

Bayesian Spike Source Localization in Extracellular Recordings using Amortized Variational Inference

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Motivation

- Spatially localizing detected spikes before classification can provide a useful, low-dimensional feature set to aid preexisting spike sorting algorithms.
- Location estimates can be utilized in downstream analysis (eg. to register recorded neurons with anatomical information [1]).
- Most current localization methods are designed for low-channel count recording devices.
- Localization methods for dense MEAs utilize cleaned extracellular action potentials (through spike-triggered averaging), disallowing their use before spike sorting
- All current localization methods are non-Bayesian.

Contribution

- A Bayesian inversion approach to spike source localization.
- Scalable inference with amortized variational inference.
- Large improvements in localization and spike sorting accuracy over the only commonly used method, *center of mass*.
- Quantitative and qualitative evaluation with both real and simulated extracellular datasets.

Model

- The source location of $s_{i,k}$ is defined as $\{(x_{s_{i,k}}, y_{s_{i,k}}, z_{s_{i,k}})\} \in \mathbb{R}^3$.
- We assume that the amplitudes decay exponentially with the distance from the source, $r: a \exp(br)$ where $a, b \in \mathbb{R}$, $r \in \mathbb{R}^+$.
- We fix the decay rate, b , to be constant for all spikes in the recording and equal to an empirical estimate from literature ([1],[2],[3]).
- The generative process of our model is as follows,

$$\begin{aligned} a_{i,k} &\sim N(\mu_{a_{i,k}}, \sigma_a), x_{s_{i,k}} \sim N(\mu_{x_{s_{i,k}}}, \sigma_x), y_{s_{i,k}} \sim N(\mu_{y_{s_{i,k}}}, \sigma_y), \\ z_{s_{i,k}} &\sim N(\mu_{z_{s_{i,k}}}, \sigma_z), \hat{r}_{i,k} = \|(\mathbf{x}_{s_{i,k}}, \mathbf{y}_{s_{i,k}}, \mathbf{z}_{s_{i,k}}) - \mathbf{p}_c\|_2, \\ \alpha_{i,k} &\sim N(a_{i,k} \exp(b\hat{r}_{i,k}), I) \end{aligned}$$

- p_c is the position of each channel on the MEA and $\alpha_{i,k}$ is the observed amplitudes.
- We refer to the augmented dataset as $\beta_{i,k}$ (as described in the full manuscript).
 - We learn our posterior via amortized variational inference (with a variational autoencoder) with a Gaussian observation model.
 - We directly optimize $a_{i,k}$ when maximizing the lower bound.
 - The evidence lower bound (the lower bound on the log marginal likelihood of the data) for each spike, $s_{i,k}$, is given by,

$$\log p(\beta_{i,k}; a_{i,k}) \geq$$

$$-\text{KL}[q_\phi(x, y, z) \parallel p_x p_y p_z] + \mathbb{E}_{q_\phi} \left[\sum_{l=1}^L \mathcal{N}(\beta_{i,k}^0 | a_{i,k} \exp(b\hat{r}_{i,k}), I) \beta_{i,k}^1 \right]$$

where KL is the KL-divergence. The location priors, p_x, p_y, p_z , are normally distributed, with means of zero and variances of 80.

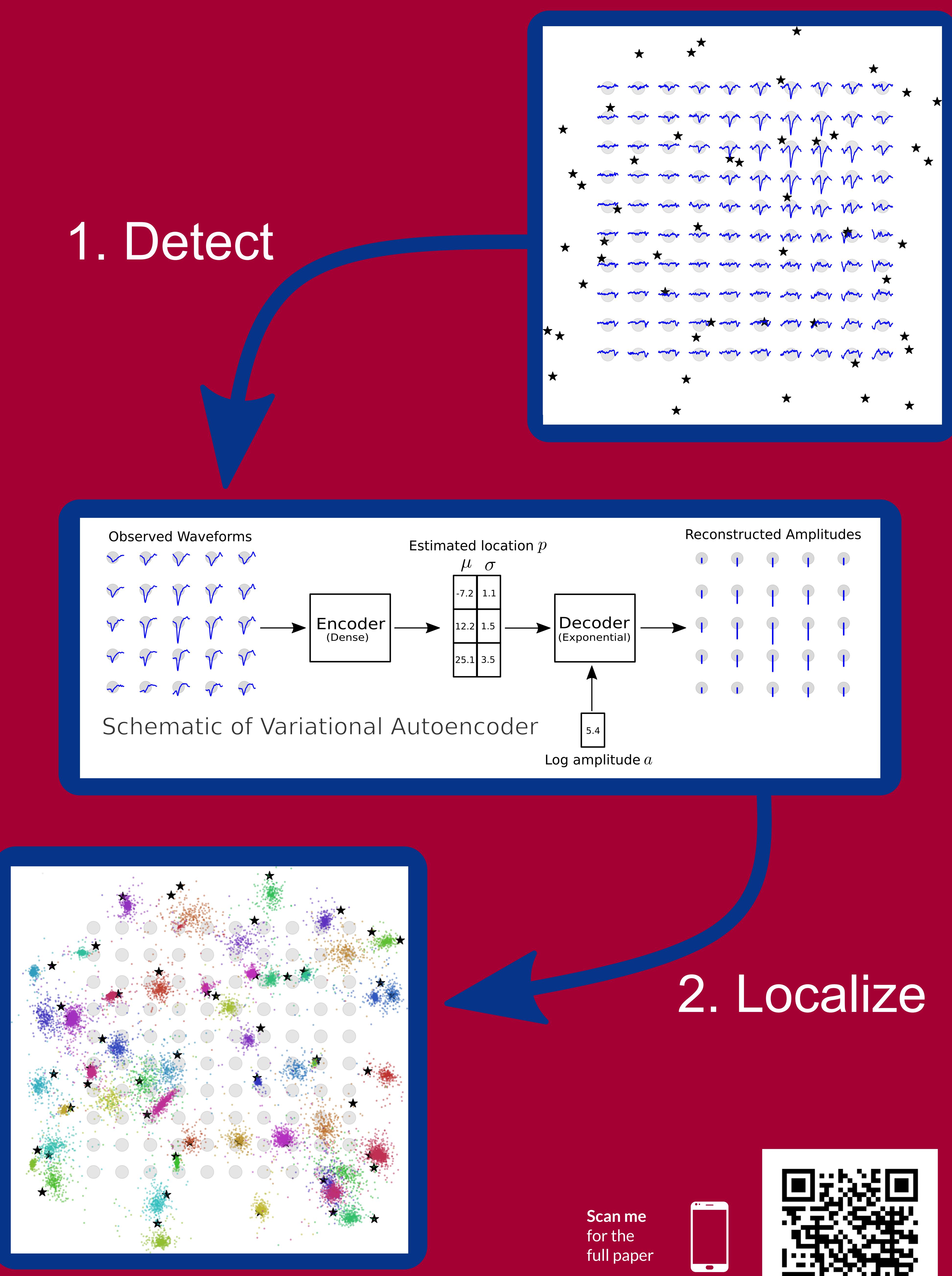
Datasets

Simulated Data

- We simulate extracellular datasets using MEArec [4].
- We simulate three 60s recordings for two probe geometries.
- The noise levels are 10μV-30μV (generated by faraway neurons).
- We use 40 excitatory cells and 10 inhibitory cells.
- We use ground truth to extract waveforms for localization.
- Quantitative evaluation of localization and spike sorting accuracy improvements over center of mass.

Real Data

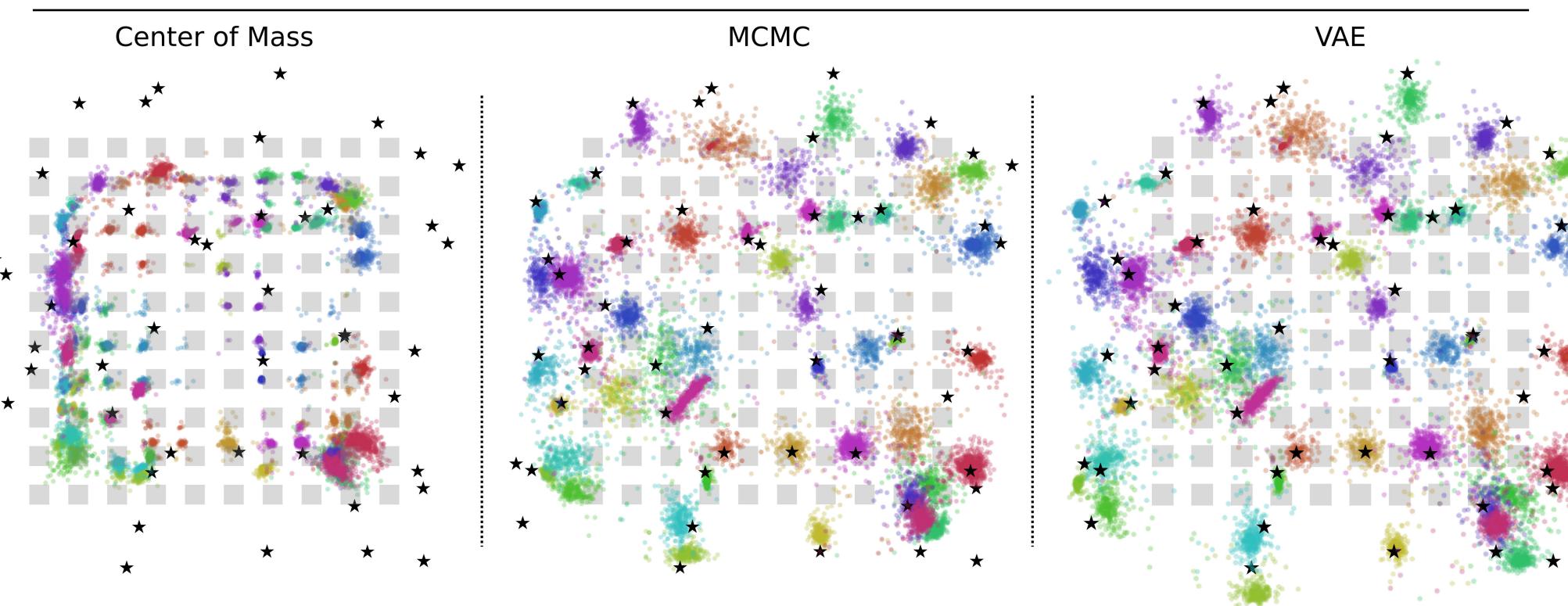
- Public data from a Neuropixels probe (6.6 million spikes) [6].
- Mouse retina data recorded with the BioCam4096 platform (2.2 million spikes) [1].
- Spike detection and sorting (with our location estimates) is done using the HerdingSpikes2 software [1].
- Qualitative evaluation of location estimates.



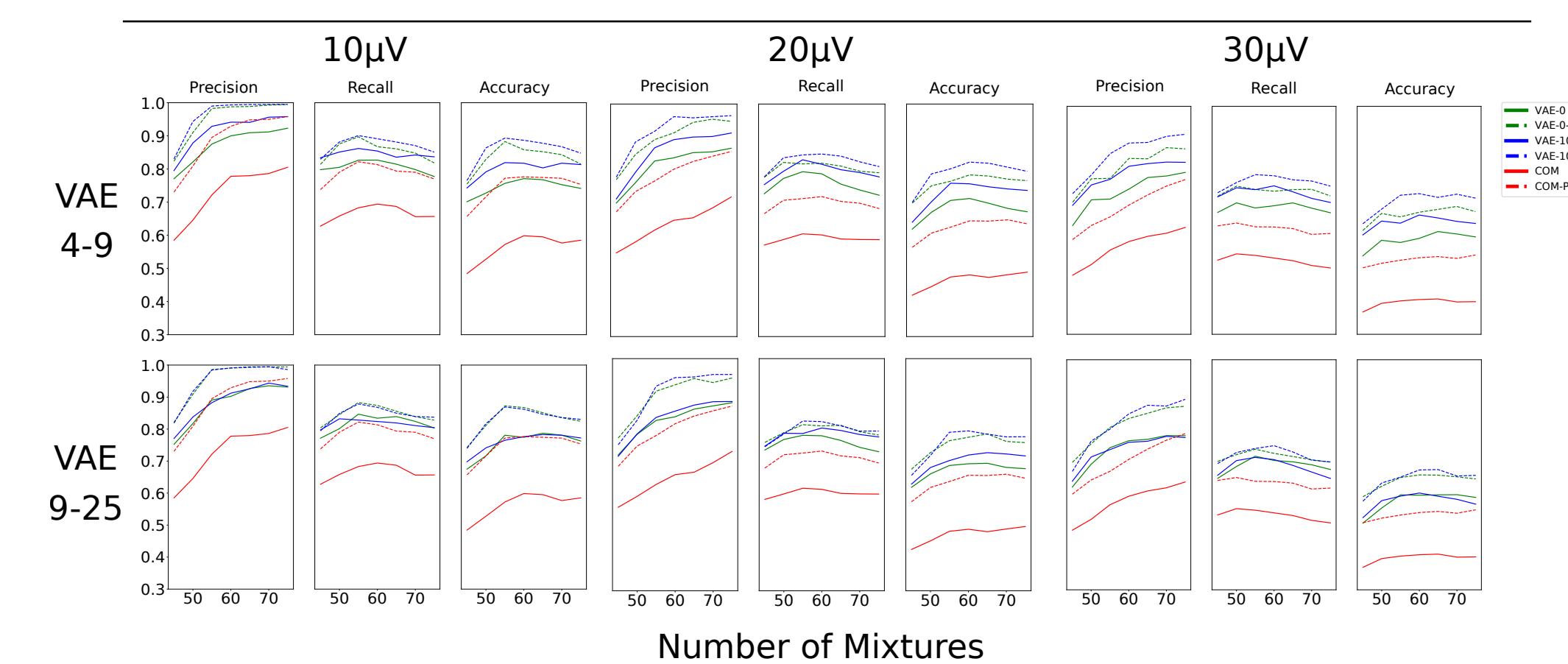
Results

Method	Observed Channels	2D Avg. Spike Distance from Soma (μm)		
		10 μV	20 μV	30 μV
COM	4	15.84±10.08	16.46±10.39	17.18±10.97
COM	9	18.05±11.42	18.59±11.67	19.22±12.1
COM	16	20.94±13.09	21.54±13.46	22.17±13.94
COM	25	23.44±14.81	24.31±15.43	25.18±15.98
MCMC	9-25	9.87±8.64	11.30±9.85	13.31±11.67
VAE - 0μV	4-9	9.21±8.00	10.40±8.97	12.05±10.35
VAE - 10μV	4-9	8.79±7.49	9.79±8.31	11.18±9.56
VAE - 0μV	9-25	8.94±7.91	10.48±9.334	12.43±11.223
VAE - 10μV	9-25	9.12±7.83	10.41±9.07	12.27±10.78

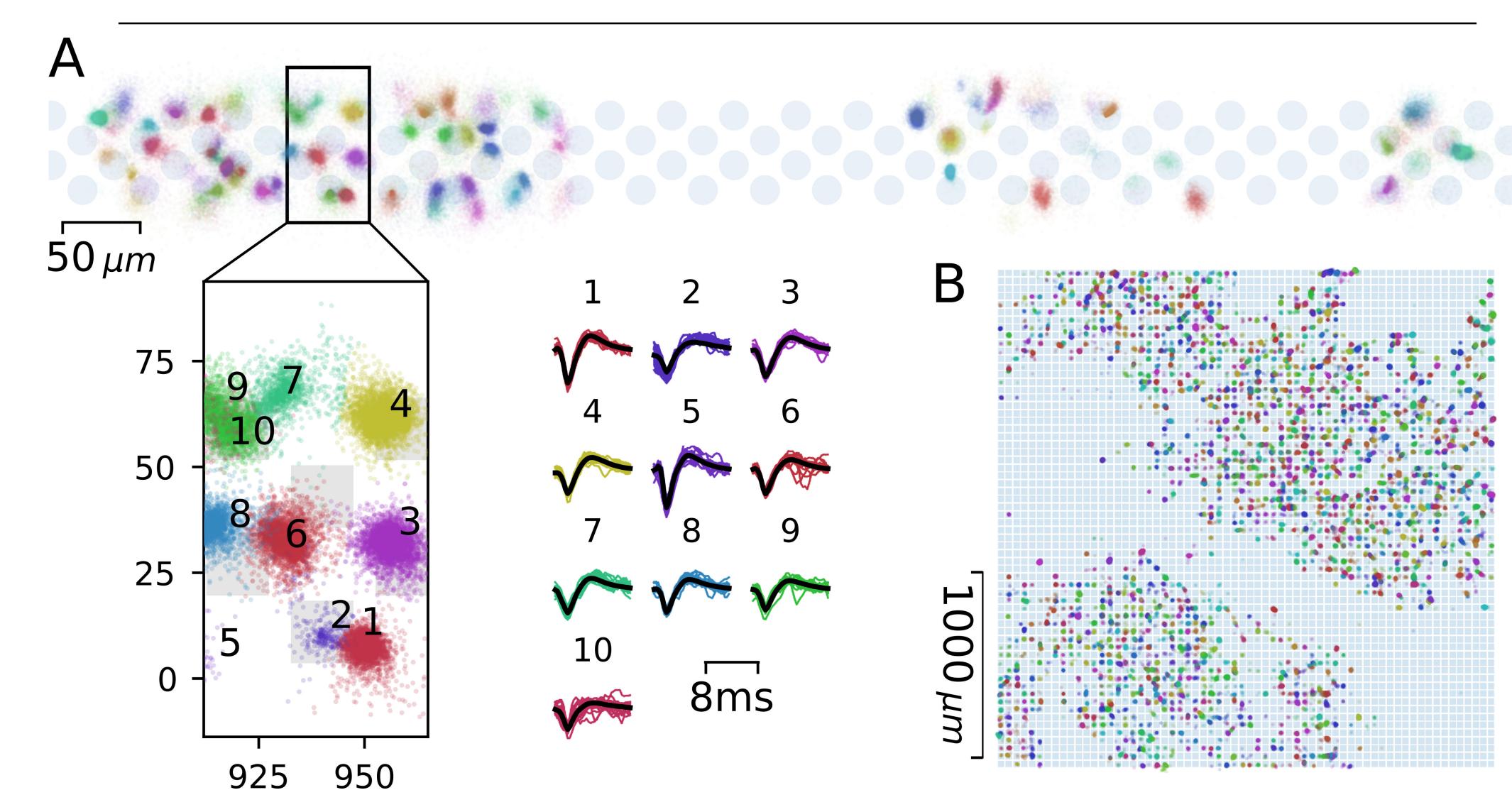
Results of the localization methods on the three simulated datasets from the square MEA with noise levels ranging from 10μV-30μV. The number next to the VAE methods in the first column is the amount of amplitude jitter that was used for the method, a hyperparameter described in the full manuscript.



The estimated spike locations for the different methods on a 10μV recording. Center of mass estimates (left) are calculated using 16 observed amplitudes. The MCMC estimated locations (middle) used 9-25 observed amplitudes for inference, and the VAE model (right) was trained on 9-25 observed amplitudes and a 10 amplitude jitter, a hyperparameter described in the full manuscript.



Spike Sorting Performance on square MEA using GMMs. We compare the sorting performance of all localization methods with and without principal components across all noise levels. For the VAE, we include the results with 0μV and 10μV amplitude jitter and with different amounts of observed channels (4-9 and 9-25). For COM, we plot the highest sorting performance (25 observed channels). The test data set had 50 neurons.



Estimated spike locations for two real recordings. A, Analysis of a one hour recording from an awake, head-fixed mouse with a Neuropixels probe. Spikes were detected and sorted using the HS2 sorting software [1] and the VAE localization. Shown is a large section of the probe, a magnification and corresponding spike waveforms from the clustered units. B, The same analysis performed on a recording from a mouse retina with a BioCam array from ref [1].

[1] Hilgen, et al. 2017. [2] Ronen, et al. 2004. [3] Charles M, et al. 1995. [4] <https://github.com/alejoe91/MEArec> [5] Srikanth et al. 2015. [6] Mora et al. 2016.