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Imaging Analysis, Bayesian

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Definition

This entry refers to Bayesian methods (Gelman et al. 1995; Bishop 2006) for making inferences about neural activity from brain imaging data. This includes data from functional magnetic resonance imaging (fMRI) (Huettel et al. 2009), magnetoencephalography (MEG), and electroencephalography (EEG) (Luck 2005). These data are unique in neuroscience in that they allow, through noninvasive methods, relations to be studied between the large-scale activity of the brain and human behavior. Statistical aspects of microscopic neural activity can be estimated through Bayesian inversion of appropriate mathematical models. The methods described below have been applied to the study of a wide range of human brain functions from low-level sensory processing and sensorimotor integration to studies of memory, emotion, and decision making (Frackowiak et al. 2003; Fig. 1).

Detailed Description

In what follows $N(x; m, V)$ denotes a multivariate Gaussian density, with mean m and covariance V, over the random variable x. Bayesian inference is used to transform prior distributions over parameters describing neuronal activity, $p(\theta)$, into posterior distributions, $p(\theta|y)$, based on neuroimaging data y.

Brain Mapping

MEG sensors, placed over the head, detect changes in magnetic fields due to changes in underlying neuronal currents. EEG electrodes, in contact with the scalp, detect voltage differences due to these same currents. For both MEG and EEG data (MEG/EEG), we can capture the relation between neuronal sources, θ, and measured signals y as a linear relation $y = L\theta$ where L is a lead field matrix derived from Maxwell's equations (Baillet et al. 2001).

These observations are assumed to be corrupted with Gaussian noise having covariance V_y. This leads to the statistical model

$$\begin{aligned} p(y|\theta) &= N(y; L\theta, V_y) \\ p(\theta) &= N(x; 0, V_\theta) \end{aligned} \tag{1}$$

Because there are many more potential brain sources (thousands) than MEG/EEG sensors (tens or hundreds), the prior $p(\theta)$ must provide sufficient constraints so that the sources can be recovered. MEG/EEG source reconstruction algorithms, such as "minimum norm," "low-resolution tomography (LORETA)," or "multiple sparse priors (MSP)," are differentiated by their priors and estimation algorithms for approximating the posterior $p(\theta|y)$ (Wipf and Nagarajan 2009; Litvak et al. 2011).

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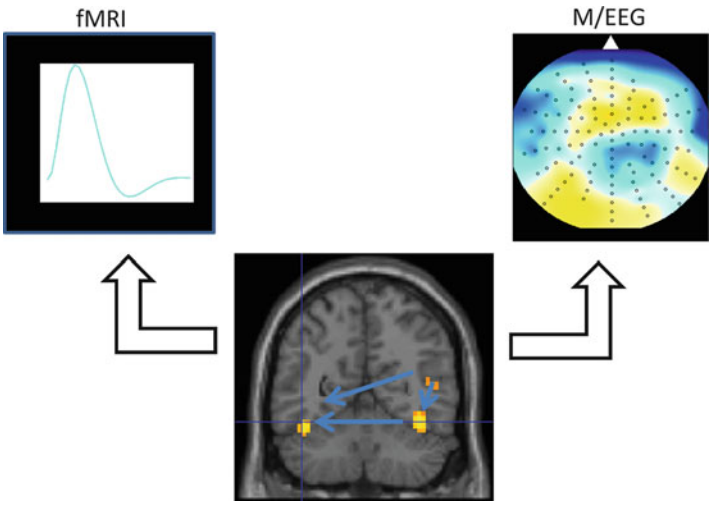

Fig. 1 Brain mapping identifies regions where experimental effect sizes are significantly nonzero (*orange*), as identified using the posterior distribution. Brain connectivity then explains activity in a set of regions using differential equation models with directed connections. For brain mapping, the parameters of interest, θ, are regional activities, and for brain connectivity, they are directed pathways (*blue*). Both approaches can be applied to data, y, from *fMRI* or *MEG*/*EEG*. For *fMRI* this requires Bayesian inversion of a forward model describing a temporal convolution and for *MEG*/*EEG* a forward model describing a spatial mapping

fMRI detects changes in neuronal activity via changes in hemodynamics and the differential magnetic properties of oxygenated versus deoxygenated blood. This is known as the blood oxygen level-dependent (BOLD) effect (Huettel et al. 2009). Given the time courses of experimental conditions, we can predict the resulting fMRI signals via temporal convolution with canonical response pro les (Friston et al. 2007b). The result of this convolution step can be captured in a design matrix X. The fMRI signal is then modeled as

$$\begin{aligned} p(Y|\theta) &= \prod_n N\left(y_n; X\theta_{\bullet n}, V_y\right) \\ p(\theta) &= \prod_k N\left(\theta_{k\bullet}; 0, V_\theta^k\right) \end{aligned} \tag{2}$$

where y_n is the fMRI time series at the nth spatial location, θ_{kn} is mean neuronal activity for experimental condition k at voxel n, and the prior covariance V_θ^k enforces local spatial smoothness constraints on the estimate of the kth neuronal response (Woolrich 2012). Inference about neuronal effect sizes can then be made from the posterior and displayed using posterior probability maps (PPMs) (Friston et al. 2007b). Bayesian methods also allow one to infer that a region has not activated (Woolrich 2012).

Brain Connectivity

Interactions among brain regions can be studied using a variety of statistical tools including structural equation modeling, regression methods, and principal or independent component analysis (Friston et al. 2007b). Studies of brain connectivity with fMRI that take a dynamical systems approach typically model time series, y, from a small number of regions (less than ten). These regions are selected based on previous analyses of imaging data or from knowledge of systems neuroscience (Kandel et al. 2000; Frackowiak et al. 2003)

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$$\begin{aligned} p(y|\theta) &= N\left(y; g(x,\theta), V_y\right) \\ \dot{x} &= \left(A + \sum_i u_i B_i\right) x + Cu \\ p(\theta) &= N(x; m_\theta, V_\theta) \end{aligned} \tag{3}$$

where $\theta = \{A, B, C, h\}$ are model parameters. Here, x is a vector of neuronal activity in multiple brain regions, $\dot{x}$ denotes the time derivative, and u is a vector of experimental stimuli. Connectivity is characterized by a set of "intrinsic connections," A; input connections, C; and modulatory connections, B. Here B specifies which intrinsic connections can be changed by contextual variables involving, for example, changes in attentional or instructional set. The overall connectivity pattern is a scientific hypothesis about the structure of the large-scale neuronal network mediating the underlying sensorimotor or cognitive function. Such hypotheses can be compared using Bayesian model selection (Penny et al. 2004).

In the above model, neuronal activity gives rise to fMRI activity by a dynamic process described by an extended Balloon (Buxton et al. 1998) and BOLD signal model. This takes the place of the linear convolution models used in mapping studies and has the advantage of accommodating, for example, nonlinear hemodynamic saturation effects. These models are not routinely used in mapping studies due to the computational expense of fitting them at large numbers of voxels. The overall dynamic model involves a set of hemodynamic state variables, state equations, and hemodynamic parameters, h. Together these equations describe a nonlinear process, $g(x, \theta)$, that converts neuronal activity into the BOLD signal.

For MEG/EEG data, dynamical connectivity models are again usually based on activity in a small number of regions

$$\begin{aligned} p(y|\theta) &= N\left(y; Lx, V_y\right) \\ \dot{x} &= f(x, u, \theta) \\ p(\theta) &= N(x; m_\theta, V_\theta) \end{aligned} \tag{4}$$

where x is a vector of neuronal activity. This activity is driven by experimental perturbations u according to a differential equation with parameters θ. Models of event-related Fifields/potentials (Luck 2005) are based on variants of the Jansen-Rit model (David et al. 2006) for describing the activity of multiple cell populations within a single cortical unit. Multiple cortical units are then connected together using anatomically realistic connection rules (Felleman and Van Essen 1991) to form large-scale networks. Priors over model parameters constrain, for example, synaptic time constants to physiological ranges. Usually, the most interesting components of the posterior distribution are those that describe changes in the long-range excitatory connections among regions (Litvak et al. 2011).

Model Inference

Bayesian inference for the above models is based on the standard corpora of approximate inference methods (Gelman et al. 1995; Bishop 2006). Due to the size of most neuroimaging data sets, with data at potentially thousands of spatial positions and hundreds of time points, deterministic methods such as variational Bayes (Bishop 2006; Friston et al. 2007a) are most often used. Methods have been developed to make inferences about families of models and effects that are consistent over a group of subjects.

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Related Terms

Q2 The fitting of differential equation models to neuroimaging data using Bayesian inference has become known as dynamic causal modeling (DCM) (Friston et al. 2003). The standard method of brain mapping based on classical inference is known as statistical parametric mapping (SPM) (Friston et al. 2007b).

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Q5	Please check if inserted volume number for Litvak et al. (2011).