Efficient sequential inference in DBNs: steps towards joint MEG/fMRI connectivity analysis

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Recently, the problem of estimating functional connectivity in the context of fMRI has been addressed using two different approaches. One approach treats the activity of regions of interest (ROI) as unobserved, but uses restrictive bilinear model to describe interactions between ROIs [4]. The other approach applies a general dynamic Bayesian network (DBN) model with multinomial conditional probability densities, but treats the state of ROIs as completely observed and uses quantized fMRI data [2].

Our goal is to employ DBN framework to allow modeling of general multiway nonlinear interactions and integration of various sources of data, while at the same time avoiding losing information at data quantization phase. A very general and a powerful framework that allows inference in such models is particle filtering (PF) [3]. Unfortunately this approach is known to be computationally expensive when the dimensionality of the problem grows.

In this work we show how to improve efficiency of PF by introducing additional data sources (MEG and fMRI joint analysis) and how to exploit the structure of the observations in the DBN to further reduce the curse of dimensionality.

We have conducted a series of simulations where given equivalent conditions we run PF tracking on a single ROI model using fMRI-only inference as well as the fused fMRI/MEG inference. The results obtained by the joint analysis provide more stable estimates given order of magnitude fewer particles (Figure 1). In practice that means greater efficiency of the joint analysis.

To improve efficiency in the case of a large number of ROIs we exploit the structure of the problem: a single observation per ROI. This structure allows us to independently explore subspaces of the state space and improve the efficiency and performance of the inference. The details of the method are presented in [1].

For the real data experiment in the multi-ROI case we have used a functional magnetic resonance imaging (fMRI) dataset [2]. As the model of the BOLD signal generation from neural activity we have used the hemodynamic forward model [4].

Voxel time courses were averaged on a per (ROI) basis using the Talairach database.

In order to obtain the underlying structure of the DBN, we have used the approach of [2]. Among the discovered DBN families we have used several most significant ones according to the cross validation

\[ \text{Figure 1: Average (across all time points) variance of estimated means of the BOLD response 1a and neural activity 1b for 800 runs. Smaller values are better. Combined analysis requires much fewer particles to achieve lower variance of the estimate.} \]

\[ \text{Figure 2: The network for a subset of regions of interest (ROIs) from the Talairach anatomical atlas database. Note that each ROI is observed through its indirect measurement by fMRI.} \]
procedure (t-test with p-value of 0.05). This resulted in a DBN of 42 hidden variables per slice. Figure 2 shows a small portion of the hidden structure of the DBN we use.

Two novel parallel PF algorithms [1] as well as conventional PF were run on this dataset for 50 time points (100 seconds with 2 seconds fMRI sampling rate). Since the ground truth for neural activity of ROIs is unknown in this dataset, for evaluation we have used cross validation log likelihood based on kernel density estimators with Gaussian kernels and automatically chosen variance value using a cross validation procedure [5]. Parallel PFs show higher score (better) although are not much different in their performance. Conventional PF has considerably lower mean score as well as a higher variance.

The results of application of our joint analysis method to the real data (visual checkerboard experiment) are displayed in Figure 3.

![Figure 3: BOLD (top) and neural activity (bottom) estimation plots. Each plot displays the ground truth averaged BOLD response (red circles) plotted with the corresponding signal estimate produced by our Bayesian sensor fusion model (blue squares). Since true neural activity is not known for the real dataset only the estimate is displayed in the bottom plots. Horizontal axes give time (seconds), while vertical axes are arbitrary units for signal response. The BOLD response is perfectly tracked by fMRI 3a as well as by the joint analysis 3c. However, MEG completely fails to track it. fMRI only analysis fails to track neural response. In both cases this is due to varying parameters of the HFM, required since the true parameters are unknown. This lead to underdetermined problem in case of fMRI, creating random results while maintaining perfect fit, and also allowed the MEG only case to drift off completely, since it was not constrained by BOLD response. The joint analysis produced the best results in BOLD response tracking and neural activity estimation.](image)

**References**


