**Conditional Random Fields for Single Cell Targeting of Neuronal ensembles**

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**Highlights <85**

- CRFs depict neuronal ensembles representing features of visual stimuli**70**

- CRFs allows identification of core neurons from each neuronal ensemble**70**

- Core neurons evoke pattern completion of optogenetically imprinted ensembles**76**

- CRFs capture changes in network dynamics induced by circuit reconfiguration**75**

**Summary 139<150**

The prediction of different states from many variables with mutual dependencies is fundamental for the creation of models in varied applications including: natural language, computer vision and bioinformatics. Such problems can be approached by structured prediction methods that combine graphical models and classification algorithms. Conditional random fields (CRFs) represent a widely used probabilistic method for structured prediction. However, CRFs application to infer the functional connectivity of biological neural networks remains unexplored. We used CRFs and graph theory in population calcium imaging from primary visual cortex (V1) of awake behaving mice to identify neuronal ensembles and predict visual stimuli. Finally, using simultaneous two-photon imaging and optogenetics we show that our approach can be used to identify core neurons from neuronal ensembles imprinted in vivo. Our method provides a powerful tool for targeting individual neurons that can influence overall network activity.

**Introduction**

The coordinated firing of neuronal populations is considered to be the substrate of sensory, behavioral and cognitive functions. These coactive neuronal groups, defined as neuronal ensembles, are assumed to generate complex circuit functions that cannot be achieved by single neurons ([Miller et al., 2014](#_ENREF_28)). Recent advances in two-photon calcium imaging and two-photon optogenetics, have made possible the recording of simultaneous activity from large ensembles of neurons while manipulating population activity with single cell resolution in awake behaving animals ([Carrillo-Reid et al., 2016](#_ENREF_9)). However, how the functional connectivity in cortical microcircuits relate to their function has been difficult to elucidate because it requires the identification of physiologically relevant neurons that can be targeted during close-loop optogenetic experiments, allowing the manipulation of learned behavioral tasks.

Graph theory has been applied to model the structural and functional organization of the brain ([Bullmore and Sporns, 2009](#_ENREF_6)). However, graphs are usually constructed with nodes representing brain regions ([He et al., 2007](#_ENREF_18)), and edges representing information flow ([Iturria-Medina et al., 2008](#_ENREF_20)). For functional analysis, many studies have constructed graphs with data from fMRI, EEG and electrode arrays, taking brain regions ([Achard and Bullmore, 2007](#_ENREF_1); [Fair et al., 2008](#_ENREF_14); [Hagmann et al., 2008](#_ENREF_16)), voxels ([Eguiluz et al., 2005](#_ENREF_13); [van den Heuvel et al., 2008](#_ENREF_43); [Zuo et al., 2012](#_ENREF_47)) or electrode position ([Downes et al., 2012](#_ENREF_12)) as nodes, and activity associations such as cross correlation, mutual information and Granger causality as edges ([Bullmore and Sporns, 2009](#_ENREF_6); [Fair et al., 2008](#_ENREF_14); [Khazaee et al., 2015](#_ENREF_21); [Micheloyannis et al., 2009](#_ENREF_27); [Wang et al., 2010](#_ENREF_44)).

On the other hand, at the single cell level graphical models have been used to describe organizing principles of artificial neural networks, identifying neurons that could have a potential role orchestrating the overall network activity ([Iturria-Medina et al., 2008](#_ENREF_20); [Sporns, 2000](#_ENREF_37)). Such graphs are usually associated with a restricted set of parameters that describe the weight and direction of edges obtained by pairwise correlations, therefore are incapable of characterizing the emergent properties of cortical ensembles described by the whole population activity. Finally, although a few studies have applied graph theory to model network organization in calcium imaging data with single cell resolution in cultures or brain slices ([Bonifazi et al., 2009](#_ENREF_5); [Gururangan et al., 2014](#_ENREF_15); [Yatsenko et al., 2015](#_ENREF_45)), it has not been applied to define the functional connectivity based on the joint probability distribution of neuronal ensembles in awake behaving animals.

Cortical ensembles in primary visual cortex consist of strongly interconnected neurons ([Carrillo-Reid et al., 2016](#_ENREF_9); [Ko et al., 2011](#_ENREF_22)), forming a network structure that can be naturally modeled with graph theory, where nodes and edges are biologically meaningful representing neurons and their connections respectively. We demonstrate that graph theory applied to CRFs allows the identification of cortical ensembles associated with different experimental conditions opening the possibility of targeting, with two-photon optogenetics, the most significant neurons from specific populations during physiological processes.

**Results**

**Identification of cortical ensembles from calcium imaging population data**

Cortical ensembles in primary visual cortex represent neuronal populations responding to specific features of visual stimuli ([Carrillo-Reid et al., 2015a](#_ENREF_7); [Carrillo-Reid et al., 2016](#_ENREF_9); [Miller et al., 2014](#_ENREF_28)). The overall activity of multiple cells at a given time window can be understood as a multidimensional array of population vectors where vectors pointing to a similar space can be considered as a group (Figure 1). We previously showed that population vectors defining a group (i.e. a cortical ensemble) can be extracted from multidimensional arrays performing singular value decomposition (SVD) ([Carrillo-Reid et al., 2015a](#_ENREF_7)). Even though SVD can identify cortical ensembles reliably, it lacks from a fully characterized model that allows the systematic study of changes in functional connectivity during different experimental conditions.

**CRFs models predict external stimuli**

CRFs model the conditional distribution *p*(**y**|**x**) for observed population activity **x** over all nodes and network states **y** with an associated graphical structure. Therefore, CRFs have been successfully applied in diverse areas such as news and finance ([Peng et al., 2011](#_ENREF_31); [Tang et al.](#_ENREF_41)), bioinformatics ([Li et al., 2008](#_ENREF_24); [Liu et al., 2006](#_ENREF_26); [Sato and Sakakibara, 2005](#_ENREF_34)), computer vision ([He et al., 2004](#_ENREF_17); [Sminchisescu et al., 2006](#_ENREF_36)) and natural language processing ([Choi et al., 2005](#_ENREF_11); [Lafferty et al., 2001](#_ENREF_23)).

In order to construct a fully characterized model from the observations, we used CRFs representing neurons and their functional connections as nodes and edges in a graph (Figure 2A). To obtain the probability estimation to observe different network states based on observed population vectors, we assume that observed activity events from each neuron were generated by nodes in a graph structure, and that each node can have two values: ‘0’ corresponding to non-activity, and an ‘1’ corresponding to neuronal activity. In this way nodes interact with each other by connecting edges, which have four possible combinations ‘00’, ‘01’, ‘10’, and ‘11’, depending on the values of the two nodes on the edge. The two values associated with nodes and the four values associated with edges are characterized by a set of parameters called node potentials (ϕ0, ϕ1) and edge potentials (ϕ00, ϕ01, ϕ10, ϕ11) correspondingly (Figure 2A). These parameters reflect the likelihood of individual values on each node and edge. The strength of synchronization between two neurons can then be represented by the term . Using part of the observation data, we obtained the model parameters and performed cross-validation on the withheld data. We then eliminated weak edges by the synchronization strength term using a threshold generated from models constructed from shuffled data. Therefore, the likelihood of the neuronal population exhibiting a specific activation pattern can be described by the normalized product of the corresponding nodes and edge potentials (Figure 2A).

To integrate the information of external stimulus with the observed data, we added a hidden node for each presented stimulus, and set it to ‘1’ when the corresponding stimulus was on and ‘0’ when the stimulus was off (Figure 2B). We then trained CRFs models using the real data with hidden nodes. In this way, the nodes that are directly connected to the hidden nodes depict different visual stimuli (Figure 2C).

CRFs model the conditional probability of network states given the observations. Therefore, by treating visual stimuli as nodes and comparing the output likelihood of observing each stimulus, such models are able to predict visual stimuli from observed data. For example, with two visual stimuli (horizontal and vertical drifting gratings), we computed the likelihood of and , corresponding to observing horizontal and vertical stimulus, separately. The relative likelihood, , can be used to predict the presented stimuli (Figure 2D, 2F). To evaluate the prediction performance, we calculated three standard measurements from the number of true positives (TP), true negatives (TN), false positives (FP) and false negatives (FN): accuracy, defined as (TP+TN)/(TP+TN+FP+FN); precision, defined as TP/(TP+FP); recall, defined as TP/(TP+FN). Predictions made from thresholding the relative likelihood give a mean accuracy of xxx (Figure 2G), with precision xxx (Figure 2H) and recall xxx (Figure 2I).

**Emergent properties depicted from CRFs graphs**

To investigate if cortical ensembles identified by CRFs represent emergent network properties that cannot be understood by single cell activity or pair correlations we compared CRFs graphs against graphs constructed from pairwise correlation values (CC graph) between neurons, using observed spikes along with hidden nodes that represent visual stimuli (Figure 3A) ([Bonifazi et al., 2009](#_ENREF_5); [Downes et al., 2012](#_ENREF_12); [Sadovsky and MacLean, 2014](#_ENREF_33); [Zuo et al., 2012](#_ENREF_47)). CC and CRFs graphs show significantly different density (Figure 3B) as well as distribution of node degrees, local clustering coefficient and centrality (Figure 4C-E). Both also show nonrandom structures indicated by a heavy tail, compared with Erdos-Renyi random graphs, which preserve the number of nodes and edges (Figure 4C-E). Thus CRFs and CC graphs differ from each other (Figure 4), indicating that CRFs graphs capture network properties that are not detected in CC graphs.

**Identification of core neurons from CRFs ensembles using graph theory**

Brain network shows both structural and functional modularization, in both macro-scale and micro-scale ([Achard et al., 2006](#_ENREF_2); [Bonifazi et al., 2009](#_ENREF_5); [Hagmann et al., 2008](#_ENREF_16); [He et al., 2007](#_ENREF_18); [Shimono and Beggs, 2015](#_ENREF_35); [Sporns et al., 2007](#_ENREF_38); [Stetter et al., 2012](#_ENREF_39); [Zuo et al., 2012](#_ENREF_47)). Network modularization is often characterized by local structures with high inter-connectivity, where a group of neurons shows dense physical or functional connections. Such structures can be described with concepts defined in different spatial scales such as cliques, communities ([Palla et al., 2005](#_ENREF_30)), hubs and modules ([Bullmore and Sporns, 2009](#_ENREF_6)).

Most of the neurons used to predict the stimuli presented interact with the hidden nodes through direct or one-step indirect connections. However, in order to design close loop optogenetic experiments targeting specific neurons it is necessary to identify core neurons from each neuronal ensemble that can represent each visual stimulus. The probability distribution of a CRF model can be factored as the product of clique potentials of maximal cliques, according to the Hammersley Clifford theorem:

where maximal cliques are complete subgraphs (fully interconnected subgraphs) that cannot be extended by adding more nodes (Figure 4A). Therefore, maximal cliques can be considered as functional units in a graph. We then examined the maximal cliques that contain at least one node that has a direct connection with the hidden nodes (Figure 4B). CC and CRF graphs show significantly different number and size of maximal cliques (Figure 4C, 4D), indicating that CRF graphs captures properties that cannot be found in CC graphs. The size of CRF maximal cliques is larger than that from Erdos-Renyi random graphs, indicating those structures cannot be considered as random. Therefore, maximal cliques can be considered as the most significant for a specific given condition.

**Significant neurons from cortical ensembles are optimal for external stimuli prediction**

Neuronal ensembles identified with CRFs and SVD consist of xxx% and xxx% cells of the total population, separately (Figure 5A, 5B), while they share xxx% cells (Figure 5C). In contrast, cells that are highly tuned to a specific orientation of visual stimuli (high OSI) consists of only xxx% of the total population and share only xxx% with CRFs ensembles (Supplementary Figure 5x) indicating that cortical ensembles are not purely orientation selective cells ([Carrillo-Reid et al., 2015b](#_ENREF_8))

We then evaluated the identified significant neurons by their performance of predicting external visual stimuli presented to the mice. To make predictions with ensemble activity, we calculated the cosine similarity between population vectors ([Carrillo-Reid et al., 2015a](#_ENREF_7)) observed in real data compared to population vectors defined by CRFs. Similarity coefficients between CRFs population vectors and real data reproduces presented stimulus (Figure 5D), and is specific to the stimulus activation periods. Prediction statistics show the CRFs defined ensembles have higher prediction accuracy, precision and recall than SVD method (Figure 5E-G), demonstrating that CRF models outperform existing ensemble identification approaches.

We next investigated whether significant neurons from cortical ensembles identified by CRFs represent the optimal group of neurons for the prediction of presented visual stimuli. To do this, we randomly resized identified cortical ensembles adding or removing elements from the significant population (Figure 6 A-D) and examined the prediction performance. The similarity between population vectors of resampled ensembles has a maximum value when ensemble size is unchanged (Figure 6A). Furthermore, the most significant neurons from cortical ensembles achieve the best accuracy, precision and recall when predicting the presented visual stimuli, compared with resized ensembles (Figure 6B-D).

So far we have shown that the most significant neurons identified by CRFs represent the optimal population to predict external visual stimuli. This fact raises the question of whether CRFs ensembles are a specific non-random subgroup. To answer this question, we randomly sampled a subset of the total neuronal population, ranging from 10% to 90% of all neurons (Figure 6 E-H). We observed that prediction performance from random groups of neurons is significantly lower than CRFs ensemble performance (Figure 6 E-H), indicating that identified ensembles are non-random structures.

**CRFs as a tool for the targeted manipulation of cortical microcircuits**

A challenging issue regarding the design of closed-loop optogenetic experiments to manipulate behavioral tasks in awake animals is the identification of core neurons that could be used to recall learned patterns. To investigate if our CRFs model based on population activity can predict changes in the functional connectivity of cortical microcircuits we compared the models generated by CRFs before and after two-photon population manipulation of a given set of neurons. Interestingly the total number of edges depicted during ongoing activity remains the same suggesting that a new ensemble has been added to the network preserving an overall architecture. It has been recently shown that the coordinated firing of an identified neuronal population imprints an artificial cortical ensemble that can be recalled later on ([Carrillo-Reid et al., 2016](#_ENREF_9)). We demonstrate that our approach also revealed the existence of highly connected neurons that are able to recall imprinted ensembles demonstrating that CRFs could be used to target specific members of ensembles that play a key role in the computational properties of cortical microcircuits (FIG 7).

**Discussion**

**Functional network reconstruction with *in vivo* two-photon calcium imaging**

In the past few decades, graph theory has been applied to characterize the structure and function of neuronal networks ([Achard and Bullmore, 2007](#_ENREF_1); [Bettencourt et al., 2007](#_ENREF_4); [Chiang et al., 2016](#_ENREF_10); [Downes et al., 2012](#_ENREF_12); [Fair et al., 2008](#_ENREF_14); [Hagmann et al., 2008](#_ENREF_16); [Iturria-Medina et al., 2008](#_ENREF_20); [Oh et al., 2014](#_ENREF_29); [Supekar et al., 2008](#_ENREF_40); [Yu et al., 2008](#_ENREF_46); [Zuo et al., 2012](#_ENREF_47)). While most of these studies operated on functional recording across multiple brain regions ([Achard and Bullmore, 2007](#_ENREF_1); [Chiang et al., 2016](#_ENREF_10); [Fair et al., 2008](#_ENREF_14); [Hinne et al., 2013](#_ENREF_19); [Zuo et al., 2012](#_ENREF_47)), only a few have focused on the properties of local cortical region properties with recording from single neurons in the region ([Bonifazi et al., 2009](#_ENREF_5); [Carrillo-Reid et al., 2015b](#_ENREF_8); [Sadovsky and MacLean, 2014](#_ENREF_33); [Stetter et al., 2012](#_ENREF_39); [Yatsenko et al., 2015](#_ENREF_45)).

The majority of methods applied to reconstructing functional connectivity in brain slices ([Sadovsky and MacLean, 2014](#_ENREF_33); [Stetter et al., 2012](#_ENREF_39)) or *in vivo* ([Carrillo-Reid et al., 2015b](#_ENREF_8); [Yatsenko et al., 2015](#_ENREF_45)) operate on the correlation matrix, and aim at recovering the functional dependencies between observed neurons. Such methods are valuable for revealing network properties such as node degrees, clustering coefficient and functional hubs, and have been applied in medical diagnosis. However, these methods are model-free, therefore are incapable of describing the probability distribution different activity states of the network. In this study, we provide a tool for modeling the functional network in mouse primary visual cortex *in vivo* by constructing conditional random field models. These models not only reveals the structure of the functional connections, but also provide a full distribution of the conditional probability of network state given the population activity, and are capable of predicting the external visual stimulus presented to the network (Figure 2).

**CRF models for identifying core neurons**

Compared with generative graphical models such as Hidden Markov Model (HMM) that represent the joint probability distribution of observation and network state, CRF, as a type of discriminative model, model only the conditional probability, therefore avoid modeling the probability distribution of observations as well as any assumptions on the potentially complex dependencies between observation variables ([Lafferty et al., 2001](#_ENREF_23)). Additionally, given the finite number of discrete population activity types, conditional distribution itself is sufficient for making predictions. Compared with other discriminative models such as Max entropy Markov model (MEMM), CRF achieves higher accuracy by using a global normalizer to overcome the local bias in MEMM induced by local normalizer ([Lafferty et al., 2001](#_ENREF_23)).

The difficulty of constructing CRF models lie in the computation of the global normalizer. With an arbitrary graph structure, this problem is often intractable. Recent advances that combines Bethe free energy approximation and Frank-Wolfe method for inference and learning model parameters allow fast and relatively accurate construction of cyclic CRF models ([Tang et al., 2016](#_ENREF_42)). This, for the first time, makes applying CRF models in datasets with hundreds of interconnected neurons possible. Constraints for applying CRF models still exist: with less than 400 frames of training data, the learned model does not achieve the best performance (Supplementary Figure x).

Compared with the SVD method, our approach of core neuron identification improved the prediction accuracy by only xxx%. One reason could be that the current algorithm of learning CRF executes structure learning step and parameter learning step separately. Therefore, the learned graphical structure and parameters may not be the globally best matching ones. It is still computational unrealistic to explore all possible structure and parameter combinations. Additionally, approximations in parameter inference also does not guarantee global optimal. Improvement on CRF learning algorithms is expected.

**Targeted optogenetics of core neurons**

It has been suggested that in large networks, node connectivity follows a scale-free power-law distribution ([Barabasi and Albert, 1999](#_ENREF_3)). In such scale-free networks, a small subset of nodes with high connectivity exists with a probability that decays exponentially with node degrees. Similarly, neuronal networks would be characterized by a subset of neurons with strong synaptic connections. Previous studies have shown evidence for the existence of such functional hubs ([Bonifazi et al., 2009](#_ENREF_5); [Hagmann et al., 2008](#_ENREF_16)). Perturbing the activity of a single hub changed the entire network dynamics ([Bonifazi et al., 2009](#_ENREF_5)), confirming the importance of functional hubs in regulating network activity.

To investigate the role of core neurons in a network, techniques for identifying and manipulating such neurons are needed. Optogenetics manipulations have been applied to show that coactivation of neuronal groups underlying physiology processes can induce relevant behavior changes ([Liu et al., 2012](#_ENREF_25)). While one-photon optogenetics activate cells in an entire area, two-photon optogenetics allow manipulating ensemble activity with single cell precision. Recently, our group demonstrated that cortical circuit reconfiguration of neuronal ensembles can be achieved by two-photon optogenetics ([Carrillo-Reid et al., 2016](#_ENREF_9)). Our method thus serves as a powerful tool of guiding the design of such optogenetic experiments, and opens up the possibility of probing the function of core neurons in cortical networks.

**Figure legends**

**Figure 1. Two-photon imaging of population activity in primary visual cortex in awake behaving mice**

(A) Illustration of the experimental setup. Mice were head fixed to a two-photon microscope, and were allowed to run on a treadmill. Visual stimuli of drifting gratings were presented on a screen to the monocular side of the mice. (B)A representative field of view with detected ROIs. Scale bar represents xxx. (C) Schematic of generating the dissimilarity matrix for finding neuronal ensembles. Binary spike vectors for each frame were normalized using TF-IDF, and the cosine distance between every pair of normalized vectors were calculated, which was further used as the input to SVD. (D) Example of visual ensemble activity identified using SVD. Red cells represent the ensemble of horizontal visual stimuli; blue cells represent the ensemble of vertical visual stimuli. (E) Activities of visual and spontaneous ensembles. Raster plot shows the extracted spikes during spontaneous activity or under visual stimuli. Mouse was shown with horizontal and vertical drifting gratings in an alternative fashion. Light red and blue vertical stripes indicate the time of horizontal and vertical stimuli, respectively. Red box highlights the activity of significant neurons for horizontal visual stimuli. Blue box highlights the activity of significant neurons for vertical visual stimuli. Black and purple box highlight significant neurons for spontaneous activity. Gray box shows the rest of the neurons. Cells in the two visual ensembles tend to be co-active during their corresponding visual stimuli, whereas cells in spontaneous ensembles exhibit patterns that are more irregular. Scale bar represents 400 frames.

**Figure 2. Conditional random field model predicts visual stimulus**

(A) Illustration of conditional random field model. Shaded nodes (x) represent the observed binary spiking state of the neurons. White nodes (y) represent true states of the neurons, and are connected by edges that indicate their mutual dependencies; node potentials are defined over the two possible states of each node, and edge potentials are defined over the four possible states of each existing edge, depending on the state of the two nodes it connects. The probability distribution of the network over all possible states can therefore be factored using the node and edge potentials. (B) Illustration of hidden nodes in a CRF model. In this case, two hidden nodes (squares) were added for the horizontal (red) and vertical (blue) visual stimuli, separately. Nodes that are directly connected to the two hidden nodes are also highlighted in the corresponding color. (C) An example of graphs constructed with hidden nodes. Nodes that are either directly connected to the hidden nodes or indirectly connected to the hidden nodes through one intermediate nodes are highlighted. Connecting edges between them are also highlighted. Square on the upper left corner corresponds to horizontal stimulus (red); square on the lower left corner corresponds to vertical stimulus (blue). (D) Example of relative log-likelihood calculated by the CRF model. Black trace shows . Gray dashed line represents 0. Light red and blue vertical stripes indicate the time of horizontal and vertical stimuli, respectively. (E) Prediction raster plot from the example in (D). Top panel shows the prediction for horizontal stimulus; bottom panel shows the prediction for vertical stimulus. (F) Relative log-likelihood during horizontal and vertical stimuli. Red box represents the distribution of relative log-likelihood during horizontal stimulus; blue box represents the vertical stimulus. Gray region represents the threshold of 3 times baseline standard deviation level. (G-I) Accuracy (G), precision (H) and recall (I) of prediction.

**Figure 3. Graph properties of CRF models and correlation-based models**

(A) An examples of graphs constructed with CRF model and with pairwise correlations (CC). In the latter case, pairwise Pearson correlations between frames were calculated, and the threshold is determined by 5% significance level of correlation values of shuffled data. Here node size is proportional to the node degree, and the edge color represents the synchrony edge potential (ф11+ ф00- ф01- ф10). (B) Graph density of CRF and CC models. (C-E) The complementary cumulative distribution of node degrees (C), local clustering coefficients (D), and eigenvector centrality (E) in CC and CRF model. Both models show more dispersed distributions than random models, while the properties of CRF model differ from CC model.

**Figure 4. Maximal clique properties of CRF models and correlation-based models**

(A) Illustration of 3, 4 and 5-cliques with corresponding adjacency matrices. (B) An example of maximal cliques that contain at least one node directly connected with the hidden nodes. The top panel highlights all the maximal cliques for horizontal stimulus; the bottom panel highlights all the maximal cliques for vertical stimulus. (C) The number of maximal cliques in CC and CRF models. (D) The complementary cumulative distribution of maximal clique sizes.

**Figure 5. Predicting visual stimuli with identified significant neurons**

(A) Examples of significant neurons identified using SVD with TF-IDF normalization and CRF models. Red and blue circles represent the ensemble cells of horizontal and vertical visual stimuli, respectively; nodes filled with red and has blue edges represents significant neurons shared between the two visual stimuli. (B) Percentage of significant neurons with SVD and CRF models. (C) Percentage of shared neurons identified by SVD and CRF models. Percentage is calculated by number of cells belong to both models divided by the sum of number of unique cells in two models. (D) Cosine similarities of frames with stimuli that match or not match the model. (E-G) Accuracy (E), precision (F) and recall (G) of predictions from different models.

**Figure 6. Ensembles are composed of groups of neurons that are specific to the stimulus**

(A) Examples of identified ensemble cells, 10% subsample of ensemble cells, randomly sampled cells of 20% ensemble cell number, and randomly sample cells of 90% ensemble cell number. Their corresponding prediction raster plot and frame cosine similarities are shown on the right. (B) Mean cosine similarity of randomly down-sampled or up-sampled ensemble groups, in frames with matching or non-matching stimulus. (C-D) Accuracy (C), precision (D) and recall (E) of predictions from randomly down-sampled or up-sampled ensemble groups. (F) Mean cosine similarity of randomly sampled cells, in frames with matching or non-matching stimulus. (G-I) Accuracy (G), precision (H) and recall (I) of predictions from randomly down-sampled or up-sampled ensemble groups.

**Experimental Procedures**

***Conditional Random Fields***

We construct a conditional random field (CRF) with the observed population activity where , and the target hidden network state , where , for samples (time points). For each sample, the conditional probability can be expressed as:

where is a vector of sufficient statistics of the distribution, is a vector of parameters, and is the partition function:

The conditional probability can be factored over a graph structure , where is the collection of nodes representing observation variables and target variables, and is the collection of subsets of . The conditional dependencies can be then written as

This model is a generalized version of Ising models, which have been previously applied to model neuronal networks ([Yu et al., 2008](#_ENREF_46)). The log-likelihood of each observation can be then written as:

Given the inferred binary spikes from raw imaging data, we construct a CRF model by two steps: (1) structure learning, and (2) parameter learning. For structure learning, we learnt a graph structure using l1-regularized logistic regression and performed structure elimination by thresholding the edge potentials ([Ravikumar et al., 2010](#_ENREF_32)). Based on the learnt structure, we use the Bethe approximation to approximate the partition function, and iterative Frank-Wolfe methods to perform parameter estimation by maximizing the log-likelihood of the observations with a quadratic regularizer ([Tang et al., 2016](#_ENREF_42)):

Cross-validation was done to find the best model parameters via model likelihood.

***Shuffling Methods***

We performed shuffling of binary data while preserving the activity level for each cell and each frame. To do this, we randomly selected two cells and two time points where they show different activity (‘0’ and ‘1’), and exchange the activity pairs across them. This procedure was repeated for a large number (2n, where n is the number of total spikes) to complete one shuffling. The activity of the stimulus-representing hidden nodes were not shuffled. For each dataset, shuffling was done for 100 times unless noted otherwise.

***Edge Elimination of CRF Graphs***

Edges in the constructed CRF models can represent both positive correlation and negative correlation. To eliminate edges that do not represent strong synchronization between neurons, we trained CRF models with 100 shuffled data, and obtained the synchronization term . We then fitted the distribution of these synchronization terms to a normal distribution, and determined a threshold by bottom 30% quantile. All edges in the real-data CRF model that show a synchronization term below the threshold were eliminated.

***Correlation-based Graphs***

To construct correlation-based graphs, we first calculated the Pearson correlation coefficients between the binary spike vectors of each pair of cells. Then, we generated correlation threshold by calculating Pearson correlation coefficients of shuffled data, fitting the coefficients to a normal distribution, and finding the 95% CDF level.

***Maximal Cliques***

Finding maximal cliques using exhaustive search methods is computationally unrealistic with a relatively large number of vertices. To find maximal cliques in an adjacency matrix efficiently, we used the Bron-Kerbosch algorithm. This algorithm recursively detects all the maximal cliques in a given graph . The algorithm starts with three sets: an empty set with currently growing maximal clique, a set with all prospective vertices connected to all vertices in , and a set with nodes that have been processed. In each call of the algorithm, a pivot vertex with the largest node degree is chosen. Since for each vertex , either the vertex or its non neighbors but not both will be in a clique, each is tested as candidate component for by recursively calling the algorithm with and restricted to the neighbors of . The algorithm then moves from to , and reports as a maximal clique when both and are empty.

***Graph properties***

Given the adjacency matrix where if node is linked to node , we investigated the following graph properties: graph density, node degrees, local clustering coefficients, and eigenvector centrality. Graph density is calculated as the number of existing edges divided by the number of total possible edges:

where *NV* is the number of vertices in the graph. Node degree is defined for node as the number of edges connected to it:

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Local clustering coefficient is defined for each node as the fraction edges connected to it over the total number of possible edges between the node's neighbors (nodes that have a direct connection with it). Eigenvector centrality is defined on the relative centrality score matrix , where

This can be written in the form of eigenvector equation:

Solving the above equation gives a set of eigenvalues and associated eigenvectors. The entry of the eigenvector associated with the largest gives the eigenvector centrality for node .

***Prediction with cosine similarity***

Identified significant neurons were represented by a binary vector over all neurons, and the entries corresponding to the ensemble members were set to 1, while the rest were set to 0. Cosine similarities between ensemble vectors and frame activity vectors were calculated, and a threshold was determined by 3 times the standard deviation of baseline noise. The cosine similarity between two frame activity vectors depicts the angle between two vectors in the high-dimensional space; orthogonal angles indicate that the active neurons in the two frames are mostly different, while small angles indicate that the active neurons are mostly the same. Frames that were significantly similar compared with the threshold were taken as stimulus-on frames.

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