Accepted Manuscript

Bayesian Optimisation of Large-Scale Biophysical Networks

J. Hadida, S.N. Sotiropoulos, R.G. Abeysuriya, M.W. Woolrich, S. Jbabdi

PII: S1053-8119(18)30170-8

DOI: 10.1016/j.neuroimage.2018.02.063

Reference: YNIMG 14764

To appear in: NeuroImage

Received Date: 2 August 2017

Revised Date: 27 February 2018

Accepted Date: 28 February 2018

Please cite this article as: Hadida, J., Sotiropoulos, S.N., Abeysuriya, R.G., Woolrich, M.W., Jbabdi, S., Bayesian Optimisation of Large-Scale Biophysical Networks, *NeuroImage* (2018), doi: 10.1016/j.neuroimage.2018.02.063.

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.



Bayesian Optimisation of Large-Scale Biophysical Networks

J. Hadida^{a,b,*}, S.N.Sotiropoulos^{a,c}, R.G.Abeysuriya^b, M.W.Woolrich^{b,1}, S.Jbabdi^{a,1}

^a Wellcome Centre for Integrative Neuroimaging (FMRIB), Nuffield Department of Clinical Neurosciences, University of Oxford

^b Wellcome Centre for Integrative Neuroimaging (OHBA), Department of Psychiatry, University of Oxford

^cSir Peter Mansfield Imaging Centre (SPMIC), School of Medicine, University of Nottingham

Abstract

The relationship between structure and function in the human brain is well established, but not yet well characterised. Large-scale biophysical models allow us to investigate this relationship, by leveraging structural information (e.q. derived from diffusion tractography) in order to couple dynamical models of local neuronal activity into networks of interacting regions distributed across the cortex. In practice however, these models are difficult to parametrise, and their simulation is often delicate and computationally expensive. This undermines the experimental aspect of scientific modelling, and stands in the way of comparing different parametrisations, network architectures, or models in general, with confidence. Here, we advocate the use of Bayesian optimisation for assessing the capabilities of biophysical network models, given a set of desired properties (e.g. band-specific functional connectivity); and in turn the use of this assessment as a principled basis for incremental modelling and model comparison. We adapt an optimisation method designed to cope with costly, high-dimensional, non-convex problems, and demonstrate its use and effectiveness. Using five parameters controlling key aspects of our model, we find that this method is able to converge to regions of high functional similarity with real MEG data, with very few samples given the number of parameters, without getting stuck in local extrema, and while building and exploiting a map of uncertainty defined smoothly across the parameter space. We compare the results obtained using different methods of structural connectivity estimation from diffusion tractography, and find that one method leads to better simulations.

Keywords: biophysical model, simulation, Bayesian optimisation, resting-state, diffusion, MEG

*Corresponding author

Email address: jhadida@fmrib.ox.ac.uk (J. Hadida) ¹Equal contribution

Preprint submitted to NeuroImage

دريافت فورى 🛶 متن كامل مقاله

- امکان دانلود نسخه تمام متن مقالات انگلیسی
 امکان دانلود نسخه ترجمه شده مقالات
 پذیرش سفارش ترجمه تخصصی
 امکان جستجو در آرشیو جامعی از صدها موضوع و هزاران مقاله
 امکان دانلود رایگان ۲ صفحه اول هر مقاله
 امکان پرداخت اینترنتی با کلیه کارت های عضو شتاب
 دانلود فوری مقاله پس از پرداخت آنلاین
 پشتیبانی کامل خرید با بهره مندی از سیستم هوشمند رهگیری سفارشات
- ISIArticles مرجع مقالات تخصصی ایران