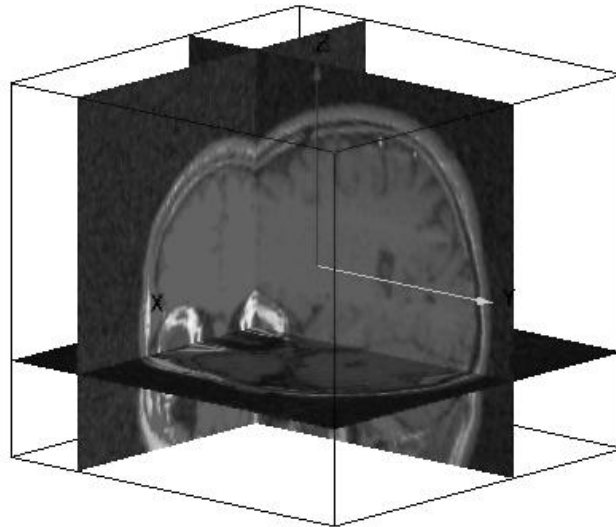


Brain MRI Tissue Segmentation with a Continuous Restricted Boltzmann Machine

Andrew Kope
Daley Lab

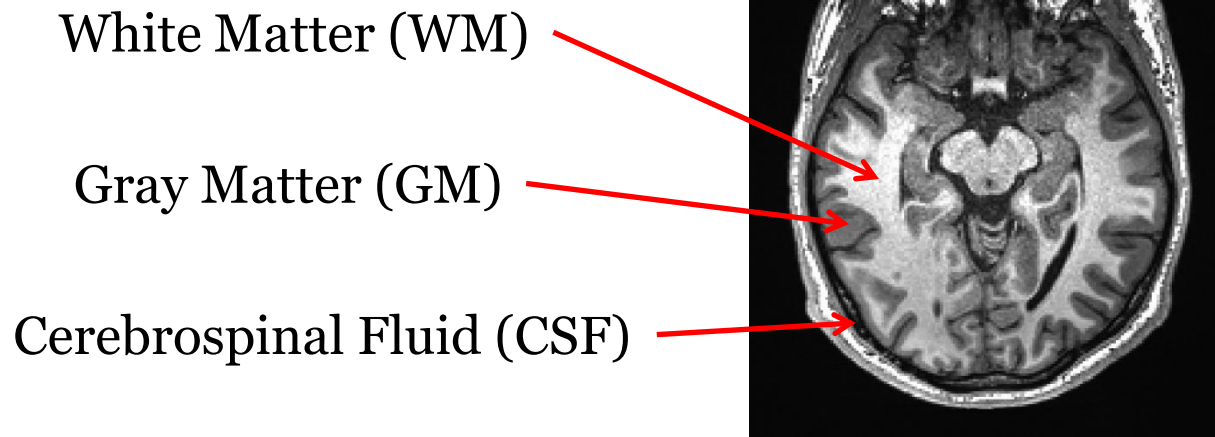
MRI Brain Scans

- 3D volumes - many 2D slices
- Only contain intensity data



MRI Brain Scans

- Three tissue types of interest



Why Perform Tissue Segmentation?

- Build population atlases
- Guide surgeons
- Monitor anatomical changes

Why Perform Tissue Segmentation?

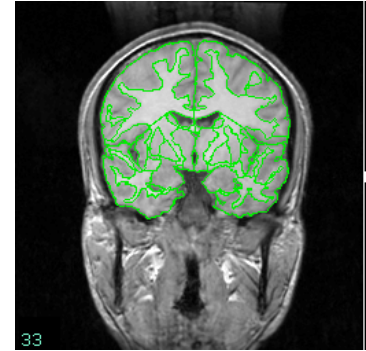
- Build population atlases
- Guide surgeons
- Monitor anatomical changes

- Traditionally done **manually**

Existing Segmentation Algorithms

- Edge Detection
- Region Growing
- K Nearest Neighbours

- Hidden Random Markov Field (FAST)
- Gaussian Probability Model (SPM5)



Justification

- There are already several good MRI tissue segmentation algorithms...

Why investigate another one?

Justification

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Why investigate another one?

- Successful only under narrow conditions

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- Require large datasets and extensive training

Justification

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Why investigate another one?

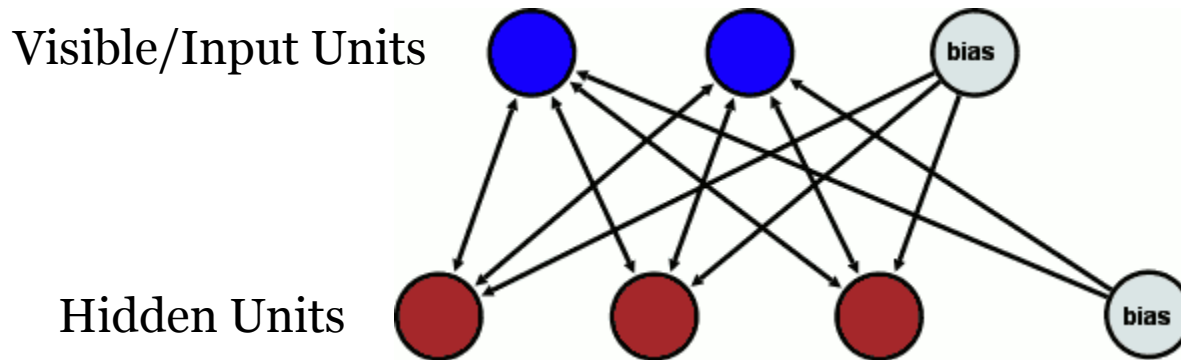
- Successful only under narrow conditions
- Require large datasets and extensive training
- Require additional 'backend' information

Ideal Algorithm:

- Robust to noise
- Require few training cases
- Trained quickly
- Store all information implicitly

The Continuous Restricted Boltzmann Machine (CRBM)

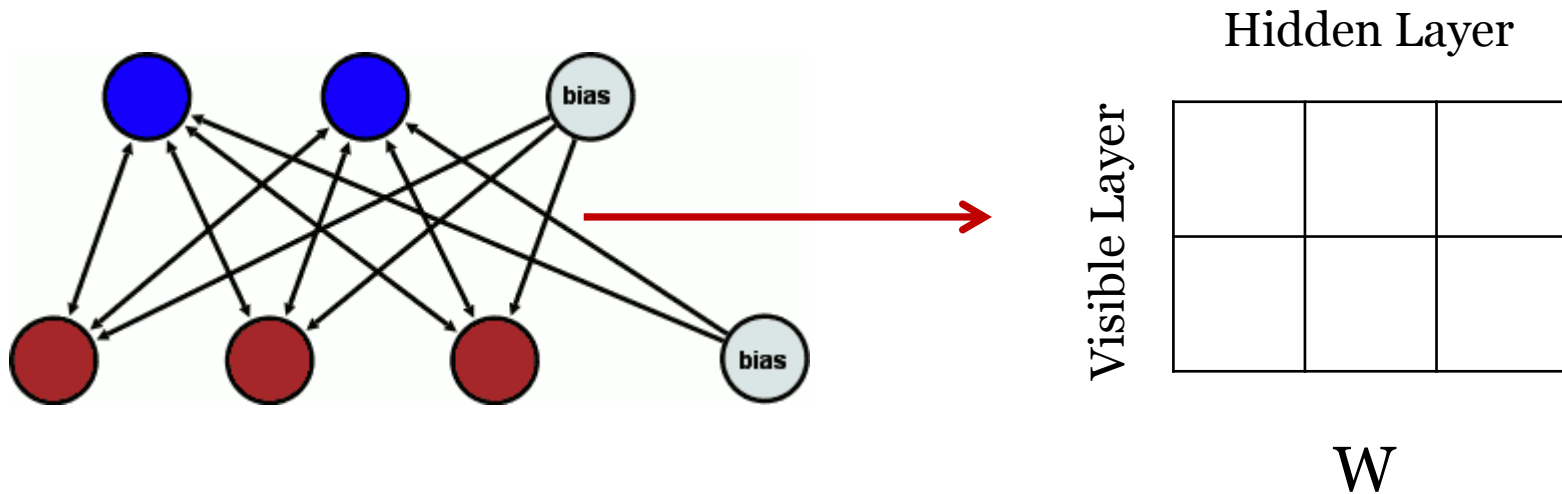
Restricted Boltzmann Machine



- Invented in 1986 by Paul Smolensky
- Popularized recently by Geoffrey Hinton

CRBM: Learning

- Let matrix W be the weights between each pair of nodes in the machine



CRBM: Learning

- Iteratively change the weights in W
- Reflect the input states in the training data

$$\begin{array}{|c|c|c|} \hline & & \\ \hline & & \\ \hline & & \\ \hline \end{array} = \begin{array}{|c|c|c|} \hline & & \\ \hline & & \\ \hline & & \\ \hline \end{array} + \begin{array}{|c|c|c|} \hline & & \\ \hline & & \\ \hline & & \\ \hline \end{array} * \begin{array}{l} \text{Learning} \\ \text{Rate} \end{array}$$

$W_{n+1} \qquad \qquad W_n \qquad \qquad CD_n$

CRBM: Learning

- Iteratively change the weights in W
- Reflect the input states in the training data

$$\begin{array}{|c|c|c|} \hline & & \\ \hline & & \\ \hline & & \\ \hline \end{array} = \begin{array}{|c|c|c|} \hline & & \\ \hline & & \\ \hline & & \\ \hline \end{array} + \begin{array}{|c|c|c|} \hline & & \\ \hline & & \\ \hline & & \\ \hline \end{array} * \begin{array}{l} \text{Learning} \\ \text{Rate} \end{array}$$

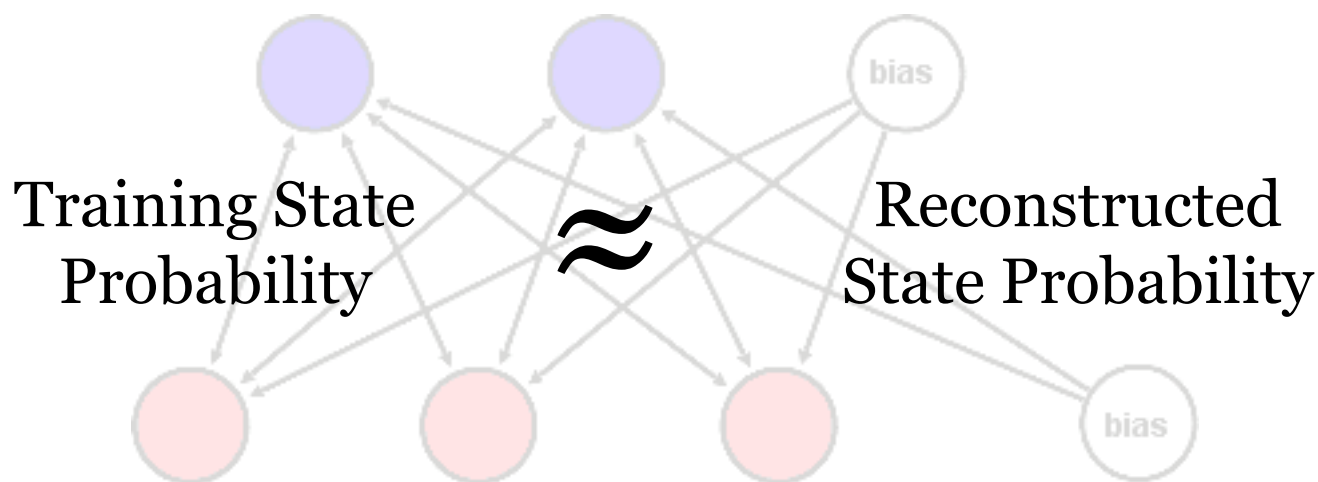
$W_{n+1} \qquad \qquad W_n \qquad \qquad CD_n$

$$\sum (\text{input states} - \text{reconstructed states})^2 < (\text{threshold})$$

Tissue Segmentation with a CRBM

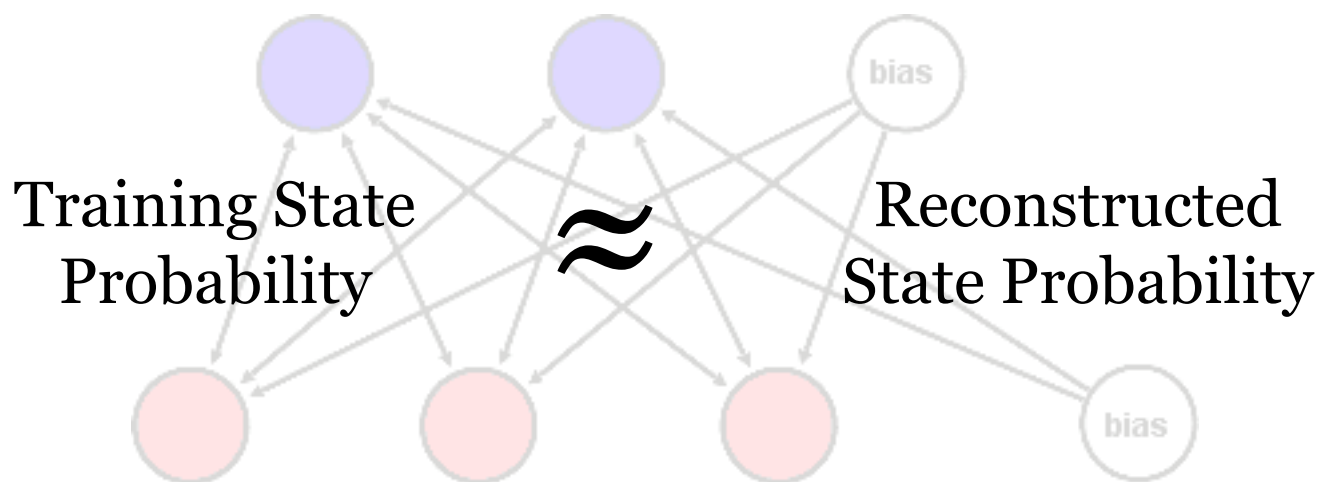
CRBM Tissue Segmentation: Theory

- “Learns” probable visible layer states



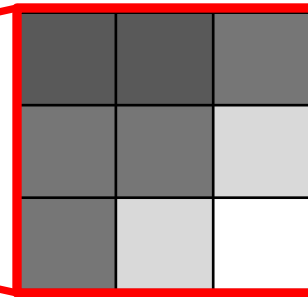
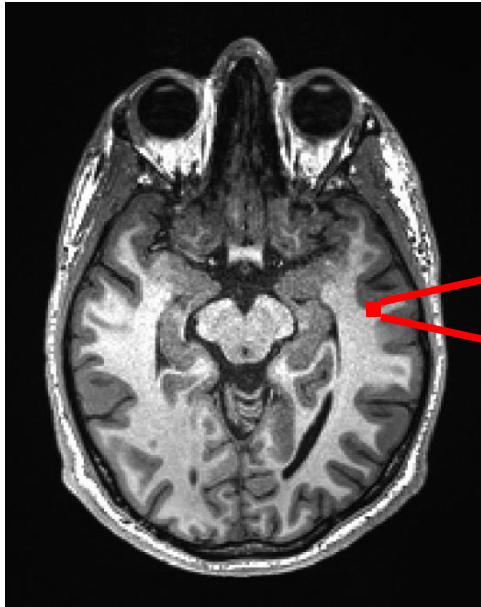
CRBM Tissue Segmentation: Theory

- “Learns” probable visible layer states



- Can reconstruct an **incomplete** input vector

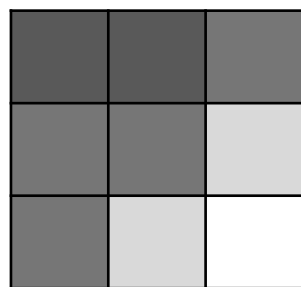
CRBM Tissue Segmentation: Training



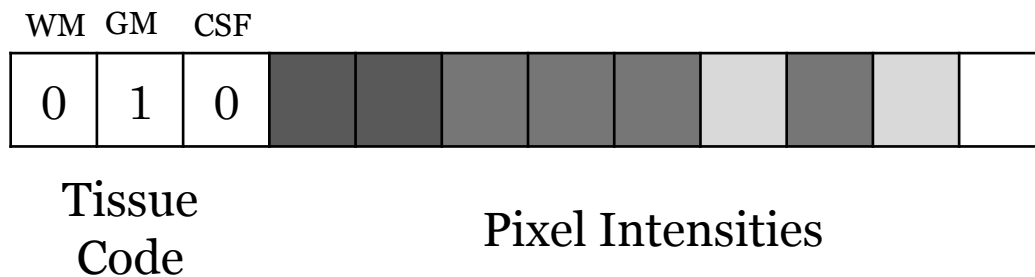
Gray Matter

CRBM Tissue Segmentation: Training

Input Vector: [tissue type code + intensities]



Gray Matter



CRBM Tissue Segmentation: Testing

- Present a partial input vector
- Reconstruct the missing tissue code



reconstruction

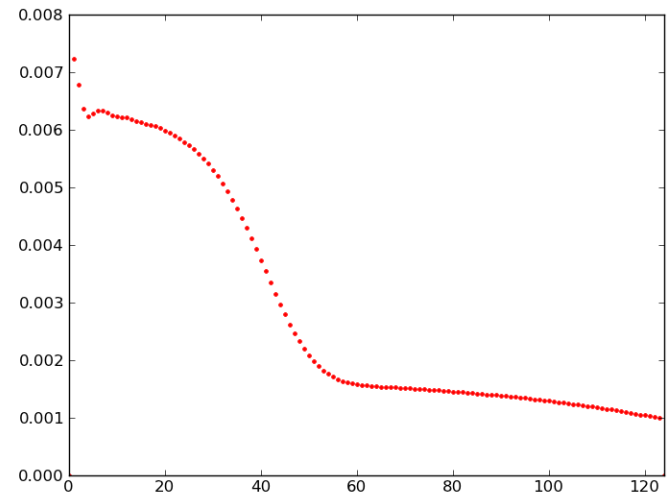


“Gray Matter”

Implementation

Test Case 1

- Hidden Units: 1000
- Learning Rate: 0.65
- Error Threshold: 0.001
- Segments GM/WM/CSF

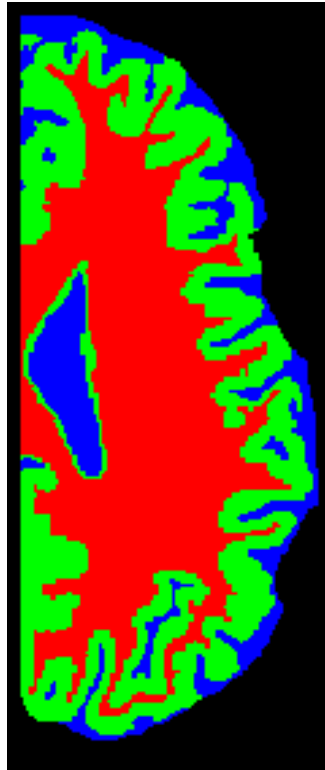


- Dataset from Western University
 - Naïve segmentation
 - 1 120x285 24bit PNG

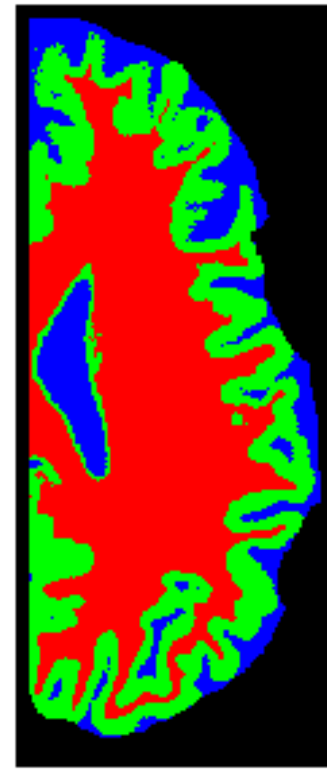
Test Case 1



MRI



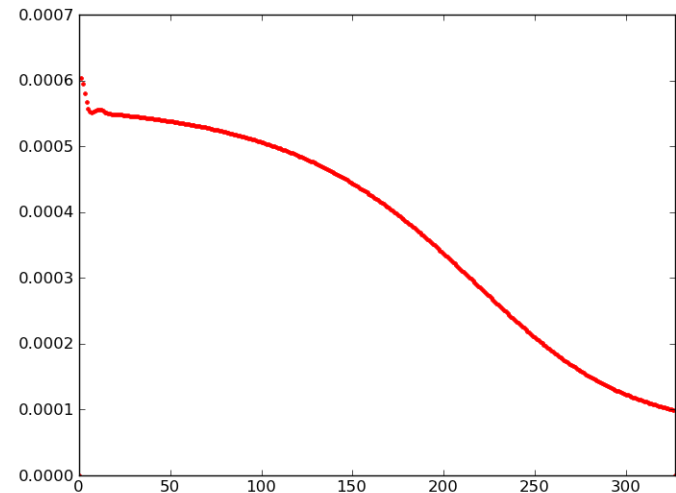
Manual
Segmentation



CRBM
Segmentation

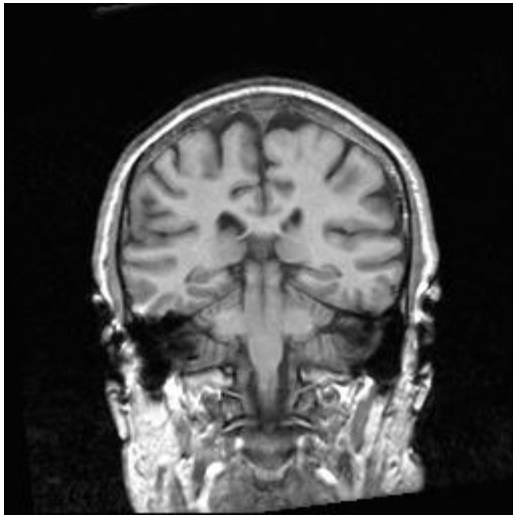
Test Case 2

- Hidden Units: 2000
- Learning Rate: 0.65
- Error Threshold: 0.0001
- Segments GM/WM



- Dataset from Massachusetts General Hospital
 - Expert segmentation
 - 28 256x256 24bit PNGs

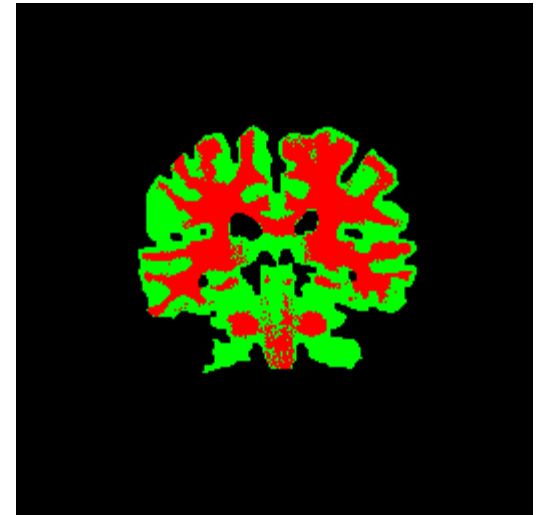
Test Case 2



MRI



Manual
Segmentation



CRBM
Segmentation

Results

- Test Case 1
 - DICE coefficient of 0.91
 - Jaccard index of 0.84
- Test Case 2
 - DICE coefficient of 0.76
 - Jaccard index of 0.61

Current Problems

- Sensitive to MRI noise and low-contrast scans
- Tissues outside cerebrum are misclassified
- Finding a good classification threshold is difficult

Future Improvements

- Improve input vectors
 - Normalize image contrast
 - Include in-volume neighbours
 - Include (x, y, z) coordinates
- Parallelize implementation
- Combine multiple datasets

References

Chung, G., Dinov, I. D., Toga, A. W., & Vese, L. A. (2010). MRI tissue segmentation using a variational multilayer approach. In K. Miller & P. Nielsen (Eds.), *Computational Biomechanics for medicine*, doi: 10.1007/978-1-4419-5874-7_2 York: Psychology Press.

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