

Robust Subspace Clustering Approach for High-Dimensional MRF: Novel Simultaneous Clustering and Dimensionality Reduction at Scale



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Introduction

- Magnetic Resonance Fingerprinting (MRF) enables simultaneous acquisition of multiple tissue property maps (e.g. T1, T2, T2*, CBV, R).
- MRF requires to store a large dictionary of high-dimensional simulated pairs of parameters and signals.
- Prior work with only T1, T2, T2* with HD-GMM: not efficient [1]
- <u>Proposed solution</u>: Scalable approach using High Dimensional Student Mixture Model to compress the signals and enable **fast and accurate map**

reconstruction.

Online learning of High Dimensional Student Mixture Model (HD-STM)

> Student mixture model: $p(\mathbf{y}; \boldsymbol{\theta}) = \sum_{k=1}^{K} \pi_k \mathcal{S}_M(\mathbf{y}; \boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k, \nu_k)$

 \succ High-Dimensional hypothesis: $\Sigma_k = \mathbf{D}_k \mathbf{A}_k \mathbf{D}_k^T$ with $\mathbf{A}_k = \text{diag}(a_1, \dots, a_{d_k}, b_k, \dots, b_k)$

> We learn HD-STM using the online EM algorithm [2]

$$p(\boldsymbol{y};\boldsymbol{\theta}) \propto \exp\left(\phi\left(\boldsymbol{\theta}\right)^{T} \boldsymbol{s}\left(\boldsymbol{y}\right) - \psi\left(\boldsymbol{\theta}\right)\right) \rightarrow \begin{cases} S_{n} = (1 - \gamma_{n})S_{n-1} + \gamma_{n}\mathbb{E}_{\boldsymbol{\Theta}_{n-1}}[\boldsymbol{s}(\boldsymbol{Y}_{n})] & \text{E-step} \\ \boldsymbol{\Theta}_{n} = \operatorname{argmax} \phi(\boldsymbol{\Theta}_{n-1})S_{n} + \Psi(\boldsymbol{\Theta}_{n-1}) & \text{M-step} \end{cases}$$



 \succ The main EM computations involve quadratic quantities that do not depend on the last $M - d_k$ columns of \mathbf{D}_k

$$(\boldsymbol{y} - \boldsymbol{\mu}_{k})^{T} \boldsymbol{\Sigma}_{k}^{-1} (\boldsymbol{y} - \boldsymbol{\mu}_{k}) = ||\boldsymbol{\mu}_{k} - P_{k} (\boldsymbol{y})||_{\boldsymbol{\widetilde{\Sigma}}_{k}^{-1}}^{2} + \frac{1}{b_{k}} ||\boldsymbol{y} - P_{k} (\boldsymbol{y})||^{2}$$

> Noting $\widetilde{\mathbf{D}}_k$ the matrix consisting of the first d_k columns of \mathbf{D}_k then the projection onto a lower dimensional space of an observation is $\hat{\mathbf{y}}_k = \widetilde{\mathbf{D}}_k^T (\mathbf{y} - \boldsymbol{\mu}_k)$

Divide & Conquer HD matching for MRF reconstruction



Results: ROI values & Maps reconstructions

Parameter	Tissue	HD-STM	Literature
T1 (ms)	WM GM	863 ± 17 1,655 ± 68	$\sim 690 - 1,100 \ \sim 1,286 - 1,393$
T2 (ms)	WM GM	$50 \pm 2 \\ 102 \pm 15$	$\sim 56 - 80$ $\sim 78 - 117$
CBV (%)	WM GM	$3.9 \pm 0.5 \\ 6.1 \pm 0.9$	$\sim 1.7 - 3.6$ $\sim 3.0 - 8.0$
R (µm)	WM GM	$5.6 \pm 0.05 \\ 5.9 \pm 0.1$	$6.8 \pm 0.3 \\ 7.3 \pm 0.3$

Mean and standard deviation of reconstructed T1, T2, CBV, and R values in white matter (WM) and gray matter (GM) across all available slices for six volunteers. Manually drawn ROIs were used, and the values are compared to literature standards in the table.



Reconstruction of six parameters (T1, T2, Δ f, B1, CBV, and R) from a single slice of one subject, comparing traditional matching, HD-STM, and HD-GMM methods.



Ínría

[1] Oudoumanessah G., Coudert T., et al. " Cluster globally, Reduce locally: Scalable efficient dictionary compression for magnetic resonance fingerprinting" 22th IEEE International Symposium on Biomedical Imaging

[2] Cappé O., and Moulines E. "On-line expectation–maximization algorithm for latent data models." *Journal of the Royal Statistical Society Series B: Statistical Methodology* 71.3 (2009): 593-613.

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Takeaway

• HD-STM can be used for any other dimension reduction task

 HD-STM can be generalized to HD mixture of Elliptical distributions [3]