## Unsupervised discovery of neural sequences in large-scale recordings



Emily Mackevicius



Andrew Bahle



Alex Williams



Shijie Gu



Natasha Denissenko



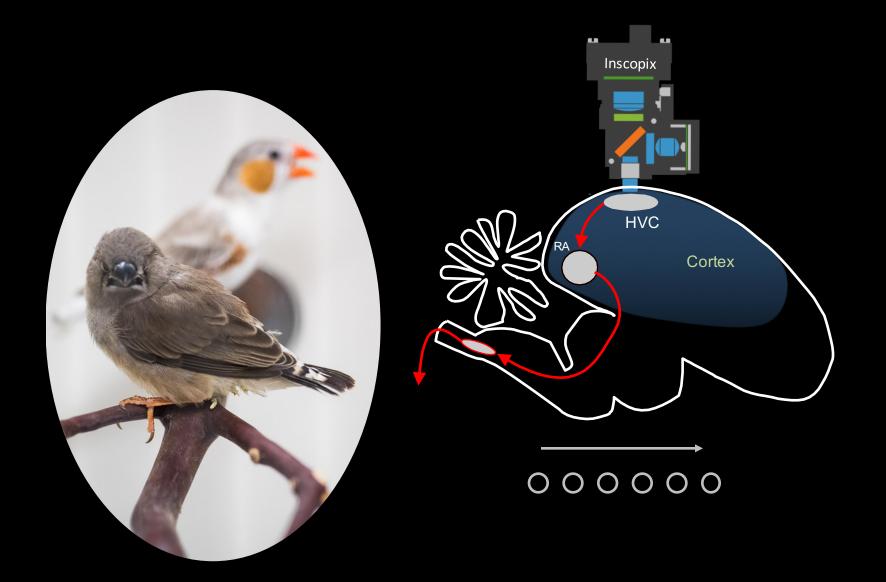
Mark Goldman

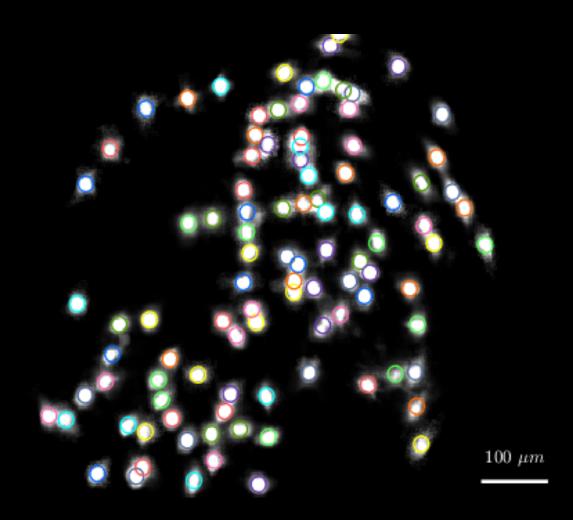


Michale Fee

github.com/Feelab/seqNMF

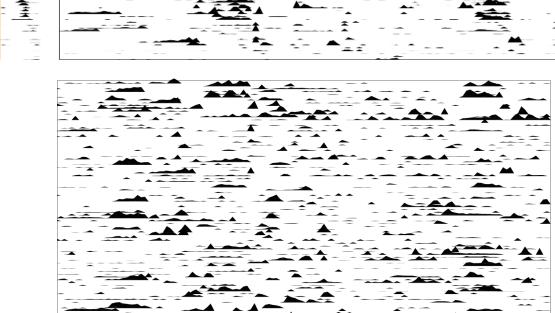
https://www.biorxiv.org/content/early/2018/03/02/273128



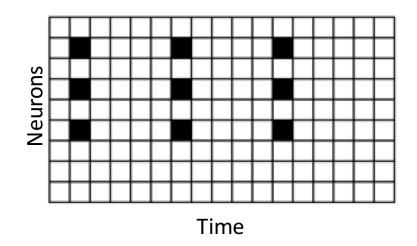


CNMF\_E cell extraction (PC Zhou, Paninski lab, with Shijie Gu)

Neurons (re-sorted)



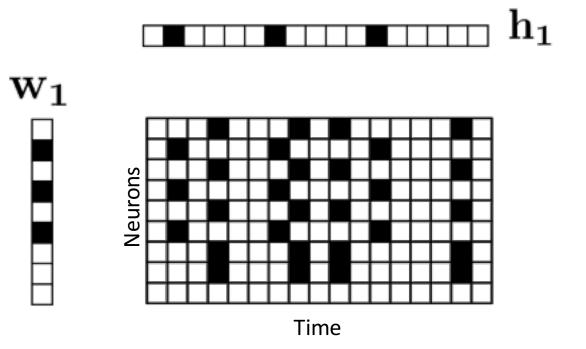
### Non-negative matrix factorization (NMF)



Non-negative matrix factorization (NMF)

(like PCA/SVD, but factors must be positive)

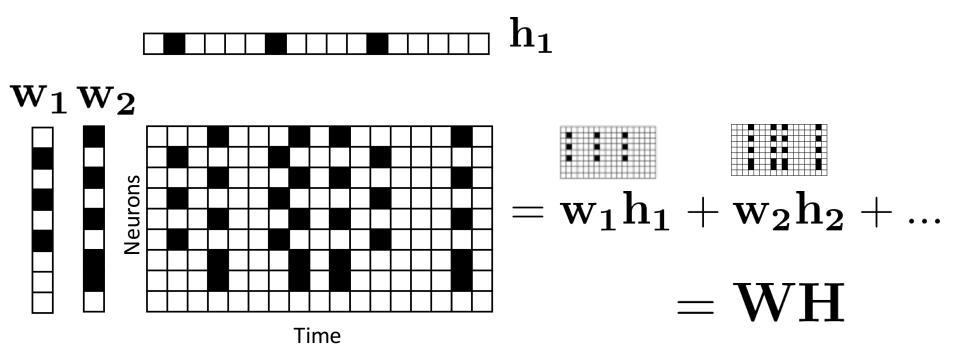
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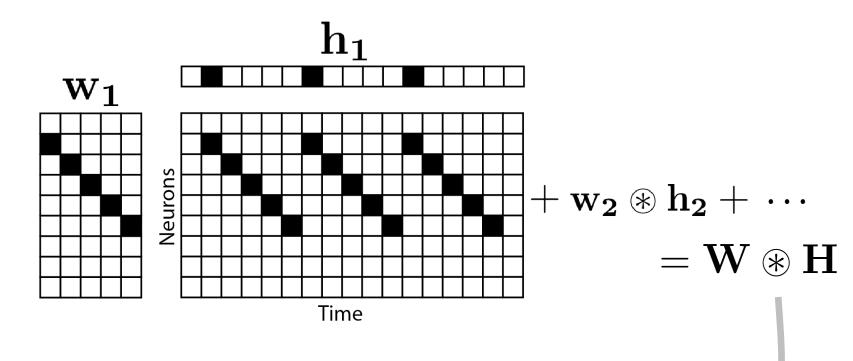
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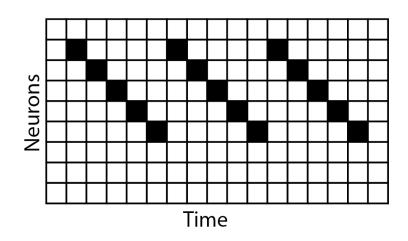
#### Convolutional NMF



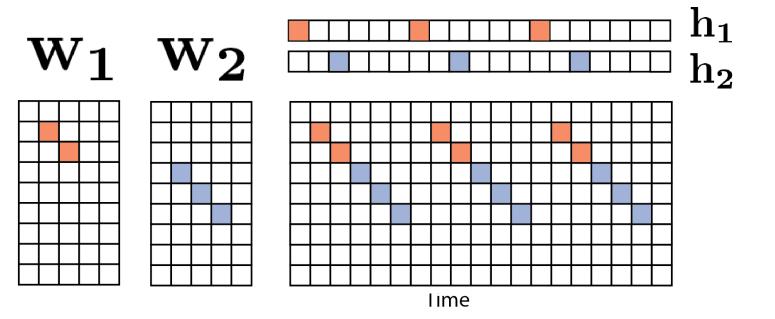
Easy to fit

$$(\widetilde{\mathbf{W}}, \widetilde{\mathbf{H}}) = \arg\min_{\mathbf{W}, \mathbf{H}} (||\mathbf{X} - \mathbf{W} \circledast \mathbf{H}||_F^2)$$

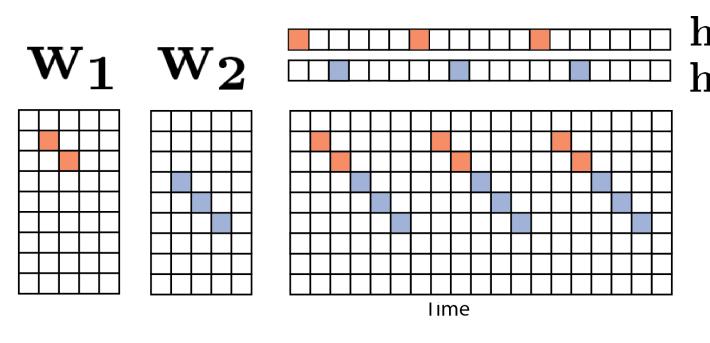
Smaragdis, 2004, 2007



$$(\widetilde{\mathbf{W}}, \widetilde{\mathbf{H}}) = \arg\min_{\mathbf{W}, \mathbf{H}} (||\mathbf{X} - \mathbf{W} \circledast \mathbf{H}||_F^2)$$

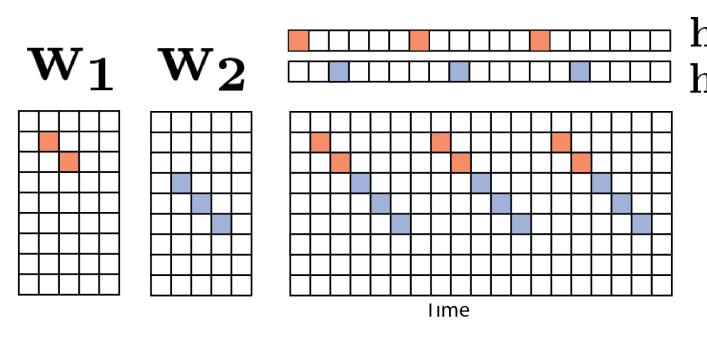


$$(\widetilde{\mathbf{W}}, \widetilde{\mathbf{H}}) = \arg\min_{\mathbf{W}, \mathbf{H}} (||\mathbf{X} - \mathbf{W} \circledast \mathbf{H}||_F^2)$$



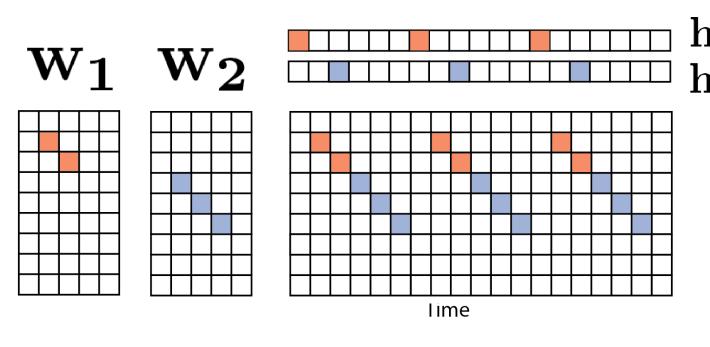
$$(\widetilde{\mathbf{W}}, \widetilde{\mathbf{H}}) = \arg\min_{\mathbf{W}, \mathbf{H}} (||\mathbf{X} - \mathbf{W} \circledast \mathbf{H}||_F^2 + \lambda \mathcal{R})$$

$$\mathcal{R} = ||\mathbf{H}\mathbf{H}^{ op}||$$



$$(\widetilde{\mathbf{W}}, \widetilde{\mathbf{H}}) = \arg\min_{\mathbf{W}, \mathbf{H}} (||\mathbf{X} - \mathbf{W} \circledast \mathbf{H}||_F^2 + \lambda \mathcal{R})$$

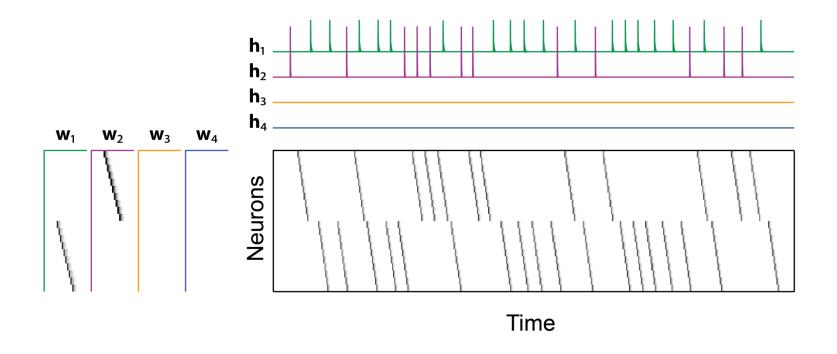
$$\mathcal{R} = ||\mathbf{H}\mathbf{S}\mathbf{H}^\top||$$



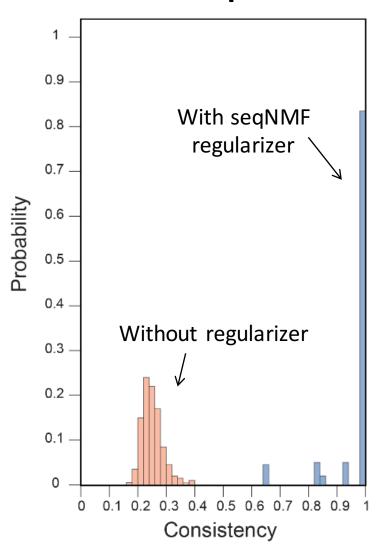
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$$\mathcal{R} = ||\mathbf{W} \circledast \mathbf{X} \mathbf{S} \mathbf{H}^{\top}||$$

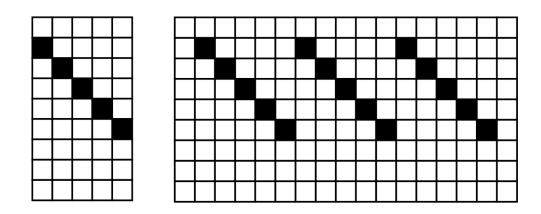
## SeqNMF robustly discovers factors in simulated data



# SeqNMF factorizations are highly consistent compared to CNMF

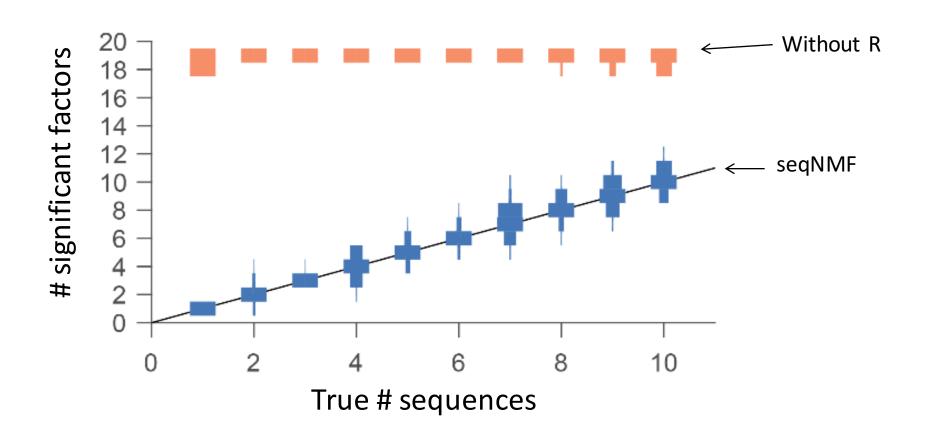


## Testing significance of each factor on held-out data

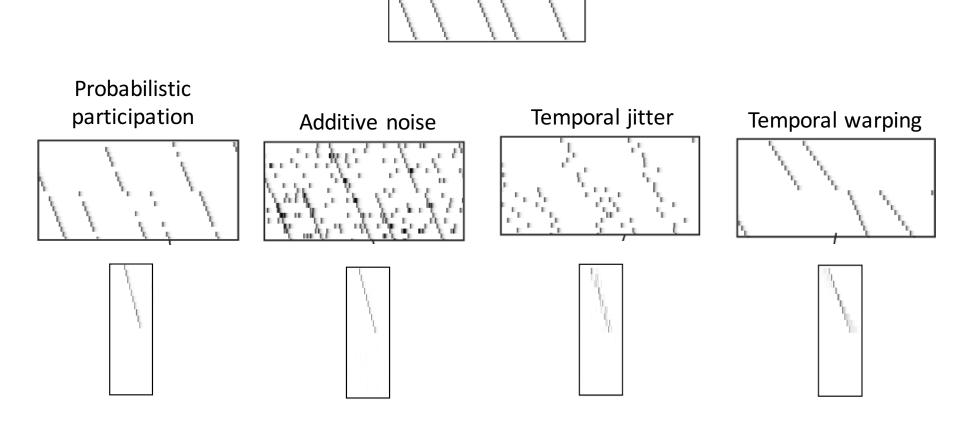


Many moments of high overlap, compared to null

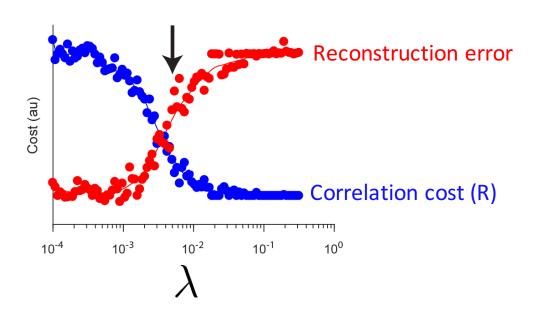
#### SeqNMF discovers the correct number of sequences



#### SeqNMF is robust to noise

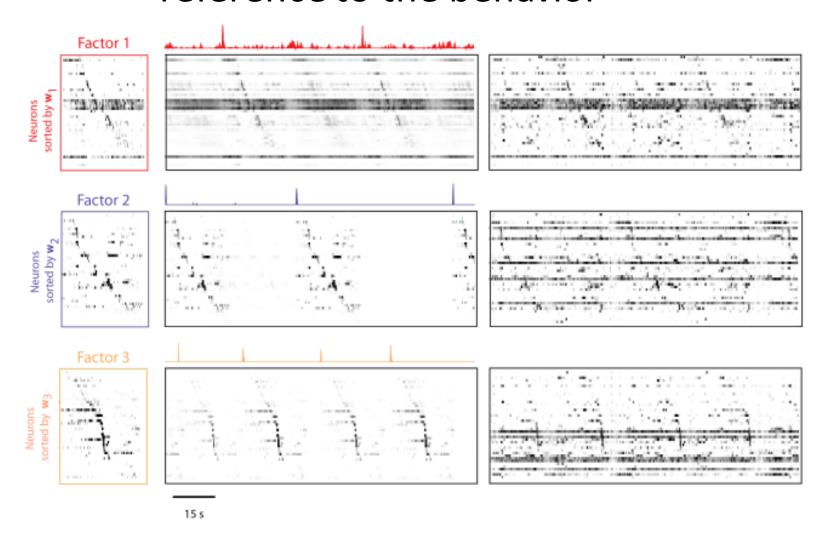


#### Method to choose lambda

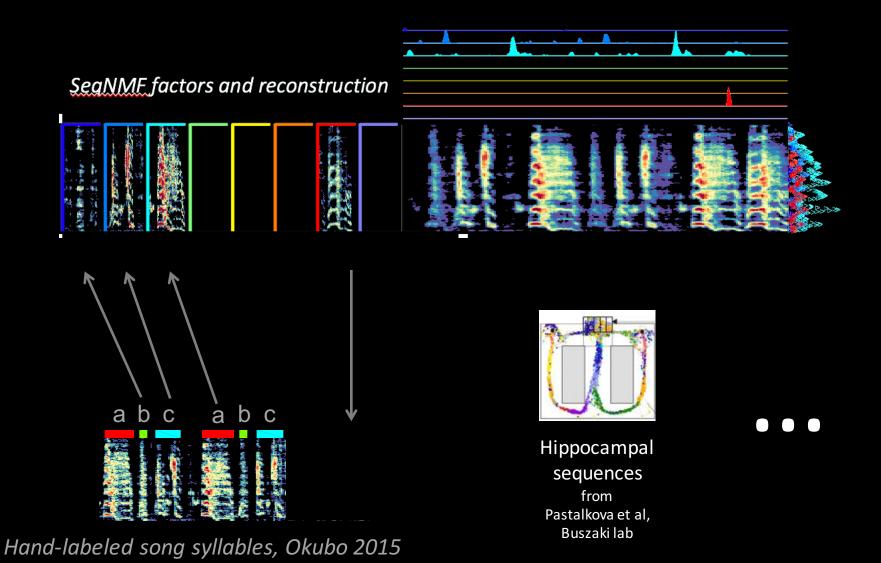


$$(\widetilde{\mathbf{W}}, \widetilde{\mathbf{H}}) = \arg\min_{\mathbf{W}, \mathbf{H}} (||\mathbf{X} - \mathbf{W} \circledast \mathbf{H}||_F^2 + \lambda \mathcal{R})$$

## SeqNMF extracts hippocampal sequences without reference to the behavior



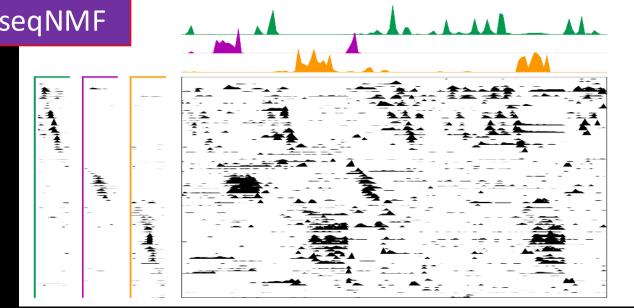
### SeqNMF is broadly applicable to many highdimensional datasets



### SeqNMF: GO FIND SEQUENCES!

github.com/Feelab/seqNMF

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