

---

# Cross-Spectral Factor Analysis

---

Neil M. Gallagher<sup>\*1</sup>, Kyle Ulrich<sup>\*2</sup>, Austin Talbot<sup>3</sup>,  
Kafui Dzirasa<sup>1,4</sup>, Lawrence Carin<sup>2</sup> and David E. Carlson<sup>5,6</sup>

<sup>1</sup>Department of Neurobiology, <sup>2</sup>Department of Electrical and Computer Engineering, <sup>3</sup>Department of Statistical Science, <sup>4</sup>Department of Psychiatry and Behavioral Sciences, <sup>5</sup>Department of Civil and Environmental Engineering, <sup>6</sup>Department of Biostatistics and Bioinformatics, Duke University

*\*Contributed equally to this work*

{neil.gallagher, austin.talbot, kafui.dzirasa,  
lcarin, david.carlson}@duke.edu

## Abstract

In neuropsychiatric disorders such as schizophrenia or depression, there is often a disruption in the way that regions of the brain communicate with one another. To facilitate understanding of network-level communication between brain regions, we introduce a novel model of multisite low-frequency neural recordings, such as local field potentials (LFPs) and electroencephalograms (EEGs). The proposed model, named Cross-Spectral Factor Analysis (CSFA), breaks the observed signal into factors defined by unique spatio-spectral properties. These properties are granted to the factors via a Gaussian process formulation in a multiple kernel learning framework. In this way, the LFP signals can be mapped to a lower dimensional space in a way that retains information of relevance to neuroscientists. Critically, the factors are *interpretable*. In addition, the proposed approach was empirically more or as predictive of genotype and behavioral context for data collected in a rodent model when compared to commonly used approaches that lack the interpretability of CSFA. CSFA provides a useful tool for understanding neural dynamics, particularly by aiding in the design of causal follow-up experiments.

## 1 Introduction

Neuropsychiatric disorders (e.g. schizophrenia, autism spectral disorder, etc.) take an enormous toll on our society [16]. In spite of this, the underlying neural causes of many of these diseases are poorly understood and treatments are developing at a slow pace [2]. Many of these disorders have been linked to a disruption of neural dynamics and communication between brain regions [10, 33]. In recent years, tools such as optogenetics [15, 26] have facilitated the direct probing of causal relationships between neural activity in different brain regions and neural disorders [28]. Planning a well-designed experiment to study spatiotemporal dynamics in neural activity can present a challenge due to the high number of design choices, such as which region(s) to stimulate, what neuron types, and what stimulation pattern to use. In this manuscript we explore how a machine learning approach can facilitate the design of these experiments by developing *interpretable* and *predictive* methods. These two qualities are crucial because they allow exploratory experiments to be used more effectively in the design of causal studies.

We explore how to construct a machine learning approach to capture neural dynamics from raw neural data during changing behavioral and state conditions. A body of literature in theoretical and experimental neuroscience has focused on linking synchronized oscillations, which are observable in LFPs and EEGs, to neural computation [18, 24]. Such oscillations are often quantified by spectral power, coherence, and phase relationships in particular frequency bands; disruption of these

relationships have been observed in neuropsychiatric disorders [20, 33]. There are a number of methods for quantifying synchrony between pairs of brain regions based on statistical correlation between recorded activity in those regions [36, 5], but current methods for effectively identifying such patterns on a multi-region network level, such as Independent Component Analysis (ICA), are difficult to transform to actionable hypotheses.

The motivating data considered here are local field potentials (LFPs) recorded from implanted depth electrodes at multiple sites (brain regions). LFPs are believed to reflect the combined local neural activity of hundreds of thousands of neurons [9]. The unique combination of spatial and temporal precision provided by LFPs allows for accurate representation of frequency and phase relationships between activity in different brain regions. Notably, LFPs do not carry the signal precision present in spiking activity from signal neurons; however, LFP signal characteristics are more consistent between animals, meaning that information gleaned from LFPs can be used to understand *population* level effects, just as in fMRI or EEG studies. Our empirical results further demonstrate this phenomenon.

Multi-region LFP recordings produce relatively high-dimensional datasets. Basic statistical tests typically perform poorly in such high dimensional spaces without being directed by prior knowledge due to multiple comparisons, which diminish statistical power [27]. Furthermore, typical multi-site LFP datasets are both “big data” in the sense that there are a large number of high-dimensional measurements and “small data” in the sense that only a few animals are used to represent the entire population. A common approach to address this issue is to describe such data by a small number of factors (e.g. dimensionality reduction), which increases the statistical power when relevant information (e.g. relationship to behavior) is captured in the factors. Many methods for reducing the dimensionality of neural datasets exist [14], but are generally either geared towards spiking data or simple general-purpose methods such as principal components analysis (PCA). Therefore, reducing the dimensionality of multi-channel LFP datasets into a set of *interpretable* factors can facilitate the construction of *testable* hypotheses regarding the role of neural dynamics in brain function.

The end goal of this analysis is not simply to improve predictive performance, but to design meaningful future causal experiments. By identifying functional and interpretable networks, we can form educated hypotheses and design targeted manipulation of neural circuits. This approach has been previously successful in the field of neuroscience [10]. The choice to investigate networks that span large portions of the brain is critical, as this is the scale at which most clinical and scientific *in vivo* interventions are applied. Additionally, decomposing complex signatures of brain activity into contributions from individual functional networks (i.e. factors) allows for models and analyses that are more conceptually and technically tractable.

Here, we introduce a new framework, denoted Cross-Spectral Factor Analysis (CSFA), which is able to accurately represent multi-region neural dynamics in a low-dimensional manifold while retaining interpretability. The model defines a set of factors, each capturing the power, coherence, and phase relationships for a distribution of neural signals. The learned parameters for each factor correspond to an interpretable representation of the network dynamics. Changes in the relative strengths of each factor can relate neural dynamics to desired variables. Empirically, CSFA discovers networks that are highly predictive of response variables (behavioral context and genotype) for recordings from mice undergoing a behavioral paradigm designed to measure an animal’s response to a challenging experience. We further show that incorporating response variables in a supervised multi-objective framework can further map relevant information into a smaller set of features, as in [30], potentially increasing statistical power.

## 2 Model Description

Here, we describe a model to extract a low-dimensional “brain state” representation from multi-channel LFP recordings. The states in this model are defined by a set of factors, each of which describes a specific distribution of observable signals in the network. The data is segmented into time windows composed of  $N$  observations, equally spaced over time, from  $C$  distinct brain regions. We let window  $w$  be represented by  $\mathbf{Y}^w = [\mathbf{y}_1^w, \dots, \mathbf{y}_N^w] \in \mathbb{R}^{C \times N}$  (see Fig 1[left]).  $N$  is determined by the sampling rate and the duration of the window. The complete dataset is represented by the set  $\mathcal{Y} = \{\mathbf{Y}^w\}_{w=1, \dots, W}$ . Window lengths are typically chosen to be 1-5 seconds, as this temporal resolution is assumed to be sufficient to capture the broad changes in brain state that we are interested in. We assume that window durations are short enough to make the signal approximately stationary.

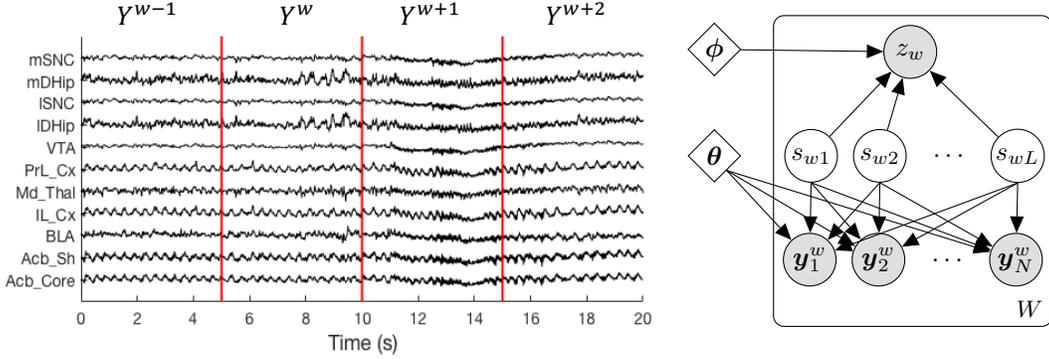


Figure 1: [left] Example of multi-site LFP data from seven brain regions, separated into time windows. [right] Visual description of the parameters of the dCSFA model.  $y_c^w$ : Signal from channel  $c$  in window  $w$ .  $z_w$ : Task-relevant side information.  $s_{w\ell}$ : Score for factor  $\ell$  in window  $w$ .  $\theta$ : Parameters describing CSFA model.  $\phi$ : Parameters of side-information classifier. Shaded regions indicate observed variables and clear represent inferred variables.

This assumption, while only an approximation, is appropriate because we are interested in brain state dynamics that occur on a relatively long time scale (i.e. multiple seconds). Therefore, within a single window of LFP data the observation may be represented by a stationary Gaussian process (GP). It is important to distinguish between signal dynamics, which occur on a time scale of milliseconds, and brain state dynamics, which are assumed to occur over a longer time scale.

In the following, the Cross-Spectral Mixture kernel [34], a key step in the proposed model, is reviewed in Section 2.1. The formulation of the CSFA model is given in Section 2.2. Model inference is discussed in Section 2.3. In Section 2.4, a joint CSFA and classification model called discriminative CSFA (dCSFA) is introduced. Supplemental Section A discusses additional related work. Supplemental Section B gives additional mathematical background on multi-region Gaussian processes. Supplemental Section C offers an alternative formulation of the CSFA model that models the observed signal as the real component of a complex signal. For efficient calculations, computational approximations for the CSFA model are described in Supplemental Section D.

## 2.1 Cross-Spectral Mixture Kernel

Common methods to characterize spectral relationships within and between signal channels are the power-spectral density (PSD) and cross-spectral density (CSD), respectively [29]. A set of multi-channel neural recordings may be characterized by the set of PSDs for each channel and CSDs for each pair of channels, resulting in a quadratic increase in the number of parameters with the number of channels observed. In order to counteract the issues arising from many multiple comparisons, neuroscientists typically preselect channels and frequencies of interest before experimental hypotheses about spectral relationships in neural datasets. Instead of directly calculating each of these parameters, we use a modeling approach to estimate the PSDs and CSDs over all channels and frequency bands by using the Cross-Spectral Mixture (CSM) covariance kernel [34]. In this way we effectively reduce the number of parameters required to obtain a good representation of the PSDs and CSDs for a multi-site neural recording.

The CSM multi-output kernel is given by

$$\mathbf{K}_{CSM}(t, t'; \mathbf{B}_q, \mu_q, \nu_q) = \text{Real} \left( \sum_{q=1}^Q \mathbf{B}_q k_q(t, t'; \mu_q, \nu_q) \right), \quad (1)$$

where the matrix  $\mathbf{K}_{CSM} \in \mathbb{C}^{C \times C}$ . This is the real component of a sum of  $Q$  separable kernels. Each of these kernels is given by the combination of a cross-spectral density matrix,  $\mathbf{B}_q \in \mathbb{C}^{C \times C}$ , and a stationary function of two time points that defines a frequency band,  $k_q(\cdot)$ . Representing  $\tau = t - t'$ , as all kernels used here are stationary and depend only on the difference between the two inputs, the frequency band for each spectral kernel is defined by a spectral Gaussian kernel,

$$k_q(\tau; \mu_q, \nu_q) = \exp \left( -\frac{1}{2} \nu_q \tau^2 + j \mu_q \tau \right), \quad (2)$$

which is equivalent to a Gaussian distribution in the frequency domain with variance  $\nu_q$ , centered at  $\mu_q$ . The matrix  $\mathbf{B}_q$  is a positive semi-definite matrix with rank  $R$ . (Note: The cross-spectral density matrix  $\mathbf{B}_q$  is also known as coregionalization matrix in spatial statistics [4]). Keeping  $R$  small for the coregionalization matrices ameliorates overfitting by reducing the overall parameter space. This relationship is maintained and  $\mathbf{B}_q$  is updated by storing the full matrix as the outer product of a tall matrix with itself:

$$\mathbf{B}_q = \tilde{\mathbf{B}}_q \tilde{\mathbf{B}}_q^\dagger, \quad \tilde{\mathbf{B}}_q \in C \times R. \quad (3)$$

Phase coherence between regions is given by the magnitudes of the complex off-diagonal entries in  $\mathbf{B}_q$ . The phase offset is given by the complex angle of those off-diagonal entries.

## 2.2 Cross-Spectral Factor Analysis

Our proposed model creates a low-dimensional manifold by extending the CSM framework to a multiple kernel learning framework [17]. Let  $t_n$  represent the time point of the  $n^{\text{th}}$  sample in the window and  $\mathbf{t}$  represent  $[t_1, \dots, t_N]$ . Each window of data is modeled as

$$\mathbf{y}_n^w = \mathbf{f}_w(t_n) + \epsilon_n^w, \quad \epsilon_n^w \sim \mathcal{N}(\mathbf{0}, \eta^{-1} \mathbf{I}_C), \quad (4)$$

$$\mathbf{F}_w(\mathbf{t}) = \sum_{l=1}^L s_{wl} \mathbf{F}_w^l(\mathbf{t}), \quad \mathbf{F}_w(\mathbf{t}) = [\mathbf{f}_w(t_1), \dots, \mathbf{f}_w(t_N)], \quad (5)$$

where  $\mathbf{F}_w(\mathbf{t})$  is represented as a linear combination functions drawn from  $L$  latent factors, given by  $\{\mathbf{F}_w^l(\mathbf{t})\}_{l=1}^L$ . The  $l$ -th latent function is drawn independently for each task according to

$$\mathbf{F}_w^l(\mathbf{t}) \sim \mathcal{GP}(\mathbf{0}, \mathbf{K}_{CSM}(\cdot; \boldsymbol{\theta}_l)), \quad (6)$$

where  $\boldsymbol{\theta}_l$  is the set of parameters associated with the  $l^{\text{th}}$  factor (i.e.  $\{\mathbf{B}_q^l, \mu_q^l, \nu_q^l\}_{q=1}^Q$ ). The  $\mathcal{GP}$  here represents a *multi-output* Gaussian process due to the cross-correlation structure between the brain regions, as in [32]. Additional details on the multi-output Gaussian process formulation can be found in Supplemental Section B.

In CSFA, the latent functions  $\{\mathbf{F}_w^l(\mathbf{t})\}_{l=1}^L$  are not the same across windows; rather, the underlying cross-spectral content (power, coherence, and phase) of the signals is shared and the functional instantiation differs from window to window. A marginalization of all latent functions results in a covariance kernel that is a weighted superposition of the kernels for each latent factor, which is given mathematically as

$$\mathbf{Y}^w \sim \mathcal{GP}(\mathbf{0}, \mathbf{K}_{CSFA}(\cdot; \boldsymbol{\Theta}, w)) \quad (7)$$

$$\mathbf{K}_{CSFA}(\tau; \boldsymbol{\Theta}, w) = \sum_{l=1}^L s_{wl}^2 \mathbf{K}_{CSM}(\tau; \boldsymbol{\theta}_l) + \eta^{-1} \delta_\tau \mathbf{I}_C. \quad (8)$$

Here,  $\boldsymbol{\Theta} = \{\boldsymbol{\theta}_1, \dots, \boldsymbol{\theta}_L\}$  is the set of parameters associated with all  $L$  factors and  $\delta_\tau$  represents the Dirac delta function and constructs the additive Gaussian noise. The use of this multi-output GP formulation within the CSFA kernel means that the latent variables can be directly integrated out, facilitating inference.

To address multiplicative non-identifiability, the maximum power in any frequency band is limited for each CSM kernel (i.e.  $\max(\text{diag}(\mathbf{K}_{CSM}(0; \boldsymbol{\theta}_l))) = 1$  for all  $l$ ). In this way, the factor scores squared,  $s_{wl}^2$ , may now be interpreted approximately as the variance associated with factor  $l$  in window  $w$ .

## 2.3 Inference

A maximum likelihood formulation for the zero-mean Gaussian process given by Eq. 7 is used to learn the factor scores  $\{\mathbf{s}_w\}_{w=1}^W$  and CSM kernel parameters  $\boldsymbol{\Theta}$ , given the full dataset  $\mathcal{Y}$ . If we let  $\boldsymbol{\Sigma}_{CSFA}^w \in \mathbb{C}^{NC \times NC}$  be the covariance matrix obtained from the kernel  $\mathbf{K}_{CSFA}(\cdot; \boldsymbol{\Theta}, w)$  evaluated at time points  $\mathbf{t}$ , we have

$$(\{\mathbf{s}_w\}_{w=1}^W, \boldsymbol{\Theta}) = \max_{\{\mathbf{s}_w\}_{w=1}^W, \boldsymbol{\Theta}} \mathcal{L}(\mathcal{Y}; \{\mathbf{s}_w\}_{w=1}^W, \boldsymbol{\Theta}) \quad (9)$$

$$\mathcal{L}(\mathcal{Y}; \{\mathbf{s}_w\}_{w=1}^W, \boldsymbol{\Theta}) = \prod_{w=1}^W \mathcal{N}(\text{vec}(\mathbf{Y}^w); \mathbf{0}, \boldsymbol{\Sigma}_{CSFA}^w), \quad (10)$$

where  $\text{vec}(\cdot)$  gives a column-wise vectorization of its matrix argument, and  $W$  is the total number of windows. As is common with many Gaussian processes, an analytic solution to maximize the log-likelihood does not exist. We resort to a batch gradient descent algorithm based on the Adam formulation [22]. Fast calculation of gradients is accomplished via a discrete Fourier transform (DFT) approximation for the CSM kernel [34]. This approximation alters the formulation given in Eq. 7 slightly; the modified form is given in Supplemental Section D. The hyperparameters of the model are the number of factors ( $L$ ), the number of spectral Gaussians per factor ( $Q$ ), the rank of the coregionalization matrix ( $R$ ), and the precision of the additive white noise ( $\eta$ ). In applications where the generative properties of the model are most important, hyperparameters should be chosen using cross-validation based on hold-out log-likelihood. In the results described below, we emphasize the predictive aspects of the model, so hyperparameters are chosen by cross-validating on predictive performance. In order to maximize the generalizability of the model to a population, validation and test sets are composed of data from complete animals/subjects that were not included in the training set.

In all of the results described below, models were trained for 500 Adam iterations, with a learning rate of 0.01 and other learning parameters set to the defaults suggested in [22]. The kernel parameters  $\Theta$  were then fixed at their values from the 500<sup>th</sup> iteration and sufficient additional iterations were carried out until the factor scores,  $\{\mathbf{s}_w\}_{w=1}^W$ , reached approximate convergence. Corresponding factor scores are learned for validation and test sets in a similar manner, by initializing the kernel parameters  $\Theta$  with those learned from the training set and holding them fixed while learning factor scores to convergence as outlined above. Normalization to address multiplicative identifiability, as described in Section 2.2, was applied to each model after all iterations were completed.

## 2.4 Discriminative CSFA

We often wish to discover factors that are associated with some side information (e.g. behavioral context). More formally, given a set of labels,  $\{z_1, \dots, z_W\}$ , we wish to maximize the ability of the factor scores,  $\{\mathbf{s}_1, \dots, \mathbf{s}_w\}$ , to predict the labels. This is accomplished by modifying the objective function to include a second term related to the performance of a classifier that takes the factor scores as regressors. We term this modified model discriminative CSFA, or dCSFA. We choose the cross-entropy error of a simple logistic regression classifier to demonstrate this, giving

$$\{\{\mathbf{s}_w\}_{w=1}^W, \Theta\} = \max_{\{\mathbf{s}_w\}_{w=1}^W, \Theta} \mathcal{L}(\mathcal{Y}; \{\mathbf{s}_w\}_{w=1}^W, \Theta) + \lambda \sum_{w=1}^W \sum_{k=0}^1 1_{z_w=k} \log \left( \frac{\exp(\phi_k \mathbf{s}_w)}{\sum_k \exp(\phi_k \mathbf{s}_w)} \right). \quad (11)$$

The first term of the RHS of (11) quantifies the generative aspect of how well the model fits the data (the log-likelihood of Section 2.2). The second term is the loss function of classification. Here  $\lambda$  is a parameter that controls the relative importance of the classification loss function to the generative likelihood. It is straightforward to include alternative classifiers or side information. For example, when there are multiple classes it is desirable to set the loss function to be the cross entropy loss associated with multinomial logistic regression [23], which only involves modifying the second term of the RHS of (11).

In this dCSFA formulation,  $\lambda$  and the other hyperparameters are chosen based on cross-validation of the predictive accuracy of the factors, to produce factors that are predictive as possible in a new dataset from other members of the population. The number of factors included in the classification and corresponding loss function can be limited to a number less than  $L$ . One application of dCSFA is to find a few factors predictive of side information, embedded in a full set of factors that describe a dataset [30]. In this way, the predictive factors maintain the desirable properties of a generative model, such as robustness to missing regressors. We assume that in many applications of dCSFA, the descriptive properties of the remaining factors matter only in that they provide a larger generative model to embed the discriminative factors in. In applications where the descriptive properties of the remaining factors are of major importance, hyperparameters can instead be cross-validated using the objective function from (11) applied to data from new members of the population.

## 2.5 Handling Missing Channels

Electrode and surgical failures resulting in unusable data channels are common when collecting the multi-channel LFP datasets that motivate this work. Fortunately, accounting for missing channels is straightforward within the CSFA model by taking advantage of the marginal properties of multivariate

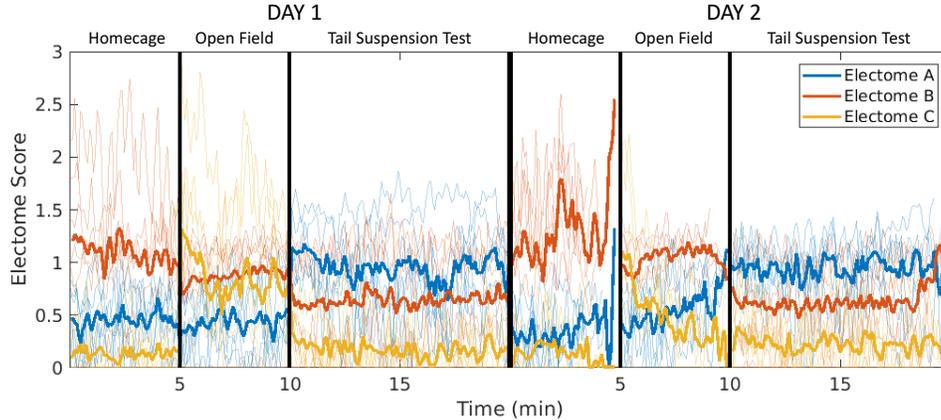


Figure 2: Scores for three different factors over the duration of a two-day experiment, for 6 different mice. Score trajectories are smoothed over time for visualization. Bold lines give score trajectory averaged over all 6 mice. These 6 mice were held out from the training set used to generate this dCSFA model and these factors.

Gaussian distributions. This is a standard approach in the Gaussian process literature [31]. Missing channels are handled by marginalizing the missing channel out of the covariance matrix in Eq. 7. This mechanism also allows for the application of CSFA to multiple datasets simultaneously, as long as there is some overlap in the set of regions recorded in each dataset. Similarly, the conditional properties of multivariate Gaussian distributions provide a mechanism for simulating data from missing channels. This is accomplished by finding the conditional covariance matrix for the missing channels given the original matrix (Eq. 8) and the recorded data.

### 3 Results

#### 3.1 Synthetic Data

In order to demonstrate that CSFA is capable of accurately representing the true spectral characteristics associated with some dataset, we tested it on a synthetic dataset. The synthetic dataset was simulated from a CSFA model with pre-determined kernel parameters and randomly generated score values at each window. Further details of the model used to generate this data is described in Supplemental Section E and Supplemental Table 2. In this way there is a known covariance matrix associated with each window of the dataset. The cross-spectral density was learned for each window of the dataset by training a randomly initialized CSFA model and the KL-divergence compared to the true cross-spectral density was computed. Hyperparameters for the learned CSFA model were chosen to match the model from which the dataset was generated.

A classical issue with many factor analysis approaches, such as probabilistic PCA [7], is the assumption of a constant covariance matrix. To emphasize the point that our method captures dynamics of the covariance structure, we compare the results from CSFA to the KL-divergence from a constant estimate of the covariance matrix over all of the windows, as is assumed in traditional factor analysis approaches. CSFA had an average divergence of  $1.0 \cdot 10^6$  compared to  $5.4 \cdot 10^7$  for the mean estimate ( $p\text{-value} = 1.7 \times 10^{-237}$ , Wilcoxon rank sum test). This indicates that, on average, CSFA provides a much better estimate of the covariance matrix associated with a window in this synthetic dataset compared to the classical constant covariance assumption.

#### 3.2 Mouse Data

We collected a dataset of LFPs recorded from 26 mice from two different genetic backgrounds (14 wild type, 12 CLOCK $\Delta$ 19). The CLOCK $\Delta$ 19 line of mice have been proposed as a model of bipolar disorder [35]. There are 20 minutes of recordings for each mouse: 5 minutes occurred while the mouse was in its home cage, 5 minutes occurred during open field exploration, and 10 minutes occurred during a tail suspension test. The tail suspension test is used as an assay of

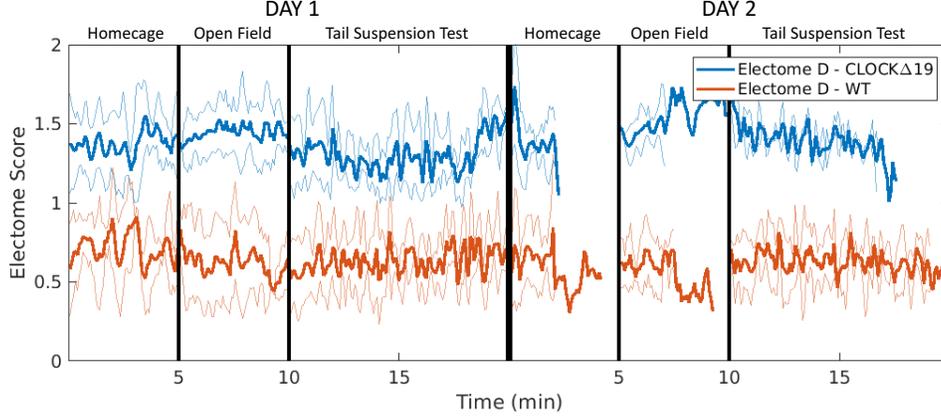


Figure 3: Scores for a single factor over the duration of a two-day experiment, for two mice each from the wild type and *CLOCK* $\Delta$ 19 genotypes. Score trajectories for mice from the *CLOCK* $\Delta$ 19 genetic background are in blue, and from a wild type background in red. Score trajectories for each mouse are smoothed in time. Bold lines give the average trace for each genotype. The data from those 4 mice were held out from the training set used to generate the dCSFA model resulting in this factor. (Note: some windows were thrown out due to noise contaminating the LFP signal, the remaining windows were concatenated for this figure, resulting in some 'empty' segments)

response to a challenging experience [1]. We learned models for CSFA and for dCSFA in two separate classification tasks: prediction of animal genotype and of the behavioral context of the recording (i.e. home cage, open field, or tail-suspension test). Following previous applications [34], the window length was set to 5 seconds and data was downsampled to 250 *Hz*. Eleven distinct brain regions were recorded: Nucleus Accumbens Core, Nucleus Accumbens Shell, Basolateral Amygdala, Infralimbic Cortex, Mediodorsal Thalamus, Prelimbic Cortex, Ventral Tegmental Area, Lateral Dorsal Hippocampus, Lateral Substantia Nigra Pars Compacta, Medial Dorsal Hippocampus, and Medial Substantia Nigra Pars Compacta. Three mice of each genotype were held out as a testing set. We choose the number of factors,  $L$ , the number of spectral Gaussians per factor (i.e. factor complexity),  $Q$ , the rank of the cross-spectral density matrix,  $R$ , and the additive noise precision,  $\eta$ , via 5-fold cross-validation, in which a CSFA model is trained for each combination of  $L \in \{10, 20, 30\}$ ,  $Q \in \{3, 5, 8\}$ ,  $R \in \{1, 2\}$ ,  $\eta \in \{5, 20\}$ , while leaving all data from a subset of animals out. Classification performance on task condition was used as the validation metric, and  $L = 21$ ,  $Q = 8$ ,  $R = 2$ ,  $\eta = 5$  was selected. For dCSFA, the first 3 factors were included in the classifier portion of each model. dCSFA was trained separately for the genotype classification and the behavioral classification. Logistic regression was used for genotype and multiple logistic regression was used for the behavioral paradigms.

We compare our CSFA and dCSFA models to several two-stage modeling approaches that are representative of techniques commonly used in the analysis of neural oscillation data [21]. Each of these approaches begins with a method for estimating the spectral content of a signal, followed by a dimension-reducing technique. Detailed descriptions of these comparison approaches are given in Supplemental Section F. The classification accuracies comparing CSFA, dCSFA, and each of the comparison methods were calculated using the test set described above; these values are shown in Table 1. For the genotype classification CSFA and dCSFA outperform the comparison methods. Figure 2 demonstrates that the predictive features learned from dCSFA clearly track the different behavioral paradigms. Importantly, while the predictive performance of the behavioral context classifier using dCSFA factor scores is barely better than the CSFA model, the classification requires *just* 3 factors, rather than 21. This is important for statistical tests and useful in experimental design. Calculating p-values for the coefficients corresponding to each factor in a logistic regression model of genotype on the *hold-out* set, the three factors learned from dCSFA to predict genotype gave p-values of 0.12,  $4.5 \cdot 10^{-47}$ , and 0.02. The strongly significant factor is visualized in Figure 4.

Model	Genotype (AUC)	Behavioral Context (Accuracy)
FFT/PCA	0.52	84.5
NP/PCA	0.82	88.1
NP/NMF	0.82	87.4
CSFA	0.85	80.8
dCSFA-21	0.86	79.6
dCSFA-3	0.75	80.1

Table 1: Classification results for genotype binary classification and experiment task multiclass classification. FFT/PCA: Magnitude of principal components of the signal FFT. NP/PCA: Principal components of a non-parametric estimate of spectral content of signal. NP/NMF: Non-negative matrix factorization of a non-parametric estimate of spectral content of signal. CSFA: CSFA factor scores. dCSFA-21: All factor scores from logistic-dCSFA model. dCSFA-3: Factor scores used in discriminative classifier for logistic-dCSFA. All numbers are reported for a lasso-logistic regression classifier, except for dCSFA-3, on which a non-regularized logistic regression classifier was used.

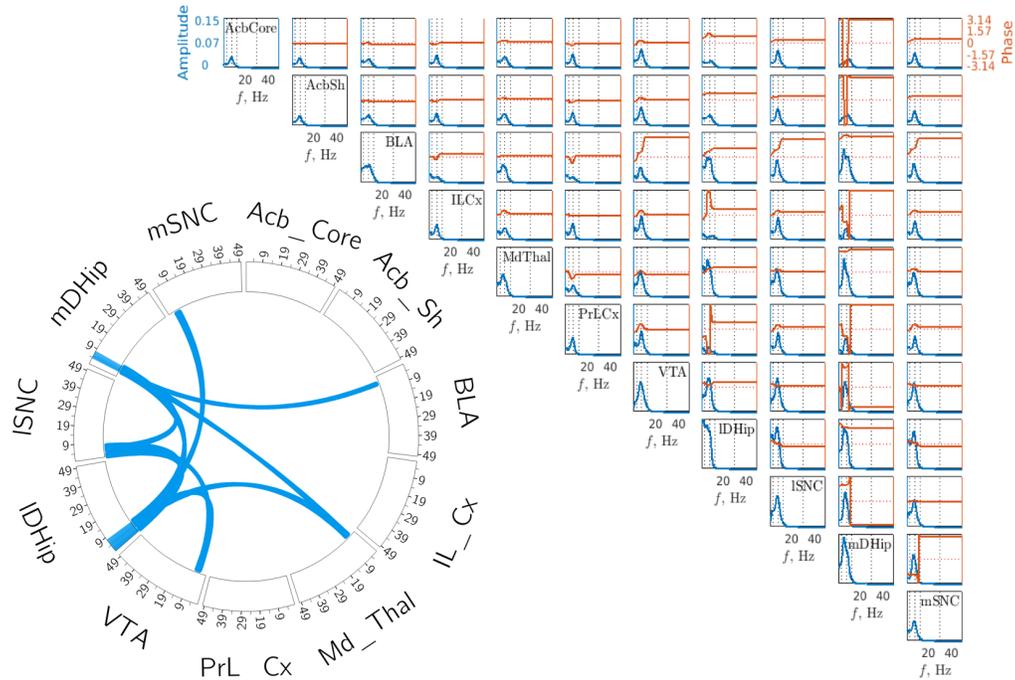


Figure 4: Visual representations of a dCSFA factor. [right] Relative power-spectral (diagonal) and cross-spectral (off-diagonal) densities associated with the covariance function defining a single factor. Amplitude reported for each frequency within a power or cross-spectral density is normalized relative to the total sum of powers or coherences, respectively, at that frequency for all factors. [left] Simplified representation of the same factor. Each 'wedge' corresponds to a single brain region. Colored regions along the 'hub' of the circle represent frequency bands with significant power within that corresponding region. Colored 'spokes' represent frequency bands with significant coherence between the corresponding pair of regions.

### 3.3 Visualization

The models generated by CSFA are easily visualized and interpreted in a way that allows neuroscientists to generate testable hypotheses related to brain network dynamics. Figure 4 shows one way to visualize the latent factors produced by CSFA. The right hand side shows the power and cross-spectra associated with the CSM kernel from a single factor. Together these plots define a distribution of multi-channel signals that are described by this one factor. Plots along the diagonal give power spectra for each of the 11 brain regions included in the dataset. The off diagonal plots show the cross spectra with the associated phase offset in orange. The phase offset implies that oscillations may originate in one region and travel to another, given the assumption that another (observed or unobserved) region is not responsible for the observed phase offset. These assumptions are not true in general, so we emphasize that their use is in hypothesis generation.

The circular plot on the bottom-left of Figure 4 visualizes the same factor in an alternative concise way. Around the edge of the circle are the names of the brain regions in the data set and a range of frequencies modeled for each region. Colored bands along the outside of the circle indicate that spectral power in the corresponding region and frequency bands is above a threshold value. Similarly, lines connecting one region to another indicate that the coherence between the two regions is above the same threshold value at the corresponding frequency band. Given the assumption that coherence implies communication between brain regions [5], this plot quickly shows which brain regions are believed to be communicating and at what frequency band in each functional network.

## 4 Discussion and Conclusion

Multi-channel LFP datasets have enormous potential for describing brain network dynamics at the level of individual regions. The dynamic nature and high-dimensionality of such datasets makes direct interpretation quite difficult. In order to take advantage of the information in such datasets, techniques for simplifying and detecting patterns in this context are necessary. Currently available techniques for simplifying these types of high dimensional datasets into a manageable size (e.g. ICA, PCA) generally do not offer sufficient insight into the types of questions that neuroscientists are interested in. More specifically, there is evidence that neural networks produce oscillatory patterns in LFPs as signatures of network activation [18]. In this work, we show that CSFA detects signatures of multi-region network activity that explain variables of interest to neuroscientists (i.e. animal genotype, behavioral context). Methods such as CSFA, which identify and interpret these signatures at a network level, are needed to form reasonable and testable hypotheses about the dynamics of whole-brain networks.

The proposed CSFA model explicitly targets known relationships of LFP data to map the high-dimensional data to a low-dimensional set of features. In direct contrast to many other dimensionality reduction methods, each factor maintains a high degree of interpretability, particularly in neuroscience applications. We emphasize that CSFA captures both spectral power and coherence across brain regions, both of which have been associated with neural information processing within the brain [19]. It is important to note that this model finds temporal precedence in random variables, rather than true causality; there are many examples where temporal precedence does not imply true causation. Therefore, we emphasize that CSFA facilitates the generation of testable hypothesis rather than demonstrating causal relationships by itself. In addition, CSFA can suggest ways of manipulating network dynamics in order to directly test their role in mental processes. Such experiments might involve closed-loop stimulation using optogenetic or transcranial magnetic stimulation to manipulate the complex temporal dynamics of neural activity captured by the learned factors.

Future work will focus on making these approaches broadly applicable, computationally efficient, and reliable. It is worth noting that CSFA describes the full-cross spectral density of the data, but that there are additional signal characteristics of interest to neuroscientists that are not described, such as cross-frequency coupling [24]; another possible area of future work is the development of additional kernel formulations that could capture these additional signal characteristics. CSFA will also be generalized to include other measurement modalities (e.g. neural spiking, fMRI) to create joint generative models.

In summary, we believe that CSFA fulfills three important criteria: 1. It consolidates high-dimensional data into an easily interpretable low-dimensional space. 2. It adequately represents the raw observed data. 3. It retains information from the original dataset that is relevant to neuroscience researchers. All

three of these characteristics are necessary to enable neuroscience researchers to generate trustworthy hypotheses about a network-level brain dynamics.

## 5 Acknowledgements

In working on this project L.C. received funding from the DARPA HIST program; K.D., L.C., and D.C. received funding from the National Institutes of Health by grant R01MH099192-05S2; K.D. received funding from the W.M. Keck Foundation.

## References

- [1] H. M. Abelaire, G. Z. Reus, and J. Quevedo. Animal models as tools to study the pathophysiology of depression. *Revista Brasileira de Psiquiatria*, 2013.
- [2] H. Akil, S. Brenner, E. Kandel, K. S. Kendler, M.-C. King, E. Scolnick, J. D. Watson, and H. Y. Zoghbi. The future of psychiatric research: genomes and neural circuits. *Science*, 2010.
- [3] M. A. Alvarez, L. Rosasco, and N. D. Lawrence. Kernels for Vector-Valued Functions: a Review. *Foundations and Trends in Machine Learning*, 2012.
- [4] S. Banerjee, B. P. Carlin, and A. E. Gelfand. *Hierarchical modeling and analysis for spatial data*. Crc Press, 2014.
- [5] A. M. Bastos and J.-M. Schoffelen. A Tutorial Review of Functional Connectivity Analysis Methods and Their Interpretational Pitfalls. *Front Syst Neurosci* 2016.
- [6] M. J. Beal. *Variational Algorithms for Approximate Bayesian Inference*. PhD thesis, University of London, United Kingdom, 2003.
- [7] C. M. Bishop. Pattern recognition. *Machine Learning*, 2006.
- [8] D. M. Blei, A. Y. Ng, and M. I. Jordan. Latent Dirichlet Allocation. *Journal of Machine Learning Research*, 2003.
- [9] G. Buzsáki, C. A. Anastassiou, and C. Koch. The origin of extracellular fields and currents—EEG, ECoG, LFP and spikes. *Nature Reviews Neuroscience*, 2012.
- [10] D. Carlson, L. K. David, N. M. Gallagher, M.-A. T. Vu, M. Shirley, R. Hultman, J. Wang, C. Burrus, C. A. McClung, S. Kumar, L. Carin, S. D. Mague, and K. Dzirasa. Dynamically Timed Stimulation of Corticolimbic Circuitry Activates a Stress-Compensatory Pathway. *Biological Psychiatry* 2017.
- [11] R. Caruana. Multitask Learning. *Machine Learning*, 1997.
- [12] B. Chen, G. Polatkan, G. Sapiro, D. Blei, D. Dunson, and L. Carin. Deep learning with hierarchical convolutional factor analysis. *IEEE Transactions on Pattern Analysis and Machine Intelligence*, 2013.
- [13] Y. Cho and L. K. Saul. Kernel methods for deep learning. In *Advances in Neural Information Processing Systems*, 2009.
- [14] J. P. Cunningham and M. Y. Byron. Dimensionality reduction for large-scale neural recordings. *Nature Neuroscience*, 2014.
- [15] K. Deisseroth. Optogenetics. *Nature Methods*, 2011.
- [16] W. W. Eaton, S. S. Martins, G. Nestadt, O. J. Bienvenu, D. Clarke, and P. Alexandre. The burden of mental disorders. *Epidemiologic reviews*, 2008.
- [17] M. Gönen and E. Alpaydm. Multiple kernel learning algorithms. *Journal of Machine Learning Research*, 2011.
- [18] A. Z. Harris and J. A. Gordon. Long-Range Neural Synchrony in Behavior. *Annual Review of Neuroscience*, 2015.
- [19] K. D. Harris and A. Thiele. Cortical state and attention. *Nature Reviews Neuroscience*, 2011.
- [20] R. Hultman, S. D. Mague, Q. Li, B. M. Katz, N. Michel, L. Lin, J. Wang, L. K. David, C. Blount, R. Chandu, and others. Dysregulation of prefrontal cortex-mediated slow-evolving limbic dynamics drives stress-induced emotional pathology. *Neuron*, 2016.
- [21] D. Iacoviello, A. Petracca, M. Spezialetti, and G. Placidi. A real-time classification algorithm for EEG-based BCI driven by self-induced emotions. *Computer Methods and Programs in Biomedicine*, 2015.
- [22] D. P. Kingma and J. Ba. Adam: A Method for Stochastic Optimization. *arXiv:1412.6980 [cs]* 2014. arXiv: 1412.6980.
- [23] C. Kwak and A. Clayton-Matthews. Multinomial logistic regression. *Nursing research*, 2002.

- [24] J. E. Lisman and O. Jensen. The Theta-Gamma Neural Code. *Neuron* 2013.
- [25] J. Mairal, P. Koniusz, Z. Harchaoui, and C. Schmid. Convolutional kernel networks. In *Advances in Neural Information Processing Systems*, 2014.
- [26] G. Miesenböck. Genetic methods for illuminating the function of neural circuits. *Current Opinion in Neurobiology*, 2004.
- [27] M. D. Moran. Arguments for rejecting the sequential Bonferroni in ecological studies. *Oikos*, 2003.
- [28] E. J. Nestler and S. E. Hyman. Animal models of neuropsychiatric disorders. *Nature Neuroscience*, 2010.
- [29] A. V. Oppenheim. *Discrete-time signal processing*. Pearson Education India, 1999.
- [30] R. Raina, Y. Shen, A. McCallum, and A. Y. Ng. Classification with hybrid generative/discriminative models. In *Advances in Neural Information Processing Systems*, 2004.
- [31] C. E. Rasmussen and C. K. I. Williams. *Gaussian Processes for Machine Learning*. the MIT Press, 2006.
- [32] Y. W. Teh, M. Seeger, and M. I. Jordan. Semiparametric Latent Factor Models. *AISTATS*, 2005.
- [33] P. J. Uhlhaas, C. Haenschel, D. Nikolić, and W. Singer. The role of oscillations and synchrony in cortical networks and their putative relevance for the pathophysiology of schizophrenia. *Schizophr Bull* 2008.
- [34] K. R. Ulrich, D. E. Carlson, K. Dzirasa, and L. Carin. GP Kernels for Cross-Spectrum Analysis. *Advances in Neural Information Processing Systems*, 2015.
- [35] J. van Enkhuizen, A. Minassian, and J. W. Young. Further evidence for clock $\delta$ 19 mice as a model for bipolar disorder mania using cross-species tests of exploration and sensorimotor gating. *Behavioural Brain Research*, 2013.
- [36] H. E. Wang, C. G. Bénar, P. P. Quilichini, K. J. Friston, V. K. Jirsa, and C. Bernard. A systematic framework for functional connectivity measures. *Front. Neurosci.*, 2014.
- [37] P. Welch. The use of fast Fourier transform for the estimation of power spectra: A method based on time averaging over short, modified periodograms. *IEEE Transactions on Audio and Electroacoustics* 1967.
- [38] A. G. Wilson, E. Gilboa, A. Nehorai, and J. P. Cunningham. Fast Kernel Learning for Multidimensional Pattern Extrapolation. *Advances in Neural Information Processing Systems*, 2014.
- [39] A. Wilson and R. Adams. Gaussian process kernels for pattern discovery and extrapolation. In *Proceedings of the 30th International Conference on Machine Learning (ICML-13)*, 2013.
- [40] M. Zhou, H. Chen, L. Ren, G. Sapiro, L. Carin, and J. W. Paisley. Non-parametric Bayesian dictionary learning for sparse image representations. In *Advances in Neural Information Processing Systems*, 2009.

## A Additional related work

The goal of this model is to design a general-purpose method for analysis of neural oscillations, specifically an interpretable generative process via a low-dimensional embedding. In machine learning, low-dimensional representations of the data are often used to capture underlying correlated structures, such as topic models [8], state-space models [6], dictionary learning [40], and deep convolutional factor analysis [12]. Due to the inherent non-linearities of oscillatory time-series, non-linear functions are convenient choices to represent this quasi-periodic data. Gaussian processes [31] provide a concise framework for placing prior distributions over these latent functions, and are increasingly being used to represent expressive features through the covariance kernel, such as deep architectures [13], convolutional factor analysis [25], or encoding arbitrary spectral densities via a Gaussian mixture [25]. This latter kernel is known as the spectral mixture (SM) covariance kernel [39], and a recent multi-task [11] extension of the SM kernel, known as the cross-spectral mixture (CSM) kernel [34], encodes the full cross-spectral density between multiple output observations within the GP framework. The CSM kernel was illustrated as an excellent tool for representing multi-output LFP data [34].

## B Multi-output Gaussian processes

A multi-output regression task includes observations from  $C$  output channels,  $\mathbf{Y} = [\mathbf{y}_1, \dots, \mathbf{y}_N] \in \mathbb{R}^{C \times N}$  at  $N$  time points. The data are modeled as

$$\mathbf{y}_n = \mathbf{f}_w(t_n). \quad (12)$$

A multi-output Gaussian process [31, 3] places a prior distribution over the latent function, given by

$$\mathbf{f}(\cdot) \sim \mathcal{GP}(\mathbf{m}(\cdot), \mathbf{K}(\cdot, \cdot; \boldsymbol{\theta})). \quad (13)$$

where the Gaussian process is defined by the mean function  $\mathbf{m}(t) \in \mathbb{R}^C$ , and the covariance function  $\mathbf{K}(t, t'; \boldsymbol{\theta}) \in \mathbb{R}^{C \times C}$ . The covariance function defines how signal in  $\mathbf{f}(\cdot)$  covaries over channels and time points, such that  $K^{c,c'}(t_n, t_{n'}; \boldsymbol{\theta}) \triangleq \text{cov}(f_c(t_n), f_{c'}(t_{n'}))$ . The mean function is often set to equal  $\mathbf{0}$ . For any set of  $N$  points  $\mathbf{t} = [t_1, \dots, t_N]$ , the values of the function  $\mathbf{f}$  are drawn from a multivariate normal distribution defined by the mean vector,  $\mathbf{M}(\mathbf{t}) = [\mathbf{m}(t_1); \dots; \mathbf{m}(t_N)] \in \mathbb{R}^{NC}$ , and the covariance matrix,  $\Sigma_K(\mathbf{t}; \boldsymbol{\theta}) \in \mathbb{R}^{NC \times NC}$ . The covariance matrix  $\Sigma_K$  is related to the covariance function  $\mathbf{K}$  in the following way:

$$\Sigma_K(\mathbf{t}; \boldsymbol{\theta}) = \begin{bmatrix} \mathbf{K}(t_1, t_1; \boldsymbol{\theta}) & \cdots & \mathbf{K}(t_1, t_N; \boldsymbol{\theta}) \\ \vdots & \ddots & \vdots \\ \mathbf{K}(t_N, t_1; \boldsymbol{\theta}) & \cdots & \mathbf{K}(t_N, t_N; \boldsymbol{\theta}) \end{bmatrix}$$

The parameters  $\boldsymbol{\theta}$  may be optimized to fit these observations by maximizing the marginal likelihood

$$\boldsymbol{\theta}^* = \arg \max_{\boldsymbol{\theta}} \log p(\mathbf{Y}|\mathbf{t}, \boldsymbol{\theta}), \quad p(\mathbf{Y}|\mathbf{t}, \boldsymbol{\theta}) = \mathcal{N}(\text{vec}(\mathbf{Y}); \mathbf{M}(\mathbf{t}), \Sigma_K(\mathbf{t}; \boldsymbol{\theta})), \quad (14)$$

where  $\text{vec}(\cdot)$  is a column-wise vectorization of its matrix-valued argument. The form of the covariance kernel constrains the types of posterior functions that may be represented by the Gaussian process. Recently, expressive covariance kernels have been explored [39, 38, 34] that are capable of representing any stationary kernel while treating  $\boldsymbol{\theta}$  as expressive features of interest extracted from the model.

## C Complex Normal Formulation

Let the observed data for a single window be  $\mathbf{Y} = [\mathbf{y}_1, \dots, \mathbf{y}_N]$ ; we drop window indexing here for simplicity. From Eq. 7 we model the data as originating from a multivariate normal distribution.

$$\mathbf{Y} \sim \mathcal{N}(\mathbf{0}, \mathbf{K}_{CSFA}(\mathbf{t}, \mathbf{t}; \boldsymbol{\Theta})). \quad (15)$$

We can consider the observed data,  $\mathbf{Y}$ , to be the real portion of a complex signal, such that

$$\tilde{\mathbf{Y}} = \tilde{\mathbf{Y}}^r + j\tilde{\mathbf{Y}}^i, \quad \tilde{\mathbf{Y}}^r = \mathbf{Y}, \quad \{\tilde{\mathbf{Y}}^r, \tilde{\mathbf{Y}}^i\} \in \mathbb{R}^{CN}, \quad (16)$$

where superscript  $r$  and  $i$  correspond to the real and imaginary components of a vector argument and  $j$  is the imaginary number. In such as case, we can represent the full complex vector  $\tilde{\mathbf{Y}}$  as arising from a multivariate circularly symmetric complex normal distribution.

$$\tilde{\mathbf{Y}} \sim \mathcal{CN}(\mathbf{0}, 2\tilde{\mathbf{K}}_{CSFA}(\mathbf{t}, \mathbf{t}; \Theta)) \quad (17)$$

$$\tilde{\mathbf{K}}_{CSFA}(\mathbf{t}, \mathbf{t}; \Theta) = \sum_{l=1}^L s_{wl}^2 \tilde{\mathbf{K}}_{CSM}(\mathbf{t}, \mathbf{t}; \theta_l) + \eta^{-1}(\mathbf{I}_N \otimes \mathbf{I}_C) \quad (18)$$

$$\tilde{\mathbf{K}}_{CSM}(\mathbf{t}, \mathbf{t}; \theta_l) = \sum_{q=1}^Q \mathbf{B}_q \otimes k_q(\mathbf{t}, \mathbf{t}; \mu_q, \nu_q), \quad (19)$$

where  $\otimes$  denotes the Kronecker product. Note that the only differences between this formulation and that given in the main text are that  $\tilde{\mathbf{K}}_{CSM}$  equal to the full complex value of the sum in Eq. 19 and that the covariance matrix in Eq. 17 is multiplied by a factor of 2.

## D DFT Approximation

The computational costs associated with calculating gradients in a CSFA model with a large number of parameters can be quite high, due to the fact that a matrix inversion is necessary for gradient calculation (see [31]). As originally described in [34], the computational costs of the CSM model can be significantly decreased by approximating the covariance matrices associated with all spectral Gaussian kernels (see Sec. 2.1) as circulant matrices. We let  $K_{ql}$  be the covariance matrix associated with the  $q^{th}$  spectral Gaussian kernel in the  $l^{th}$  factor at time points  $\mathbf{t}$ . By definition,  $K_{ql}$  is a symmetric Toeplitz matrix, such that it is uniquely identified by its first column,  $\mathbf{c}$ . We get a circulant matrix approximation of  $K_{ql}$  by generating a new first column,  $\tilde{\mathbf{c}}$ , by reflecting the first  $\lfloor \frac{N}{2} + 1 \rfloor$  elements of  $\mathbf{c}$  to the last  $\lfloor \frac{N}{2} + 1 \rfloor$ . The resulting matrix,  $\tilde{K}_{ql}$ , is diagonalizable by the discrete Fourier transform (DFT) in the following way. Letting  $\mathbf{U}$  be the  $N \times N$  unitary DFT matrix, and  $\delta$  be the sampling period associated with time points  $\mathbf{t}$ , we have

$$\mathbf{U}^\dagger \tilde{K}_{ql} \mathbf{U} = \Lambda_{\tilde{K}_{ql}} = \text{diag}(\delta^{-1} S(\omega)), \quad (20)$$

where  $\omega$  is the vector of frequencies corresponding to the DFT transformation over  $\mathbf{t}$ , and  $S(\cdot)$  is the power spectral density associated with  $\tilde{\mathbf{c}}$ . In this way, we only need to perform computation on the diagonal matrix  $\Lambda_{\tilde{K}_{ql}}$ , rather than on the full matrix  $K_{ql}$ . As the sampling rate and window length approach infinity there is no error in approximating  $K_{ql}$  with  $\tilde{K}_{ql}$  [34], due to sufficient resolution of the DFT frequency bins.

CSFA can take advantage of the same approximation, when formulated in the following way. Letting  $\mathbf{Z}$  denote the DFT of the observed data, we have

$$\mathbf{Z} \sim \mathcal{CN}(\mathbf{0}, 2\mathbf{\Sigma}(\omega, \omega; \Theta)) \quad (21)$$

$$\mathbf{\Sigma}(\omega, \omega; \Theta) = (\mathbf{I}_C \otimes \mathbf{U})^\dagger \tilde{\mathbf{K}}_{CSFA}(\mathbf{t}, \mathbf{t}; \Theta) (\mathbf{I}_C \otimes \mathbf{U}) \quad (22)$$

$$\approx \eta^{-1}(\mathbf{I}_N \otimes \mathbf{I}_C) + \sum_{l=1}^L s_l^2 \sum_{q=1}^Q \mathbf{B}_{ql} \otimes \Lambda_{\tilde{K}_{ql}}(\omega; \mu_{ql}, \nu_{ql}). \quad (23)$$

This approximation results in a covariance matrix,  $\mathbf{\Sigma}$ , that is block diagonal, significantly reducing the cost of the matrix inversion necessary for computing gradients.

## E Artificial Dataset Parameterization

To generate our synthetic dataset we generated random draws from a CSFA model with 4 channels and 5 latent factors, each factor containing a single spectral Gaussian component. The parameters for the original CSFA model from which the data were generated are given in Table 2. We simulated 5000 time windows of 5s sampled at 500Hz. For each window a random subset of scores were nonzero with 40% of the scores being nonzero on average for any given window. The non-zero scores were independently drawn from a uniform distribution, then normalized such that the sum of squared scores for each window added to one. This normalization scheme gives approximately unit variance for the signal in each window.

Factor	Spectral Gaussian Mean (Hz)	Spectral Gaussian Variance (Hz <sup>2</sup> )	Channel Weights	Channel Shifts
1	6	1	$[e^{2.25} e^2 0 0]$	$[0 0 0 -\pi/2]$
2	6	1	$[0 0 e^2 e^{1.75}]$	$[0 0 0 \pi/2]$
3	10	1	$[e e e e]$	$[0 \pi/4 \pi/2 3\pi/4]$
4	20	5	$[0 e e^{0.75} 0]$	$[0 0 \pi/2 0]$
5	3	1	$[e^{2.5} e^{2.5} e^{2.25} e^{2.75}]$	$[0 -\pi/8 -\pi/4 -3\pi/8]$

Table 2: Parameter values for simulated CSFA dataset

## F Comparison Methods

To provide a comparison of our method we describe three alternative approach to classifying side information using the power and cross spectra. Just like CSFA, we divide the recording in to a series of time windows. In the first method, each window was simply converted to the spectral domain via Fourier transform, and then principal components analysis (PCA) was applied to the absolute value of the vectorized form of 5500 covariates. We refer to this first method in the text as FFT/PCA.

In the remaining two methods, for each window we estimate the power spectra for each channel, and coherence for each pair of channels, independently using Welch’s method [37], a non-parametric method for obtaining a denoised estimate of the power spectra. Letting  $F$  equal the number of frequencies used and  $C$  equal the number of channels, this gives us a high dimensional  $(F * (C + 1) * C/2)$  representation of the brain dynamics for each window (ignoring directionality). In our second method, this dimensionality is reduced using PCA. That method is referred to in the text as NP/PCA (i.e. non-parametric spectral estimation and PCA). Dimensionality is reduced in the third method using a non-negative matrix factorization (NMF). We refer to this approach in the text as NP/NMF. This approach is more similar to CSFA because we end up with all positive factors as well as non-negative loadings (scores). The number of factors used in each model was chosen using the same cross-validation scheme as described in section 2.3 for the CSFA hyperparameters.

A large advantage of all of these methods is the computational cost is significantly lower than CSFA. However, these methods lose the interpretability of CSFA. First of all these are nonparametric estimates of the power and cross spectra which means that there are no constraints between the estimate (variations in cross spectra are independent from the other channels). With both PCA and NNM the factors are not sparsified in any way, which means that every factor involves every frequency in every channel. This means that interpreting the factors requires interpreting a combination of every frequency and coherence. This contrasts with CSFA where, by using parametric spectral Gaussian distributions and coregionalization matrices, the few parameters have strong significance.