CRBMseg: Brain MRI Tissue Segmentation with a Continuous Restricted Boltzmann Machine

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Introduction

We present a novel algorithm for automated brain tissue segmentation on anatomical MRI volumes which employs a continuous restricted Boltzmann machine, called CRBMseg. We also present the results of a pilot performance test on simulated MRI scanner data, and discuss future refinements and threats to the algorithm's validity.

Motivation

Segmentation of brain magnetic resonance imaging (MRI) volumes into distinct tissue types has several applications, including building population atlases of brain tissue types, guiding surgeons in the operating room, and monitoring anatomical changes in the brain.

Existing brain MRI tissue segmentation algorithms such as FAST and SPM5-segment leave room for performance improvements in both processing time and segmentation accuracy; Tsang et al. (2008) tested FAST and SPM5-segment, finding misclassification rates of approximately 10%.

Performance

Trained on a dataset of 23245 pixels, our algorithm was able to classify brain tissues in a small test dataset with a misclassification rate of 9%. Below are data describing CRBMseg's performance on the large simulated testing dataset described in the results section:

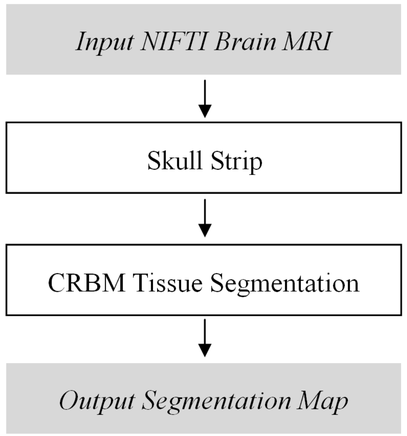
Slice	Dice Coefficient [1]
21	0.780140379851
41	0.784768025255
61	0.761341743422
81	0.757848224837
101	0.766559995837
121	0.761158260411
141	0.754797637145

1. Dice's coefficient measures set agreement, and is given by the formula D(A,B) = 2 |A and B| / (|A| + |B|)

Algorithm

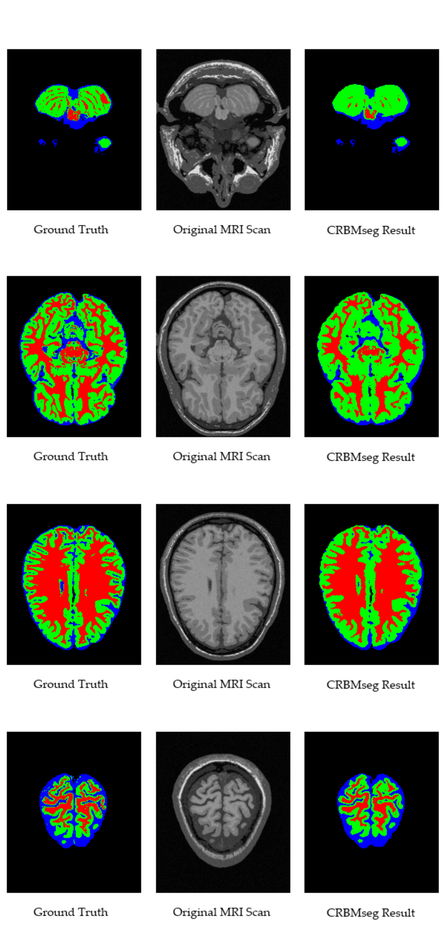
The CRBMseg algorithm uses a two step pipeline to perform the tissue segmentation of an input brain MRI scan. Given an input NIFTI scan, the brain is first isolated from the rest of the image. The scan is then segmented into white matter, gray matter, and cerebrospinal fluid using a continuous restricted Boltzmann machine (CRBM, Hinton & Salakhutdinov, 2006).

To determine the tissue type of a given voxel, the CRBM receives an input vector containing that voxel's intensity, the intensities of its 26 in-volume neighbours, and a blank tissue type code; the CRBM then reconstructs the voxel's tissue type code.



Results

We conducted a pilot performance test of the CRBMseg algorithm on simulated brain MRI data from the Montreal Neurological Institute BrainWeb database (Cocosco et al., 1997). The CRBM was first trained on noiseless data; once training was complete, it was used to segment a novel simulated scan.



Threats

- **The test dataset doesn't use real scanner data.** The BrainWeb dataset provides a ground truth tissue segmentation map, which no other dataset of manually segmented images can provide; having a ground truth map allows us to assess of the performance of the algorithm with perfect knowledge of the 'true' tissue type of each voxel.
- **The current performance of CRBMseg doesn't match other algorithms on large datasets.** The CRBMseg algorithm is still in development. Presented here are the results of a pilot performance test; future refinements of the algorithm to improve both segmentation accuracy and efficiency are planned.

Future Directions

- Fine tune input and training parameters
- Validate with real data
- Parallelize on GPU

References

Cocosco, C.A., Kollokian, V., Kwan, R.K.-S., Evans, A.C. (1997). BrainWeb: Online interface to a 3D MRI simulated brain database. *Proceedings of 3rd International Conference on Functional Mapping of the Human Brain*. Copenhagen. Retrieved from http://www.bic.mni.mcgill.ca/brainweb/

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Thanks

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