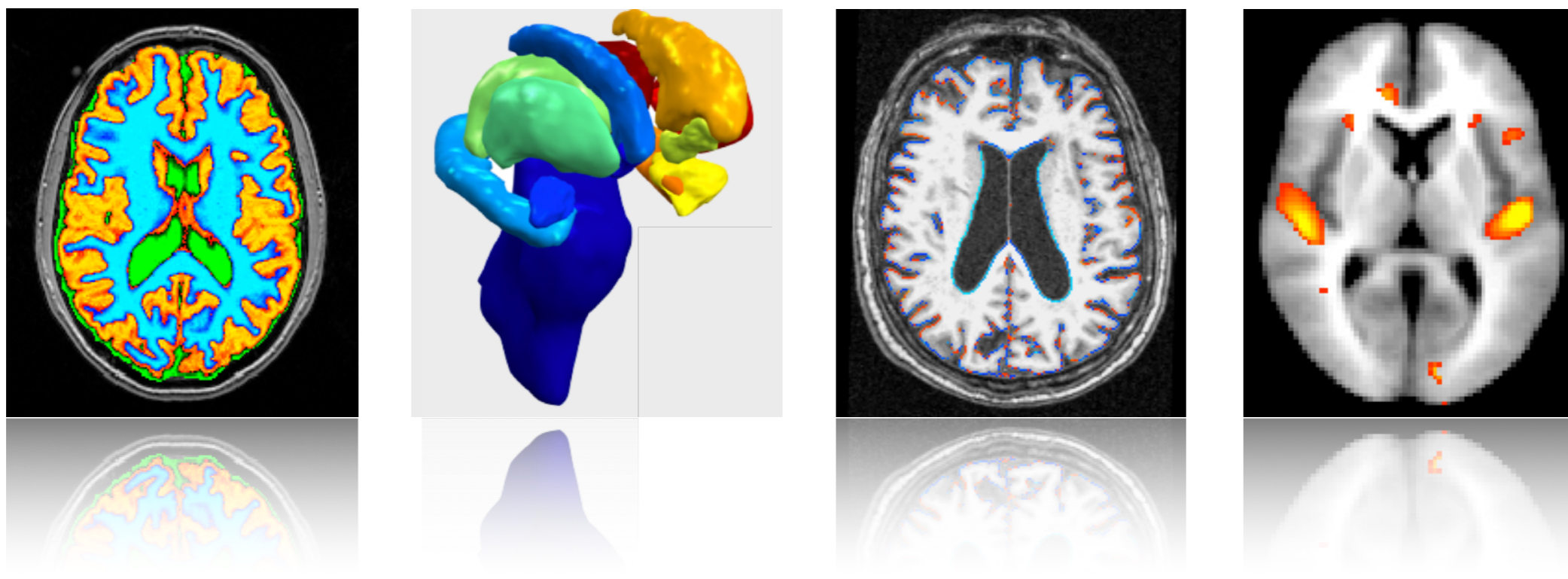




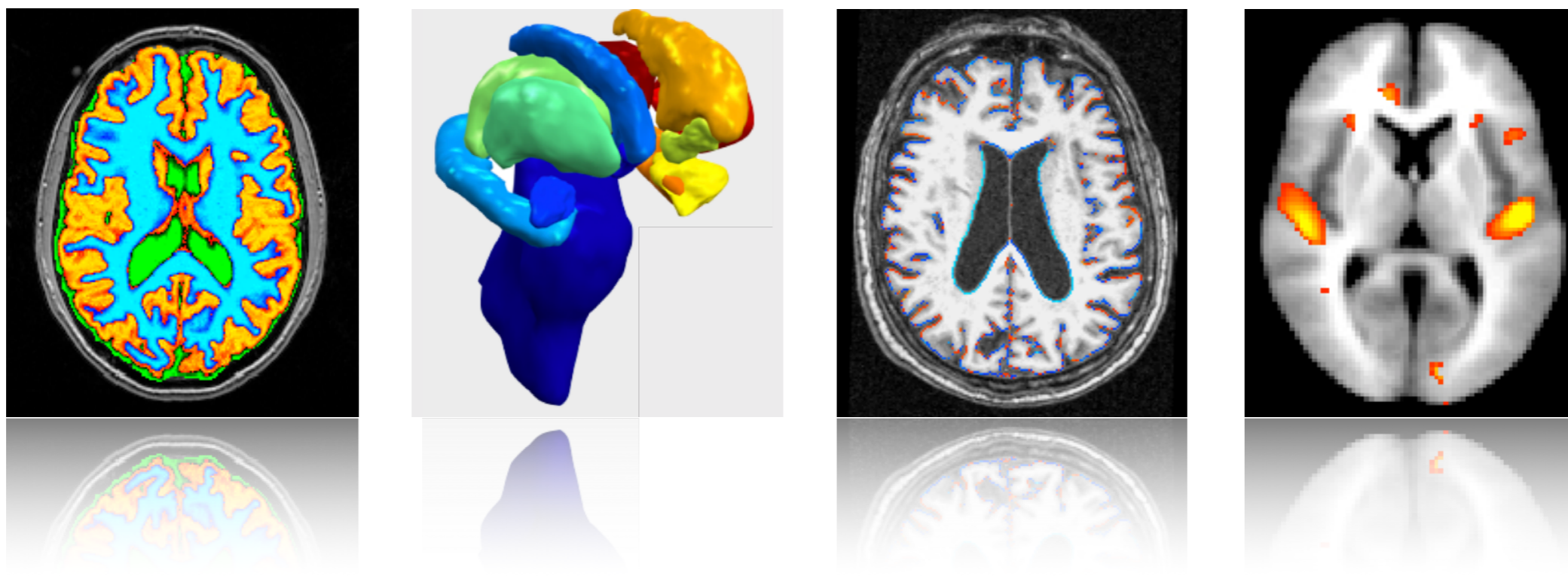
Structural Segmentation



- FAST tissue-type segmentation
- FIRST sub-cortical structure segmentation
- BIANCA segmentation of white matter lesions
- FSL-VBM voxelwise grey-matter density analysis
- SIENA/SIENAX global atrophy estimation



Structural Segmentation



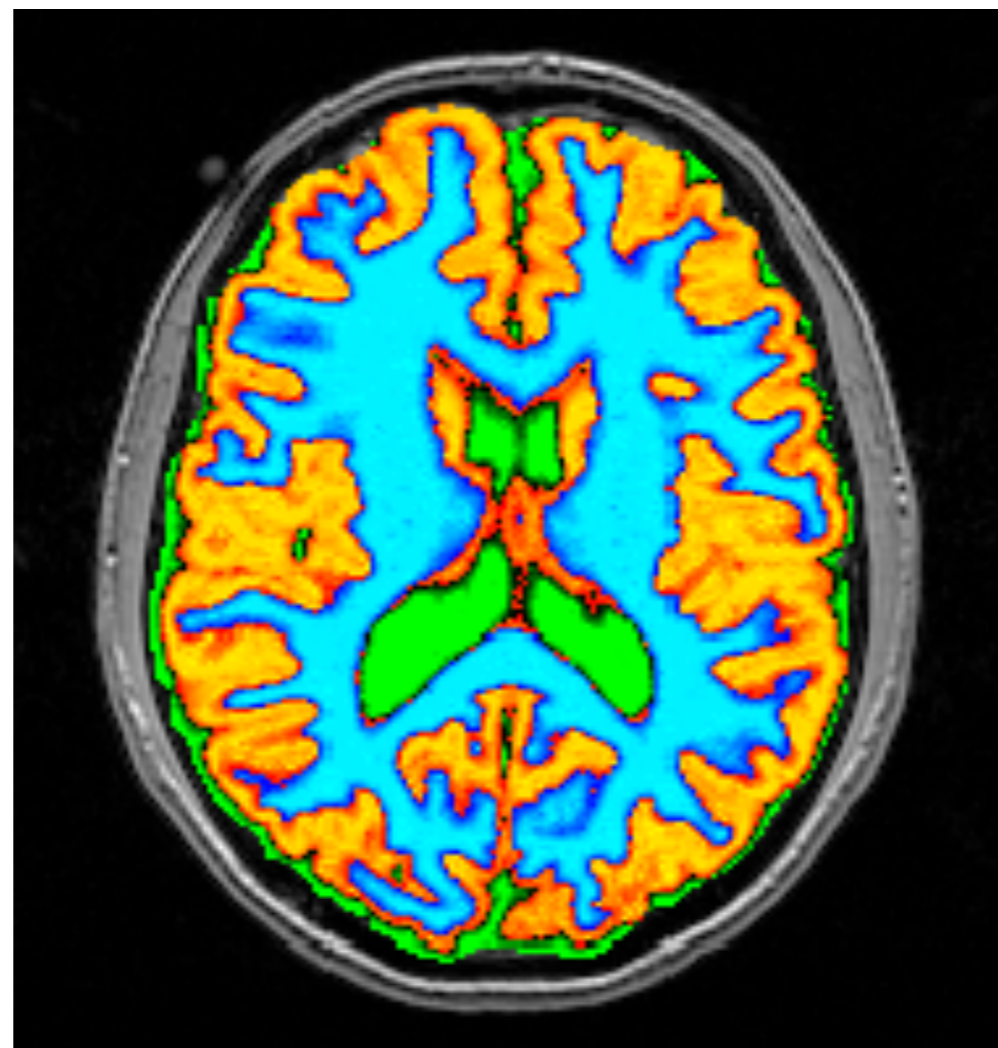
- FAST tissue-type segmentation
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- SIENA/SIENAX global atrophy estimation



FAST

FMRIB's Automated Segmentation Tool

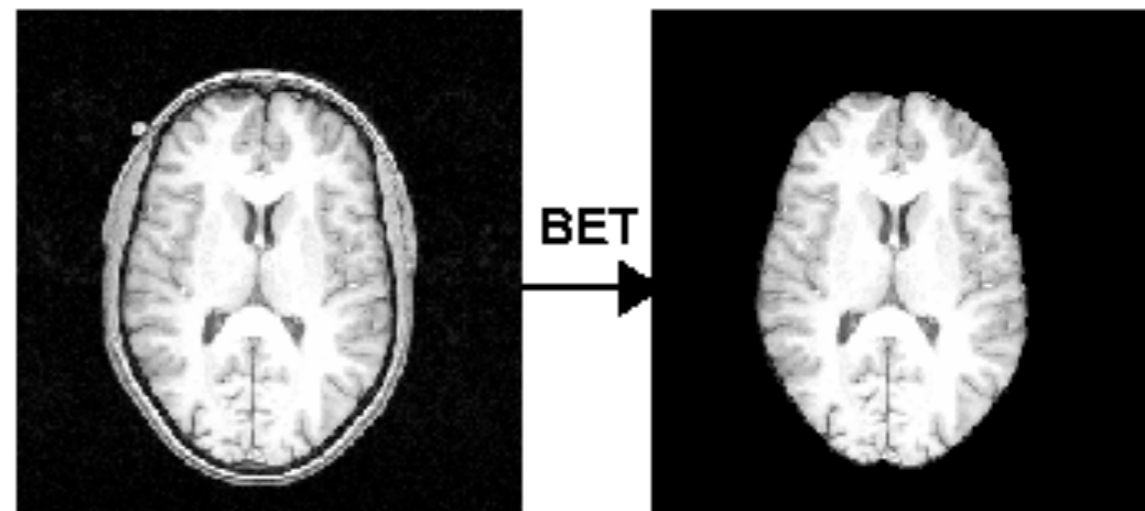
generic tissue-type segmentation and bias
field correction



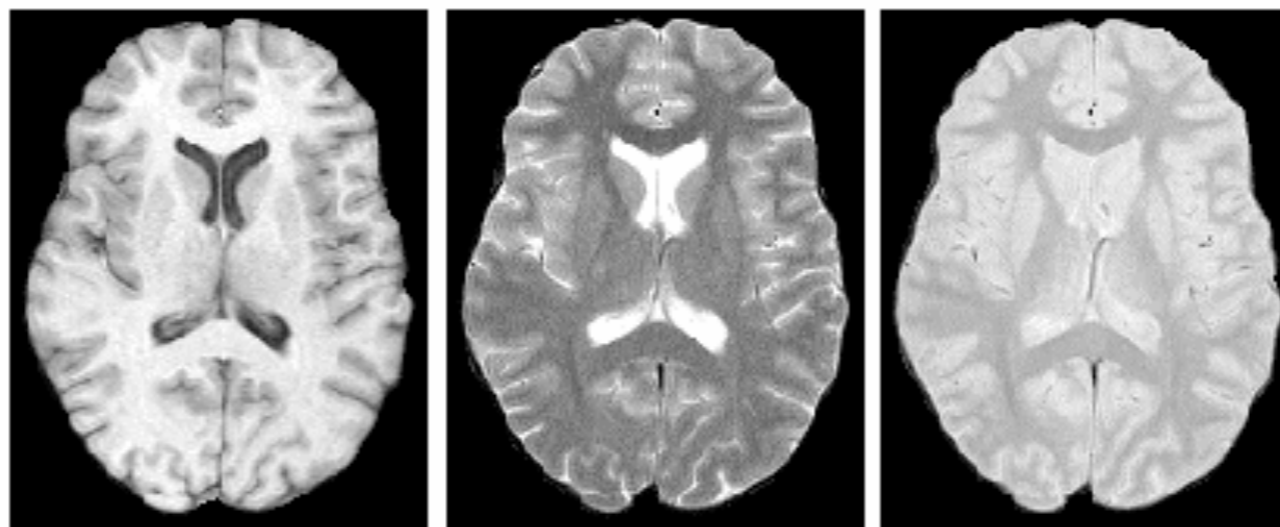


FAST: Input

- First use BET to remove non-brain
All volumetric results are *highly sensitive* to errors here.
For *bias-field correction alone* the errors do not matter that much



- Input is normally a single image (T1, T2, proton-density...)
- Or several inputs (“multichannel”)
- For multi-channel, all must be pre-aligned (FLIRT)

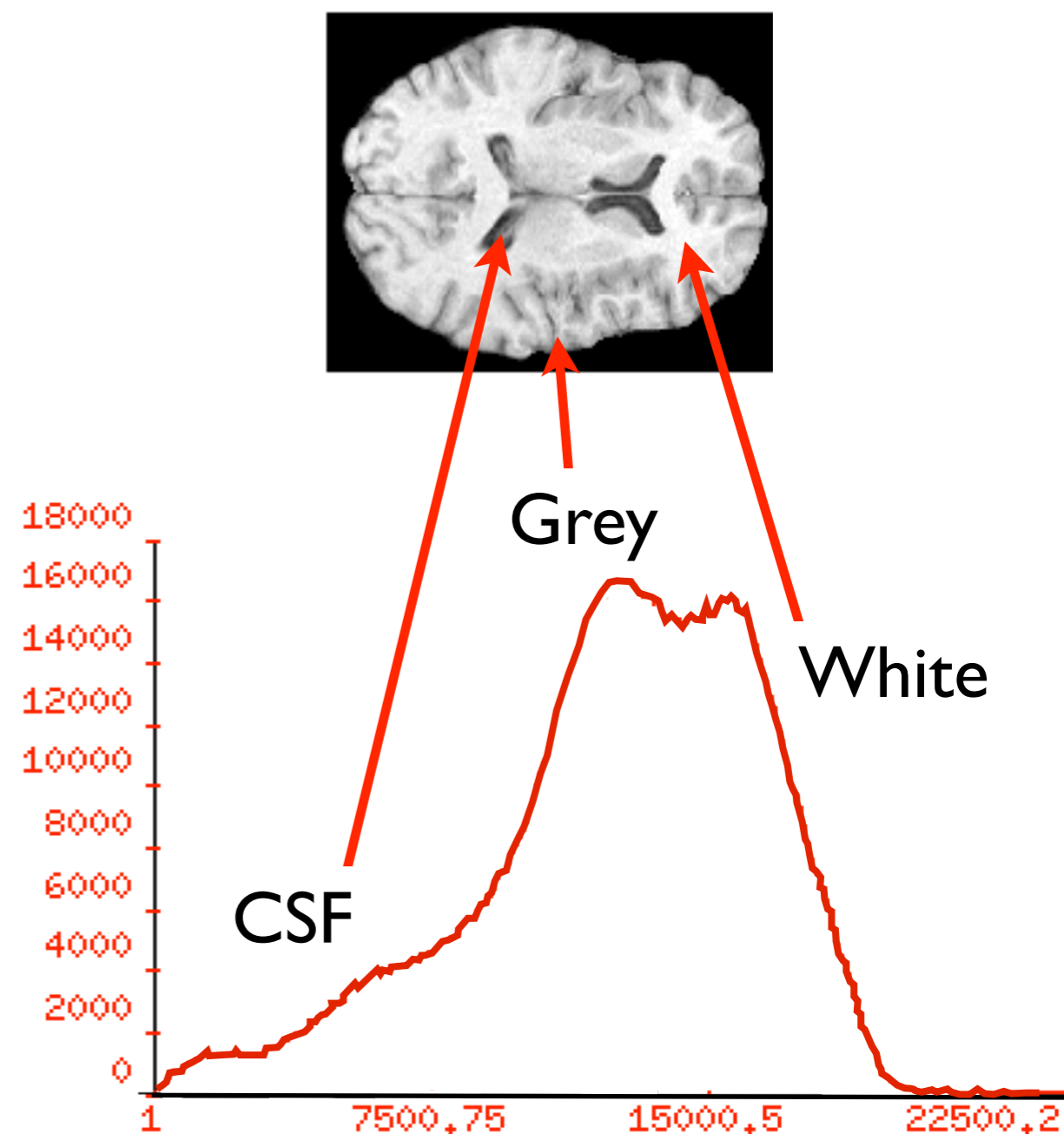




Intensity Model

tissue intensity distributions

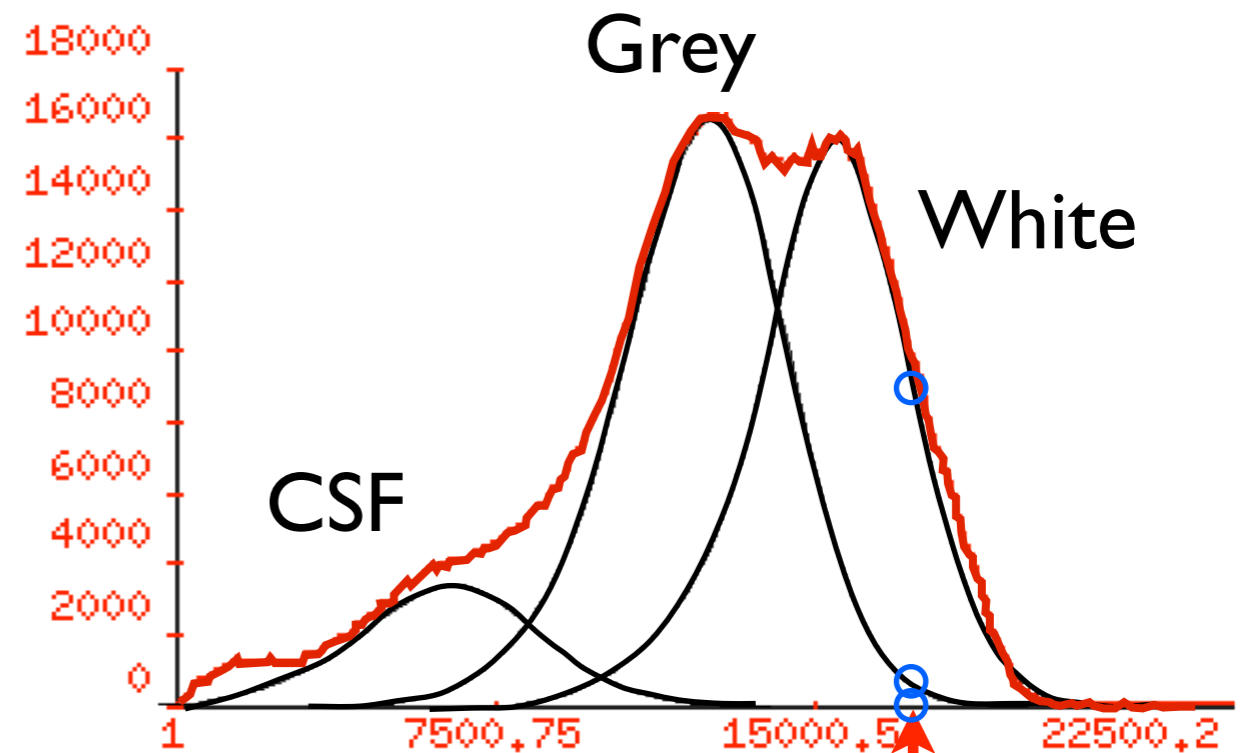
- Histogram = voxel count vs. intensity
- Model = mixture of Gaussians
- If well separated, have clear peaks; then **segmentation** easy
- Overlap worsened by:
 - Bias field
 - Blurring
 - Low resolution
 - Head motion
 - Noise





Probability Model

- Histogram = probability distribution function
- Model = mixture of Gaussians
- Probability determined for each tissue class



For example:

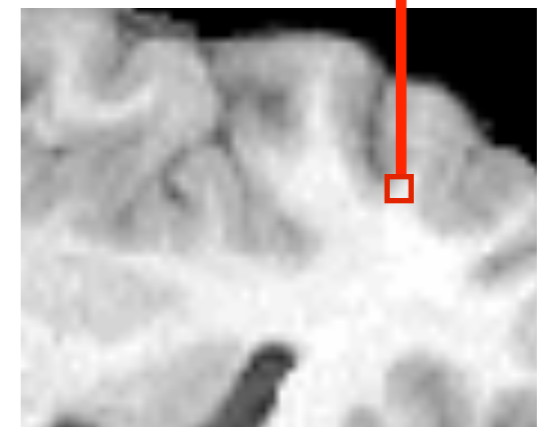
Voxel near WM/GM border

$P(\text{CSF})$ near zero

$P(\text{GM})$ low

$P(\text{WM})$ moderate

Intensity = 17203

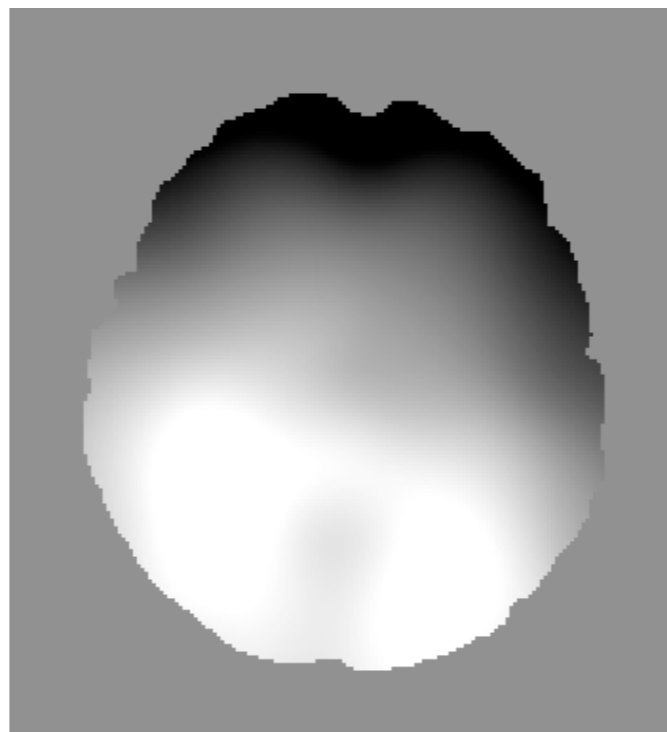




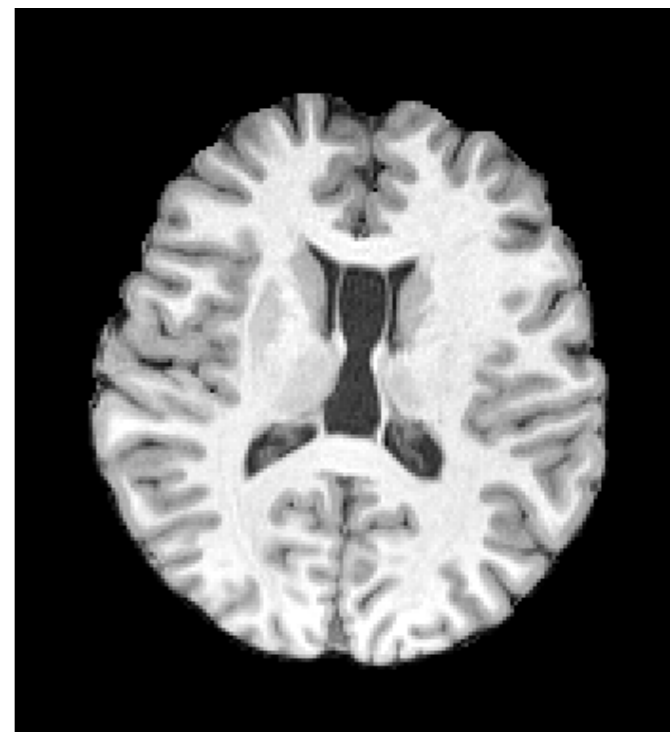
Bias Field Correction



Original



Bias



Restored

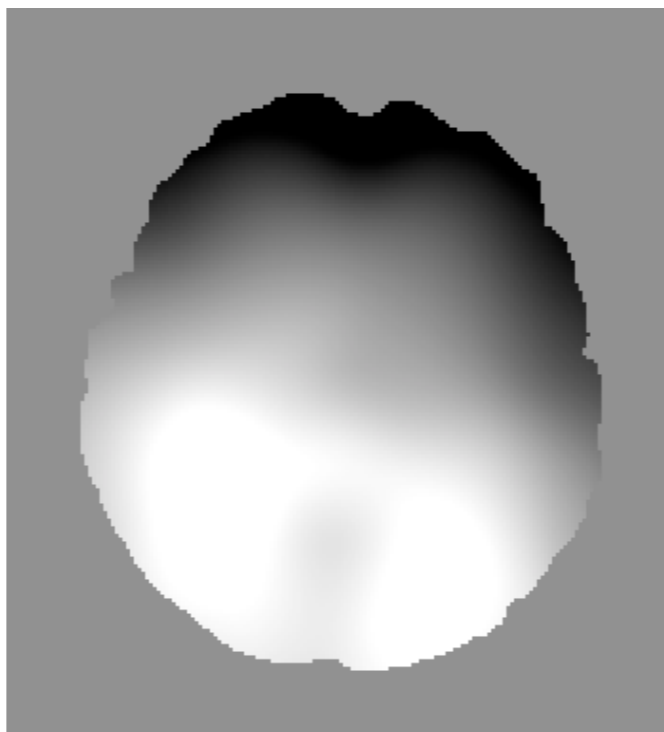
- MRI RF (radio-frequency field) inhomogeneity causes intensity variations across space
- Causes problems for segmentation
- Need to remove bias field before or during segmentation
- Becomes more common and problematic at high field



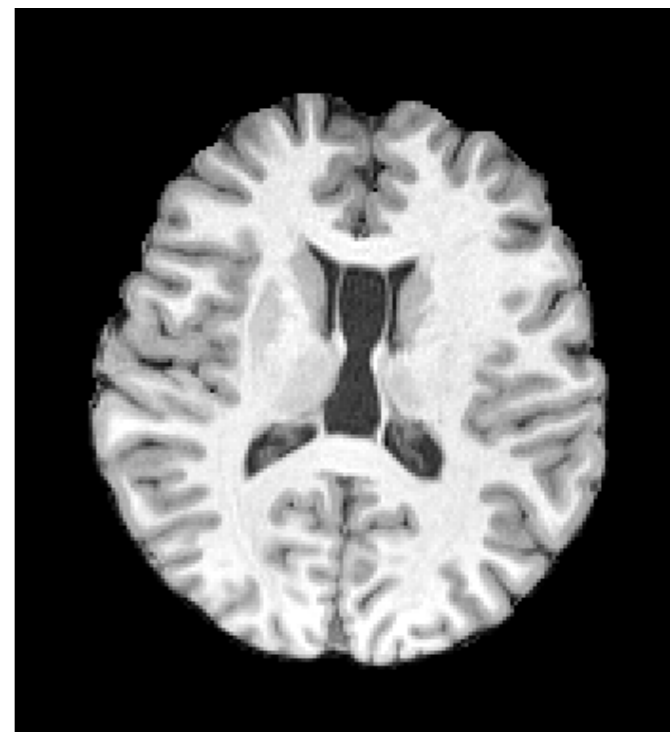
Bias Field Correction



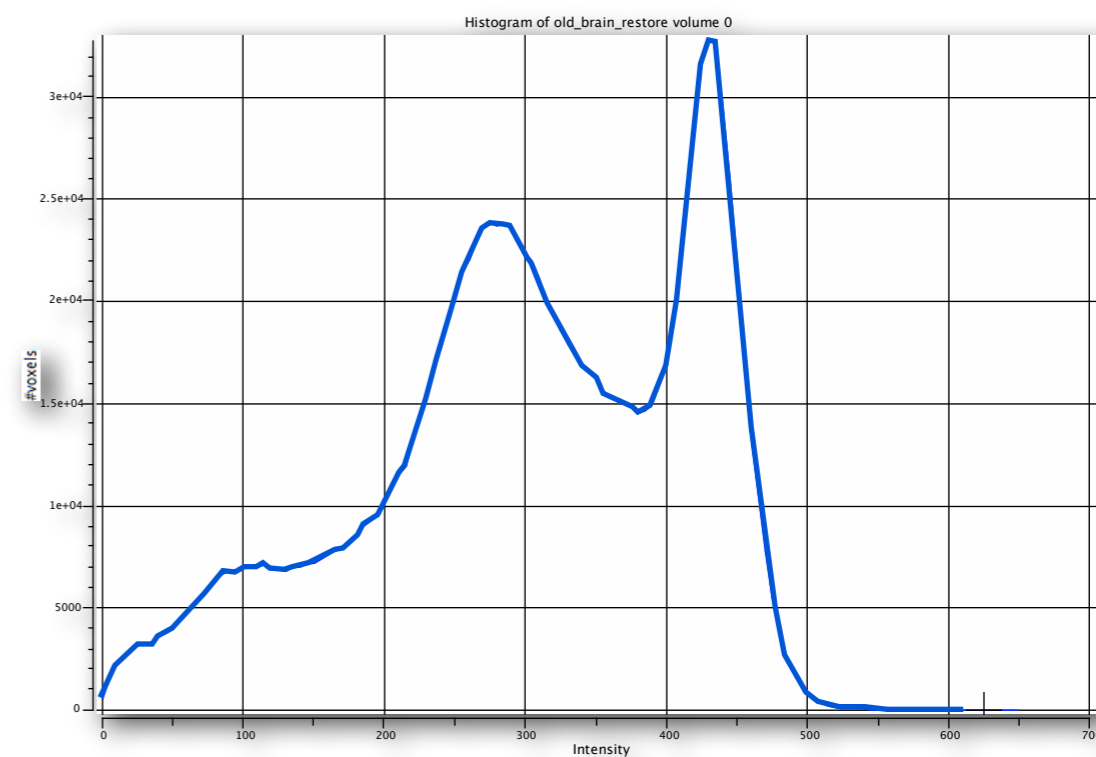
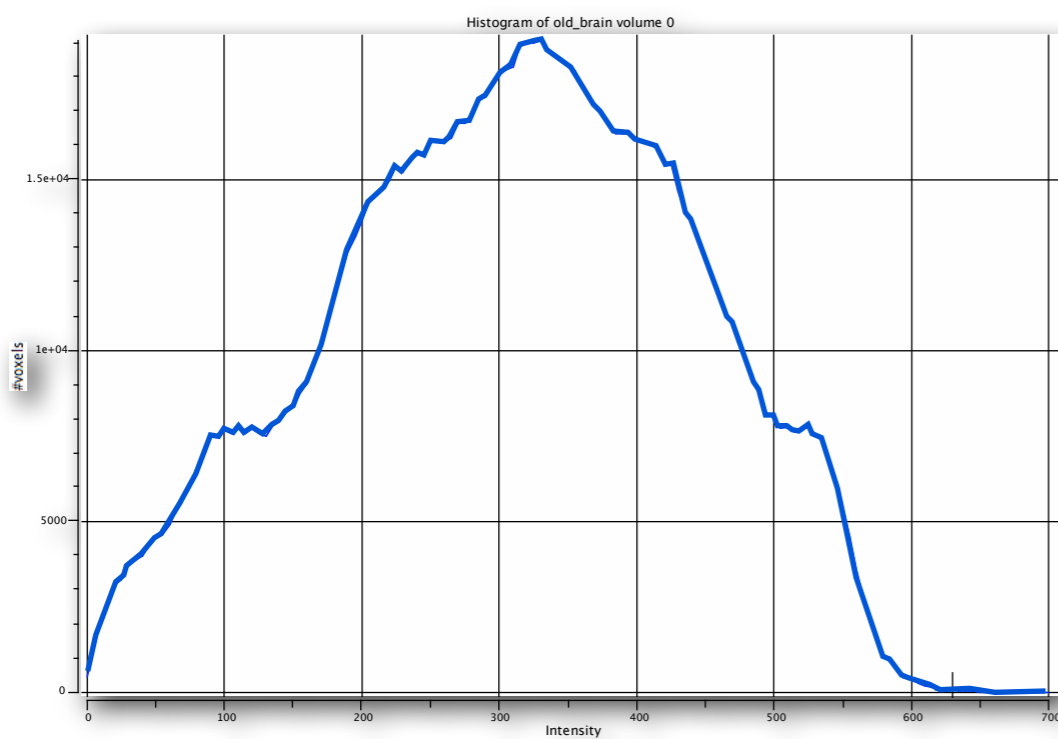
Original



Bias



Restored

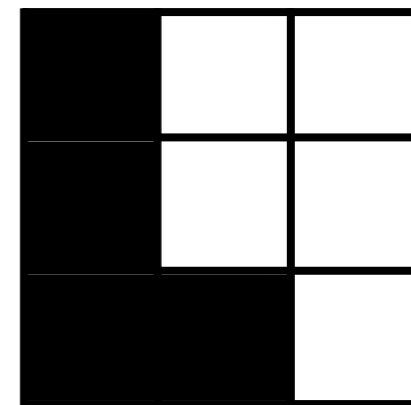


Histograms

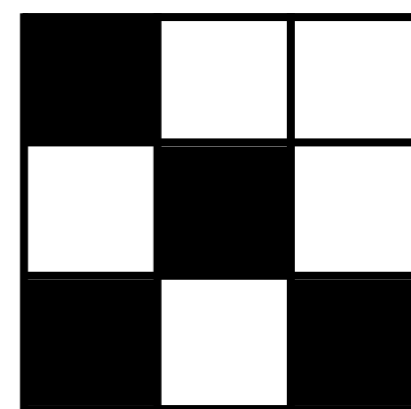


Use Spatial Neighbourhood Information (MRF)

- Neighbourhood information: “if my neighbours are grey matter then I probably am too”
- Simple classifiers (like K-means) do not use spatial neighbourhood information
- More robust to noise
- Need the right balance between believing neighbours or intensity



Likely configuration
High probability



Unlikely configuration
Low probability



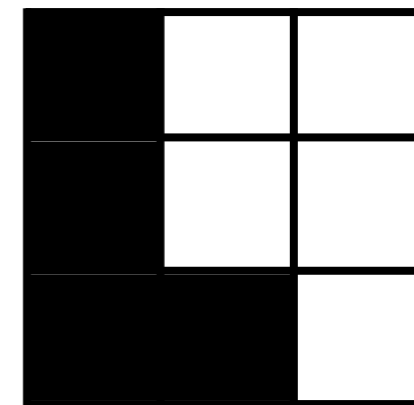
Use Spatial Neighbourhood Information (MRF)

Combine with probability based on Gaussian Mixture Model:

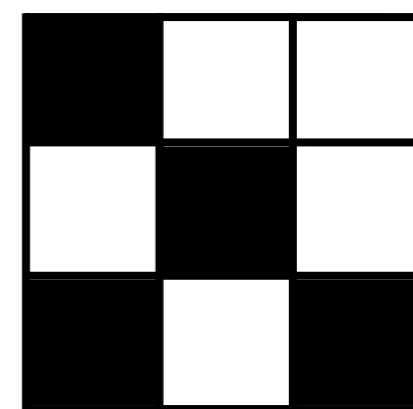
$$\text{Final log probability} = \log p(\text{intensity}) + \beta \log p(\text{MRF})$$

Final result depends on β value

This is user-adjustable



Likely configuration
High probability

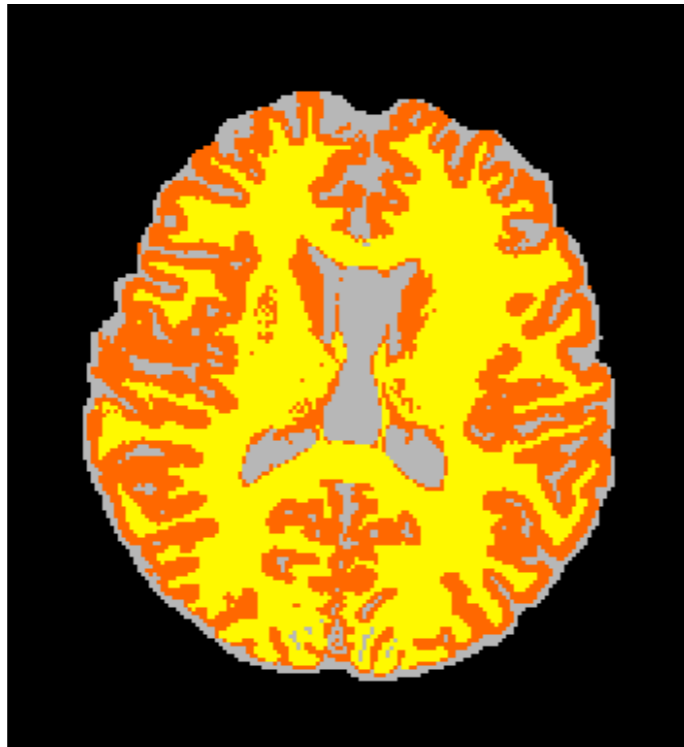


Unlikely configuration
Low probability

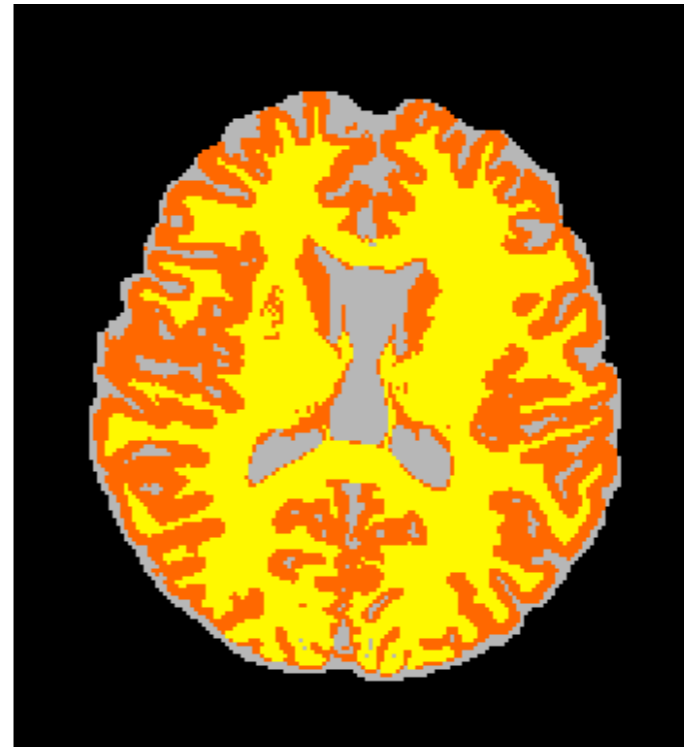


Effect of MRF Weighting

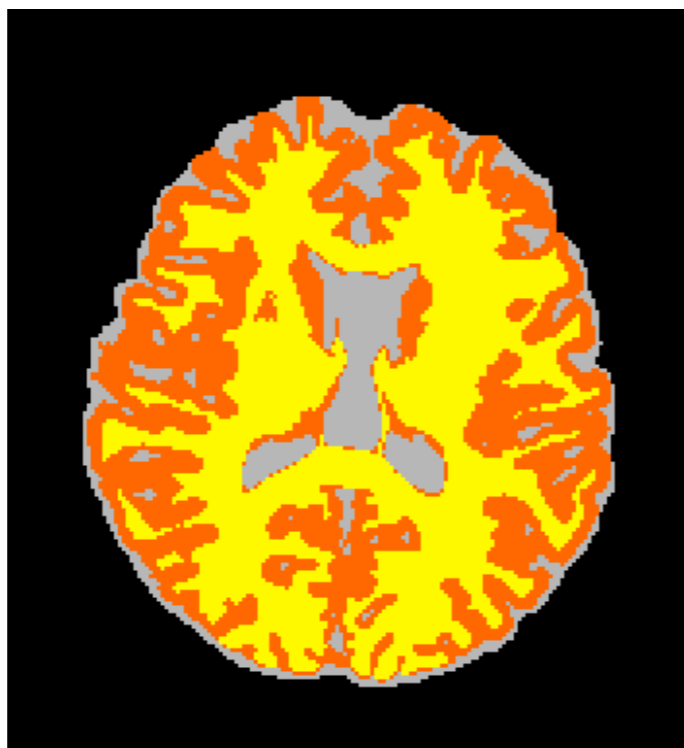
$\beta=0$



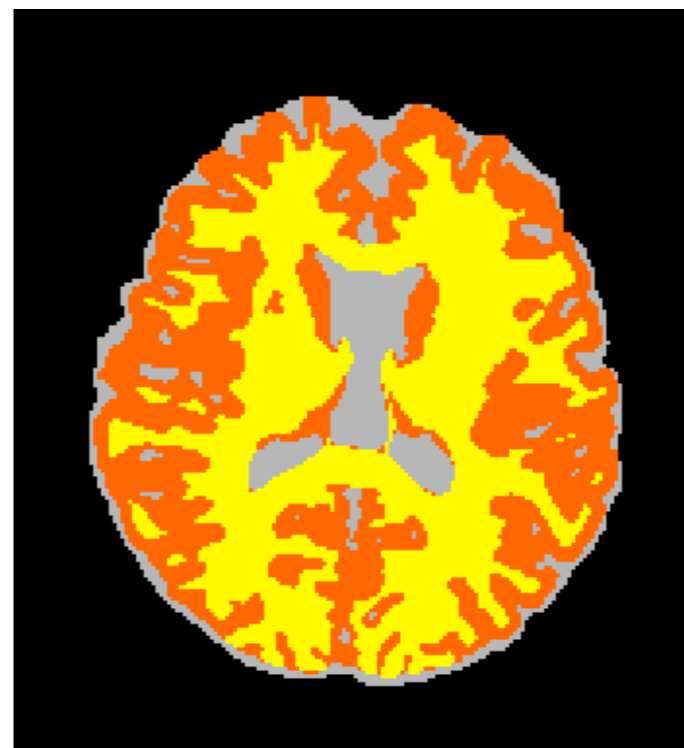
$\beta=0.1$



$\beta=0.3$



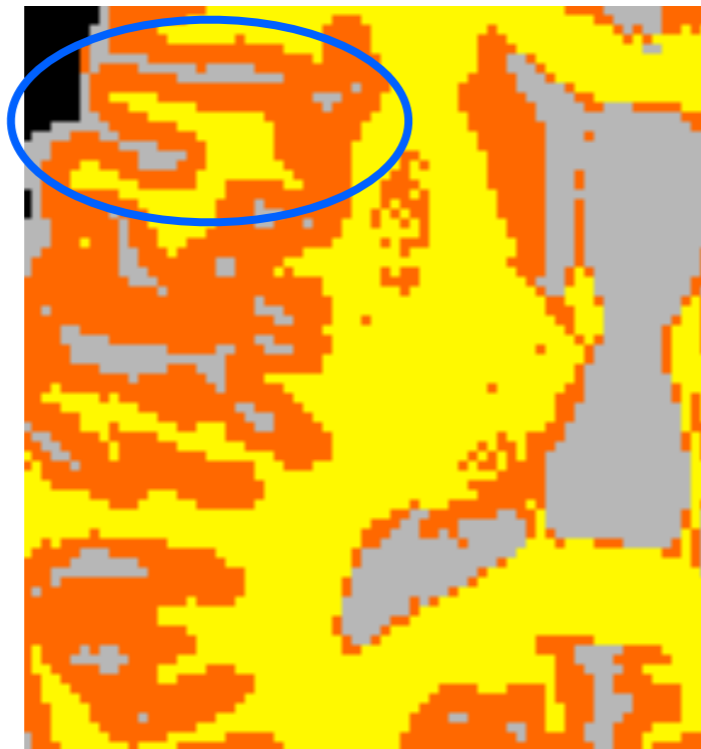
$\beta=0.5$





Effect of MRF Weighting

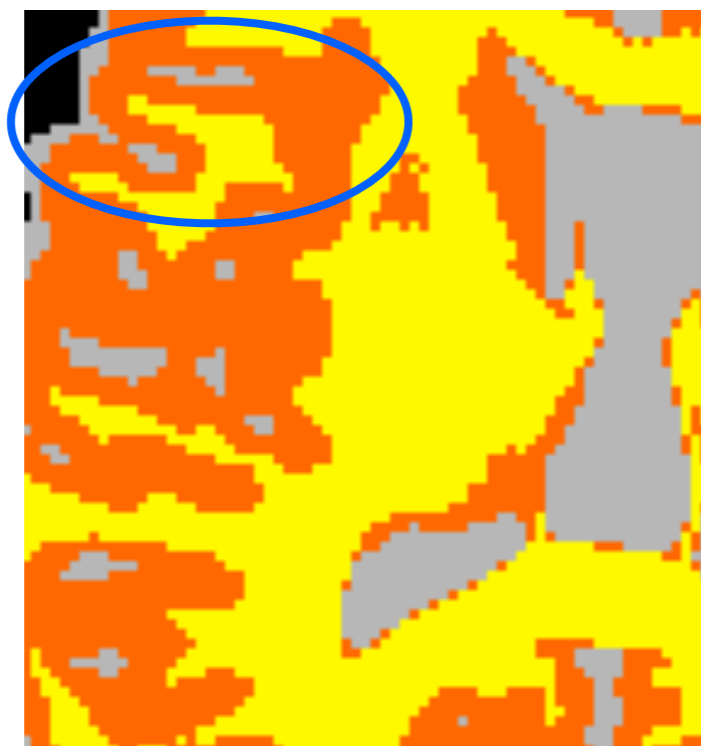
$\beta=0$



$\beta=0.1$



$\beta=0.3$



$\beta=0.5$

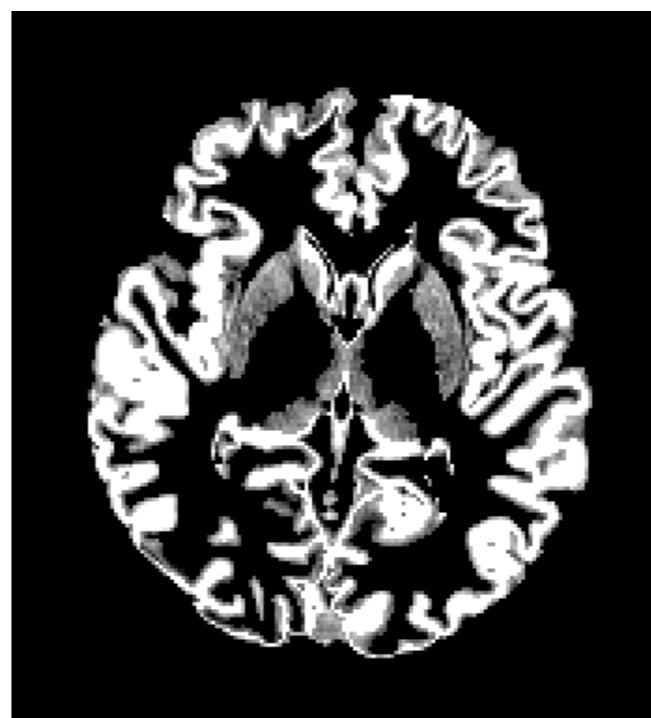
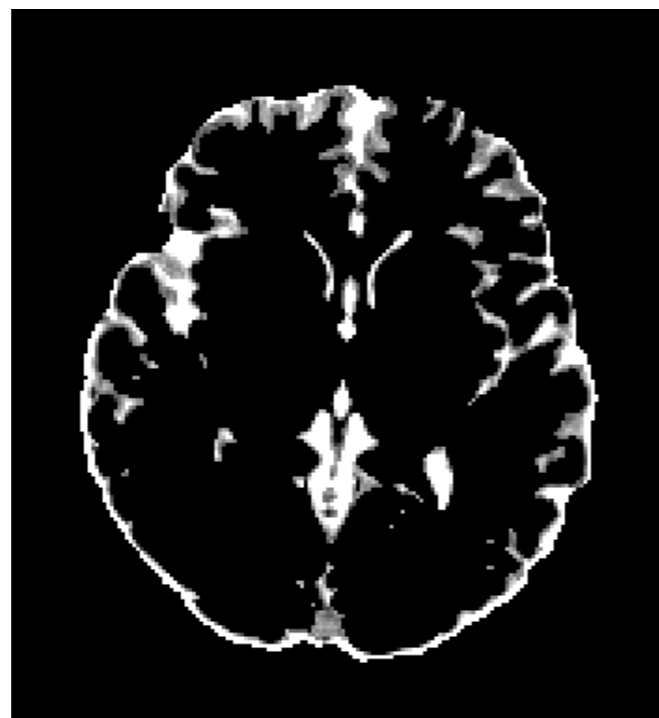




Partial Volume Modelling

- A better model is what fraction of each voxel is tissue X?
- “partial volume” = fraction of CSF, GM or WM

PVE
CSF, GM, WM



Image



“Hard”
Segmentation



PVE (GM)

- This **substantially improves accuracy of volume estimation**



FAST - The Overview

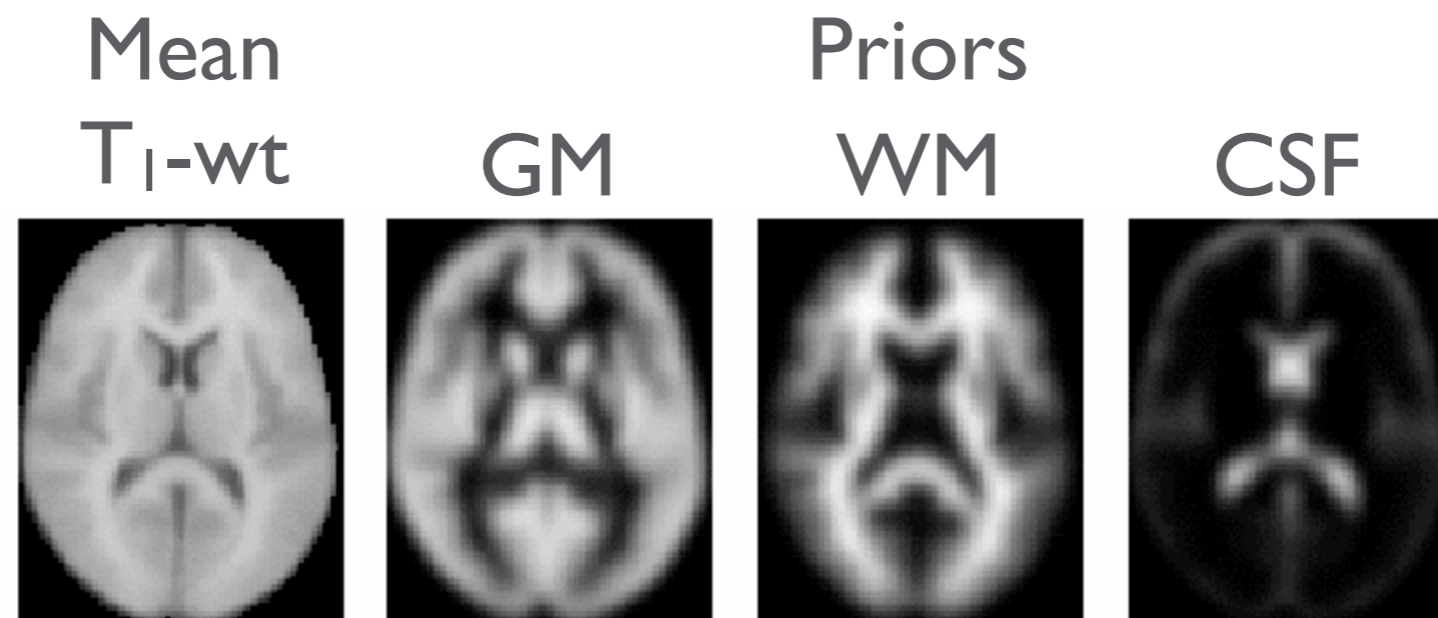
- Initial (approximate) segmentation
 - Tree-K-means
- Iterate
 - Estimate bias field
 - Estimation segmentation; iterate
 - Update segmentation (intensity + MRF)
 - Update tissue class parameters (mean and standard deviation)
- Apply partial volume model
 - MRF on mixel-type (how many tissues)
 - PV Estimation





Optional Use of Priors (tissue probability maps)

- Segmentation priors = average of many subjects' segmentations
- Can use priors to weight segmentation, but can skew results (e.g. due to misalignment)
- FAST does not use priors by default
- If bias field is very bad, priors can be turned on to help initial segmentation (alternatively, do more iterations)
- Can also be turned on to feed into final segmentation (e.g. to aid segmentation of deep grey ... but see FIRST)





Other Options

FAST:

- **Bias field smoothing (-l)**
 - vary spatial smoothing of the bias field (e.g. less smooth for high field strength)
- **MRF beta (-H)**
 - vary spatial smoothness of the segmentation (default 0.1)
- **Iterations (-I)**
 - vary number of main loop iterations (default 4)



FAST

FMRIB's Automated Segmentation Tool

Summary

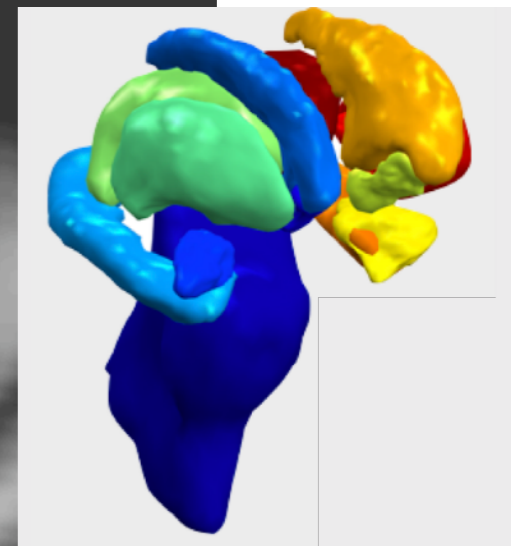
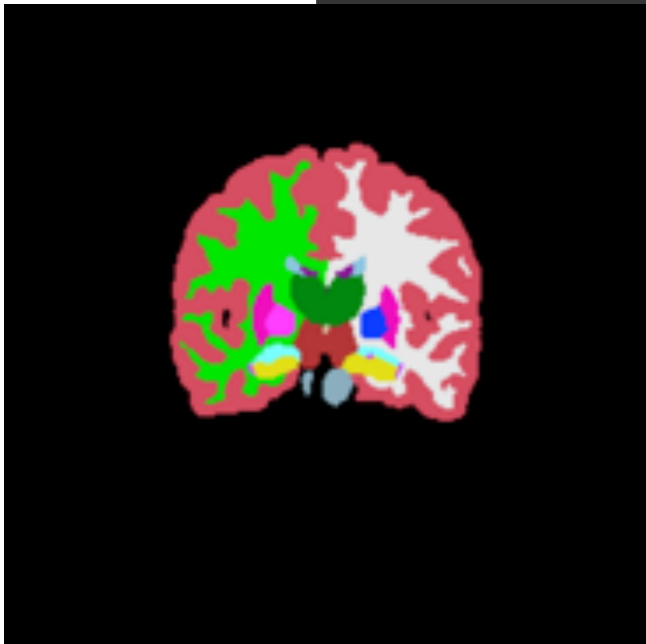
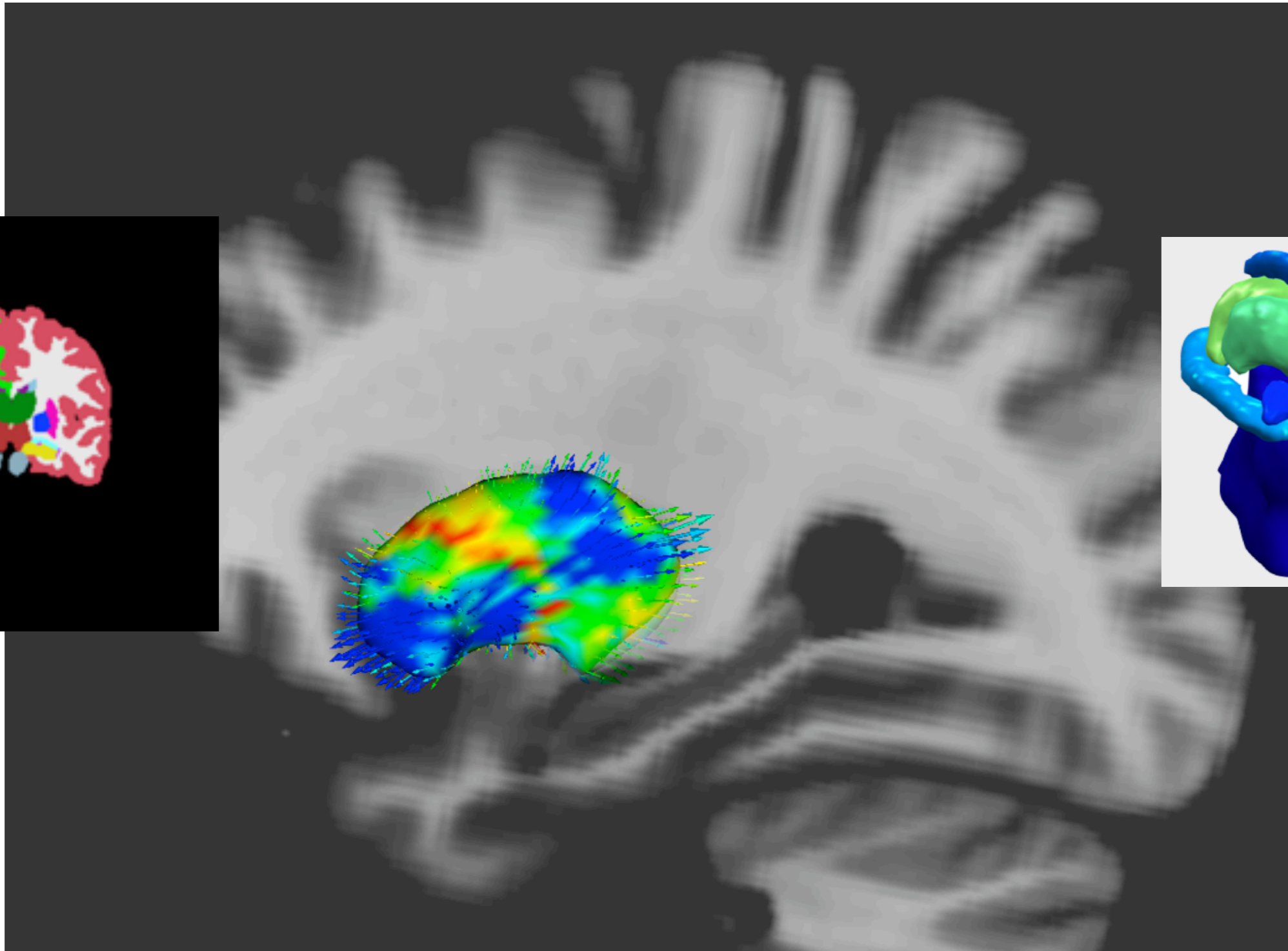
- Typically use a single T1-weighted image
 - Multichannel is an option
- Segments into three main tissue-types:
 - Grey Matter, White Matter and CSF
- Models and corrects for bias field
 - **Can be used just for bias field correction**
- Combines intensity and neighbourhood information
- Partial Volumes Estimates (PVE) are most useful and more accurate for volume calculations
- Can use priors, but can cause bias, so not the default
- Have several adjustable parameters to optimise output



FIRST

FMRIB's Integrated Registration & Segmentation Tool

Segmentation of subcortical brain structures





FIRST

FMRIB's Integrated Registration & Segmentation Tool

Segmentation of subcortical brain structures

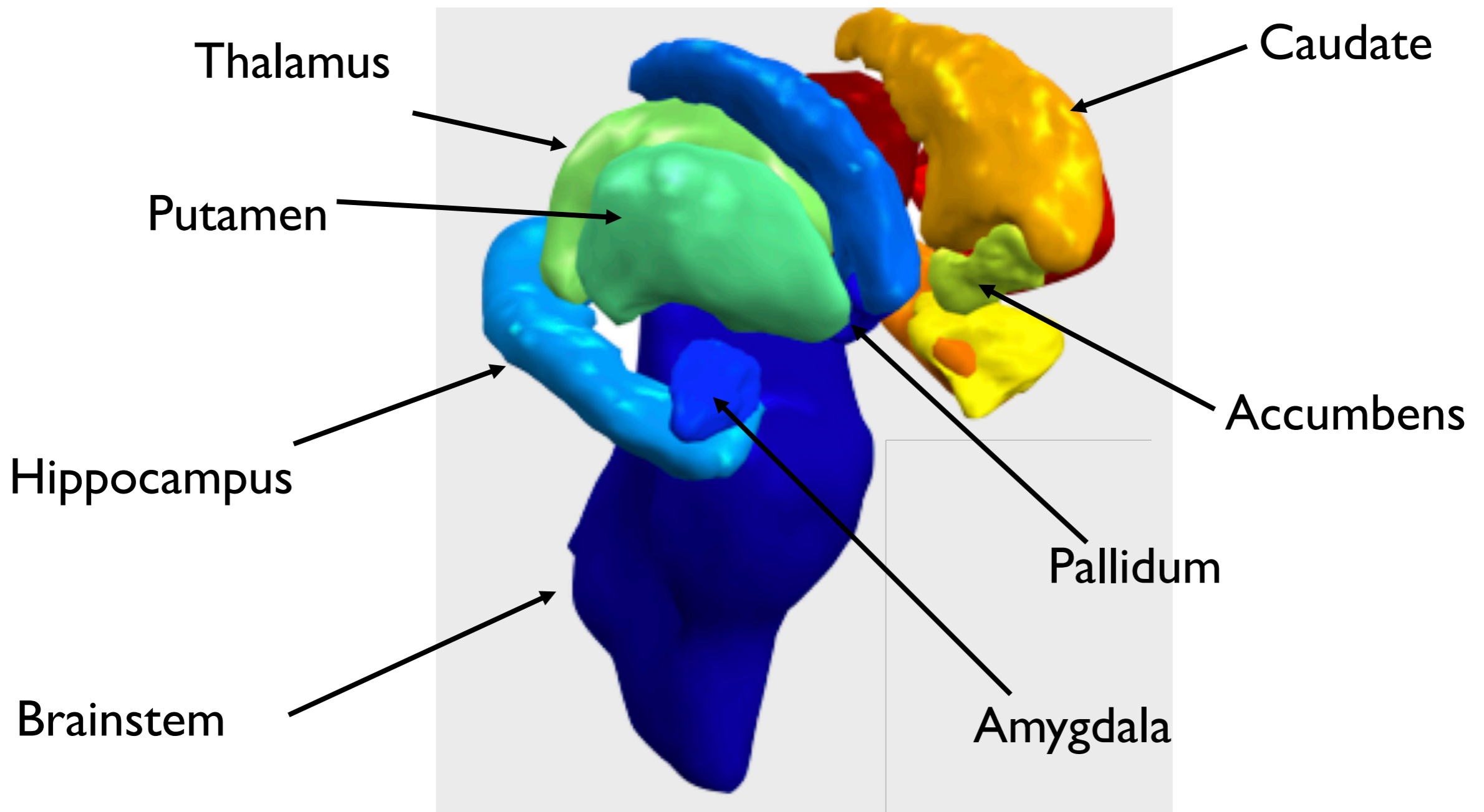




Sub-Cortical Structure Models

Incorporate prior anatomical information via explicit shape models

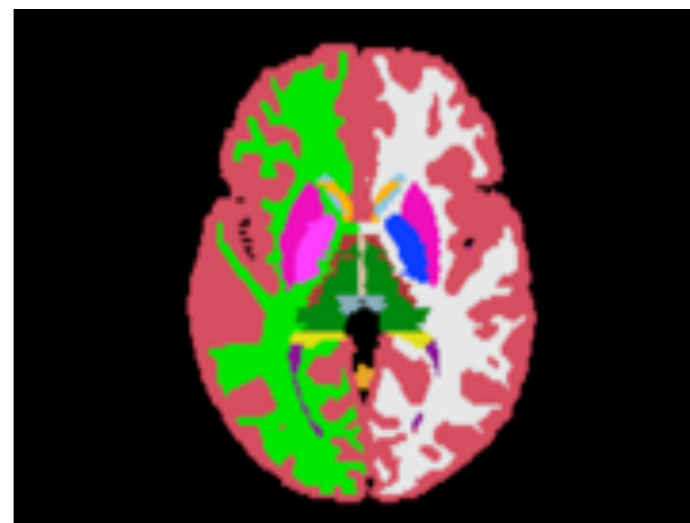
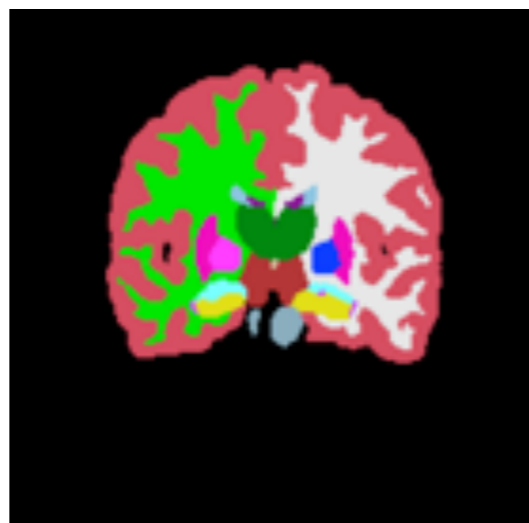
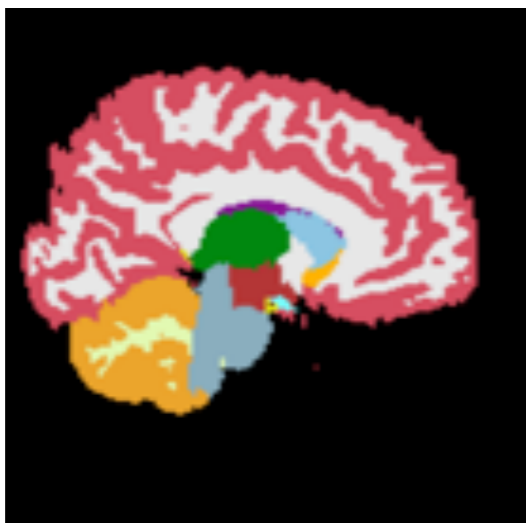
Have 15 different sub-cortical structures (left/right separately)





Training Data

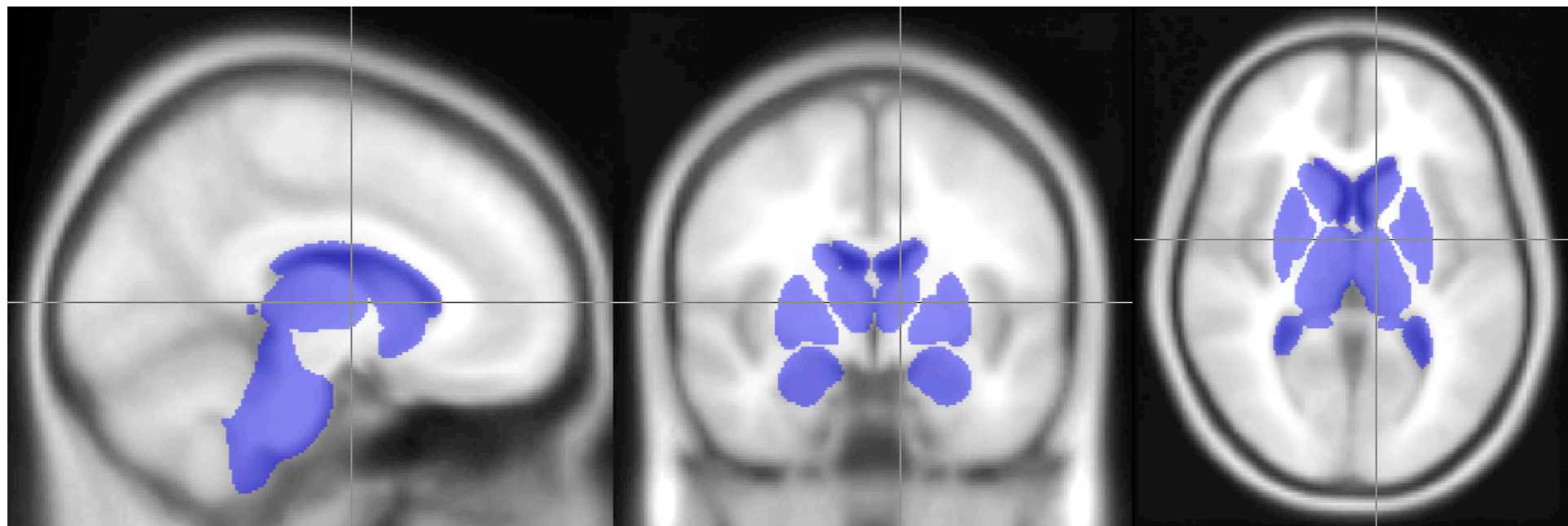
- Manual segmentations courtesy of David Kennedy, Center for Morphometric Analysis (CMA), Boston
- 336 complete data sets
- T_1 -weighted images only
- Age range 4 to 87
 - Adults: Ages 18 to 87, Controls, schizophrenia, AD
 - Children: Ages 4 to 18, Controls, ADHD, BP, prenatal cocaine exposure, schizophrenia.





Model Training : Alignment to MNI152 space

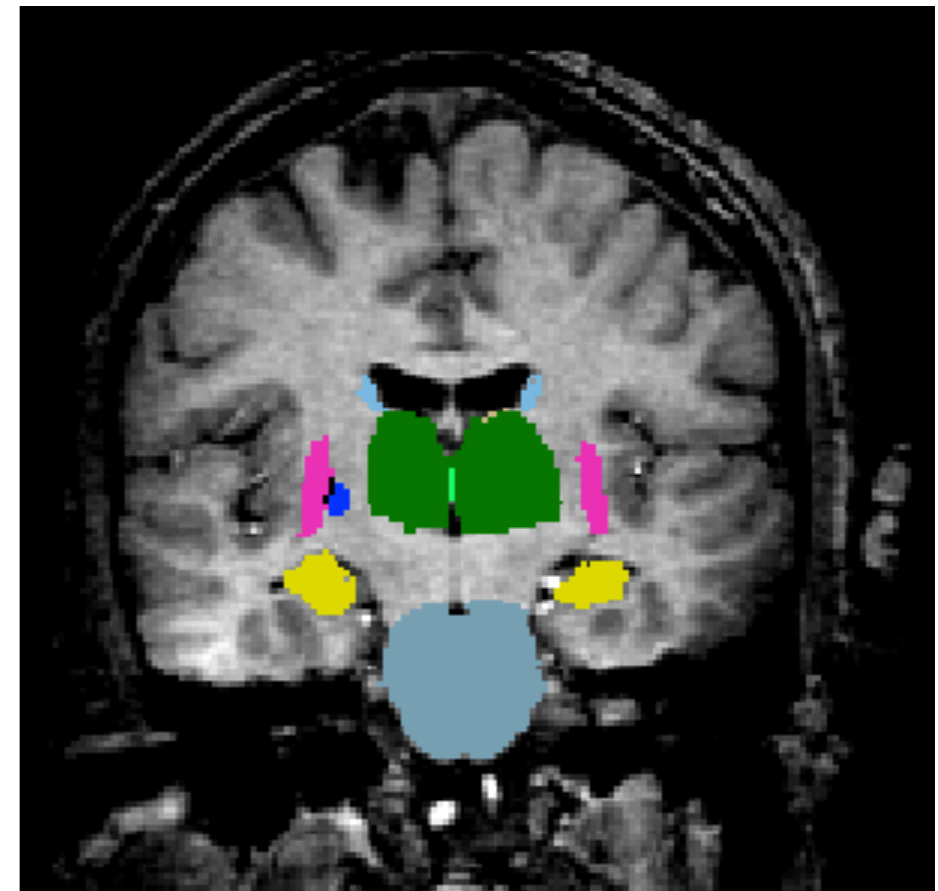
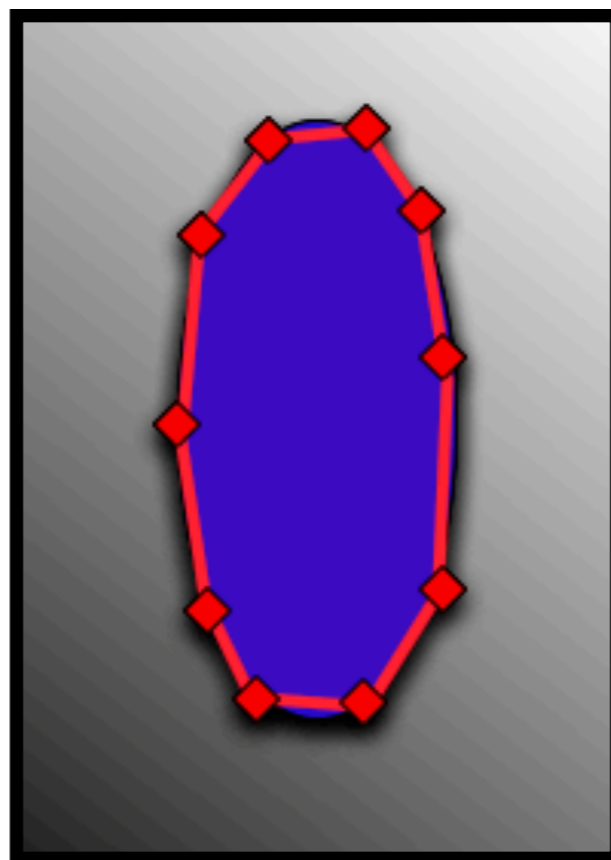
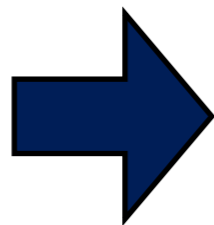
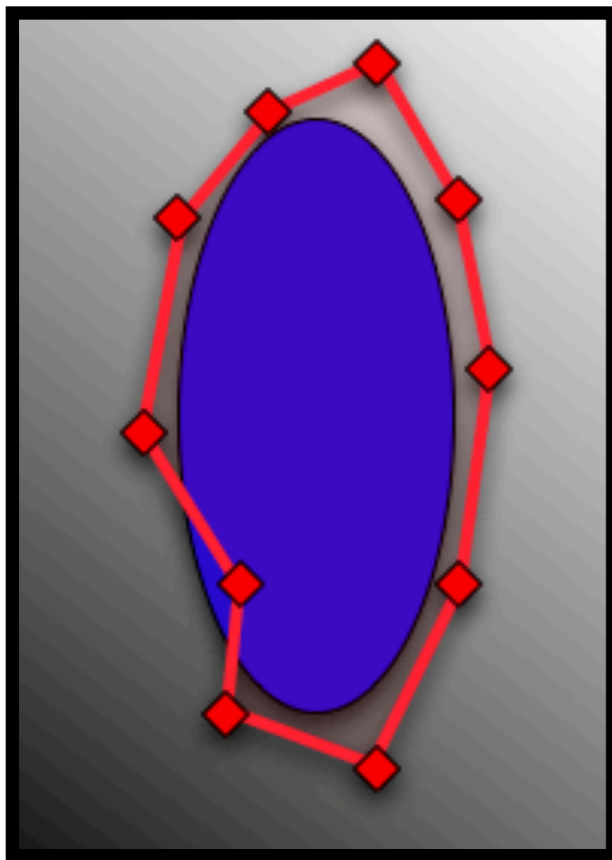
- All CMA data affine-registered to MNI152 space
 - 1mm resolution, using FLIRT
- 2-stage process:
 - Whole head 12 DOF affine
 - 12 DOF affine with MNI-space sub-cortical mask





Deformable Models

- Model: 3D mesh
- Use anatomical info on shape & intensity (from training)
- Deformation: iterative displacement of vertices
- Maintain point (vertex) correspondence across subjects





The Model: Shape

- Model average shape (from vertex locations)
- Also model/learn *likely variations* about this mean
 - modes of variation of the population; c.f. PCA
 - also call eigenvectors
- Average shape and the modes of variation serve as prior information (known before seeing the new image that is to be segmented)
 - formally it uses a Bayesian formulation



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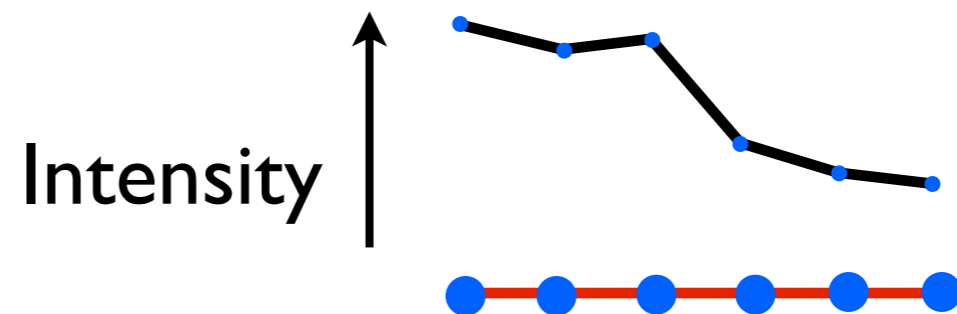
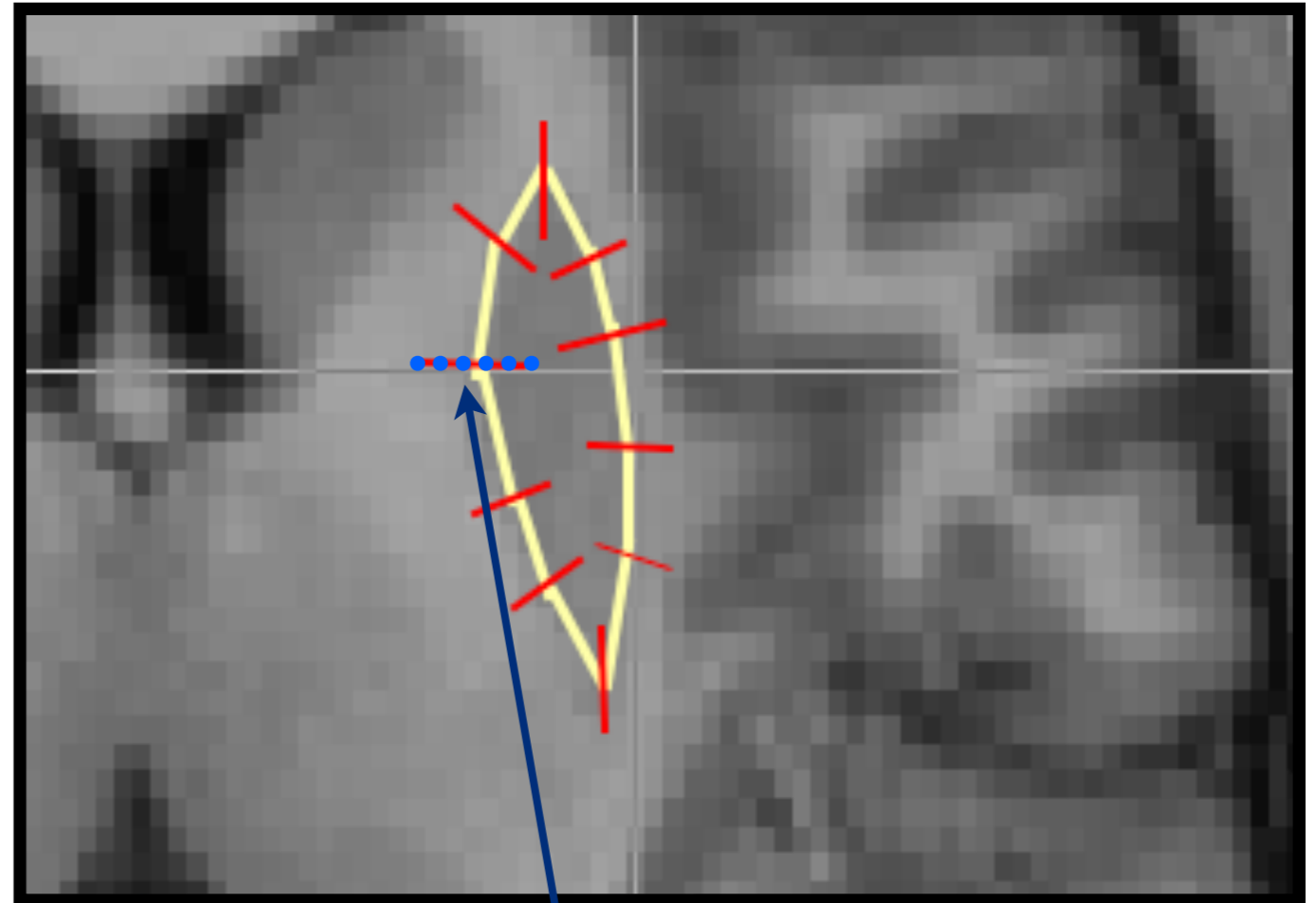
$$X = \overset{\text{mean}}{\mu_X} + \overset{\text{Singular values}}{UD} \overset{\text{Shape parameters}}{b_X}$$

Eigenvectors (modes)



The Model: Intensity

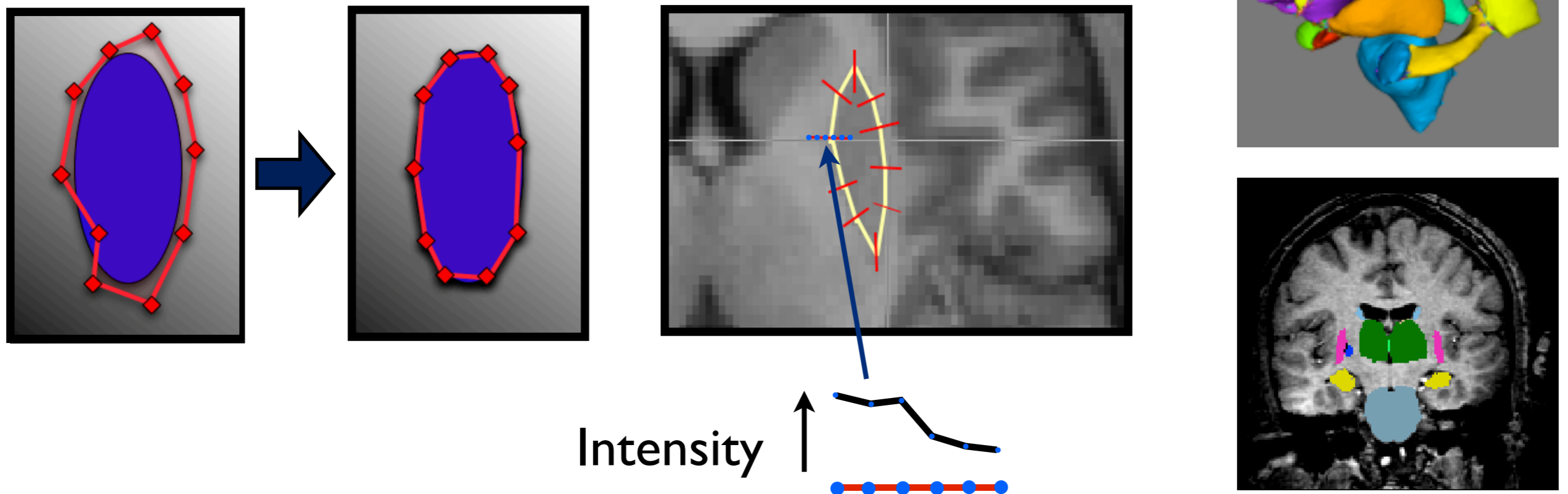
- Intensity is then sampled along the **surface normal** and stored
- Learn average intensity and “modes of variation”
- Aside: the intensities are re-scaled to a common range and the mode of the intensities in the structure is subtracted





FIRST - Model

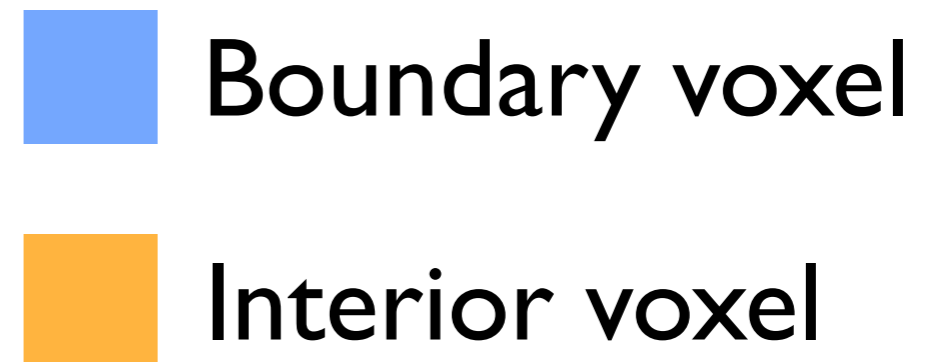
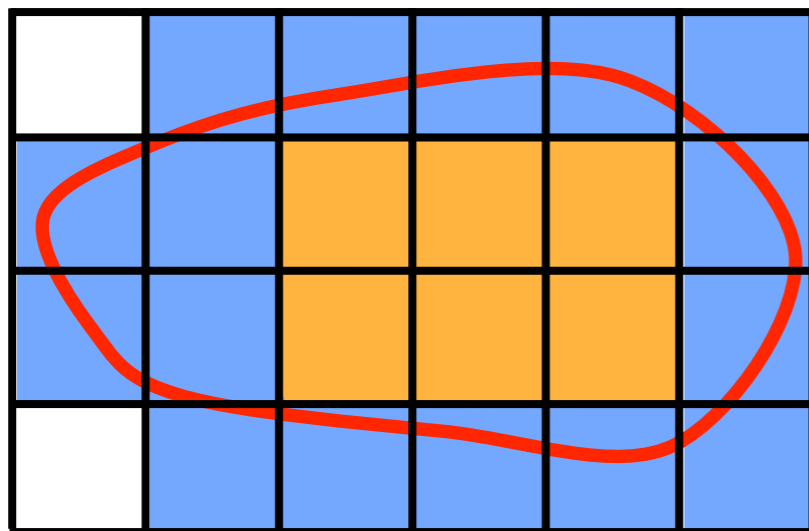
- Model: 3D mesh
- Training the model: learn average shape/intensity and likely variations (“modes of variation”) about both
- Fitting the model: Find the “best” shape by searching along modes of variation and uses intensity match to judge fitting success





Boundary Correction

- FIRST models all structures by meshes
- Converting from meshes to images gives two types of voxels:
 - boundary voxels
 - interior voxels
- Boundary correction is necessary to decide whether the boundary voxels should belong to the structure or not
- Default correction uses FAST classification method and is run automatically (uncorrected image is also saved)
 - ensures that neighbouring structures do not overlap

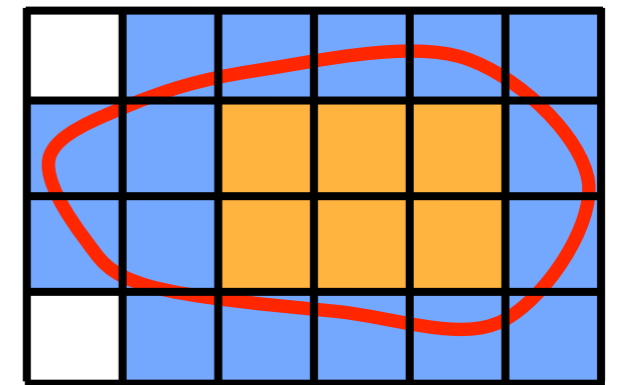




FIRST - Output/Analyses

- Volumetric analysis

- FIRST converts meshes to images applying boundary correction to decide whether boundary voxels belong to the structure or not

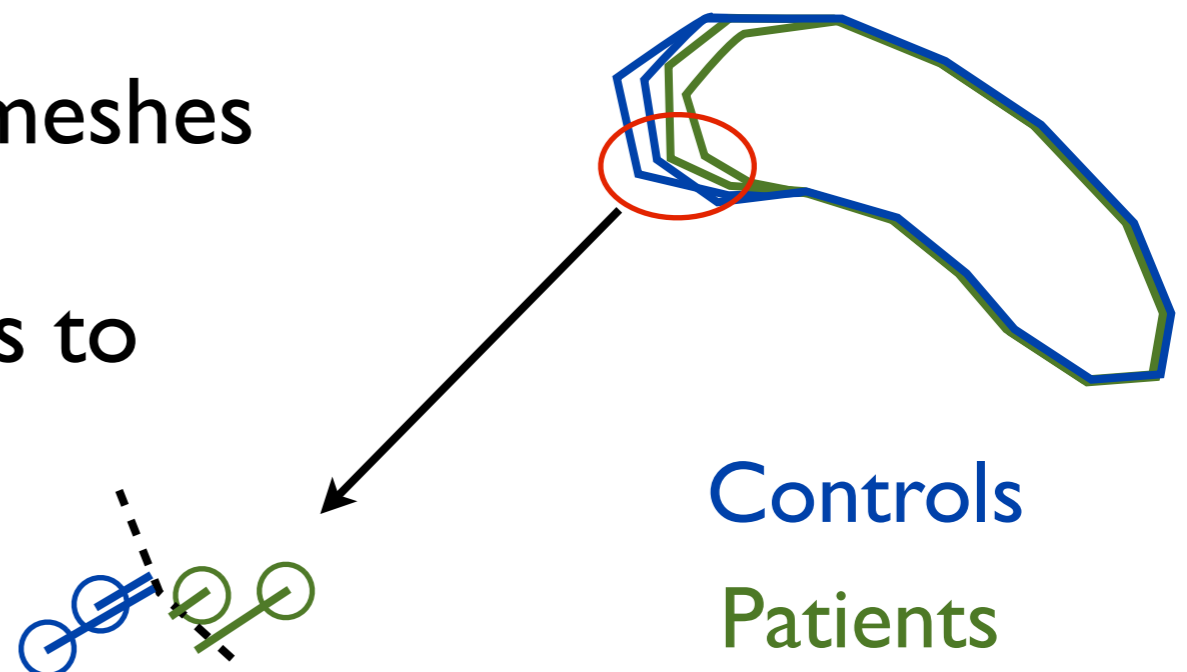


■ Boundary voxel

■ Interior voxel

- Vertex analysis

- FIRST models all structures by meshes
- Consider each vertex in turn
- Do a test on distance of vertices to average shape





Running FIRST

- Inputs:
 - T₁-weighted image
 - Model (built from training data) - provided with FSL
- Applying FIRST
 - A single command: **run_first_all**
 1. registers image to MNI152 1mm template
 2. fits structure models (meshes) to the image
 3. applies boundary correction (for volumetric output)
- Analysis:
 - Use command: **first_utils**
 - volumetric analysis (summary over whole structure)
 - vertex analysis (localised change in shape and/or size)
 - randomise (with multiple comparison correction)

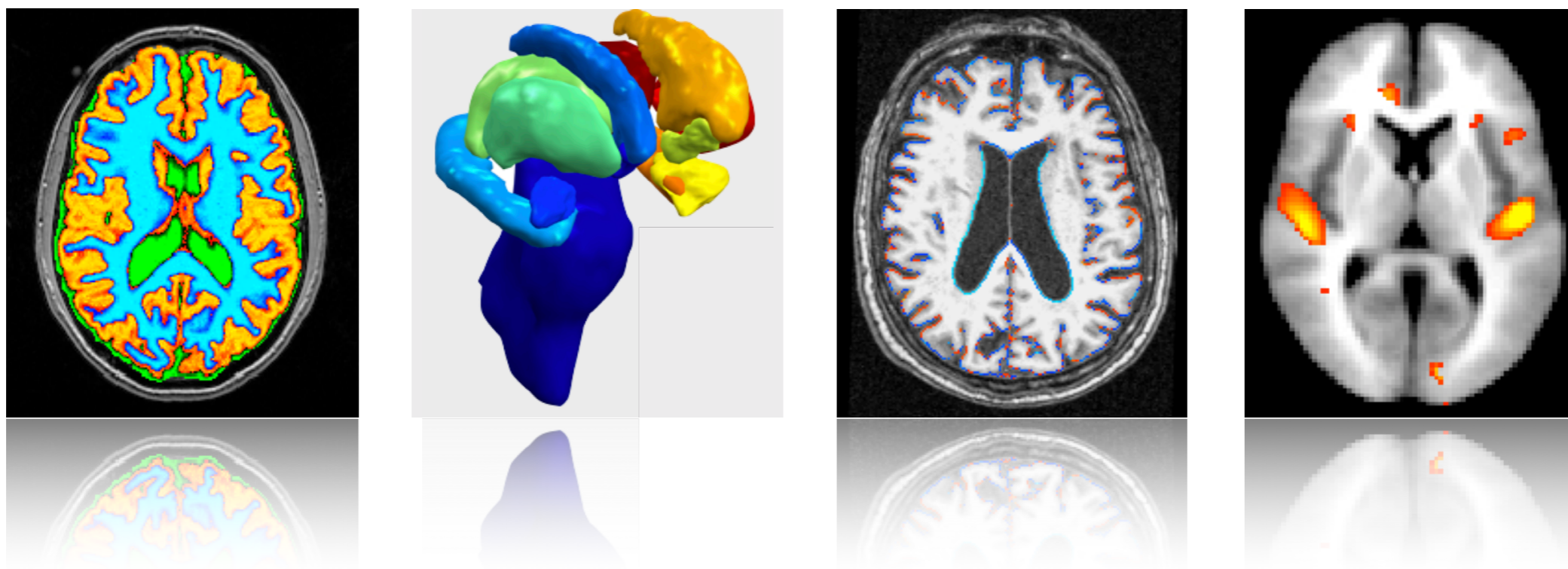


fsl_anat - Anatomical processing script

- General pipeline for processing anatomical images with FSL tools
- Specific features:
 - Brain extraction is registration-based (alternative to bet)
 - Bias-field correction improved (especially for strong bias-fields).
- The stages in the pipeline (in order) are:
 - reorient the images to MNI: **fslreorient2std**
 - automatically crop the image: **robustfov**
 - bias-field correction: **fast**
 - registration to standard space (linear and non-linear): **flirt** + **fnirt**
 - registration-based brain-extraction: **fnirt**
 - tissue-type segmentation: **fast**
 - subcortical structure segmentation: **first**
- Run-time depends on image resolution (30-90' would be typical).



After the break...



- FAST tissue-type segmentation
- FIRST sub-cortical structure segmentation
- BIANCA segmentation of white matter lesions
- FSL-VBM voxelwise grey-matter density analysis
- SIENA/SIENAX global atrophy estimation