

Validation of dynamical whole-brain models in high-dimensional spaces



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Introduction

- Simulating the resting-state brain dynamics mathematical whole-brain models allows for describing a subject's brain activity by a set of interpretable model simulated functional **parameters** and connectivity.
- However, computational challenges in parameter optimization constrain highdimensional model studies and their level of model personalization.
- 2 mathematical optimization algorithms to explore high-dimensional moderate parameter spaces computational costs, and validate wholebrain models by optimizing between 2 and 103 free model parameters simultaneously.
- Aim: To gain an insight into the behavior of high-dimensional whole-brain models and their potential utility for personalized simulations of human brain dynamics.

- 272 subjects (Human Connectome Project [1]) with individual empirical structural and functional connectivity (eSC and eFC, resp.)
- Brain atlases: Schaefer 100 (Sch100) [2] and Harvard-Oxford 0% (HO0Thr) [3] atlases with N = 100 and N = 96cortical regions, resp.
- Computational model: Kuramoto model [4] of coupled phase oscillators
- Phase dynamics of brain region $i \in \{1, ..., N\}$: $\dot{\theta}_i(t) = 2\pi f_i + \frac{c}{N} \sum_{j=1}^{N} k_{ij} \sin(\theta_j (t - \tau_{ij}) - \theta_i(t)) + \sigma \eta_i(t)$ simulated BOLD signals simulated FC (sFC)

Model validation:

Pearson Correlation (sFC,eFC) > MAXIMIZATION

Detecting optimal, subject-specific model parameters:

- C and τ free, $\sigma = 0.3$ fixed, f_i from empirical BOLD: **2D**
- C, τ and σ free, f_i from empirical BOLD: **3D**
- C, τ , σ and f_i free: 103D (Sch100) / 99D (HO0Thr)

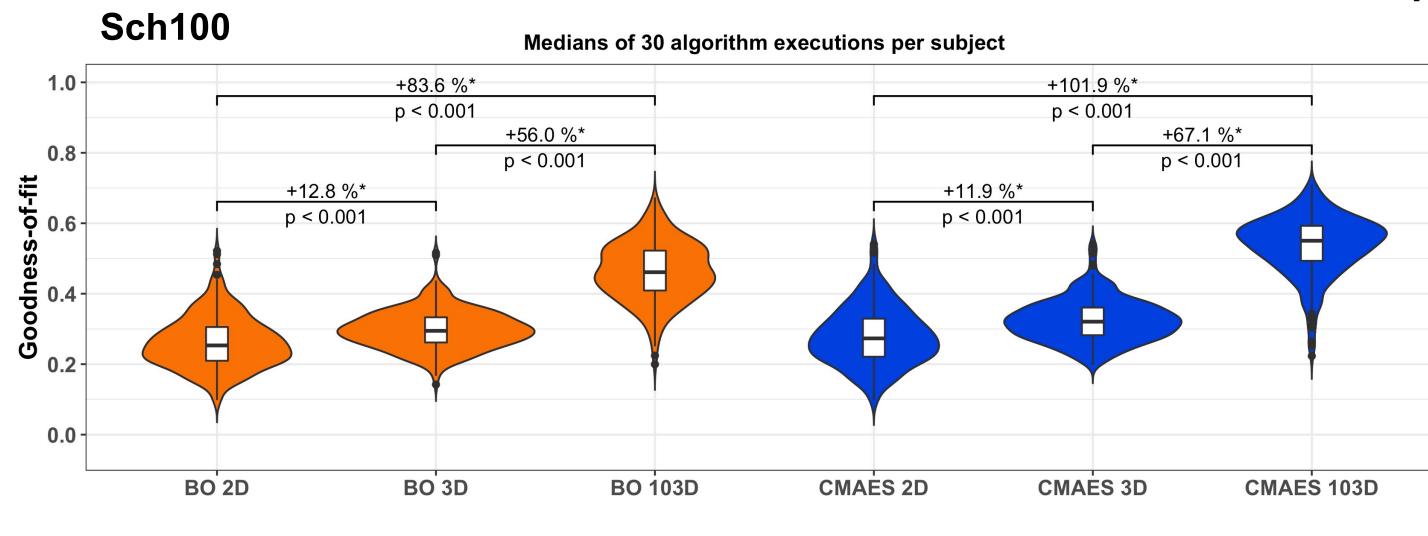
Methods **Model variables Description Description Model variables** Coupling delay (signal transmission time) Phase of region *i* at $\theta_i(t)$ between region *i* and time t Free parameter of Average fiber path natural frequency PL_{ii} length between region (0.01 - 0.1 Hz) ofi and jregion i Free parameter of Free parameter of global coupling global delay strength Relative coupling $k_{ij} = \frac{SC_{ij}}{\langle SC \rangle}$ Free parameter of strength between noise intensity region *i* and *j* Number of Independent noise streamlines between SC_{ij} perturbation of region $\eta_i(t)$ region i and j in the i at time t eSC matrix Simulated BOLD $sin(\theta_i)$ <.> Averaging operator signal of region i

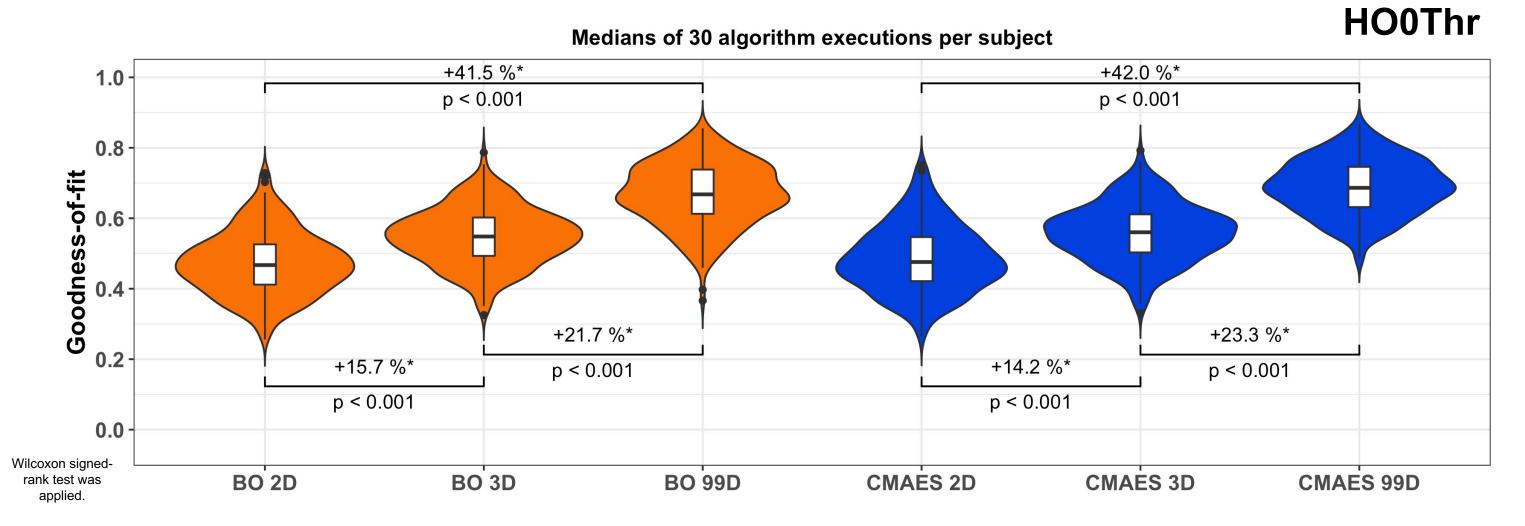
methods:

Covariance Matrix Adaptation Evolution Strategy (CMAES) [5]: Global population-based optimization technique, best trial solutions from every iteration (generation) are selected to form **Optimization** the distribution mean of the population for the next step Bayesian Optimization (BO) [6]: Sequential design strategy for global optimizations of black-box functions, probabilistic surrogate model for the goal function, adjusted after every new function evaluation

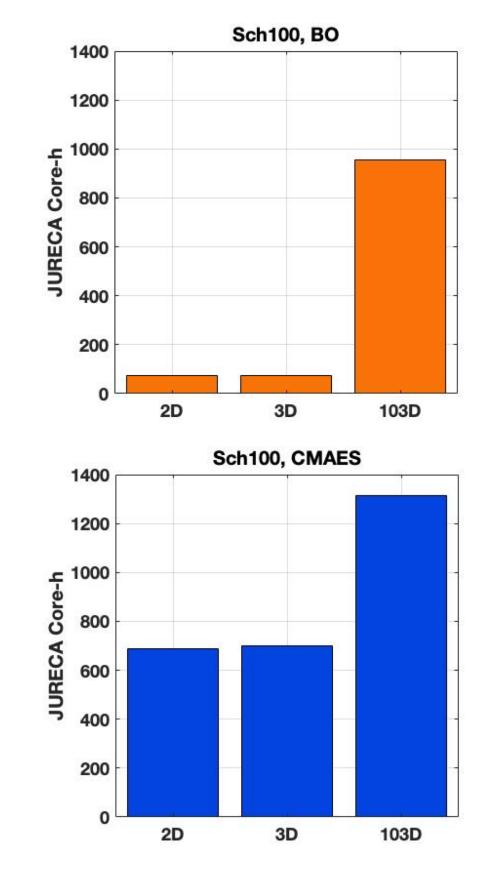
Results

#1: Goodness-of-fit for personalized model simulations

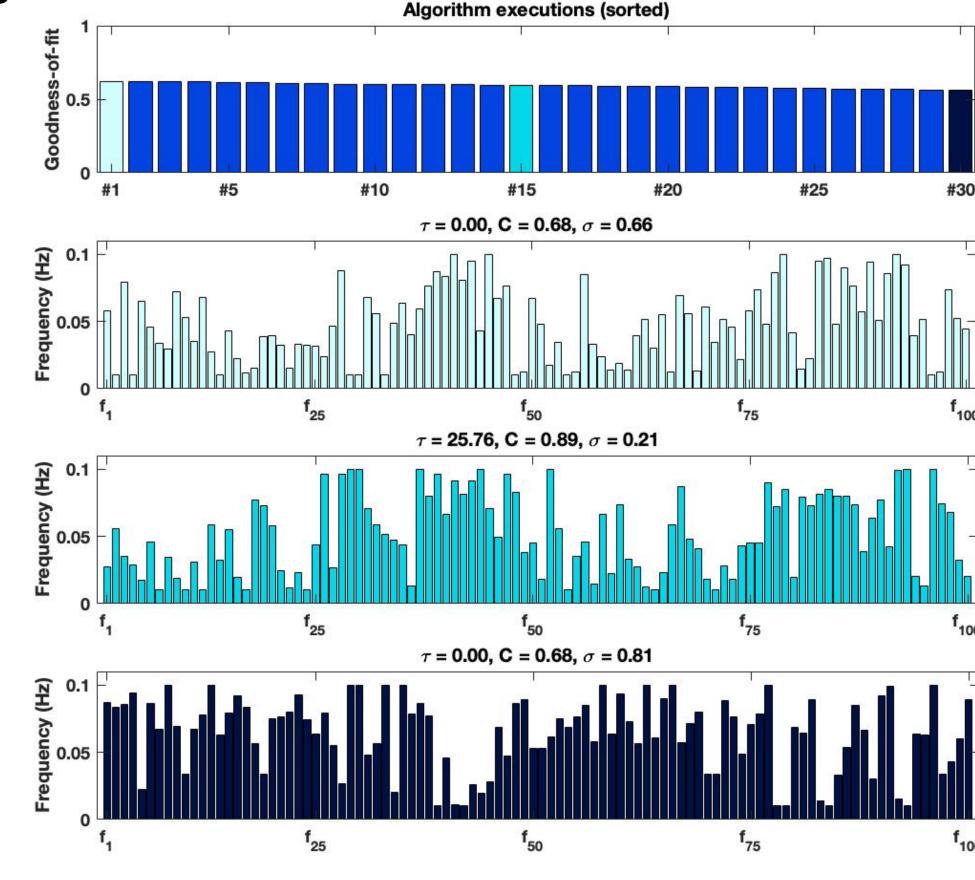




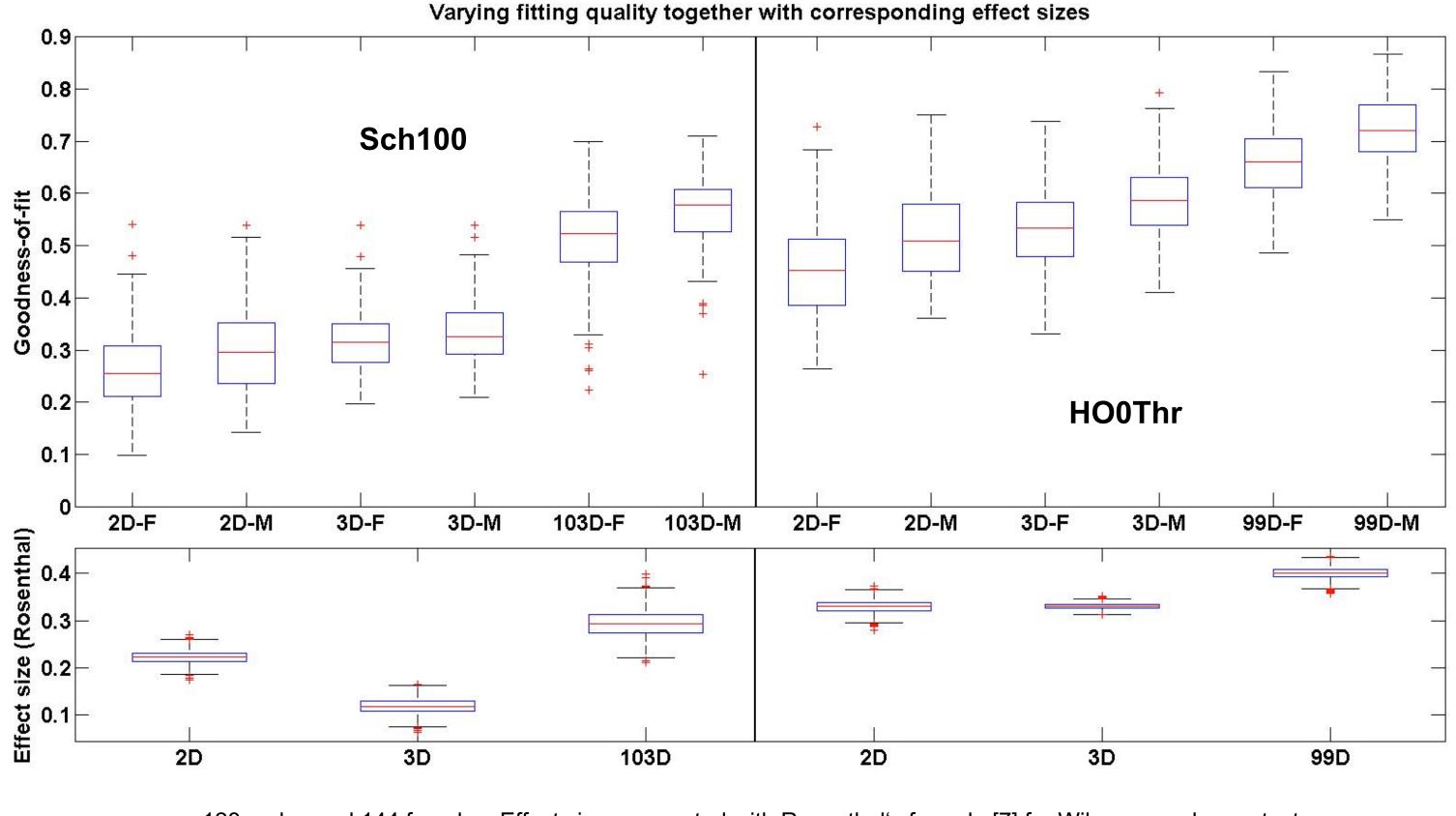
#2: Mean resource consumption per subject for 30 algorithm executions



#3: Example of high-dimensional simulation outcomes for one subject



#4: Differentiation between males (M) and females (F) on simulated data



128 males and 144 females. Effect sizes computed with Rosenthal's formula [7] for Wilcoxon rank-sum test.

Discussion

Summary:

Empirical measurements can be much better replicated by high-dimensional models than by low-dimensional ones.

A high goodness-of-fit can be obtained for several configurations of "optimal" model parameters, which are thus **less reliable** in high-dimensional cases.

Differences between males and females appear to be more pronounced in data simulated by high-dimensional models.

Conclusions:

- New horizons for personalized brain modeling can be opened up by mathematical optimization algorithms which enable the exploration of whole-brain models in high-dimensional parameter spaces.
- Multiple algorithm executions per subject are necessary in view of the complexity of high-dimensional parameter spaces and the unfeasibility of a confirmatory grid search.

Outlook:

- High-dimensional brain models properly validated bear a huge potential for more precise and personalized studies.
- The manifold on which the optimal parameters seem to be located remains a hot topic for further investigations.
- The location of **optimal model parameters** might serve as an individual subject's personal profile.

References: [1] Van Essen et al. (2013). "The WU-Minn Human Connectome Project: an overview." Neuroimage 80: 62-79. [2] Schaefer et al. (2018). "Local-Global Parcellation of the Human Cerebral Cortex from Intrinsic Functional Connectivity MRI." Cerebral Cortex 28(9): 3095-3114. [3] Desikan et al. (2006). "An automated labeling system for subdividing the human cerebral cortex on MRI scans into gyral based regions of interest." Neuroimage 31(3): 968-980. [4] Cabral et al. (2011). "Role of local network oscillations in resting-state functional connectivity." Neuroimage 57(1): 130-139. [5] Hansen (2006). "The CMA Evolution Strategy: A Comparing Review." In: "Towards a New Evolutionary Computation." Studies in Fuzziness and Soft Computing 192. Springer, Berlin, Heidelberg. [6] Martinez-Cantin (2014). "BayesOpt: A Bayesian Optimization, Experimental Design and Bandits." Journal of Machine Learning Research 15: 3735–3739. [7] Rosenthal & Rosnow (1991). "Essentials of behavioral research" (2nd ed.). New York: McGraw-Hill.