Localized compression of grey matter maps for age prediction in healthy and clinical populations

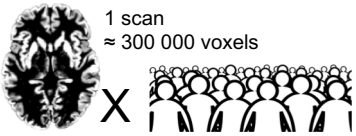
Sarah Genon[1,2*], Deepthi Varikuti[1,2*], Aristeidis Sotiras[3], Holger Schwender[4], Felix Hoffstaedter[1,2], Kaustubh Patil[1,2], Christiane Jockwitz[5], Svenja Caspers[5], Susanne Moebus[6], Katrin Amunts[5], Christos Davatzikos[3], Simon Eickhoff[1,2]

*Equally contributed

[1]Institute of Neuroscience and Medicine (INM-7: Brain and Behaviour), Research Centre Jülich, Germany
[2]Institute of Systems Neuroscience, Heinrich Heine University Düsseldorf, Germany
[3]University of Pennsylvania, Philadephia, United States
[4]Mathematical Institute, Heinrich Heine University Düsseldorf, Germany
[5]Institute of Neuroscience and Medicine (INM-1), Research Centre Jülich, Germany
[6]Institute of Medical Informatics, Biometry and Epidemiology, University of Duisburg-Essen, Germany

Introduction

- **Predicted age can be used as a marker of brain degeneration** [1]
- **Dimensionality reduction** is critical:



- Compression that promotes prediction accuracy is crucial, but compression that promotes **accuracy and** allows post-hoc **interpretability** is better
- Compression should promote biologically plausible units
- We examined compression based on
  - **Functional parcellation**
  - **Non-negative factorization (NMF) of structural data**

Methods

- **Compression & test healthy datasets:**

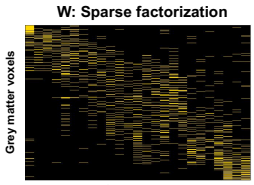
1000brains	Mixed
unisite	multisite
n = 693	n = 1084
age: 55-75	age: 18-81

- **Clinical validation dataset:** ADNI

HC	MCI	IMCI	AD
n = 244	n = 64	n = 184	n = 163
55-90	55-87	56-92	56-91

- **Grey Matter (GM) computation:** Voxel-based morphometry (VBM8): normalization, unified segmentation, modulation for non-linear normalization, 8mm FWHM smoothing
- **Age prediction regression model:** by fitting LASSO regression
  - on the coefficient matrix obtained from the respective NNMF
  - on the coefficient matrix obtained by projecting a cohort's data on the respective other cohort's components
  - on the parcels' mean GM
- **Evaluation of model generalization:** 10-fold cross-validation replicated 25 times
  Prediction accuracy: Mean Absolute Error (MAE)
- **GM Factorization: OPNMF**

Factorizes high dimensional voxel wise data of all subjects (X) into two non-negative matrices, X ≈ WH
➔ sparse factorization (the dictionary)
➔subject-specific loading coefficients



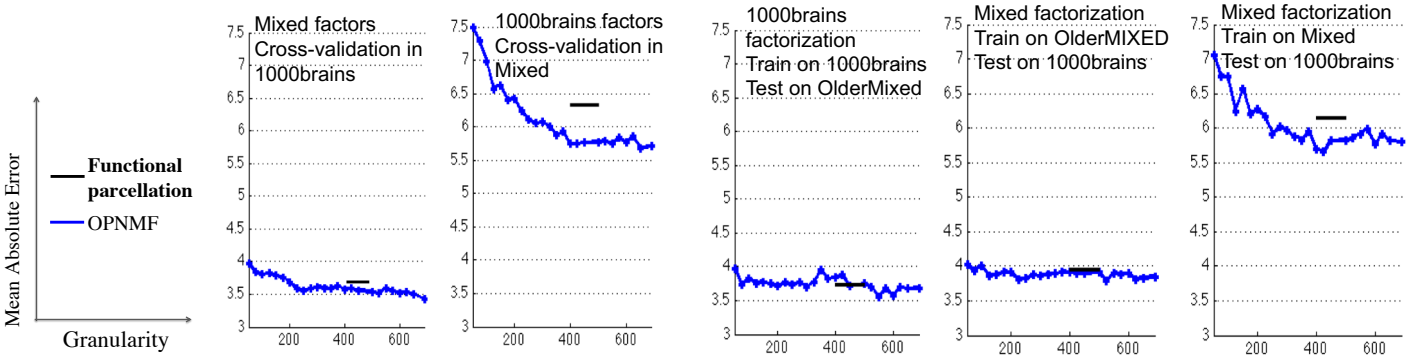
Factors' range: 50-690

- **Functional parcellation:**

Resting-state based parcellations of the Cerebral Cortex [2] and subcortical structures [3]

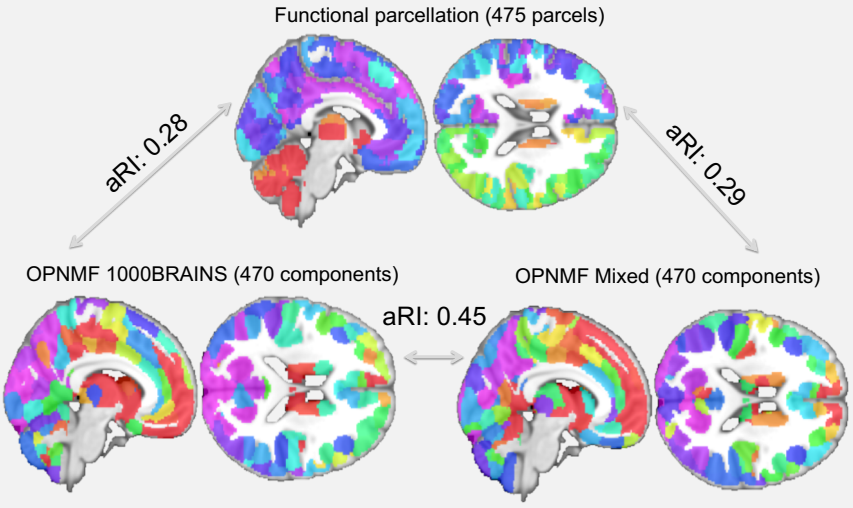
Results

Age prediction performance of OPNMF and functional parcellation

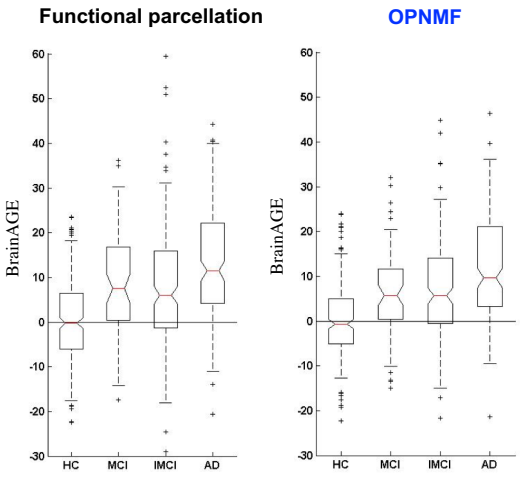


Similarity between functional parcellation and OPNMF parcellations

(measured with adjusted Rand Index, aRI)



BrainAGE prediction in ADNI by models trained on 1000brains



Discussion

- OPNMF: Convergence of the spatial pattern as well as good prediction performance when the factorization of one dataset has been projected onto another dataset argue for the **biological validity** and **transferability** of the factorization
- RS-parcellation: Compression of GM maps based on a functional representation (resting-state-based parcellation) offers comparable prediction performance (than OPNMF compression) in both healthy and clinical datasets

But OPNMF-based compression can slightly outperform resting-state-based parcellation.

- The best compression of GM data should be based on structural data, but, alternatively, opting for a representation based on functional parcellation should not dramatically impact on the prediction performance.

References:
[1] Franke, K., et al., Estimating the age of healthy subjects from T 1-weighted MRI scans using kernel methods: Exploring the influence of various parameters. Neuroimage, 2010. 50(3): p. 883-892
[2] Schaefer, A., et al., Local-Global Parcellation of the Human Cerebral Cortex from Intrinsic Functional Connectivity MRI. Cereb Cortex, 2017: p. 1-20. [3] Bellec, P., et al., Multi-level bootstrap analysis of stable clusters in resting-state fMRI. Neuroimage, 2010. 51(3): p. 1126-39.

Acknowledgments: This study was supported by the Deutsche Forschungsgemeinschaft (DFG, GE 2835/1-1, EI 816/4-1), the National Institute of Mental Health (R01-MH074457), the Helmholtz Portfolio Theme 'Supercomputing and Modeling for the Human Brain', and the European Union's Horizon 2020 Research and Innovation Programme under Grant Agreement No. 720270 (HBP SGA1) and No. 785907 (HBP SGA2).