Paradigm Free Mapping vs Total Activation

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Abstract

Here's where the fantastic abstract will go.

Keywords: fMRI deconvolution, paradigm free mapping, total activation

1. Introduction

- Talk about our motivation for this paper.
- We could mention iCAPs Neuron, and papers with applications like PFM, TA, clinical patient papers with iCAPs.
- Apart from [[Richard F. Betzel]]'s work [1, 2, 3], we could mention the connection with the [[Multiplication of Temporal Derivatives]] method [4, 5].
  - These are basically calculating the derivative, which is the same as applying a high-pass filter and calculating the correlation.

Here is a sample reference: [6].

2. Theory

- What is deconvolution and different formulations presented as a review.
- Analysis vs synthesis
  - TA paper but without the spatial regularization
  - PFM paper
  - In Gitelman it's an **H** multiplied by a Fourier term.

The hemodynamic response to neuronal activity at time t can be modeled as the convolution with a finite impulse response function of the neuronal signal $s_{t-\tau}$ at time $t-\tau$ with the hemodynamic response function h_τ:

$$y_t = \Sigma_t h_\tau s_{t-\tau}, \tag{1}$$

where y_t is the measured BOLD signal on a given voxel. This equation can be reformulated in matrix notation as $\mathbf{y} = \mathbf{Hs}$ where $\mathbf{H} \in \mathbb{R}^{NxN}$ is the HRF in Toeplitz matrix form, and N is the number of frames of the fMRI acquisition.

Functional MRI data analyses are often directed to disentangling and understanding the neural processes that occur among brain regions. However, interactions in the brain are expressed, not at the level of hemodynamic responses, but at the neural level. Thus, an intermediate step that estimates the underlying neuronal activity is necessary for such analyses. Given the nature of the fMRI BOLD signal, the appropriate approximation of the neuronal activity can be obtained by means of deconvolution with an assumed hemodynamic response [6]. Hence, the maximum likelihood estimate of the hemodynamic response to the underlying neural activity can be calculated using the ordinary least-squares estimator that minimizes the residual sum of squares between the modeled (**Hs**) and measured (**y**) signals. Yet, the estimates of the neuronal activity **s** must be constrained with a regularization term to attenuate the collinearity of the design matrix **H**.

2.1. Paradigm Free Mapping

Paradigm Free Mapping (PFM) builds upon the signal model introduced in (1); i.e., the BOLD signal is the result of convolving the underlying neural activity with the hemodynamic response, and proposes to estimate the activity-inducing signal by solving the following regularization problem [7, 8, 9]:

$$\hat{\mathbf{y}} = \arg\min_{\mathbf{y}} \frac{1}{2}\|\mathbf{y} - \mathbf{Hs}\|_F^2 + \Omega(\mathbf{s}) \tag{2}$$

where $\Omega(\mathbf{s})$ is the regularization term.

Assuming that single-trial BOLD responses are the result of brief bursts of neuronal activation, the activity-inducing signal **s** must be a sparse vector. Thus, sparse estimates of **s** could be obtained by substituting $\Omega(\mathbf{s})$ in (3) with an L_0-norm and solving the optimization problem [10]. However, due to the convolution model defined in (3), finding the optimal solution to the problem demands an

exhaustive search across all possible combinations of the columns of the design matrix $\mathbf{H}$. Hence, a pragmatic solution is to solve the optimization problem with the use of an L_1-norm, or LASSO [11], which is a convex function and therefore provides fast convergence to the optimal solution.

$$\hat{\mathbf{y}} = \arg\min_{\mathbf{y}} \frac{1}{2}\|\mathbf{y} - \mathbf{H}\mathbf{s}\|_F^2 + \lambda\|\mathbf{s}\|_1 \quad (3)$$

where λ regulates how sparse the optimal solution is. The PFM formulation provides enough flexibility to

2.2. Total Activation

Even though based on the same signal model as PFM, Total Activation (TA) proposes to use a linear differential operator L_h that inverts the hemodynamic system based on activelets to recover the activity-inducing signal $\mathbf{s}$ [12, 13]:

$$L_h\{x\}(t) = s(t) \quad (4)$$

where x is the neuronal-related signal; i.e., the activity inducing signal $\mathbf{s}$ convolved with the HRF, and L_h is defined as

$$L_h = \prod_{i=1}^{M_1}(D - \alpha_i I)(\prod_{j=1}^{M_2}(D - \gamma_j I))^{-1} \quad (5)$$

where D is the derivative operator, $\alpha_i (i = 1, \ldots, M_1)$ define the zeros of the filter, $\gamma_j (j = 1, \ldots, M_2)$ represent the poles, I is the identity matrix and $M_1 > M_2$.

$$\hat{\mathbf{x}} = \arg\min_{\mathbf{x}} \frac{1}{2}\|\mathbf{y} - \mathbf{x}\|_F^2 + \mathcal{R}(\mathbf{x}) \quad (6)$$

where $\mathbf{y}$ is the fMRI data and $\mathcal{R}(\mathbf{x})$ is the regularization term.

3. Results

- Methods on how we're doing simulations and results (with simulations and experimental data)
  - Different SNRs and maybe even use CAPs
  - Selection of HRF explained if both use the same but it's different from what's used for simulating.
    - What happens? For example with gamma for simulating.
  - Selection of regularization parameter
    - Present with real data on a voxel

4. Discussion

- Pros and cons of each formulation: analysis vs synthesis
- Link with other approaches
- Finish with conclusions and a moving forward
  - We have to refine the deconvolution
  - HRF variability there are three: conference proceeding by Philippe, ISBI 2012 by césar, and Farouj with a different formulation. Say conceptual differences among those.
  - Mention stability-selection [14]
  - Debiasing
  - Connected to debiasing other deconvolution algorithms that are based on a norm lower than 1.

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