Brain MRI Segmentation Using an Expectation-Maximization Algorithm

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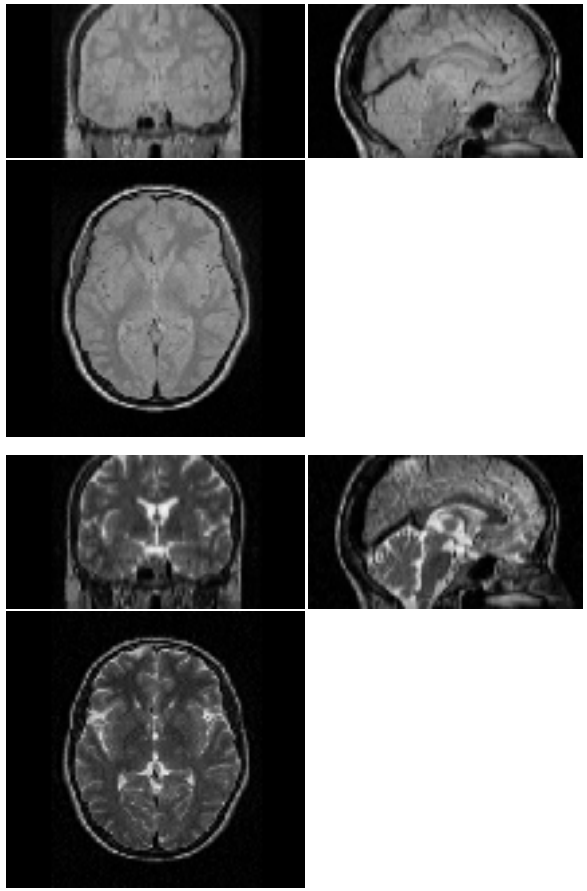
MRI of the brain

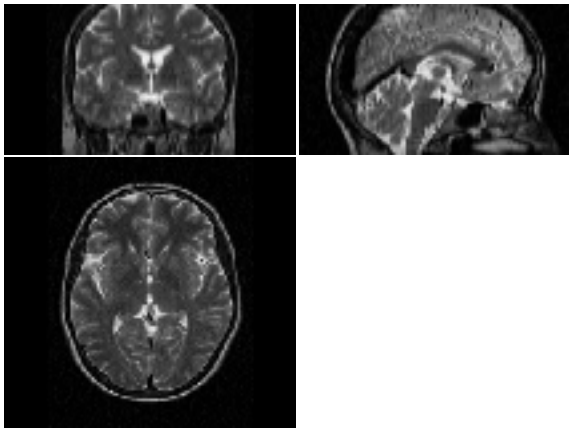
- Magnetic Resonance (MR) imaging of the brain:
  - Three-dimensional (3-D)
  - High soft tissue contrast
  - High spatial resolution
  - Possibly multi-spectral

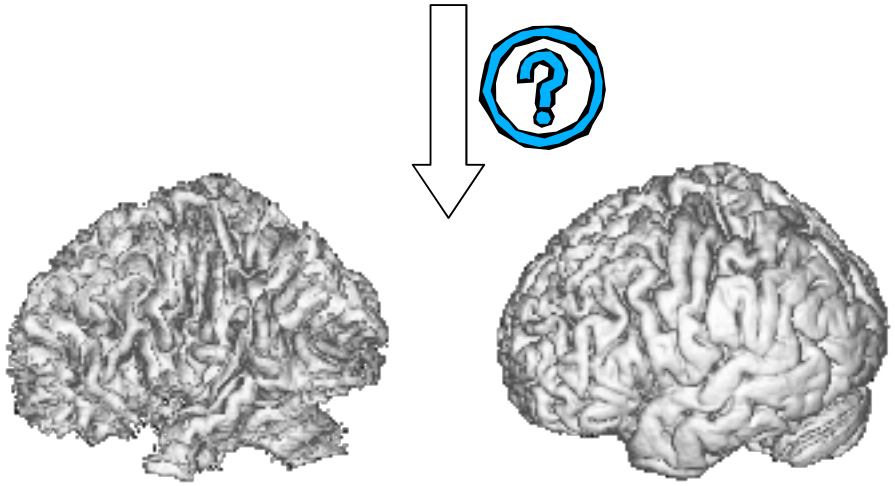


→ Non-invasive quantitative measurements possible

Segmentation of brain MRI

- Radiotherapy planning
- Surgical planning
- Image-guided interventions
- Visualizations
- Studying brain diseases
- Clinical drug trials
- ...





How to segment brain MRI?

Manual delineation by a human expert

- difficult to accurately delineate complex 3-D structures
- extremely time-consuming
- considerable inter- and intra-rater variability
- multi-spectral input is hard to interpret

→ Routine analysis is impractical

→ Need for automated procedures

Overview

- The mixture model and the EM algorithm
- A probabilistic brain atlas
- Modeling MR bias fields
- Multiple Sclerosis lesion segmentation
- Partial volume segmentation
- Discussion and future directions

Overview

- ***The mixture model and the EM algorithm***
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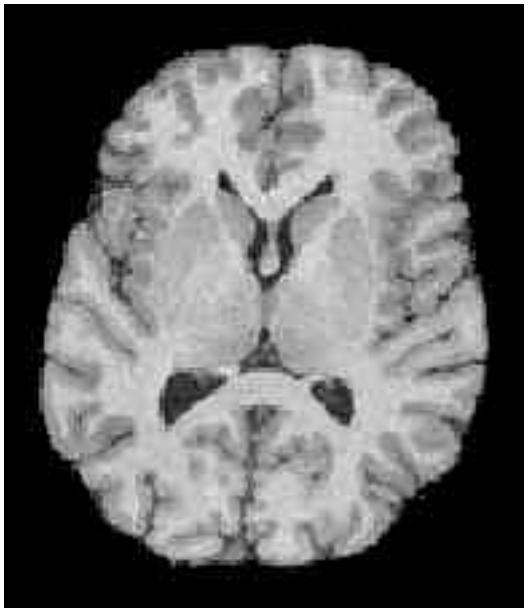
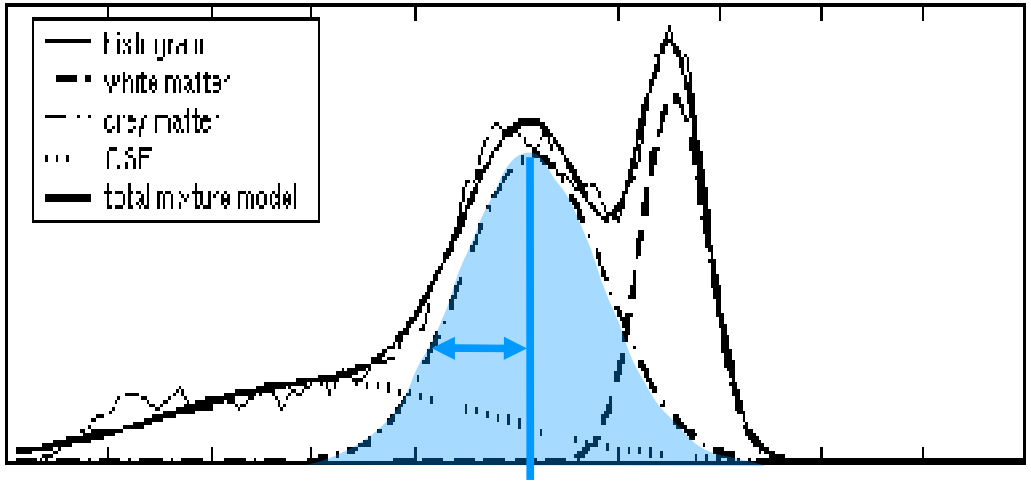
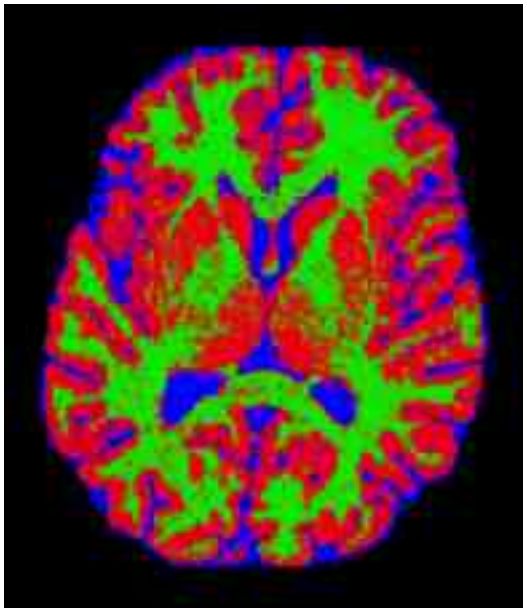
The Gaussian mixture model

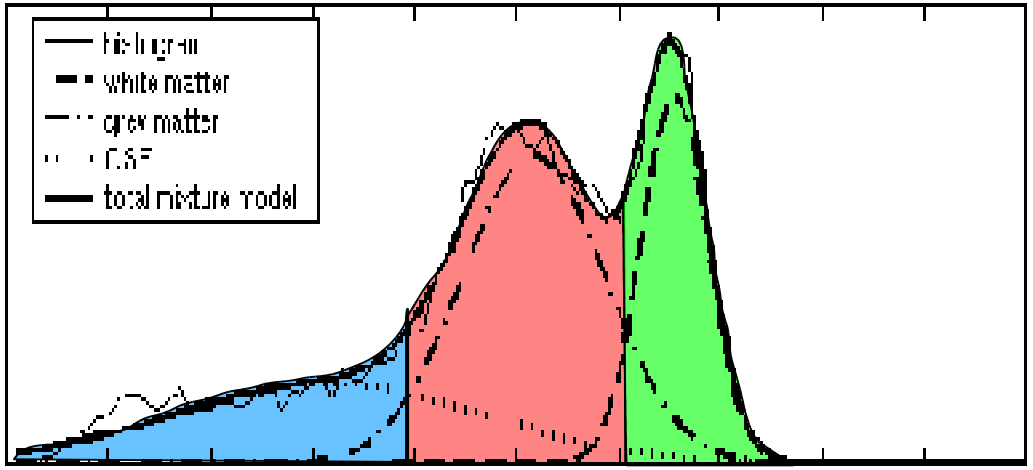




- Intensity distributions of white matter, gray matter and CSF are modeled as Gaussian distributions
  - mean = average intensity
  - variance = variation around the average intensity

The Gaussian mixture model





Once the mean and variance of each tissue type is known, voxels can be classified based on their intensity

How to obtain model parameters?

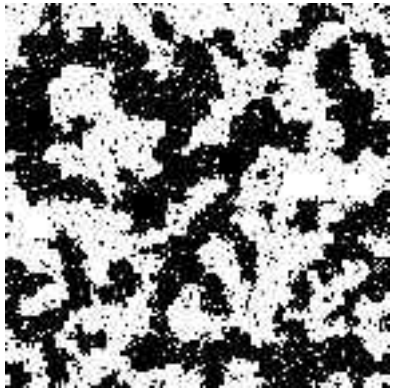
- Interactively select representative voxels for each tissue type
  - Train model once and apply it to hundreds of scans
  - Needs to be re-done for every new pulse-sequence
  - Not fully reproducible
  - In clinical trials: inter-scan variations in the intensity distributions of the tissue types
    - Hardware fluctuations of MR scanners over time
    - Multi-center trials may involve different scanners

Can we estimate the model parameters automatically from each individual scan?

More formal image model

$f(\boldsymbol{L} \mid \Phi_L)$

spatial model

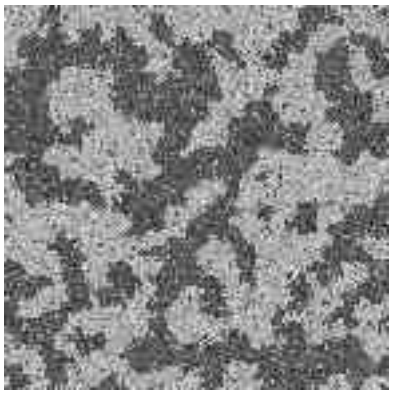


$\boldsymbol{L} = \{l_j\}$

label of voxel j

$f(\boldsymbol{Y} \mid \boldsymbol{L}, \Phi_Y)$

intensity model



$\boldsymbol{Y} = \{y_j\}$

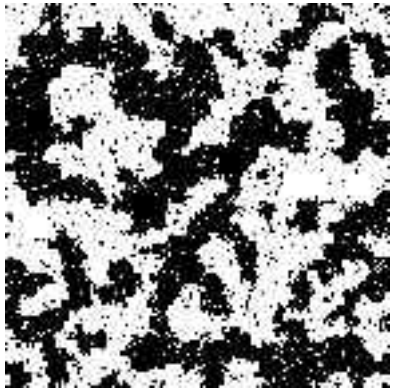
intensity of voxel j

- Total model parameters: $\Phi = \{\Phi_Y, \Phi_L\}$
- Overall model: $f(\boldsymbol{Y} \mid \Phi) = \sum_{\boldsymbol{L}} f(\boldsymbol{Y} \mid \boldsymbol{L}, \Phi_Y) f(\boldsymbol{L} \mid \Phi_L)$

Spatial model

$f(\boldsymbol{L} \mid \Phi_L)$

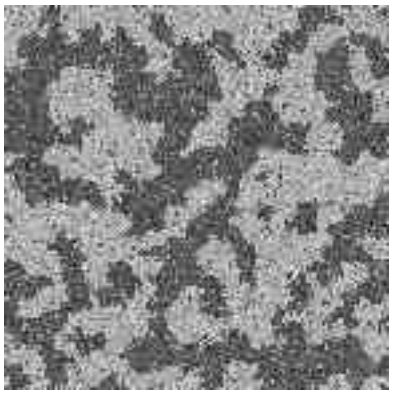
spatial model



$\boldsymbol{L} = \{l_j\}$

$f(\boldsymbol{Y} \mid \boldsymbol{L}, \Phi_Y)$

intensity model



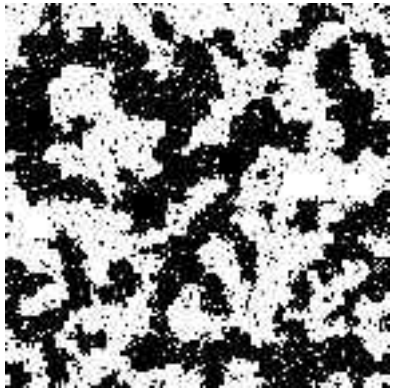
$\boldsymbol{Y} = \{y_j\}$

- Assume that the label of each voxel is drawn independently from the labels of other voxels, with probability π_k for tissue type k
- The spatial model parameters are then: $\Phi_L = \{\pi_k\}$

Intensity model

$f(\boldsymbol{L} \mid \Phi_L)$

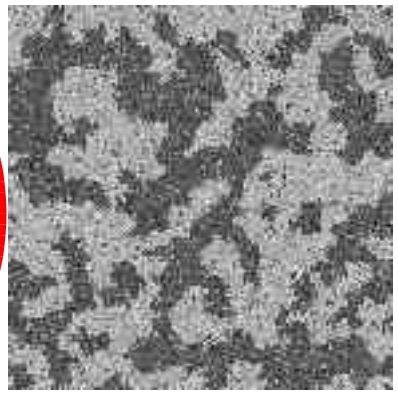
spatial model



$\boldsymbol{L} = \{l_j\}$

$f(\boldsymbol{Y} \mid \boldsymbol{L}, \Phi_Y)$

intensity model



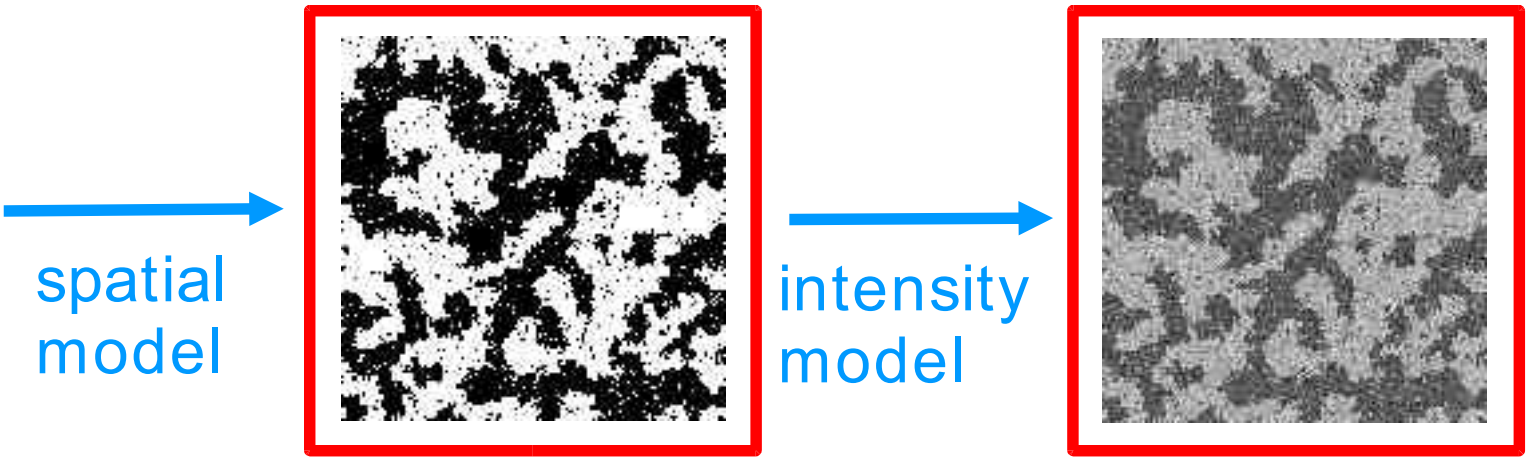
$\boldsymbol{Y} = \{y_j\}$

- Assume that the intensity of a voxel is conditionally independent from the intensity of other voxels, given its tissue label: $f(\boldsymbol{Y} \mid \boldsymbol{L}, \Phi_Y) = \prod_j f(y_j \mid l_j, \Phi_Y)$
- Assume that the intensity distribution of tissue type k is normally distributed with mean $\boldsymbol{\mu}_k$ and covariance $\boldsymbol{\Sigma}_k$
- The intensity model parameters are then: $\Phi_Y = \{\boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k\}$

Parameter estimation

- Given an image, estimate the so-called Maximum-Likelihood parameters
  = parameters that maximize $\log f(\mathbf{Y} \mid \Phi)$
  = parameters that best explain the data
- Cannot be solved with closed-form expressions
- Expectation-Maximization (EM) algorithm *[Dempster et al., 1977]* provides a very intuitive iterative parameter estimation scheme

Expectation-Maximization algorithm



- If the tissue labels (“missing data”) were known, parameter estimation would be straightforward
- EM algorithm iteratively fills in the missing data and updates the parameters accordingly

Expectation-Maximization algorithm

- Iterative optimization algorithm
  - *Expectation step:* find the function

Likelihood with the missing tissue labels filled in

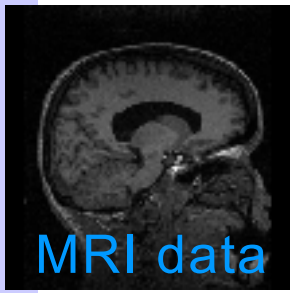
$$Q(\Phi \mid \Phi^{(m)}) = E_{\boldsymbol{L}}[\log f(\boldsymbol{Y}, \boldsymbol{L} \mid \Phi) \mid \boldsymbol{Y}, \Phi^{(m)}]$$

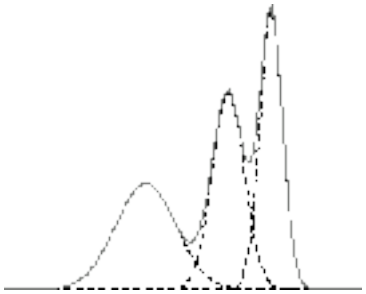
Expectation over the missing tissue labels based on the current parameter estimation and the observed data

  - *Maximization step:* find

$$\Phi^{(m+1)} = \arg\max_{\Phi} Q(\Phi \mid \Phi^{(m)})$$

Expectation step



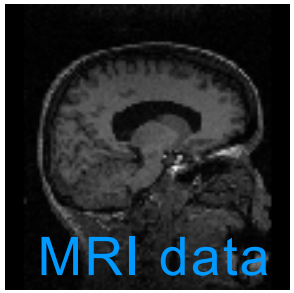


Statistical classification of the image voxels based on the current parameter estimation

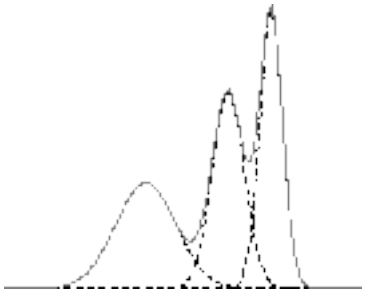
$$f(l_j \mid \boldsymbol{Y}, \Phi^{(m)}) = \frac{f(\boldsymbol{y}_j \mid l_j, \Phi_Y^{(m)}) \cdot \pi_{l_j}^{(m)}}{\sum_k f(\boldsymbol{y}_j \mid l_j = k, \Phi_Y^{(m)}) \cdot \pi_k^{(m)}}$$

- Bayes' rule
- “soft” classification

Maximization step



Parameter re-estimation based on the current classification

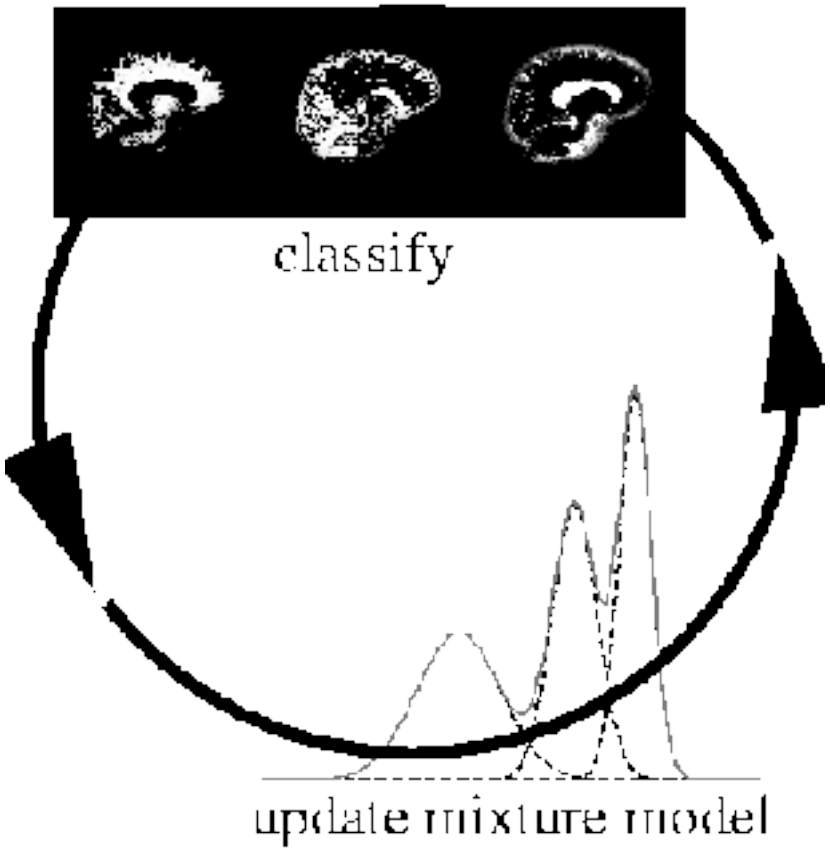


$$\boldsymbol{\mu}_k^{(m+1)} = \frac{\sum_j f(l_j=k \mid \mathbf{Y}, \Phi^{(m)}) \cdot \mathbf{y}_j}{\sum_j f(l_j=k \mid \mathbf{Y}, \Phi^{(m)})}$$

$$\boldsymbol{\Sigma}_k^{(m+1)} = \frac{\sum_j f(l_j=k \mid \mathbf{Y}, \Phi^{(m)}) \cdot (\mathbf{y}_j - \boldsymbol{\mu}_k^{(m+1)}) \cdot (\mathbf{y}_j - \boldsymbol{\mu}_k^{(m+1)})^t}{\sum_j f(l_j=k \mid \mathbf{Y}, \Phi^{(m)})}$$

$$\pi_k^{(m+1)} = \frac{\sum_j f(l_j=k \mid \mathbf{Y}, \Phi^{(m)})}{N}$$

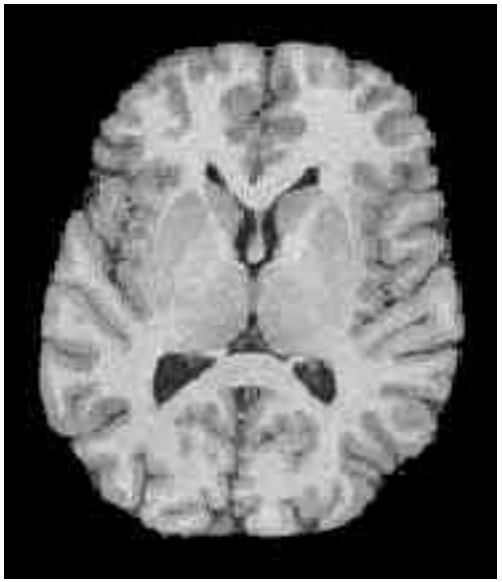
EM algorithm summarized

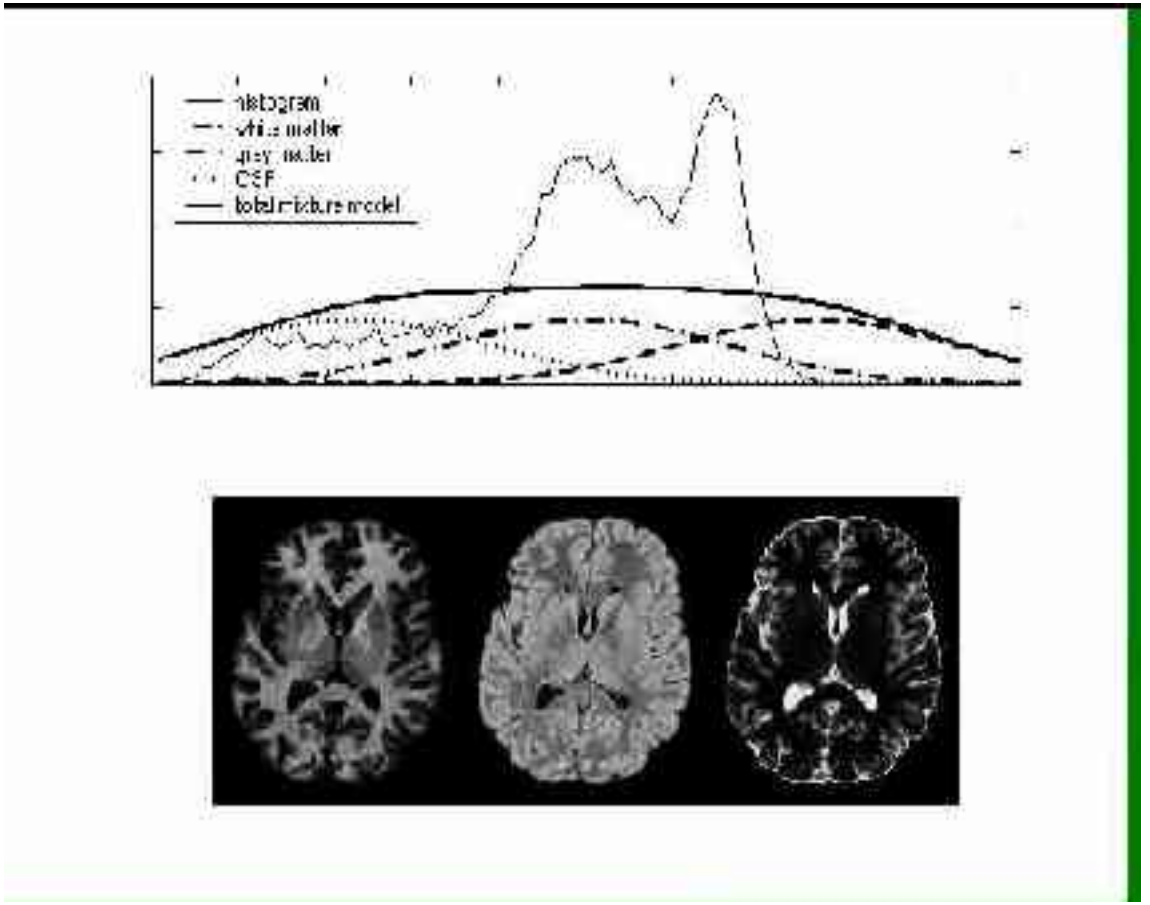


Simultaneous classification and parameter estimation

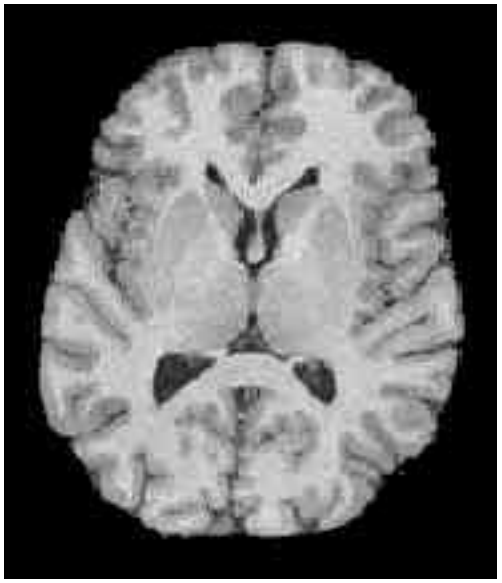
Likelihood is guaranteed to increase at each iteration

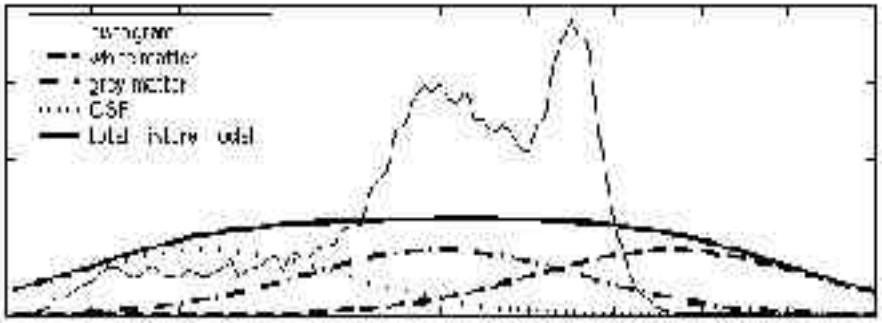
Example

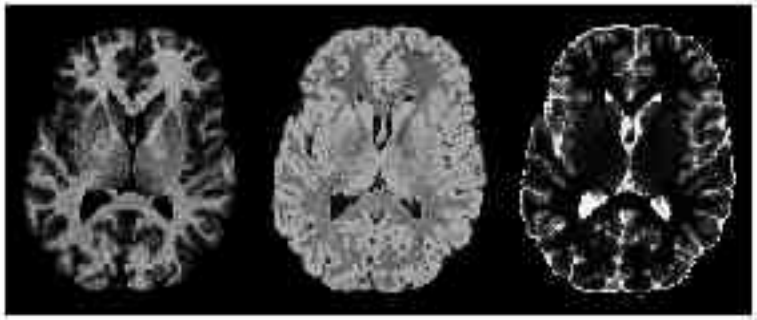



histogram
white matter
gray matter
CSF
total mixture model

Example







- But how to extract the intra-cranial volume?
- But how to initialize automatically ?

Overview

- The mixture model and the EM algorithm
- ***A probabilistic brain atlas***
- Modeling MR bias fields
- Multiple Sclerosis lesion segmentation
- Partial volume segmentation
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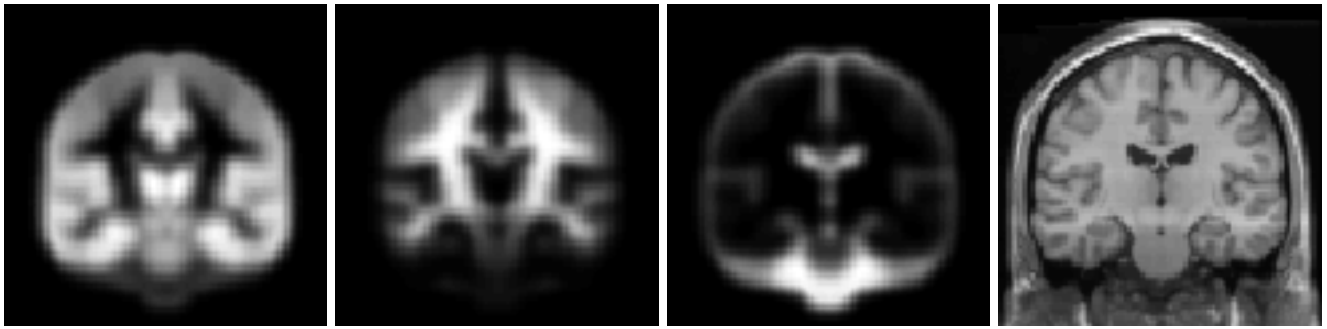
Expected location of tissue types

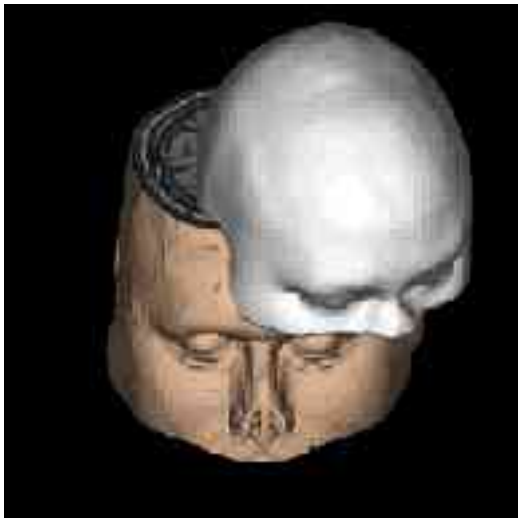


gray matter probability | white matter probability | CSF probability | Atlas template

- Average of many binary white matter, gray matter and CSF segmentations after affine normalization
- Expected location of major tissue types in a healthy young population in a standardized coordinate frame
- Source: Montréal Neurological Institute

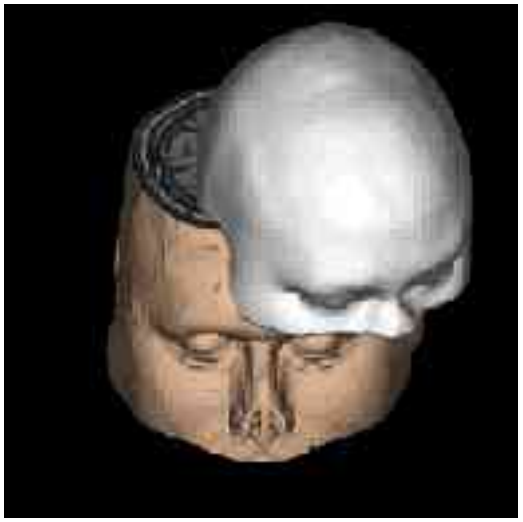
Atlas registration

- Atlas needs to be brought into spatial correspondence with the image under study before it can be used
- Affine transformations (translation, rotation, scale and skew)
- This can be done fully automatically by maximizing the so-called Mutual Information between the atlas template and the study image



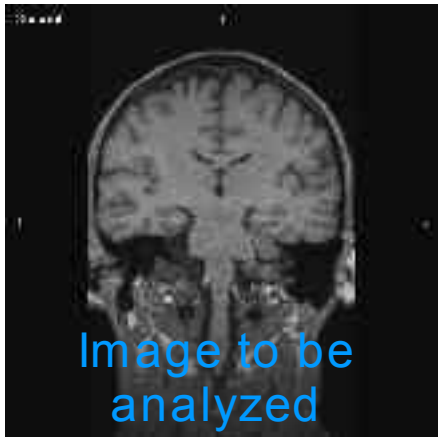
Atlas registration

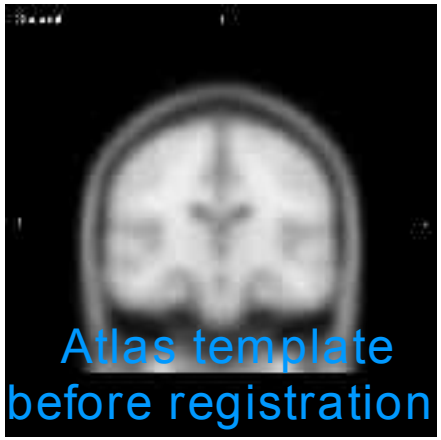
- Mutual Information measures the statistical dependence between two images *[Maes et al., 1997] [Wells et al., 1996a]*
- Is assumed maximal when the images are correctly aligned
- Makes very few assumptions about the intensities in the images to be co-registered

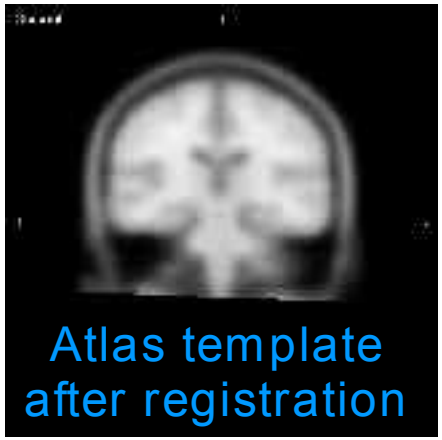


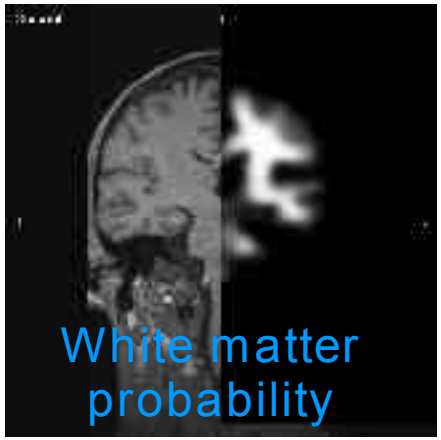
→ Fully-automated registration of the atlas template with the images under study, regardless of the pulse-sequence used.

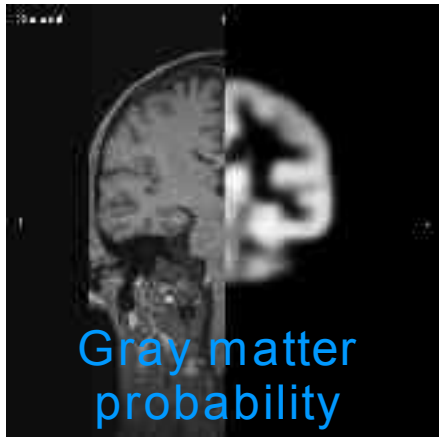
Atlas registration

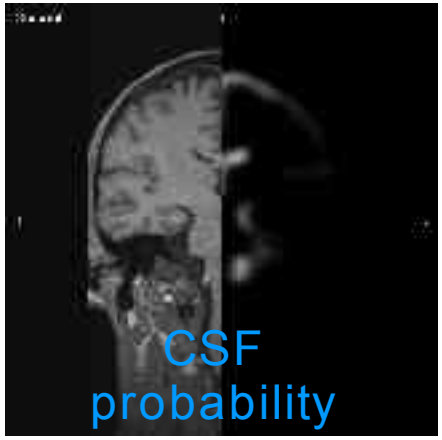








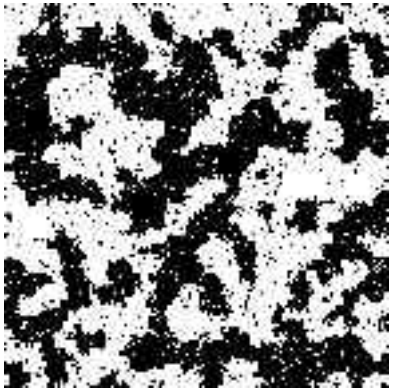




Improved spatial model

$f(\boldsymbol{L} \mid \Phi_L)$

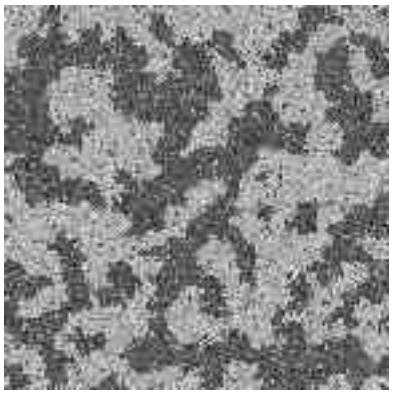
spatial model



$\boldsymbol{L} = \{l_j\}$

$f(\boldsymbol{Y} \mid \boldsymbol{L}, \Phi_Y)$

intensity model



$\boldsymbol{Y} = \{y_j\}$

- The prior probability for tissue type k π_k is provided by the statistical brain atlas
- Depends now on the location in the brain!
- No unknown spatial model parameters Φ_L to be estimated

Resulting EM algorithm

- Expectation step:

$$f(l_j \mid \boldsymbol{Y}, \Phi^{(m)}) = \frac{f(\boldsymbol{y}_j \mid l_j, \Phi_Y^{(m)}) \cdot \pi_{l_j}^{(m)}}{\sum_k f(\boldsymbol{y}_j \mid l_j = k, \Phi_Y^{(m)}) \cdot \pi_k^{(m)}}$$

Classification takes prior knowledge into account

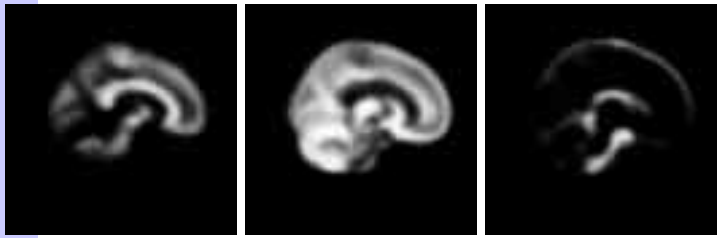
Classification is moderated by the statistical brain atlas
[Ashburner and Friston, 1997]

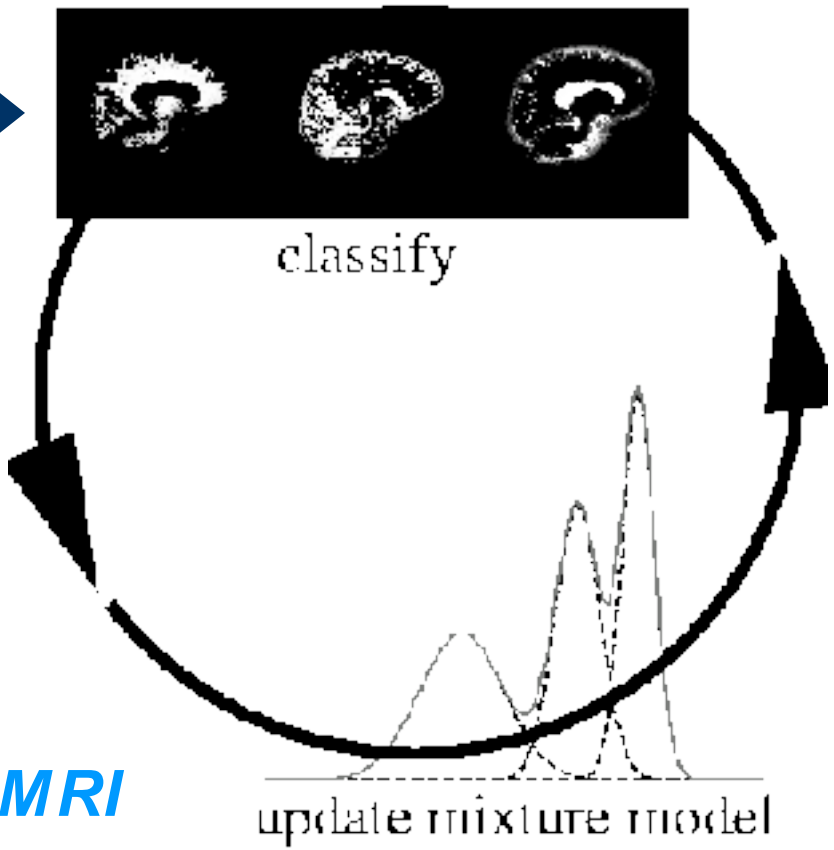
This effectively introduces geometrical constraints into the statistical classification

→ Makes the algorithm more robust

- Maximization step: remains the same

Fully-automated segmentation





Atlas initializes EM algorithm

Atlas provides a rough brain mask => no need for brain stripping in a pre-processing step

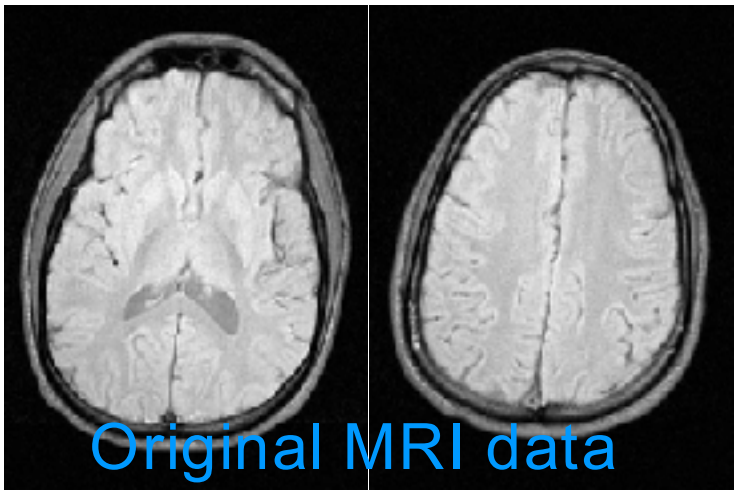
Fully automated, pulse sequence adaptive brain MRI segmentation

Overview

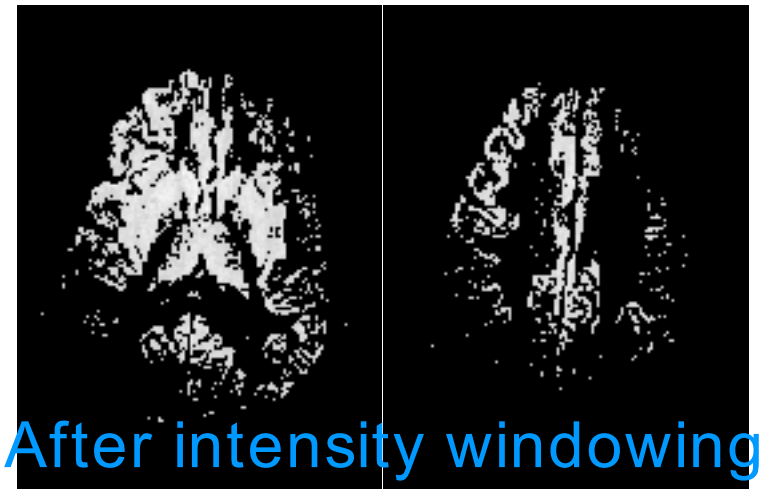
- The mixture model and the EM algorithm
- A probabilistic brain atlas
- ***Modeling MR bias fields***
- Multiple Sclerosis lesion segmentation
- Partial volume segmentation
- Discussion and future directions

MR field inhomogeneity

- MRI-specific imaging artifact
  - Equipment limitations
  - Patient-induced electrodynamic interactions
- Results in non-uniform tissue intensities
- Also called “bias field”



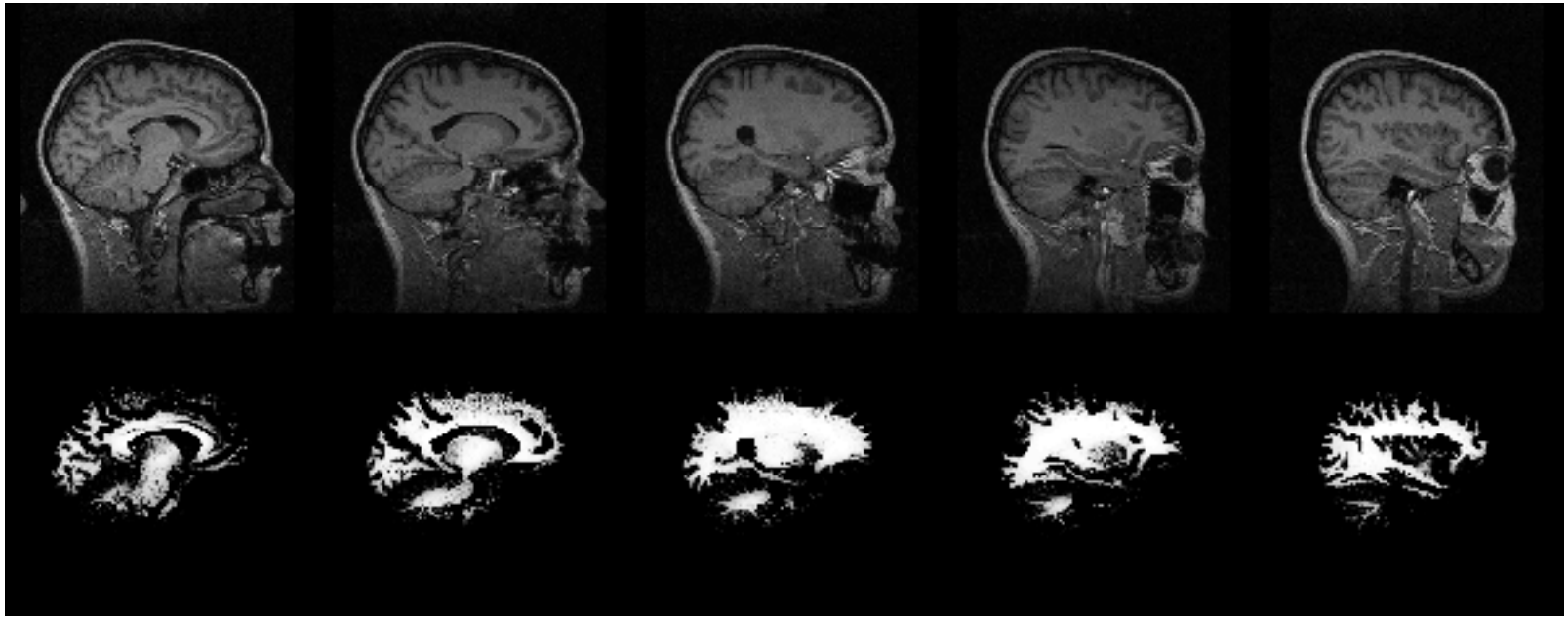
Original MRI data



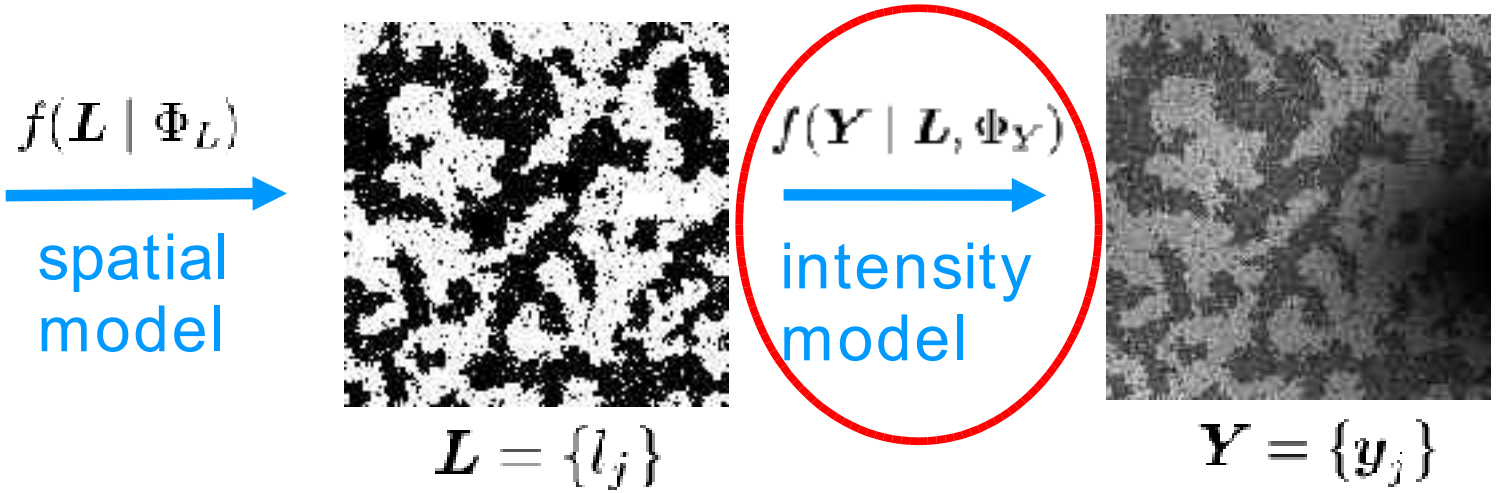
After intensity windowing

MR field inhomogeneity

- Causes segmentation errors in the automated EM segmentation procedure



Improved intensity model

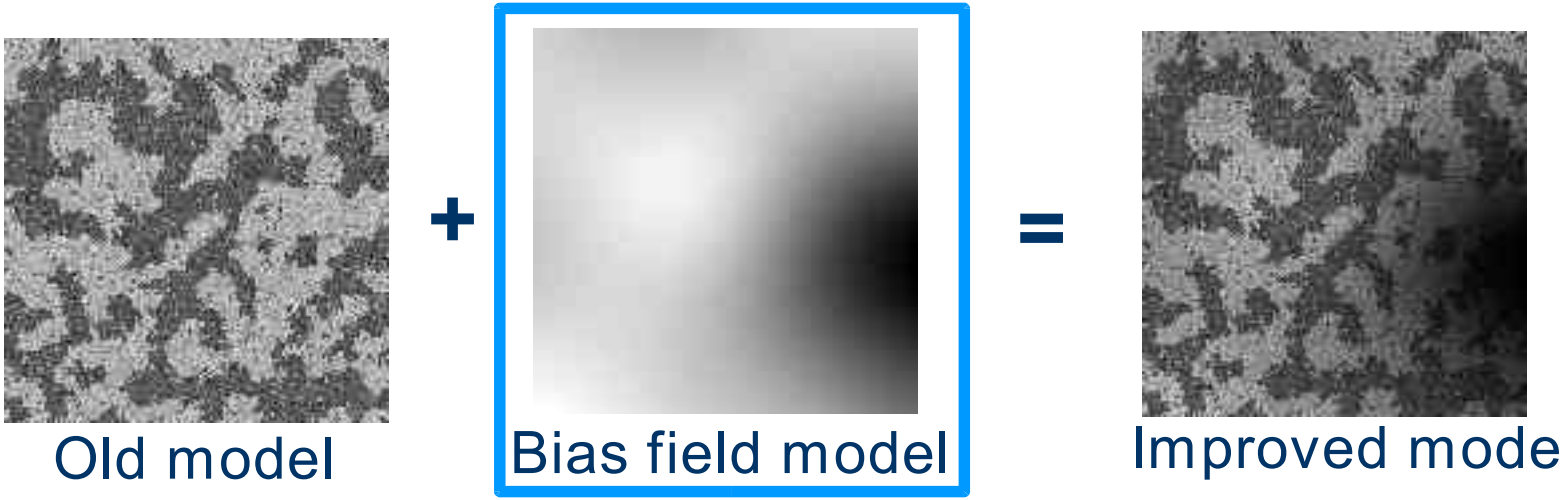


Include an explicit model for the bias field in the intensity model

[Van Leemput et al., 1999], based on *[Wells et al., 1996b]*

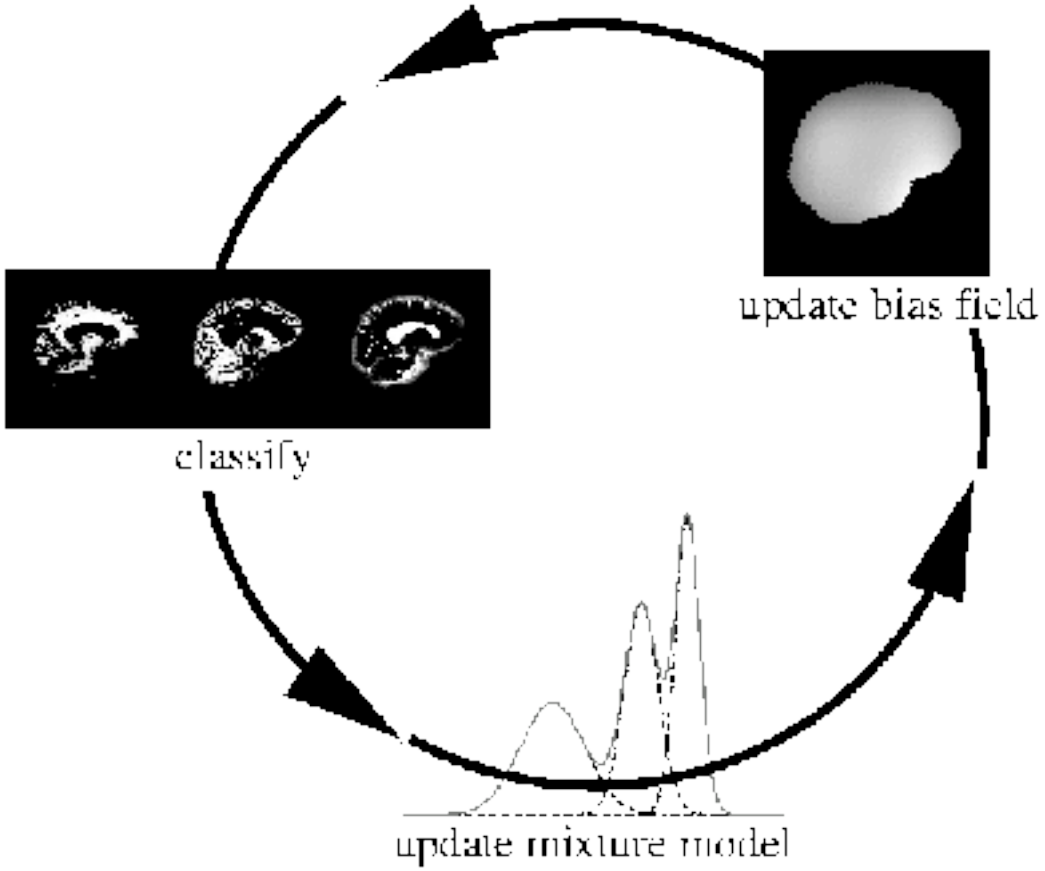
Improved intensity model

- Bias field is usually assumed to be multiplicative
- After logarithmic transformation => bias field becomes additive



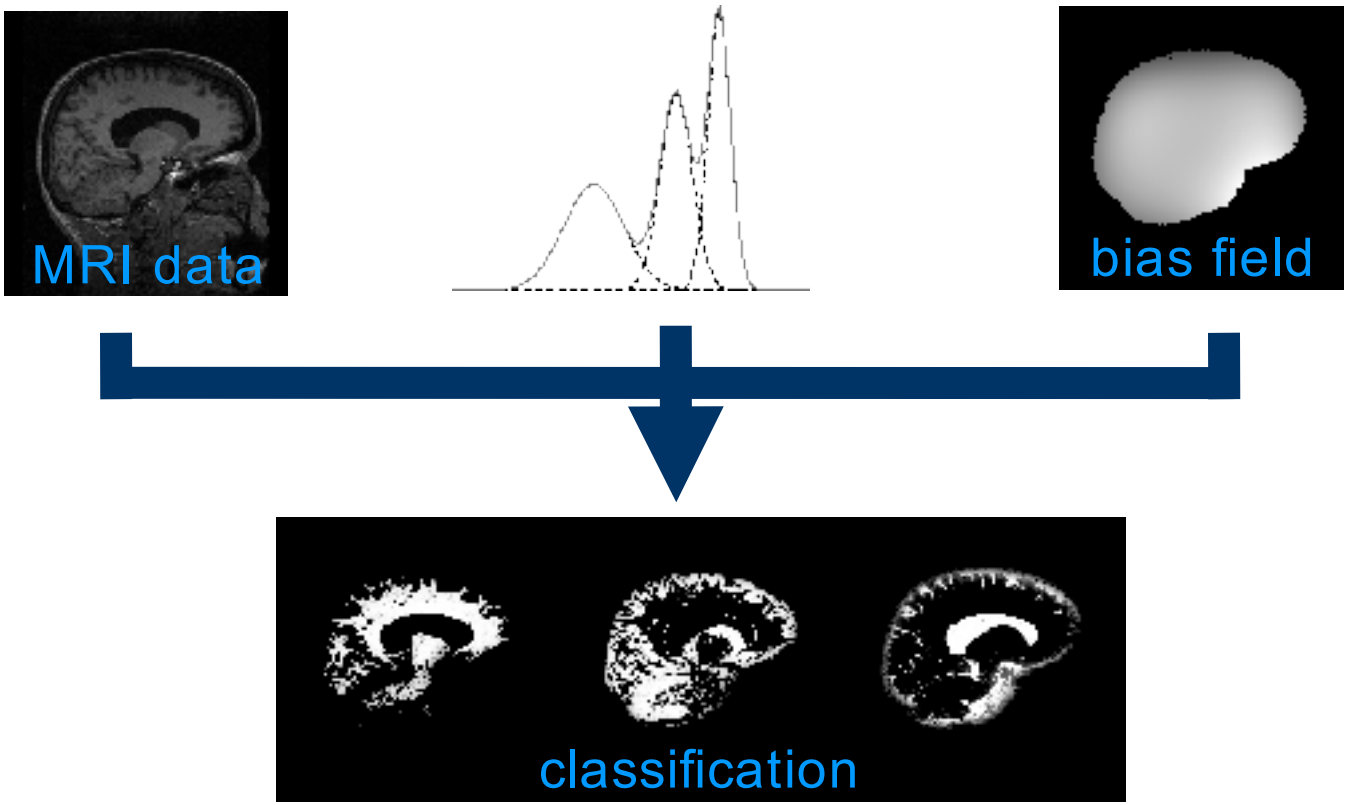
- Fourth-order polynomial
- Parameters need to be estimated as well

Resulting EM algorithm

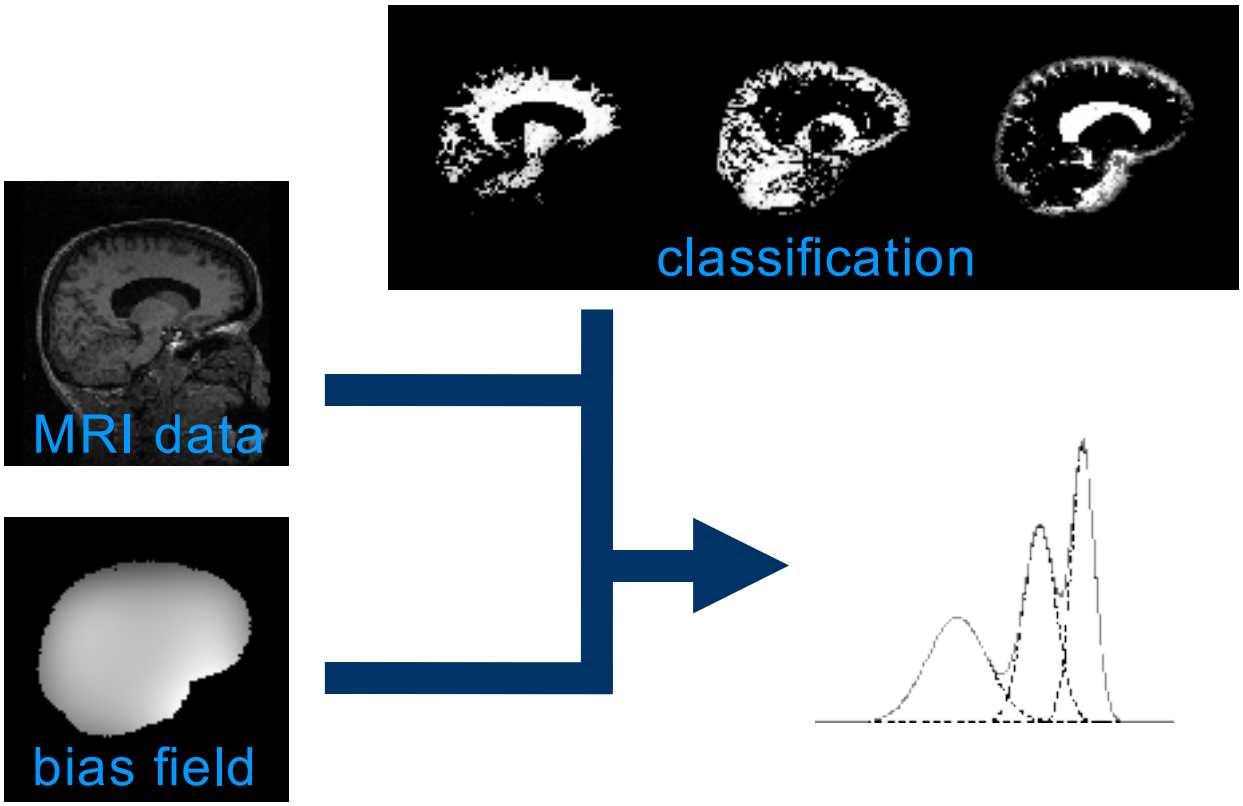


Three-step
EM algorithm

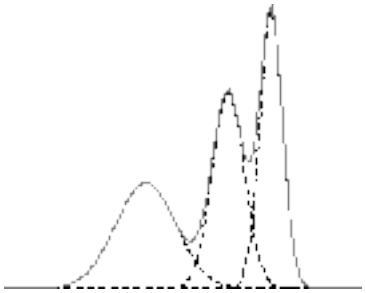
E-step: classification

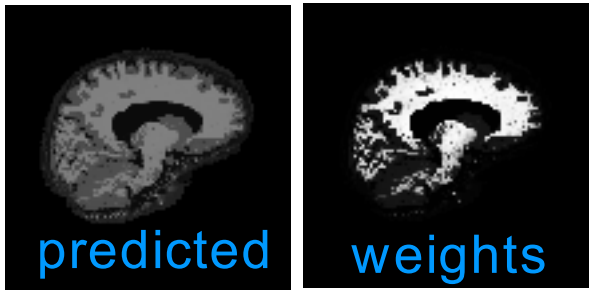


M-step part 1: distribution estimation



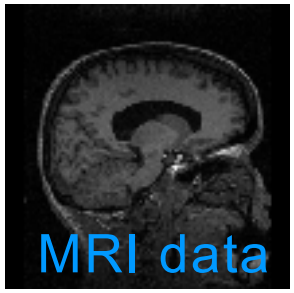
M-step part 2: bias field estimation

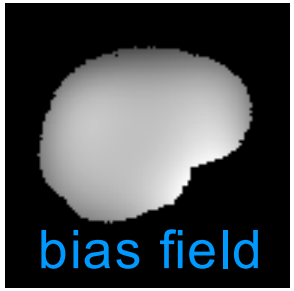




$$w_j = \sum_k \frac{f(l_j{=}k \mid \boldsymbol{y_j}, \Phi)}{\sigma_k^2}$$

M-step part 2: bias field estimation





Bias field is computed primarily from tissues with a narrow intensity distribution, and is extrapolated to regions where it cannot be confidently estimated

Weighed least-squares fit

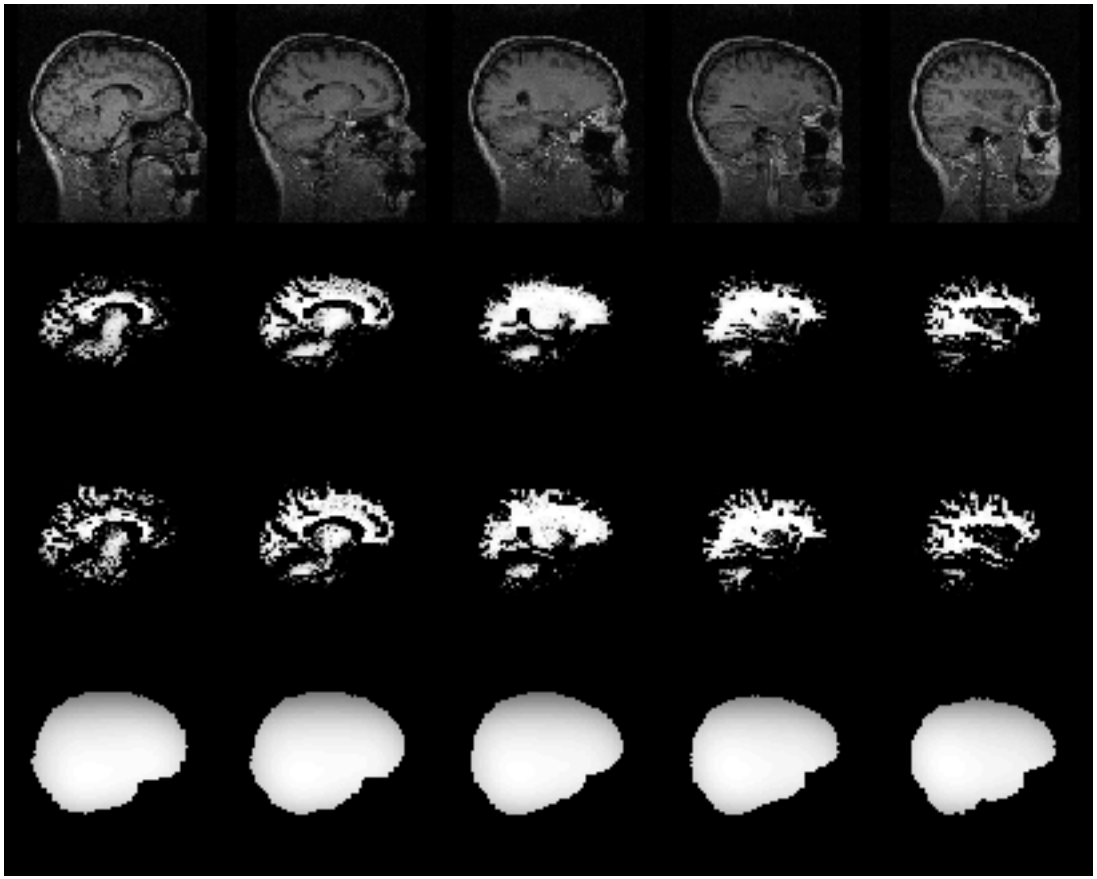
Example 1

MRI data

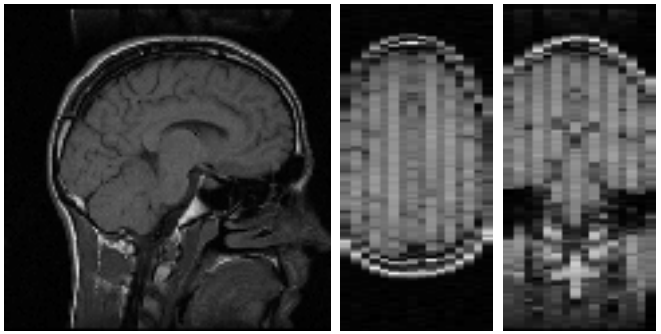
White matter without bias field model

White matter with bias field model

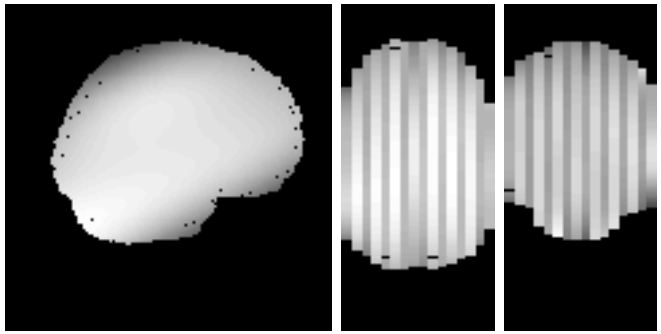
Estimated bias field



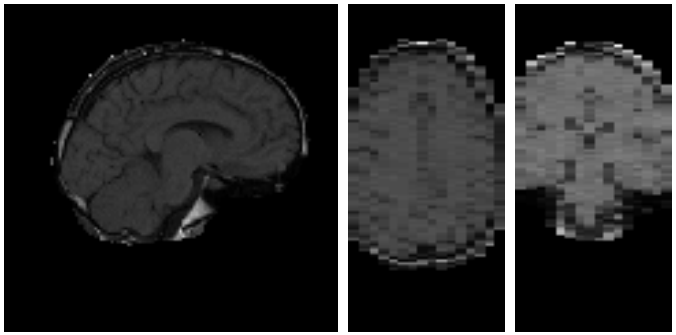
Example 2: 2-D multi-slice sequence



MRI data



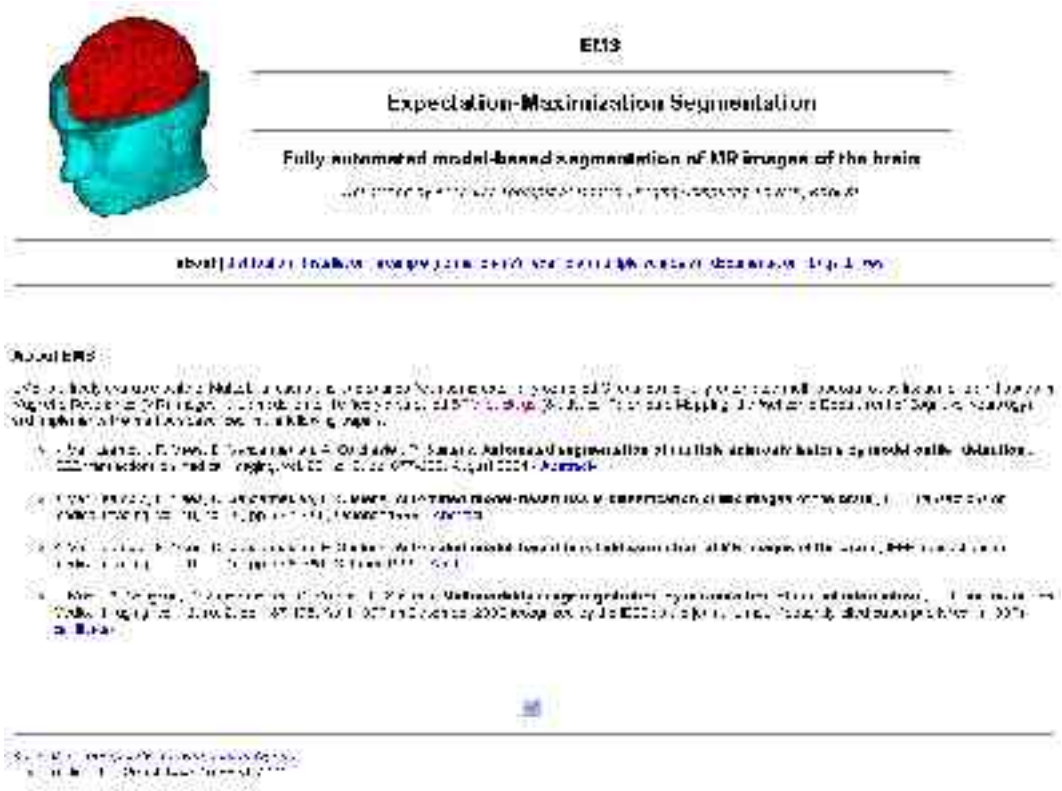
Estimated bias field



Bias-corrected MRI data

Implemented in ”EMS” software

Freely available from the website of the Medical Image Computing group, K.U.Leuven, Belgium: bilbo.esat.kuleuven.ac.be



Unifying Statistical Classification and Geometrical Models – MICCAI 2003

Overview

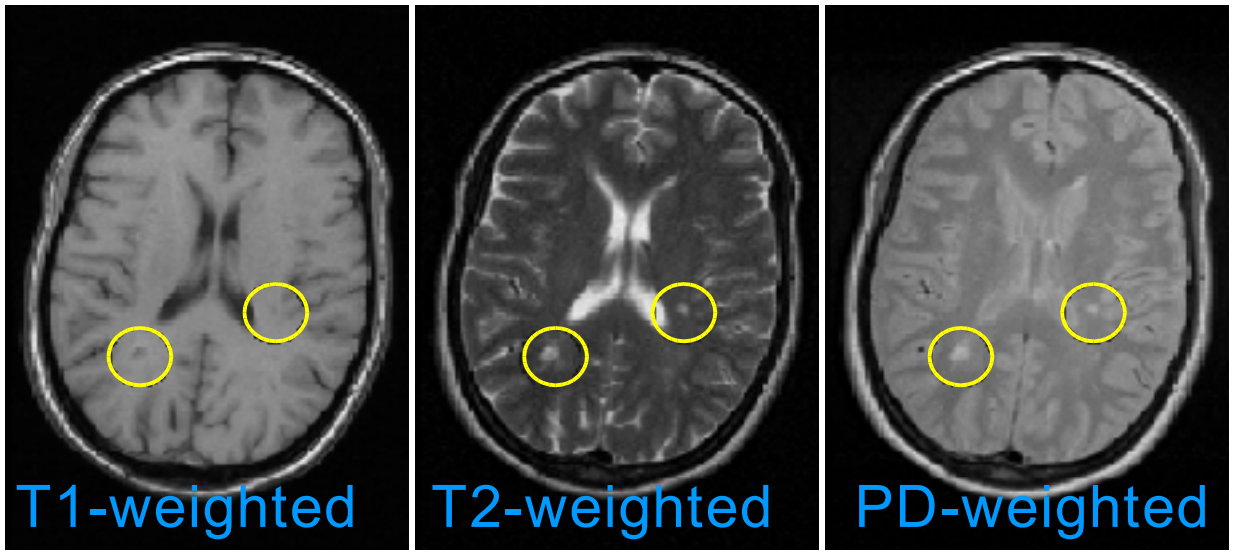
- The mixture model and the EM algorithm
- A probabilistic brain atlas
- Modeling MR bias fields
- ***Multiple Sclerosis lesion segmentation***
- Partial volume segmentation
- Discussion and future directions

Multiple Sclerosis (MS)

- Common disease of young adults
- Primarily affects white matter
- Cause?
  - environmental factors
  - genetic susceptibility
- Relapsing-remitting
  - Relapse, stabilization, (partial) recovery
- Primary progressive

MRI in Multiple Sclerosis

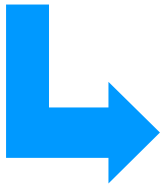
- MRI depicts abnormalities in 95% of patients



- Diagnosis accompanied by confirmatory MRI

MRI in Multiple Sclerosis

- Assessing progression
- Monitoring effect of a new drug therapy
  - MS lesion segmentation from MRI
  - More sensitive and more objective marker than neurological disability scales
  - Primary outcome of preliminary clinical trials

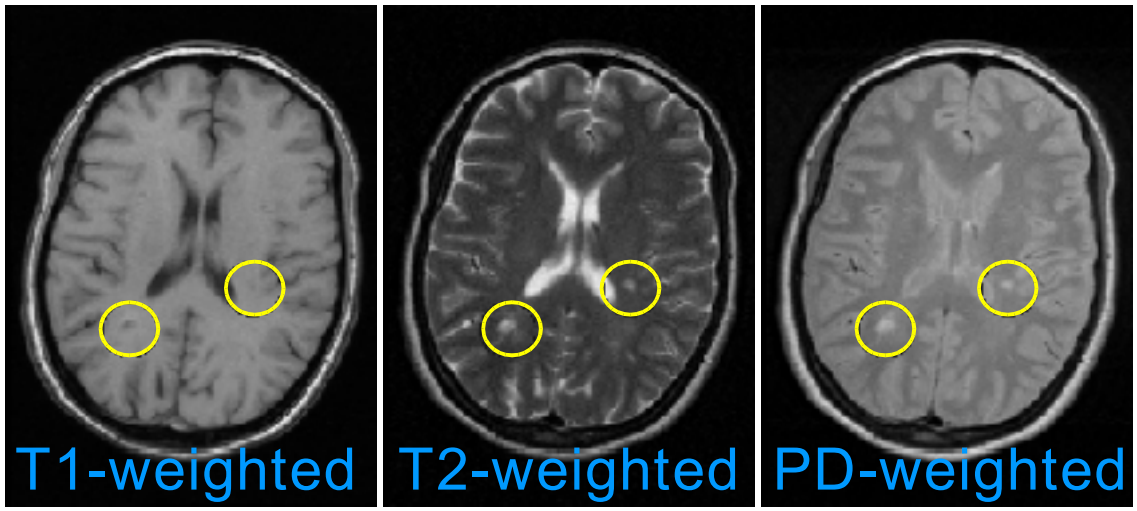


Manual analysis????

- many hundreds of scans
- inter- and intra-rater variability

Need for automated tools

Including MS lesion model????



- Widely varying appearance in MRI
  → difficult to model
- Not every individual scan contains lesions
  → difficult to estimate model parameters

Lesions as model outliers

Detect lesions as voxels that are not well explained by the model for normal brain MRI

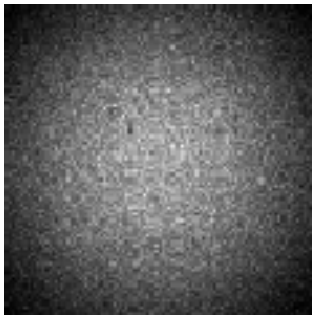
Requires knowledge of the model parameters

But estimation of those model parameters is difficult in the presence of lesions!

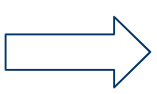
Parameter estimation?

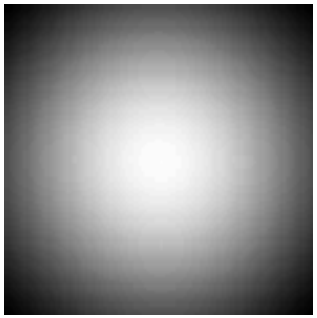
- Consider case of one tissue type
- Simulated data with known bias field
- Estimate bias field using Maximum-Likelihood (ML) parameter estimation:

maximize $\sum_j \log f(\boldsymbol{y}_j \mid \Phi)$

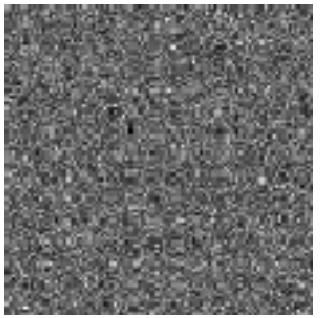


synthetic data





estimated bias field

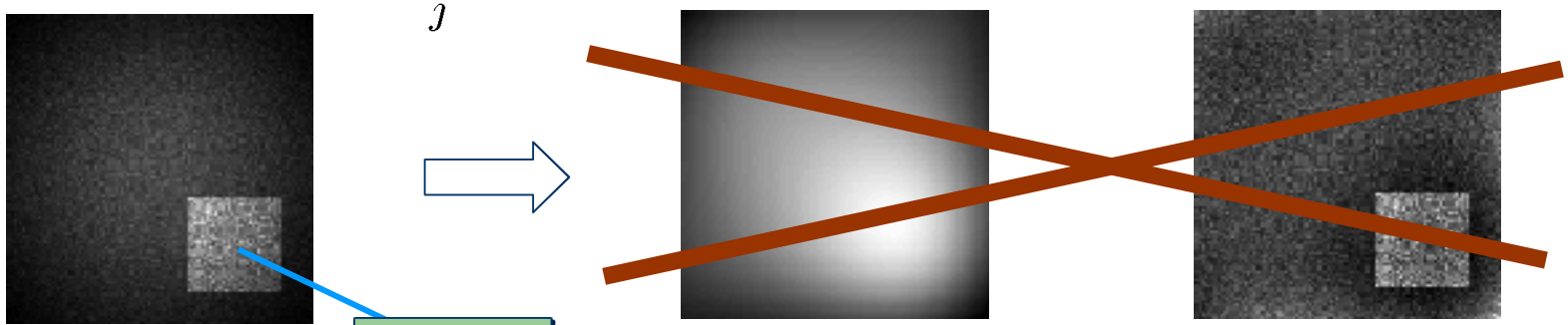


corrected data

Parameter estimation?

- Consider case of one tissue type
- Simulated data with known bias field
- Estimate bias field using Maximum-Likelihood (ML) parameter estimation:

maximize $\sum_j \log f(\boldsymbol{y}_j \mid \Phi)$



Robust statistics

- Model outliers should have a reduced weight on the parameter estimation
- M-estimator: $\sum_j \log f(\boldsymbol{y}_j \mid \Phi) \Longrightarrow \sum_j \log \left(f(\boldsymbol{y}_j \mid \Phi) + \lambda \right)$
- Iterative parameter estimation ("W-estimator")

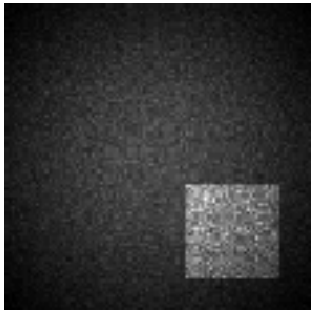
<u>step 1:</u> calculate "typicality" weights

$$t_j^{(m)} = \frac{f(\boldsymbol{y}_j \mid \Phi^{(m-1)})}{f(\boldsymbol{y}_j \mid \Phi^{(m-1)}) + \lambda}$$

<u>step 2:</u> maximize

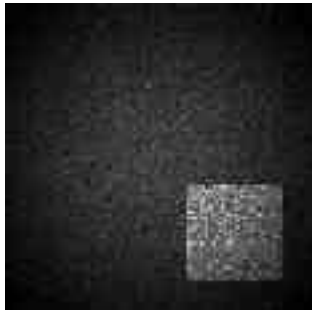
$$\sum_j t_j^{(m)} \log f(\boldsymbol{y}_j \mid \Phi)$$

Robust statistics

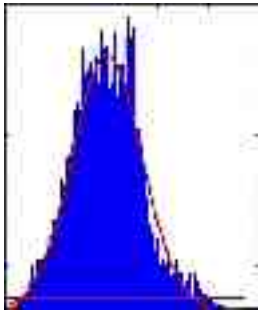


synthetic data

estimated bias field

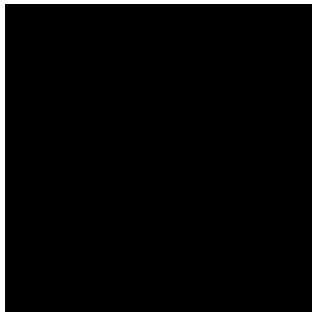


corrected data



histogram corrected data

"typicality"
= weight in
parameter estimation

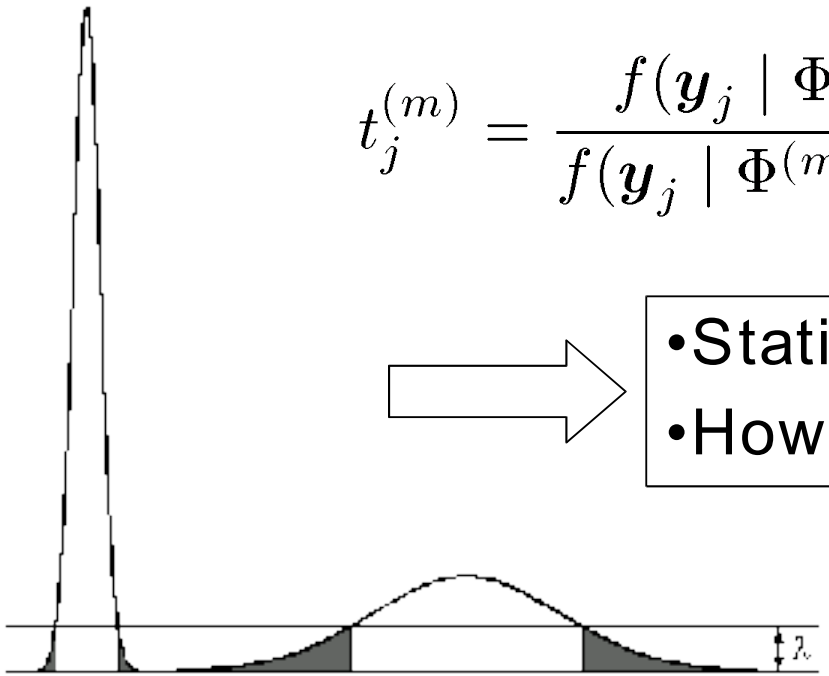


1 - "typicality"
= outlier belief

Applied to MS lesion segmentation

- Extension to multiple tissues
- Outlier belief depends on covariances of classes

$$t_j^{(m)} = \frac{f(\boldsymbol{y}_j \mid \Phi^{(m-1)})}{f(\boldsymbol{y}_j \mid \Phi^{(m-1)}) + \lambda}$$

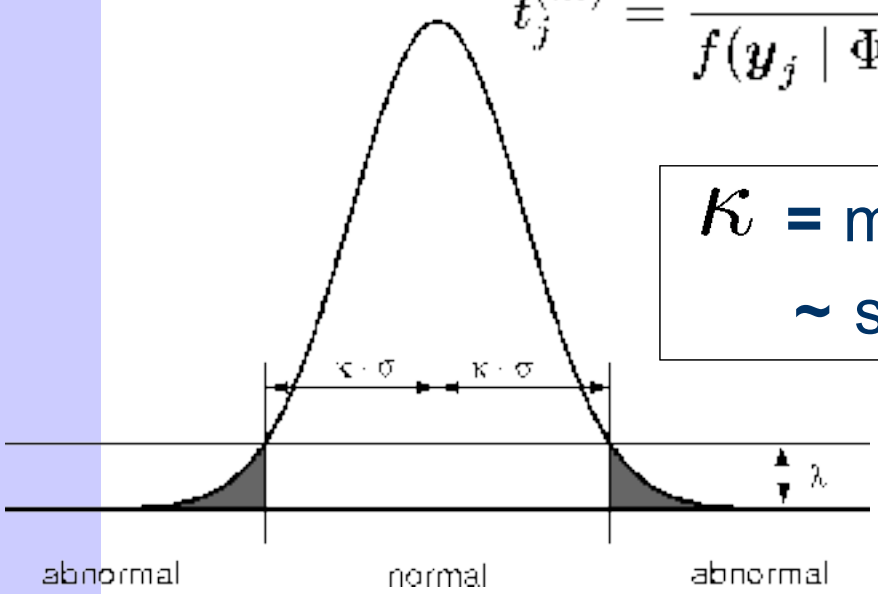


- Statistical meaning?
- How to choose λ ?

Applied to MS lesion segmentation

- Heuristic adaptation that takes the size of the covariance matrices into account
- Re-parameterization to more easily interpretable κ

$$t_j^{(m)} = \frac{f(\boldsymbol{y}_j \mid \Phi^{(m-1)})}{f(\boldsymbol{y}_j \mid \Phi^{(m-1)}) + \frac{1}{\sqrt{(2\pi)^C |\boldsymbol{\Sigma}^{(m-1)}|}} \exp(-\frac{1}{2}\kappa^2)}$$

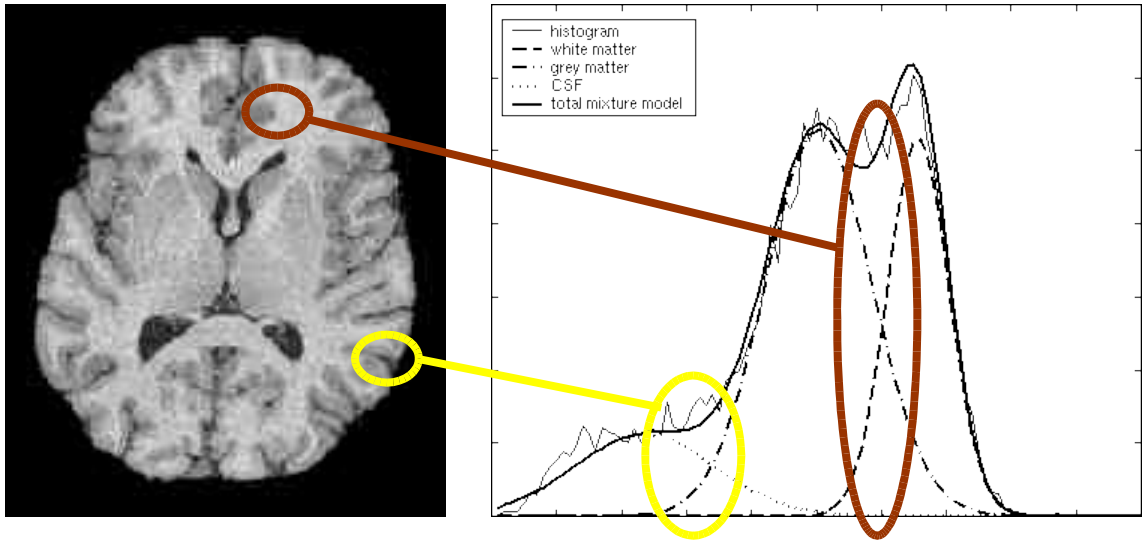


κ = mahalanobis distance threshold

~ statistical significance level

MS lesions are not the only model outliers...

- Partial volume voxels are also model outliers
  - On the edge between two or more tissue types
  - Mix several tissue types
  - Violate model assumptions (cf. later)



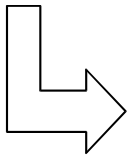
Separating MS lesions from partial volume voxels

- Exploit prior knowledge about MS lesions
  - MS lesions are hyperintense on PD and T2

Constraints on intensity

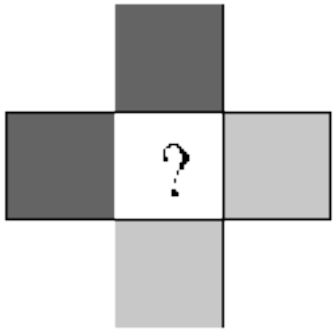
  - 95% of MS lesions are white matter lesions

Constraints on location

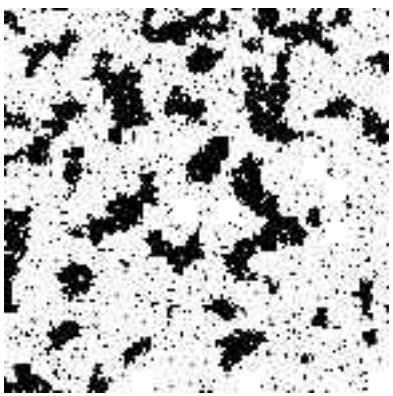


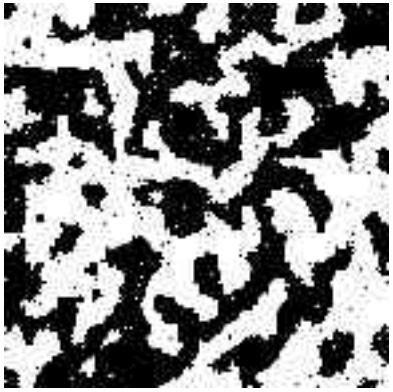
Markov random field model
[Li, 1995]

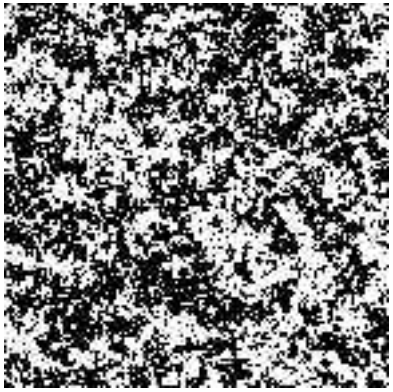
Markov random field (MRF) model



Tissue type in a voxel is statistically dependent on the tissue type of neighboring voxels



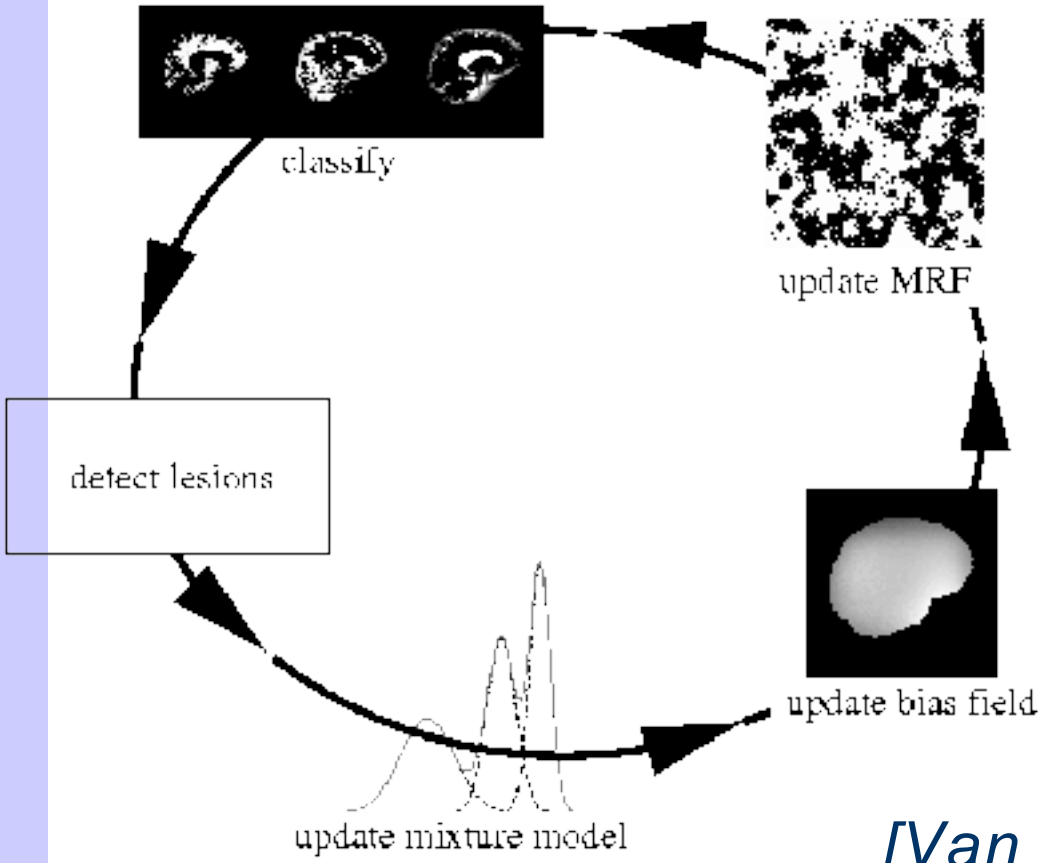




Typical MRF samples, for different MRF parameter sets

Can be used to confine lesions to locations close to white matter

Fully-automated MS lesion segmentation



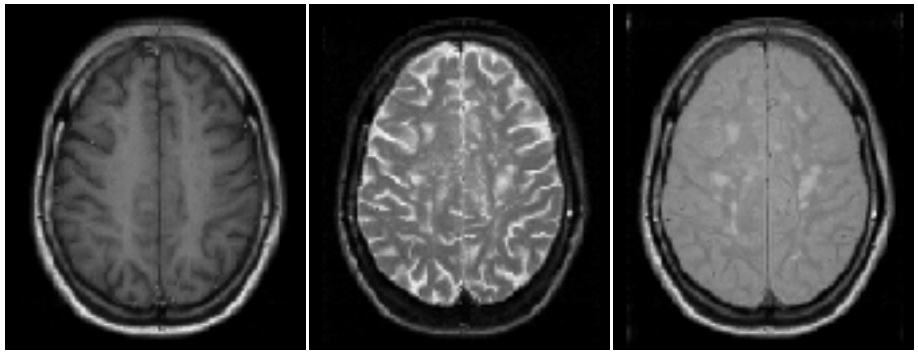
- Model parameters are only estimated from normal tissues
- Model adapts itself to each individual scan
- No need for pre- or post-processing
- Only one parameter to be specified: significance level κ

[Van Leemput et al., 2001]

Validation

- Data from clinical trial
  - 50 MS patients scanned every month during 1 year
  - T1-, T2- and PD-weighted MR images
  - European Commission funded research project BIOMORPH
- Automated segmentations compared to expert MS lesion delineations

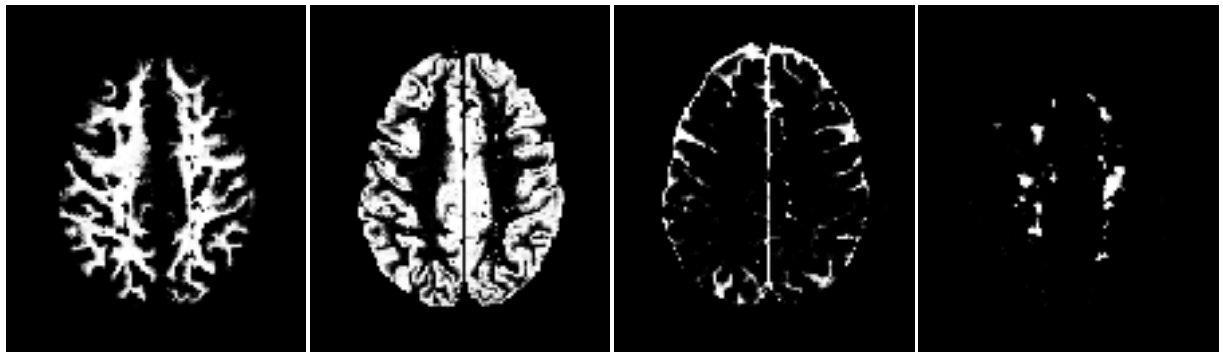
Validation



T1 T2 PD

Expert lesion delineation

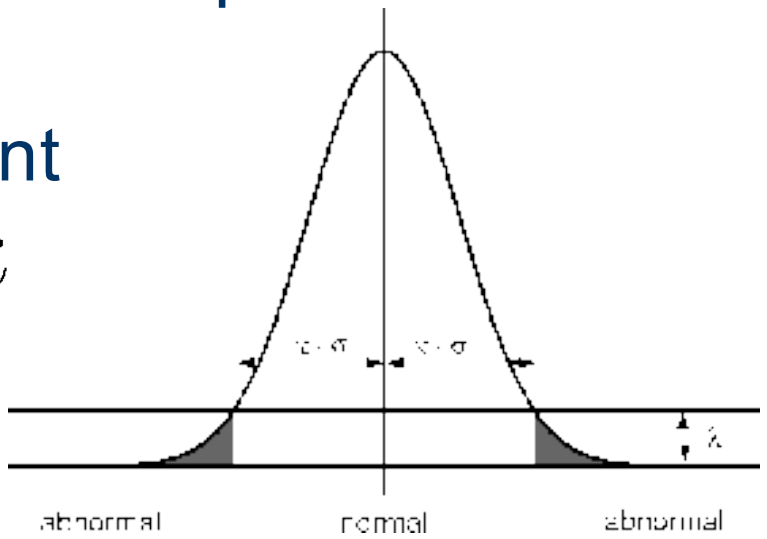
Automated segmentation



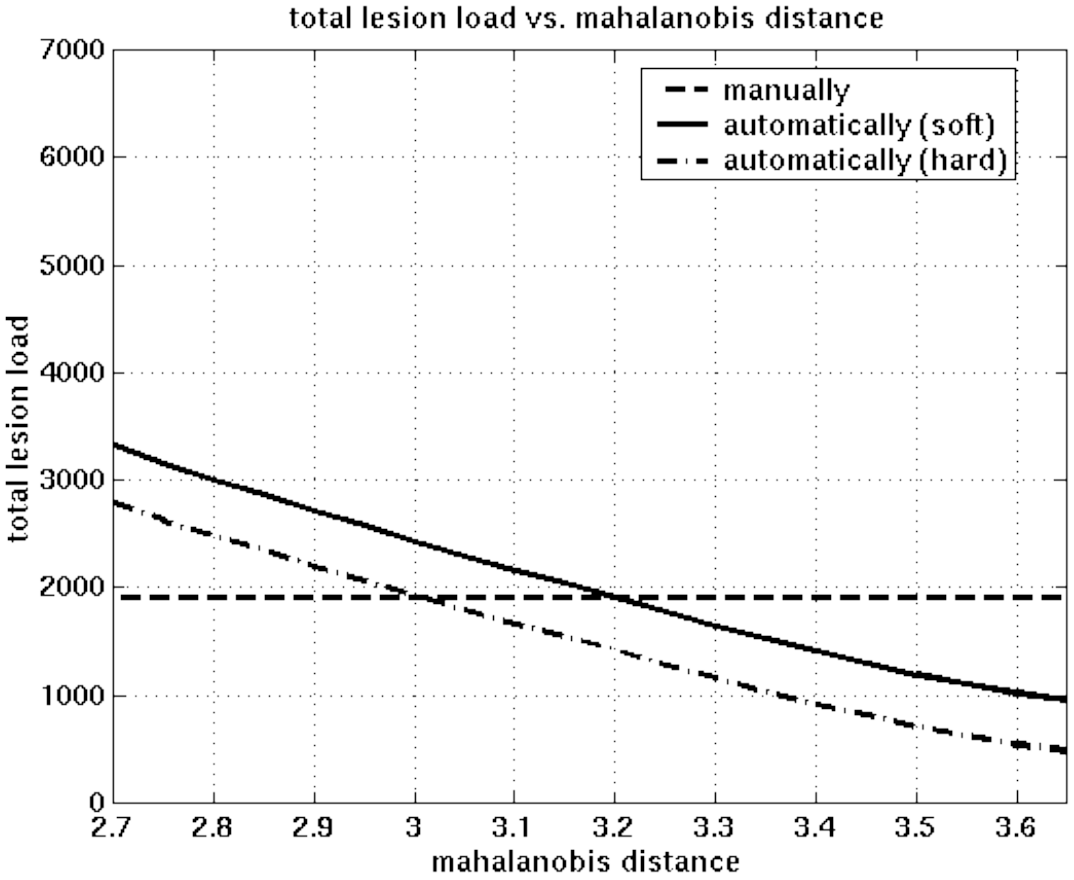
White matter Gray matter CSF MS lesions

Total lesion load (TLL)

- Total lesion volume per scan
- For 10 patients, 2 consecutive time points were analyzed by a human expert
- Expert TLL estimation compared to automated TLL estimation
- Evaluated for different significance levels κ

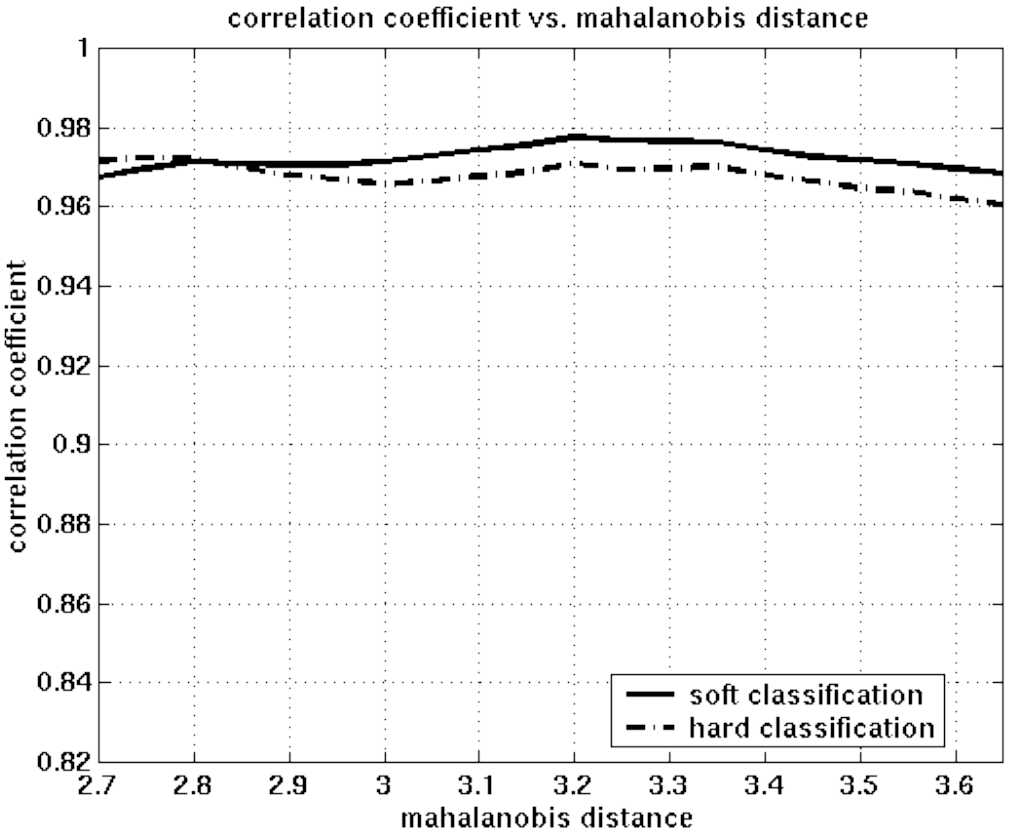


Total lesion load (TLL)



Average automated TLL decreases from 150% to 25% of expert estimates as κ increases

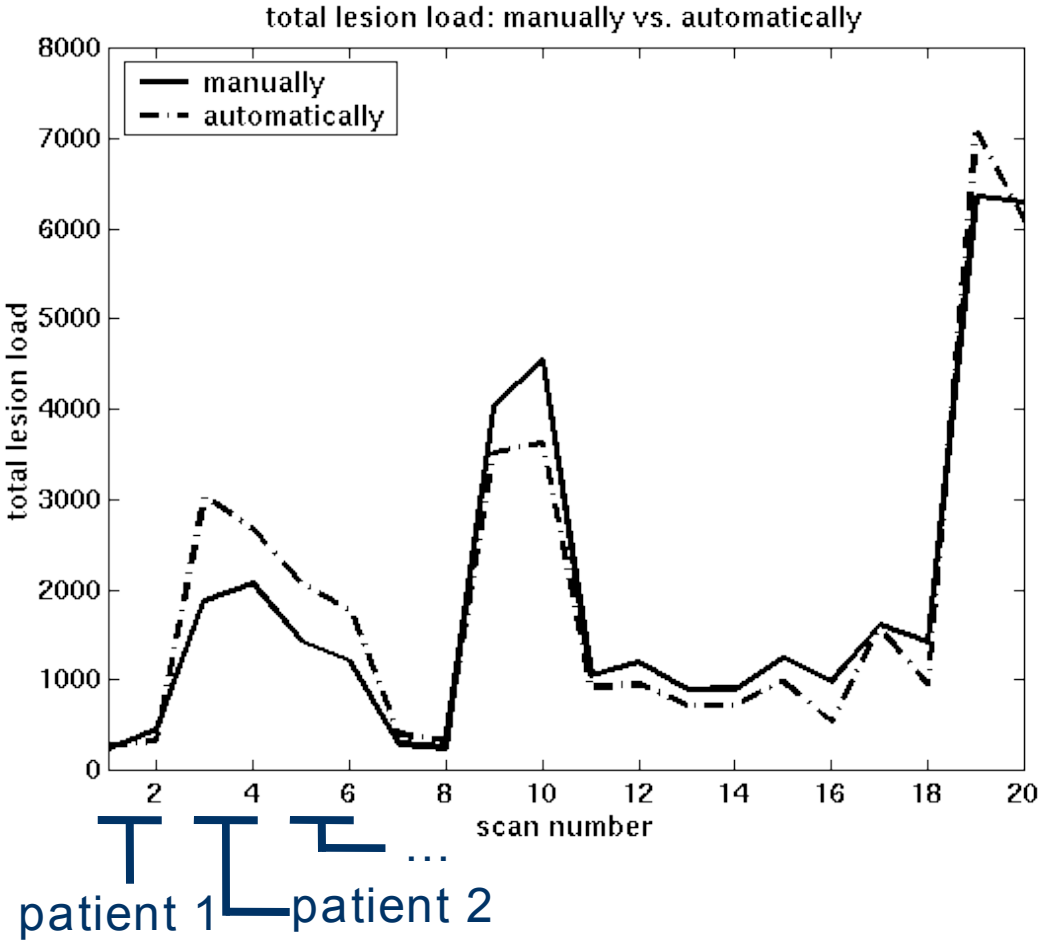
Total lesion load (TLL)



But correlation coefficient is always very high (0.96-0.98)

Exact choice of κ is unimportant in clinical trials assessing change in lesion volume

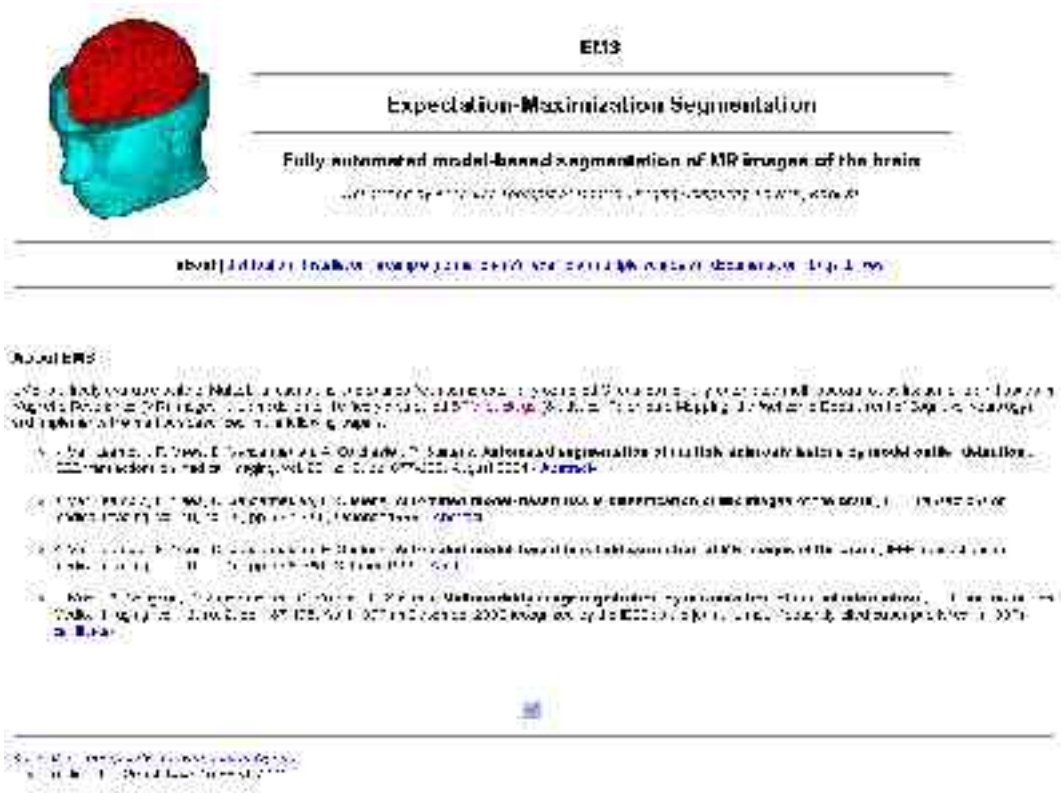
Total lesion load (TLL)



- For case κ = 3.0
- Agreement in direction of change in 9/10 cases

Implemented in ”EMS” software

Freely available from the website of the Medical Image Computing group, K.U.Leuven, Belgium: bilbo.esat.kuleuven.ac.be



Unifying Statistical Classification and Geometrical Models – MICCAI 2003

Overview

- The mixture model and the EM algorithm
- A probabilistic brain atlas
- Modeling MR bias fields
- Multiple Sclerosis lesion segmentation
- ***Partial volume segmentation***
- Discussion and future directions

Partial volume segmentation

- Assumed so far that each voxel belongs to one single tissue type
- In reality, many voxels in brain MR images are a mixture of several tissue types at the same time
  - Complex shape of the tissue interfaces in the brain
  - Limited spatial resolution of MRI
- "Partial volume (PV) effect"

Partial volume segmentation

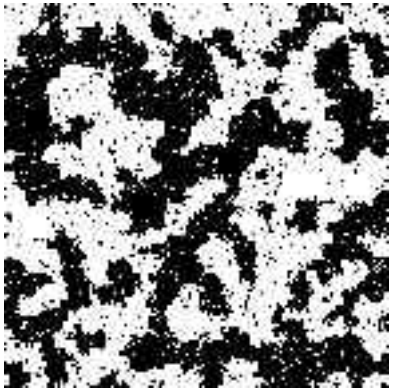
- Consistently misplacing the tissue borders in a 1 mm isotropic brain MRI with a single pixel in each slice results in large volume errors *[Niessen et al., 1999]*:
  - ~ 30% for white matter
  - ~ 40% for gray matter
  - ~ 60% for CSF
- Partial volume voxels make lesion segmentation by outlier detection more difficult

→ Need to explicitly model the partial volume effect

Improved image model

$f(\boldsymbol{L} \mid \Phi_L)$

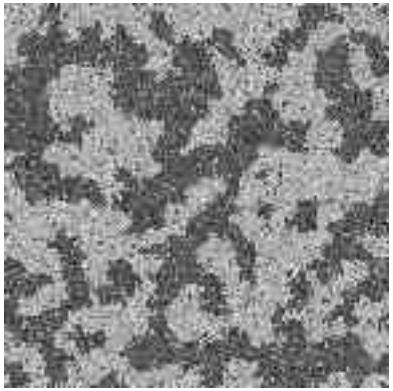
spatial model



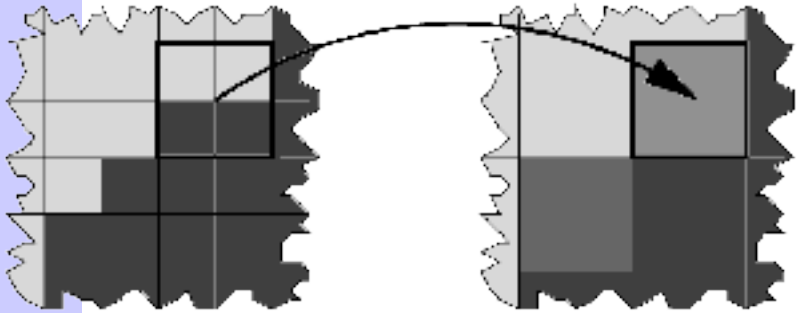
$\boldsymbol{L} = \{l_j\}$

$f(\boldsymbol{Y} \mid \boldsymbol{L}, \Phi_Y)$

intensity model



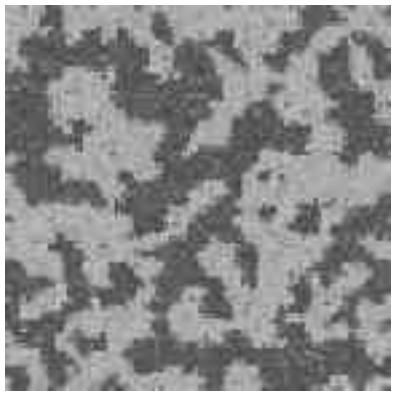
$\boldsymbol{Y} = \{y_j\}$



Original image grid

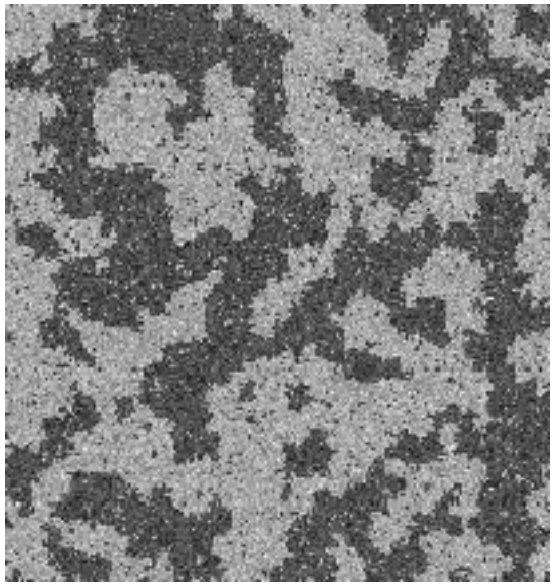
Downsampled image grid

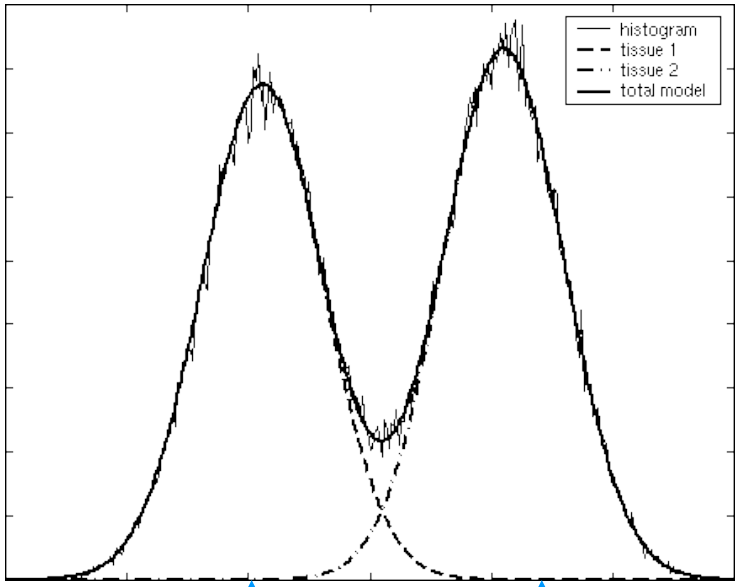
downsample



$\tilde{\boldsymbol{Y}}$

Before downsampling...

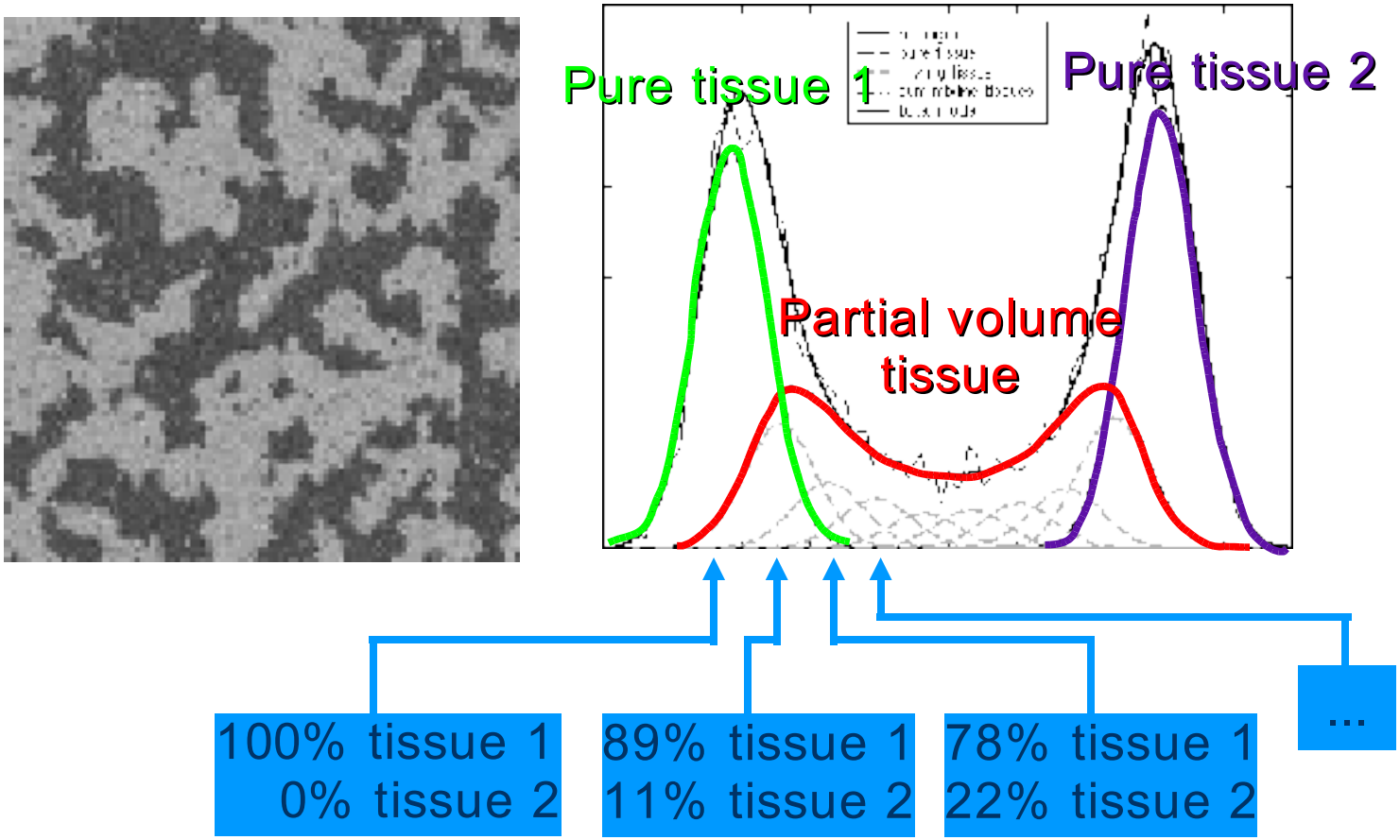




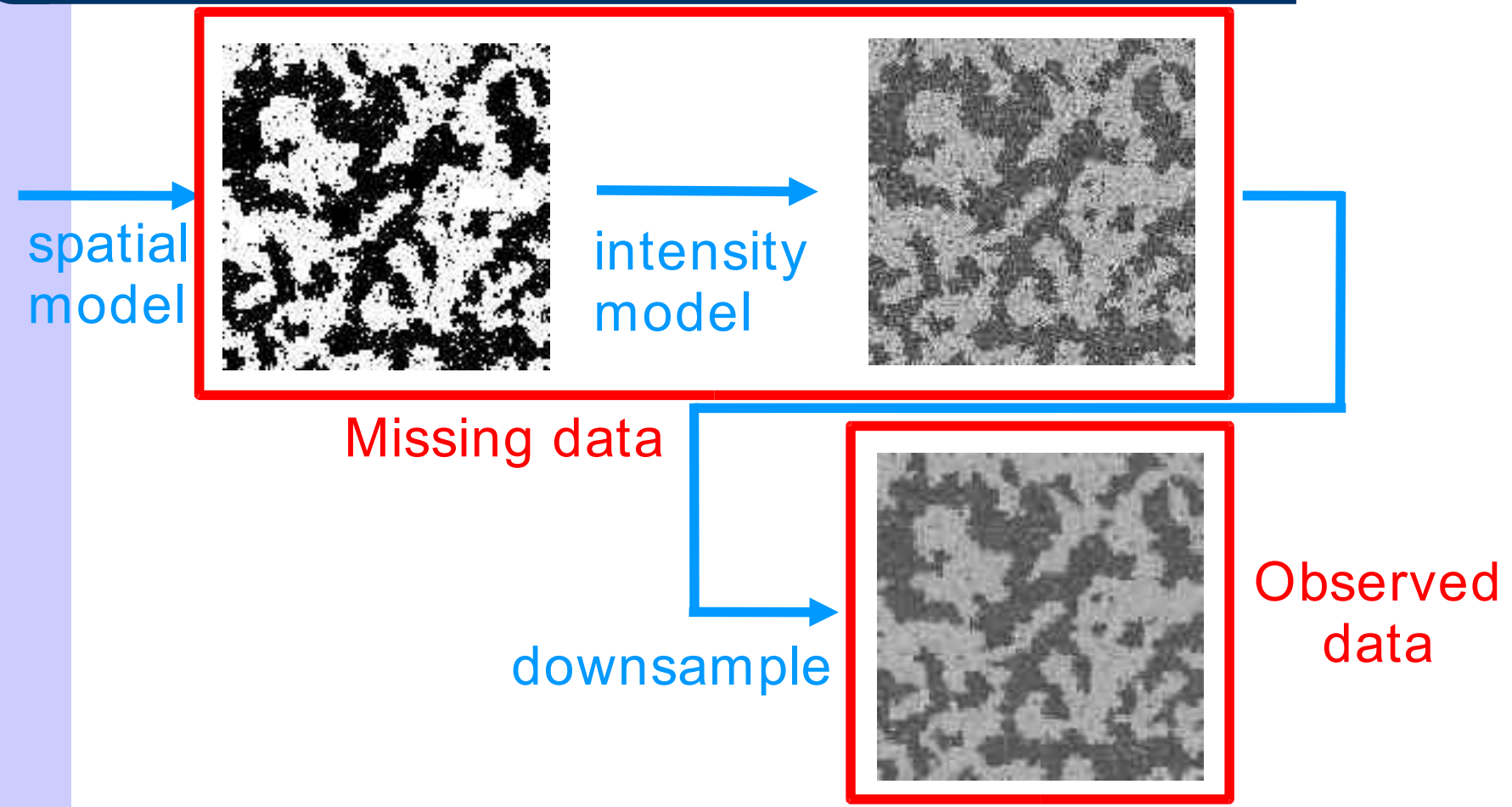
100% tissue 1
0% tissue 2

0% tissue 1
100% tissue 2

... after downsampling (3x)



Expectation-Maximization algorithm



Expectation-Maximization algorithm

- *Expectation step:* find the function

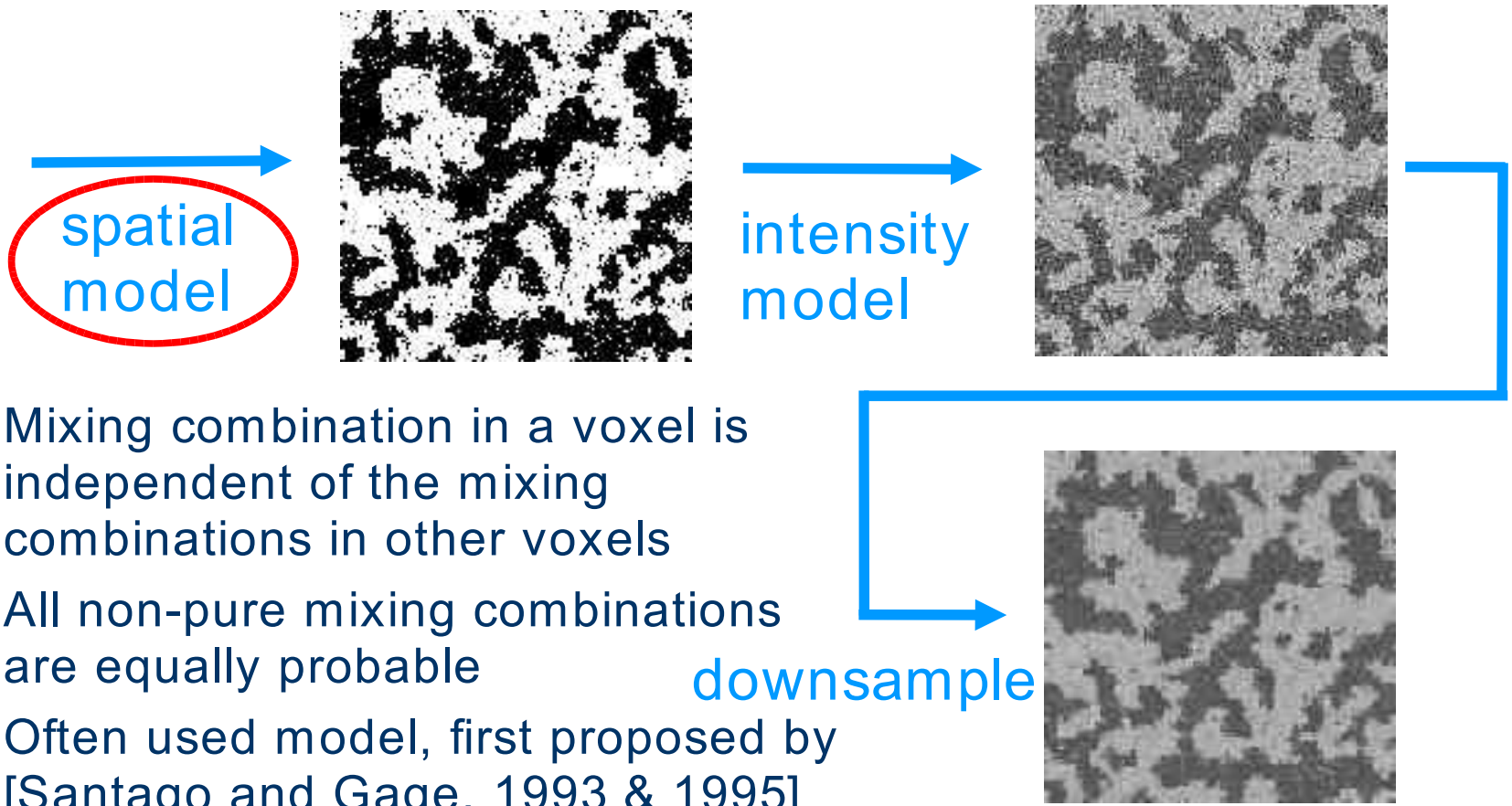
$$Q(\Phi \mid \Phi^{(m)}) = E_{\boldsymbol{L},\boldsymbol{Y}}\left[\log f(\boldsymbol{L},\boldsymbol{Y} \mid \Phi) \mid \tilde{\boldsymbol{Y}}, \Phi^{(m)}\right]$$

  Involves a partial volume image classification:
  - Not only probability for pure tissues
  - But also probability for e.g. 22% of tissue 1 and 78% of tissue 2
- *Maximization step:* find

$$\Phi^{(m+1)} = \arg\max_{\Phi} Q(\Phi \mid \Phi^{(m)})$$

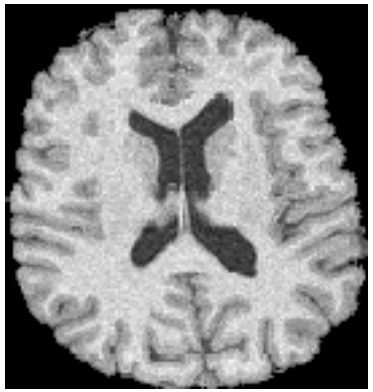
→ Unifying framework for PV segmentation literature *[Van Leemput et al., 2003]*

Spatial model 1

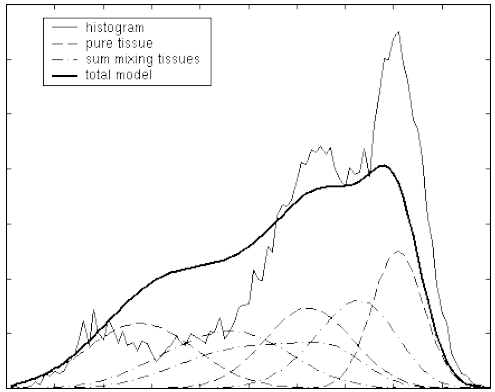


- Mixing combination in a voxel is independent of the mixing combinations in other voxels
- All non-pure mixing combinations are equally probable
- Often used model, first proposed by [Santago and Gage, 1993 & 1995]

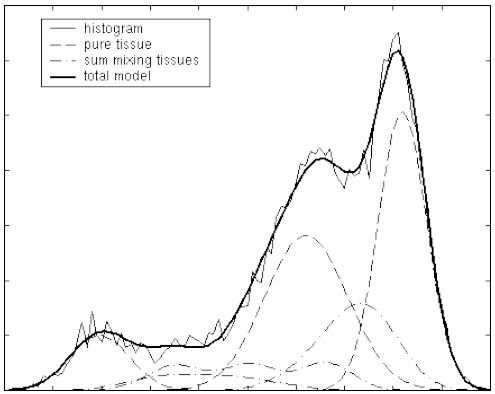
Spatial model 1



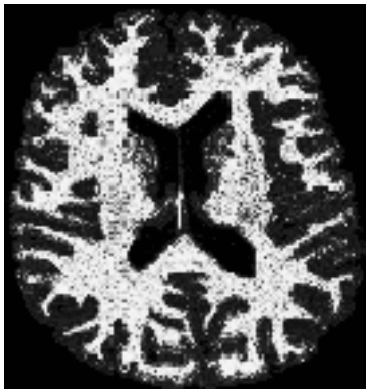
T1, 1x1x1 mm³



Parameter initialization



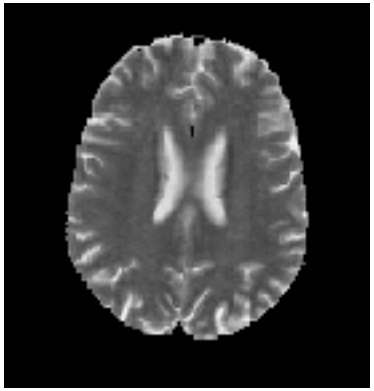
EM parameter estimation



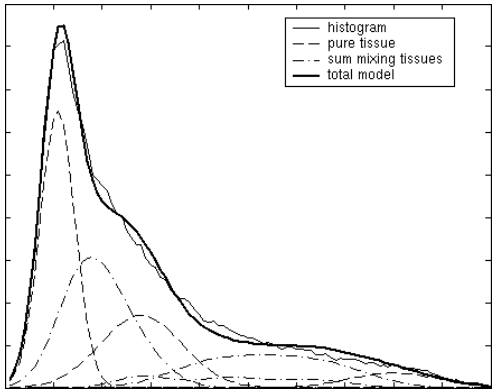
White matter fraction

White-gray matter PV voxels

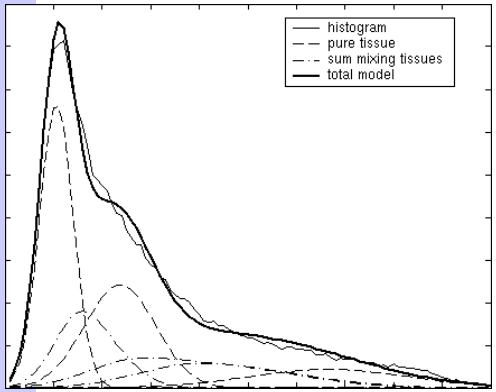
Spatial model 1



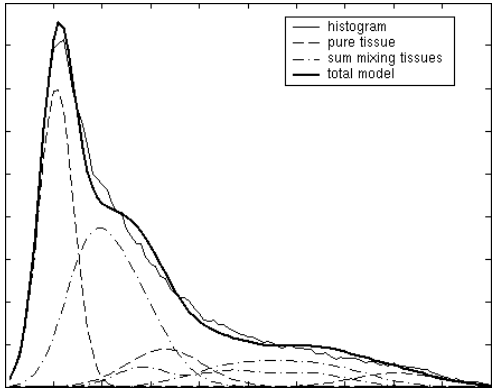
T2, 1,18 x 1,18 x 3 mm³



EM parameter estimation 1



EM parameter estimation 2

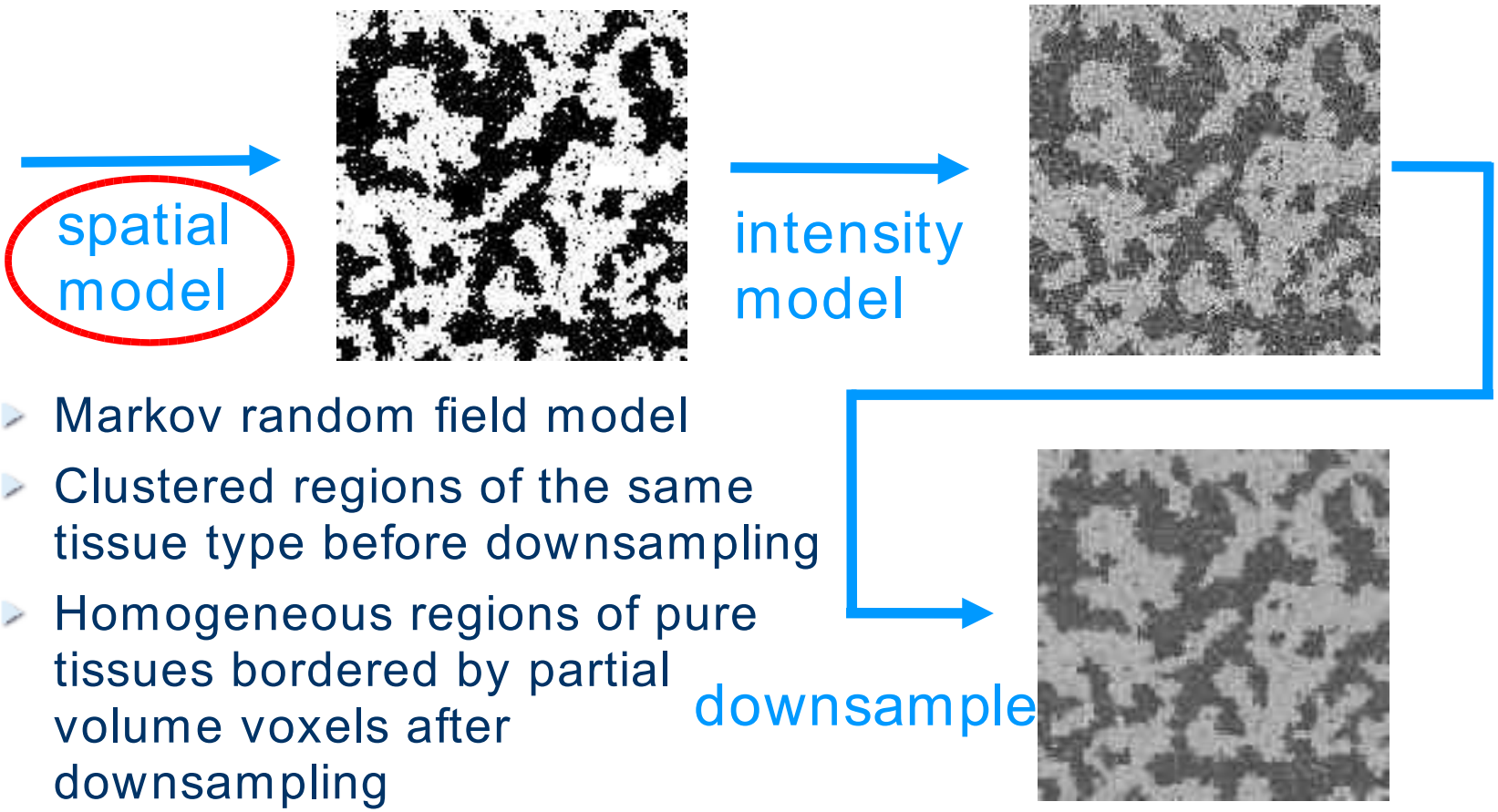


EM parameter estimation 3

- Slight modifications in the initialization result in different parameter estimations
- Fully histogram-based method but histogram alone is not sufficient
- The “true” parameter estimation is the one that provides a meaningful classification

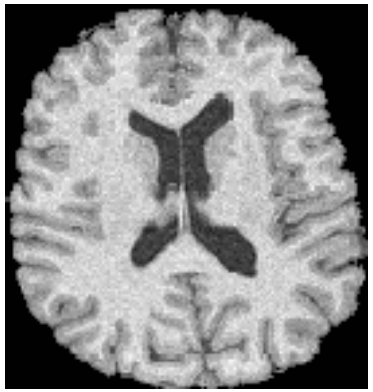
→ Spatial information needed

Spatial model 2

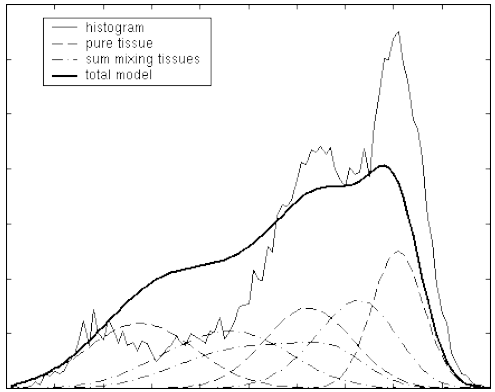


- Markov random field model
- Clustered regions of the same tissue type before downsampling
- Homogeneous regions of pure tissues bordered by partial volume voxels after downsampling

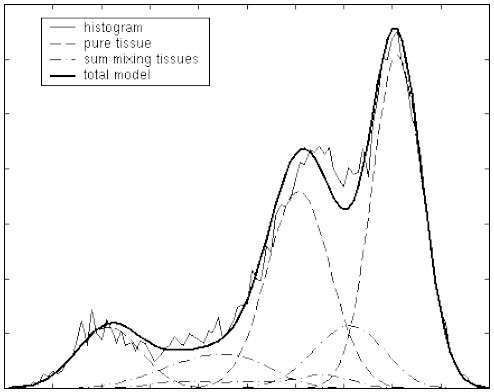
Spatial model 2



T1, 1x1x1 mm³



Parameter initialization

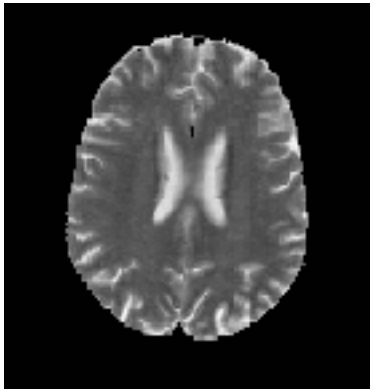


EM parameter estimation

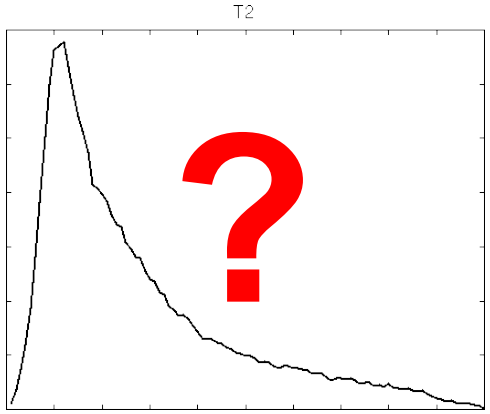
White matter fraction

White-gray matter PV voxels

Spatial model 2



T2, 1,18 x 1,18 x 3 mm³



EM parameter estimation?

- MRF model tends to minimize the boundary length between tissues
- This discourages classifications from accurately following the complex shape of the tissue interfaces
- MRF over-smooths the classifications in cases where the intensity information doesn't prevent it

→ In order to solve this, better spatial models are needed to describe the spatial distribution of tissues in the brain

Overview

- The mixture model and the EM algorithm
- A probabilistic brain atlas
- Modeling MR bias fields
- Multiple Sclerosis lesion segmentation
- Partial volume segmentation
- ***Discussion and future directions***

Expectation-Maximization algorithm

- Image classification performed simultaneously with model parameter estimation:
  - Intuitive algorithm that interleaves classification with model parameter estimation
  - Allows to integrate prior geometrical knowledge into the classification in a natural fashion
- After automated initialization with a statistical atlas, the classifier re-trains itself on each individual scan
  - Segments images of arbitrary pulse-sequences without user intervention

Intensity model

- Each tissue has a typical intensity and tissue-specific intensity variations
- MR bias fields can be explicitly modeled
- Lesions can be detected as model outliers
  - This allows to explicitly exclude lesions from model parameter estimations (e.g. bias field correction)
- The partial volume effect can be explicitly modeled

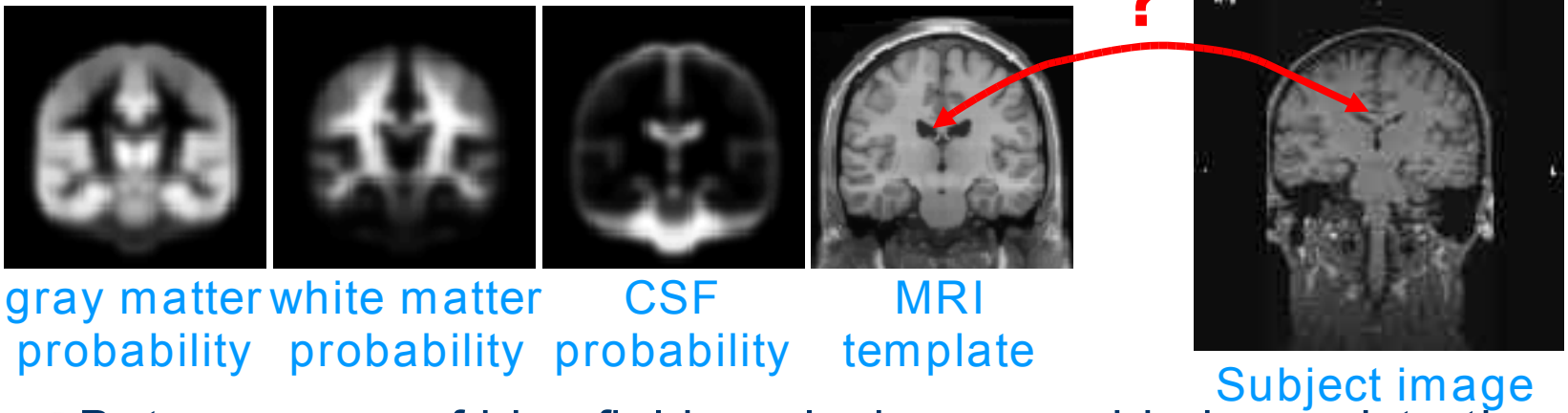
⟶ The intensity model is already quite complete

Spatial model

- Affine atlas registration provides only a rough brain mask => misclassifications of non-brain tissues as brain tissue
- Affine atlas registration does not allow to segment brain MR images with large shape differences (e.g. dramatically enlarged ventricles)
- White matter/gray matter/CSF atlas does not allow further parcellation of the brain
- More sophisticated models are needed for robust partial volume segmentation => atlas-based?
  - Deformable registration *[Maes et al., 1999] [Marroquin et al., 2002][Pohl et al., 2002][D'Agostino et al., 2003]*

Future research directions?

- Deformable atlas registrations are performed by minimizing a registration metric between an MRI template associated with the atlas and the image to be segmented



  - But presence of bias fields or lesions may hinder registration
  - Many deformable registration algorithms require similar intensities in the two images
  - Mutual Information based deformable registration is still difficult

Future research directions?

- Deformable registration is performed to help the segmentation, but the segmentation could in turn help the registration
- Deformation field as model parameters in the image model, to be estimated by the EM-algorithm?
- Simultaneous registration and segmentation would eliminate the need for an atlas template

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