**Identification and Targeting of Cortical Ensembles with Probabilistic Graphical Models**

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**Highlights**

- Conditional Random Fields (CRFs) model network properties of cortical ensembles

- CRFs infer cortical ensembles that predict different visual stimuli

- High-ranked neurons in CRFs have pattern completion capability

- CRFs capture network reconfiguration induced by two-photon optogenetic stimulation

**Summary**

A fundamental problem for machine learning in applications including natural language processing, computer vision and bioinformatics is the prediction of internal states from measurements of variables with mutual dependencies. One solution is the implementation of structured prediction methods that combine graphical models and classification algorithms, such as Conditional random fields (CRFs). However, the application of CRFs to infer the network properties of neural ensembles remains unexplored. We used CRFs in population calcium imaging data from primary visual cortex (V1) of awake head-fixed mice to identify cortical ensembles and predict visual stimuli. Using simultaneous two-photon imaging and two-photon optogenetics we show that CRFs identify high-ranked neurons from artificially imprinted ensembles with pattern completion capability. Our method can also capture functional changes in network activity evoked by single cell targeting. CRFs models could be broadly used for deciphering functional changes of neural circuits.

**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 ([Miller et al., 2014](#_ENREF_30)). Recent advances in two-photon calcium imaging and two-photon optogenetics have made possible the imprinting and recalling of cortical ensembles with single cell resolution in awake animals ([Carrillo-Reid et al., 2016](#_ENREF_9)). However, how the activation of specific groups of neurons relates to the function of cortical microcircuits has been difficult to elucidate. This is partly because it requires the online identification of single cells that can be targeted during close-loop optogenetic experiments, potentially under interventional 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_7)). However, graphs are usually constructed with nodes representing brain regions ([He et al., 2007](#_ENREF_19)), and edges representing information flow ([Iturria-Medina et al., 2008](#_ENREF_22)). 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_15); [Hagmann et al., 2008](#_ENREF_17)), voxels ([Eguiluz et al., 2005](#_ENREF_14); [van den Heuvel et al., 2008](#_ENREF_47); [Zuo et al., 2012](#_ENREF_51)) or electrode position ([Downes et al., 2012](#_ENREF_13)) as nodes, and activity associations such as cross correlation, mutual information and Granger causality as edges ([Bullmore and Sporns, 2009](#_ENREF_7); [Fair et al., 2008](#_ENREF_15); [Khazaee et al., 2015](#_ENREF_23); [Micheloyannis et al., 2009](#_ENREF_29); [Wang et al., 2010](#_ENREF_48)).

In addition, 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_22); [Sporns, 2000](#_ENREF_40)). 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 optimal network structure underlying the whole population activity. Finally, 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_16); [Yatsenko et al., 2015](#_ENREF_49)), but these methods have not been applied to define the optimal configuration of neuronal ensembles that allows the prediction of different visual stimuli in awake animals.

Cortical ensembles in primary visual cortex consist of strongly interconnected neurons ([Carrillo-Reid et al., 2016](#_ENREF_9); [Ko et al., 2011](#_ENREF_24)), forming a network structure that can be intuitively modeled with graph theory, where nodes and edges are biologically meaningful, representing neurons and their connections respectively. Here, we demonstrate that CRFs allow the identification of cortical ensembles associated with different experimental and physiological conditions, opening the possibility of targeting with single cell resolution the most significant neurons from specific populations during microcircuit computations.

**Results**

**CRFs applied to calcium imaging population data**

CRFs model the conditional distribution *p*(**y**|**x**) of a network, where **x** represents observations and **y** represents true labels associated with a graphical structure ([Sutton and McCallum, 2012](#_ENREF_44)). Since no assumptions are made on **x**, CRFs can accurately describe the conditional distribution with complex dependencies in observation variables associated with a graphical structure that is used to constrain the interdependencies between labels. Therefore, CRFs have been successfully applied in diverse areas of machine learning such as news ([Peng et al., 2011](#_ENREF_33)), bioinformatics ([Li et al., 2008](#_ENREF_26); [Liu et al., 2006](#_ENREF_27); [Sato and Sakakibara, 2005](#_ENREF_36)), computer vision ([He et al., 2004](#_ENREF_18); [Sminchisescu et al., 2006](#_ENREF_39)) and natural language processing ([Choi et al., 2005](#_ENREF_11); [Lafferty et al., 2001](#_ENREF_25)).

In order to construct a structured model from population activity with single cell resolution, we used CRFs representing neurons and their functional connections as nodes and edges in a graph, respectively (Figure 1A). To estimate the probability of different network states from observed population vectors (Figure S1), 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 and edge potentials correspondingly (Figure 1A). These parameters are also known as potential functions and reflect the scores of individual values on each node and edge. Using part of the observation data, we first estimate model parameters and then perform cross-validation on held-out data. The final normalized product of the corresponding nodes and edge potentials describes the likelihood that a given neuronal population exhibits a specific activation pattern.

To integrate information of the external stimulus along with the observed neuronal data, we added an additional node for each type of stimulus that was presented to the animal. This node was set to ‘1’ when the corresponding stimulus was on and ‘0’ when the stimulus was off (Figures 1A and 1B). The general and mathematical properties of CRF models obtained with added nodes did not significantly differ from CRF models obtained without added nodes (density: baseline model 14.74% ± 3.40%, add node model 13.39% ± 3.08%; node strength: baseline model -0.3259 ± 0.2053, add node model -0.3378 ± 0.2122; node degree: baseline model 0.0603 ± 0.0224, add node model 0.0547 ± 0.0208; local clustering coefficient: baseline model 0.3161 ± 0.0276, add node model 0.3009 ± 0.0289; centrality: baseline model 0.3692 ± 0.1232, add node model 0.3661 ± 0.1233; Figure S2). In both conditions, CRFs modeled the conditional probability of network states given the observations. Therefore, by treating visual stimuli as added nodes and comparing the output likelihood of observing each stimulus, we were able to predict visual stimuli from observed data. In this way, the nodes directly connected to the added nodes represent different visual stimuli. For example, given two visual stimuli (horizontal or vertical drifting gratings), the likelihood corresponding to observing each stimulus is defined by , and . Thus, the relative likelihood can be used to classify the presented stimuli (mean ± SEM relative likelihood from an example experiment: 0.3663 ± 0.1106 for horizontal stimulus, -0.4944 ± 0.0793 for vertical stimulus; Figure 1C and Figure 1E). To evaluate the classification performance, we examined the receiver operating characteristic (ROC) curve of the two stimuli (Figure 1D) as well as the area under curve (AUC, mean ± SEM: 0.8319 ± 0.0184 for horizontal, 0.8455 ± 0.0098 for vertical; Figure 1F). We also 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); and recall, defined as TP/(TP+FN) (accuracy: 0.9254 ± 0.0156 for horizontal, 0.9172 ± 0.0160 for vertical; precision: 0.8262 ± 0.0484 for horizontal, 0.9387 ± 0.0329 for vertical; recall: 0.8651 ± 0.0210 for horizontal, 0.6344 ± 0.1367 for vertical). Using these measurements, we demonstrated that CRFs are able to predict the orientations of drifting-gratings.

**Identification of the most representative neurons from cortical ensembles based on CRFs**

It has been shown that coactive cortical ensembles represent neuronal populations with modular properties ([Carrillo-Reid et al., 2015](#_ENREF_8); [Carrillo-Reid et al., 2016](#_ENREF_9); [Cossart et al.](#_ENREF_12); [Mao et al.](#_ENREF_28); [Miller et al., 2014](#_ENREF_30)). Structural and functional modularization, in both macro-scale and micro-scale levels, are characterized by local structures with high inter-connectivity, where a group of neurons shows dense physical or functional connections ([Achard et al., 2006](#_ENREF_2); [Bonifazi et al., 2009](#_ENREF_5); [Hagmann et al., 2008](#_ENREF_17); [He et al., 2007](#_ENREF_19); [Shimono and Beggs, 2015](#_ENREF_38); [Sporns et al., 2007](#_ENREF_41); [Stetter et al., 2012](#_ENREF_42); [Zuo et al., 2012](#_ENREF_51)). Such structures can be described by different concepts such as cliques, communities ([Palla et al., 2005](#_ENREF_32)), hubs and modules ([Bullmore and Sporns, 2009](#_ENREF_7)).

In order to design close-loop optogenetic experiments with single cell resolution, it is necessary to identify these cortical modules formed by the most representative neurons from cortical ensembles that can efficiently represent different visual stimuli. The classification nature of CRFs provides a convenient way to define the most representative neurons from cortical ensembles. For each neuron, we set its activity to be either ‘1’ or ‘0’ in all population activity vectors of the dataset, and compared the output likelihood using the inferred CRF models (Figure 2A). Then, we calculated single neuron preference by binarizing the likelihood difference (Figure 2B). Since representative neurons are likely to be strongly connected with each other, we defined the node strength in CRFs models as the summation of terms on all connecting edges for each node in the graph (Figure 2C). In this way, we defined the most representative neurons from cortical ensembles as the neurons that can be used to predict each visual stimulus with higher performance and have high node strength (Figure 2D and 2E). To demonstrate the general applicability of our method, we analyzed publically open datasets (Allen Brain Observatory) that contains several visual stimuli types with different experimental settings, and showed that our method was able to find the most representative neurons for each visual stimulus in those datasets (TF = 1: AUC 0.8586 ± 0.0204, accuracy 0.9106 ± 0.0284, precision 0.9896 ± 0.0085, recall 0.6399 ± 0.1133; TF = 2: AUC 0.8508 ± 0.0202, accuracy 0.9097 ± 0.0241, precision 0.9705 ± 0.0217, recall 0.6422 ± 0.1223; TF = 4: AUC 0.8057 ± 0.0255, accuracy 0.8615 ± 0.0301, precision 0.9037 ± 0.0919, recall 0.4639 ± 0.1222; TF = 8: AUC 0.7446 ± 0.0276, accuracy 0.8278 ± 0.0272, precision 0.8493 ± 0.1072, recall 0.3390 ± 0.1218; TF = 15: AUC 0.6509 ± 0.0225, accuracy 0.7695 ± 0.0267, precision 0.0660 ± 0.1487, recall 0.1791 ± 0.0885; Figure S3).

**Classification performance of the most representative cortical ensembles**

We next investigated whether these most representative neurons from cortical ensembles have the better performance for the prediction of visual stimuli. To do so, we randomly resized the population vectors containing the most representative neurons from cortical ensembles by adding or removing elements from the group, and examined the prediction performance. The similarity function and prediction performance of population vectors formed with the most representative neurons from cortical ensembles has a maximum value when the size of population vectors is unchanged (similarity 0.2887 ± 0.0212; AUC 0.9383 ± 0.0074; n = 20 ensembles; mean ± SEM; Figures 3A-3C). Furthermore, population vectors from the most representative neurons from cortical ensembles achieve the best accuracy, precision and recall when predicting the presented visual stimuli, compared with resized ensembles (accuracy 0.8367 ± 0.0143; precision 0.6175 ± 0.0402; recall 0.9067 ± 0.0165; Figure S5).

So far we have shown that population vectors formed with the most representative neurons from cortical ensembles identified by CRFs represent the optimal population to predict external visual stimuli. This fact raises the question of whether such population vectors are a specific non-random subgroup. To answer this question, we randomly sampled a subset of the number of most representative cells from cortical ensembles, ranging from 10% to 100%. We observed that the prediction performance from random groups of neurons is significantly lower than the most representative population vectors (Figures 3D-3F and S5), indicating that the most representative neurons from cortical ensembles are non-random population vectors.

**Comparison with previously used approaches**

The population vectors formed by the most representative neurons from cortical ensembles identified with CRFs have comparable prediction performance with previously used methods for cortical ensemble classification ([Carrillo-Reid et al., 2015](#_ENREF_8); [Carrillo-Reid et al., 2016](#_ENREF_9)) (Figure 4A-4E) or groups of neurons with high orientation selectivity index (OSI) (Figure S5A-S5E; mean ± SEM AUC: CRF 0.9383 ± 0.0074, SVD 0.9111 ± 0.0103, OSI 0.9341 ± 0.0087; accuracy: CRF 0.8367 ± 0.0143, SVD 0.8448 ± 0.0157, OSI 0.9217 ± 0.0136; precision: CRF 0.6175 ± 0.0402, SVD 0.6724 ± 0.0446, OSI 0.8353 ± 0.0343; recall: CRF 0.9067 ± 0.0165, SVD 0.8097 ± 0.0245, OSI 0.8650 ± 0.0294). On the other hand, the most representative neurons from cortical ensembles identified with CRFs share 51.29% ± 5.51% cells with the SVD ensembles, and are composed of a mixed population of cells with high OSI and cells with low OSI (shared 42.34% ± 3.84%; Figure S5F and S5G), indicating that the most representative neurons from cortical ensembles identified with CRFs are not purely orientation selective cells. Interestingly, the percentage of neurons from SVD ensemble and with high OSI was not significantly different from the size of population vectors defined by the most representative neurons (CRF 11.43% ± 0.95%, SVD 10.49% ± 1.35%, OSI 12.56% ± 2.26%; Figure 4H and Figure S5H) suggesting that few neurons need to be targeted to manipulate the network activity of cortical microcircuits.

**Targeted manipulation of cortical microcircuits using CRFs models**

It has been recently shown that the repetitive activation of an identified neuronal population with two-photon optogenetics imprints an artificial cortical ensemble that can be recalled later on by specific members of the ensemble ([Carrillo-Reid et al., 2016](#_ENREF_9)). Since CRFs can be used to identify the most representative neurons from cortical ensembles, we hypothesize that our approach could also be used for the identification of neurons with pattern completion capability from artificially imprinted cortical ensembles.

Neurons with pattern completion capability represent highly connected neurons. Similar to representative neurons, we used the parameters from CRFs obtained from simultaneous two-photon imaging and two-photon optogenetic experiments with single cell resolution (Figure 5A) and defined high-ranked neurons as the ones with strong node strength and high AUC values (Figure 5B). Indeed, single-cell two-photon optogenetic stimulation of high-ranked neurons was able to evoke pattern completion of imprinted ensembles, whereas low-ranked neurons were unable to recall imprinted ensembles (Figure 5C). These experiments demonstrated that neurons with pattern completion capability have stronger graph connectivity with other members of artificially imprinted cortical ensembles. Thus, CRFs could be used to target single neurons that play a key role in the computational properties of cortical microcircuits.

**Reconfiguration of cortical ensembles depicted by CRFs**

We have shown that high-ranked neurons have pattern completion capability that is a reflection of graph connectivity inferred from CRFs. To investigate if our approach can also describe the changes in network properties of these high-ranked neurons induced by cortical ensemble reconfiguration, we compared the models generated by CRFs before and after two-photon population manipulation of a given set of neurons for several times (Figure 6A), an experimental protocol that builds new coactive ensembles ([Carrillo-Reid et al., 2016](#_ENREF_9)). To visualize the change in graph connectivity induced by the imprinting protocol in neurons with pattern completion capability we construct isomorphic graphs from the CRFs models and arrange them in a circular configuration (Figure 6B) demonstrating that high-ranked neurons increased their graph connectivity with the imprinted ensemble. Moreover, after the ensemble is imprinted, neurons with pattern completion capability show better predictive performance and higher node strength (Figure 6C), demonstrating that the parameters inferred from CRFs can be used to study changes in network properties of specific neurons. Interestingly, the connection density of the neurons belonging to the imprinted ensemble was also increased (Figure 6D). However, the graphical properties of CRFs before and after population photostimulation remained stable both within the imprinted network (node strength: pre -0.1596 ± 0.0311, post -0.2291 ± 0.0496; node degree: pre 0.0365 ± 0.0059, post 0.0445 ± 0.0053; local clustering coefficient: pre 0.2602 ± 0.0221, post 0.2850 ± 0.0415; centrality: pre 0.3168 ± 0.0499, post 0.4024 ± 0.0588; Figure 6E-6H) and in the whole network (node strength: pre -0.2527 ± 0.0379, post -0.2164 ± 0.0294; node degree: pre 0.0377 ± 0.0034, post 0.0400 ± 0.0031; local clustering coefficient: pre 0.2753 ± 0.0188, post 0.2487 ± 0.0207; centrality: pre 0.3094 ± 0.0281, post 0.3369 ± 0.0306; Figure S6), suggesting that imprinted ensembles have been added to cortical microcircuits but preserving a balance with the overall network structure.

The fact that CRFs were able to describe changes in the reconfiguration of cortical neurons demonstrates the potential of structured prediction methods to study the modulation of neuronal microcircuits induced by external perturbations or pathological conditions.

**Discussion**

**Analysis of network properties in cortical microcircuits**

In this study, we provide a tool for modeling network properties of mouse primary visual cortex *in vivo* using conditional random fields. Structured prediction methods not only reveal the structure of the functional connections, but also provide the conditional probability of the interactions between neurons to find network states capable of predicting sensory stimuli with different properties (Figure 1).

In the past 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_13); [Fair et al., 2008](#_ENREF_15); [Hagmann et al., 2008](#_ENREF_17); [Iturria-Medina et al., 2008](#_ENREF_22); [Oh et al., 2014](#_ENREF_31); [Supekar et al., 2008](#_ENREF_43); [Yu et al., 2008](#_ENREF_50); [Zuo et al., 2012](#_ENREF_51)). While most of these studies operated on functional recordings across multiple brain regions ([Achard and Bullmore, 2007](#_ENREF_1); [Chiang et al., 2016](#_ENREF_10); [Fair et al., 2008](#_ENREF_15); [Hinne et al., 2013](#_ENREF_20); [Zuo et al., 2012](#_ENREF_51)), only a few have focused on the general network properties of cortical circuits with recordings from single neurons ([Bonifazi et al., 2009](#_ENREF_5); [Sadovsky and MacLean, 2014](#_ENREF_35); [Stetter et al., 2012](#_ENREF_42); [Yatsenko et al., 2015](#_ENREF_49)).

The majority of methods applied to infer network properties in brain slices ([Cossart et al., 2003](#_ENREF_12); [Ikegaya et al., 2004](#_ENREF_21); [Mao et al., 2001](#_ENREF_28); [Sadovsky and MacLean, 2014](#_ENREF_35); [Stetter et al., 2012](#_ENREF_42)) or *in vivo* ([Yatsenko et al., 2015](#_ENREF_49)) operate on the correlation matrix, and aim to recover the functional dependencies between observed neurons. Such methods are valuable for revealing some properties such as node degrees, clustering coefficients or functional hubs. However, these methods are model-free, therefore are incapable of describing the overall network dynamics based on the probability distribution of neuronal ensembles. Our method provides an alternative by directly modeling the statistical dependencies of each node.

**CRFs graph models identify neuronal ensembles**

Compared with generative models that make assumptions on the dependencies between all the observation variables from the model, CRFs only model the hidden system states dependent on observed features. Since no independence assumptions are made between observed variables, CRFs avoid potential errors under these assumptions introduced by unobserved common inputs of the neuronal population. Additionally, given the finite number of network states described by population activity, the conditional distribution is sufficient for making predictions, both for the population state and for identifying representative cells in each state. One popular example of generative models for functional connectivity is the Ising model or the more generalized Potts model ([Tavoni et al.](#_ENREF_46); [Yu et al., 2008](#_ENREF_50)). The generative nature of these models restricts their ability to model arbitrary dependencies between observed variables. Compared with other discriminative finite-state models such as Maximum Entropy Markov Models (MEMM), CRFs use global normalizers to overcome the local bias in MEMM induced by local normalizers, and have been shown to achieve higher accuracy in applications such as sequence labeling ([Lafferty et al., 2001](#_ENREF_25)). Therefore, CRFs appear to be promising for modeling cortical functional connectivity and for identifying the most representative neurons from cortical ensembles.

The difficulty of constructing CRFs lies in the computation of global normalizers. With an arbitrary graph structure, this problem is often intractable. Recent advances that combines Bethe free energy approximation and Frank-Wolfe methods for inference and learning model parameters allow fast and relatively accurate construction of cyclic CRFs ([Tang et al., 2016](#_ENREF_45)). Thus, CRFs can be applied to datasets with thousands of interconnected neurons. However, a main constraint for applying CRFs is the number of samples in the training dataset.

**Comparison with classification algorithms to detect cortical ensembles**

Compared with the previously used descriptive methods for neuronal ensemble identification ([Carrillo-Reid et al., 2015](#_ENREF_8)), our approach modestly improved prediction performance (Figure 4). One reason could be that current CRF learning algorithms separately perform the structure learning and parameter learning steps. Therefore, the learned graphical structure and parameters may not be the globally best matching ones. However, it is still computational unrealistic to explore all possible structures and parameter combinations. Additionally, approximations during the parameter learning step can sometimes compromise the global optimality guarantees.

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 S1). We previously showed that population vectors defining a group (i.e. a cortical ensemble) can be extracted from multidimensional arrays by performing singular value decomposition (SVD) ([Carrillo-Reid et al., 2015](#_ENREF_8)). Even though SVD can identify cortical ensembles reliably, it lacks a structured model that allows the systematic study of changes in network properties.

**Physiological significance of single cell targeting with optogenetic stimulation**

Electrical stimulation of visual cortex has been used for decades as an attempt to provide useful visual sensations to patients that have lost the functionality of their eyes ([Brindley Gs Fau - Lewin and Lewin, 1986](#_ENREF_6)). The sensations produced by electrical stimulation of the visual cortex were termed phosphenes since they represented bright spots. A challenging issue regarding prostheses is the training of patients using devices with a large number of electrodes ([Shepherd and Shivdasani, 2013](#_ENREF_37)). Our results suggest that after a given network have been inferred, the identification of neurons with pattern completion capability could be used to reduce the number of active points that require stimulation. The further development of network models based on population activity that can predict a given set of features embedded in visual stimuli will be crucial for the fine manipulation of cortical ensembles.

It has been shown that the connectivity of diverse systems described by graphs with complex topologies follow a scale-free power-law distribution ([Barabasi and Albert, 1999](#_ENREF_3)). Scale-free networks are characterized by the existence of a small subset of nodes with high connectivity ([Carrillo-Reid et al., 2015](#_ENREF_8)). Similarly, cortical ensembles described by CRFs could be characterized by a subset of neurons with strong synaptic connections. The existence of neurons with pattern completion capability has been demonstrated in previous studies where perturbing the activity of single neurons was able to change the overall network dynamics ([Bonifazi et al., 2009](#_ENREF_5); [Carrillo-Reid et al., 2016](#_ENREF_9); [Hagmann et al., 2008](#_ENREF_17)).

We demonstrated that the parameters defined by CRFs models could be used in the design of closed loop experiments with single cell resolution to investigate the role of a specific subpopulation of neurons in a given cortical microcircuit during different behavioral events.

**Figure legends**

**Figure 1. Classification of visual stimuli using CRFs**

(A) Schematic representation of CRFs. Circles represent neurons. Squares represent added nodes depicting visual stimuli. Shaded nodes (x) represent observed data. 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 factorized using the node and edge potentials. (B) Example of a CRF graph constructed from real data. In this case, added nodes (squares) represent horizontal (red) and vertical (blue) drifting-gratings. First- and second-degree connections with added nodes are highlighted in the corresponding color. Scale bar: 50μm. (C) Top: relative likelihood calculated by CRFs. Gray region represents 3 S.D. Bottom: temporal course of ensemble classification for horizontal (top) and vertical (bottom) drifting-gratings. Colored stripes indicate visual stimuli. Scale bar: 10 seconds. (D) ROC curve of predicting horizontal and vertical stimuli using the relative likelihood. Dashed line represent random chance. (E) Mean likelihood difference during horizontal and vertical visual stimuli (p=9.1864e-170). (F) Area under curve (AUC) in ROC curves for horizontal and vertical stimuli (p=0.6991). (G) Accuracy (p=0.8048), (H) precision (p=0.5268) and (I) recall (p=0.3828) for vertical and horizontal drifting-gratings. (n = 7 mice; n = 7 ensembles per stimulus; Wilcoxon signed rank-test; \*\*\*p<0.001). For conceptual model of population vector, see Figure S1; for the properties of models without added node, see Figure S2.

**Figure 2. Identification of cortical ensembles with CRFs**

(A) Schematic representation of ensemble identification from CRF models. The activity of the neuron is set to ‘1’ or ‘0’ at each frame, and the likelihood and of modified population vectors is calculated. Edge color tone represents the strength of ; node color represents node strength. (B) An example of likelihood difference (bottom panel) and predictions (top panel) for high activity frames from a neuron belonging to a cortical ensemble representing horizontal drifting-gratings (red). (C) Schematic representation of high and low node strength neurons from CRF models. (D) The most representative neurons from cortical ensembles for two visual stimuli were defined as neurons with high predictive power (represented by AUC) and strong node strength. AUC of neurons in the imaged population were calculated by predicting the horizontal (left, red) and vertical (right, blue) visual stimuli. A cross-validated threshold was defined for AUC, and a threshold for node strength was defined from CRF models of shuffled data. (E) Spatial map of the most representative cortical ensembles from CRFs for horizontal (red, left) and vertical (blue, right) drifting-gratings. Scale bar: 50μm. For CRF methods applied in the Allen Brain Observatory datasets with more orientations of drifting-gratings, see Figure S4.

**Figure 3. CRF cortical ensembles are the most representative ones for visual stimuli identification**

(A) Cosine similarity between population vectors representing the most representative cortical ensembles identified with CRFs for a given visual stimuli. Each most representative cortical ensemble was randomly down-sampled or up-sampled (orange). The cosine similarity of population vectors belonging to different visual stimuli is shown in gray. (B) AUC and (C) ROC curves of predictions from randomly down-sampled or up-sampled most representative cortical ensembles, calculated by using the similarity values to predict the time of visual stimuli. (D) Cosine similarity between population vectors of randomly sampled cells. (E) AUC and (F) ROC curves of predictions from randomly chosen ensembles. (n = 6 mice; n = 20 ensembles; Wilcoxon signed rank-test; \*p<0.05; \*\*p<0.01; \*\*\*p<0.001) For randomly down- or up-sample ensembles (A-C), statistical tests were down by comparing resampled ensembles with the original ensembles (indicated with black triangle); for random chosen ensembles (D-F), statistical tests were down by comparing random ensembles with the original ensembles. Data presented as box plots displaying median and 25th and 75th quantiles; whiskers indicate the most extreme data points not considering outliers. For more statistics of random ensembles, see Figure S4.

**Figure 4. Comparison of prediction performance with CRF, SVD ensembles and high OSI cells**

(A) ROC curves of the classification result with SVD, CRF and high OSI cells. Dashed line represent random chance. (B) Area under curve (AUC) of ROC curves (p=0.0657). (C) Accuracy (p=0.5458), (D) precision (p=0.3915) and (E) recall (p=0.0028) of predictions for each visual stimuli using the three methods. (F) Percentage of shared neurons between CRF and SVD ensembles. Percentage is calculated by number of cells that belong to both methods divided by the total number of unique cells in both methods. (G) Examples of the most representative neurons from CRF (orange) and SVD (gray) cortical ensembles. Circles represent neurons of horizontal (left) and vertical (right) visual stimuli, respectively. Neurons shared between CRF and SVD ensembles are represented by orange dots circled by gray. Scale bar represents 50μm. (H) Percentage from the total population size representing representative ensemble neurons from CRF and SVD methods (p=0.0865). (n = 6 mice; n = 20, 19 for CRF and SVD ensembles respectively; Wilcoxon signed rank-test; \*p<0.05; \*\*p<0.01; \*\*\*p<0.001; n.s. p>0.05).

**Figure 5. High-ranked neurons from CRF models have pattern completion capability**

(A) CRF graphical model from simultaneous two-photon imaging and two-photon optogenetic single cell stimulation. Squares depict added nodes representing 10 stimulation trials of different neurons. High-ranked neurons are highlighted in red. Edge color tone represents the strength of ; node color represents the node strength. Scale bar: 50μm. (B) Node strengths and the AUC values of neurons in the imprinted ensemble for the single cell photostimulation. AUC values were calculated by predicting the photostimulation time of the recalling neuron using the cosine similarity of population vector of each individual neuron in the imprinted ensemble. Neuron in red represents the same high-ranked neuron highlighted in red in (A); neuron in blue represents the same low-ranked neuron highlighted in blue in (A). Dashed line and gray region represent the mean ± S.D. of AUC values and node strength from random groups with the same size as the imprinted ensemble predicting the photostimulation time of the recalling neuron. (C) Two-photon optogenetic single cell stimulation of targeted high-ranked neurons (left) was able to recall imprinted ensembles demonstrating pattern completion capability. Stimulation of low-ranked neurons (right) was not able to induce pattern completion of imprinted ensembles. Scale bar: 50μm.

**Figure 6. Reconfiguration of cortical microcircuits induced by two-photon optogenetic population manipulation**

(A) CRF graphical models trained with data from simultaneous two-photon imaging and two-photon optogenetic single cell stimulation of a high-ranked neuron with pattern completion capability before (left) and after (right) two-photon optogenetic population imprinting. Square on bottom left represents added node for single cell stimulation (10 trials). Edge color tone represents the strength of ; node color represents the node strength. Node size represents the node degree. Scale bar: 50μm. (B) The connection density of the stimulated neuron with other members of the imprinted ensemble before (left) and after (right) photostimulation trials. Red dot represents the stimulated neuron. (C) Node strength and classification AUC of the stimulated neuron for single cell stimulation before (left) and after (right) photostimulation trials. Dashed lines represent the AUC of random groups with the same size as imprinted ensemble predicting the time of single cell photostimulation. (D) Graph density, (E) node strength, (F) node degree, (G) clustering coefficient and (H) centrality values of the imprinted ensemble before (black) and after (blue) imprinting protocol remained stable indicating that the imprinted ensemble reconfigured the network structure preserving the global network properties (n = 74 neurons; Wilcoxon signed rank-test ; n.s. p>0.05). Global properties of the whole network remain unchanged too (Figure S6).

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**STAR methods**

**KEY RESOURCES TABLE**

(Need a separate file for key resources table)

Code for training CRF models can be found at <https://github.com/kuitang/fwmatch-public>.

**CONTACT FOR REAGENT AND RESOURCE SHARING**

Further information and requests for resources and reagents should be directed to and will be fulfilled by the Lead Contact, Luis Carrillo-Reid ([lc2998@columbia.edu](mailto:lc2998@columbia.edu)).

**EXPERIMENTAL MODELS AND SUBJECT DETAILS**

None.

**METHOD DETAILS**

**Spike detection of Allen Institute Brain Observatory dataset**

Calcium traces and dF/F were obtained using the SDK provided by Allen Institute. Then, dF/F values of the top and bottom 30% were removed to obtain a baseline activity, and a threshold was defined by the mean of the baseline plus 5 times standard deviation of baseline values. Spikes were detected as time points where dF/F values are higher than the threshold.

**Conditional Random Fields**

We construct a conditional random field (CRF) as previously published ([Tang et al., 2016](#_ENREF_45)), using indicator feature vector where , for each edge and node, and the target binary population activity vector , 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_50)). 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 learned a graph structure using -regularized neighborhood-based logistic regression ([Ravikumar et al., 2010](#_ENREF_34)):

,

where

.

Here is a regularization parameter that controls the density of constructed structure. Then, a graph structure is learnt by thresholding the edge potentials with a given density preference . Edges with potential values within top quantile were kept as the final structure. It is worth noting that although could bias the result, varying does not lead to density values that differ much. This is probably because of the sparse nature of the obtained Ising model.

Based on the learned 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_45)):

Here is a regularization that controls the learnt parameters. Cross-validation was done to find the best , and via model likelihood. We varied with 6 values between 0.002 and 0.5, d with 6 values between 0.25 and 0.3, and with 5 values between 10 and 10000, all sampled uniformly. To obtain the best model parameters, 90% data were used for training, while 10% data were withheld for cross-validation. The best model parameters were determined by calculating the likelihood of the withheld data and selecting the parameter set with a locally maximum likelihood in the parameter space.

**Node strength**

We define the node strength as the sum of the ‘11’ term of edge potentials from all connecting edges:

Here denotes the number of connecting edges for node . The defined node strength reflects the importance of a given cell in co-activating with other cells.

**Shuffling method**

To generate shuffled models, we first randomize the spike raster matrices while preserving the activity per cell and per frame. Then, we trained CRF models using the shuffled spike matrices, with the cross-validated , and from the real model. This procedure is repeated 100 times. Random level of node strength is determined by mean ± S.D. of mean node strengths from all shuffled models.

**Identifying the most representative cortical ensembles**

To find the most representative cortical ensembles for each condition, we iterate through all the neurons and identify their contribution in predicting stimulus conditions with the population. To this end, for the neuron in population, we set its activity to be ‘1’ and ‘0’ in turn, in all M frames. With the two resulting population vectors in the frame among all samples, we calculate the likelihood of them coming from the trained CRF model:

Then, we computed the likelihood difference vector

and calculated the standard receiver operating characteristic (ROC) curve with the ground truth as the timing of each presented visual stimuli. The prediction ability of all nodes for all presented stimuli is then represented by an area under curve (AUC) matrix , where represents the AUC value of node predicting stimulus . Additionally, we calculated the node strength of each neuron in the CRF model.

The most representative cortical ensemble for stimulus is defined by the following procedure: (1) find the nodes that has maximum value at column ; (2) vary a threshold between 0.5 and 0.9 with a step size of 0.05, and take all the nodes in (1) that has AUC values larger than the threshold; (3) take the population vector of the resulting nodes, calculate the cosine similarity with the binary data, predict timing of stimulus from the cosine similarity (see next session for details), and calculate accuracy of prediction; (4) threshold AUC values with the cross-validated threshold from (3) that results in the best accuracy; (5) shuffle the spike matrix for 100 times while preserving the activity per neuron and per frame, and train separate CRF models on shuffled data; (6) threshold the node strength of all nodes from (4) by the mean plus standard deviation of node strength from shuffled models; (7) the final representative cells are the remaining cells.

**Prediction with cosine similarity**

Identified most representative cortical ensembles 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 baseline plus 3 times the standard deviation of noise. The cosine similarity between two frame activity vectors depicts the angle between population vectors in a high-dimensional space.

**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 the node.

**QUANTIFICATION AND STATISTICAL ANALYSIS**

CRF models were trained using the Columbia Yeti shared HPC cluster. MATLAB R2016a (MathWorks) were used for data analysis. Statistical details of each specific experiments, including the statistical methods, the meaning and value of n, and the significance level can be found in figure legends.

**DATA AND SOFTWARE AVAILABILITY**

The analysis of simultaneous two-photon imaging and two-photon optogenetic stimulation data was performed from experiments previously published ([Carrillo-Reid et al., 2016](#_ENREF_9)).

We also used a publicly available dataset from the Allen Brain Observatory (<http://observatory.brain-map.org/visualcoding>) along with the SDK for extracting related information (<http://alleninstitute.github.io/AllenSDK/>) by Allen Institute of Brain Science. The experiments IDs are: 511507650, 511509529, 511510650, 511510670, 511510718, and 511510855.

All data processing, analysis and plotting code in this paper can be found at <https://github.com/hanshuting/graph_ensemble>.

**Supplementary Information**

**Supplementary Figure S1. Cortical ensembles as a representation of multidimensional population vectors obtained with two-photon calcium imaging**

(A) Schematic representation of active neurons at different frames. Black dots represent active neurons at different times (left). Binary raster plot representing the overall network activity of observed neurons (right). Population vectors capture the coordinated activity of a given neuronal ensemble. (B) Population vectors can be understood as a multidimensional array in which clusters of population vectors taken from different times define network states.

**Supplementary Figure S2. Added nodes does not affect graph properties**

(A) CRF graphs of baseline model (no added nodes) and the added node model, trained with the same experiment. Edge color represents ; node color represents node strength. Node size represents the node degree. Scale bar represents 50μm. (B) Graph densities (n=6 mice), (C) node strength (p=0.9650), (D) node degrees (p=0.6826), (E) clustering coefficients (p=0.0839) and (F) centrality (p=0.9570) comparison between the two models (n = 6 mice; Wilcoxon signed rank-test; n.s. p>0.05).

**Supplementary Figure S3. CRF ensembles are able to predict multiple stimuli**

(A) An example of constructed CRF models from the Allen Brain Observatory dataset, with four orientations of drifting grating stimuli (squares). Edge color indicates the strength of inferred connections; node size indicates the node degrees. (B) Temporal course of ensemble classification for four drifting-gratings. Colored stripes indicate visual stimuli. Scale bar represents 200 frames. (C) Two examples of ROC curves of CRF models trained with temporal frequency 1 Hz predicting visual stimuli with temporal frequency 1, 2, 4, 8 and 15 Hz. Horizontal (left) and vertical (right) stimuli prediction are shown here. (D) AUC (p= 0.6923, 0.0098, 2.642e-05, 1.5449e-06) (E) accuracy (p=0.8653, 0.0275, 0.0010, 4.6488e-06), (F) precision (p= 0.4183, 0.3039, 0.0373, 0.0001) and (G) recall (p=1, 0.0458, 0.0006, 3.557e-05) of prediction with CRF model trained with temporal frequency 1Hz, on datasets with visual stimulus temporal frequency 1, 2, 4, 8, and 15Hz. (n = 4 mice; Wilcoxon signed rank-test; \*p<0.05; \*\*p<0.01; \*\*\*p<0.001)

**Supplementary Figure S4. CRF ensembles are the most representative cells for predicting corresponding visual stimuli**

(A) Accuracy, (B) precision and (C) recall of predictions from randomly down-sampled or up-sampled CRF ensembles, calculated by using the similarity values to predict the time of visual stimuli. (D) Accuracy, (E) precision and (F) recall of predictions from randomly chosen ensembles. (n = 6 mice; n = 20 ensembles; Wilcoxon signed rank-test; \*p<0.05; \*\*p<0.01; \*\*\*p<0.001)

**Figure S5. Comparison of prediction performance with CRF ensembles and high OSI cells**

(A) ROC curves of the classification result with SVD ensembles and high OSI cells. Dashed line represent random chance. (B) Area under curve (AUC) of ROC curves (p=0.9461). (C) Accuracy (p=0.0001), (D) precision (p=0.0002) and (E) recall (p=0.3104) of predictions for each visual stimuli using the three methods. (F) Percentage of shared neurons between CRF ensembles and high OSI cells. Percentage is calculated by number of cells that belong to both methods divided by the total number of unique cells in both methods. (G) Examples of the most representative neurons from cortical ensembles identified using CRF (orange), and high OSI cells (gray). Circles represent neurons of horizontal (left) and vertical (right) visual stimuli, respectively. Neurons shared between CRF and high OSI cells are represented by orange dots circled by gray. Scale bar represents 50μm. (H) Percentage from the total population size representing representative ensemble neurons from CRF methods and high OSI cells (p=0.5075). (n = 6 mice; n = 20 CRF and OSI ensembles; Wilcoxon signed rank-test; \*: p<0.05; \*\*: p<0.01; \*\*\*: p<0.001; n.s. p>0.05).

**Supplementary Figure S6. Global network properties of cortical microcircuits induced by two-photon optogenetic population manipulation**

(A) Density, (B) node strength, (C) node degree, (D) clustering coefficients and (E) centrality values of the whole network remain unchanged after the imprinting protocol. (n = 74 neurons; Wilcoxon signed rank-test; n.s. p>0.05).