

# When Less is More: Improvements in Medical Image Segmentation through Spatial Sub-Sampling

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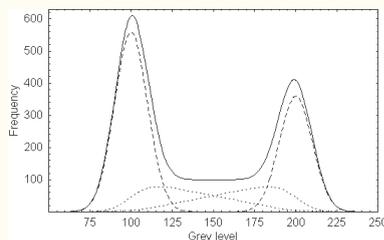
## Introduction

Segmentation of medical image data sets can be performed by fitting a model to the intensity histogram of the data, but this approach must be sub-optimal as it discards all spatial information.

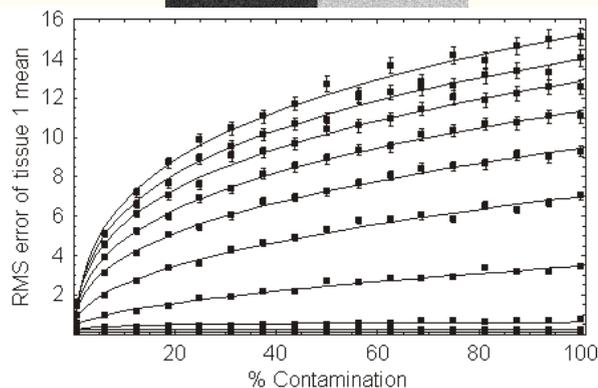
Here we sub-sample the data using the current intensity model at each stage of the fitting process, in order to obtain a largely uncontaminated sample of each pure tissue from which to estimate the tissue model parameters.

## Method

The segmentation algorithm fits a model to the intensity histogram consisting of Gaussian distributions, describing pure tissues, and uniform distributions convolved with Gaussians, describing allowed partial volume contributions.



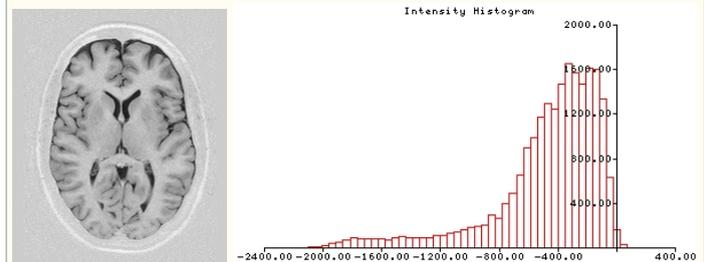
At each iteration of the EM fitting, the current tissue model is used to produce a volume map of each pure tissue. These are binarized, then blurred to prevent imposing hard cuts on the histogram, which would introduce bias. The voxels in the map region are then used to estimate the parameters for the relevant tissue in the next EM iteration.



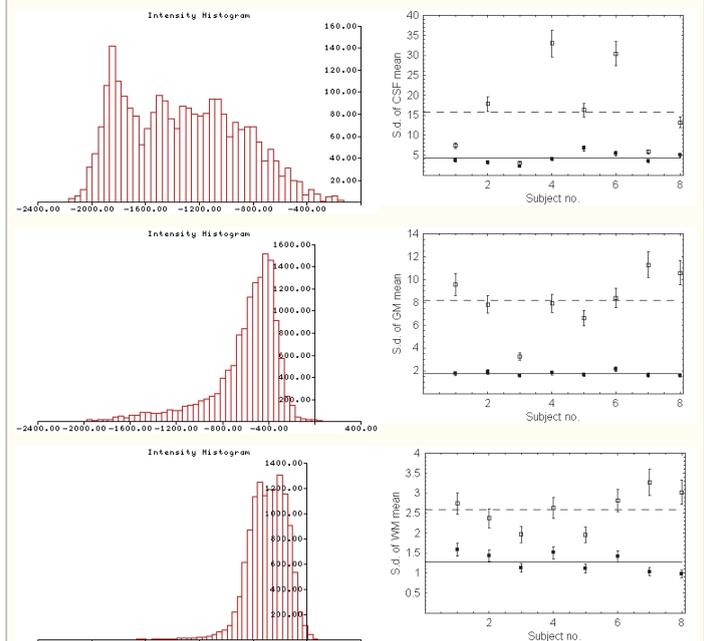
1000 iteration Monte-Carlo: reduction in RMS errors on tissue 1 (left) mean as contamination with tissue 2 (right) is reduced in the simulated data (top), for noise levels from 10 to 100% of the separation between the mean intensities of the tissues.

## Results

IRTSE MR images were collected from eight normal subjects, and Monte-Carlo experiments performed. Gaussian noise with an s.d. equal to the image noise was added, and the segmentation applied using a three-tissue model containing terms for GM, WM and CSF. 100-iteration MCs were performed both with and without spatial sub-sampling, and the standard deviations of the estimated mean tissue intensities were compared.



Example IRTSE MR image (left) and intensity histogram (right).



Sub-sampled histograms (left) and parameter stabilities (right) for segmentations without (open points) and with (filled points) spatial sub-sampling.

## Conclusion

Spatially directed sub-sampling of the data can improve the accuracy of the tissue model parameter estimation without introducing bias.

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