Cluster analysis for brain PET image segmentation

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Introduction

- Our aim is to study methods for the cluster analysis of the time activity curves in a dynamic PET brain study.
- Previous work in PET image segmentation using cluster analysis include e.g. :
    - Ashburner et al. (Academic Press 1996)
    - Wong. et al. (IEEE Nucl. Sci. 2002)
    - Chen et al. (IPMI-2001)
- Applications include automatic extraction of reference regions for computing parametric images (Chen et al.).

Methods

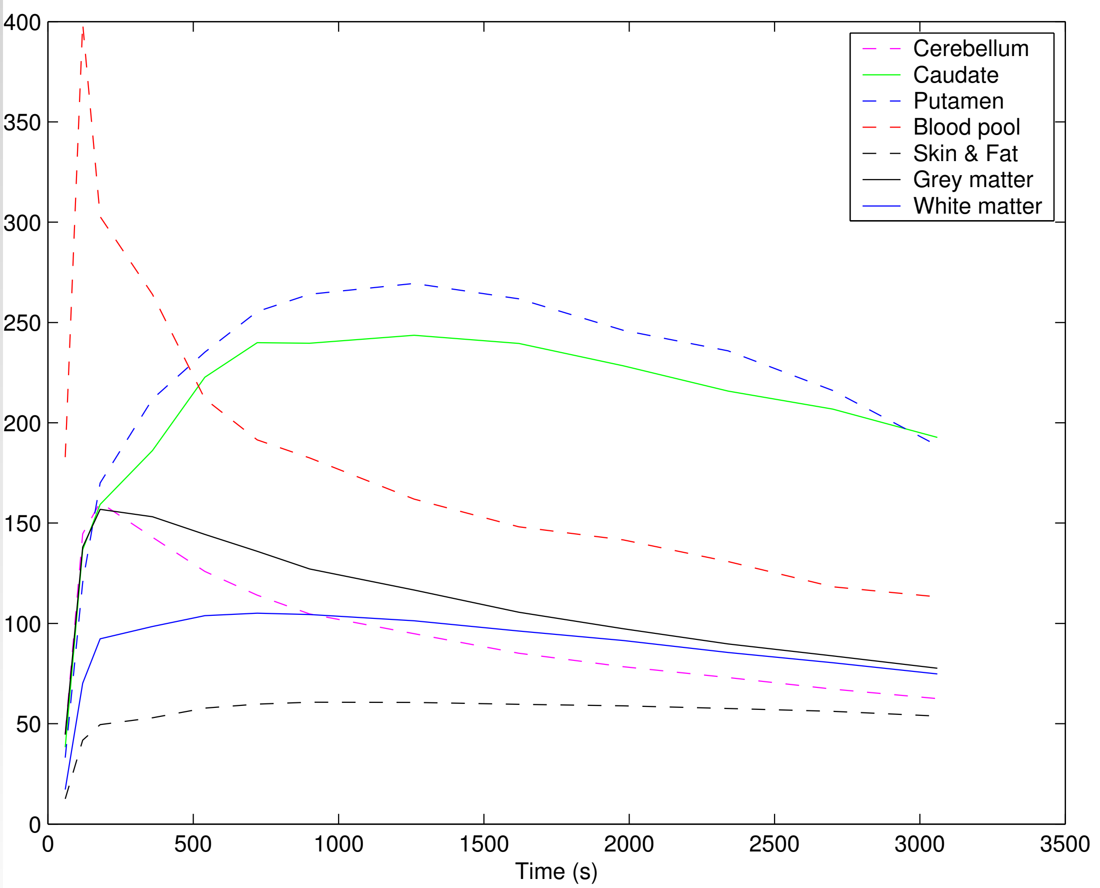
- The aim was to compare pattern recognition methods for the PET segmentation.
- Three methods were selected:
  - EM-algorithm for clustering based on data description by a finite mixture of Gaussian densities
  - The fuzzy C-means (FCM) algorithm for fuzzy clustering
  - Independent Component Analysis (ICA)

Material

- The radiopharmaceutical considered was C-11 labeled Raclopride.
- 1 dynamic Monte Carlo simulated phantom image based on the anatomical Zubal phantom and the SORTEO Monte Carlo PET simulator (Reilhac et al. 2004 IEEE-TNS) .
- 5 dynamic brain PET studies, healthy subjects, from Turku PET centre
- Each dynamic volume contained 13 frames.

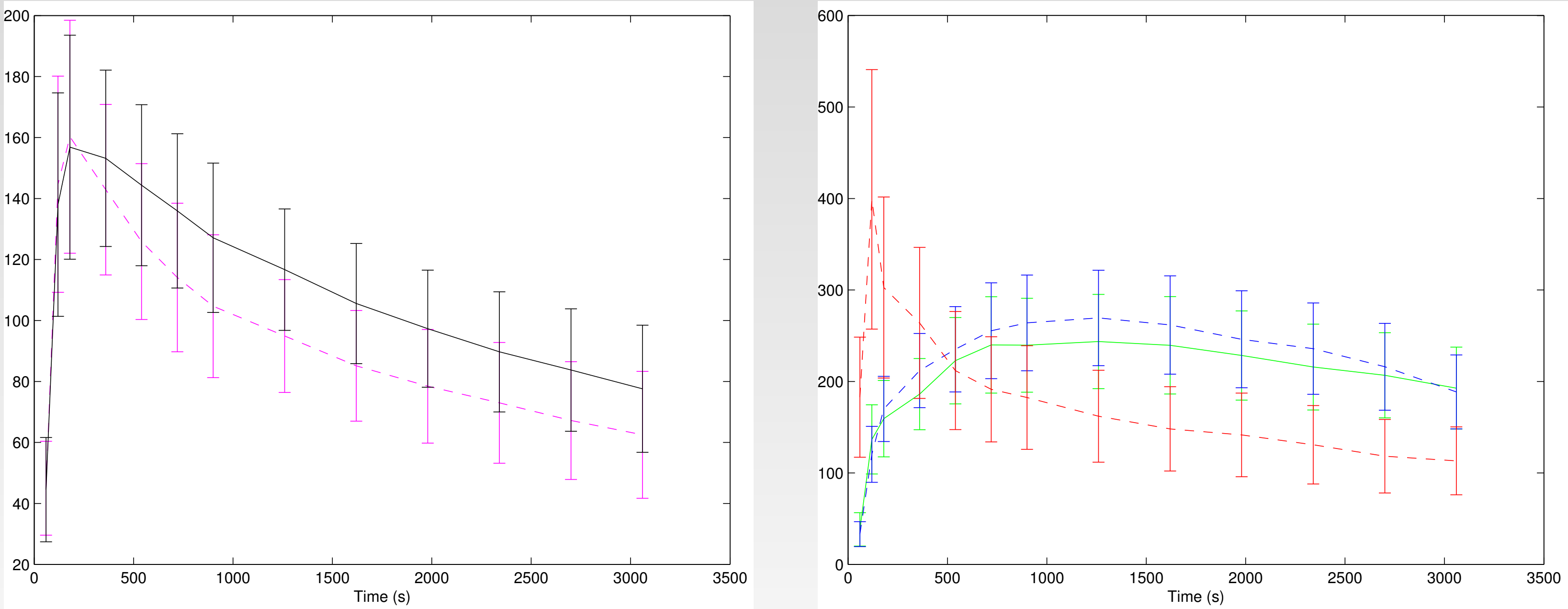
TACs

TACs for different brain structures calculated based on the SORTEO phantom and the ground truth anatomy.



Within class variation

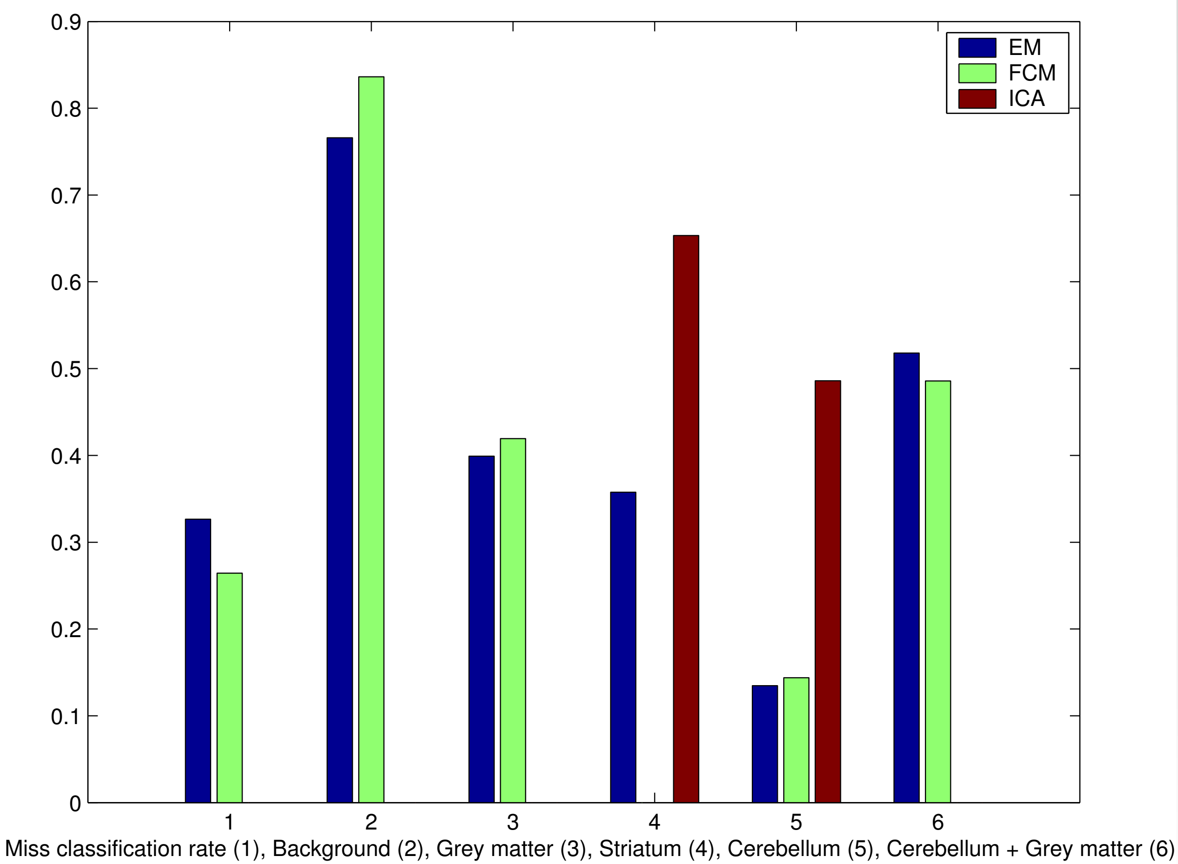
Plots with standard deviations of class conditional marginal densities. From these it is clear that the class overlap is notable if considering a single time activity value.



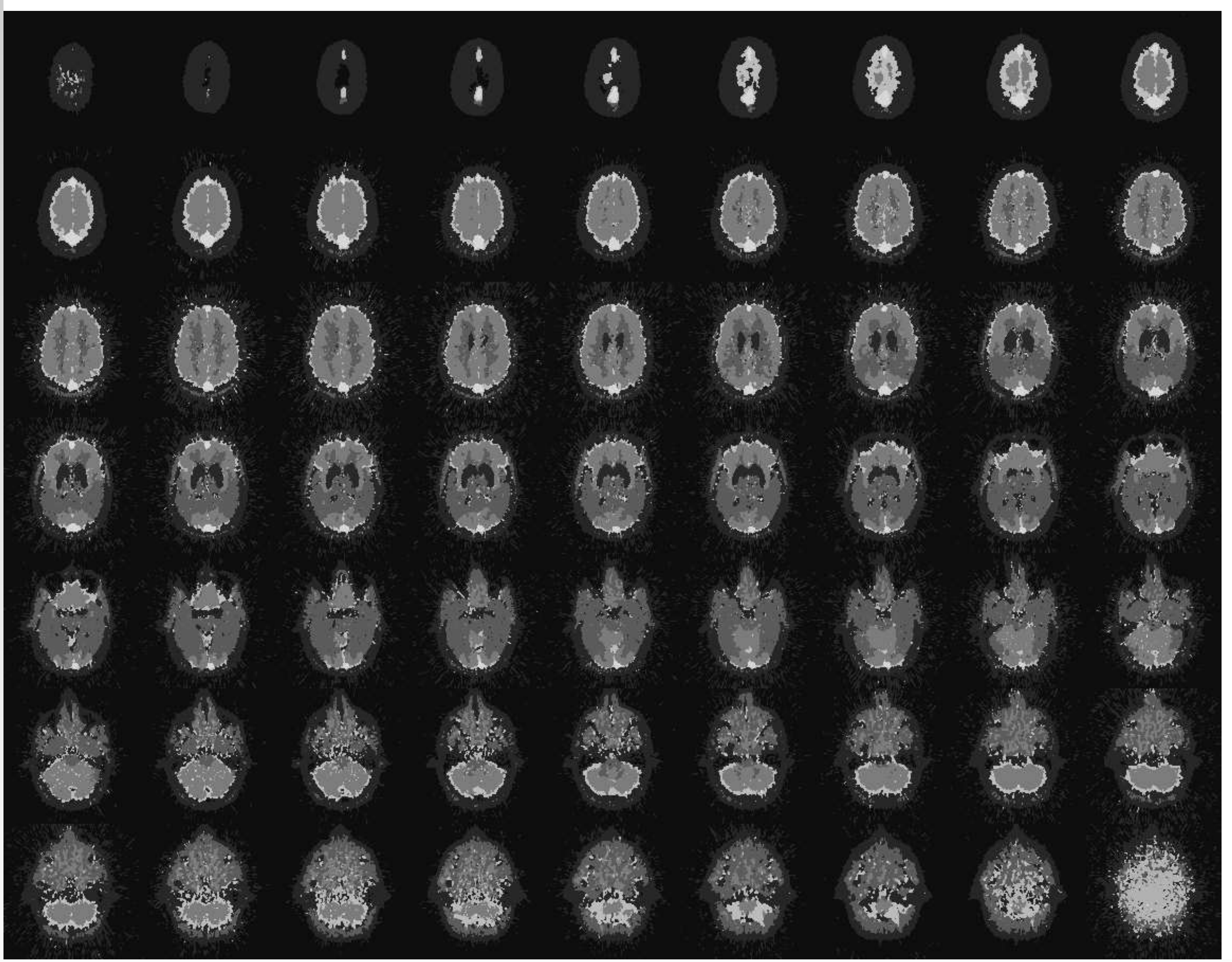
Colors of TACs are the same as in the previous slide.

Quantitative results

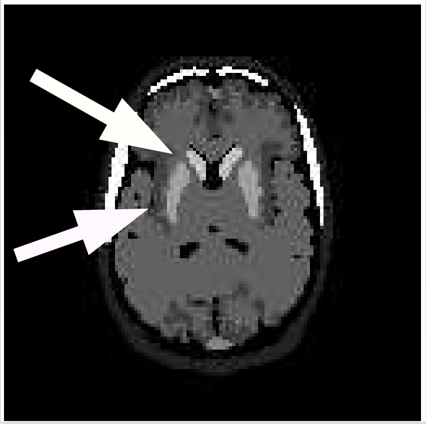
With Monte Carlo phantom, the quantitative results were measured using the Tanimoto coefficient as a performance index.



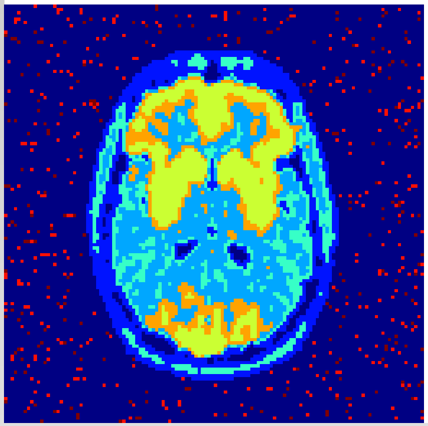
Phantom results: EM



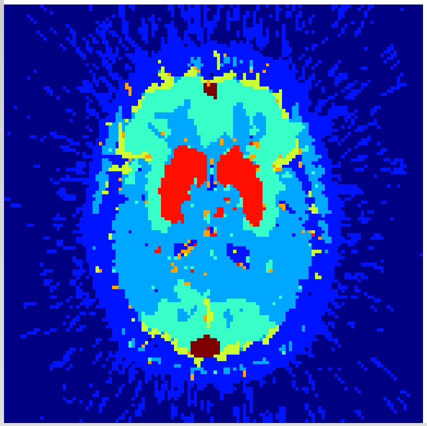
Phantom results



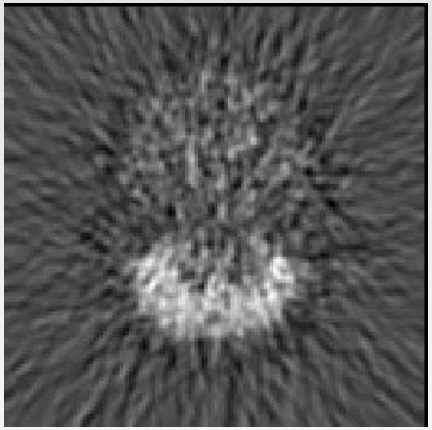
Ground truth



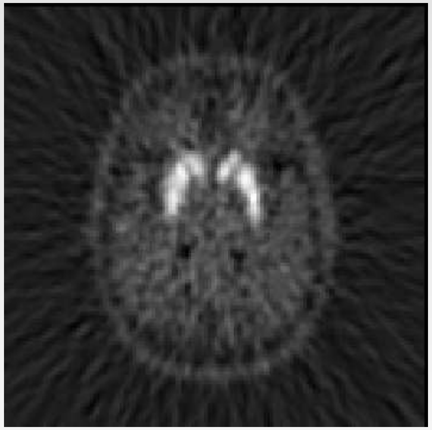
FCM



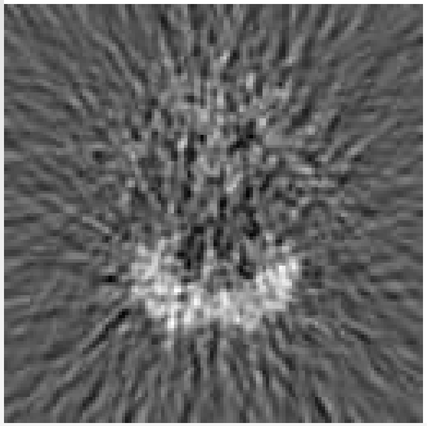
EM



ICA (ns bind)



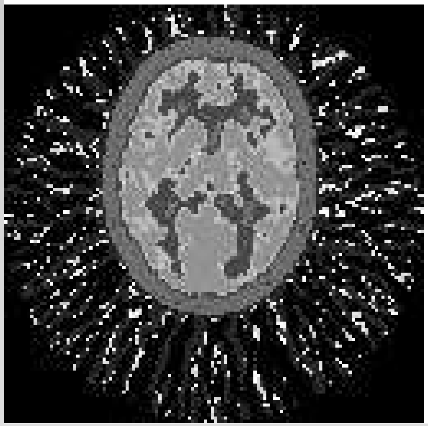
ICA (s-bind)



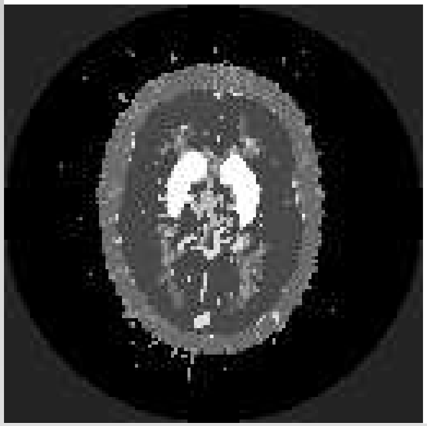
ICA (blood pool)

Results with real data

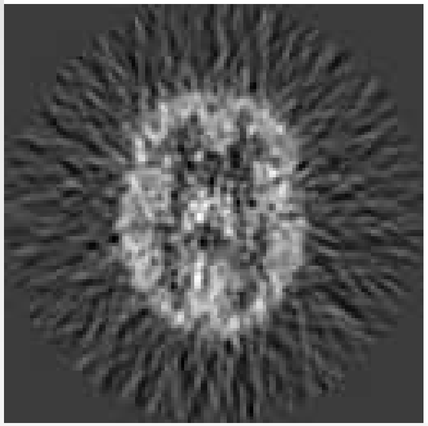
Ground truth



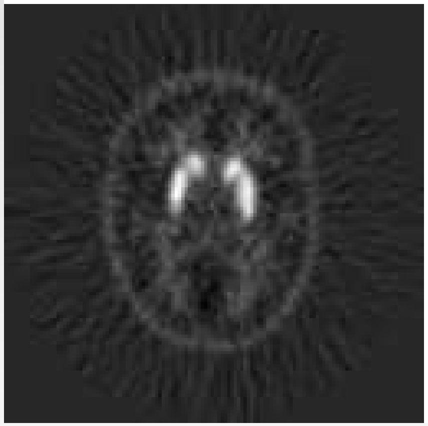
FCM



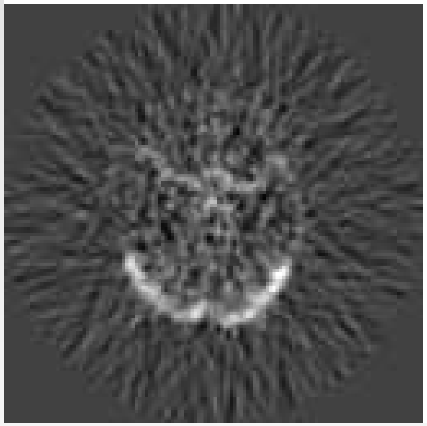
EM



ICA (ns bind)



ICA (s-bind)



ICA (blood pool)

Conclusions

- The most accurate results were produced by ICA, but the level of automation was lower with it than with the other methods. Both cerebellum and striatum could be extracted from the phantom study with ICA. Cerebellum was not well extracted from real PET brain studies.
- The EM algorithm was reasonably good in extraction of the striatum, but cerebellum was not differentiated well from the gray matter.
- The FCM was the least successful method of the three.

Acknowledgments

- Thanks to Anthonin Reilhac from Montreal Neurological Institute for the Monte Carlo simulated phantom.