Neural Mass Spatio-Temporal Modeling from High-Density Electrode Array Recordings

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Abstract—Neural mass models provide an attractive framework for modeling complex behavior in cortical circuits. The models are based on describing the dynamics of large neural populations through the space and time evolution of a small number of key aggregate statistical quantities. Fitting these models to electrode array recordings can provide insight into connectivity and structure of neural circuits as well as the response of these circuits to stimuli. However, neural mass models are fundamentally nonlinear dynamical systems with large numbers of hidden states, and validating the models on actual recordings and estimating the key parameters remains challenging. This work proposes a novel method for systematically identifying neural mass models that is particularly well-suited for high-density micro-electrocorticographic (µECoG) data. The methodology requires minimal assumptions on the model, and can automatically uncover the underlying components in the neural populations. We discuss possible applications to in vivo recordings from feline visual cortex using a recently-developed, high-density 360 contact flexible electrode array with 500 µm inter-electrode spacing.

I. INTRODUCTION

Understanding information processing in cortical circuits demands models that are analytically tractable but sufficiently rich to capture the complex dynamics and responses to stimuli. Neural mass models provide an attractive solution for this purpose by describing the behavior of large populations of neurons via a small number of aggregate statistical quantities [1]–[5]. These models have been successful in explaining a wide range of complex spatio-temporal phenomena observed in actual neural systems [6]. In addition, since the models are based on statistically averaging behavior over regions of cortical circuits, the models are ideally suited for modeling data from recordings of spatially averaged neural activity such as voltage sensitive dyes, EEG and ECoG [7]–[9].

Recent years have seen tremendous advances in electrode array technologies in terms of spatial and temporal resolution as well as area [10]–[13]. These developments offer a unique opportunity to fit these neural mass models from experimental measurements, which can in turn provide insights into the types of neural cells present in the cortex, their composition and interactions and their response to stimuli. However, validating neural mass models and identifying the key model parameters from high-density electrode array data remains mathematically challenging. The models typically have several hidden states per location to model layers of inhibitory and excitatory activities. Moreover, the evolution and interactions between these neural layers are fundamentally nonlinear.

Current methods to fit these models to neural recordings often require very specific modeling assumptions, with limited numbers of free parameters. Model fitting uses a combination of linear approximations and exhaustive search and simulation to match key statistical quantities [8], [14]. This work presents a systematic methodology for identifying a very general class of nonlinear neural mass models from ECoG data that can be readily applied to current high resolution arrays.

II. SYSTEM MODEL

The model we consider is similar to the group latent autoregressive (gLARA) model of [15] with added parameters for the nonlinearity. Specifically, we consider a network of interacting populations of neurons spread over a cortical area measured by an µECoG electrode array at N locations. Time is discretized into T steps, and we let \( x_{ik}(t) \) be the mean activity of \( k \)-th neural population in the \( i \)-th probe at time \( t \). We let \( y_{i}(t) \) denote the response of the \( i \)-the probe in time \( t \), and we assume that this response is a linear combination of the underlying activities

\[
y_{i}(t) = \sum_{k=1}^{K} C_{k} x_{ik}(t),
\]

for some coefficients \( C_{k} \). Following a standard neural mass model [4], we assume that the activities follow an nonlinear diffusion-type process of the form,

\[
x_{ik}(t+1) = (1 - \alpha_{k}) x_{ik}(t) + \sum_{k} A_{k} f(x_{ik}(t), \lambda_{k}) + \sum_{j} W_{ijk} x_{jk}(t) + s_{ik}(t),
\]

where \( \alpha_{k} \) represents a decay time constant for the \( k \)-th neural population, \( A_{k} \) is a matrix of local interactions between neural populations in the same region, and \( W_{ijk} \) represent interconnections from neural population \( k \) between two locations \( i \) and \( j \). The function \( f(x_{it}, \lambda_{k}) \) is a nonlinear excitation function with unknown parameters \( \lambda_{k} \). This formulation is very general and can incorporate a large number of nonlinear models. For example, for a sigmoidal saturation function function,
which is commonly used in these models, one can use a two-dimensional parametrization \( \lambda_k = (\lambda_{k1}, \lambda_{k2}) \) with the function

\[
 f(x_{ik}, \lambda_k) = \frac{1}{1 + \exp(\lambda_{k1} x_{ik} + \lambda_{k2})}.
\]

### III. Parameter Estimation via Expectation Maximization

The problem is to estimate the model parameters which we represent as a set

\[
 \theta := \{ W_{ijk}, \lambda_k, A_{k\ell}, C_k \},
\]

which includes the parameters \( W_{ijk} \) for the connectivity, \( \lambda_k \) for the nonlinear activation functions, and \( A_{k\ell} \) and \( C_k \) for the linear dynamics. Ideally, we would like to compute the maximum likelihood (ML) estimate of the parameter given by

\[
 \hat{\theta} := \arg \max_{\theta} p(y|\theta),
\]

where \( y = \{y_i(t)\} \) is the set of all measured probe values and \( p(y|\theta) \) is the likelihood of \( y \) given the parameter set \( \theta \). Unfortunately, exact computation of (4) is intractable due to the presence of the hidden states \( x_{ik}(t) \). Hence, we instead approximately estimated \( \theta \) with a standard expectation-maximization (EM) algorithm [16]. Similar methods have been applied in the context of micro-level connectivity mapping from fluorescent calcium imaging [17], [18] as well as fitting of the parameters in the gLARA model in [15].

The EM method generates a sequence of estimates \( \theta^\ell, \ell = 1, 2, \ldots \) for the ML estimator (4) by alternating between the following two steps:

- **E-step:** In this step, we fix the parameters \( \theta^k \), and estimate the the posterior distributions of the hidden states \( x_{ik}(t) \). That is, we compute the posterior distributions

\[
 p(x|y, \theta = \theta^\ell),
\]

where \( x = \{x_{ik}(t)\} \) is the set of all hidden states. This is essentially a filtering problem.

- **M-step:** Given the posterior distributions of the hidden states, we update the parameter estimate via the maximization

\[
 \theta^{\ell+1} = \arg \max_{\theta} \mathbb{E} \left[ \log p(x|y, \theta) \mid y, \theta = \theta^\ell \right]
\]

where \( x = \{x_{ik}(t)\} \) is the set of all hidden states in the model and the expectation is with respect to the posterior distribution (5) computed in the E-step.

The computationally challenging aspect of the estimation is the E-step since this involves filtering in a high-dimensional non-linear system. Specifically, if there are \( N \) probe locations and \( K \) populations, there are \( NK \) states in the dynamical system (2). In the application below, we are considering a high-density arrays where \( N = 360 \) with \( K = 2 \) to 4 cell types. Filtering at these dimensions can become intractable, even using simplified methods such as extended Kalman filtering. We instead propose to use a distributed filtering algorithm based on [19] based on Gaussian approximations of loopy belief propagation as in [20], [21]. In the context of the model (2) with observations (1), these methods reduce the \( NK \)-dimensional state estimation into a sequence of \( N \) \( K \)-dimensional problems.

For the M-step, the parameters \( W_{ijk}, A_{ij} \) and \( C_i \) are all linear in the state updates (2) and observations (1). Thus, the M-step optimization of these parameters can be found with a least squares. We also consider imposing sparsity constraints on the connectivity \( W_{ijk} \) as performed in [22], [23].

Since the EM method generally only convergences to a local minima, the method is potentially sensitive to the initial condition. We initialize the parameters based on a linear model using a subspace identification process [24].

### IV. Proposed Applications in Flexible Electrode Arrays

We propose to validate the methods on in vivo \( \mu \)ECoG recordings from a high-density electrode array placed on the surface of a feline visual cortex [12]. Unlike earlier arrays such as [9], this array is both flexible and non-penetrating, enabling the arrays to be scaled-up to record and stimulate larger areas of the cortex without damage, and to allow translation to human use. The array consists of 20 x 18 elements with 500 \( \mu \)m spacing sampled at 277 Hz.

Fitting the parameters in (1) and (2) can identify the composition of neuron types (e.g. inhibitory and excitatory) and their interactions. There are two potential applications: First, in one experiment, models are also fit during pharmacoologically-induced epileptic seizures to predict spatial wave patterns on during seizure onset. In the second experiment, we will fit the model to visual stimuli to understand the response of the cortex.

### References


