



fMRI

Preprocessing

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Contents

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- * Between-subject: Normalise/Segment
- * Between-subject: Dartel
- * Between-subject: Smoothing

Image registration

Most “preprocessing” involves aligning images together.

Two components:

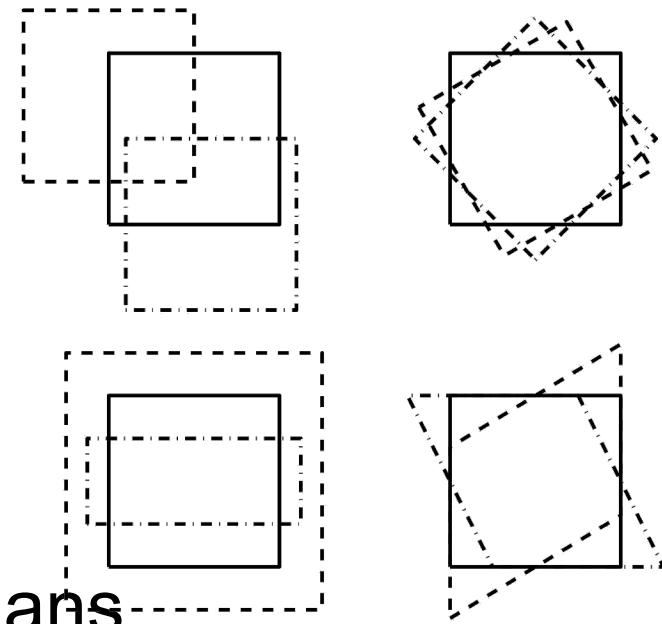
- **Registration** - i.e. Optimise the parameters that describe spatial transformations between the images.
- **Transformation** - i.e. Re-sample according to the determined transformation parameters.

Rigid-body transformations

- * Assume that brain of the same subject doesn't change shape or size in the scanner.
 - * Head can move, but remains the same shape and size.
 - * Some exceptions:
 - * Image distortions.
 - * Brain slops about slightly because of gravity.
 - * Brain growth or atrophy over time.
- * If the subject's head moves, we need to correct the images.
 - * Do this by image registration.

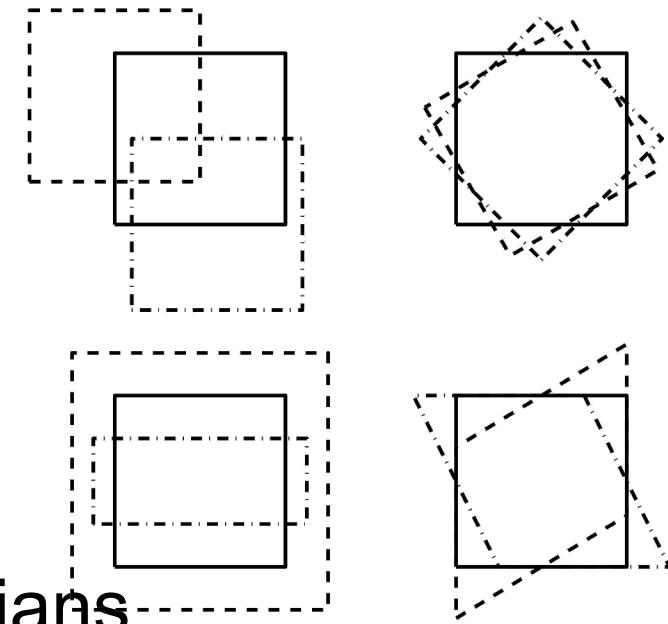
2D affine transforms

- * Translations by t_x and t_y
 - * $x_1 = x_0 + t_x$
 - * $y_1 = y_0 + t_y$
 - * Rotation around the origin by Θ radians
 - * $x_1 = \cos(\Theta) x_0 + \sin(\Theta) y_0$
 - * $y_1 = -\sin(\Theta) x_0 + \cos(\Theta) y_0$
 - * Zooms by s_x and s_y
 - * $x_1 = s_x x_0$
 - * $y_1 = s_y y_0$
- * Shear
 - * $x_1 = x_0 + h y_0$
 - * $y_1 = y_0$



2D affine transforms

- * Translations by t_x and t_y
 - * $x_1 = 1 x_0 + 0 y_0 + t_x$
 - * $y_1 = 0 x_0 + 1 y_0 + t_y$
- * Rotation around the origin by Θ radians
 - * $x_1 = \cos(\Theta) x_0 + \sin(\Theta) y_0 + 0$
 - * $y_1 = -\sin(\Theta) x_0 + \cos(\Theta) y_0 + 0$
- * Zooms by s_x and s_y :
 - * $x_1 = s_x x_0 + 0 y_0 + 0$
 - * $y_1 = 0 x_0 + s_y y_0 + 0$



*Shear

- * $x_1 = 1 x_0 + h y_0 + 0$
- * $y_1 = 0 x_0 + 1 y_0 + 0$

3D rigid-body transformations

- * A 3D rigid body transform is defined by:
 - * 3 translations - in X, Y & Z directions
 - * 3 rotations - about X, Y & Z axes
- * The order of the operations matters

$$\begin{pmatrix} 1 & 0 & 0 & X_{\text{trans}} \\ 0 & 1 & 0 & Y_{\text{trans}} \\ 0 & 0 & 1 & Z_{\text{trans}} \\ 0 & 0 & 0 & 1 \end{pmatrix} \times \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & \cos\Phi & \sin\Phi & 0 \\ 0 & -\sin\Phi & \cos\Phi & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix} \times \begin{pmatrix} \cos\Theta & 0 & \sin\Theta & 0 \\ 0 & 1 & 0 & 0 \\ -\sin\Theta & 0 & \cos\Theta & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix} \times \begin{pmatrix} \cos\Omega & \sin\Omega & 0 & 0 \\ -\sin\Omega & \cos\Omega & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix}$$

Translations

Pitch
about x axis

Roll
about y axis

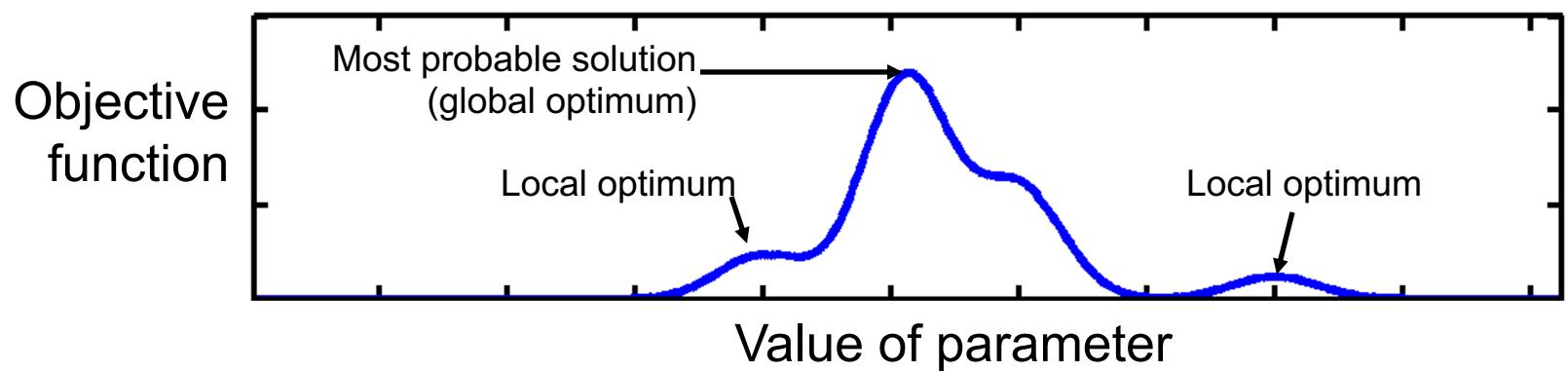
Yaw
about z axis

Voxel-to-world transforms

- * Affine transform associated with each image
 - * Maps from voxels ($x=1..n_x$, $y=1..n_y$, $z=1..n_z$) to some world coordinate system. e.g.,
 - * Scanner co-ordinates - images from DICOM toolbox
 - * T&T/MNI coordinates - spatially normalised
- * Registering image B (source) to image A (target) will update B's voxel-to-world mapping
 - * Mapping from voxels in A to voxels in B is by
 - * A-to-world using M_A , then world-to-B using M_B^{-1}
 - * $M_B^{-1} M_A$

Optimisation

- * Image registration is done by optimisation.
- * Optimisation involves finding some “best” parameters according to an “objective function”, which is either minimised or maximised
- * The “objective function” is often related to a probability based on some model



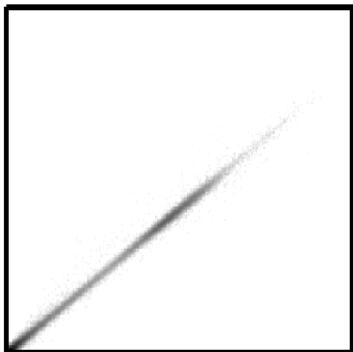
Optimisation

- * Because registration only finds a *local optimum*, some manual reorienting of the images may be needed before doing anything else in SPM.

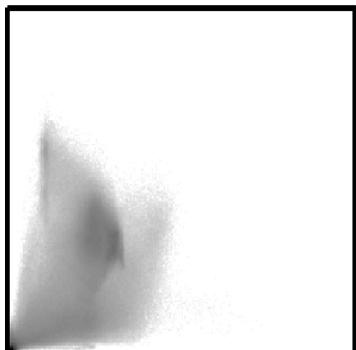
An MNI-space image from spm12/canonical directory.



Objective functions



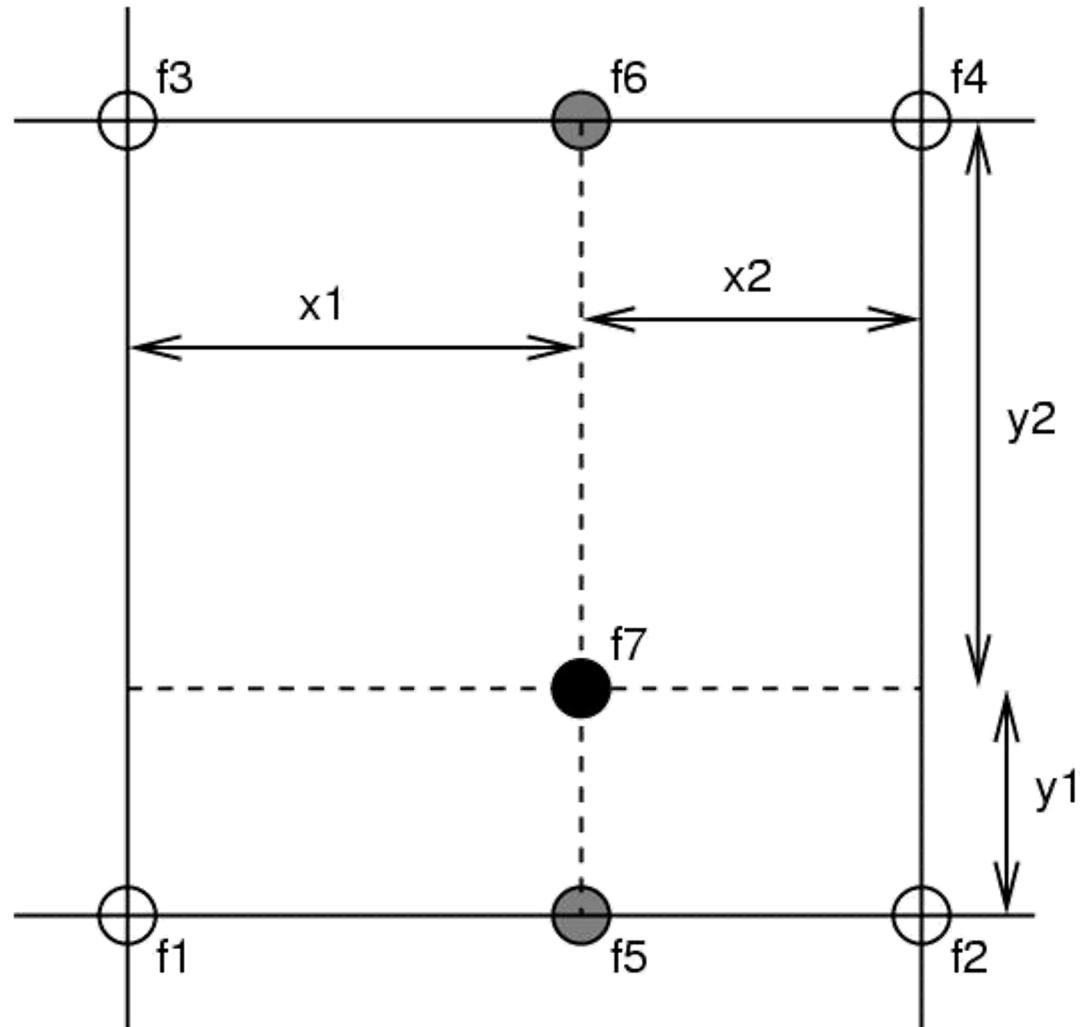
- * Intra-modal
 - * Mean squared difference (minimise)
 - * Normalised cross correlation (maximise)



- * Inter-modal (or intra-modal)
 - * Mutual information (maximise)
 - * Normalised mutual information (maximise)
 - * Entropy correlation coefficient (maximise)

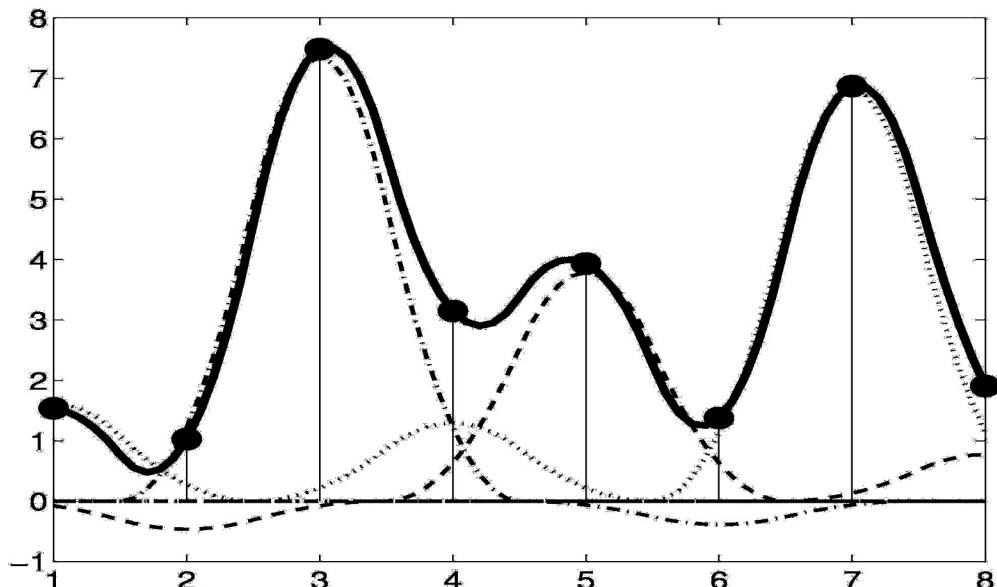
Simple interpolation

- * Nearest neighbour
 - * Take the value of the closest voxel
- * Tri-linear
 - * Just a weighted average of the neighbouring voxels
 - * $f_5 = f_1 x_2 + f_2 x_1$
 - * $f_6 = f_3 x_2 + f_4 x_1$
 - * $f_7 = f_5 y_2 + f_6 y_1$

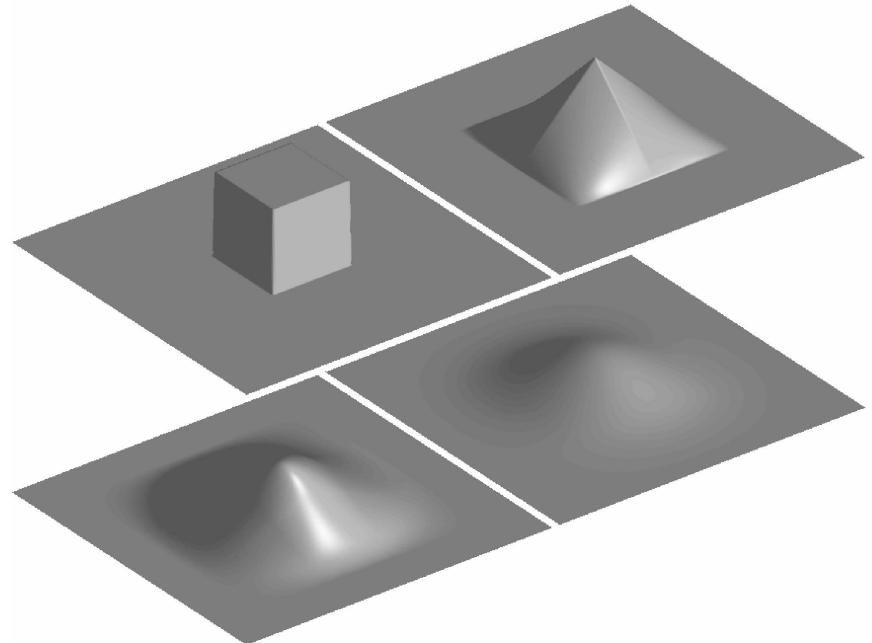


B-spline interpolation

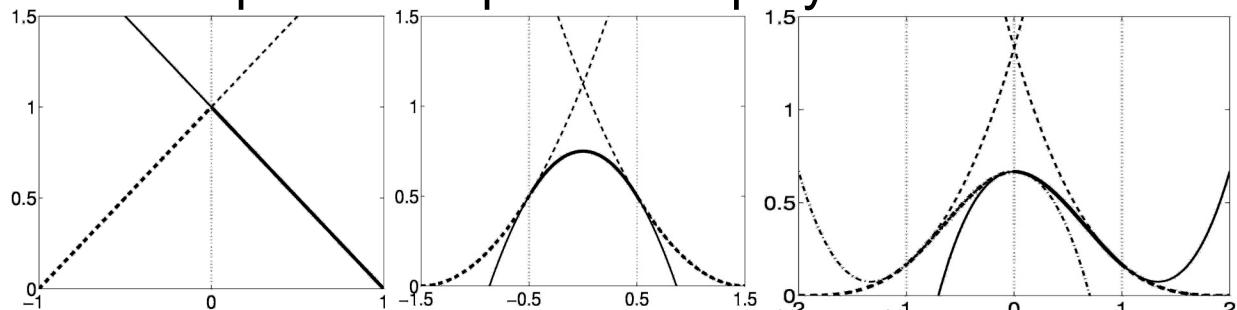
A continuous function is represented by a linear combination of basis functions



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

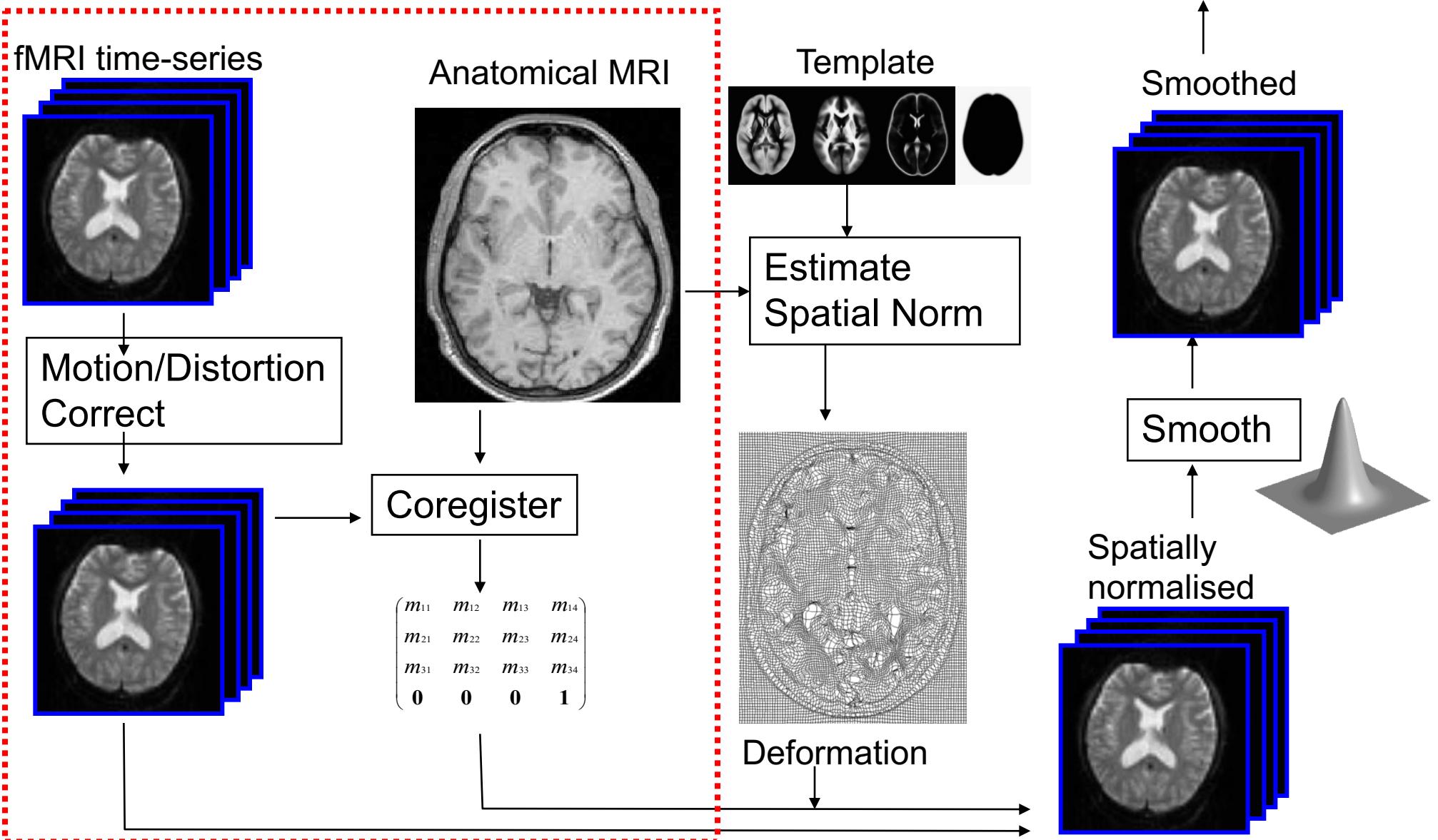


B-splines are piecewise polynomials



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

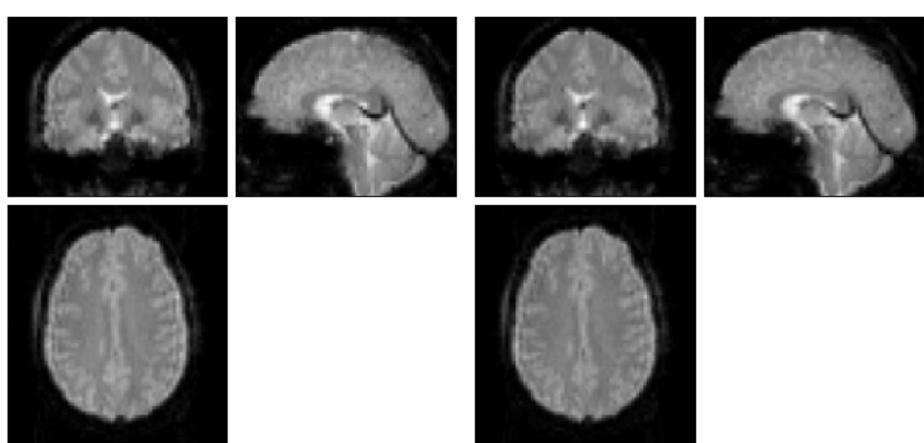
Pre-processing overview



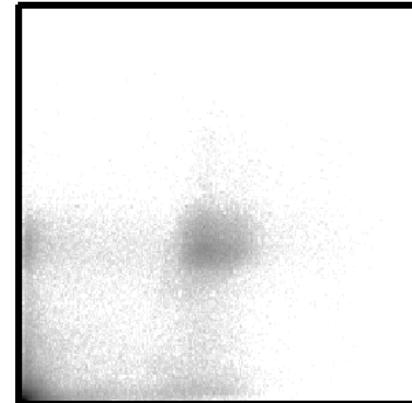
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- * Within-subject: EPI Distortion Correction
- * Within-subject: Coregistration
- * Between-subject: Normalise/Segment
- * Between-subject: Dartel
- * Between-subject: Smoothing

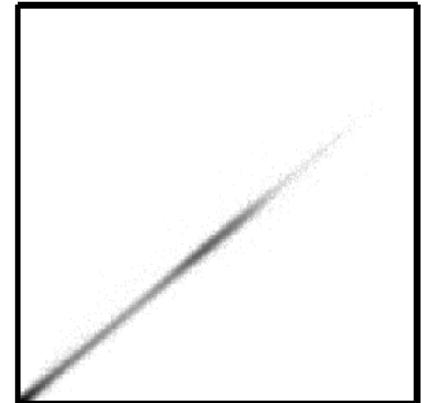
Mean-squared difference



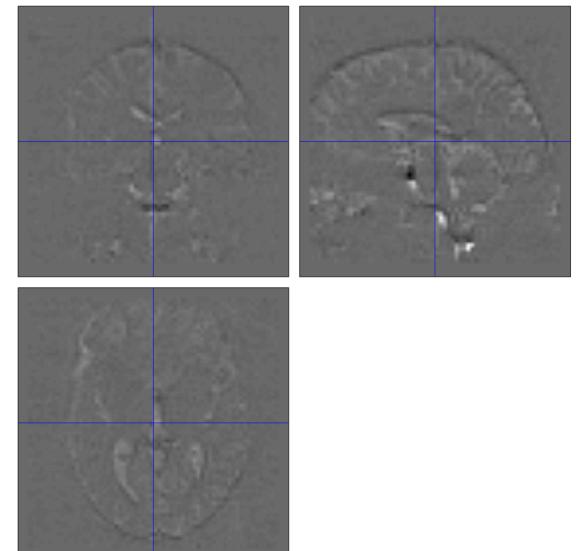
Original Joint Histogram



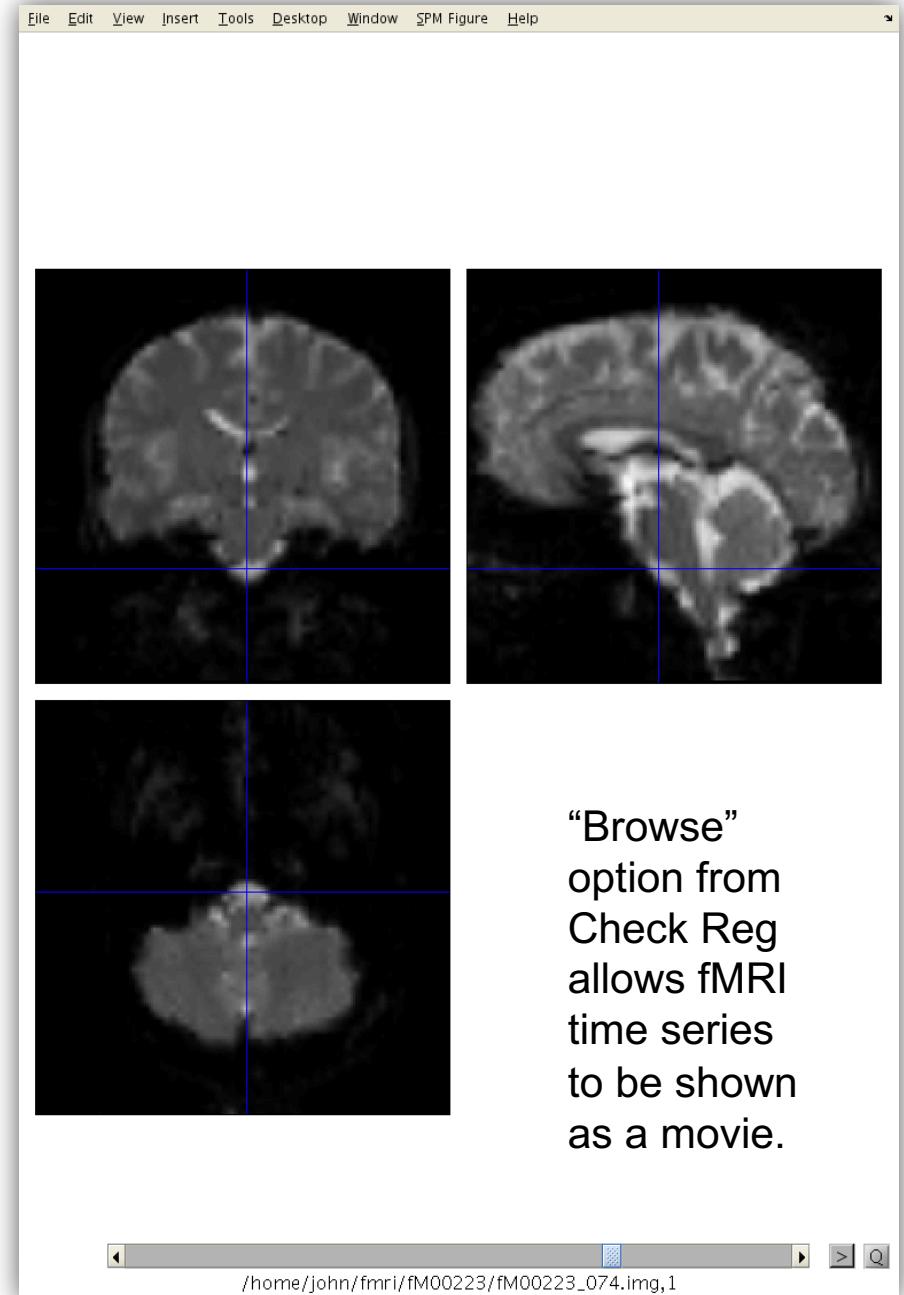
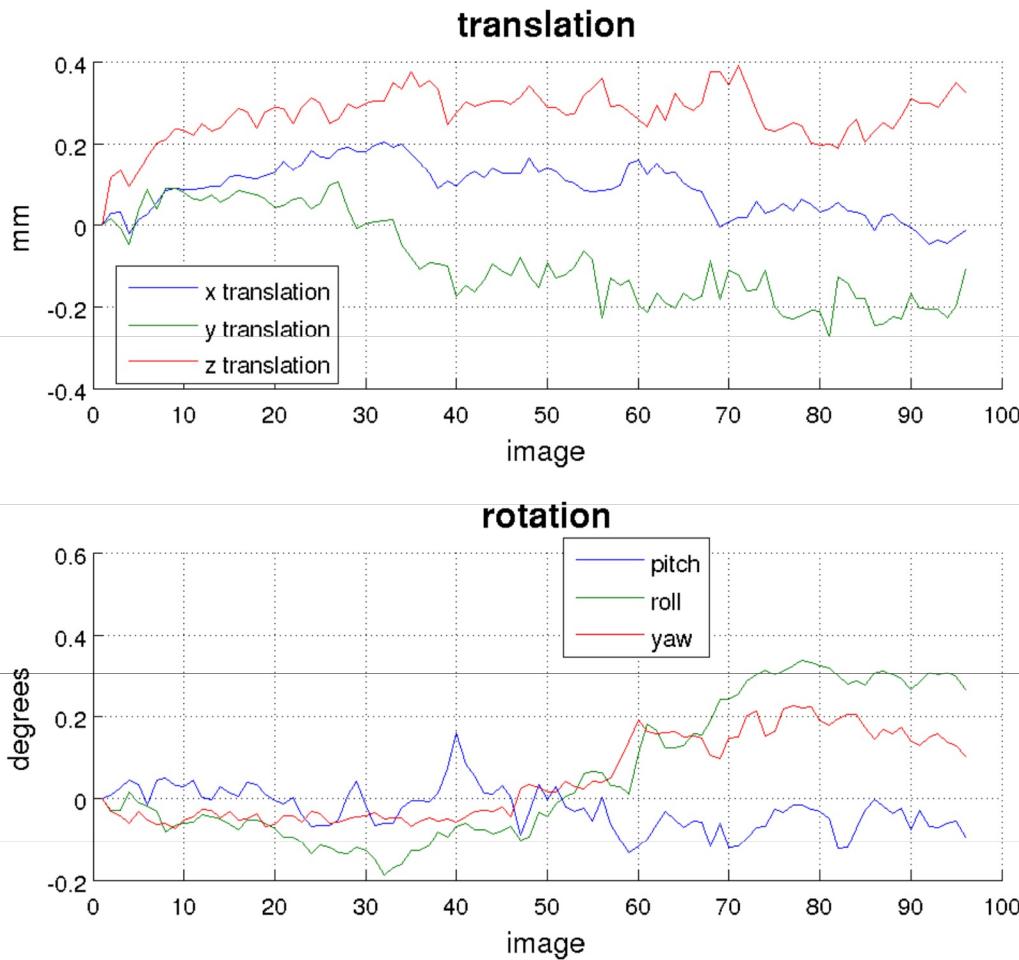
Final Joint Histogram



- * Minimising mean-squared difference works for intra-modal registration (realignment)
- * Simple relationship between intensities in one image, versus those in the other
 - * Assumes normally distributed differences



Motion estimates



Residual errors from aligned fMRI

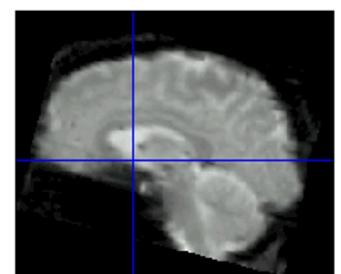
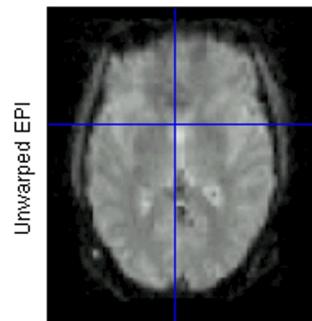
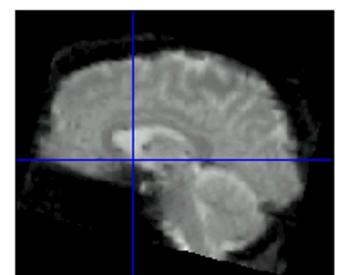
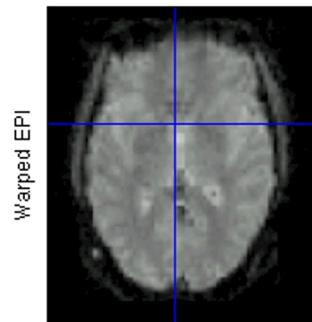
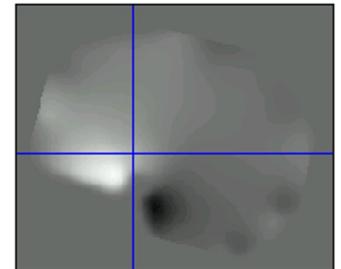
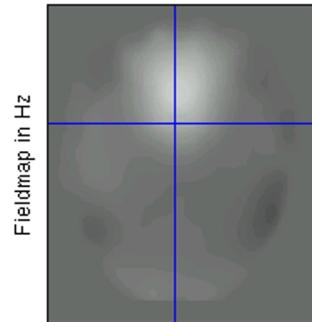
- * Re-sampling can introduce interpolation errors
 - * especially tri-linear interpolation
- * Gaps between slices can cause aliasing artefacts
- * Slices are not acquired simultaneously
 - * rapid movements not accounted for by rigid body model
- * Image artefacts may not move according to a rigid body model
 - * image distortion
 - * image dropout
 - * Nyquist ghost
- * BOLD signal changes influence the estimated motion.
- * Functions of the estimated motion parameters can be modelled as confounds in subsequent analyses

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 - * Movement by distortion interaction
- * Within-subject: Coregistration
- * Between-subject: Normalise/Segment
- * Between-subject: Dartel
- * Between-subject: Smoothing

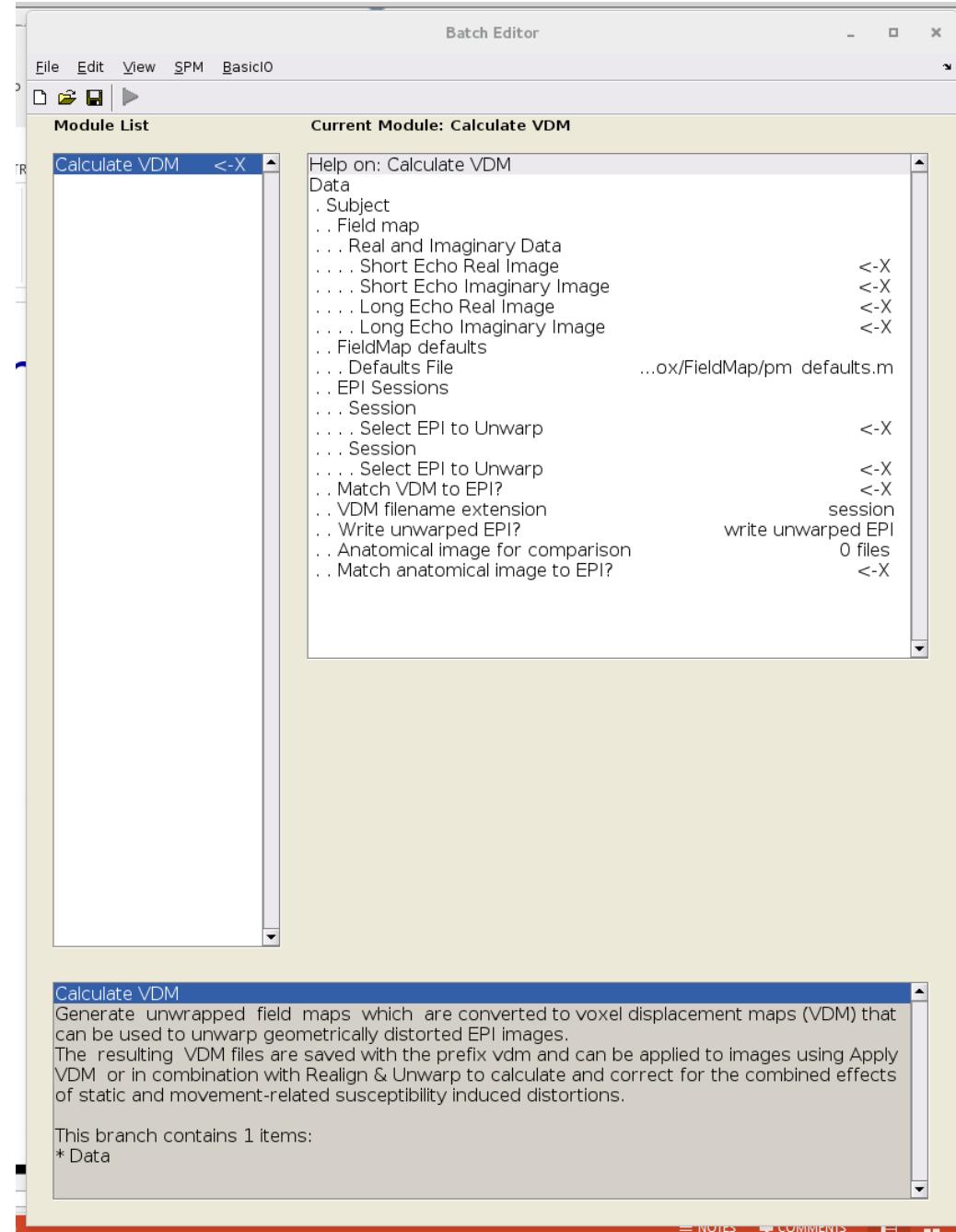
EPI distortion

- * Magnetic susceptibility differs among tissues.
- * Greatest difference is between air and tissue.
- * Subject disrupts B_0 field, rendering it inhomogeneous
- * Distortions in phase-encode direction



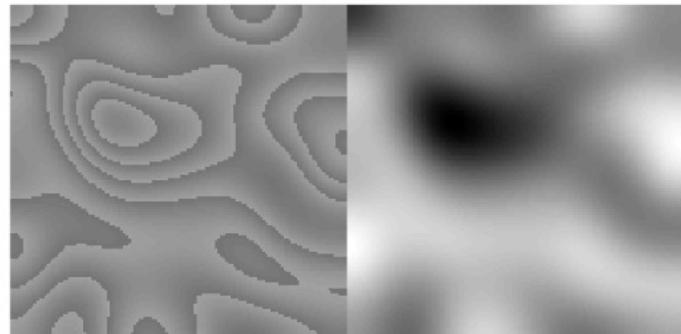
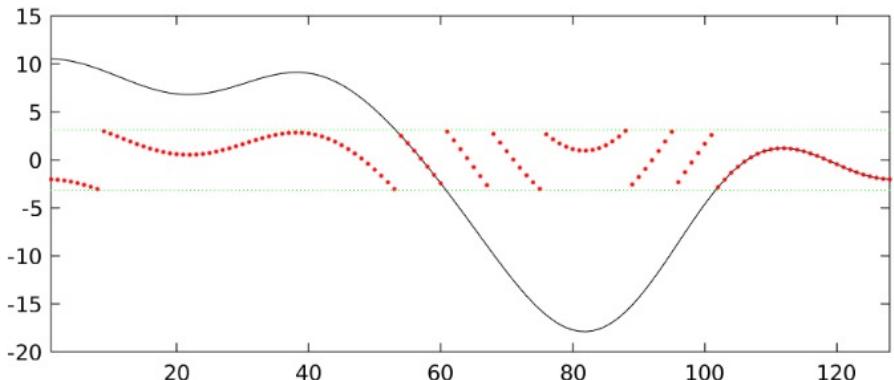
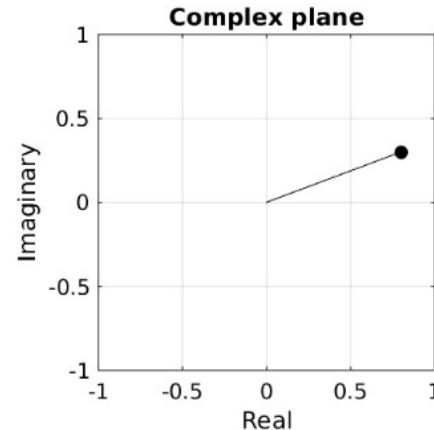
FieldMap toolbox

- * Computes a voxel-displacement map (VDM) from fieldmap scans.
- * Used to correct distortions in EPI.



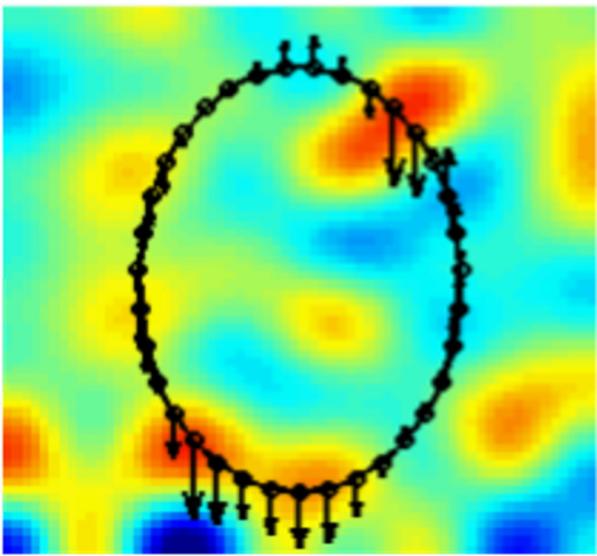
Phase unwrapping

- * Phase of complex data used.
- * $-\pi/2 < \text{phase} < \pi/2$
- * Phase-unwrapping needed.
 - * Part that is most likely to go wrong.
 - * Phase is poorly defined when magnitude is small relative to noise.

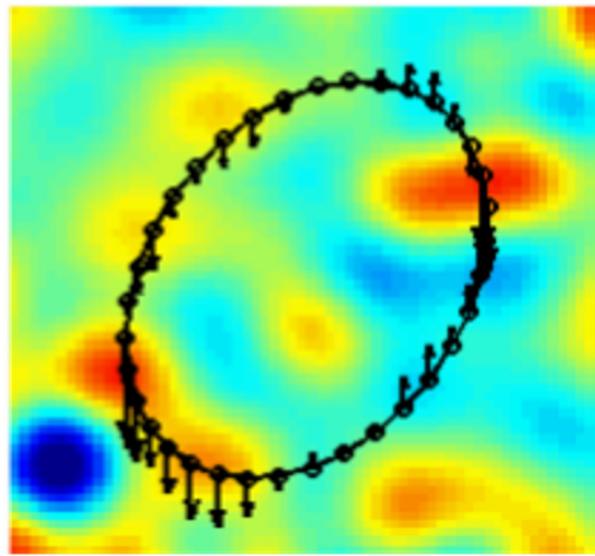


Movement-by-distortion interaction

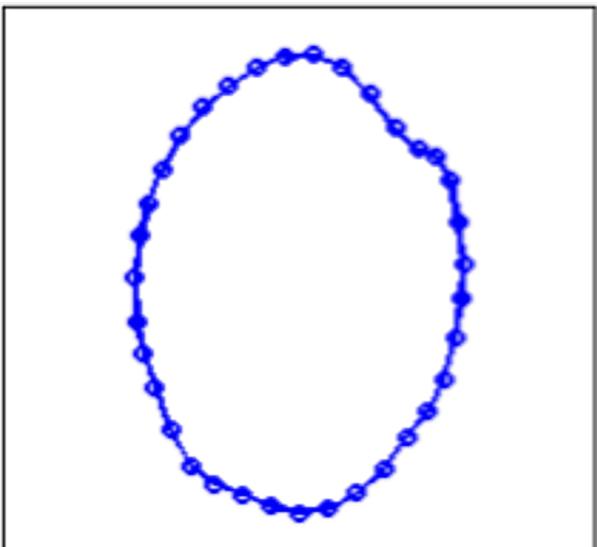
Original position



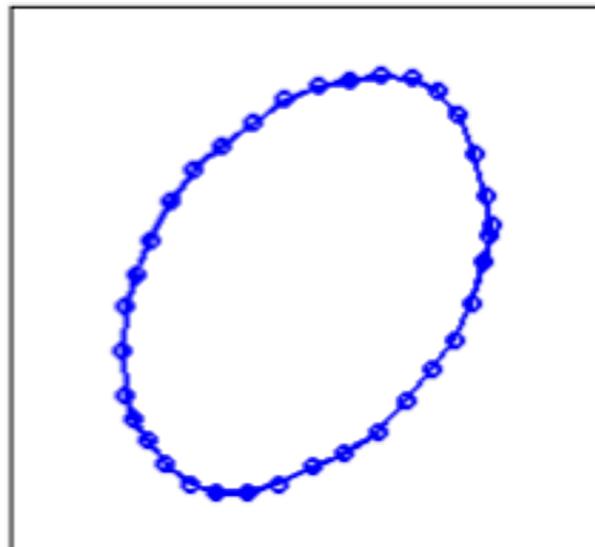
After rotation



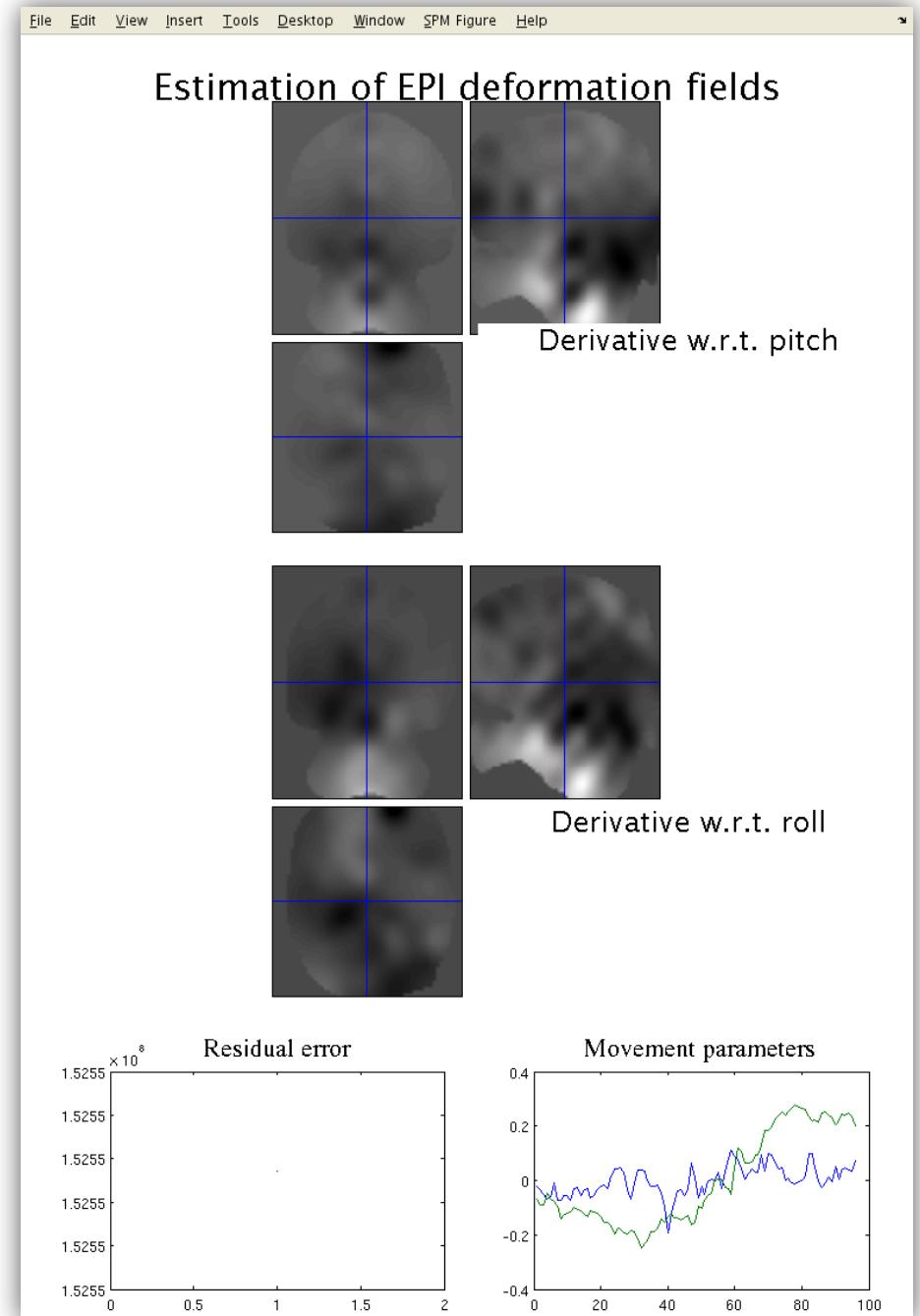
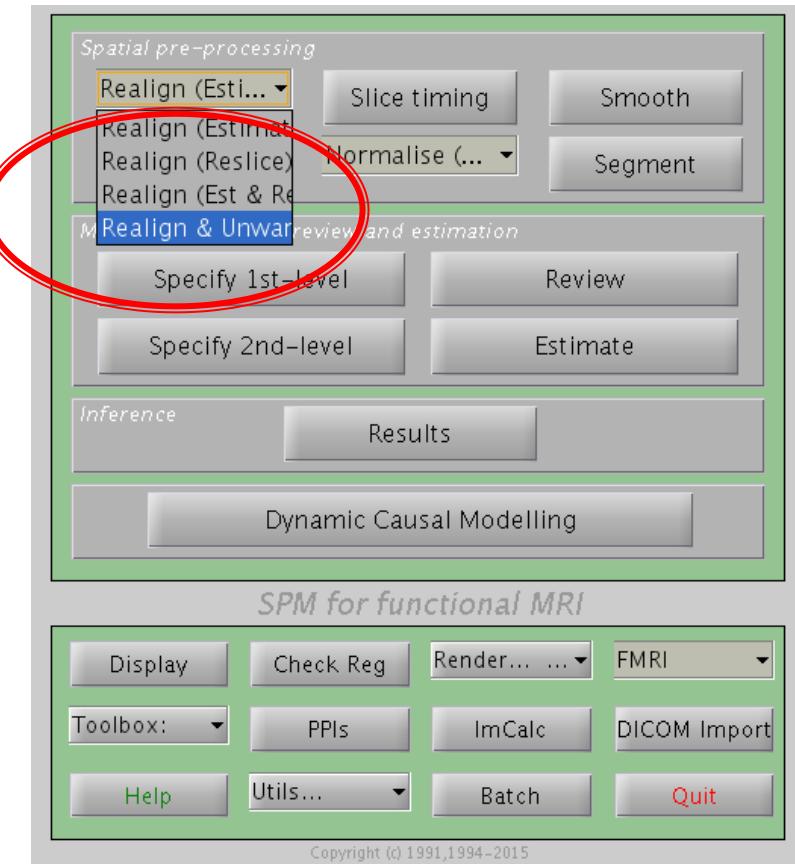
Original position



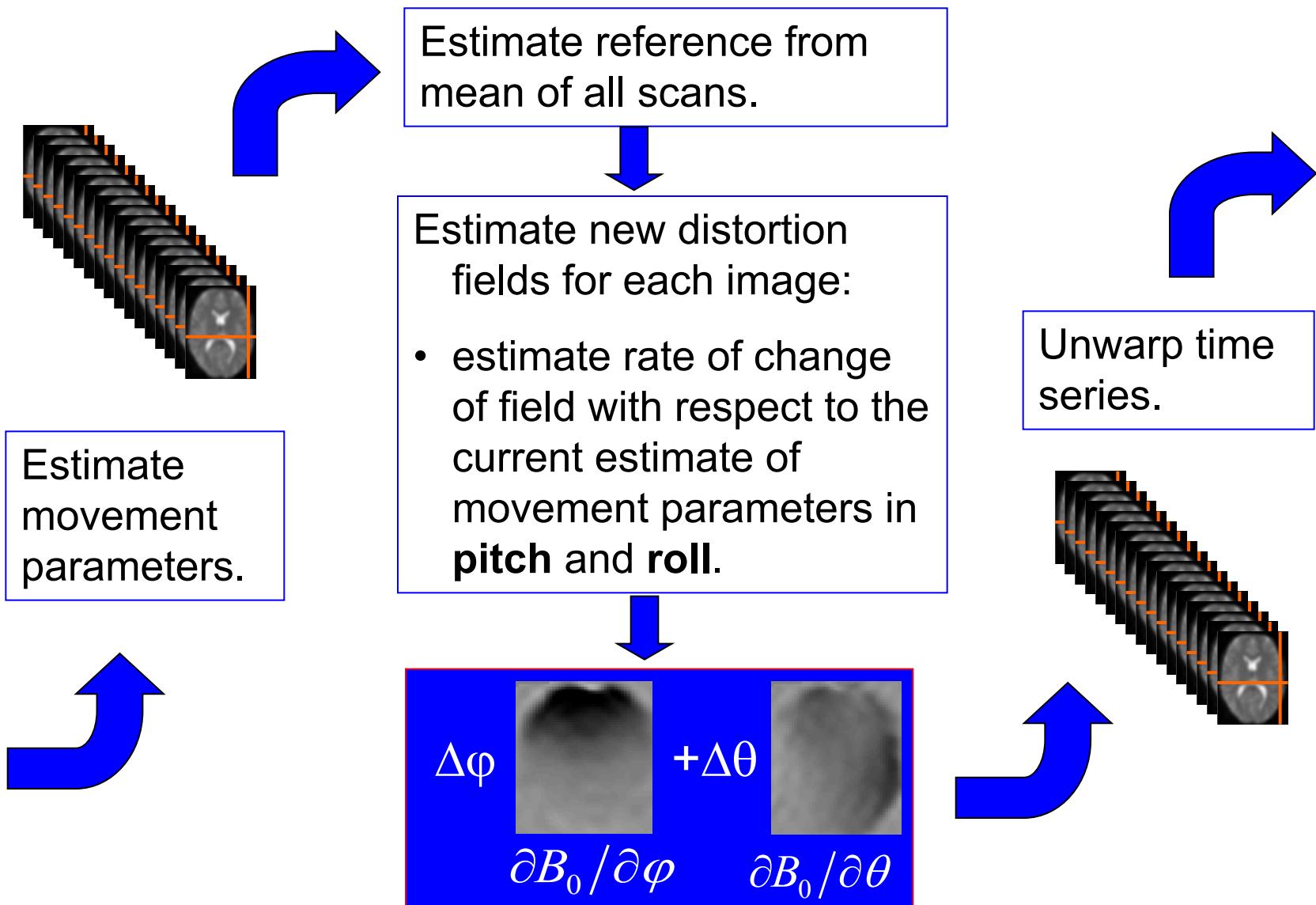
After rotation



Realign & Unwarp



Correcting for distortion changes

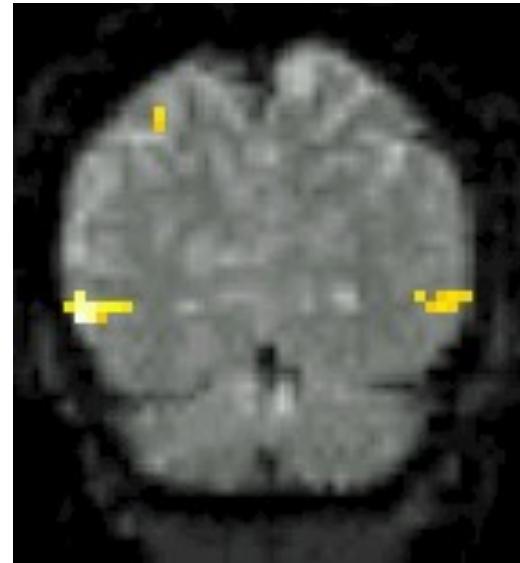


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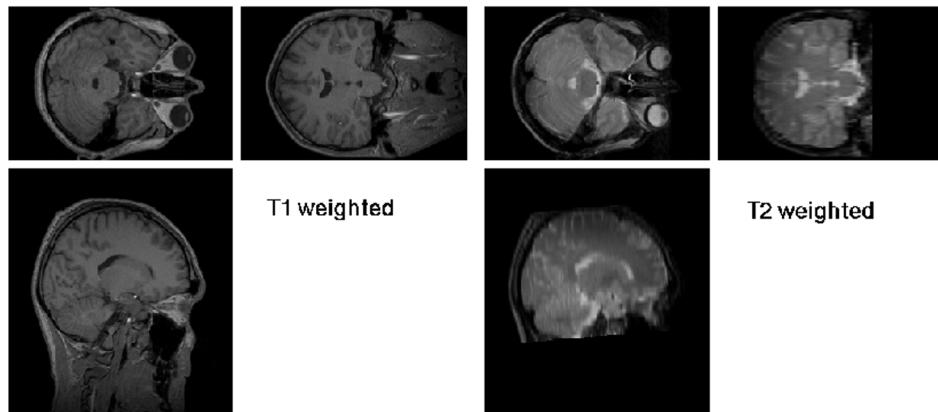
- * Preliminaries
- * Within-subject: Realignment
- * Within-subject: EPI Distortion Correction
- * **Within-subject: Coregistration**
 - * Coregistration by maximising mutual information
- * Between-subject: Normalise/Segment
- * Between-subject: Dartel
- * Smoothing

Coregistration

- Inter-modal registration.
- Match images from same subject but different modalities:
 - anatomical localisation of single subject activations
 - achieve more precise spatial normalisation of functional image using anatomical image.

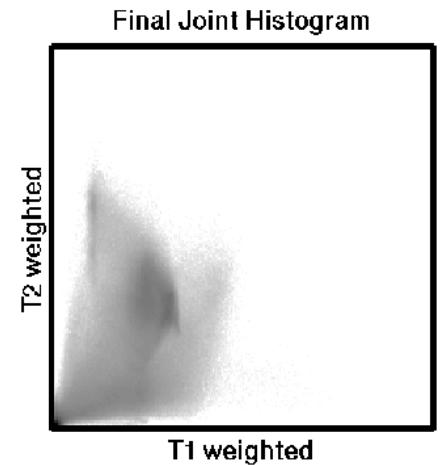
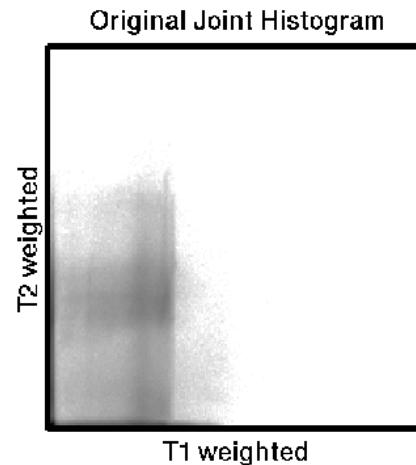


Coregistration maximises Mutual Information



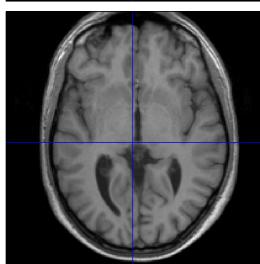
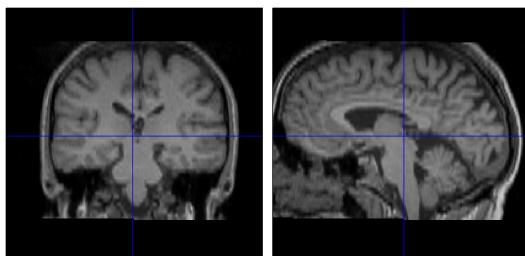
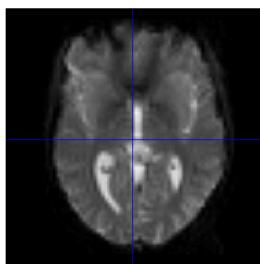
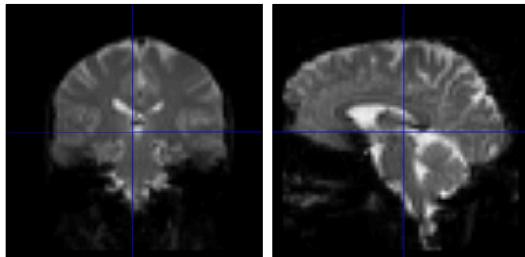
T1 weighted

T2 weighted

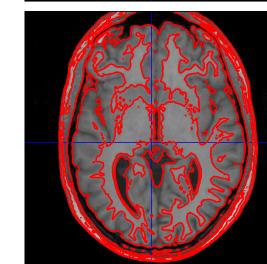
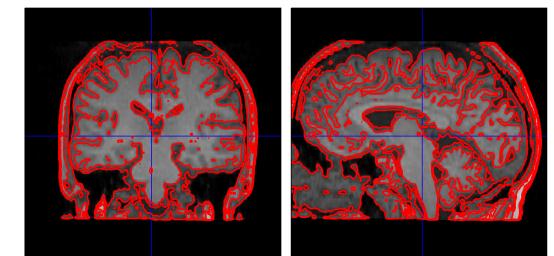
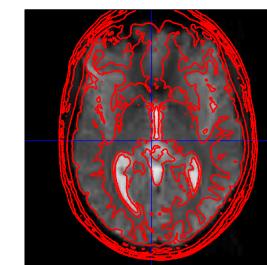
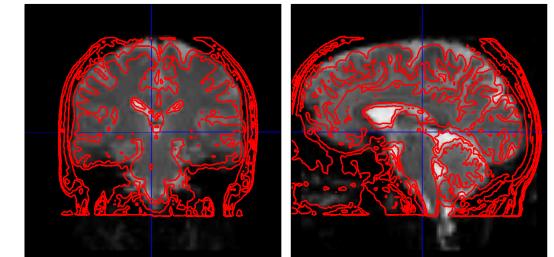


- * Used for between-modality registration
- * Derived from joint histograms
- * $MI = \int_{ab} P(a,b) \log_2 [P(a,b)/(P(a) P(b))]$
 - * Related to entropy: $MI = -H(a,b) + H(a) + H(b)$
 - * Where $H(a) = -\int_a P(a) \log_2 P(a)$ and $H(a,b) = -\int_a P(a,b) \log_2 P(a,b)$

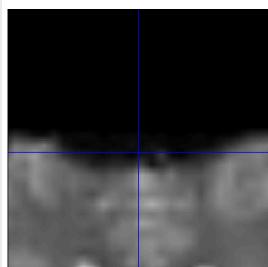
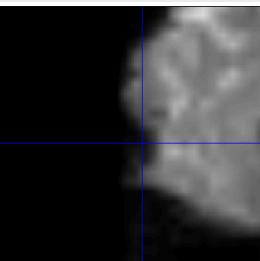
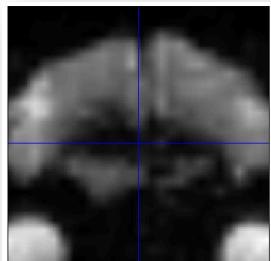
“Check Reg” to assess alignment



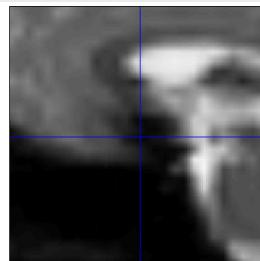
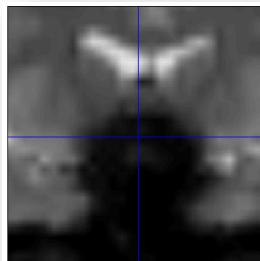
Check Reg allows
contours from one image
to be shown
superimposed on another



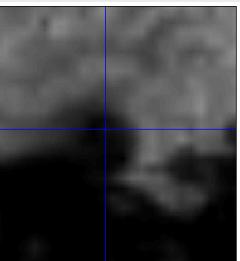
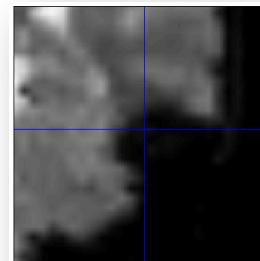
EPI dropout and distortion



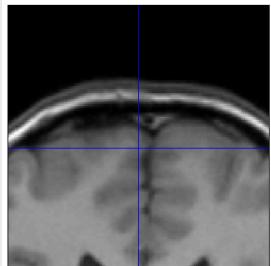
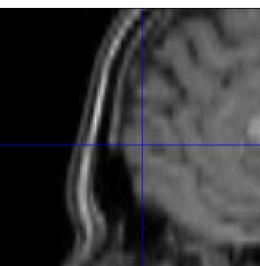
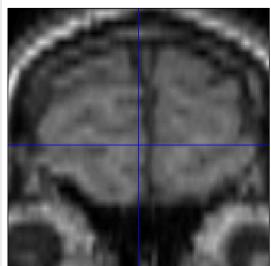
EPI



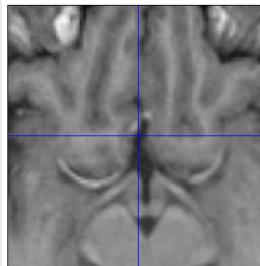
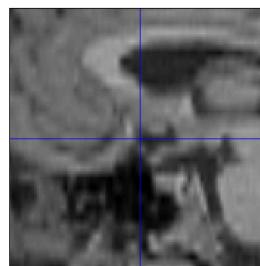
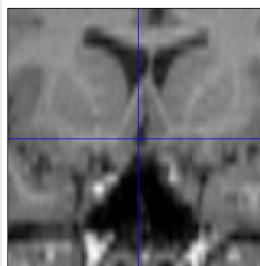
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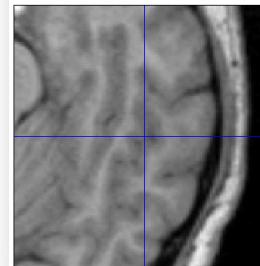
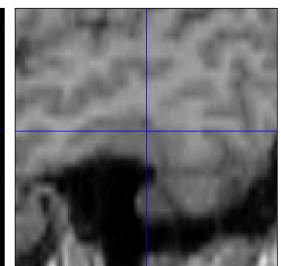
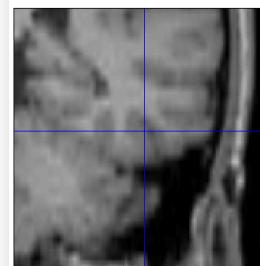
EPI



structural



structural



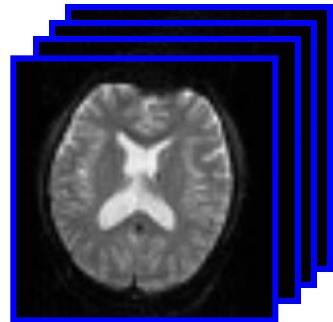
structural

References

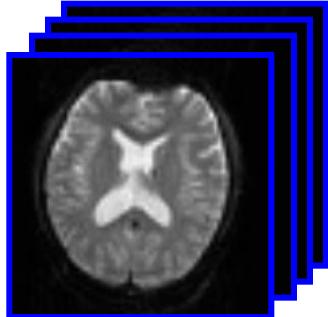
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- * Andersson et al. *Modeling geometric deformations in EPI time series*. Neuroimage 13:903-919 (2001).
- * Hutton et al. *Image distortion correction in fMRI: a quantitative evaluation*. NeuroImage 16:217-240 (2002).

Pre-processing overview

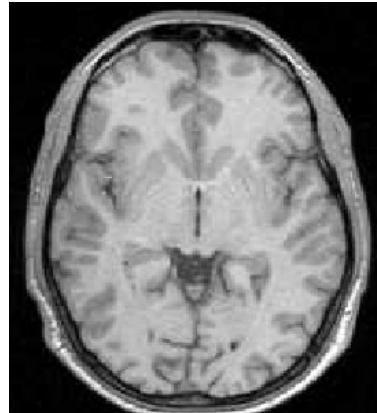
fMRI time-series



Motion Correct



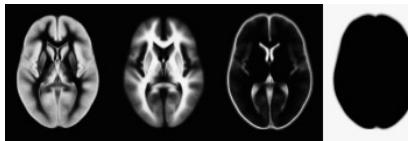
Anatomical MRI



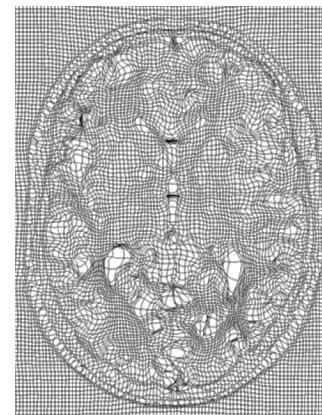
Coregister

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

Template



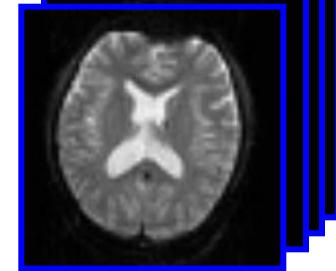
Estimate
Spatial Norm



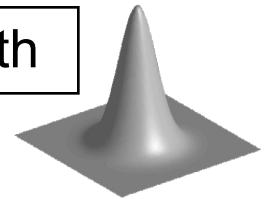
Deformation

Statistics or
whatever

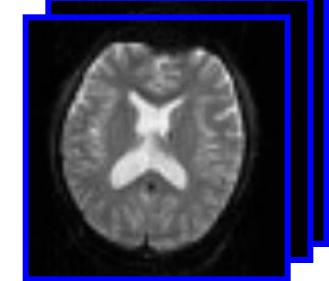
Smoothed



Smooth

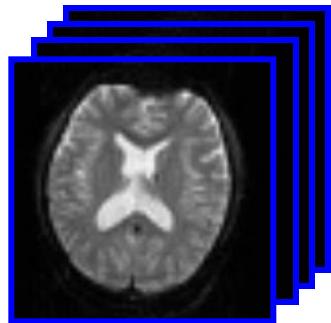


Spatially
normalised

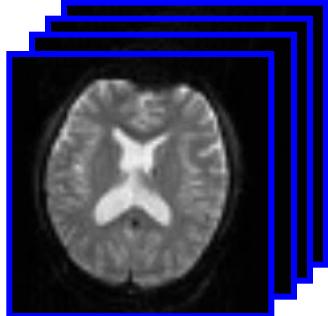


Alternative pipeline

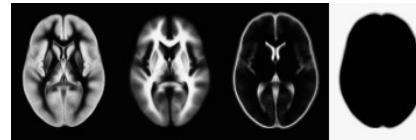
fMRI time-series



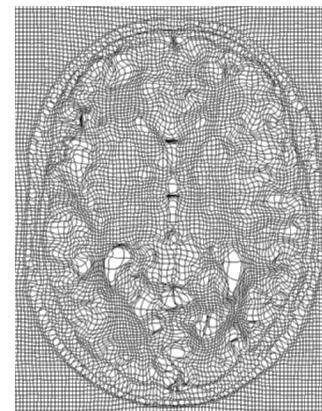
Motion Correct



Template



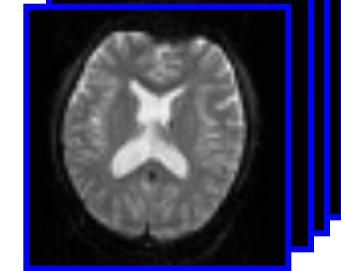
Estimate
Spatial Norm



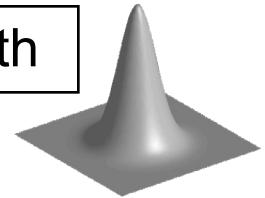
Deformation

Statistics or
whatever

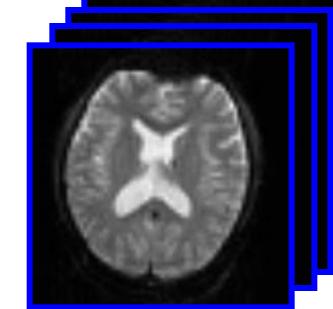
Smoothed



Smooth



Spatially
normalised



Contents

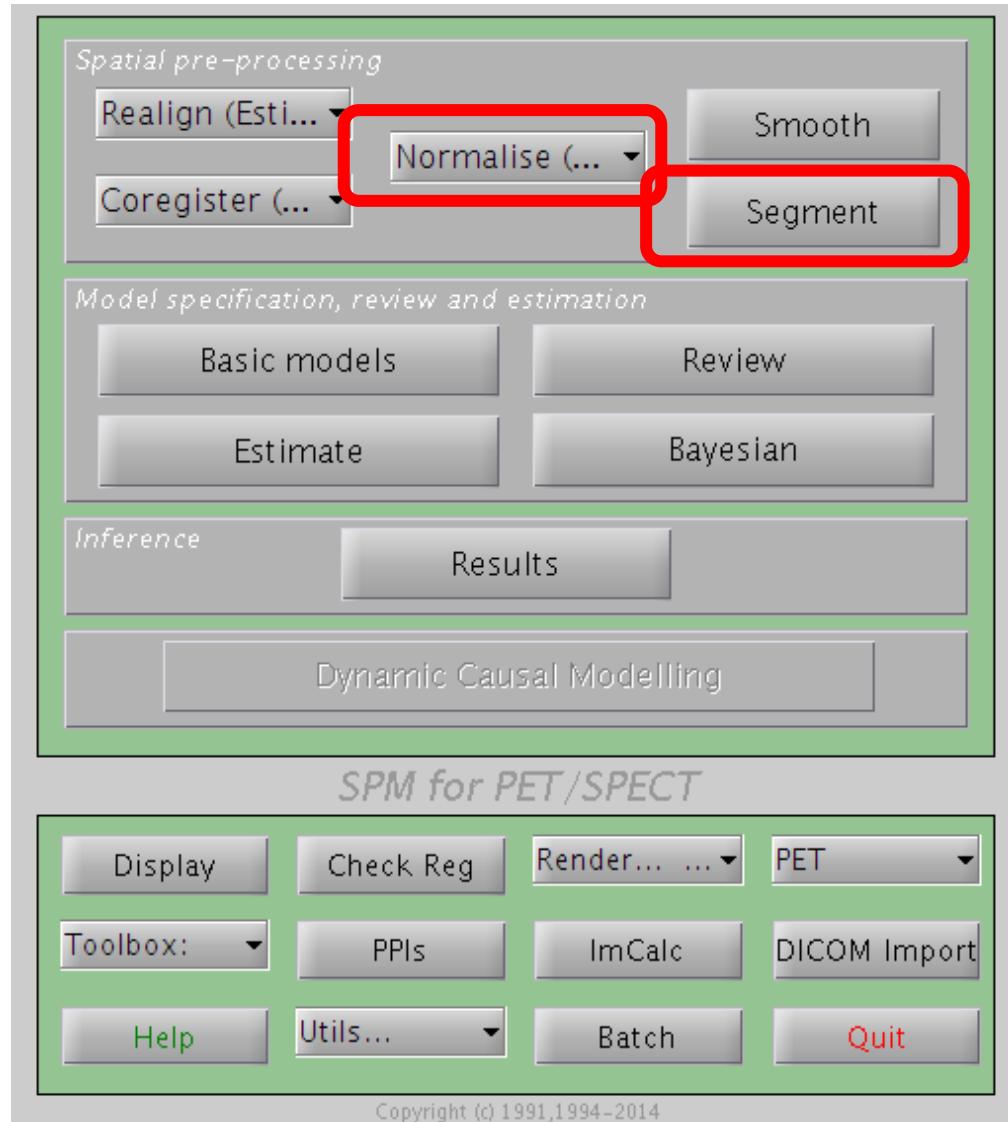
- * Preliminaries
- * Within-subject: Realignment
- * Within-subject: EPI Distortion Correction
- * Coregistration
- * **Between-subject: Normalise/Segment**
 - Use segmentation routine for spatial normalisation**
 - * Gaussian mixture model
 - * Intensity non-uniformity correction
 - * Deformed tissue probability maps
- * Between-subject: Dartel
- * Between-subject: Smoothing

Spatial normalisation

- * Brains of different subjects vary in shape and size.
- * Need to bring them all into a common anatomical space.
 - * Examine homologous regions across subjects
 - * Improve anatomical specificity
 - * Improve sensitivity
 - * Report findings in a common anatomical space (eg MNI space)
- * In SPM12, alignment is achieved by matching grey matter with grey matter and white matter with white matter.
 - * With possible alignment of other tissues.

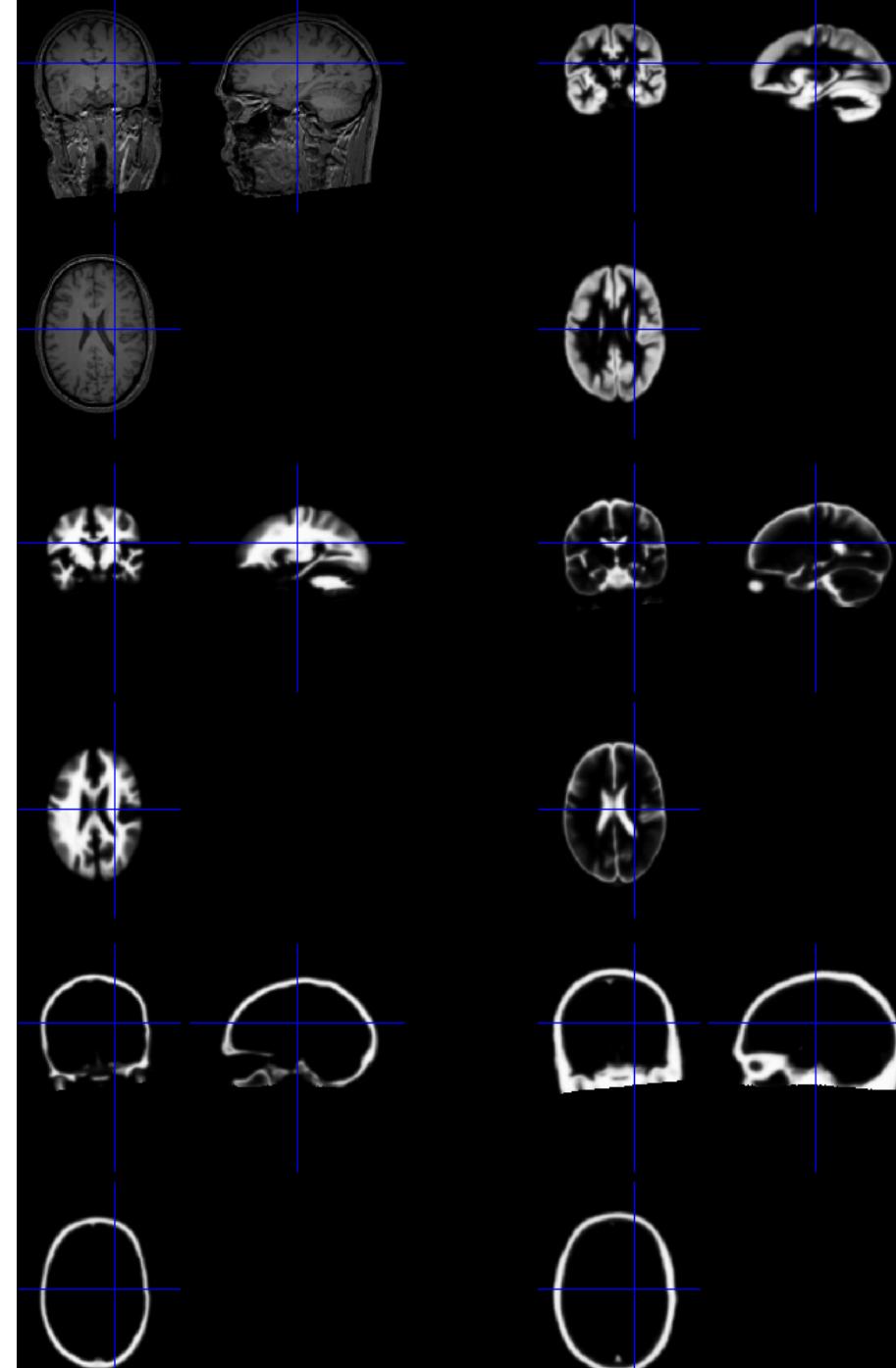
Normalise/Segment

- * This is the same algorithm as for tissue segmentation.
- * Combines:
 - * Mixture of Gaussians (MOG)
 - * Bias Correction Component
 - * Warping (Non-linear Registration) Component



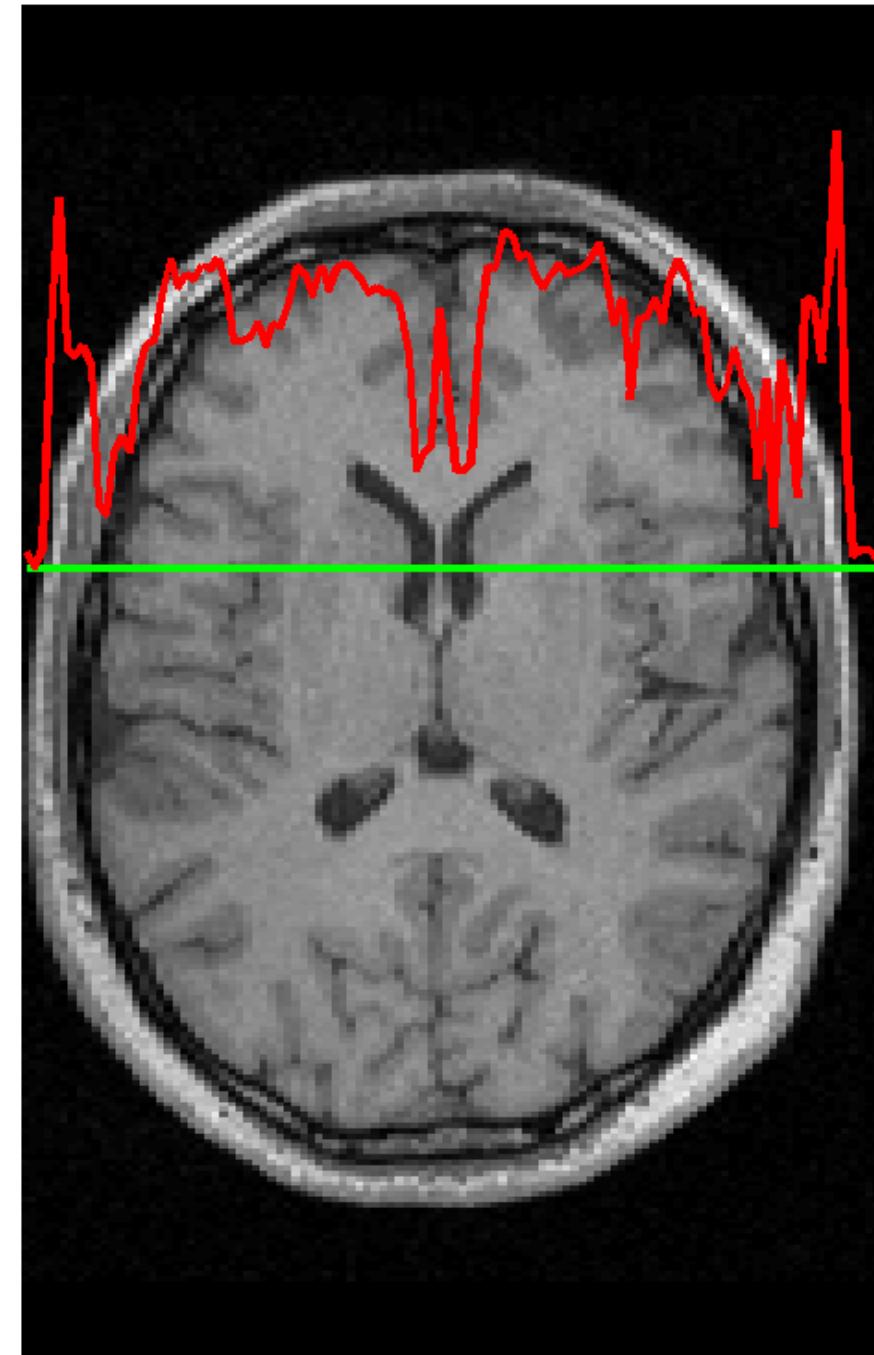
Spatial normalisation

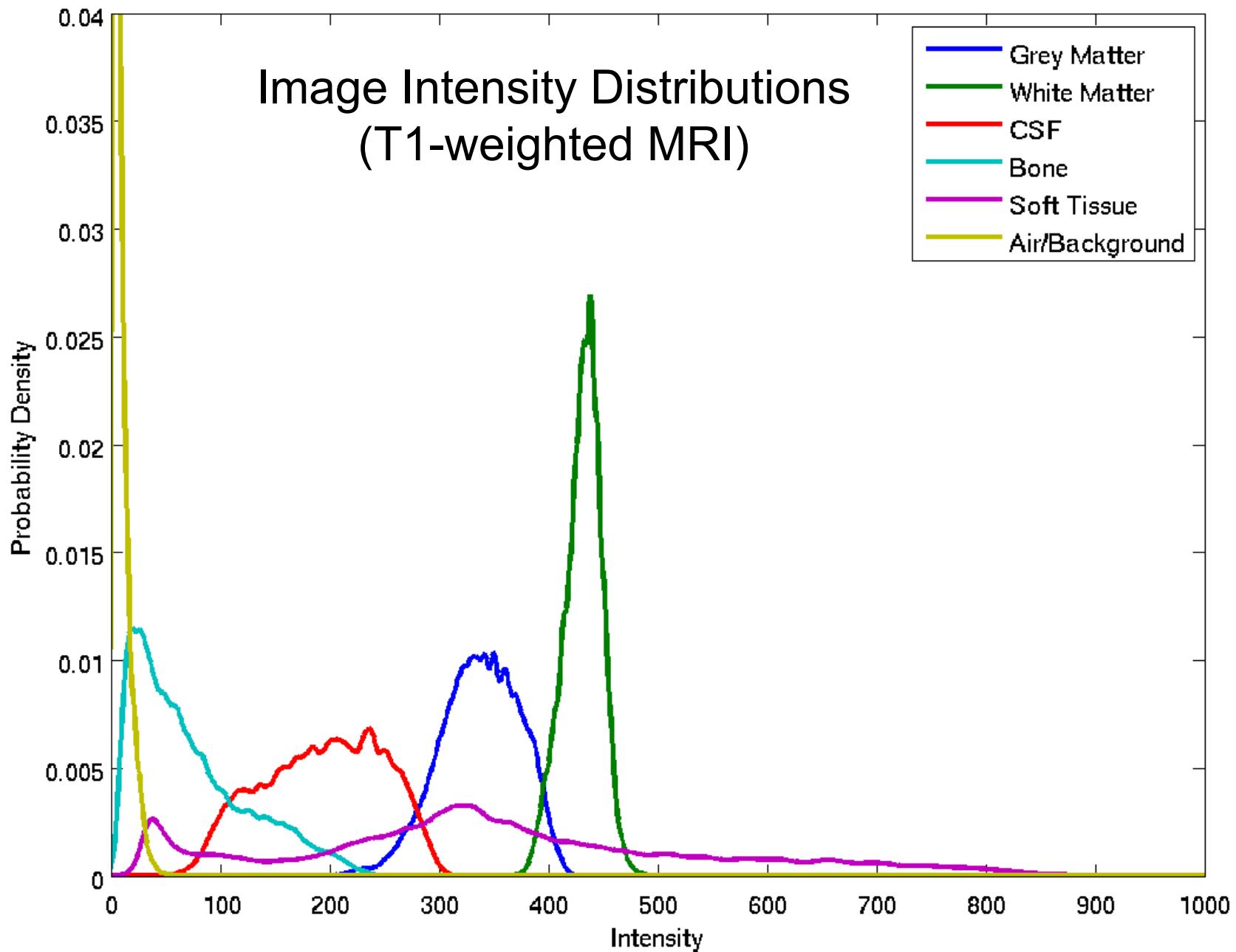
- * Default spatial normalisation in SPM12 estimates nonlinear warps that match tissue probability maps to the individual image.
- * Spatial normalisation achieved using the inverse of this transform.



Segmentation

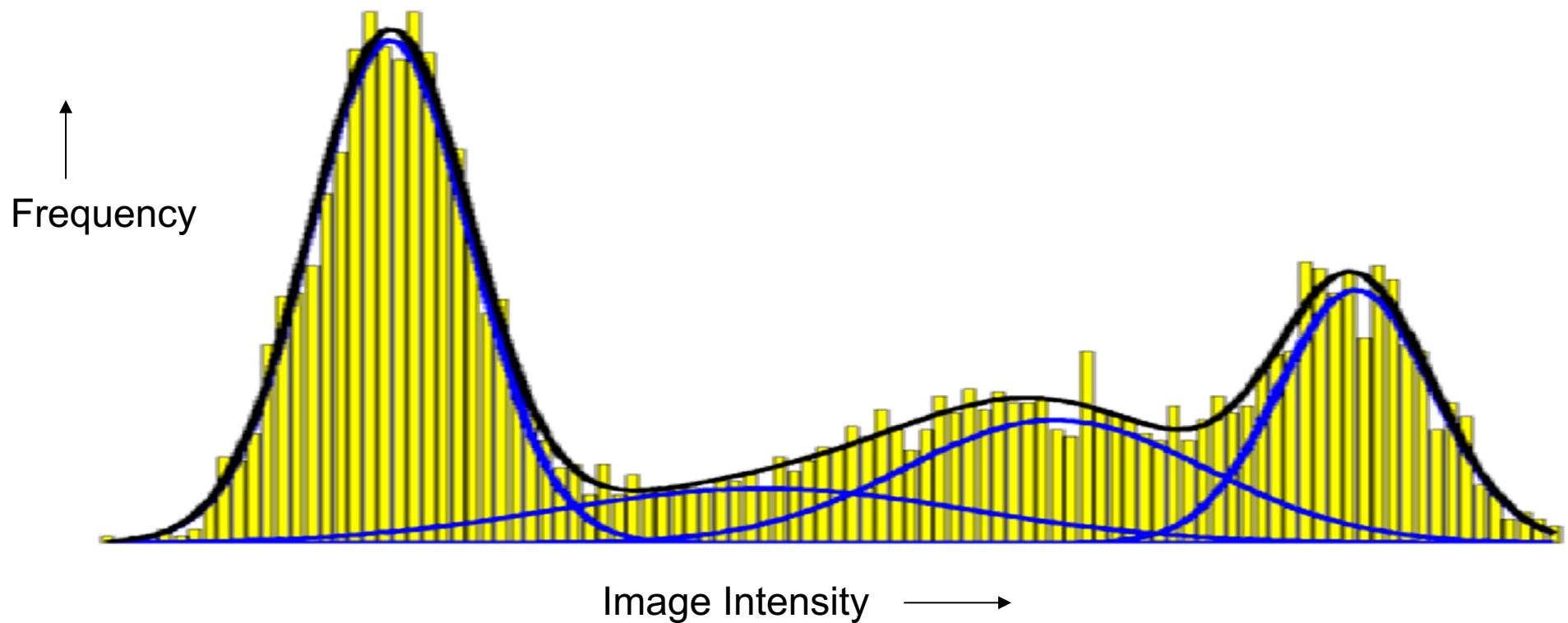
- * Segmentation in SPM12 also estimates a spatial transformation that can be used for spatially normalising images.
- * It uses a **generative model**, which involves:
 - * Mixture of Gaussians (MOG)
 - * Warping (Non-linear Registration) Component
 - * Bias Correction Component





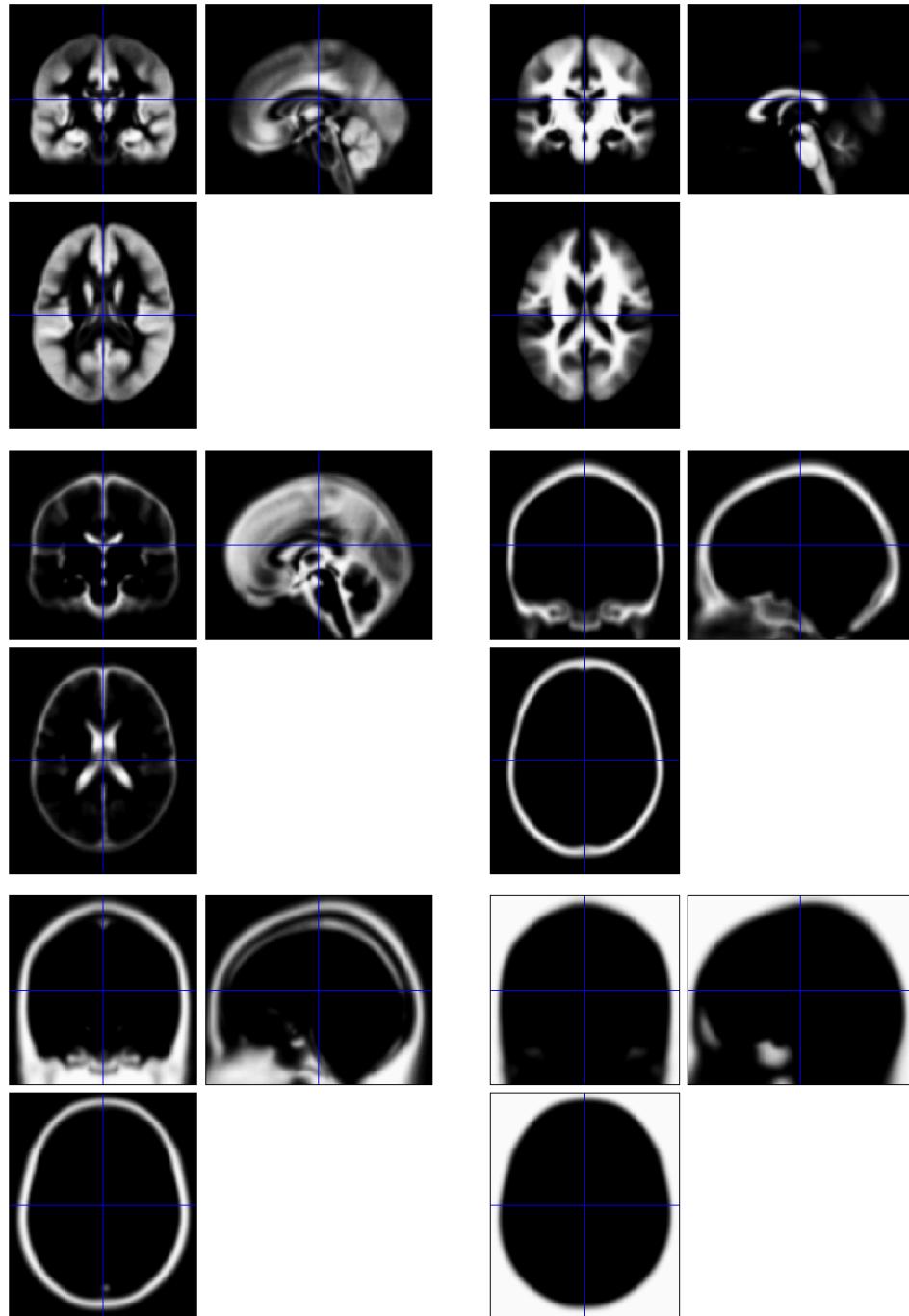
Modelling tissue intensities

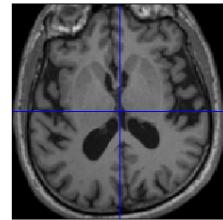
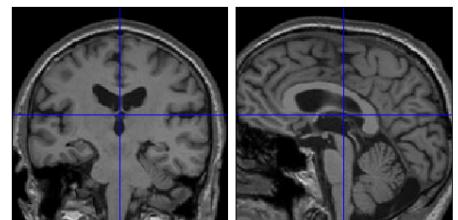
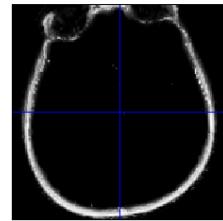
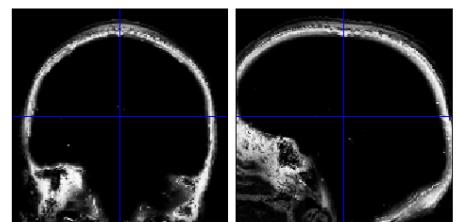
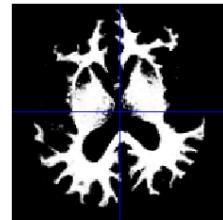
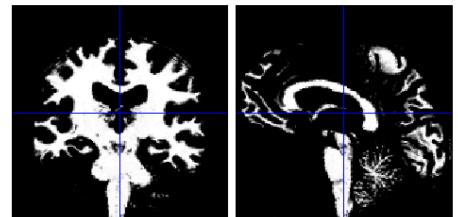
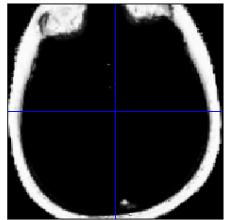
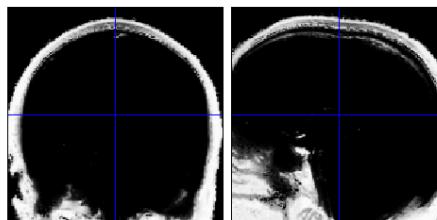
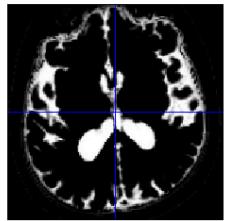
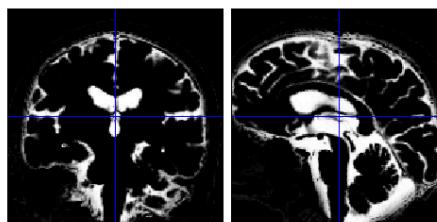
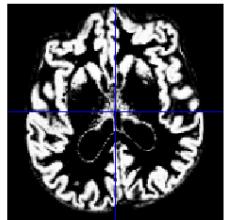
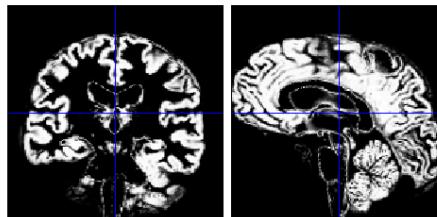
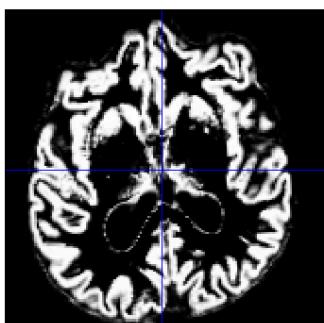
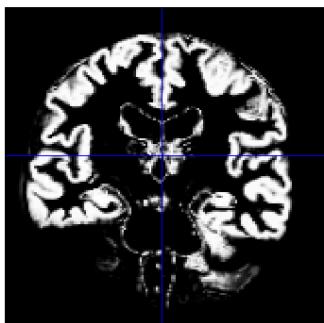
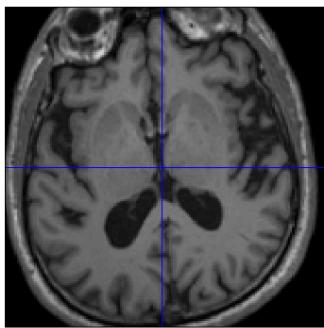
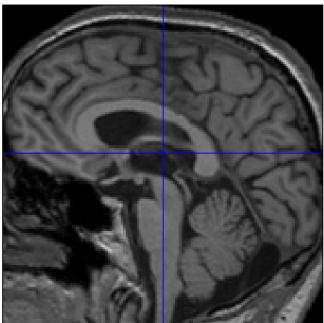
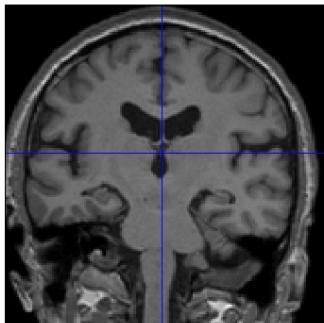
- * Classification is based on a ***Mixture of Gaussians*** model (MOG), which represents the intensity probability density by a number of Gaussian distributions.



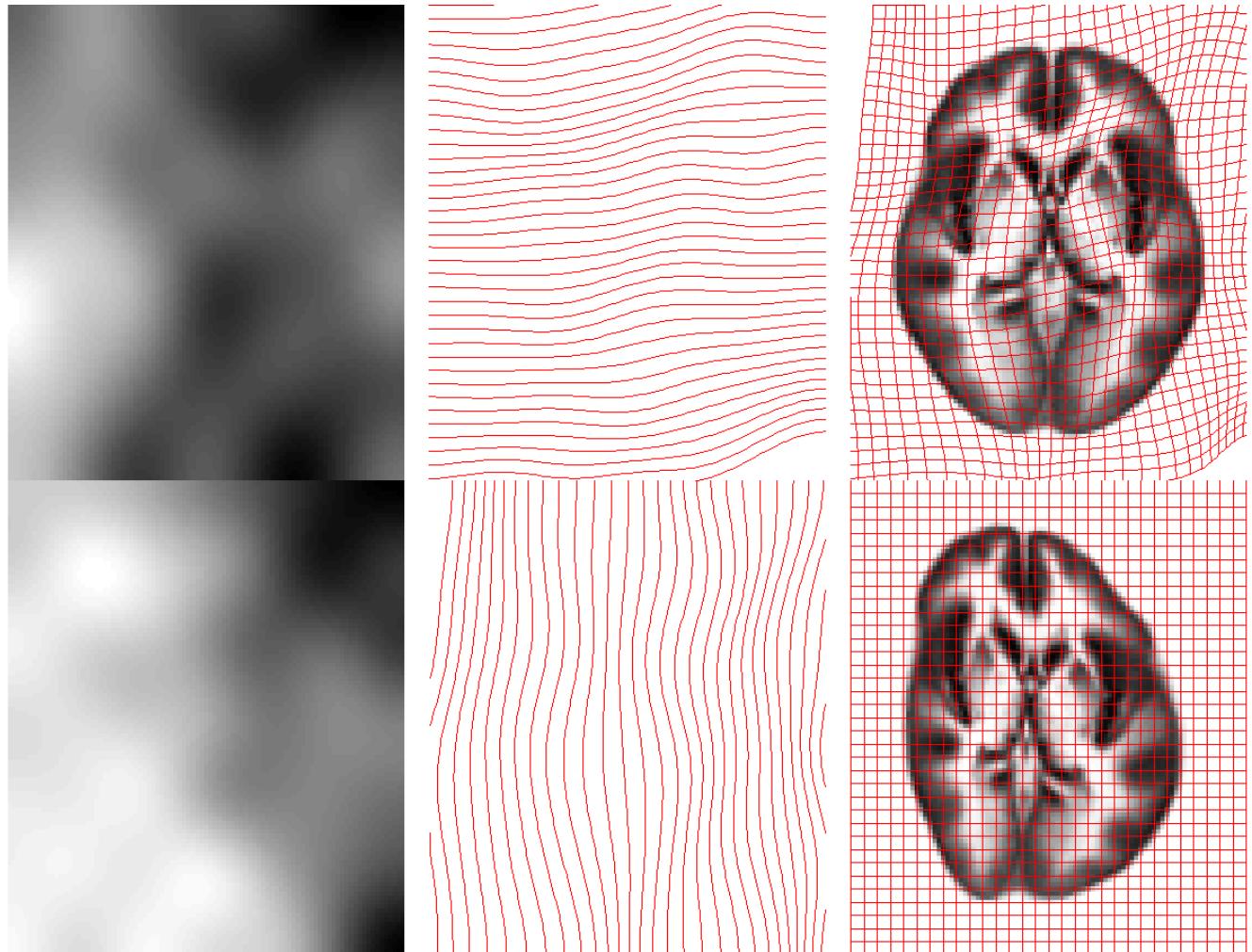
Tissue probability maps in SPM12

Includes additional non-brain tissue classes (bone, and soft tissue)

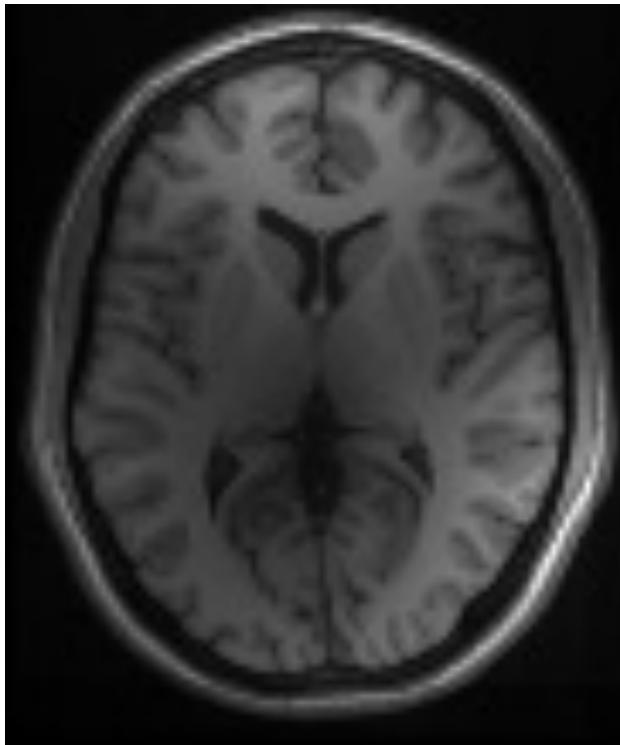
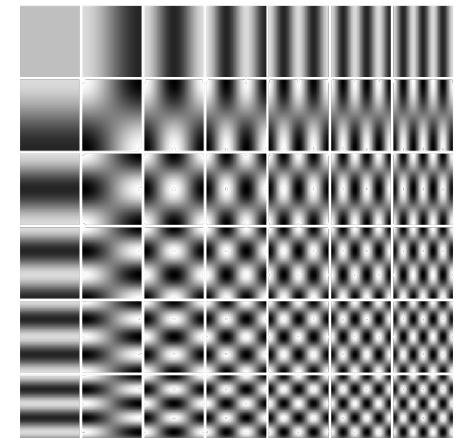




Modelling deformations



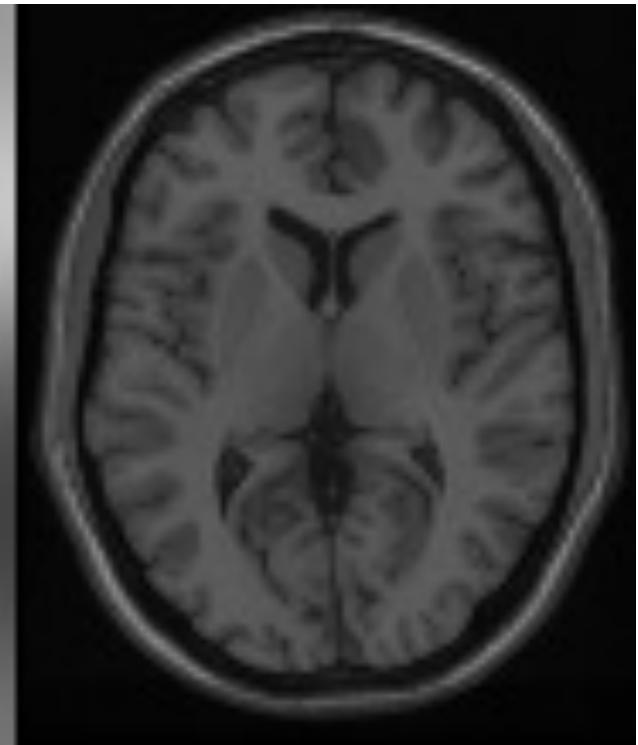
Modelling a bias field



Corrupted image

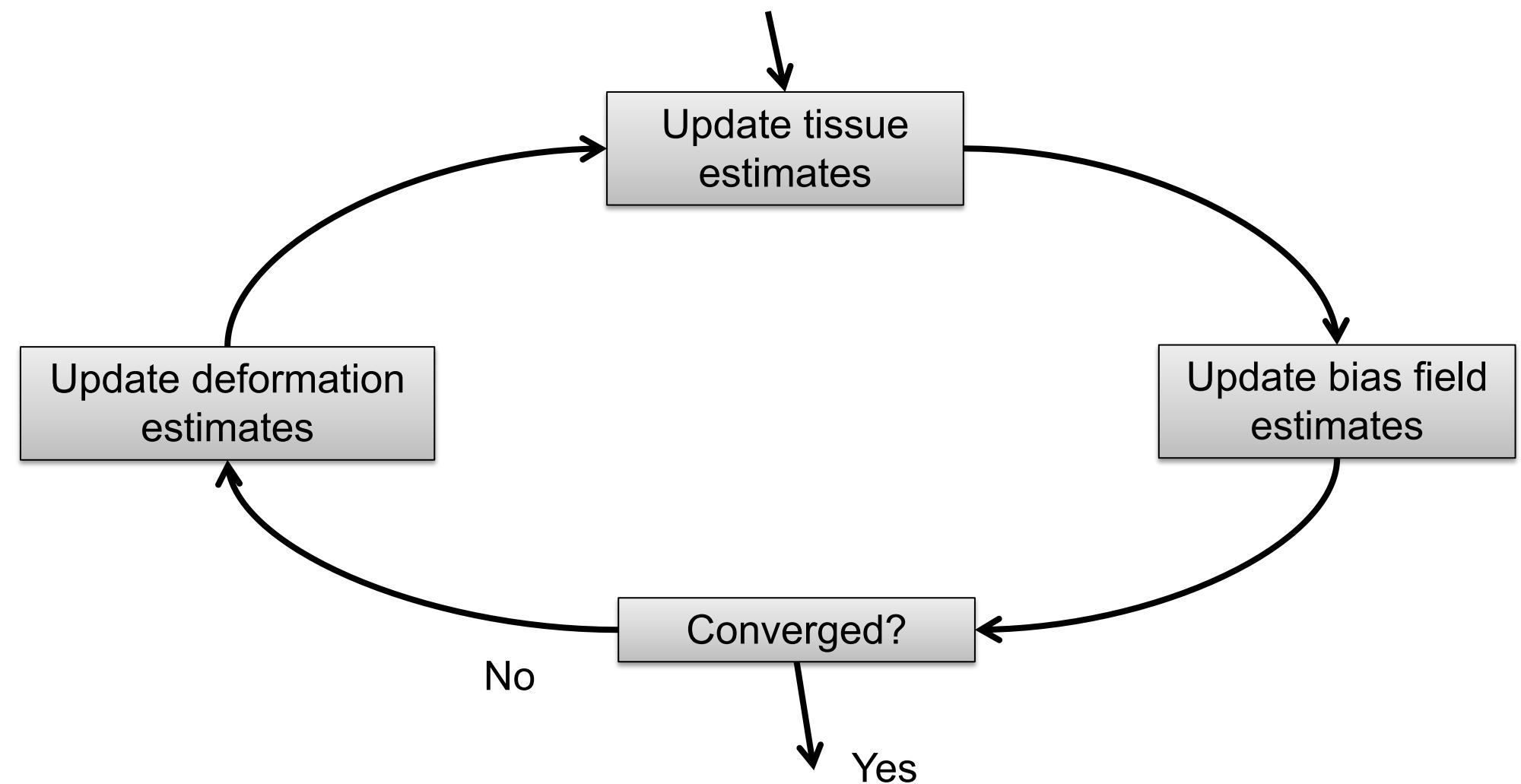


Bias Field



Corrected image

Iterative optimisation scheme

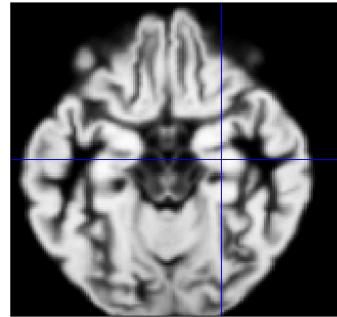
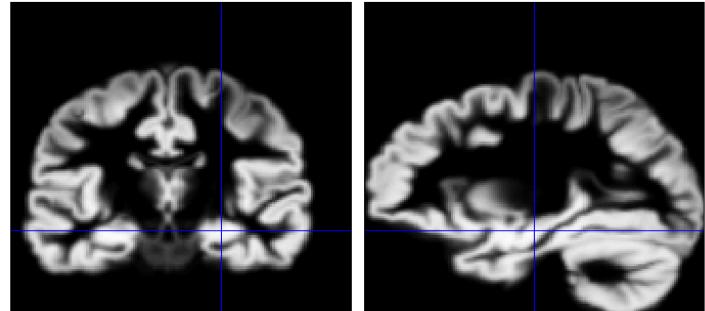


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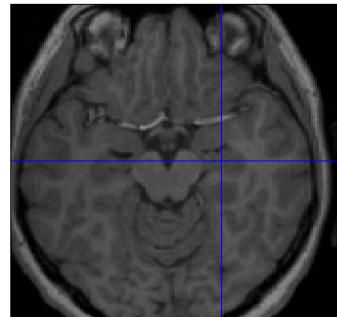
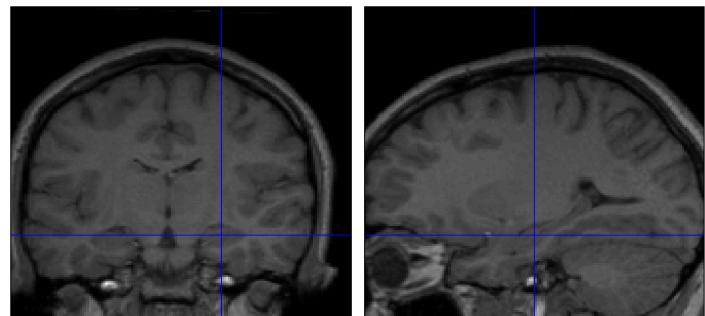
- * Preliminaries
- * Within-subject: Realignment
- * Within-subject: EPI Distortion Correction
- * Within-subject: Coregistration
- * Between-subject: Normalise/Segment
- * **Between-subject: Dartel**
 - * Velocity field parameterisation
 - * Objective function
 - * Template creation
 - * Examples
- * Between-subject: Smoothing

Dartel image registration

- * Uses fast approximations
 - * Deformation integrated using scaling and squaring
- * Uses Levenberg-Marquardt optimiser
 - * Multi-grid matrix solver
- * Matches GM with GM, WM with WM etc
- * Diffeomorphic registration takes about 30 mins per image pair (121×145×121 images).

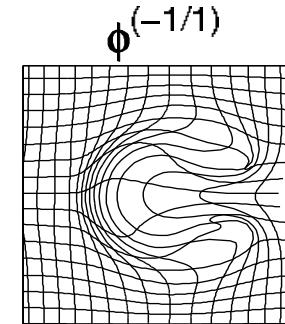
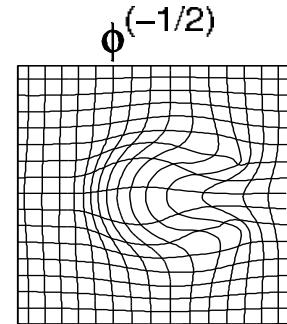
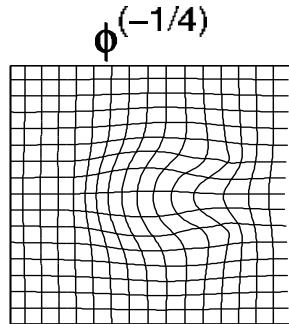
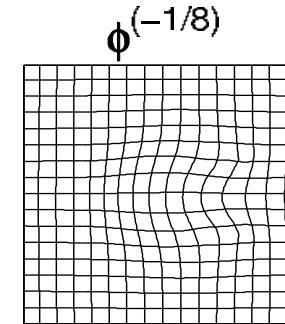
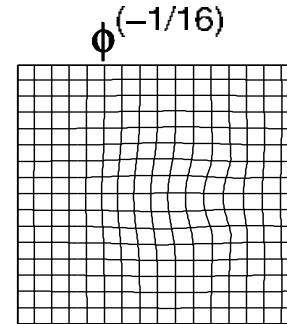
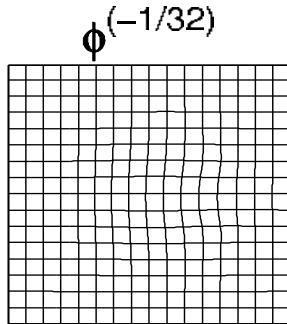
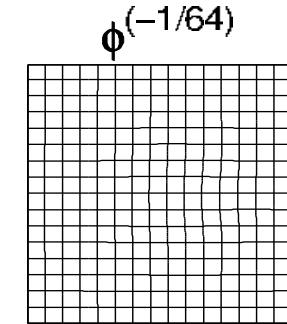
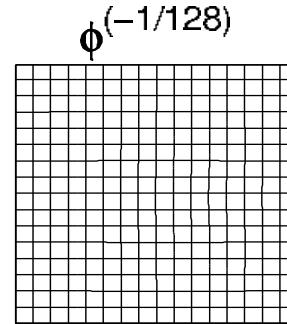
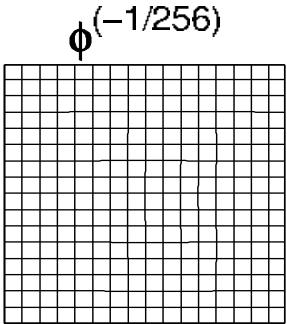


Grey matter template warped to individual



Individual scan

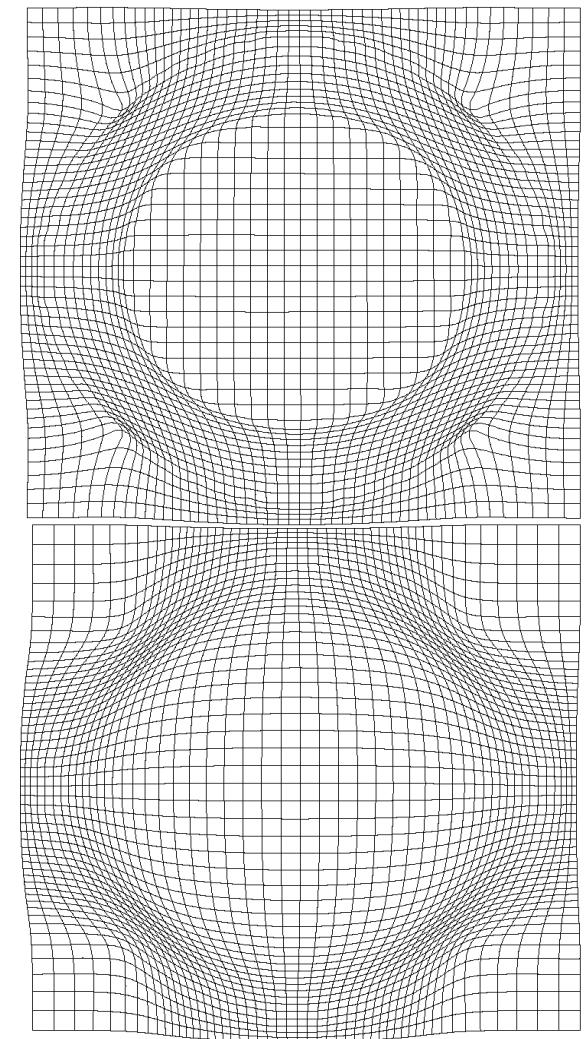
Scaling and squaring example



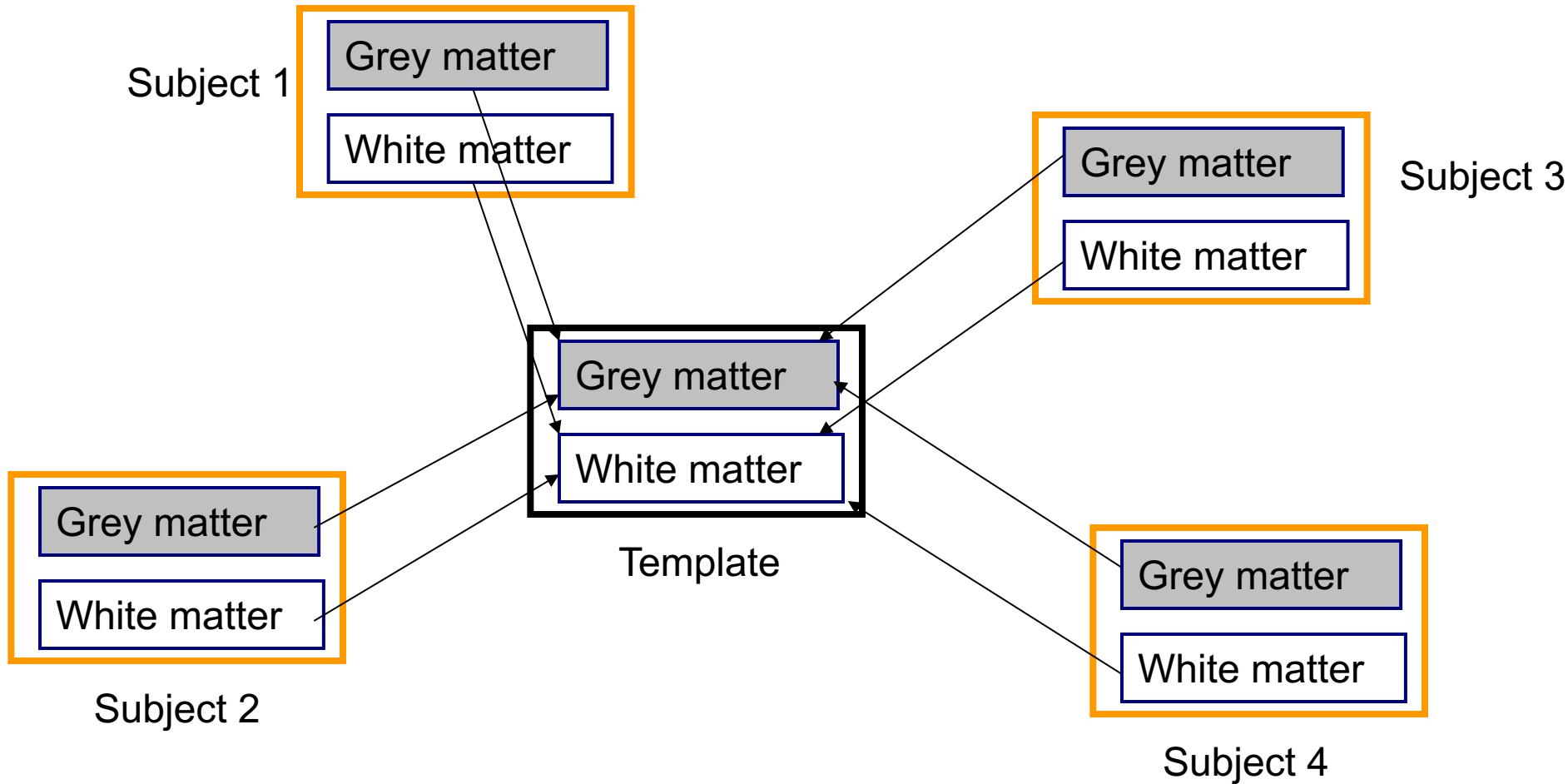
Registration objective function

- * Simultaneously minimize the sum of:
 - * **Matching Term**
 - * Drives the alignment of the images.
 - * Multinomial assumption
 - * **Regularisation term**
 - * A measure of deformation roughness
 - * Keeps the warps spatially smooth.
- * A balance between the two terms.

Effect of different forms of regularisation



Simultaneous registration of GM to GM and WM to WM

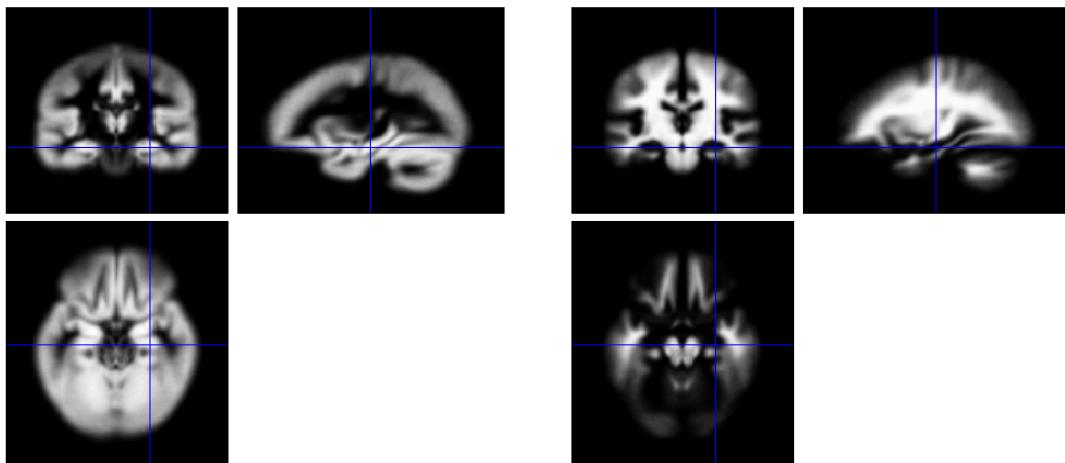


Template

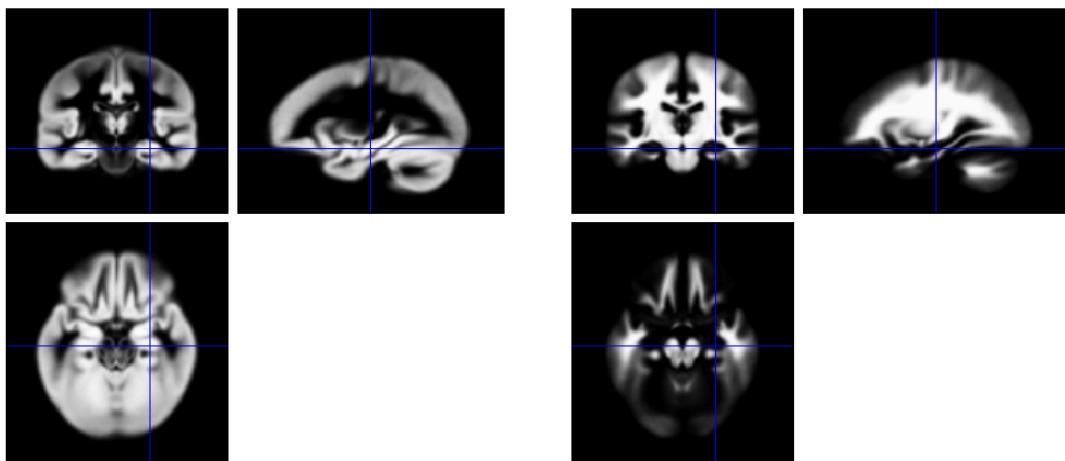
Iteratively generated
from 471 subjects

Began with rigidly
aligned tissue
probability maps

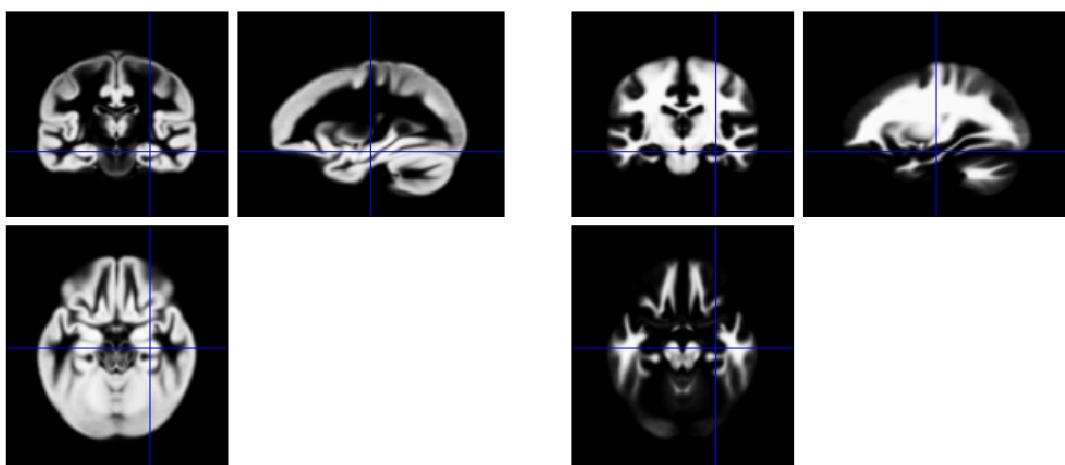
Initial
Average

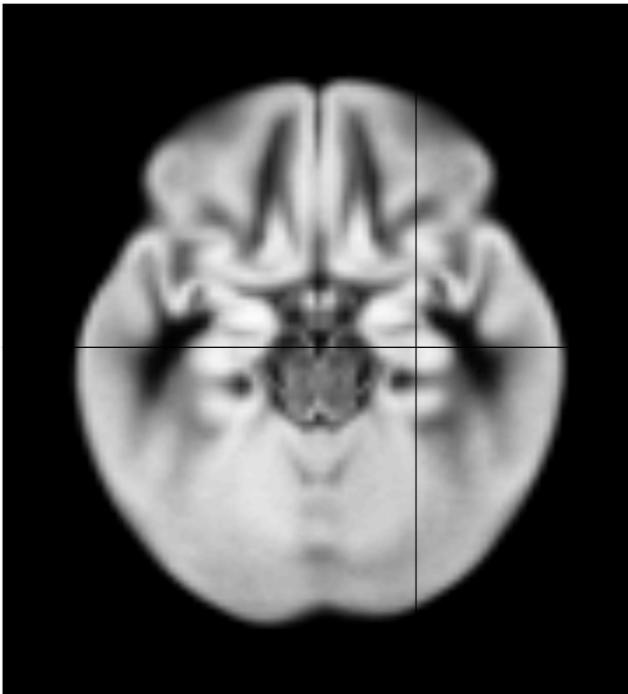
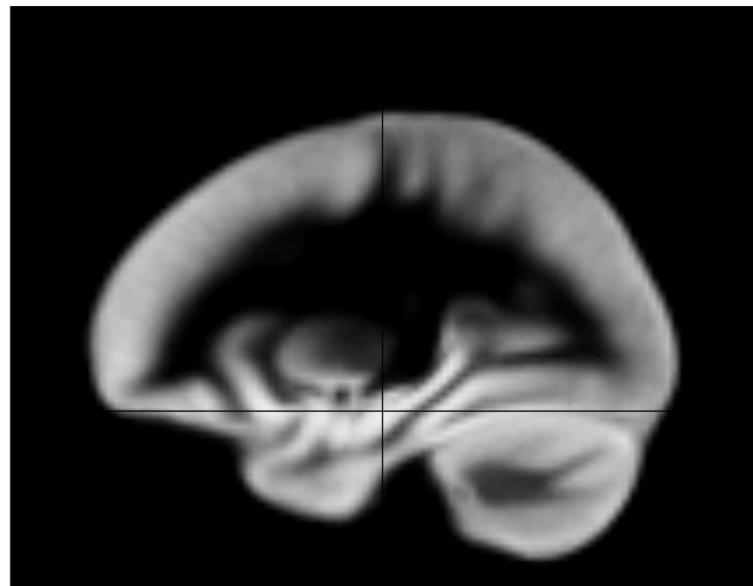
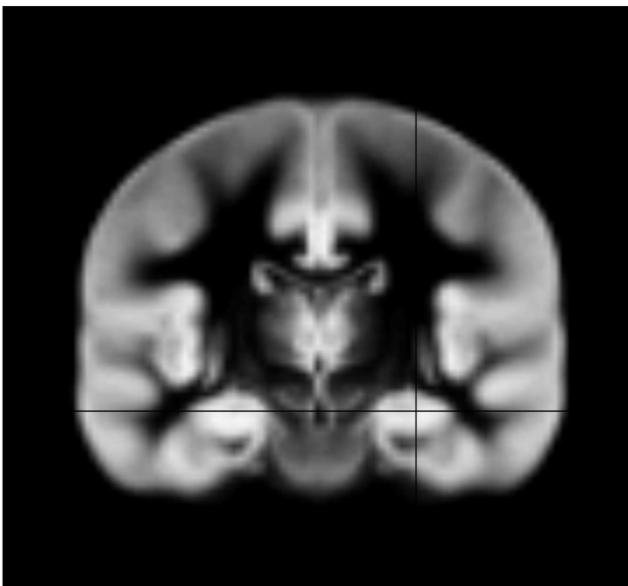


After a few
iterations

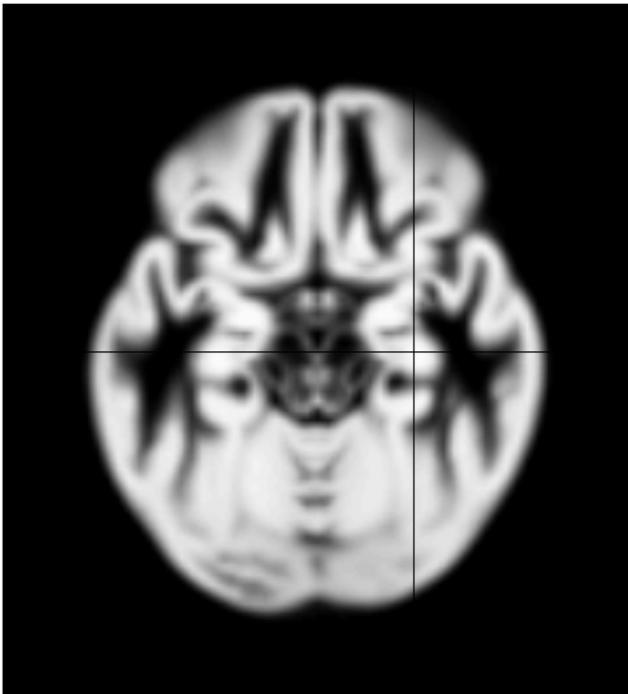
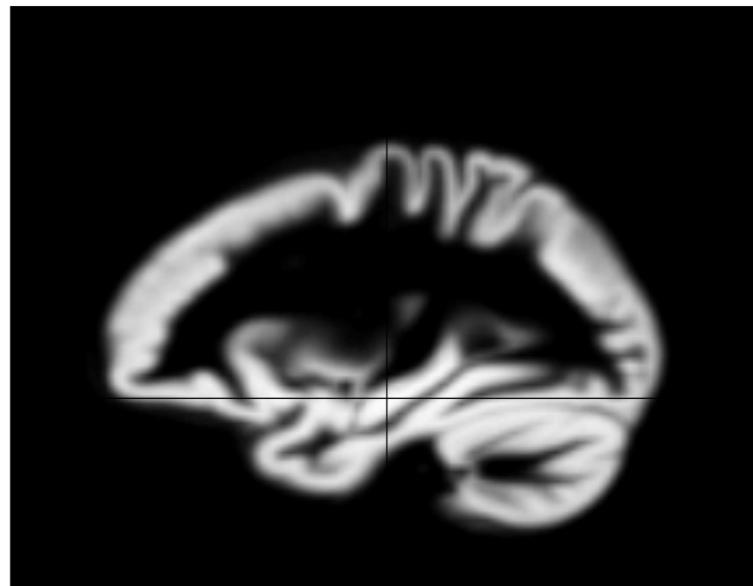
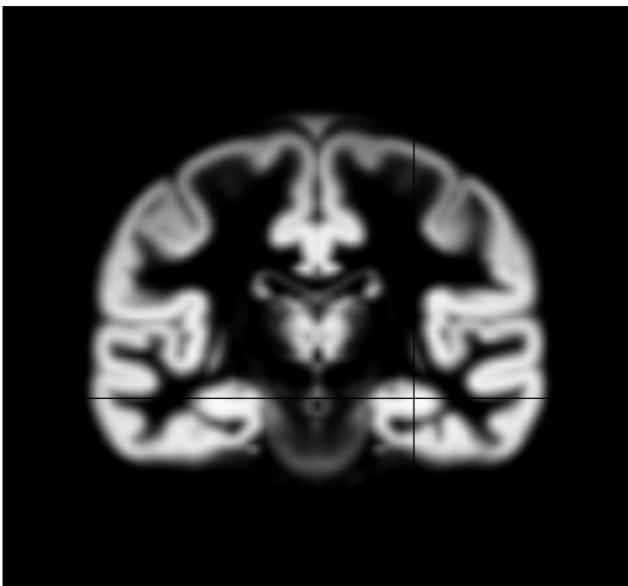


Final
template



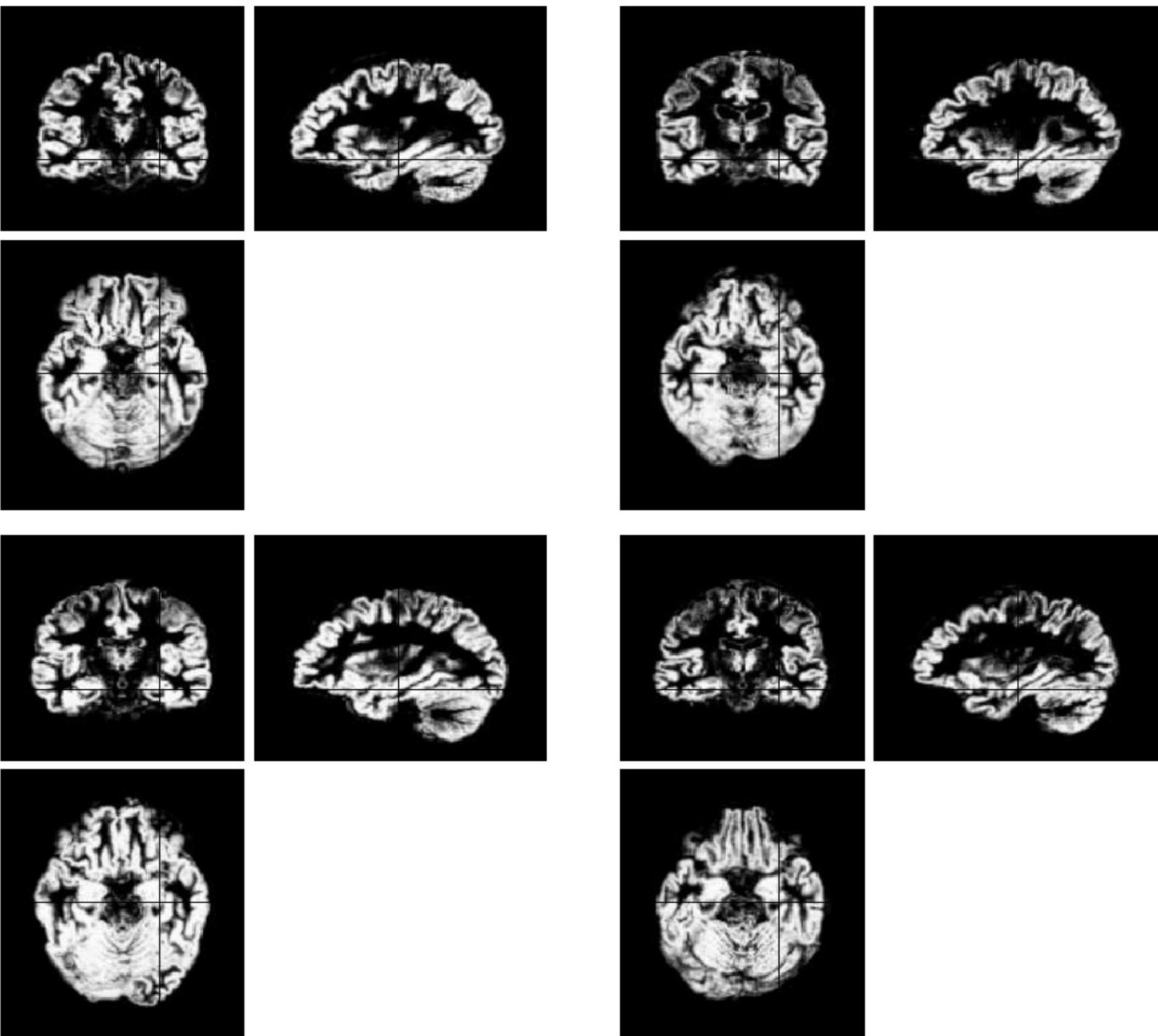


Grey matter
average of 452
subjects – affine

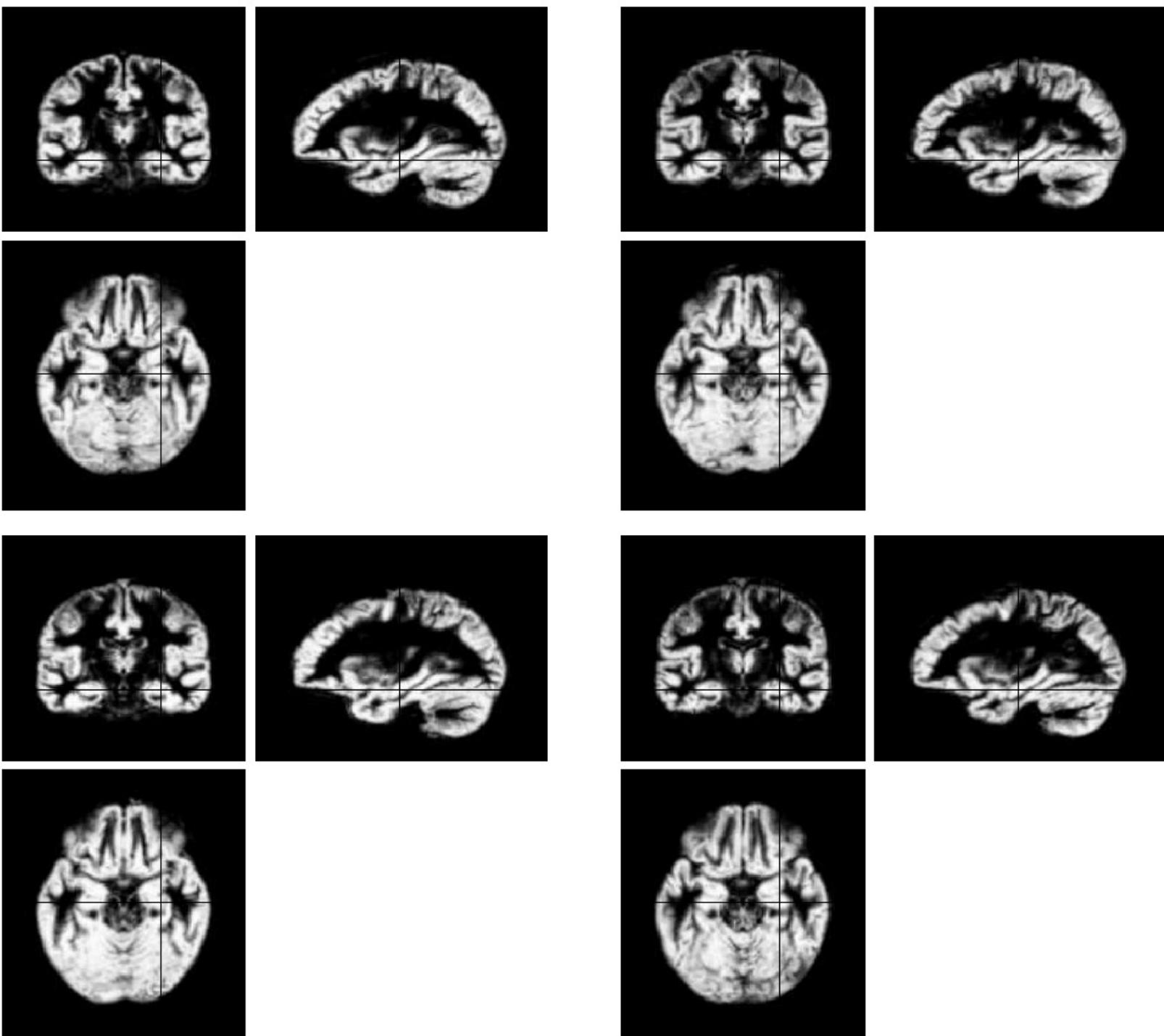


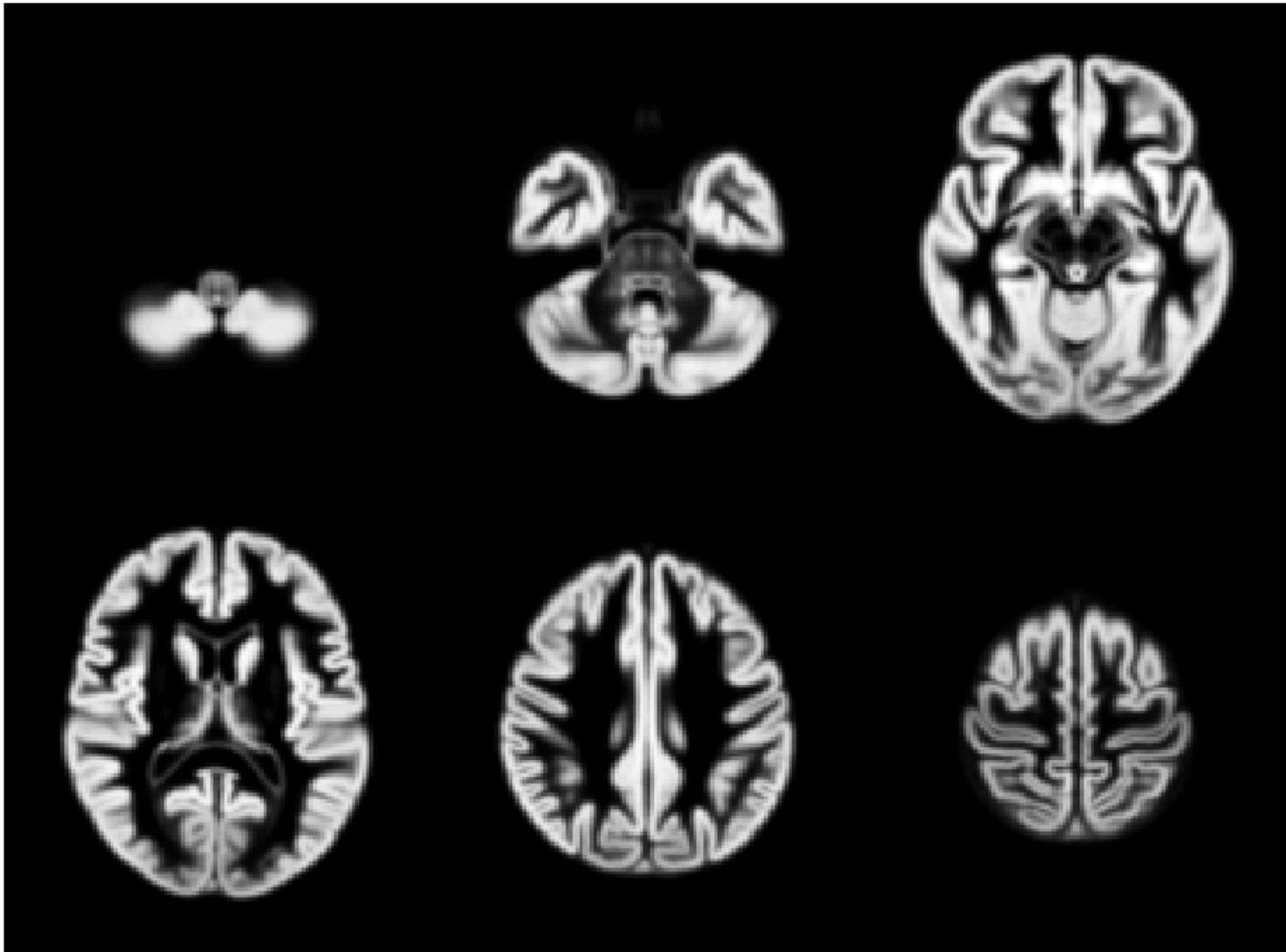
Grey matter
average of 471
subjects

Initial
GM images

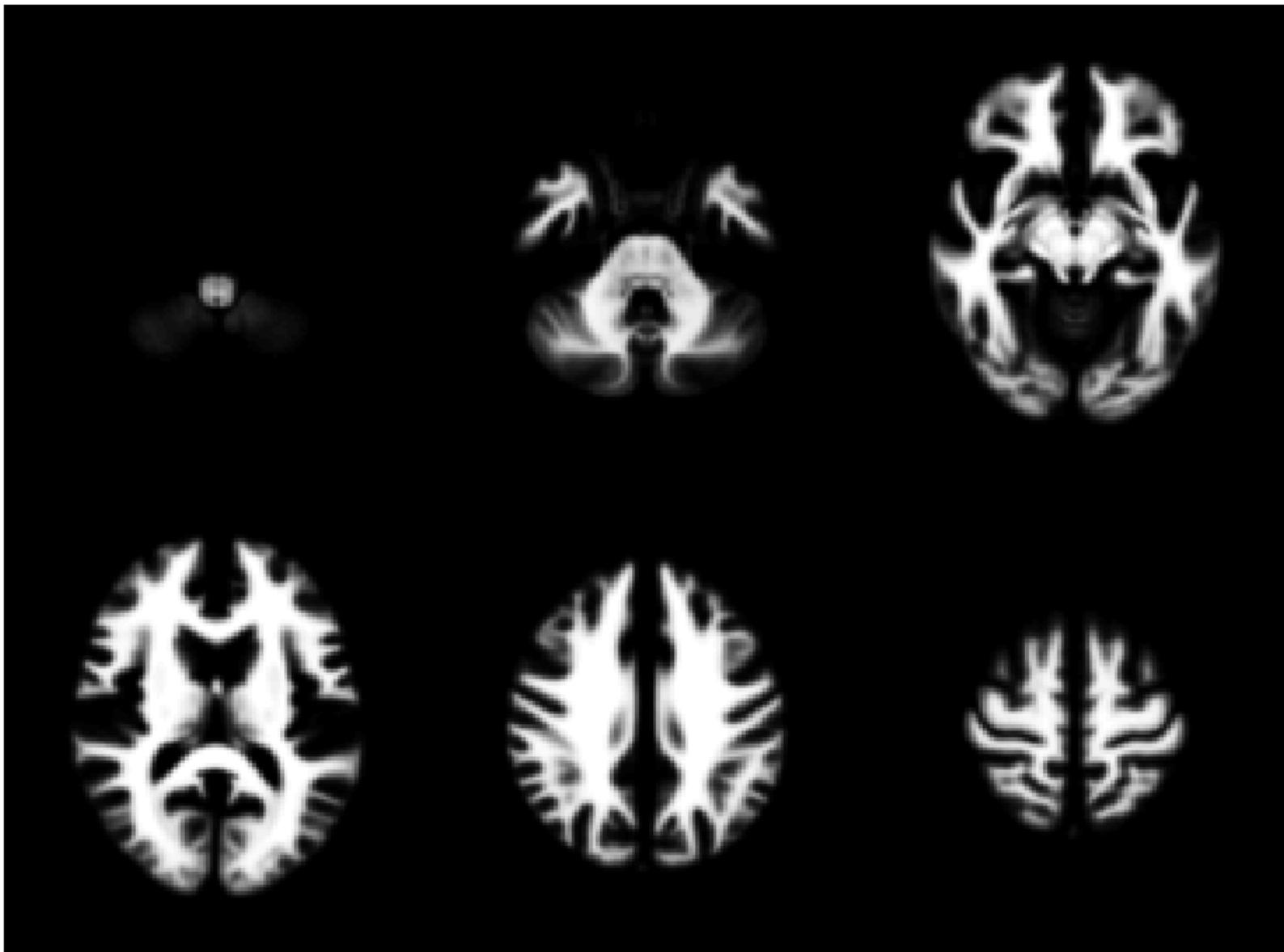


Aligned
GM images

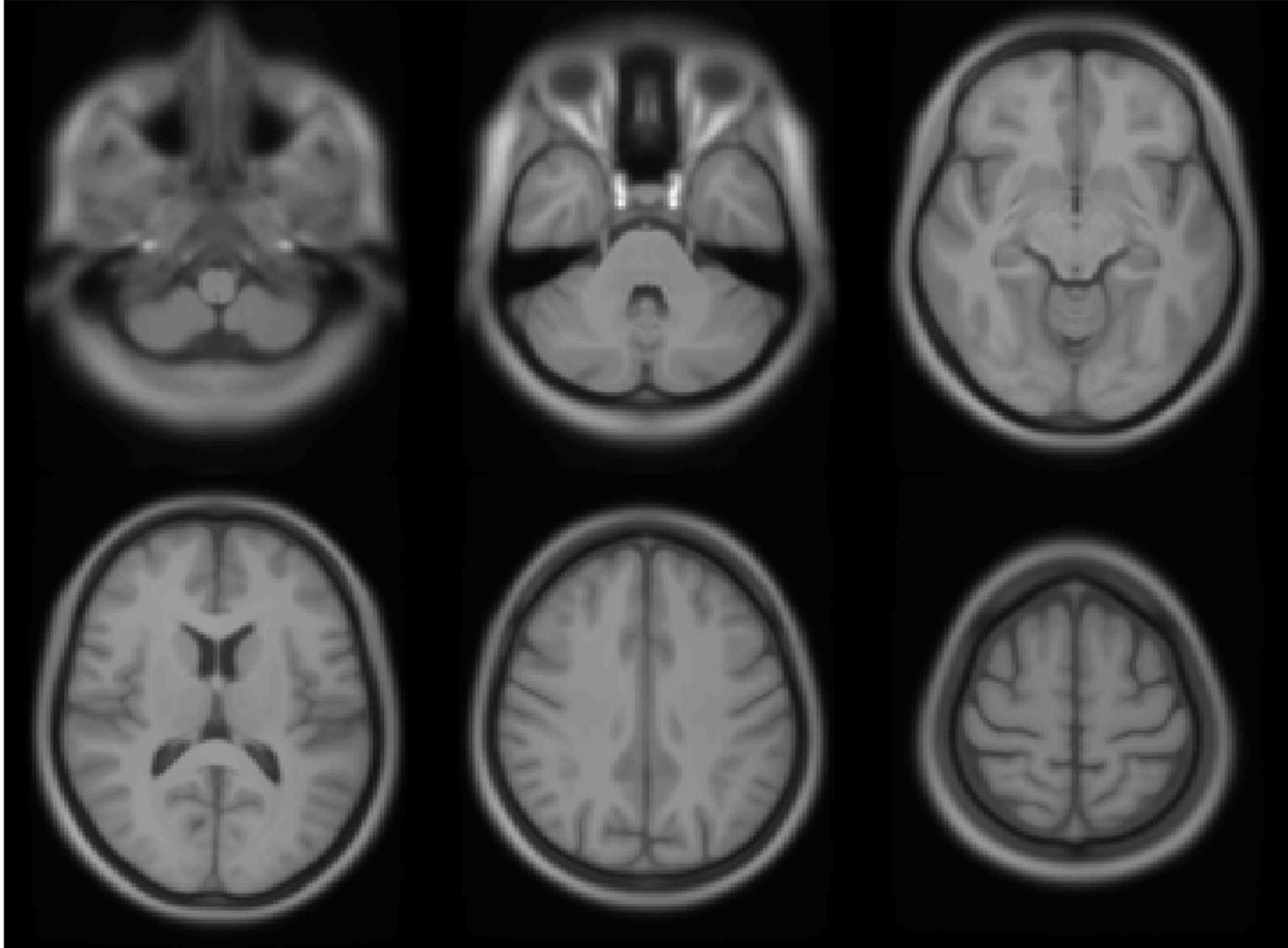




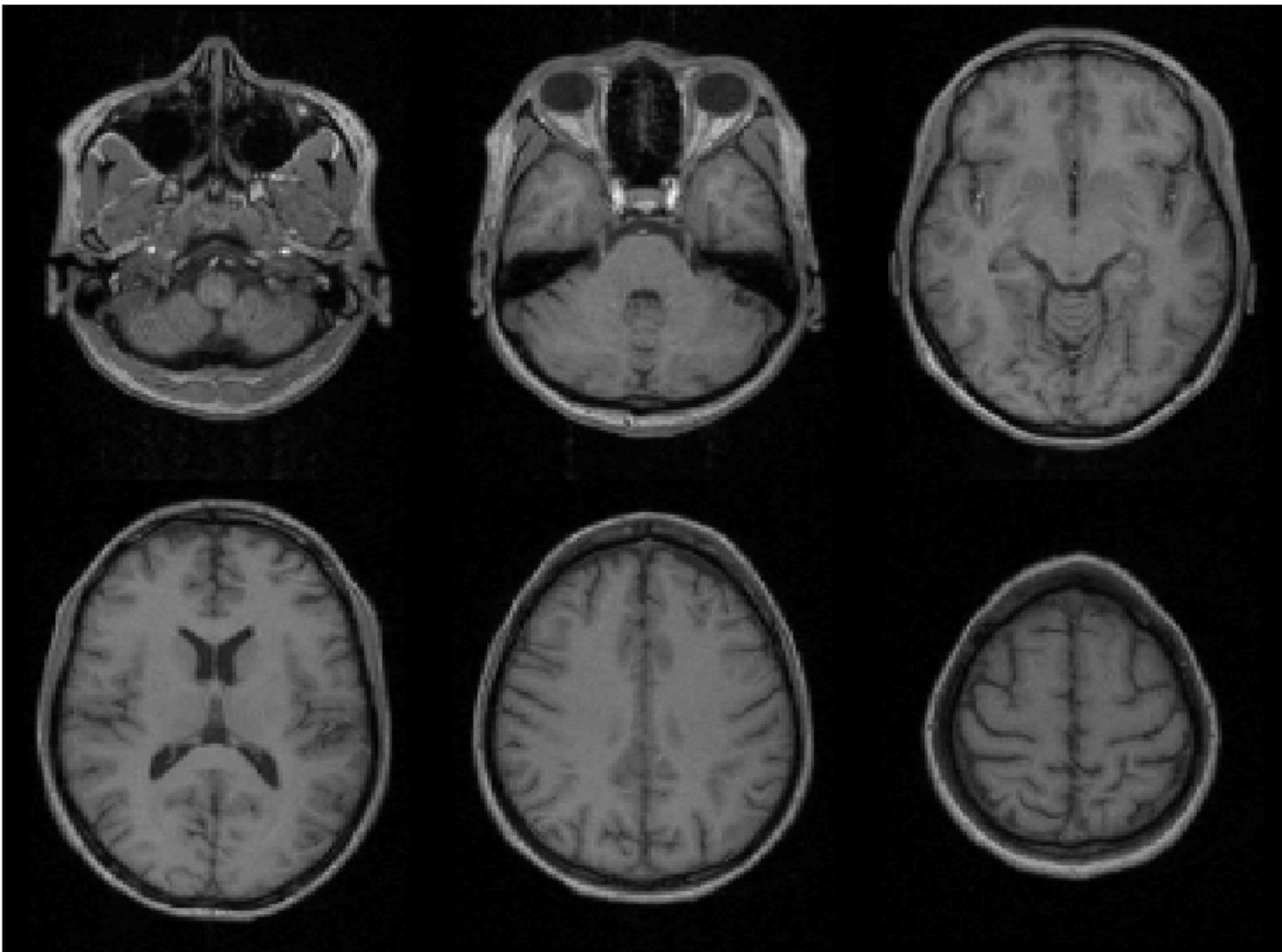
471 Subject Average



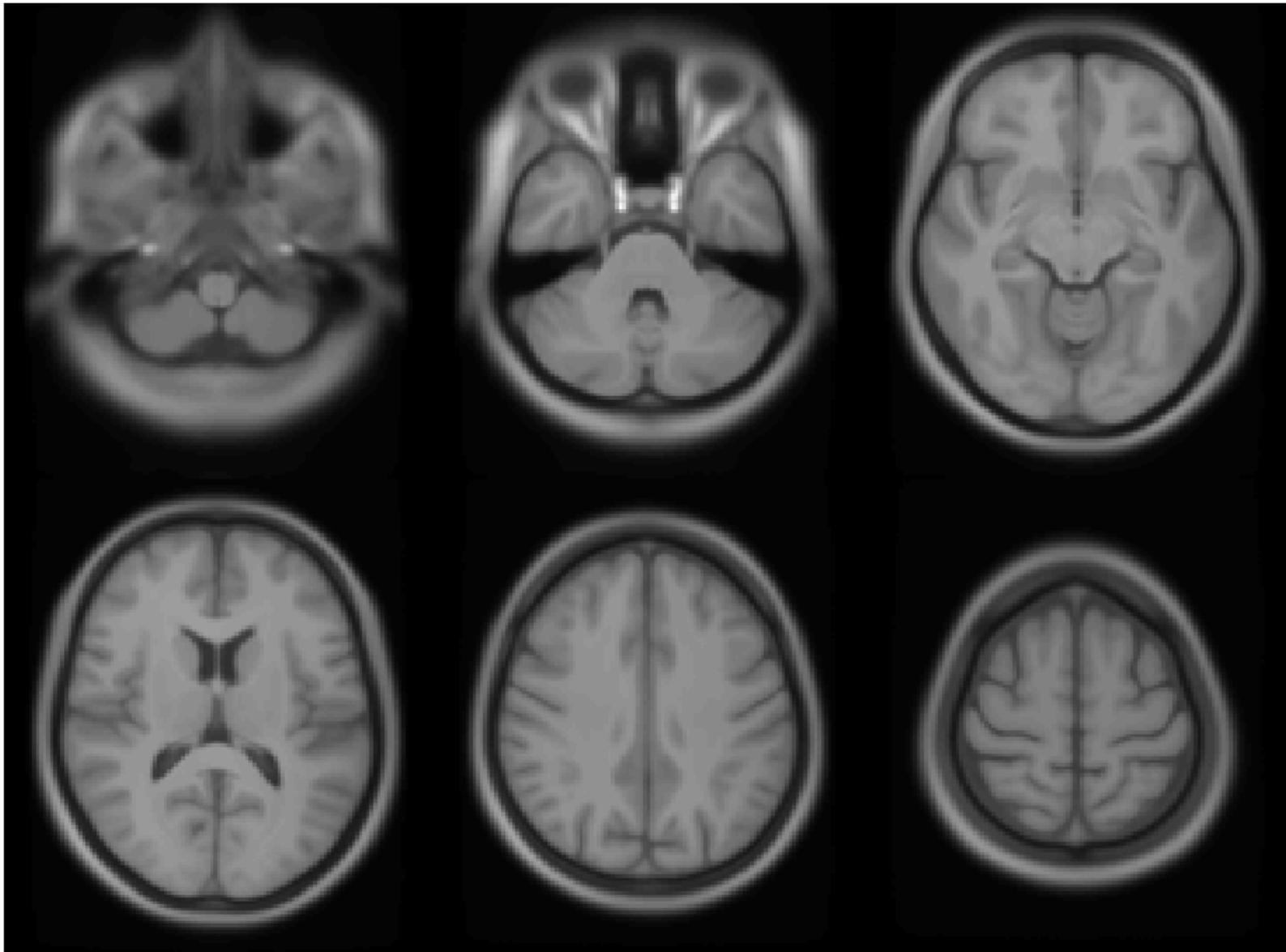
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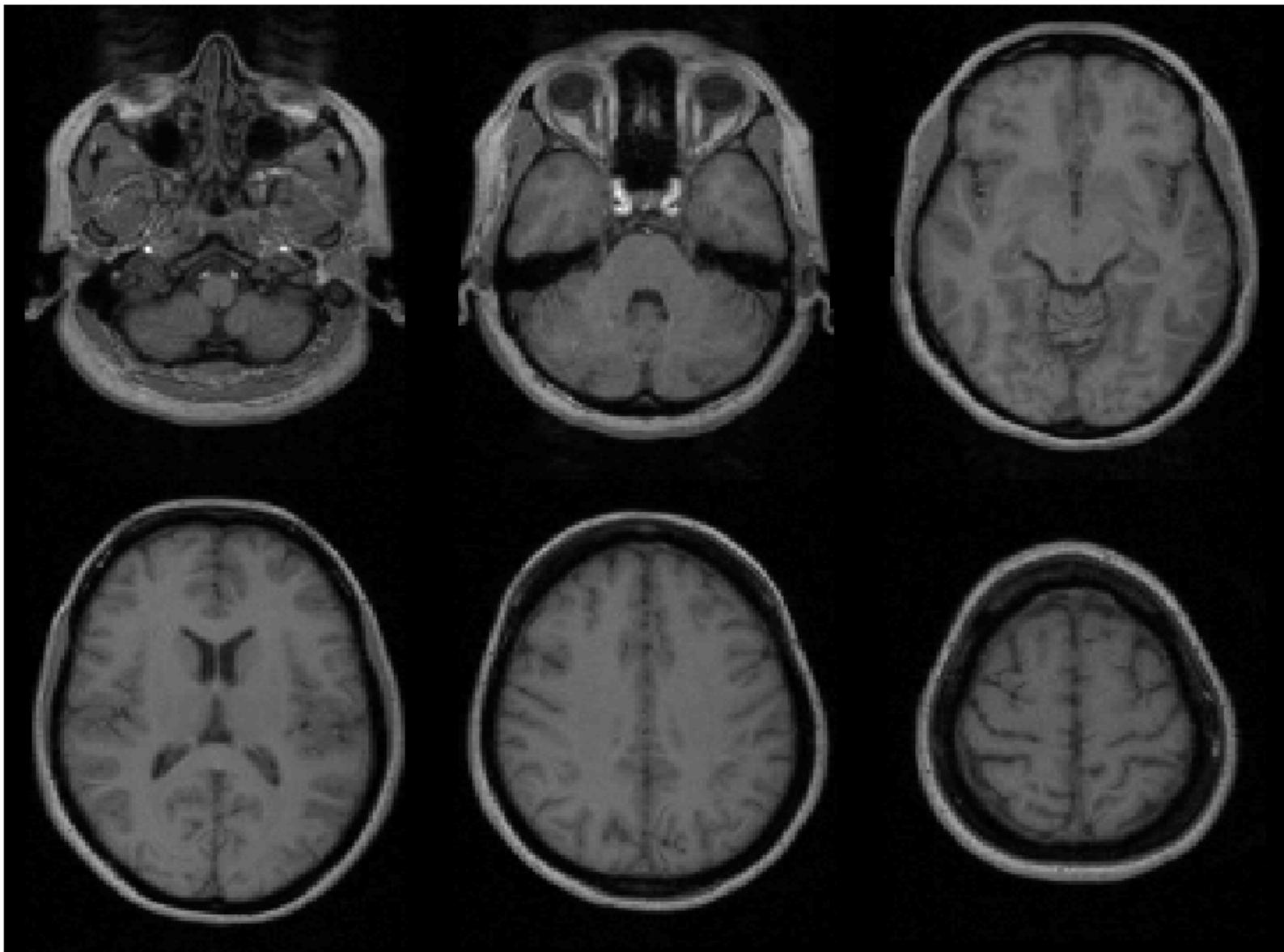
471 Subject Average



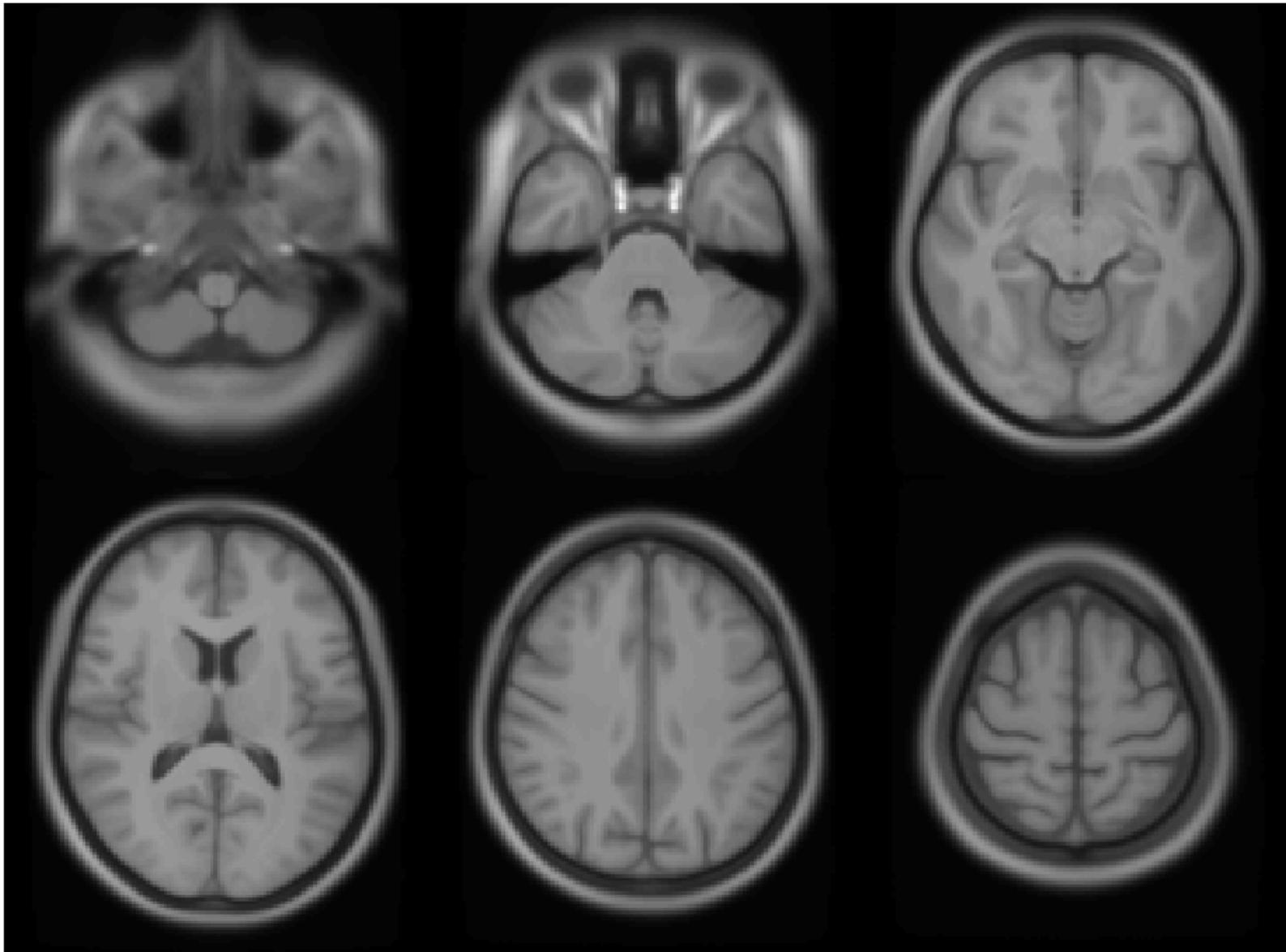
Subject 1



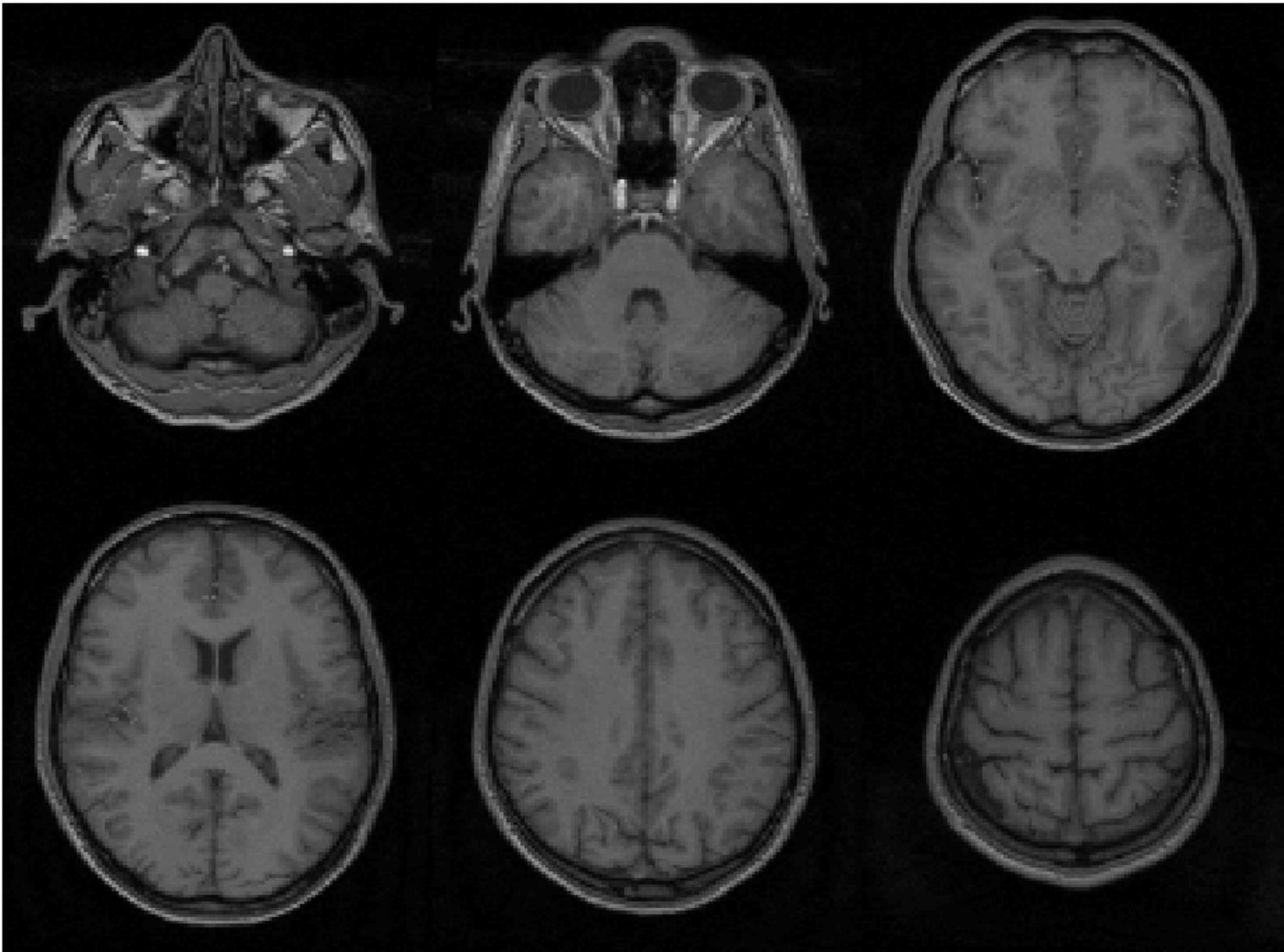
471 Subject Average



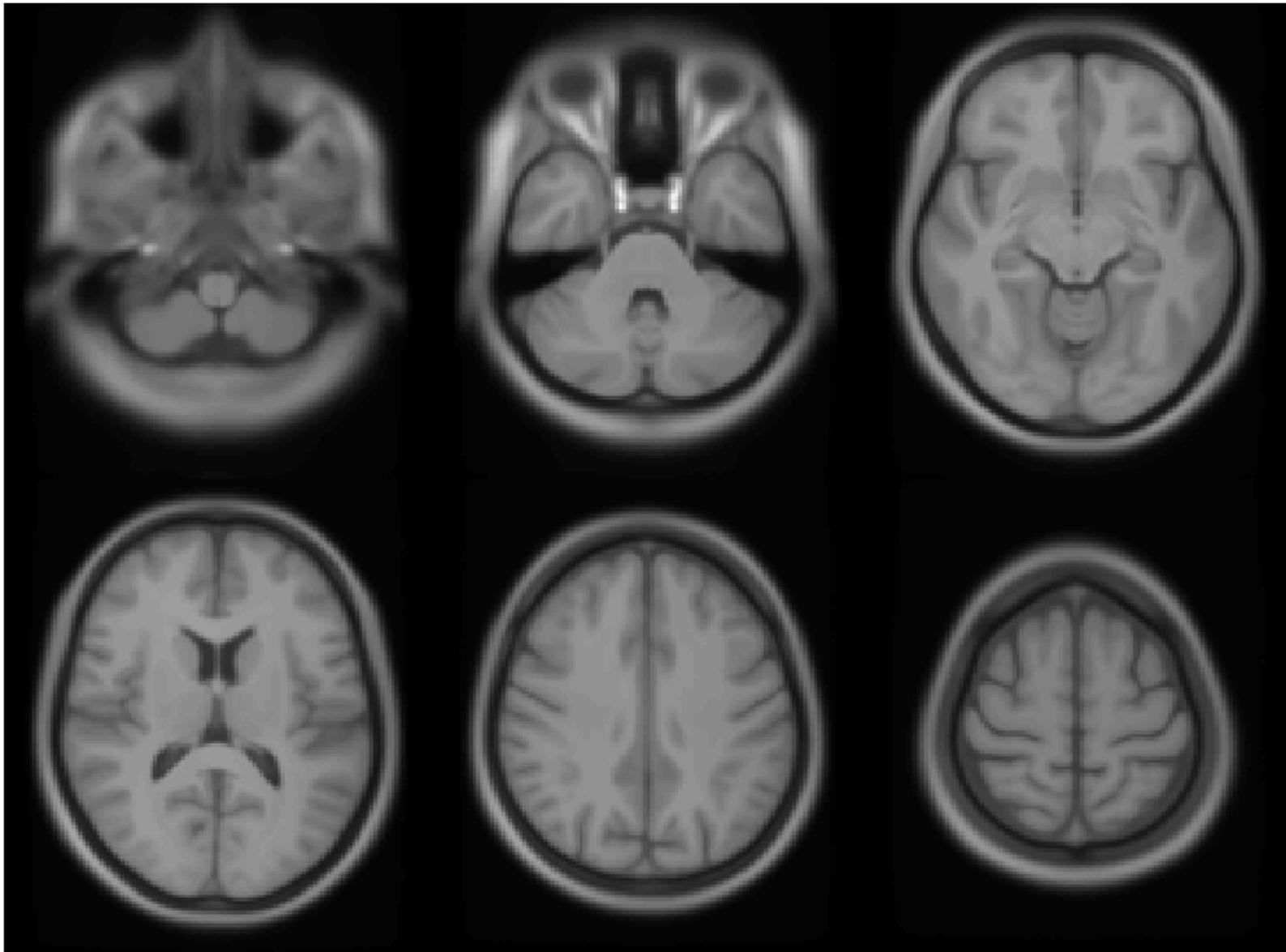
Subject 2



471 Subject Average

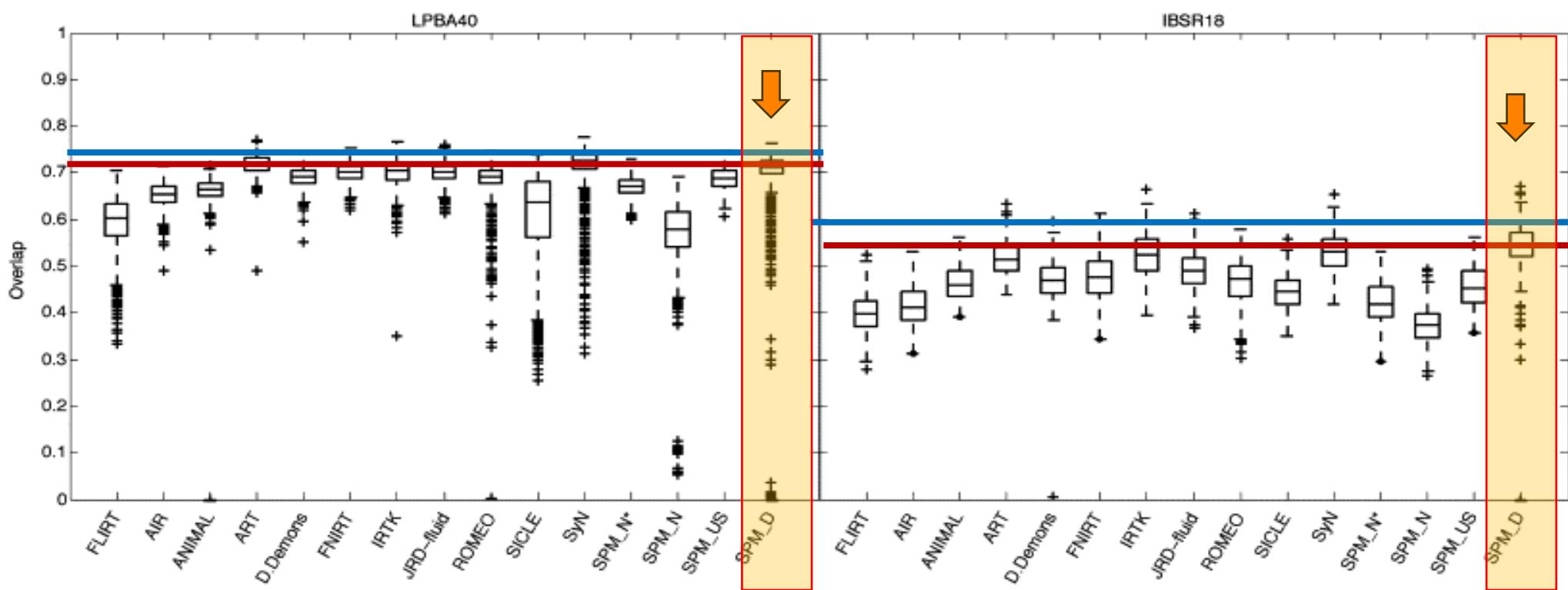
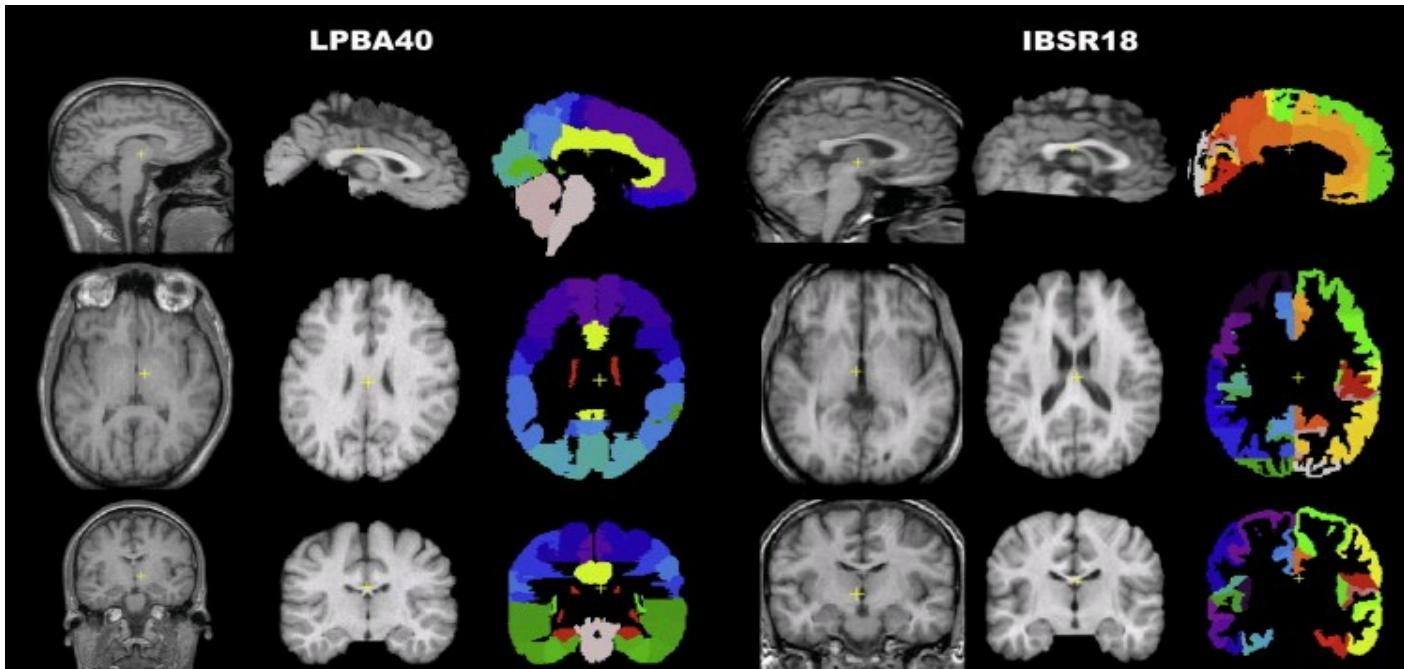


Subject 3



471 Subject Average

Evaluations of nonlinear registration algorithms



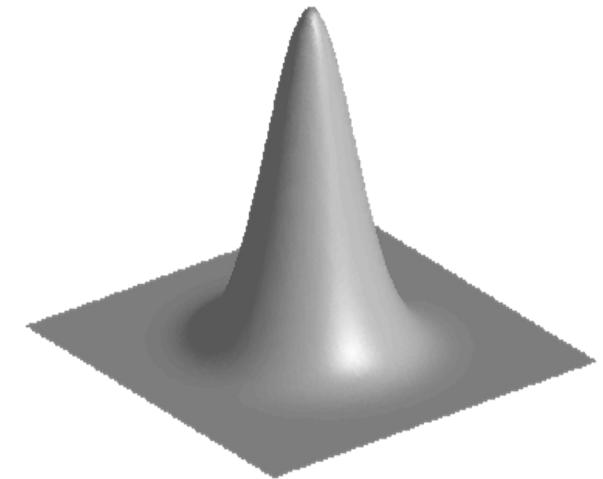
Contents

- * Preliminaries
- * Within-subject: Realignment
- * Within-subject: EPI Distortion Correction
- * Within-subject: Coregistration
- * Between-subject: Normalise/Segment
- * Between-subject: Dartel
- * **Between subject: Smoothing**
 - * Compensating for inaccuracies in inter-subject alignment

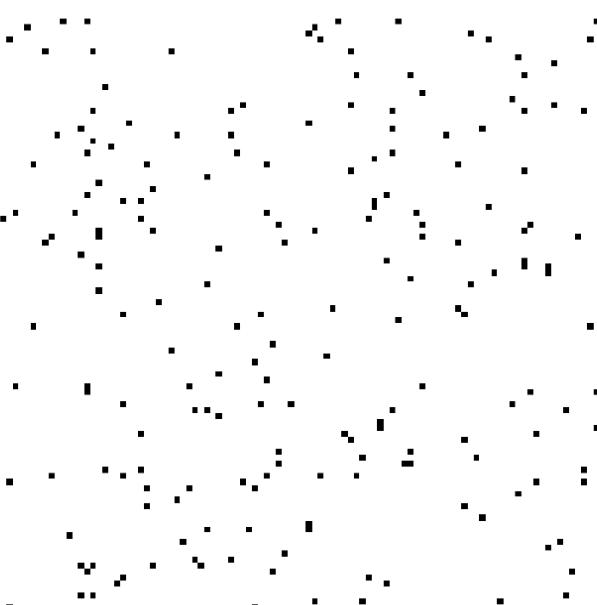
Smooth

Blurring is done by **convolution**.

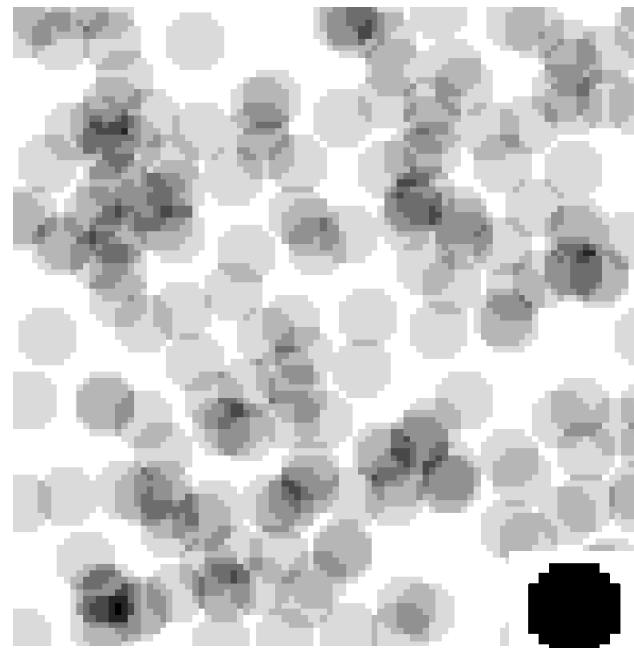
Each voxel after smoothing effectively becomes the result of applying a weighted region of interest (ROI).



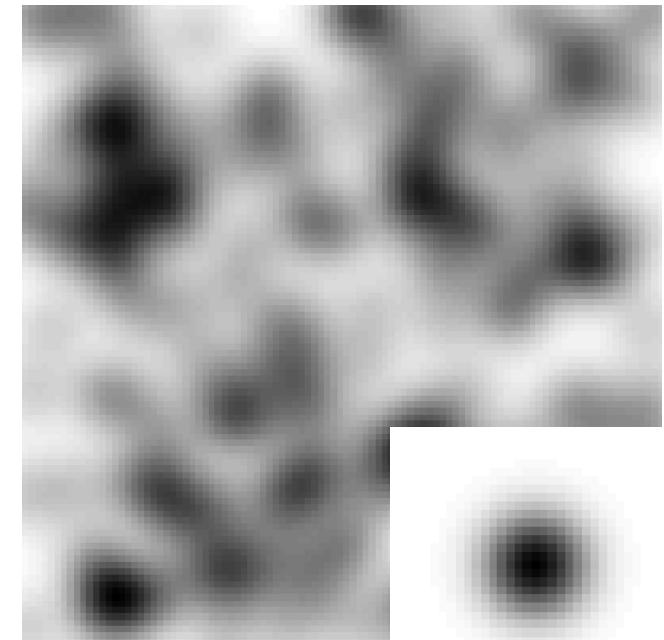
Before convolution



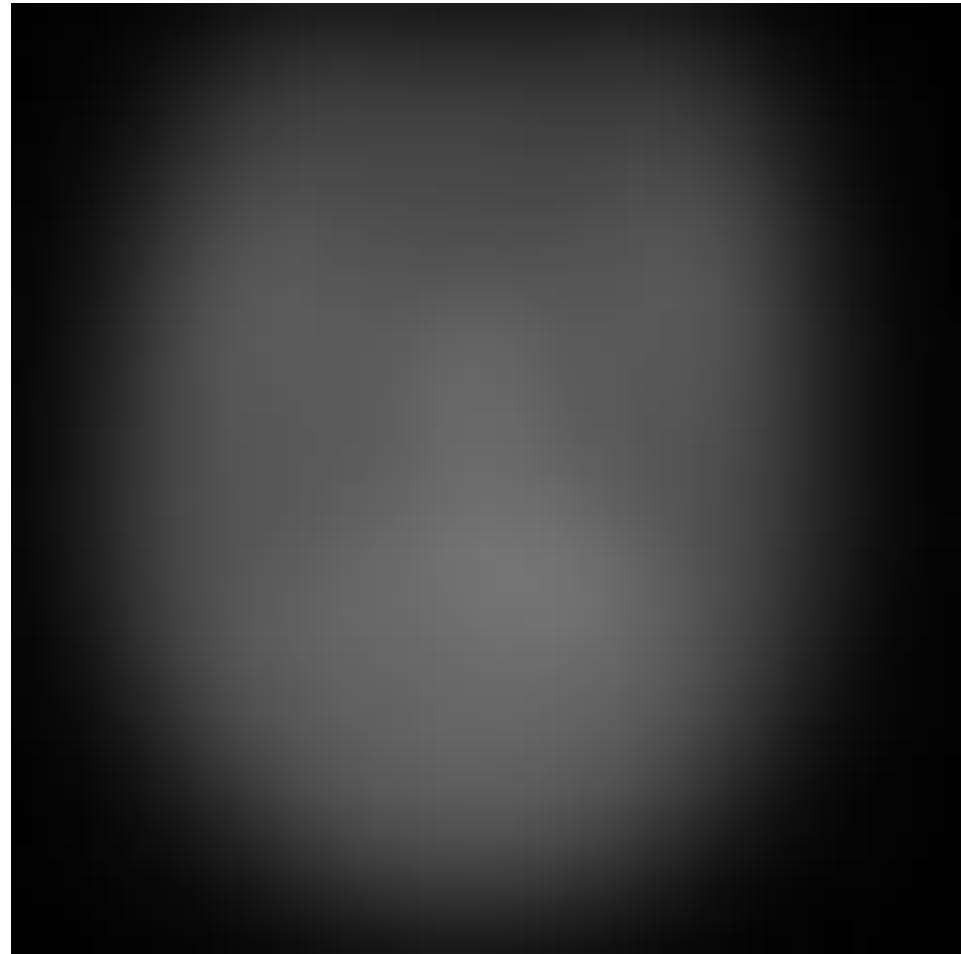
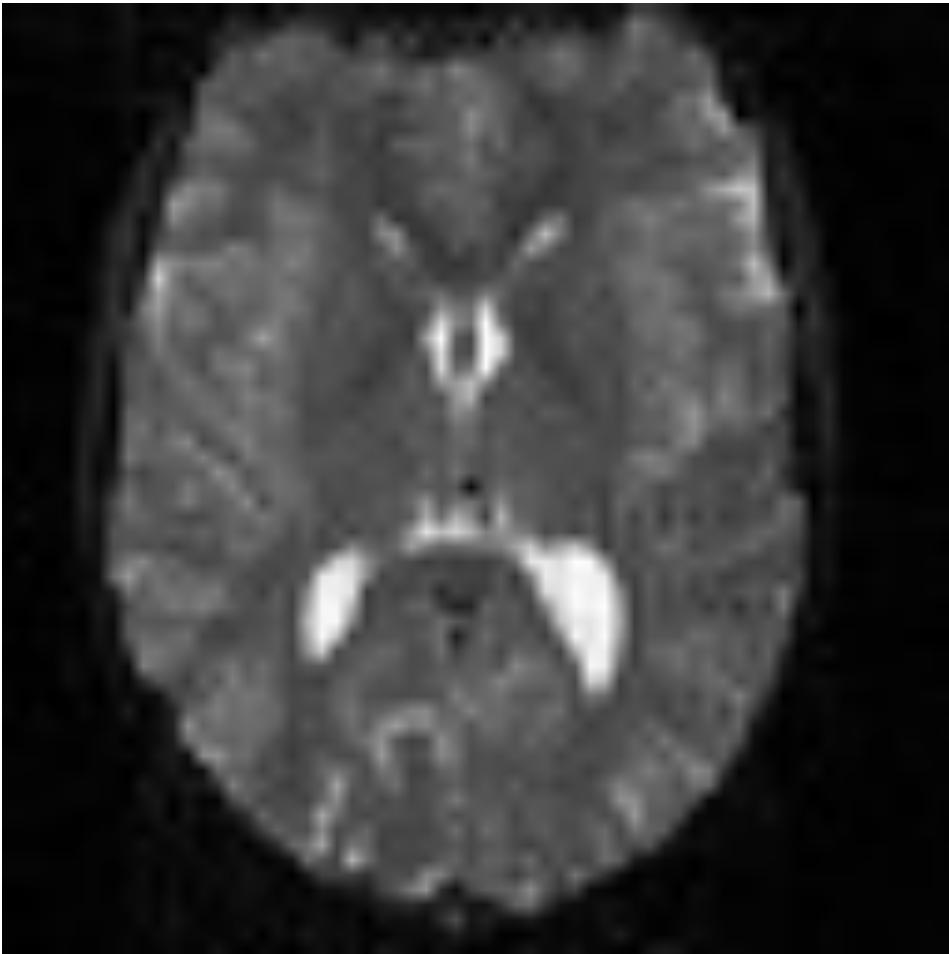
Convolved with a circle



Convolved with a Gaussian



Smooth



References

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