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Simultaneous estimation of population receptive field and hemodynamic parameters from single point BOLD responses using Metropolis-Hastings sampling

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ABSTRACT

We introduce a new approach to Bayesian pRF model estimation using Markov Chain Monte Carlo (MCMC) sampling for simultaneous estimation of pRF and hemodynamic parameters. To obtain high performance on commonly accessible hardware we present a novel heuristic consisting of interpolation between precomputed responses for predetermined stimuli and a large cross-section of receptive field parameters. We investigate the validity of the proposed approach with respect to MCMC convergence, tuning and biases. We compare different combinations of pRF - Compressive Spatial Summation (CSS), Dumoulin-Wandell (DW) and hemodynamic (5-parameter and 3-parameter Balloon-Windkessel) models within our framework with and without the usage of the new heuristic. We evaluate estimation consistency and log probability across models. We perform as well a comparison of one model with and without lookup table within the RStan framework using its No-U-Turn Sampler. We present accelerated computation of whole-ROI parameters for one subject. Finally, we discuss risks and limitations associated with the usage of the new heuristic as well as the means of resolving them. We found that the new algorithm is a valid sampling approach to joint pRF/hemodynamic parameter estimation and that it exhibits very high performance.

Introduction

Modelling is an important domain of science in general and a recurring topic in population receptive field (pRF) research in particular, where functional magnetic resonance imaging (fMRI) serves as evidence acquisition method. Classical approaches such as those by Dumoulin and Wandell (2008) and Kay et al. (2013) focus on point estimates of parameters in predefined models motivated by physiology and empirical evidence. In the recent work of Zeidman et al. (2016) authors introduce the formalism of Bayesian Model Selection in order to root pRF model choices in an objective quantitative measure such as Variational Free Energy. Furthermore, the proposed formulation employs a Balloon-Windkessel model for joint estimation of pRF and hemodynamic parameters. The main limitation of this approach lies in the assumption about the form of the posterior distribution of parameters, in this case Gaussian. The method is characterized as well by high computational requirements – the reference implementation of the algorithm is reported to require about 100 s per voxel to converge which renders its use problematic on modern PCs with exception of high-end multi-core cluster setups (the authors give an example of 192-core cluster used to estimate 14,395 voxels) or small regions of interest. A Bayesian approach using slice-sampling Monte Carlo method with fixed Hemodynamic Response Function (HRF) was recently described in Quax et al. (2016). Similarly to the variational method the sampling approach quantifies how variable the underlying receptive field is by using the uncertainty of the posterior estimate except with the added advantage of not imposing any particular form on the posterior probability distribution. The authors underline the importance of their method's capability to estimate variability – rendered particularly relevant by the fact that receptive fields are not rigid over time, but can change due to attention effects or task demands (Klein et al., 2014). The main contribution of our work is a new approach to Bayesian pRF model estimation combining the best characteristics of the above methods – inclusion of the Balloon-Windkessel hemodynamic model, Dumoulin-Wandell and compressive spatial summation (CSS) pRF models and using sampling for

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model inversion therefore not imposing any form on the posterior. Furthermore in order to address potential obstacles due to high performance requirements we introduce a novel heuristic for solving the Dumoulin-Wandell pRF model by using interpolation across a lookup table containing precomputed responses for given stimuli and a large number of predefined receptive field parameters. This enables us to massively parallelize the algorithm using a graphics processing unit (GPU) implementation of the Markov Chain Monte Carlo (MCMC) scheme. Our algorithm offers choice between existing pRF models – Dumoulin-Wandell model (Dumoulin and Wandell, 2008) and compressive spatial summation (CSS) model of pRF introduced in Kay et al. (2013) and for BOLD generation between well-established Balloon-Windkessel model (Buxton et al., 1998; Friston et al., 2000; Irikura et al., 1994; Mayhew et al., 1998), its 3-parameter version (Stephan et al., 2007) used in the recent implementation of Dynamic Causal Modelling (DCM) in Statistical Parametric Mapping (SPM) toolbox as well as a fixed user-provided HRF. Our algorithm is presented and discussed along with introduction of QPrf – its freely available implementation in the form of a standalone toolbox (https://github.com/sadaszewski/qprf) available with source code under the terms of GNU GPLv3 license. We demonstrate CSS-pRF/Balloon-Windkessel model inversion using the new heuristic and compare it to a classical two-stage method. Furthermore, we compare different combinations of pRF (CSS, classical Dumoulin-Wandell) and hemodynamic (5-parameter and 3-parameter Balloon) models within QPrf and against existing Bayesian inversion software (BayespRF). Finally, we discuss risks and limitations associated with usage of the new heuristic as well as means of resolving them.

Visual field mapping consists of measuring responses to rings and wedges stimuli presented at varying visual field locations. Within each voxel the experimenter estimates the visual field position that produces the largest fMRI response. However, in reality the population of neurons in such voxel responds (with varying intensity) to a whole range of visual field locations. The region of visual space that stimulates the voxel is called the population receptive field (pRF) (Victor et al., 1994). The pRF method can provide estimates for receptive field location, size, orientation, laterality and surround suppression (Kay et al., 2013; Zeidman et al., 2016). To this end a series of stimuli is specifically designed to differentiate between the above parameters. Temporal responses are then used to fit model values with best support from the observed data (evidence).

In Dumoulin and Wandell (2008) the authors propose a quantitative approach for estimating population receptive field (pRF) parameters using a model-based coarse-to-fine optimization scheme. The pRF model is defined as two-dimensional Gaussian with means corresponding to pRF position in the visual field and a scalar covariance matrix with diagonal values equal to (pRF size)^2. Subsequently, model parameters are varied in order to match functional magnetic resonance imaging (fMRI) time series obtained using wedges, rings and lines stimuli displayed in a series of animations. In order to do so - Frobenius inner product of stimuli and pRF Gaussian is convolved with a space-invariant hemodynamic response function (HRF) and the residual sum of squares (RSS) between the simulation and the data is iteratively minimized starting from a seed point determined by exhaustive search on predefined parameter grid.

This model is the base for further elaboration in Kay et al. (2013) leading to the compressive spatial summation (CSS) approach. While measuring BOLD responses to a set of contrast patterns, the authors discover systematic deviation from linearity. The data are more accurately explained by a model in which a compressive static nonlinearity is applied after linear spatial summation. The authors conclude that the nonlinearity is present in early visual areas (e.g., V1, V2) and increases in anterior extrastriate areas (e.g., LO-2, VO-2). The effect of compressive spatial summation has been analyzed in terms of changes in the position and size of a viewed object. It is stated that compressive spatial summation is consistent with tolerance to changes in position and size, an important characteristic of object representation. A similar grid-based fitting approach is used for estimating parameters of the CSS-extended pRF model.

The CSS-pRF approach is characterized by simplicity and relatively good speed/accuracy of fit in most cases. Some of its shortcomings however are that it: i. provides only point estimates of the parameters; ii. does not account for spatial HRF variation (which, as acknowledged by the authors, may introduce systematic errors in pRF size estimates); iii. uses an explicit HRF model based on two gamma functions which do not allow for robust estimation of more informative hemodynamic parameters introduced by the Balloon-Windkessel model (Buxton et al., 1998).

The advancement proposed by this work is a Bayesian approach to joint estimation of pRF and hemodynamic parameters full posterior distributions using a forward signal generation model and Markov Chain Monte Carlo (MCMC) sampling. Furthermore, due to the computational costs incurred by MCMC, an optimized implementation using OpenCL is presented which allows one to take advantage of modern Graphics Processing Units (GPUs) in order to keep the processing time within the same order of magnitude as previous method while providing richer and more robust results.

Materials and methods

PRF model

A population receptive field (pRF) is the region of the visual field within which stimuli evoke responses from a local population of neurons. In Dumoulin and Wandell (2008) the authors proposed a model of neuronal population receptive field defined by a two-dimensional Gaussian function:

$$g(x,\ y) = e^{-\frac{(x-x_0)^2+(y-y_0)^2}{2\sigma^2}} \tag{1}$$

where *(x0, y0)* is the receptive field center and σ is the Gaussian standard deviation. Subsequently, the predicted pRF response *r(t)* is defined as sum of cells in element-wise (Hadamard) product of effective stimulus *s(x, y, t)* and the Gaussian *g(x, y)*:

$$r(t) = \sum_{x,\ y} s(x,\ y,\ t)g(x,y) \tag{2}$$

The BOLD signal time series prediction *p(t)* is then obtained by convolving *r(t)* with a model hemodynamic response function (HRF) *h(t)*:

$$p(t) = r(t)*h(t) \tag{3}$$

This model is further elaborated in Kay et al. (2013) leading to compressive spatial summation (CSS) approach (Fig. 1), which defines *r(t)* as:

$$r(t) = g\left(\sum_{x,y} s(x,y,t)g(x,y)\right)^n \tag{4}$$

where *g* is a gain parameter and *n* is an exponent parameter. This additional compressive static nonlinearity has been proven to better explain experimental data.

In contrast to previous studies, we use the CSS component for modelling the pRF response but instead of using convolution with a spatially invariant canonical HRF to obtain the predicted BOLD time series in [3], we employ the Balloon-Windkessel model described in the following section. We do this to account for per-voxel variability of parameters determining hemodynamic response.

Balloon-Windkessel model

The hemodynamic model (Fig. 2) used in this study is a combination of the Balloon model and regional cerebral blood flow (rCBF) model as introduced in Friston et al. (2000) and used for dynamic causal modelling (Friston et al., 2003). The remainder of this section contains a brief summary of the model.