

The structure of population responses in V1 and V4 responding to natural stimuli

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Introduction

1. In visual areas of primates, neurons activate in parallel while the animal is engaged in a behavioral task.
2. Macaques visualized two consecutive stimuli that were either the same or different, while recorded with laminar arrays across the cortical depth in V1 and V4.
3. We decoded correct choice behavior from neural populations of simultaneously recorded units. Utilizing decoding weights, we test the influence of the structure of the population code on pairwise dynamics.

Methods

The spike train of a single neuron is a binary vector of zeros and ones,

$$o_{n,j}(t_k) = \begin{cases} 1, & \text{if neuron } n \text{ in trial } j \text{ spikes during the } k\text{-th millisecond} \\ 0, & \text{otherwise} \end{cases} \quad (1)$$

where $n = 1, \dots, N$ is the neural index, $j = 1, \dots, J$ is the trial index and $k = 1, \dots, K$ is the time index with step of 1 millisecond.

The spike count: $x_{n,j} = \sum_{k=1}^K o_{n,j}(t_k)$

Z-scored spike counts:

$$\tilde{x}_{n,j} = \frac{x_{n,j} - \langle x_{n,j} \rangle_j}{\sqrt{\text{Var}_j(x_{n,j})}} \quad (2)$$

One sample for the classifier (N-dimensional vector):

$$\tilde{s}_j = [\tilde{s}_{1,j}, \tilde{s}_{2,j}, \dots, \tilde{s}_{N,j}] \quad (3)$$

The optimization problem of the linear SVM [1]:

$$L_p = \frac{1}{2} \mathbf{w}^T \mathbf{w} - \sum_{j=1}^J \lambda_j [y_j (\mathbf{w}^T \tilde{\mathbf{x}}_j + b) - 1] \quad (4)$$

where \mathbf{w} is the vector of weights, b is the offset of the separating hyperplane from the origin, λ_j is the Lagrange multiplier and y_j is the class label in trial j , $y_j \in \{-1, 1\}$.

Vector of weights:

$$\mathbf{w} = \sum_{q=1}^Q \lambda_q y_q \tilde{\mathbf{x}}_q \quad (5)$$

where $\tilde{\mathbf{x}}_q$ are support vectors $Q < J$. The vector of decoding weights, $\mathbf{w} = [w_1, w_2, \dots, w_N]$, associates the activity of each neuron with its role for classification in the N -dimensional space of inputs.

Balanced accuracy:

$$BAC = \frac{TP}{2(TP + FN)} + \frac{TN}{2(TN + FP)} \quad (6)$$

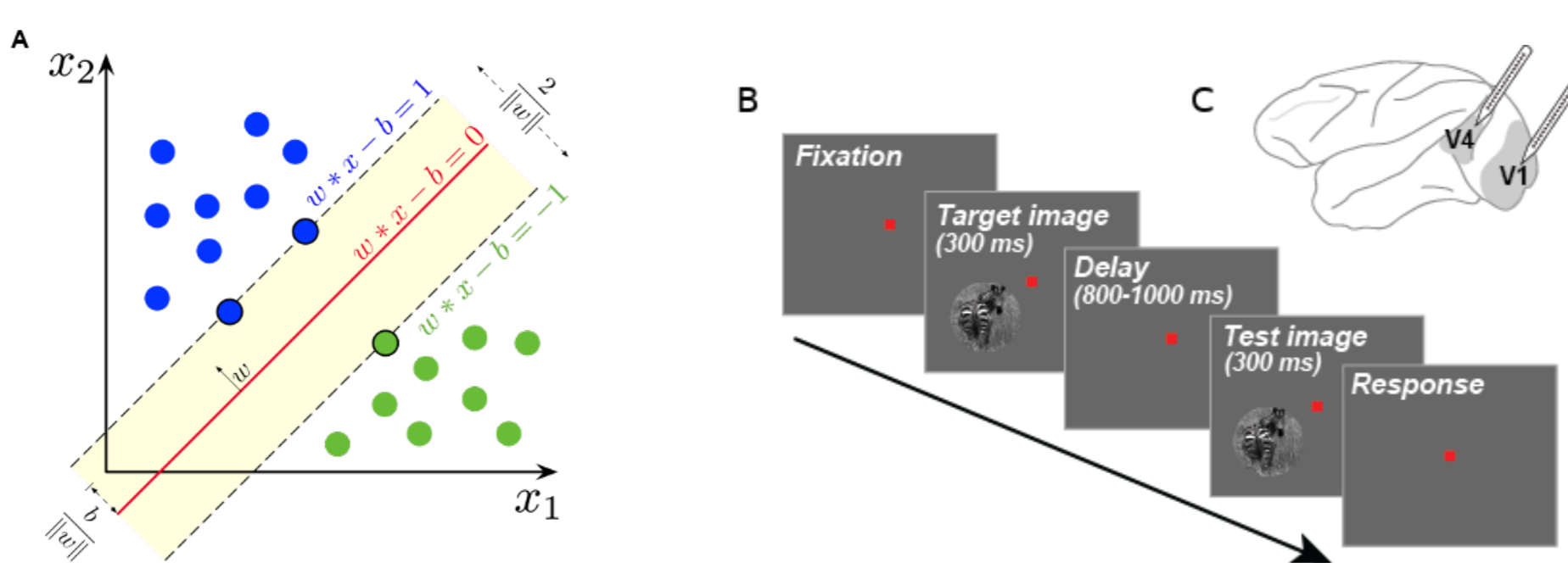


Fig. 1: A) Schema of the linear SVM. B) Experimental paradigm. Macaques visualized the target and the test stimulus, interleaved with the delay period. The multiunit signal in V1 and V4 was captured with linear arrays. C) Schema of recording sites and laminar arrays.

Results

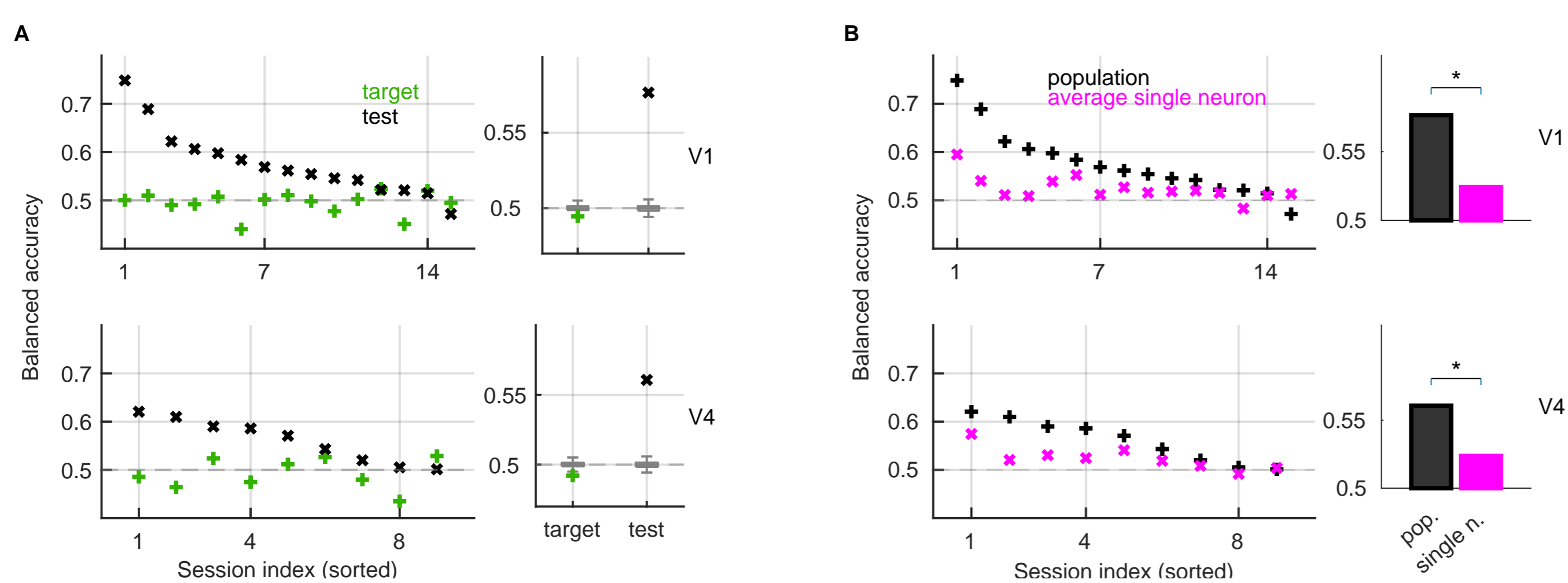


Fig. 2: The population predicts the behavior better than an average single neuron. A) Balanced accuracy during the target (green) and the test epoch (black). B) Balanced accuracy during the test epoch for the population model (black) and the average single neuron model (magenta).

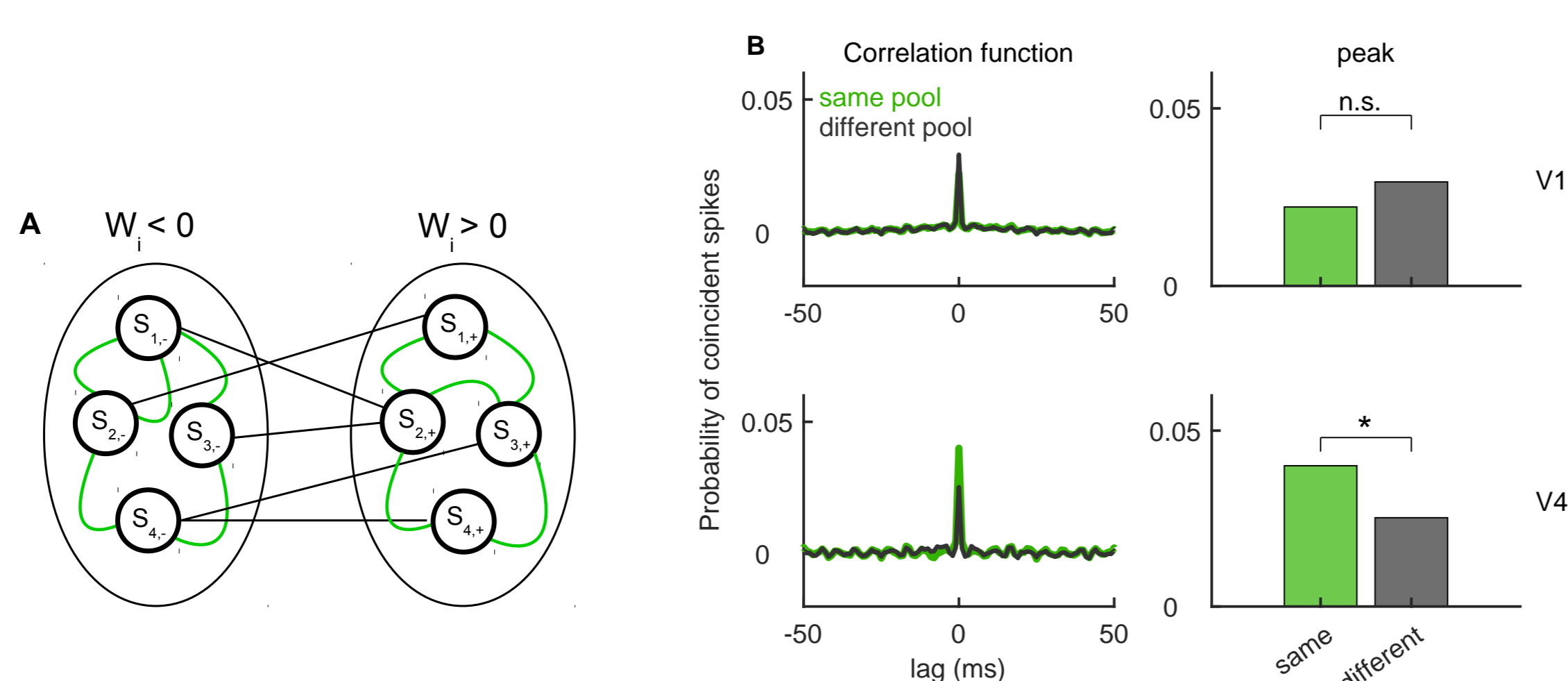


Fig. 3: Neurons are more strongly synchronized within coding pools compared to across coding pools in V4, but not in V1. A) Schema of coding pools, separating neurons with positive and negative weights. B) Left: Average correlation function for pairs of neurons within (green) and across coding pools (black). Right: Peak of the correlation function.

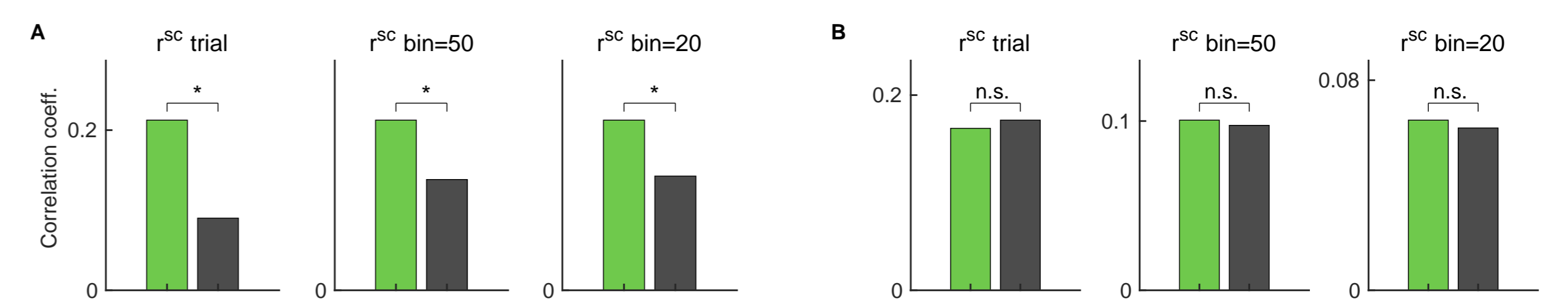


Fig. 4: Neurons are more strongly correlated within coding pools compared to across coding pools in V4, but not in V1. A) Correlations of trial-to-trial variability (left) and of binned spike counts with 50 ms (middle) and 20 ms bins (right) in V4. B) Same in V1.

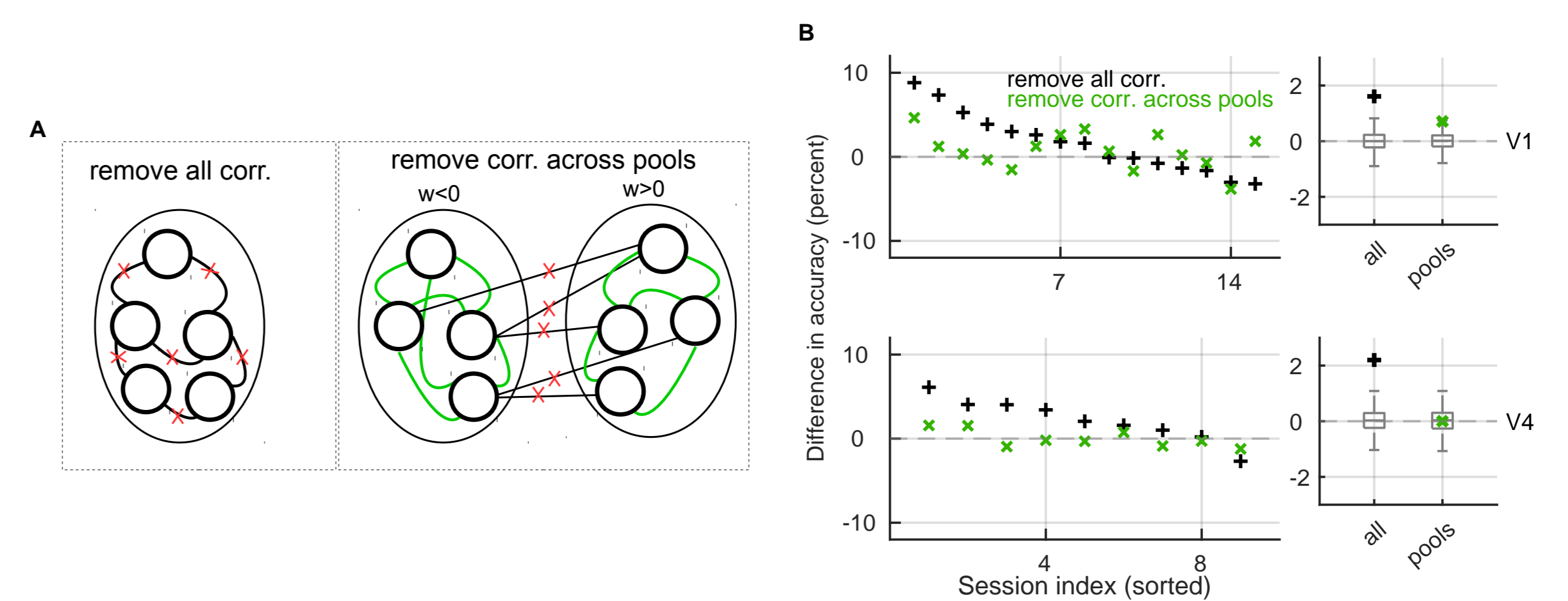


Fig. 5: Correlations within the same coding pool are harmful for the decoder, while correlations across coding pools do not have a significant influence. A) Schema of removing the correlation structure across all neurons (left) and across coding pools (right). B) Difference of the balanced accuracy between the model with removed noise correlations and the regular model. We show results of models with removed correlations across all neurons (black) and selectively only across the coding pools (green).

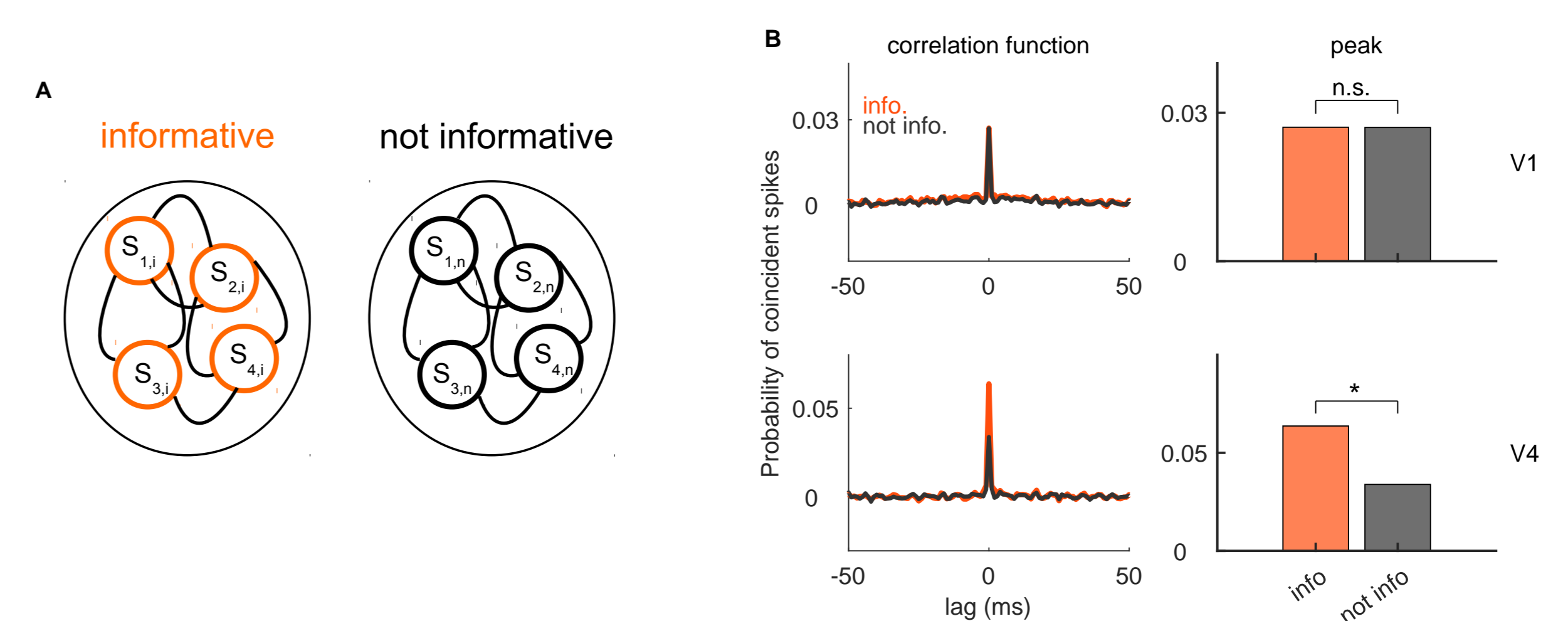


Fig. 6: Informative neurons are more strongly synchronized than uninformative neurons in V4, but not in V1. A) Schema of informative and uninformative neurons. B) Left: Average correlation function between informative (orange) and uninformative neurons (black). Right: Peak of the correlation function.

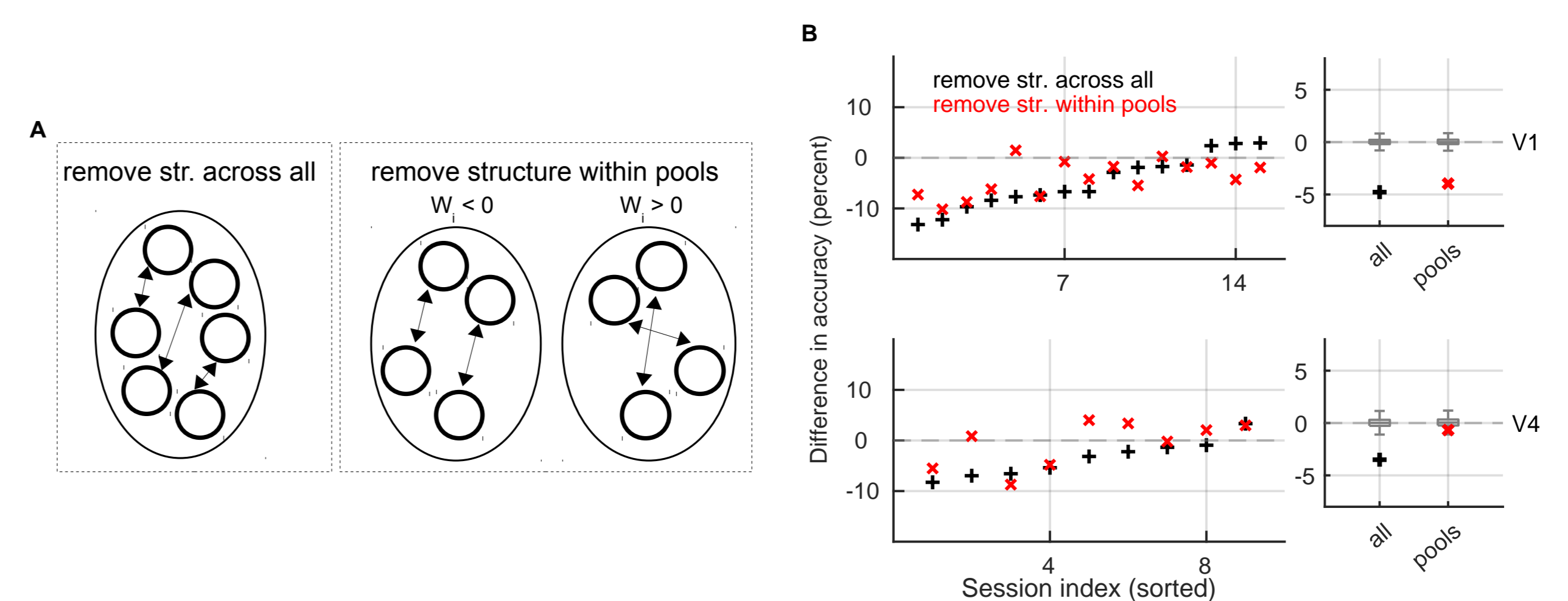


Fig. 7: In V1, the structure across all neurons matters, while in V4, only the structure within the coding pool is important. A) Schema of removal of the structure of population responses across all neurons (left) and within coding pools (right). B) Difference of the balanced accuracy between the model with removed structure and the regular model. We show results of models with structure removed across all neurons (black) and selectively within the coding pools (green).

Conclusions

- Heterogeneous structure of population responses contributes substantially to the performance of the decoder.
- The structure of spike counts is reflected in pair-wise synchrony and correlations in V4 but not in V1.

Pre-prints on bioRxiv

- [1] Koren, Andrei, Hu, Dragoi, Obermayer, Heterogeneous structure shapes pair-wise correlations on different time scales, bioRxiv
 [2] Koren, Andrei, Hu, Dragoi, Obermayer, Reading-out task variables from parallel spike trains in single trials, bioRxiv

References

- [1] Vapnik, V. N., & Vapnik, V. (1998). Statistical learning theory (Vol. 1). New York: Wiley. [2] Koren, V., & Denève, S. (2017). Computational Account of Spontaneous Activity as a Signature of Predictive Coding. PLoS computational biology, 13(1), e1005355 [3] Boerlin, M., Machens, C. K., & Denève, S. (2013). Predictive coding of dynamical variables in balanced spiking networks. PLoS computational biology, 9(11), e1003258.