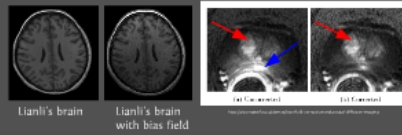


# MRI Bias Field Correction Based on Tissue Labeling

Lianli Liu, Jiyang Chu, Jie Li, Zhen Zeng  
4.25.2014

## Problem: Bias Field Correction

- Intensity inhomogeneity in MRI
  - imperfect RF profiles, patient induced inhomogeneity...
  - Human eyes: robust
  - Image analysis algorithms: intensity based methods are very sensitive to such intensity variation
- Motivation
  - Correct bias field and improve the accuracy of other image analysis results



## Outline

- Related Work
- Replication
  - A fuzzy c-means (FCM) based algorithm for intensity inhomogeneity correction and segmentation of MR images, by Chen et al. [1]
- Extension
  - Geometric Context from a Single Image, by Heim et al. [2]
- Experiment Results & Discussions
- Conclusion
- Q&A

## Extension:

### Geometric Context from a Single Image

**Their Goal:** Supervised learning on **scene** classification

**Highlights:** Superpixels provide the spatial support that allows us to compute some basic first-order statistics (e.g. texture and shape)

**Our Goal:** Supervised learning on **tissue** labeling

→ compared to our goals, we made some modifications based on the original paper (e.g. features)

**Next:**

- Our motivation centered on tissue labeling
- Integration of scene labeling with bias field correction

## Replication:

### A fuzzy c-means (FCM) based algorithm for intensity inhomogeneity correction and segmentation of MR images

**Goal:** Remove bias field and segment MR images automatically

**Approach:**

- Intensity-based bias field correction
- Segmentation with FCM

**Experimental Results (tissue labels):**

- Brain T1
- Brain T2
- Brain T2\*
- Brain T2\*
- Brain T2\*

**High-contrast Results (strong bias):**

- Brain T1
- Brain T2
- Brain T2\*
- Brain T2\*
- Brain T2\*

## Related Work

### Prospective Methods

- Existing Methods
  - Phantom based
  - Multiscale
  - Special Sequences
- Pros
  - accurate in modeling systematic error
- Cons
  - cannot remove patient induced inhomogeneity

### Retrospective Methods

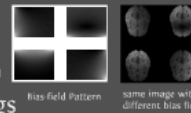
- Existing Methods
  - Filtering methods
  - Surface fitting methods
  - Segmentation based methods
  - Histogram sharpening methods
- Pros
  - more general for different sources of bias
  - easy to implement
- Cons
  - ill-posed inverse problem

## Experiments

### Dataset

#### Synthetic Data

- no-bias T1 image and tissue label from BrainWeb ISI
- Artificial bias field using Prof. Feiden's code [6]



### Experiment settings

- Train and Test**
- Training set: 50 Images \* 5 patterns (no bias + 4 bias patterns)
  - Test set: 200 Images \* 5 patterns

#### Quantitative evaluation metrics

- Tissue label accuracy: average labeling accuracy of each pixel
- Normalized Root Mean Square Error of estimated bias field

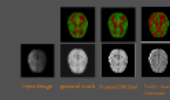
#### Baseline

- Fuzzy C-means based bias field correction



## Experiments

### Qualitative Result



### Segmentation Result



### Robust Analysis

Method	Accuracy	RMSE	Time
FCM	0.85	0.15	10s
Proposed	0.92	0.08	15s

### Bias Field Correction

Method	RMSE	Accuracy
FCM	0.15	0.85
Proposed	0.08	0.92

## Conclusion

- Our proposed algorithm provides more **robust tissue labeling** and **bias field estimation** than traditional intensity based method.
- Mature techniques from **other areas** can be really helpful in image processing

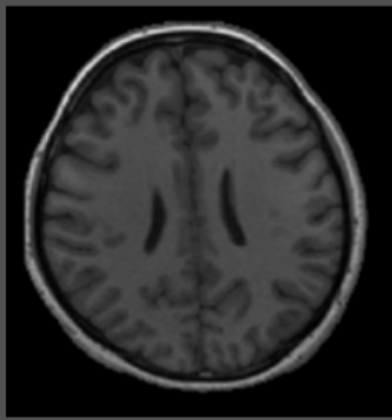
# **MRI Bias Field Correction Based on Tissue Labeling**

Lianli Liu, Jiyang Chu, Jie Li, Zhen Zeng

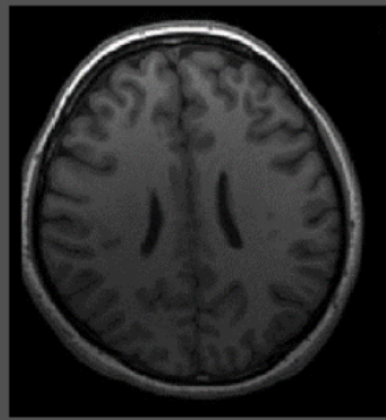
4.25.2014

# Problem: Bias Field Correction

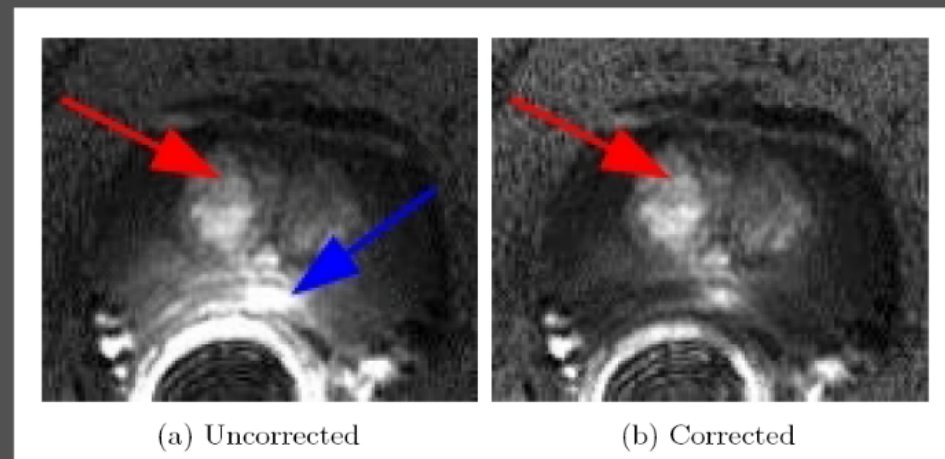
- Intensity inhomogeneity in MRI
  - imperfect RF profiles, patient induced inhomogeneity...
  - Human eyes: robust
  - Image analysis algorithms: intensity based methods are very sensitive to such intensity variation
- Motivation
  - Correct bias field and improve the accuracy of other image analysis results



Lianli's brain



Lianli's brain  
with bias field



<http://vip.uwaterloo.ca/demos/bias-field-correction-endorectal-diffusion-imaging>

# Outline

- **Related Work**

- **Replication**

A fuzzy c-means (FCM) based algorithm for intensity inhomogeneity correction and segmentation of MR images, by Chen et al. [1]

- **Extension**

Geometric Context from a Single Image, by Hoiem et al. [2]

- **Experiment Results & Discussions**

- **Conclusion**

- **Q&A**

[1] W. Chen and M. L. Giger, "A fuzzy c-means (fcm) based algorithm for intensity inhomogeneity correction and segmentation of mr images," in Biomedical Imaging: Nano to Macro, 2004. IEEE International Symposium on, pp. 1307-1310, IEEE, 2004. [http://ieeexplore.ieee.org/xpls/abs\\_all.jsp?arnumber=1398786](http://ieeexplore.ieee.org/xpls/abs_all.jsp?arnumber=1398786).  
[2] D. Hoiem, A. A. Efros, and M. Hebert, "Geometric context from a single image," in Computer Vision, 2005. ICCV 2005. Tenth IEEE International Conference on, vol. 1, pp. 654-661, IEEE, 2005. [http://ieeexplore.ieee.org/xpls/abs\\_all.jsp?arnumber=1541316&tag=1](http://ieeexplore.ieee.org/xpls/abs_all.jsp?arnumber=1541316&tag=1).

# Related Work

## Prospective Methods

- Existing Methods
  - Phantom based
  - Multicoil
  - Special Sequences
- Pros
  - accurate in modeling systematic error
- Cons
  - cannot remove patient induced inhomogeneity

## Retrospective Methods

- Existing Methods
  - Filtering methods
  - Surface fitting methods
  - Segmentation based methods
  - Histogram sharpening methods
- Pros
  - more general for different sources of bias
  - easy to implement
- Cons
  - ill-posed inverse problem

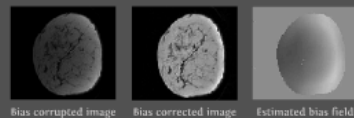
# Replication:

## A fuzzy c-means (FCM) based algorithm for intensity inhomogeneity correction and segmentation of MR images

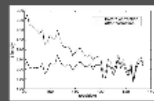
Chen et al. [1]

### Goal

Estimate bias field and segment MR images simultaneously



Bias corrupted image Bias corrected image Estimated bias field



Intensity distribution

\* Images taken from Chen et al [1]

6

### Approach

#### Fuzzy c-means based bias field estimation

- Minimize the following objective function  $J(u, \beta)$  by updating  $u, \beta$  iteratively

$$J(u, \beta) = \sum_{k=1}^K \sum_{i=1}^N u_{ki}^m |x_i - \mu_k|^2 + \lambda \sum_{k=1}^K \sum_{i=1}^N u_{ki}^m |x_i - \mu_k|^2$$

$\mu_k$  and  $\lambda$  are the dipole moment  $\mu_k$  and the regularization parameter  $\lambda$ , respectively.  $x_i$  is the intensity of tissue  $k$  at MRI voxel  $i$ ,  $u_{ki}$  is bias field at  $k$ .

8

#### Regularization of bias field estimation

- Laplacian regularization to encourage smoothness
 
$$J(u, \beta) = \sum_{k=1}^K \sum_{i=1}^N u_{ki}^m |x_i - \mu_k|^2 + \lambda \sum_{k=1}^K \sum_{i=1}^N u_{ki}^m |x_i - \mu_k|^2 + \gamma \sum_{k=1}^K \sum_{i=1}^N u_{ki}^m |\nabla \mu_k|^2$$
- Penalized least square regression to deal with scale problem between error item and smooth item
 
$$\mu_k = \frac{\sum_{i=1}^N u_{ki}^m x_i}{\sum_{i=1}^N u_{ki}^m + \gamma}$$
- Solve for smooth bias field
 
$$\beta = \frac{\sum_{i=1}^N u_{ki}^m x_i}{\sum_{i=1}^N u_{ki}^m + \gamma}$$
- 1D B-spline smoothing

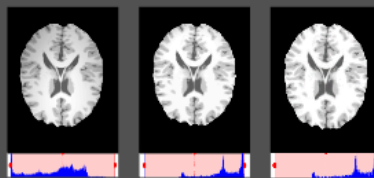
9

7

### Replication Results (weak bias)

Replicated works:

- FCM: fuzzy c-means segmentation
- FCM-B: fuzzy c-means based bias field correction



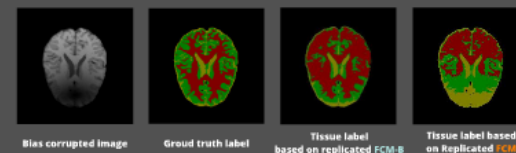
T1 image corrupted by bias field and histogram Corrected T1 results and histogram Ground truth T1 and histogram

10

### Replication Results (strong bias)

Replicated works:

- FCM: fuzzy c-means segmentation
- FCM-B: fuzzy c-means based bias field correction



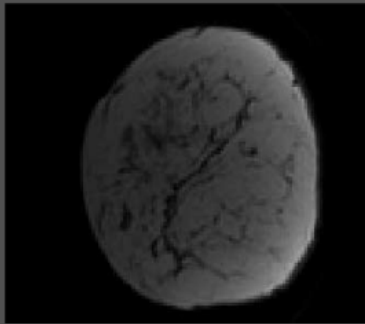
Bias corrupted image Ground truth label Tissue label based on replicated FCM-B Tissue label based on Replicated FCM

We need **better** segmentation algorithm!

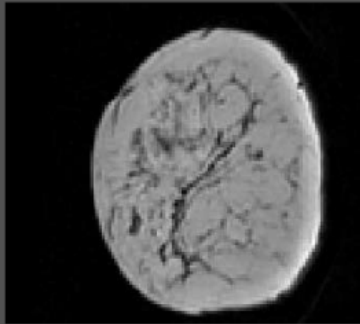
11

# Goal

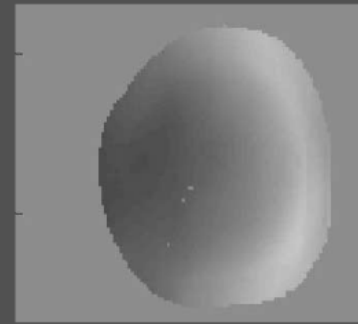
Estimate bias field and segment MR images simultaneously



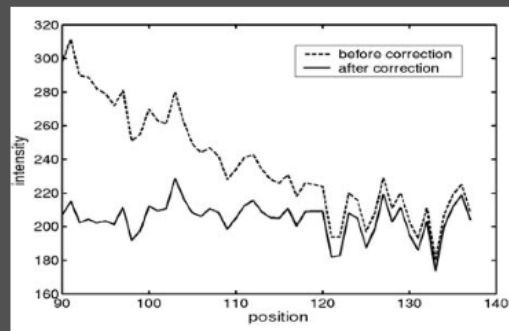
Bias corrupted image



Bias corrected image



Estimated bias field



Intensity distribution

\* images taken from Chen et al. [1]

# and segmentation of MR images

Chen et al. [1]

## Approach

### ■ Fuzzy c-means based bias field estimation

- Minimize the following objective function  $J(u, c, b)$  by updating  $x, c, b$  iteratively

$$J(u, c, b) = \sum_{i=1}^c \sum_{k=1}^N u_{ik}^m D(x_k - c_i - b_k) + \alpha \sum_{i=1}^c \sum_{k=1}^N u_{ik}^m D(\bar{x}_k - c_i - b_k)$$

$u_{ik}$ : membership of voxel  $k$  belongs to tissue type  $i$ ,  $m$ : fuzzy degree,  
 $c_i$ : prototype of tissue  $i$ ,  $x_k$ : MRI voxel value,  $b_k$ : bias field at  $k$

8

### ■ Regularization of bias field estimation

- Laplacian regularization to encourage smoothness

$$J(u, c, b) = \sum_{i=1}^c \sum_{k=1}^N u_{ik} D(x_k - c_i - b_k) + \alpha \sum_{i=1}^c \sum_{k=1}^N u_{ik} D(\bar{x}_k - c_i - b_k) + \gamma \|\nabla b\|_2^2$$

- Penalized least square regression to deal with scale problem between error item and smooth item

$$\hat{b} = \arg \min \|\hat{b} - \hat{b}^0\|_2^2 + \gamma \|\nabla \hat{b}\|_2^2$$

- Solve for smooth bias field

$$\hat{b}^0 = \arg \min \sum_{i=1}^c \sum_{k=1}^N u_{ik} D(x_k - c_i - b_k) - \alpha \sum_{i=1}^c \sum_{k=1}^N u_{ik} D(\bar{x}_k - c_i - b_k)$$

- 3D B-Spline smoothing

$$\hat{b}^0 \rightarrow \hat{b}$$

9

7

## Replication Results (strong bias)

Replicated works:



## ■ Fuzzy c-means based bias field estimation

- Minimize the following objective function  $J(u, c, b)$  by updating  $x, c, b$  iteratively

$$J(u, c, b) = \sum_{i=1}^c \sum_{k=1}^N u_{ik}^m D(x_k - c_i - b_k) + \alpha \sum_{i=1}^c \sum_{k=1}^N u_{ik}^m D(\bar{x}_k - c_i - b_k)$$

$u_{ik}$  : membership of voxel  $k$  belongs to tissue type  $i$ ,  $m$ : fuzzy degree,  
 $c_i$ : prototype of tissue  $i$ ,  $x_k$ : MRI voxel value,  $b_k$  : bias field at  $k$

## ■ Regularization of bias field estimation

- Laplacian regularization to encourage smoothness

$$J(u, c, b) = \sum_{i=1}^c \sum_{k=1}^N u_{ik} D(x_k - c_i - b_k) + \alpha \sum_{i=1}^c \sum_{k=1}^N u_{ik} D(\bar{x}_k - c_i - b_k) + \gamma \|\nabla b\|_2^2$$

- Penalized least square regression to deal with scale problem between error item and smooth item

$$\hat{b} = \arg \min \left\| \hat{b} - \hat{b}^0 \right\|_2^2 + \gamma \left\| \nabla \hat{b}^0 \right\|_2^2$$

- Solve for smooth bias field

$$\hat{b}^0 = \arg \min \sum_{i=1}^c \sum_{k=1}^N u_{ik} D(x_k - c_i - b_k) + \alpha \sum_{i=1}^c \sum_{k=1}^N u_{ik} D(\bar{x}_k - c_i - b_k)$$

- 3D B-Spline smoothing

$$\hat{b}^0 \rightarrow \hat{b}$$

# and segmentation of MR images

Chen et al. [1]

## Approach

### ■ Fuzzy c-means based bias field estimation

- Minimize the following objective function  $J(u, c, b)$  by updating  $x, c, b$  iteratively

$$J(u, c, b) = \sum_{i=1}^c \sum_{k=1}^N u_{ik}^m D(x_k - c_i - b_k) + \alpha \sum_{i=1}^c \sum_{k=1}^N u_{ik}^m D(\bar{x}_k - c_i - b_k)$$

$u_{ik}$ : membership of voxel  $k$  belongs to tissue type  $i$ ,  $m$ : fuzzy degree,  
 $c_i$ : prototype of tissue  $i$ ,  $x_k$ : MRI voxel value,  $b_k$ : bias field at  $k$

8

### ■ Regularization of bias field estimation

- Laplacian regularization to encourage smoothness

$$J(u, c, b) = \sum_{i=1}^c \sum_{k=1}^N u_{ik} D(x_k - c_i - b_k) + \alpha \sum_{i=1}^c \sum_{k=1}^N u_{ik} D(\bar{x}_k - c_i - b_k) + \gamma \|\nabla b\|_2^2$$

- Penalized least square regression to deal with scale problem between error item and smooth item

$$\hat{b} = \arg \min \|\hat{b} - \hat{b}^0\|_2^2 + \gamma \|\nabla \hat{b}\|_2^2$$

- Solve for smooth bias field

$$\hat{b}^0 = \arg \min \sum_{i=1}^c \sum_{k=1}^N u_{ik} D(x_k - c_i - b_k) - \alpha \sum_{i=1}^c \sum_{k=1}^N u_{ik} D(\bar{x}_k - c_i - b_k)$$

- 3D B-Spline smoothing

$$\hat{b}^0 \rightarrow \hat{b}$$

9

7

## Replication Results (strong bias)

Replicated works:

# Replication Results (weak bias)

## Replicated works:

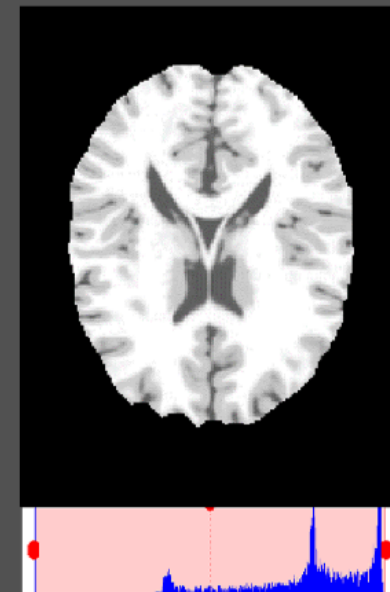
- **FCM**: fuzzy c-means segmentation
- **FCM-B**: fuzzy c-means based bias field correction



T1 image corrupted by bias field and histogram



Corrected T1 results and histogram

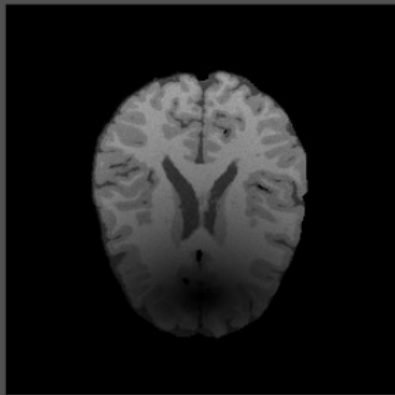


Ground truth T1 and histogram

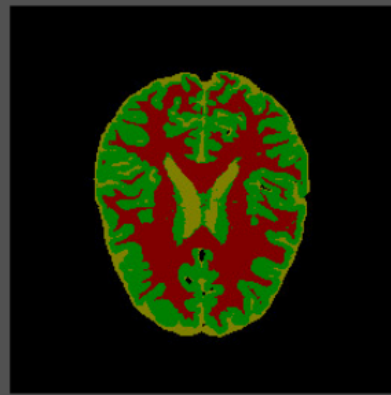
# Replication Results (strong bias)

## Replicated works:

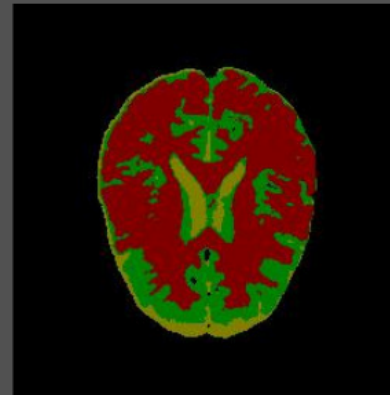
- **FCM**: fuzzy c-means segmentation
- **FCM-B**: fuzzy c-means based bias field correction



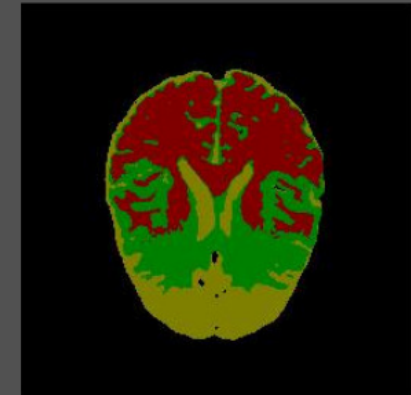
Bias corrupted image



Ground truth label



Tissue label  
based on replicated **FCM-B**



Tissue label based  
on Replicated **FCM**

We need **better** segmentation algorithm!

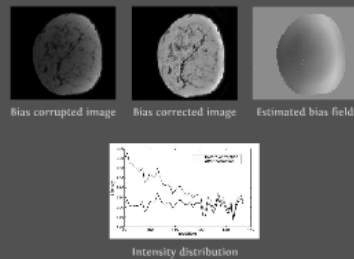
# Replication:

## A fuzzy c-means (FCM) based algorithm for intensity inhomogeneity correction and segmentation of MR images

Chen et al. [1]

### Goal

Estimate bias field and segment MR images simultaneously



\* images taken from Chen et al [1]

6

### Approach

#### Fuzzy c-means based bias field estimation

- Minimize the following objective function  $J(u, \beta)$  by updating  $u, \beta$  iteratively

$$J(u, \beta) = \sum_{k=1}^K \sum_{i=1}^N u_{ki} D(x_i, \beta_k) + \alpha \sum_{k=1}^K \sum_{i=1}^N u_{ki} D(\beta_k, \lambda_k)$$

$x_i$  and  $\beta_k$  are the input voxel  $i$  and the bias field  $\beta_k$  at  $k$ th fuzzy degree of membership of tissue  $k$ ;  $\lambda_k$ : MRI voxel value,  $\beta_k$ : bias field at  $k$

8

#### Regularization of bias field estimation

- Laplacian regularization to encourage smoothness
 
$$J(u, \beta) = \sum_{k=1}^K \sum_{i=1}^N u_{ki} D(x_i, \beta_k) + \alpha \sum_{k=1}^K \sum_{i=1}^N u_{ki} D(\beta_k, \lambda_k) + \gamma \|\nabla \beta_k\|_2^2$$
- Penalized least square regression to deal with scale problem between error item and smooth item
 
$$\beta_k = (X_k^T X_k + \lambda I)^{-1} X_k^T y_k$$
- Solve for smooth bias field
 
$$\beta_k = (X_k^T X_k + \lambda I)^{-1} X_k^T y_k + \alpha \sum_{i=1}^N u_{ki} (x_i - \beta_k)$$
- 1D B-spline smoothing

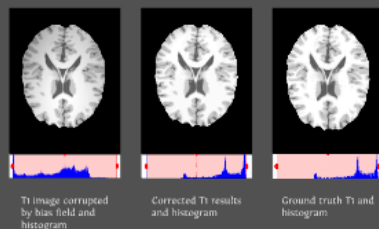
9

7

### Replication Results (weak bias)

Replicated works:

- FCM: fuzzy c-means segmentation
- FCM-B: fuzzy c-means based bias field correction

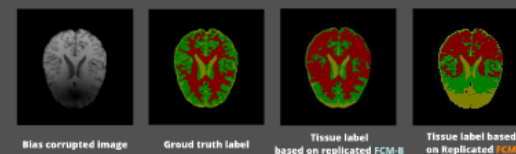


10

### Replication Results (strong bias)

Replicated works:

- FCM: fuzzy c-means segmentation
- FCM-B: fuzzy c-means based bias field correction



We need **better** segmentation algorithm!

11

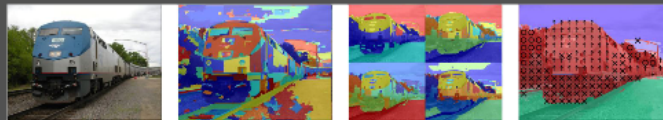
# Extension:

## Geometric Context from a Single Image

Hoiem et al. [2]

### Their Goal

Supervised learning on **scene structure** labeling



green-ground  
red-vertical  
blue-sky  
within vertical stcture: X=solid, O=porous  
by Hoiem et al. [2]

### Highlight

Superpixels provide the spatial support that allows us to compute some basic first-order statistics (e.g. texture and shape)

### Our Goal

Supervised learning on **tissue** labeling

→ Compared to our goals, we made some modifications based on the original paper (e.g. features)

- Next**
- Our replication tailored to tissue labeling
  - Integration of tissue labeling with bias field correction

13

## Their Goal

Supervised learning on **scene structure** labeling



green=ground  
red=vertical  
blue=sky  
within vertical stcture: X=solid, O=porous  
by Hoiem et al. [2]

## Highlight

Superpixels provide the spatial support that allows us to compute some basic first-order statistics (e.g. texture and shape)

## Our Goal

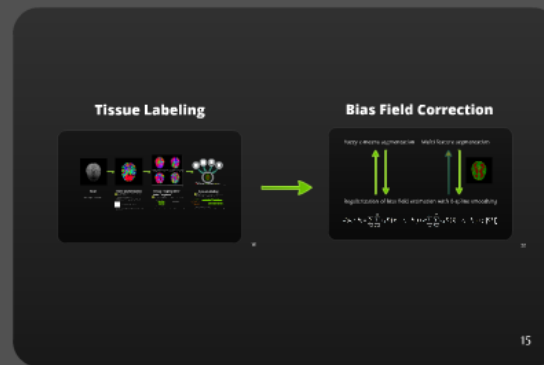
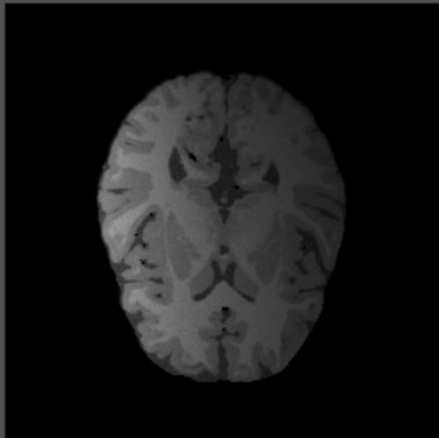
Supervised learning on **tissue** labeling

→ Compared to our goals, we made some modifications based on the original paper (e.g. features)

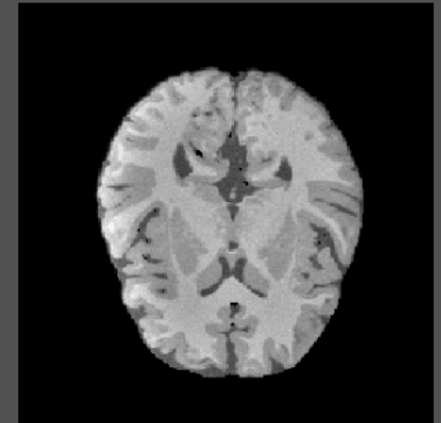
- Next**
- Our replication tailored to tissue labeling
  - Integration of tissue labeling with bias field correction



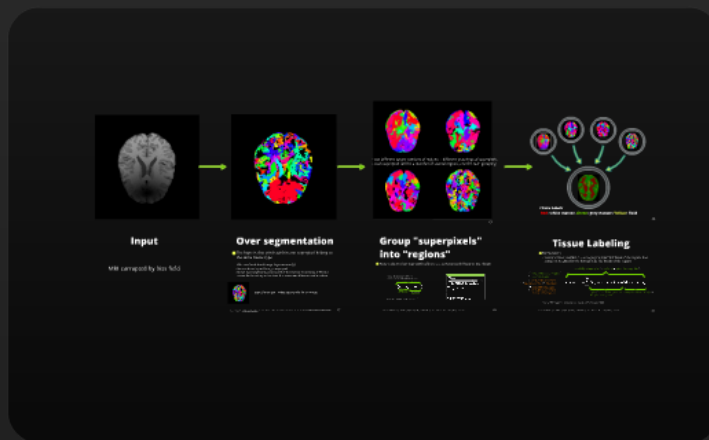
**input**



**output**

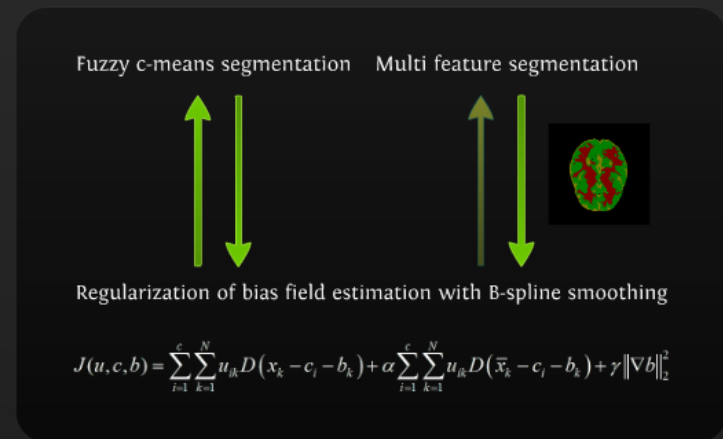


## Tissue Labeling



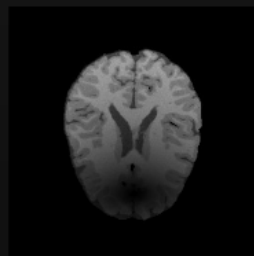
16

## Bias Field Correction



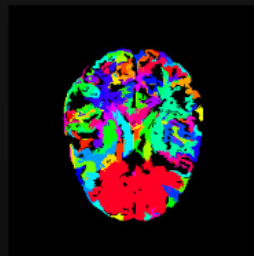
22

# Tissue Labeling



## Input

MRI corrupted by bias field



## Over segmentation

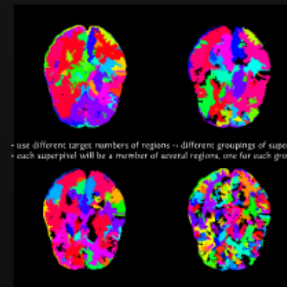
The hope is that pixels within one superpixel belong to the same tissue type

Efficient Graph-based Image Segmentation III

- Start with each pixel being a superpixel
- Merge two neighboring superpixels if the minimum statistical difference across the boundary is less than the maximum difference within them



typically we get 10,000 superpixels for an image



## Group "superpixels" into "regions"

Regions (larger than superpixels) show as a compact useful feature (e.g. shape)



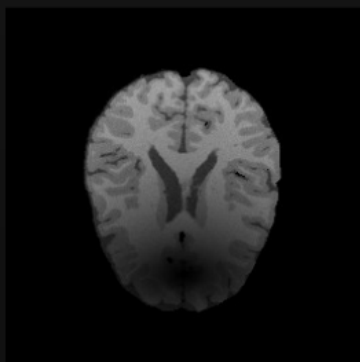
## Tissue Labeling

Formulation

Superpixel label confidence = average of label likelihoods of the regions that contain it, weighted by the homogeneity likelihood of the regions

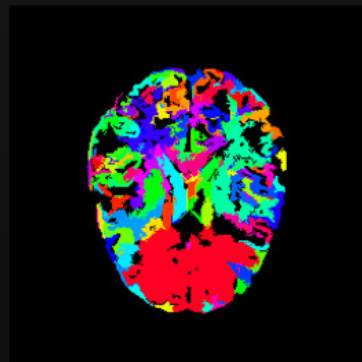
$$C_i = \frac{1}{|R_i|} \sum_{r \in R_i} \frac{L_r}{|R_r|} \cdot H_r$$

where  $C_i$  is the confidence of superpixel  $i$ ,  $R_i$  is the set of regions containing  $i$ ,  $L_r$  is the label likelihood of region  $r$ ,  $|R_r|$  is the number of superpixels in region  $r$ , and  $H_r$  is the homogeneity likelihood of region  $r$ .



## Input

MRI corrupted by bias field



## Over segmentation

- The hope is that pixels within one superpixel belong to the same tissue type

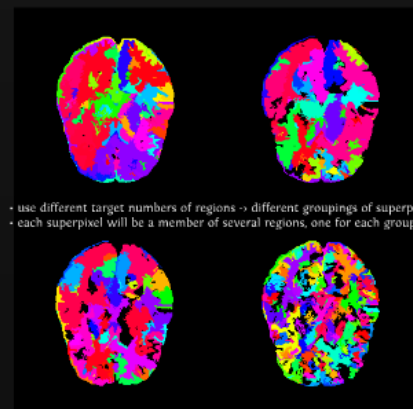
Efficient Graph-based Image Segmentation [3]

- Start with each pixel being a superpixel
- Merge two neighboring superpixels if the minimum intensity difference across the boundary is less than the maximum difference within them



typically we get  $\approx 400$  superpixels for an image

[3] Efros, A. A., and T. S. Sapiro. "Efficient graph-based image segmentation." *International journal of computer vision* 71, no. 3 (2004): 169-184. doi:10.1023/B:VISI.0000024298.80602.8d



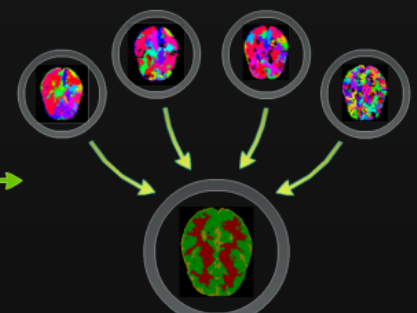
- use different target numbers of regions  $\rightarrow$  different groupings of superpixels
- each superpixel will be a member of several regions, one for each grouping

## Group "superpixels" into "regions"

- Regions (larger than superpixels) allow us to compute useful features (e.g. shape)



[4] Sapiro, T. S., and A. A. Efros. "Efficient graph-based image segmentation." *International journal of computer vision* 71, no. 3 (2004): 169-184. doi:10.1023/B:VISI.0000024298.80602.8d



**Tissue Labels**  
 Red: white matter; Green: grey matter; Yellow: fluid

## Tissue Labeling

### Formulation

- Superpixel label confidence = averaging the label likelihoods of the regions that contain it, weighted by the homogeneity likelihoods of the regions

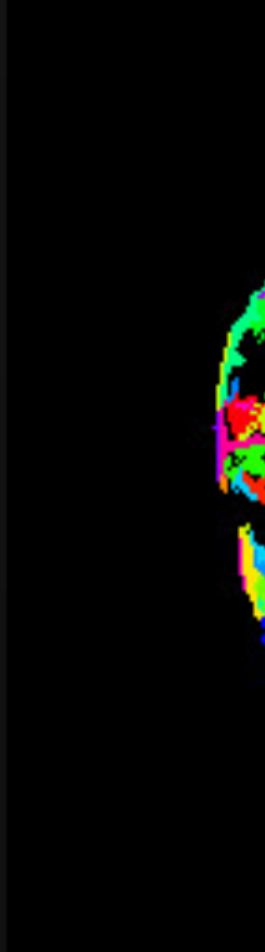
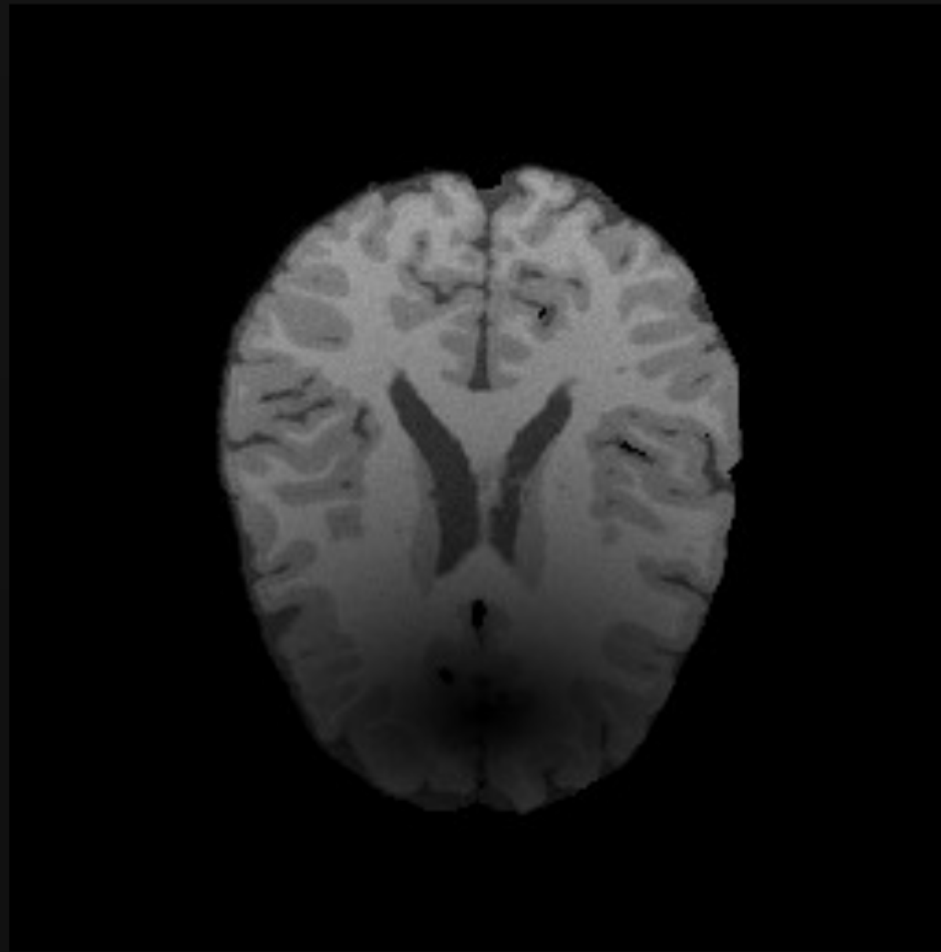
probability of superpixel  $\rightarrow$  labeled as  $r$  given the image data  $\rightarrow$

$$P(y_i = r | x_i) = \sum_{k=1}^K P(y_i = r | x_i, h_k) = \sum_{k=1}^K P(y_i = r | x_i, h_k) \cdot P(h_k | x_i)$$

$K$ : # of hypotheses  
 $h_k$ : region that contains the superpixel for the  $k$ -th hypothesis  
 $r$ : tissue label of the region  
 $x_i$ : image intensity of the region  
 $h_k$ :  $\forall x \in x_i$  the region is homogeneous

trained by logistic regression form of Adaboost [4]

[4] Sapiro, T. S., and A. A. Efros. "Efficient graph-based image segmentation." *International journal of computer vision* 71, no. 3 (2004): 169-184. doi:10.1023/B:VISI.0000024298.80602.8d



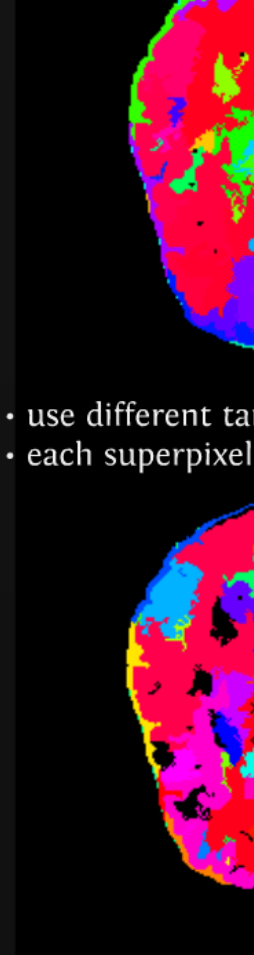
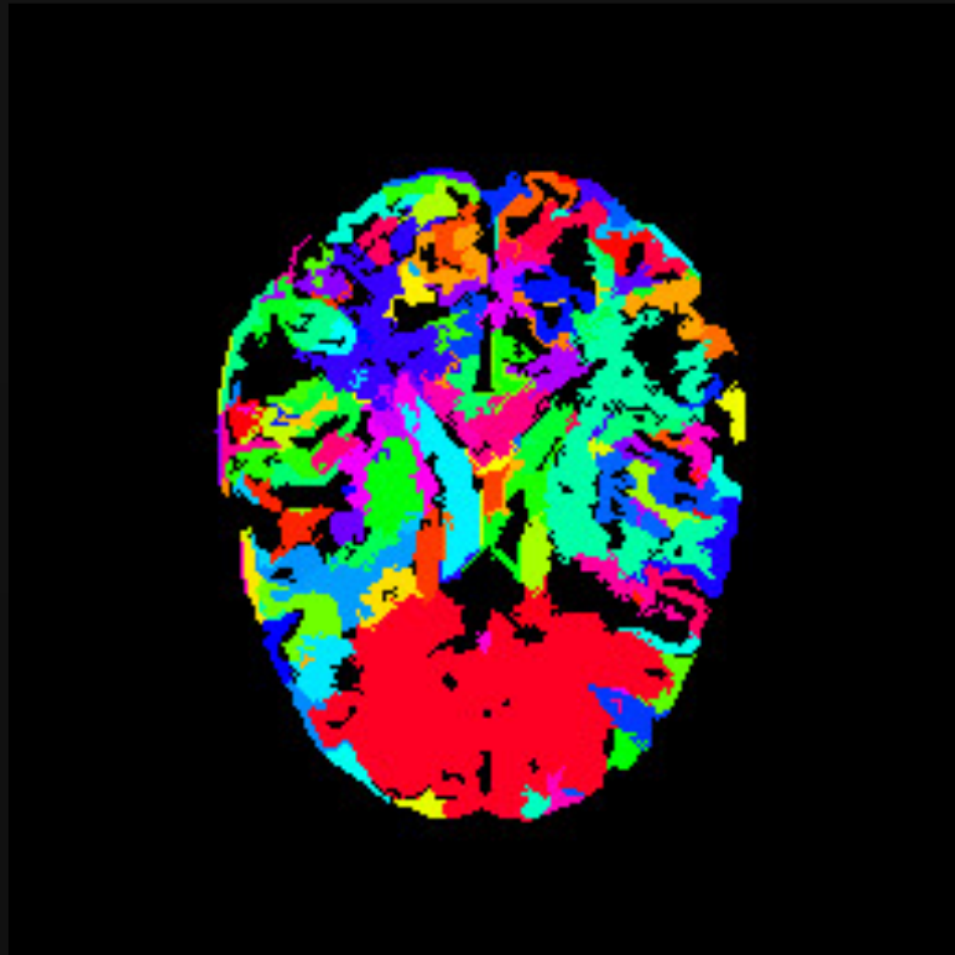
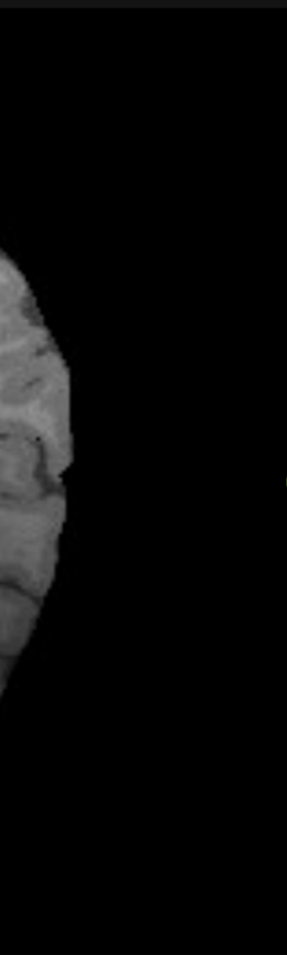
**Input**

MRI corrupted by bias field

**Over**

■ The hope is that the segmentation will be the same tissue

- Efficient Graph-Based
- Start with each pixel
- Merge two neighboring pixels across the boundary



- use different target number of superpixels
- use different target number of superpixels for each superpixel

## Over segmentation

- The hope is that pixels within one superpixel belong to the same tissue type

Efficient Graph-Based Image Segmentation [3]

- Start with each pixel being a superpixel
- Merge two neighboring superpixels if the minimum intensity difference across the boundary is less than the maximum difference within them

## Group into

- Regions (larger)

• eg. target number of superpixels  
• Group superpixels

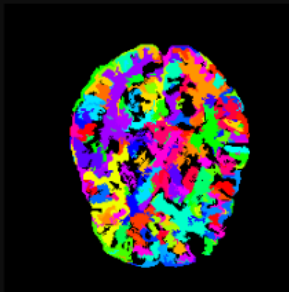
field

# Over segmentation

- The hope is that pixels within one superpixel belong to the same tissue type

Efficient Graph-Based Image Segmentation [3]

- Start with each pixel being a superpixel
- Merge two neighboring superpixels if the minimum intensity difference across the boundary is less than the maximum difference within them



typically we got  $\approx 400$  superpixels for an image

[3] P. F. Felzenszwalb and D. P. Huttenlocher, "Efficient graph-based image segmentation," International Journal of Computer Vision, vol. 59, no. 2, pp. 167-181, 2004. <http://www.cs.cornell.edu/~dph/papers/seg-ijcv.pdf>  
source available online: <http://cs.brown.edu/~pff/segment/>

# Group "superpixels" into "regions"

- Regions (larger than superpixels) allow us to compute useful features (e.g. shape)


- eg. target number of regions = 50
- Group superpixels into regions based on

likelihood of two superpixels  $i, j$  have the same label

$$P(y_i = y_j | |x_i - x_j|)$$

$x_i$ : tissue label of superpixel  $i$  ; absolute differences of  
 $x_j$ : tissue label of superpixel  $j$  ; features of superpixel  $i$   
 $x_i$ : features of superpixel  $i$  ;

trained by logistic regression form of Adaboost [4]

Feature Description
Intensity I1: T1 intensity
Texture  X1: LM filters: mean absolute response (15 filters) X2: LM filters: histogram of maximum responses (15 bins)
Location L1: normalized x and y, mean L2: relative location to center point. L3: relative distance to center point
Shape S1: number of pixels in a superpixel S2: normalized area in image S3: ratio of width by height of a superpixel

[4] M. Collins, R. Schapire, and Y. Singer, "Logistic regression, adaboost and bregman distances," Machine Learning, vol. 48, no. 1-3, 2002.



- eg. target number of regions = 50
- Group superpixels into regions based on

likelihood of two superpixels  $i, j$  have the same label

$$P(y_i = y_j | |\mathbf{x}_i - \mathbf{x}_j|)$$

$y_i$  : tissue label of superpixel  $i$   
 $y_j$  : tissue label of superpixel  $j$

absolute differences of  
 $x_i$  : features of superpixel  $i$   
 $x_j$  : features of superpixel  $j$

trained by logistic regression form of Adaboost [4]

## Feature Description

### Intensity

I1: T1 intensity

### Texture



LM filter bank, Vision Geometry Group,  
University of Oxford  
<http://www.robots.ox.ac.uk/~vgg/research/texclass/filters.html>

X1: LM filters: mean absolute response (15 filters)

X2: LM filters: histogram of maximum responses (15 bins)

### Location

L1: normalized x and y, mean

L2: relative location to center point.

L3: relative distance to center point

### Shape

S1: number of pixels in a superpixel

S2: normalized area in image

S3: ratio of width by height of a superpixel

# Group "superpixels" into "regions"

- Regions (larger than superpixels) allow us to compute useful features (e.g. shape)


- eg. target number of regions = 50
- Group superpixels into regions based on

likelihood of two superpixels  $i, j$  have the same label

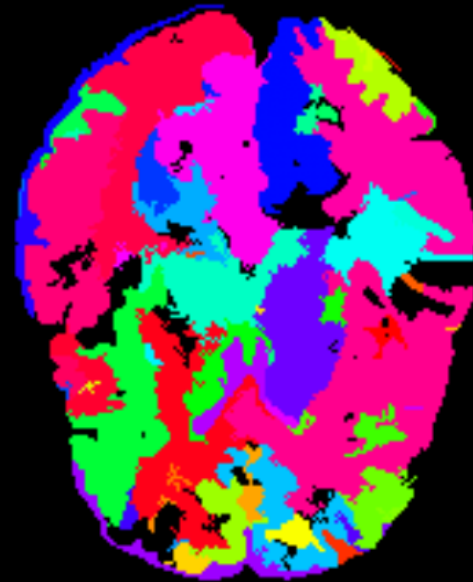
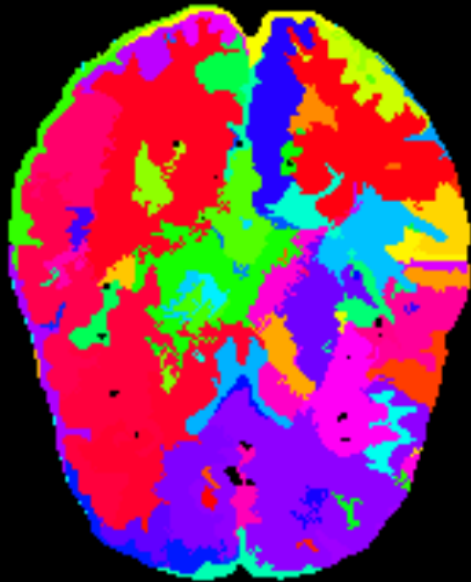
$$P(y_i = y_j | |x_i - x_j|)$$

$x_i$ : tissue label of superpixel  $i$  ; absolute differences of  
 $x_j$ : tissue label of superpixel  $j$  ; features of superpixel  $i$   
 $x_j$ : features of superpixel  $j$

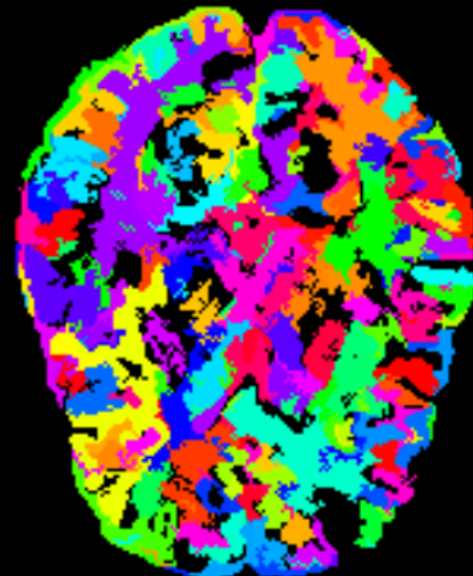
trained by logistic regression form of Adaboost [4]

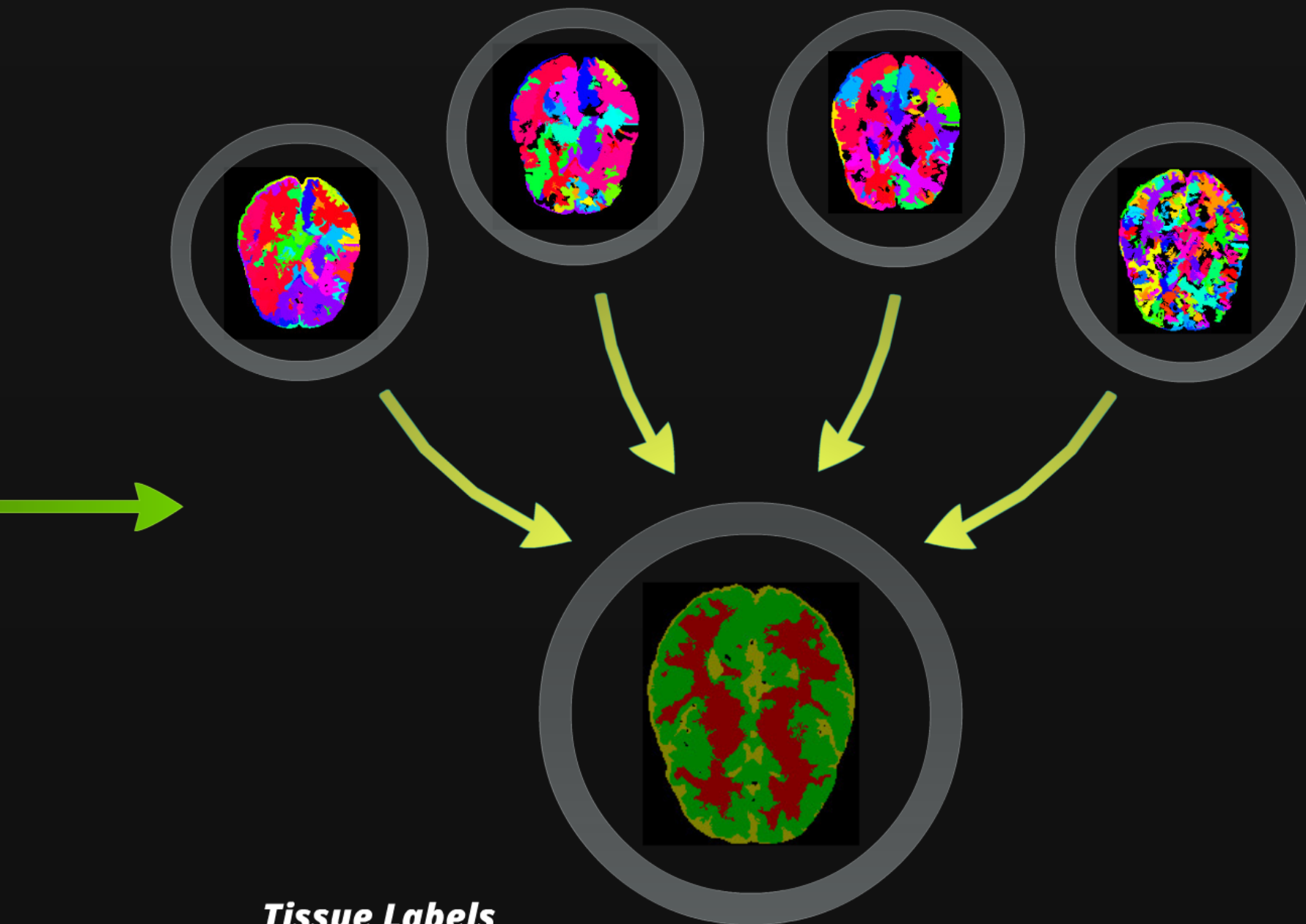
Feature Description
Intensity I1: T1 intensity
Texture  X1: LM filters: mean absolute response (15 filters) X2: LM filters: histogram of maximum responses (15 bins)
Location L1: normalized x and y, mean L2: relative location to center point. L3: relative distance to center point
Shape S1: number of pixels in a superpixel S2: normalized area in image S3: ratio of width by height of a superpixel

[4] M. Collins, R. Schapire, and Y. Singer, "Logistic regression, adaboost and bregman distances," Machine Learning, vol. 48, no. 1-3, 2002.



- use different target numbers of regions -> different groupings of superpixels
- each superpixel will be a member of several regions, one for each grouping





***Tissue Labels***

**Red:** white matter; **Green:** grey matter; **Yellow:** fluid

# Tissue Labeling

## ■ Formulation

- Superpixel label confidence = averaging the label likelihoods of the regions that contain it, weighted by the homogeneity likelihoods of the regions

probability of superpixel  $i$  labeled as  $v$  given the image data  $x$

$y_i$  : tissue label of superpixel  $i$

$n_h$  : # of hypothesis

$j^i$  : region that contains the  $i^{th}$  superpixel for the  $j^{th}$  hypothesis

$y_{ji}$  : tissue label of the region

$h_{ji}$  : homogeneity of the region

$h_{ji} = homo$  : the region is homogeneous

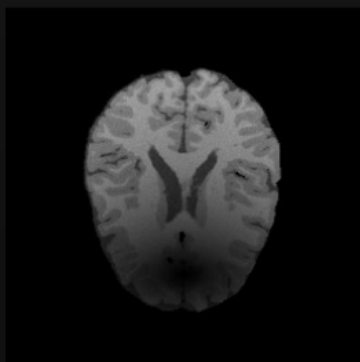
$$C(y_i = v | \mathbf{x}) = \sum_j^{n_h} P(y_{ji} = v | \mathbf{x}, h_{ji} = homo) P(h_{ji} = homo | \mathbf{x})$$

region  $ji$  label confidence given that the region is homogeneous

homogeneity likelihood of region  $ji$

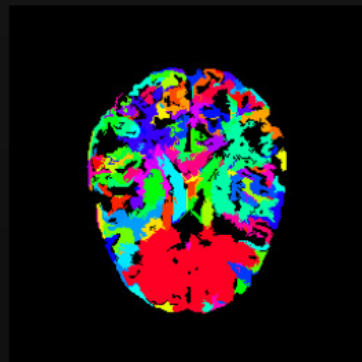
trained by logistic regression form of Adaboost [4]

[4] M. Collins, R. Schapire, and Y. Singer. "Logistic regression, adaboost and bregman distances," Machine Learning, vol. 48, no. 1-3, 2002.



## Input

MRI corrupted by bias field



## Over segmentation

- The hope is that pixels within one superpixel belong to the same tissue type

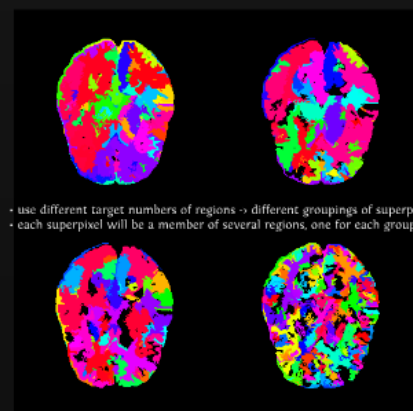
Efficient Graph-based Image Segmentation [3]

- Start with each pixel being a superpixel
- Merge two neighboring superpixels if the minimum intensity difference across the boundary is less than the maximum difference within them



typically we get  $\approx 400$  superpixels for an image

[3] Efros, A. A., and T. S. Lee. "Efficient graph-based image segmentation." *Proceedings of the IEEE conference on computer vision and pattern recognition*. 2004.



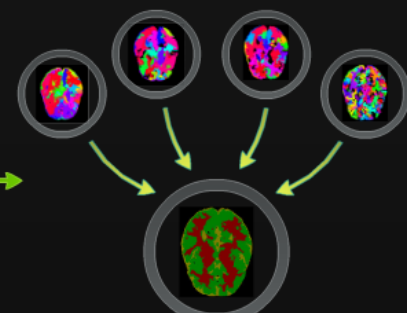
- use different target numbers of regions -> different groupings of superpixels
- each superpixel will be a member of several regions, one for each grouping

## Group "superpixels" into "regions"

- Regions (larger than superpixels) allow us to compute useful features (e.g. shape)



[4] Felzenszfeld, A., and P. H. Huttenlocher. "Efficient graph-based image segmentation." *International journal of computer vision* 59(2): 167-181, 2004.



**Tissue Labels**  
 Red: white matter; Green: grey matter; Yellow: fluid

## Tissue Labeling

### Formulation

- Superpixel label confidence = averaging the label likelihoods of the regions that contain it, weighted by the homogeneity likelihoods of the regions

probability of superpixel  $\cdot$  labeled as  $\mu$  given the image data  $\cdot$

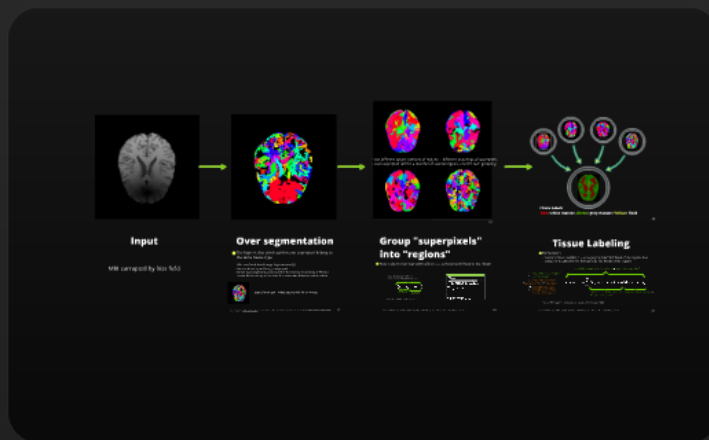
$$P(\mu | x) = \sum_{r \in R} P(\mu | r) \cdot P(r | x)$$

$\mu$ : tissue label of superpixel  
 $R$ : set of regions  
 $P(\mu | r)$ : region that contains the superpixel for the  $\mu$  tissue label  
 $P(r | x)$ : homogeneity of the region  
 $\mathbf{h}_r$ :  $\mathbf{h}_r = \mathbf{h}(\mathbf{x}_r)$ : the region's homogeneity  
 $P(r | x) = \frac{1}{Z} \exp(-\lambda \sum_{i,j \in r} |x_i - x_j|)$

trained by logistic regression form of Adaboost [4]

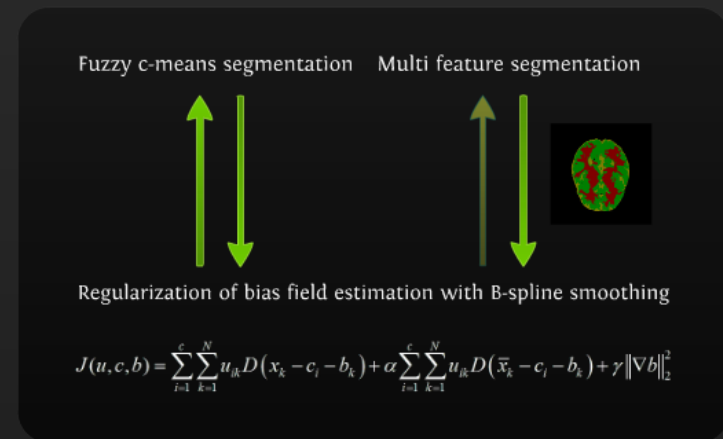
[4] Felzenszfeld, A., and P. H. Huttenlocher. "Efficient graph-based image segmentation." *International journal of computer vision* 59(2): 167-181, 2004.

## Tissue Labeling



16

## Bias Field Correction



22

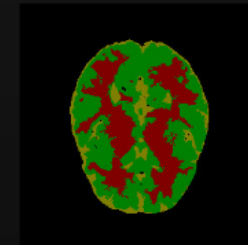
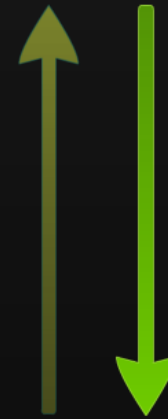
$$J(u, c, b) = \sum_{l=1}^c \sum_{k=1}^N u_{lk} D(x_k - c_l - b_k) + \alpha \sum_{l=1}^c \sum_{k=1}^N u_{lk} D(\bar{x}_k - c_l - b_k) + \gamma \|\nabla b\|_2^2$$



# Bias Field Correction

Fuzzy c-means segmentation

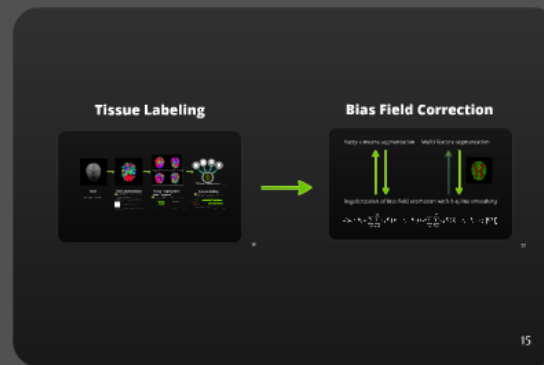
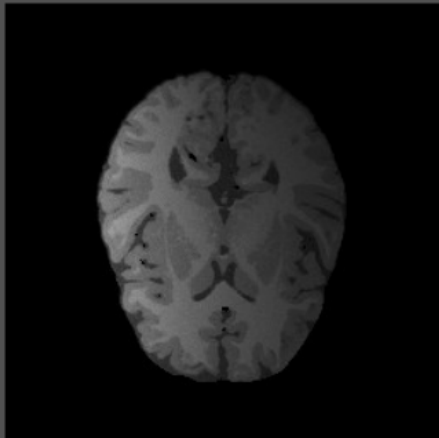
Multi feature segmentation



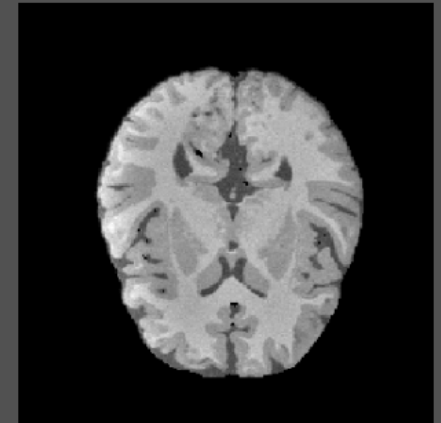
Regularization of bias field estimation with B-spline smoothing

$$J(u, c, b) = \sum_{i=1}^c \sum_{k=1}^N u_{ik} D(x_k - c_i - b_k) + \alpha \sum_{i=1}^c \sum_{k=1}^N u_{ik} D(\bar{x}_k - c_i - b_k) + \gamma \|\nabla b\|_2^2$$

**input**



**output**

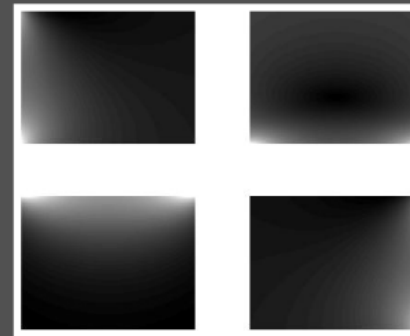


# Experiments

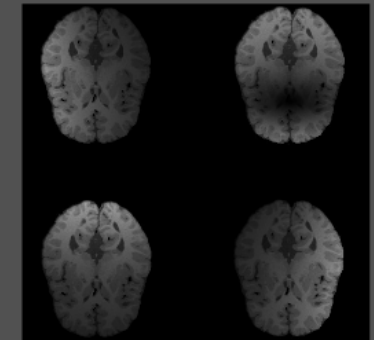
## ■ Dataset

### Synthetic Data

- no-bias T1 image and tissue label from BrainWeb [5]
- Artificial bias field using Prof. Fessler's code [6]



Bias-field Pattern



same image with different bias field

## ■ Experiment settings

### Train and Test

- Training set: 50 images \* 5 patterns (no bias + 4 bias pattern)
- Test set: 200 images \* 5 patterns

### Quantitative evaluation metric

- Tissue label accuracy: average labeling accuracy of each pixel
- Normalized Root Mean Square Error of estimated bias field

### Baseline

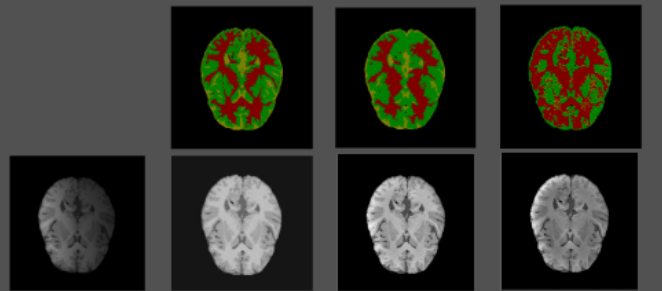
- Fuzzy C-means based bias field correction

[5]: <http://brainweb.bic.mni.mcgill.ca/brainweb/>

[6]: <http://web.eecs.umich.edu/~fessler/code/index.html>

# Experiments

## Qualitative Result



Input Image   ground truth   Proposed Method   Fuzzy c-means Bias Correction

25

## Segmentation Result

Methods	Fuzzy C-Means	Fuzzy C-Means with bias field correction	Multi-segmentation
Image with no bias	82.1%	76.7%	79.2%
Image with bias	22.3%	31.6%	73.4%

- 40% of improvement in segmentation is achieved
- Multi-features is more robust to tissue labeling in image with bias field.

26

## Robust Analysis

### Ablation study on features

Features	All	intensity	texture	location	shape
without the feature	-	68.7%	72.7%	71.3%	73.0%
With only the feature	73.4%	63%	71.2%	63.9%	46.2%

### Bias Pattern Cross Testing

- Classifier trained on clean data
  - is most sensitive to bias field.
  - relies more on intensity information.
- Classifier trained on single pattern
  - encodes pattern information.
  - performs best on same pattern data.
  - still good enough for other pattern.
- Classifier trained on mix data
  - is the most robust one across all pattern.
  - rely less on pattern information.

train data \ test data	No Bias	Pattern 1	Pattern 2	Pattern 3	Pattern 4	mix
No Bias	0.81468	0.56713	0.68967	0.6954	0.56636	0.79186
Pattern 1	0.37195	0.79230	0.68240	0.71486	0.66233	0.76642
Pattern 2	0.47871	0.52011	0.76098	0.65522	0.51161	0.69857
Pattern 3	0.43051	0.64506	0.74934	0.77822	0.64108	0.75796
Pattern 4	0.39920	0.64886	0.67136	0.71172	0.77258	0.75851

Green: The best classifier for a data set. Yellow: The second best classifier for a data set.

27

## Bias Field Correction

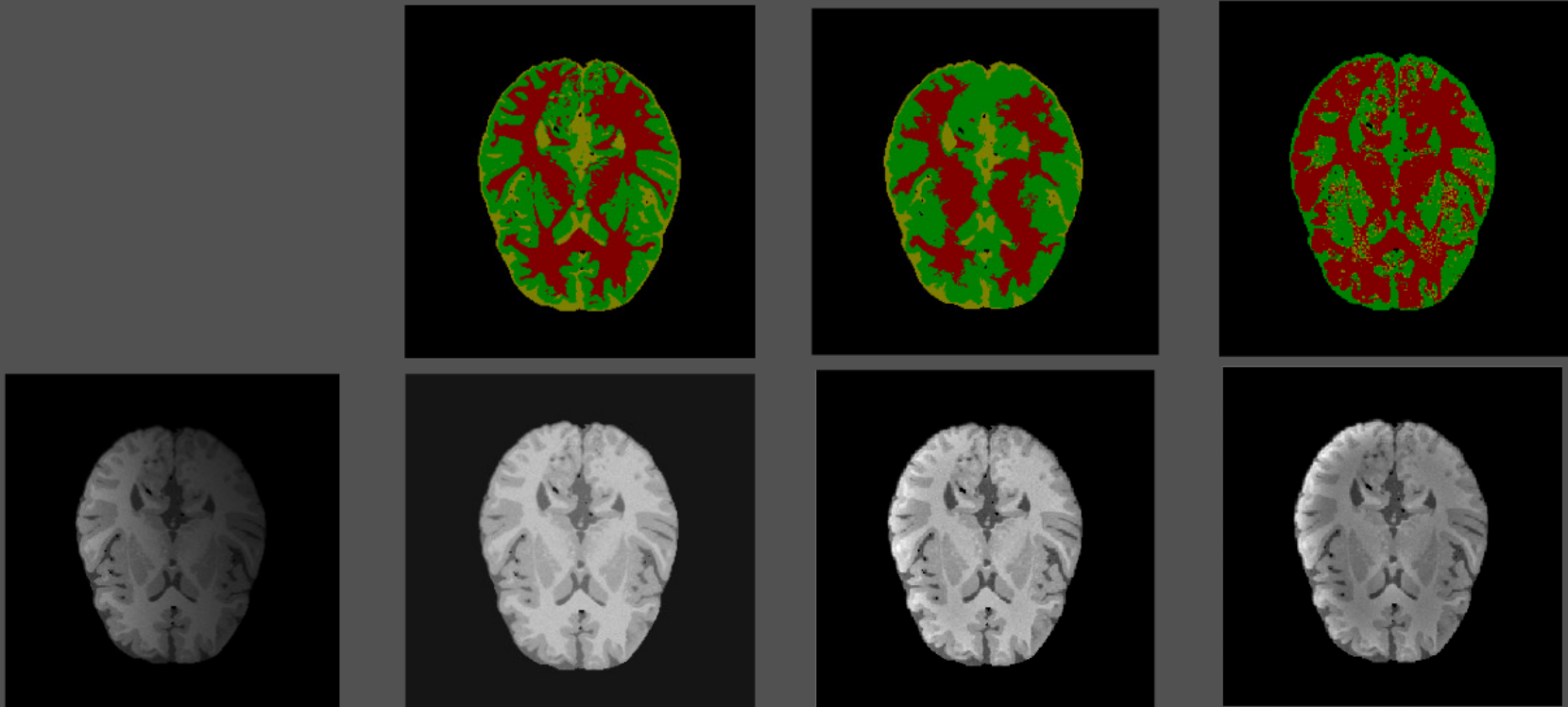
### NRMSE between estimated bias field and ground truth

Bias Pattern	Pattern 1	Pattern 2	Pattern 3	Pattern 4
Proposed method	0.1789	0.4300	0.1470	0.1568
Fuzzy c-means	0.1944	0.4995	0.1643	0.1860

- Our approach provides a better estimation on bias field.
- When the bias field is stronger, the performance improvement is more obvious (e.g. Pattern 2).

28

# Qualitative Result



Input Image

ground truth

Proposed Method

Fuzzy c-means Bias  
Correction

# Segmentation Result

Methods	Fuzzy C-Means	Fuzzy C-Means with bias field correction	Multi-segmentation
Image with no bias	82.1%	76.7%	79.2%
Image with bias	22.3%	31.6%	73.4%

- **40%** of improvement in segmentation is achieved
- Multi-features is more robust to tissue labeling in image with bias field.

# Robust Analysis

## Ablation study on features

Features	All	intensity	texture	location	shape
without the feature	-	68.7%	72.7%	71.3%	73.0%
With only the feature	73.4%	63%	71.2%	63.9%	46.2%

## Bias Pattern Cross Testing

- Classifier trained on clean data
  - is most sensitive to bias field.
  - relies more on intensity information.
- Classifier trained on single pattern
  - encodes pattern information.
  - performs best on same pattern data.
  - still good enough for other pattern.
- Classifier trained on mix data
  - is the most robust one across all pattern.
  - rely less on pattern information.

train data \ test data	No Bias	Pattern 1	Pattern 2	Pattern 3	Pattern4	mix
No Bias	0.81468	0.56713	0.68967	0.6954	0.56636	0.79186
Pattern 1	0.37195	0.79230	0.68240	0.71486	0.66233	0.76642
Pattern 2	0.47871	0.52011	0.76098	0.65522	0.51161	0.69857
Pattern 3	0.43051	0.64506	0.74934	0.77822	0.64108	0.75796
Pattern 4	0.39920	0.64886	0.67136	0.71172	0.77258	0.75851

Green: The best classifier for a data set Yellow: The second best classifier for a data set

# Bias Field Correction

## NRMSE between estimated bias field and ground truth

Bias Pattern	Pattern 1	Pattern 2	Pattern 3	Pattern 4
Proposed method	<b>0.1789</b>	<b>0.4300</b>	<b>0.1470</b>	<b>0.1568</b>
Fuzzy c-means	0.1944	0.4995	0.1643	0.1860

- Our approach provides a better estimation on bias field.
- When the bias field is stronger, the performance improvement is more obvious (e.g. Pattern 2).



# Conclusion

- Our proposed algorithm provides more **robust tissue labeling** and **bias field estimation** than traditional intensity based method.
- Mature techniques from **other areas** can be really helpful in image processing