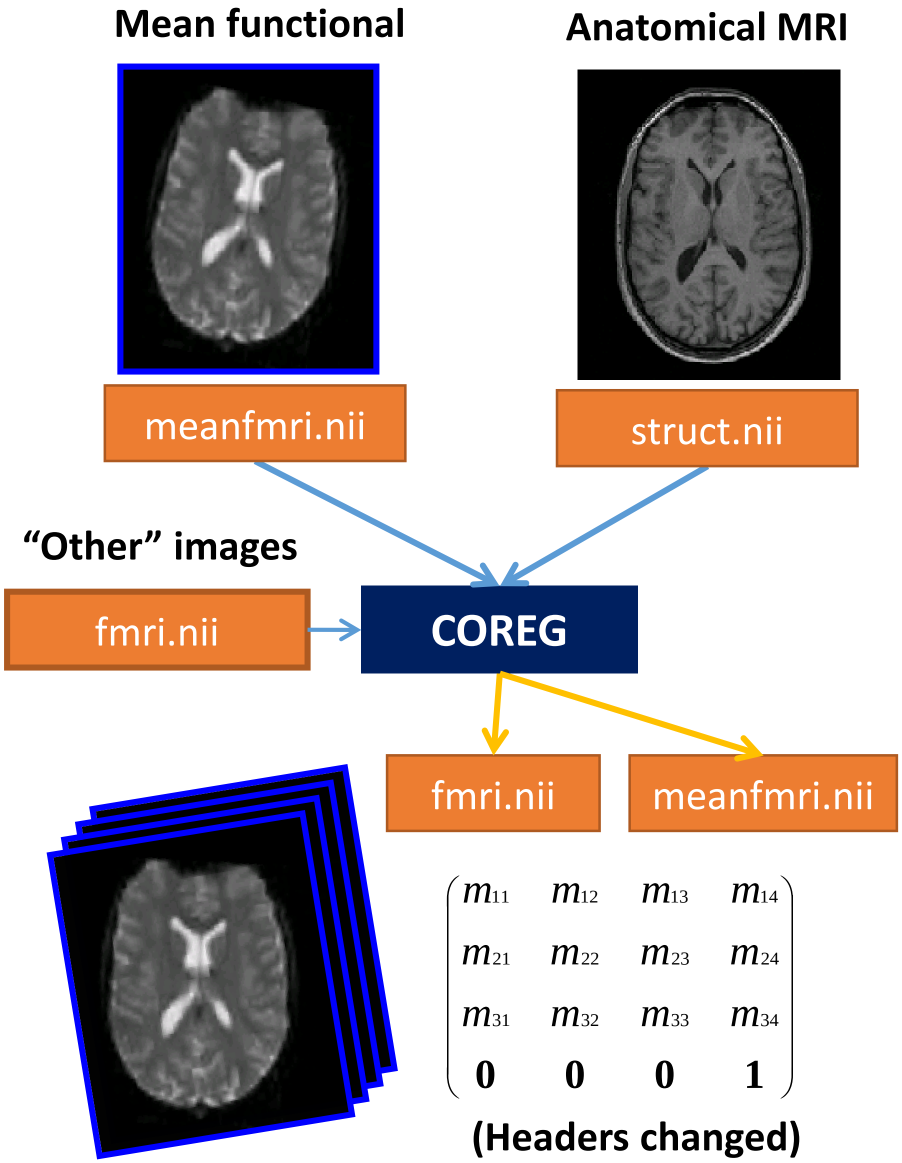
(unchanged)

(Headers changed)

Mean functional

Motion corrected

Co-registration



Mean functional

Anatomical MRI

meanfmri.nii

struct.nii

“Other” images

fmri.nii

COREG

fmri.nii

meanfmri.nii

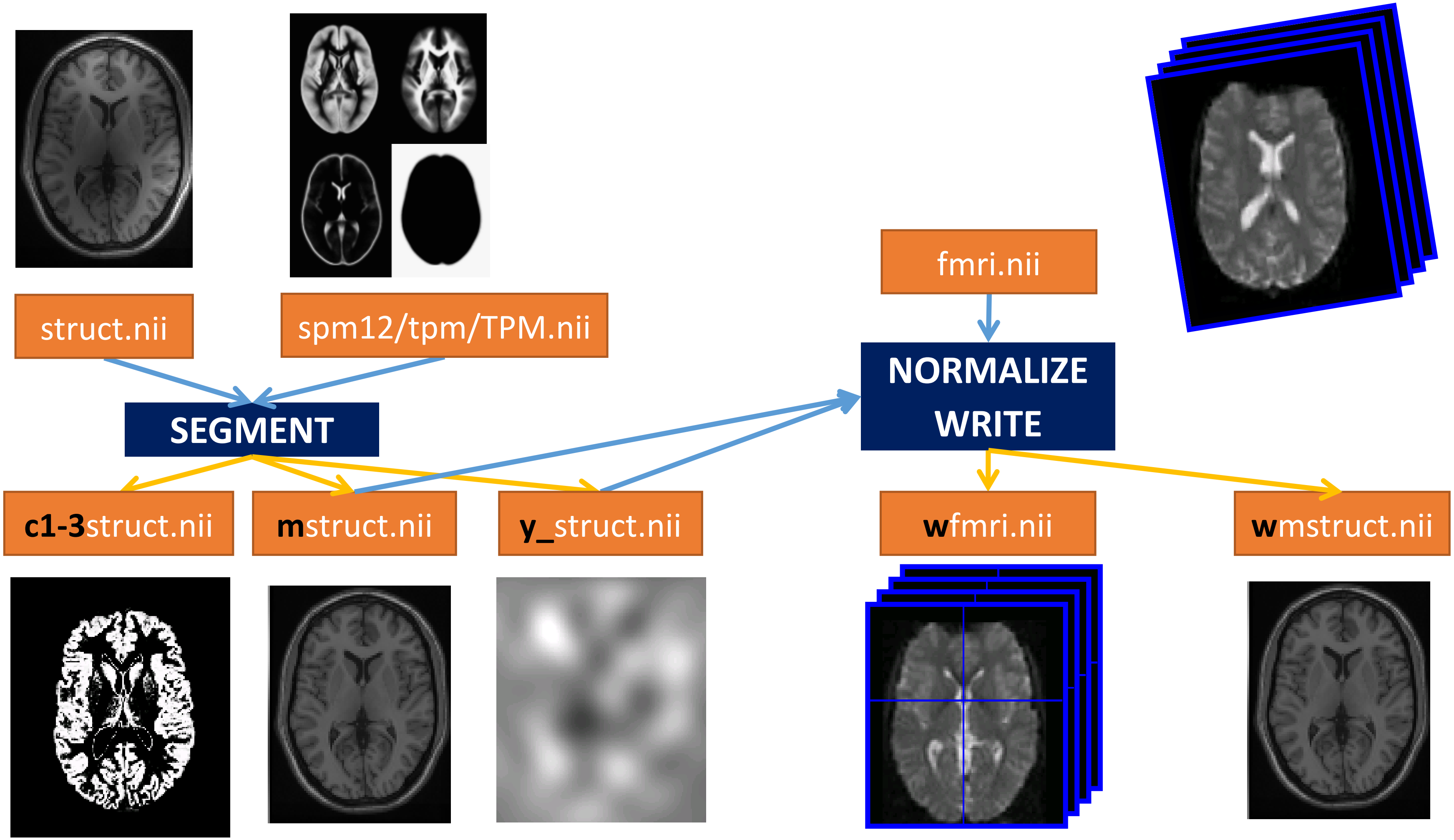
$$\begin{pmatrix} m_{11} & m_{12} & m_{13} & m_{14} \\ m_{21} & m_{22} & m_{23} & m_{24} \\ m_{31} & m_{32} & m_{33} & m_{34} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{1} \end{pmatrix}$$

(Headers changed)

Co-registered

- Goal: Match geometry of functional and structural images from same subject
  - Structural = high-resolution, geometrically correct image for later normalisation
- How: Find affine transformation (rotation/translation/shear/scaling) that maximizes mutual information (similarity) between both images
  - Note: The role of functional and structural image could be reversed in this operation
    Reference = header unchanged
    Source = header will be changed

Normalisation: Unified Segmentation



Anatomical MRI

Standard Space Tissue Probability Maps

Co-registered functional

struct.nii

spm12/tpm/TPM.nii

SEGMENT

c1-3struct.nii

mstruct.nii

y_struct.nii

fmri.nii

NORMALIZE WRITE

wfmri.nii

wmstruct.nii

Segmented Image

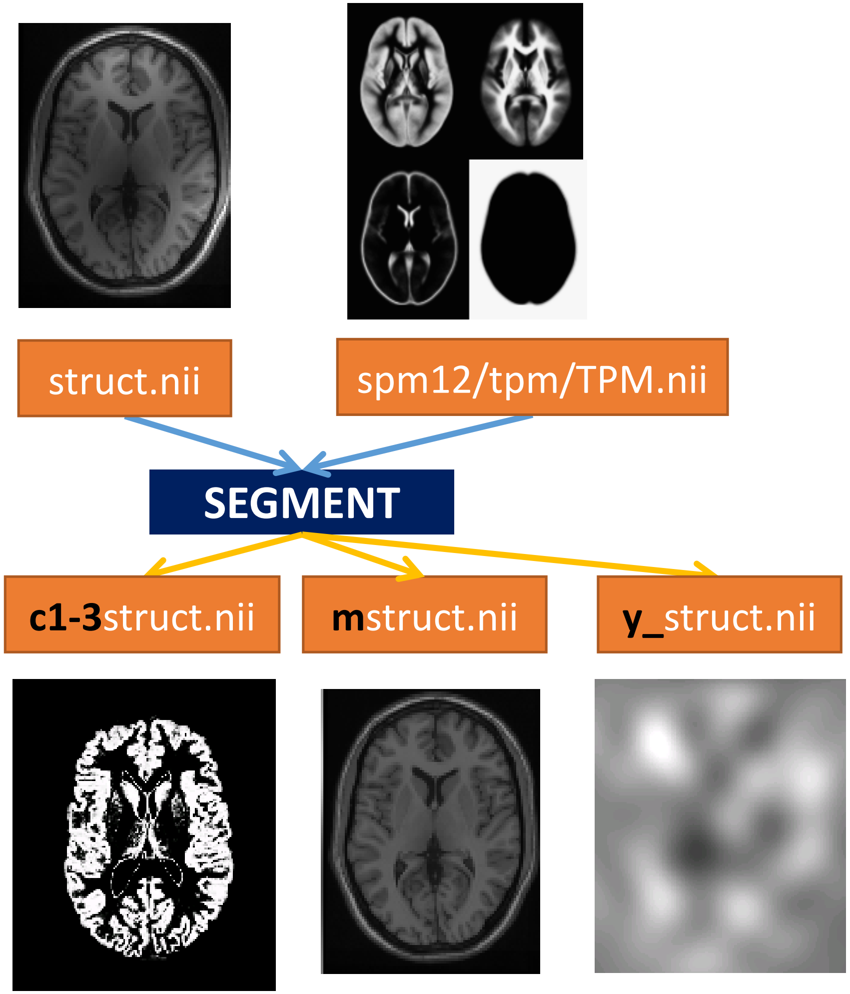
Bias-corrected Structural

Deformation Fields

Normalized Functional (MNI Space)

Normalized Structural

Normalisation I: Compute Segmentation/Deformation Fields



Anatomical MRI

Standard Space Tissue Probability Maps

struct.nii

spm12/tpm/TPM.nii

SEGMENT

c1-3struct.nii

mstruct.nii

y_struct.nii

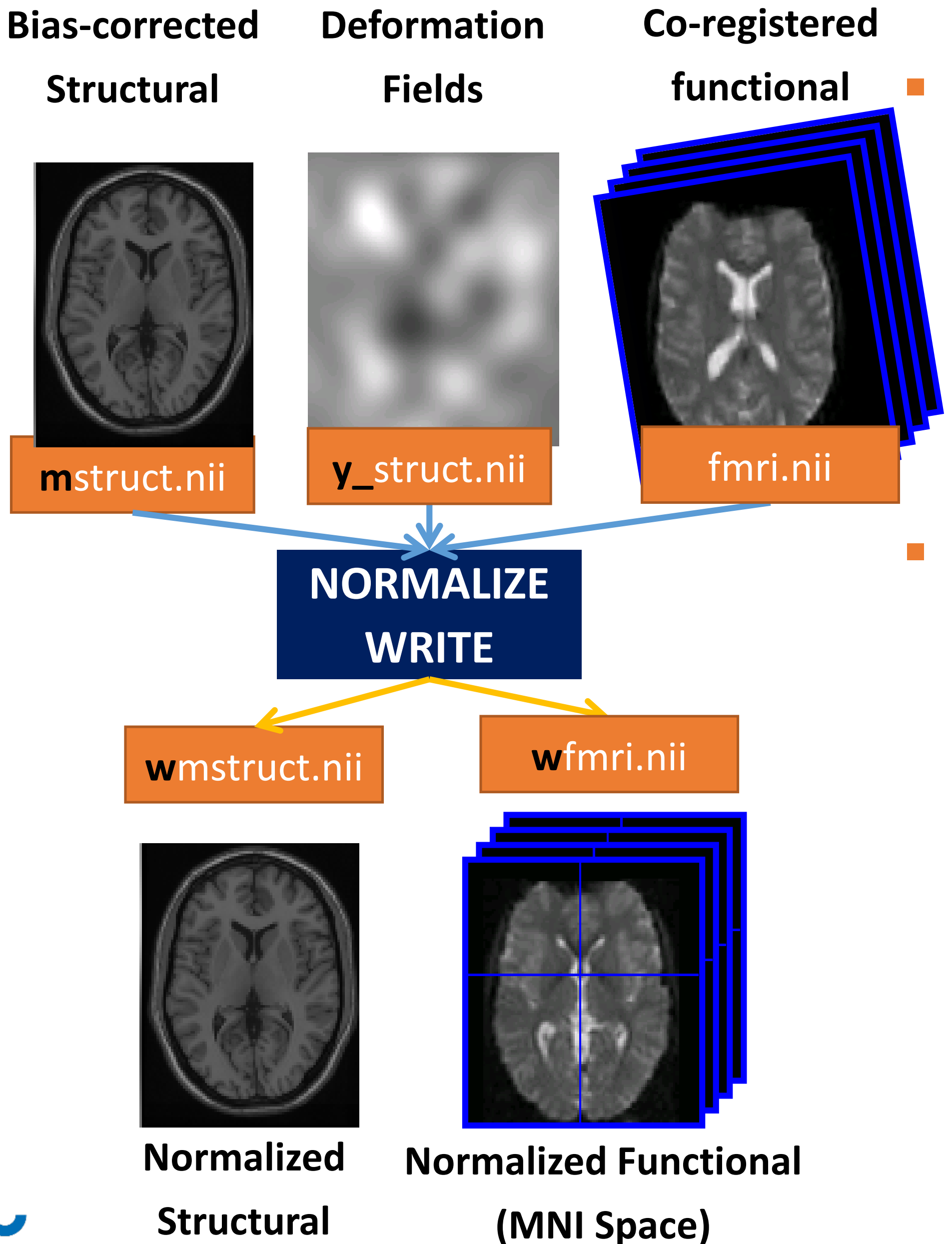
Segmented Image

Bias-corrected Structural

Deformation Fields

- Goal: Match geometry of subject brain to standard space (for group studies)
  - Integrated with segmentation, since mapping individual tissue classes is more robust
- How: Find non-linear transformation (deformation field) that makes tissue class distribution in structural image most plausible
  - Assuming coil inhomogeneity (bias), and deformations of reasonable anatomy
  - Note: uses a Bayesian maximum a posteriori estimation, where standard space tissue probability maps (TPMs) are the priors

Normalisation II: Warp via Write



Bias-corrected Structural

Deformation Fields

Co-registered functional

mstruct.nii

y_struct.nii

fmri.nii

NORMALIZE WRITE

wmstruct.nii

wfmri.nii

Normalized Structural

Normalized Functional (MNI Space)

- Goal: Write out functional/structural image in standard space for multi-subject statistical analysis
  - to report findings in common anatomical space (e.g. MNI)
- How: Applies estimated deformation fields from Unified Segmentation to all functional and structural data
  - Deformation fields have a displacement vector for each image voxel that tells where it should be moved to in standard space

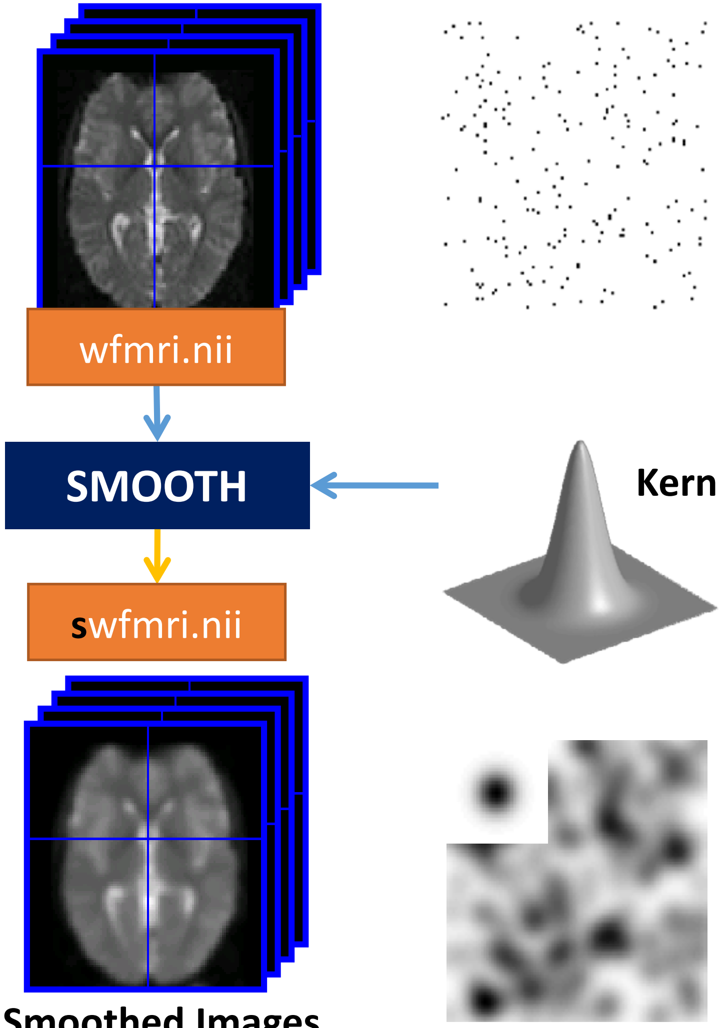
Smoothing

Input →

Output →

Normalized Functional

(MNI Space)



Smoothed Images

(Ready for Stats!)

- Goal: Increase sensitivity by reducing thermal noise and inter-subject variability in functional images
  - Plus a couple of more sophisticated reasons, e.g. matched-filter theorem, smoothness of residual random field for FWE-correction
- How: Convolution ("Blurring") with a 3D Gaussian kernel
  - Each voxel effectively becomes a weighted average of its surroundings (interpolation)
  - Typical full width at half maximum: 2-3 voxel

SPM Image File Prefixes `xfmri.nii/mat`

Prefix	**Meaning**	**Typicallly applied to**
`a`	Slice-timing corrected	functional
`m`	Bias-field corrected (*m*odulated)	structural
`mean`	*Mean* of time-series	functional
`r`	*R*e-sliced (change image matrix, reset hdr)	both
`s`	*S*moothed	functional
`u`	*U*nwarped (during realign/FieldMap Tool)	functional
`y_`	Deformation field	structural
`w`	Normalized (*w*arped with deformation field)	both

SPM File Operations in Matlab Command Window

Operation	Matlab/SPM command
Retrieve multiple file names	`fNames = spm_select('FPList', pwd, '^sM.*\.img$');`
Plot Image(s) with SPM	`spm_check_registration(fNames)`
Load image header(s)	`hdr = spm_vol(fNames);`
Load Image Matrix	`X = spm_read_vols(hdr);`
Inspect Batch in Batch Editor	`spm_jobman('interactive', ...` `matlabbatch);`
Run Batch from command line	`spm_jobman('initcfg'); %1st time` `spm_jobman('run',matlabbatch);`