

Neural Data Science **Spike sorting & evaluation**

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Data briefs

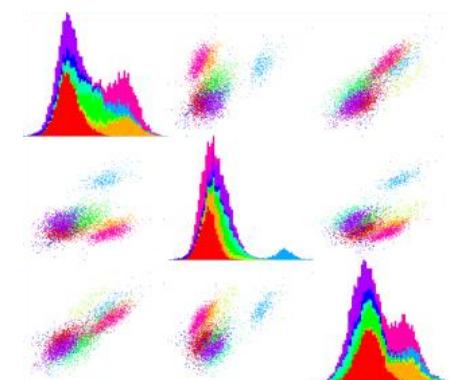
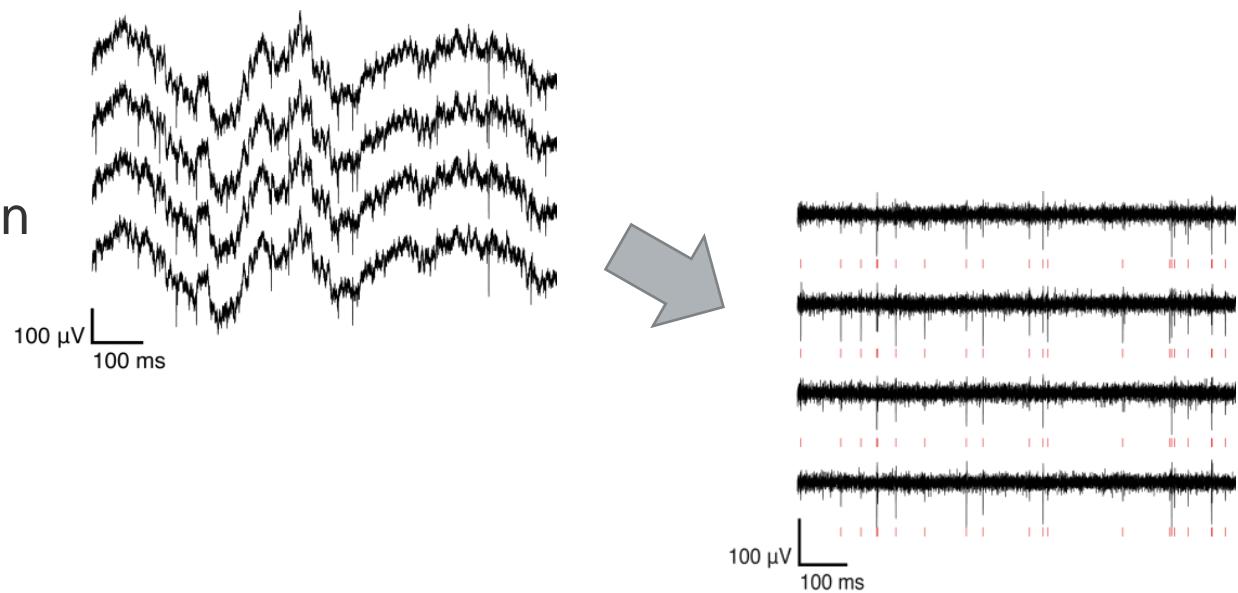
What was the average life expectancy in Europe and Africa

- 1800?
- 1950?
- 2015?



Spike sorting

- Raw data
- Spike detection
- Feature extraction
- Clustering
- Verification



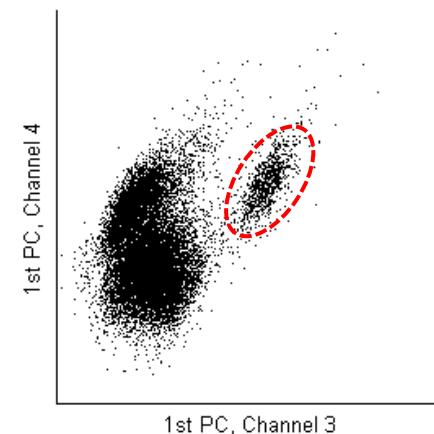
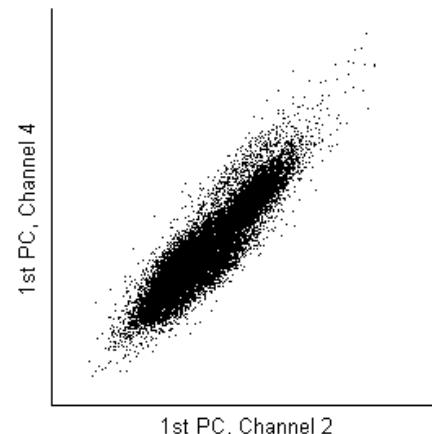
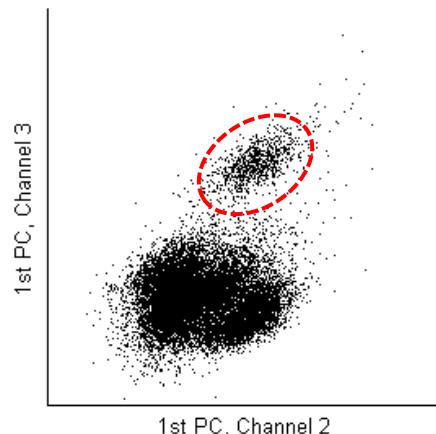
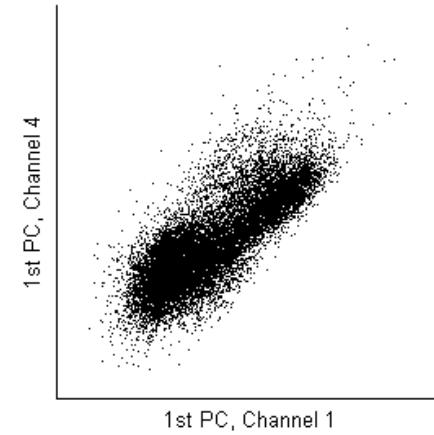
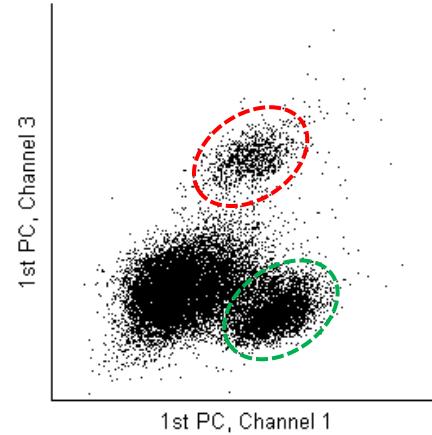
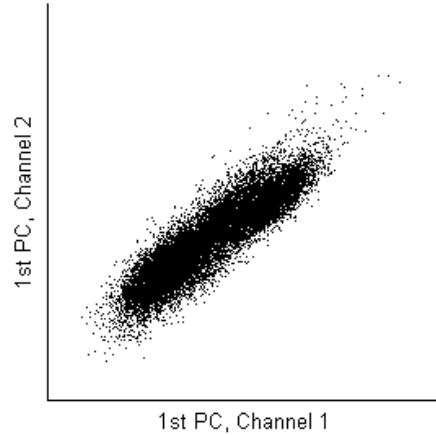


Spike sorting



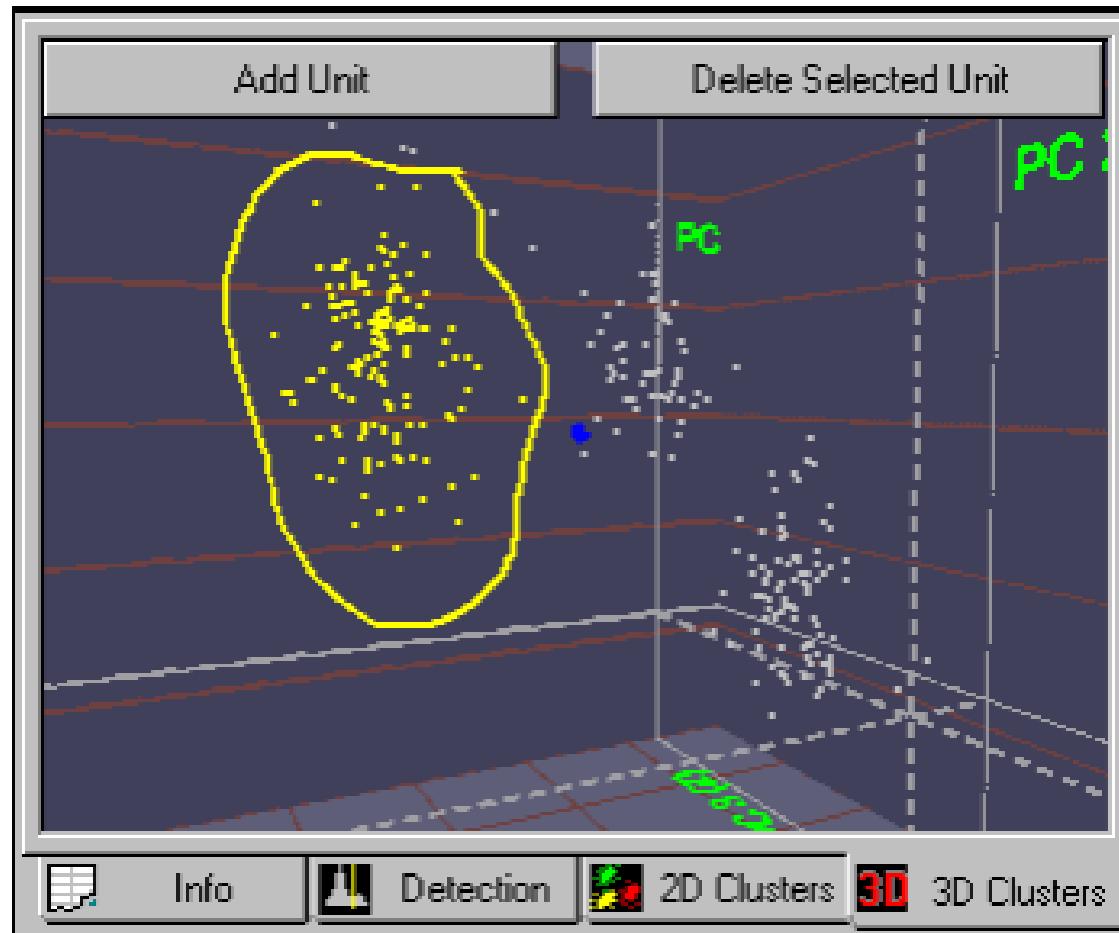


Scatter plot





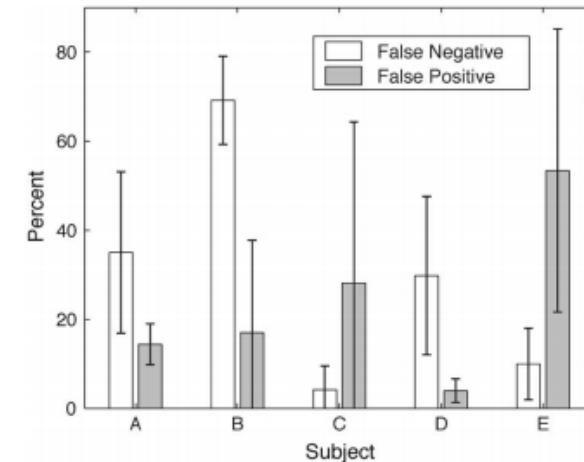
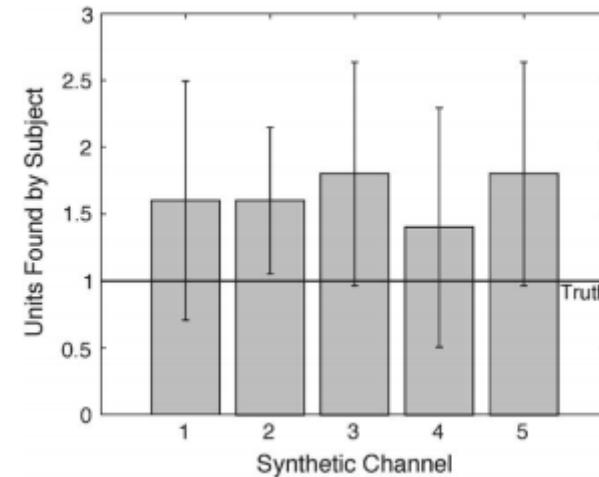
Manual cluster cutting





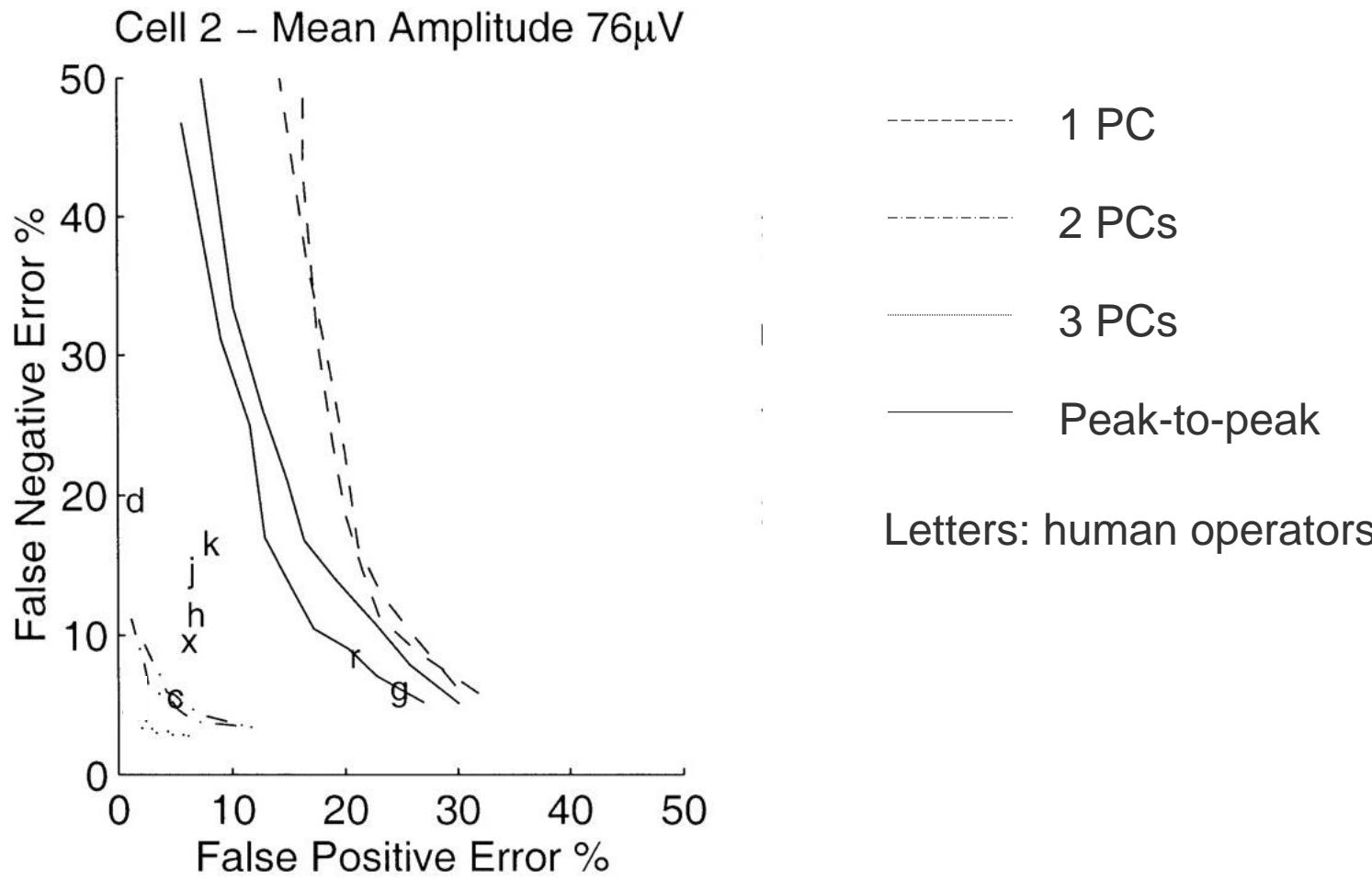
Why is that not a good idea?

- Subjective
- High error rates
- Suboptimal boundaries
- Time consuming
- Not reproducible
- Not model based





Problems of manual sorting



Harris et al. (2000), J Neurophysiology

Automatic clustering

- Objective
- Model-based
- Reproducible
- Quantifiable

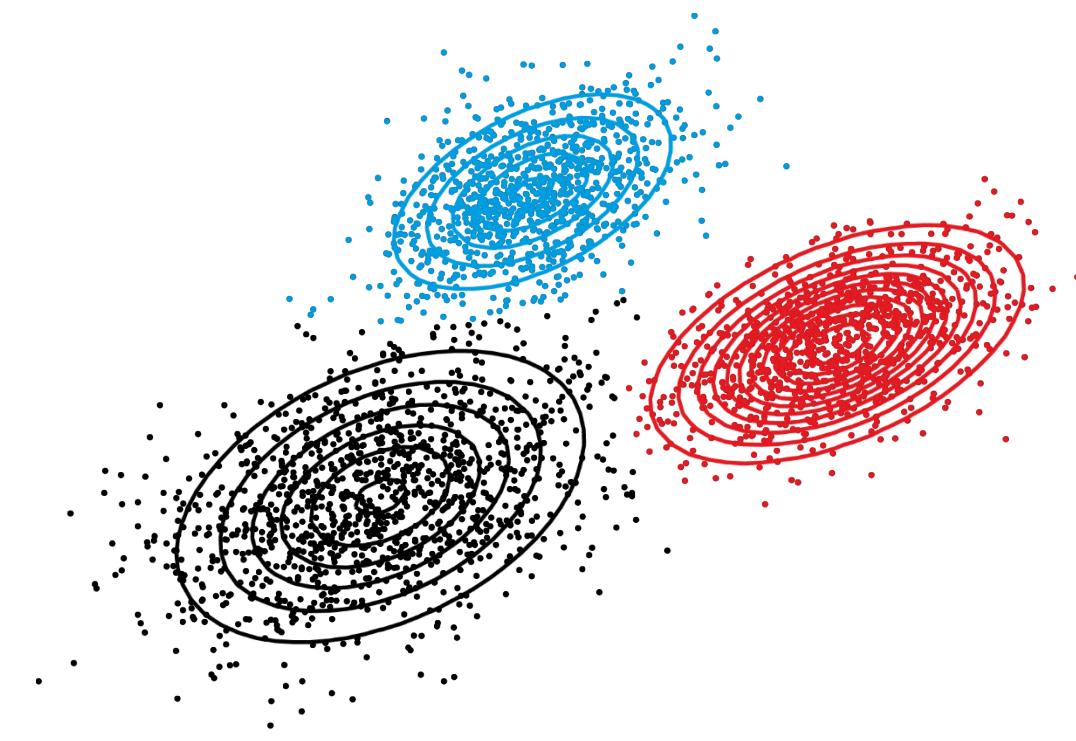
- K-Means
- Mixture of Gaussian
- Others?



Which algorithm?

Gaussian mixture model

$$p(x) = \sum_k \rho_k \mathcal{N}(x | m_k, S_k)$$





Log Likelihood

$$\ln p(x|\mu, \Sigma, \pi) = \sum_n \ln \sum_k \pi_k \mathcal{N}(x_n | \mu_k, \Sigma_k)$$

π_k Mixing coefficient of cluster k

μ_k Mean of cluster k

Σ_k Covariance of cluster k

Expectation maximization (EM)

- Finds maximum likelihood estimate of latent variable model
- Parameters: θ
Latent variables: Z
Data: X
- Alternate until convergence:

1. **E step**

Estimate latent variables Z given the current set of parameters θ

2. **M step**

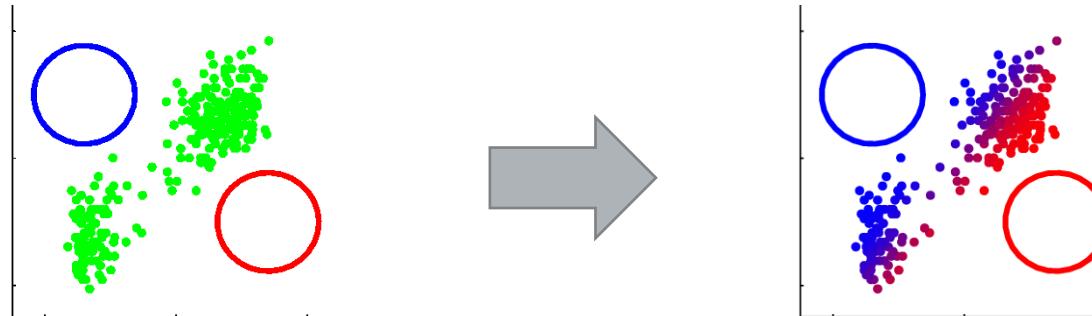
Update parameters θ to maximize the likelihood given current estimate of the latent variables Z



E-Step

Evaluate “responsibilities” with current parameter values
(posterior probability of a data point to belong to cluster k)

$$\gamma_{k,n}^{new} = \frac{\pi_k \mathcal{N}(x_n | \mu_k, \Sigma_k)}{\sum_j \pi_j \mathcal{N}(x_n | \mu_j, \Sigma_j)}$$





M-step

Update means:

$$\mu_k^{new} = \frac{1}{N_k} \sum_n \gamma_{k,n} x_n$$

Update covariances:

$$\Sigma_k^{new} = \frac{1}{N_k} \sum_n \gamma_{k,n} (x_n - \mu_k^{new})(x_n - \mu_k^{new})'$$

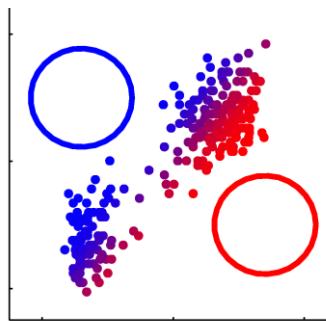
Update mixing coefficients:

$$\pi_k^{new} = \frac{N_k}{N}$$

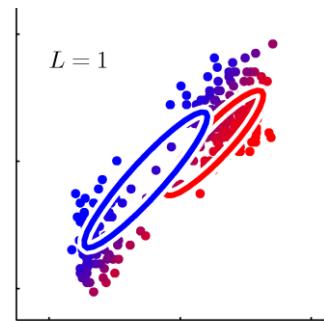
$$N_k = \sum_n \gamma_{k,n}$$



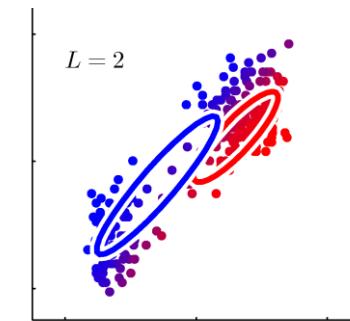
M-step



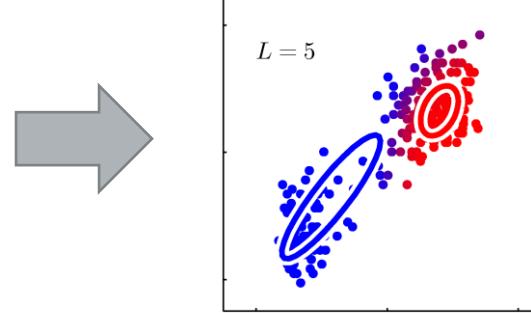
Initialization



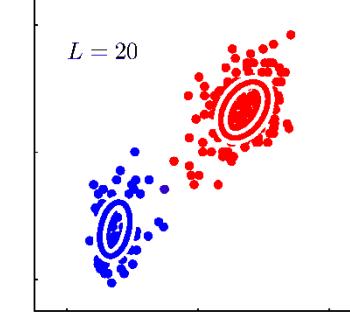
Step 1



Step 2



Step 5



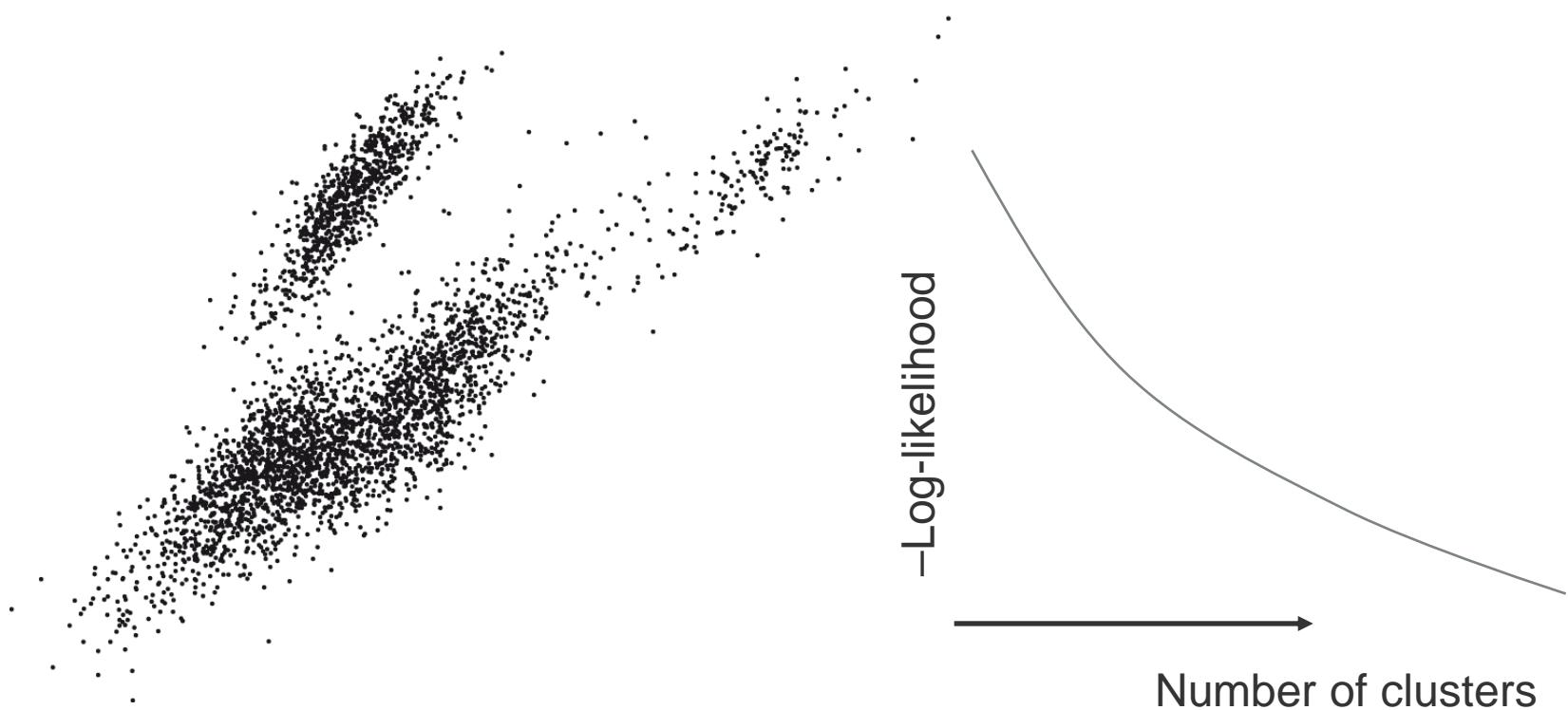
Step 20

Open issues

- How do you determine the number of clusters?
- How do you deal with local maxima?
- How do we work with outliers?
- What about clusters whose mean can drift over time?
- What about spikes occurring simultaneously?



How to determine the number of clusters?



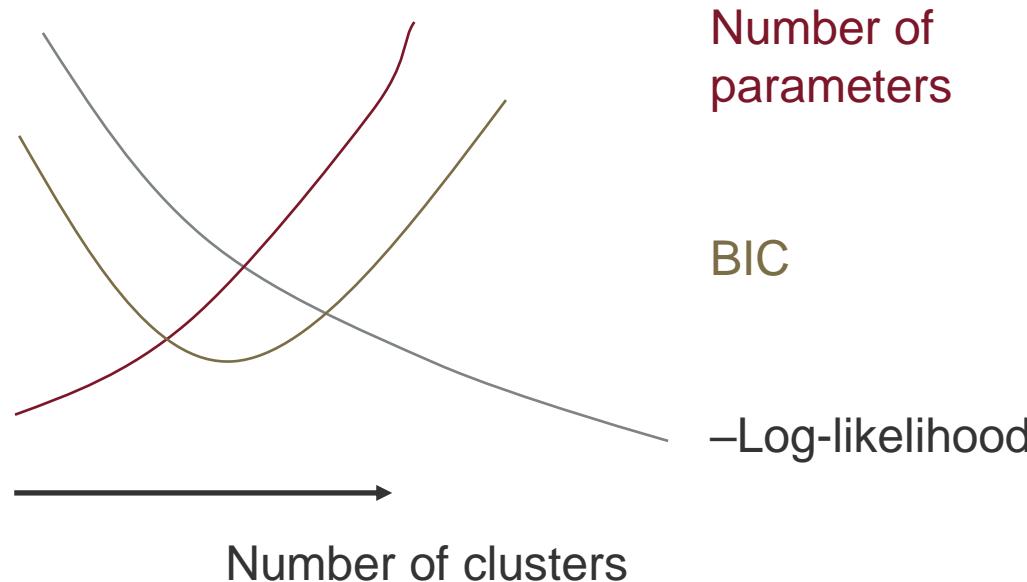


Dealing with model complexity

Penalize number of parameters!

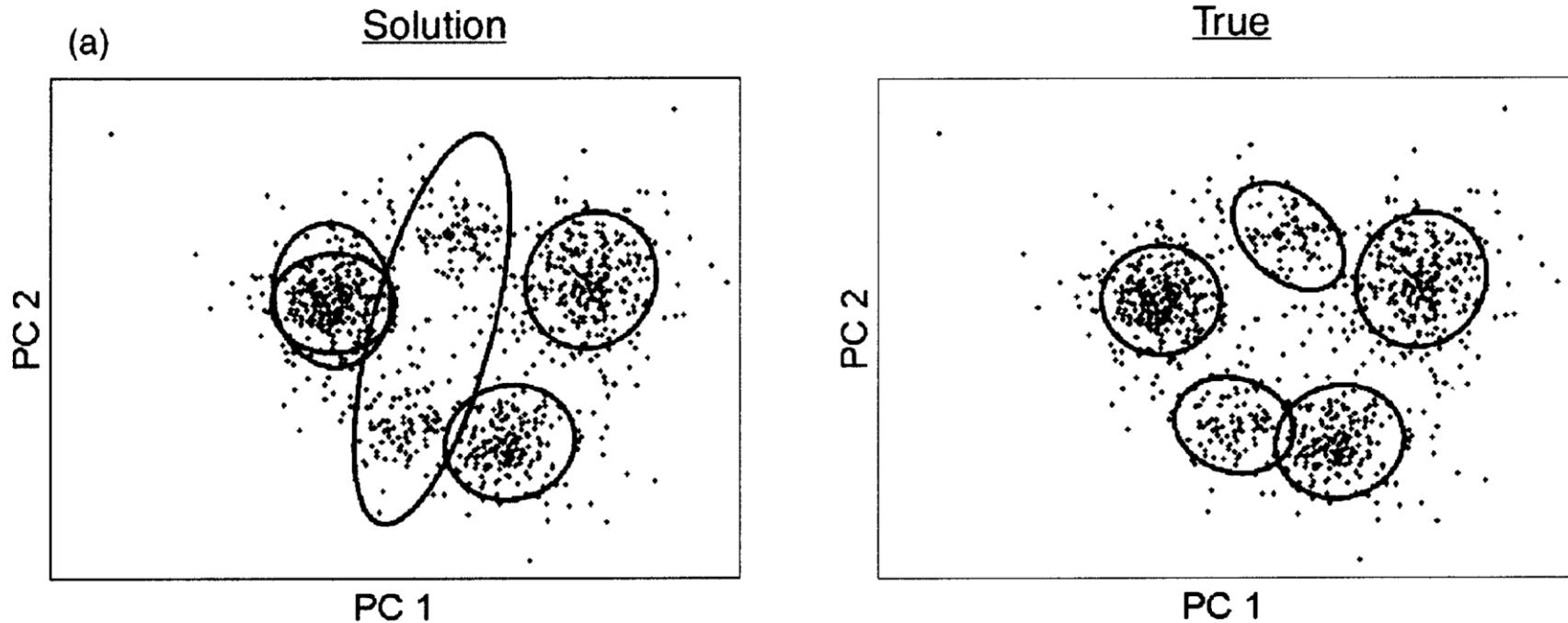
Use Bayesian Information Criterion (or similar)

$$BIC = -2 \ln p(x | \mu_{opt}, \Sigma_{opt}, \pi_{opt}) + P \ln N$$





Dealing with local maxima

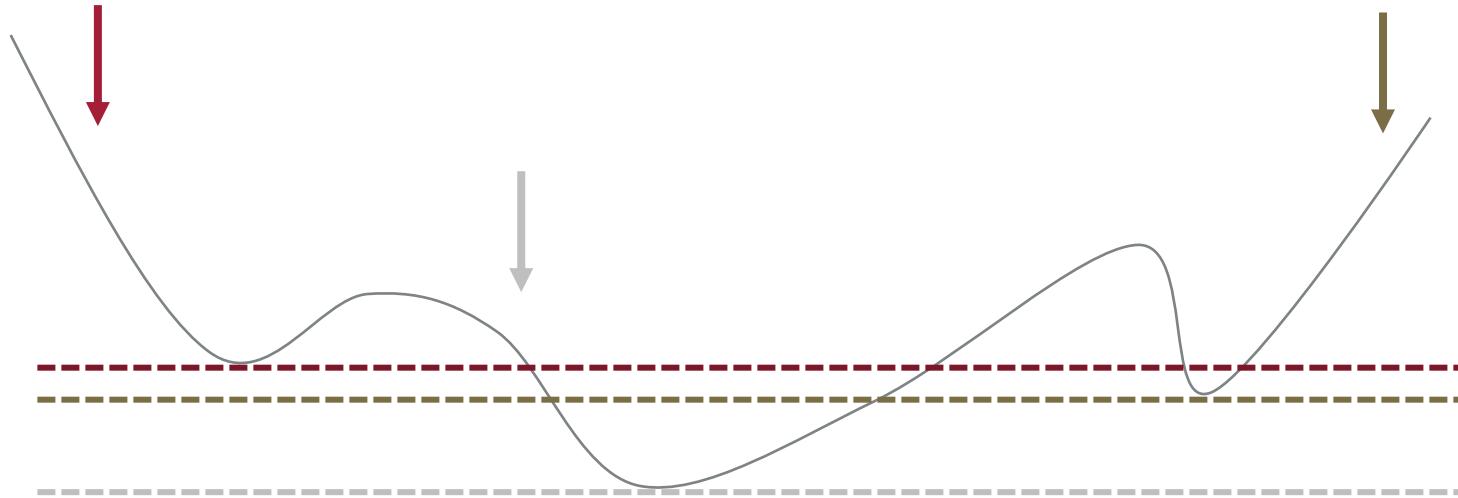


Possible solutions:

- Pick the best result among multiple independent runs
- Split-and-merge



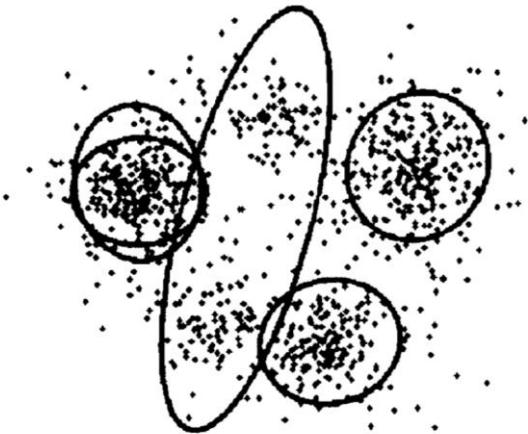
Restarting to Avoid local Minima





Split and Merge

- After EM has converged, test whether BIC is decreased by:
- **Splitting** a cluster
 - For a candidate, run 'partial EM' with two components instead of one, keeping all other components fixed
- **Merging** two clusters
 - Compute new model with two clusters combined into one

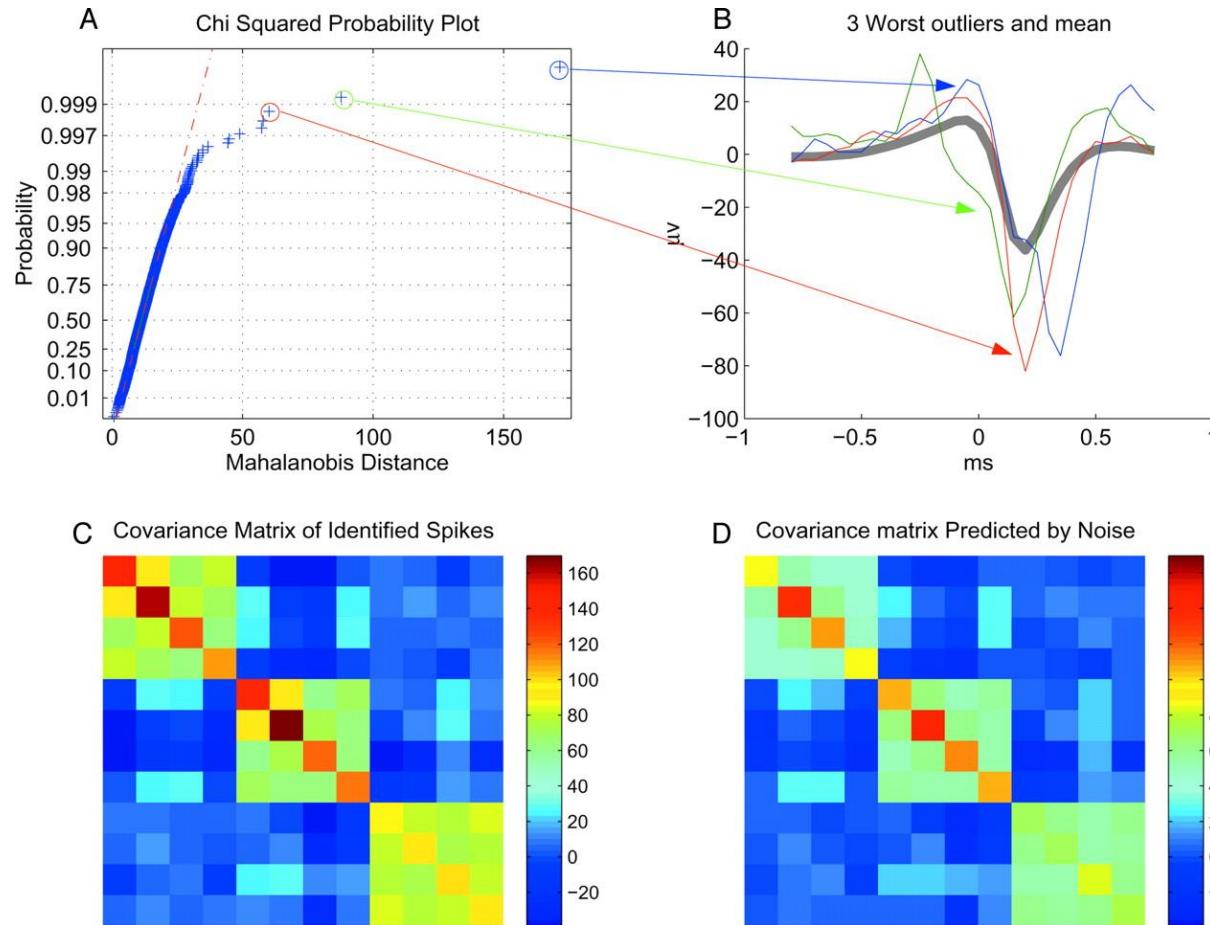


From Shoham et al.
2003



Problem: Outliers

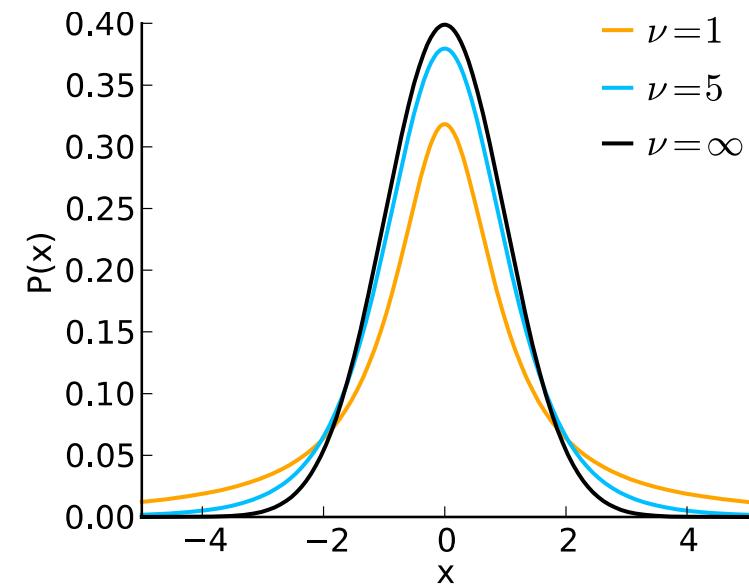
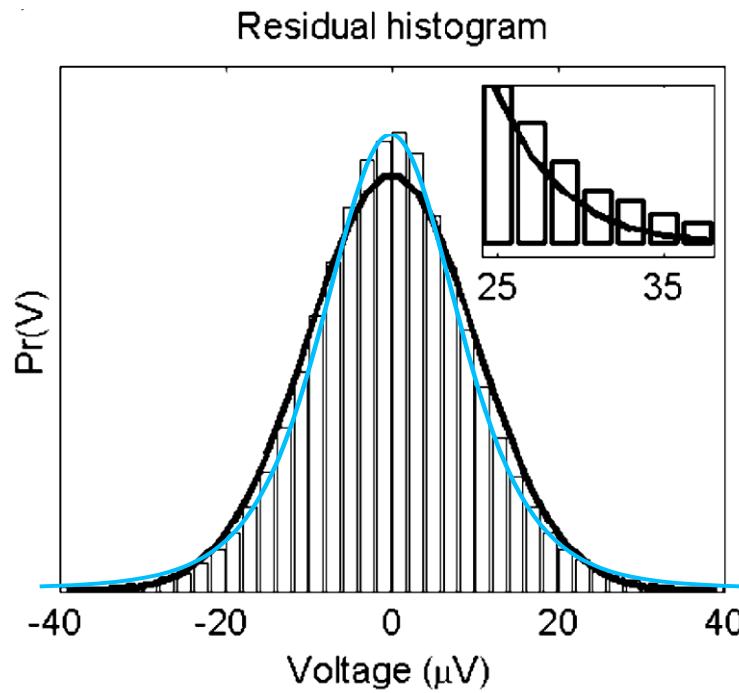
$$D = \sqrt{(x - \mu)^T C^{-1} (x - \mu)}$$





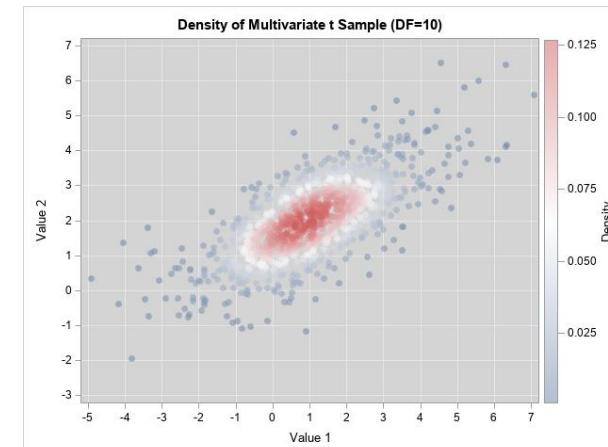
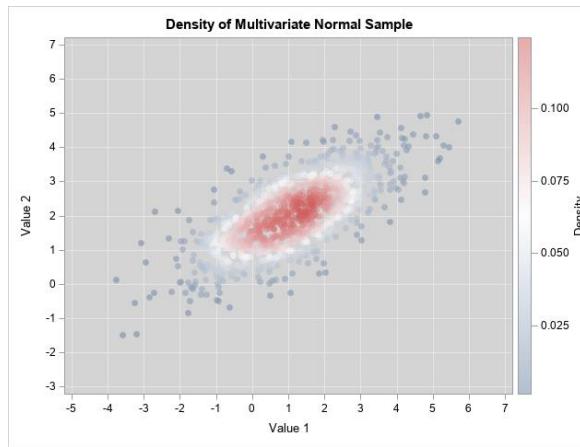
Problem: Outliers

Replace Gaussian mixtures by multivariate t-distributions





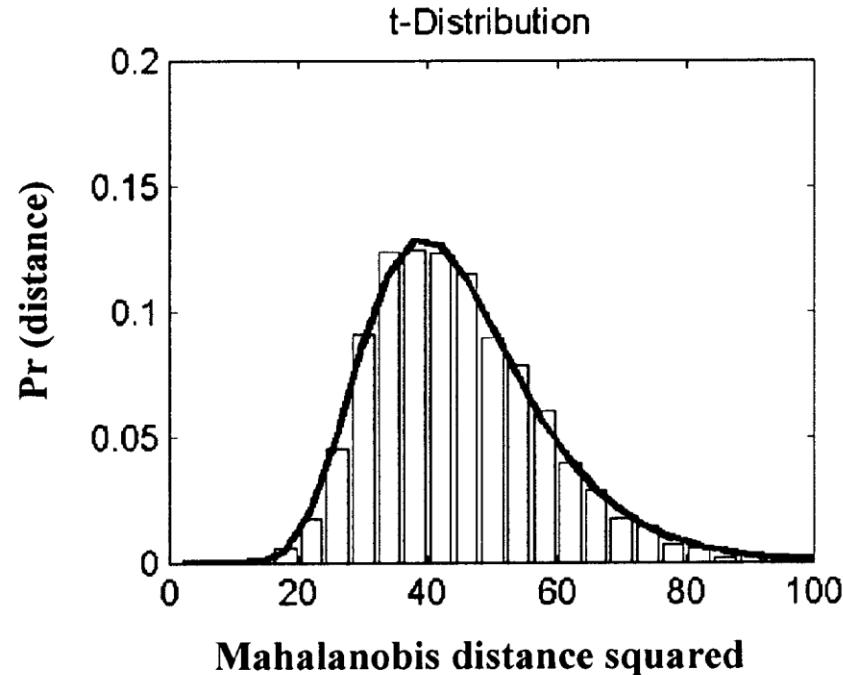
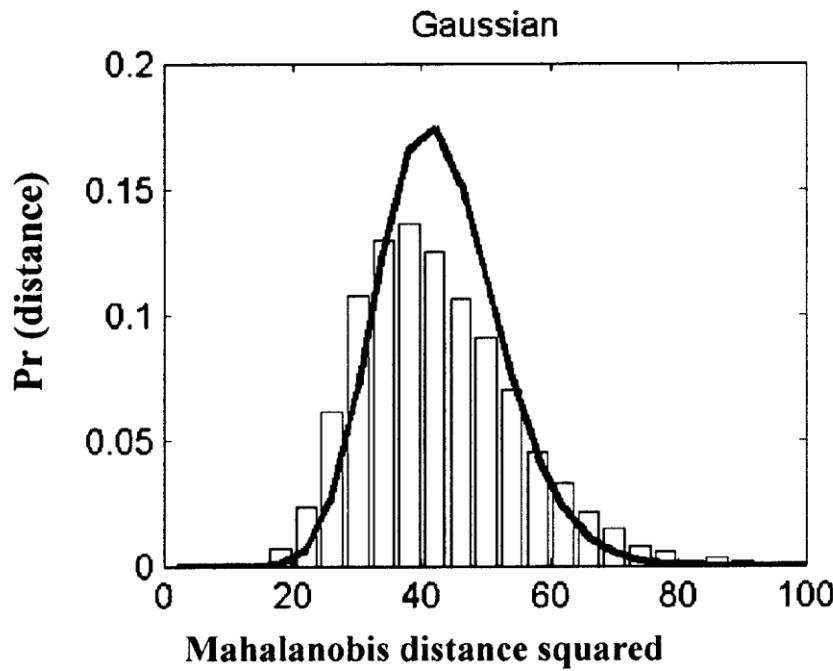
Problem: Outliers



$$f(x) = \frac{\Gamma((\nu+p)/2)}{\Gamma(\nu/2)(\nu\pi)^{p/2}|\Sigma|^{1/2}} \left(1 + \frac{1}{\nu}(x - \mu)^T \Sigma^{-1} (x - \mu)\right)^{-(\nu+p)/2}$$

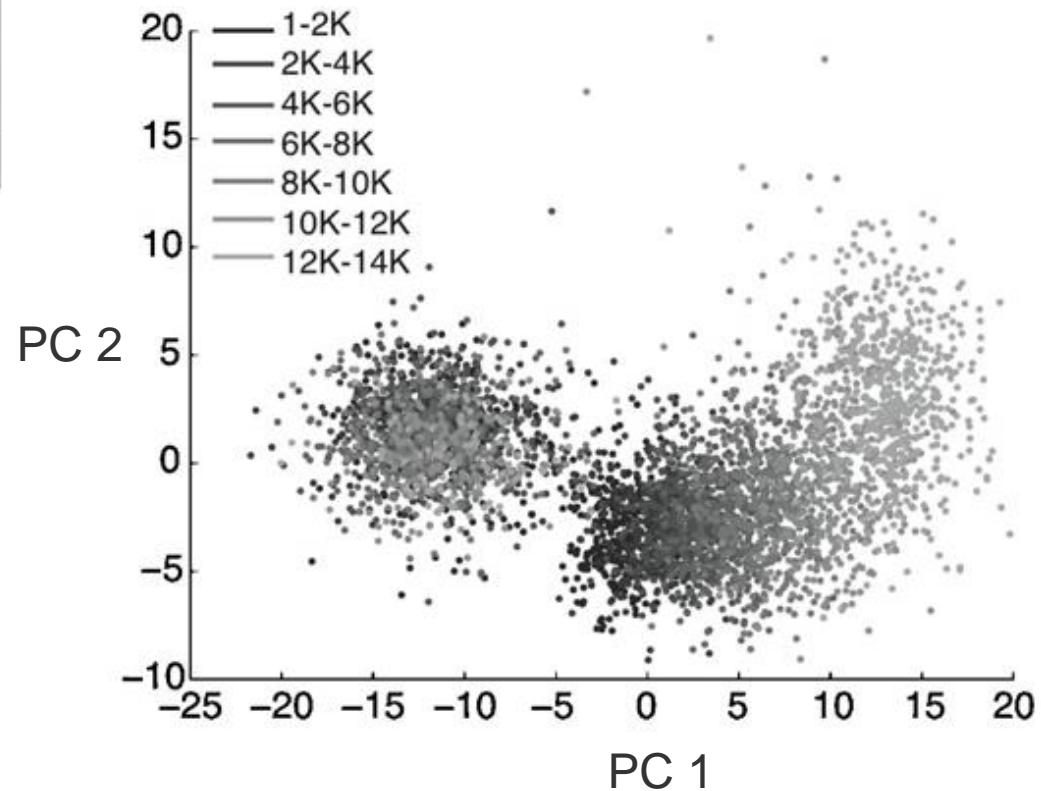
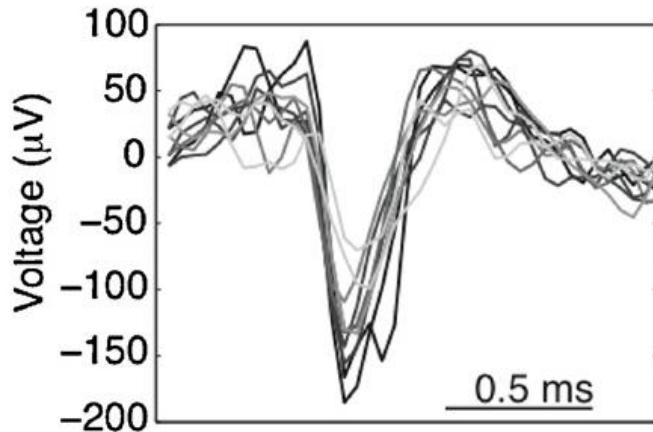


t-distributions fit data better





Problem: Waveform drift



Kalman filter mixture model

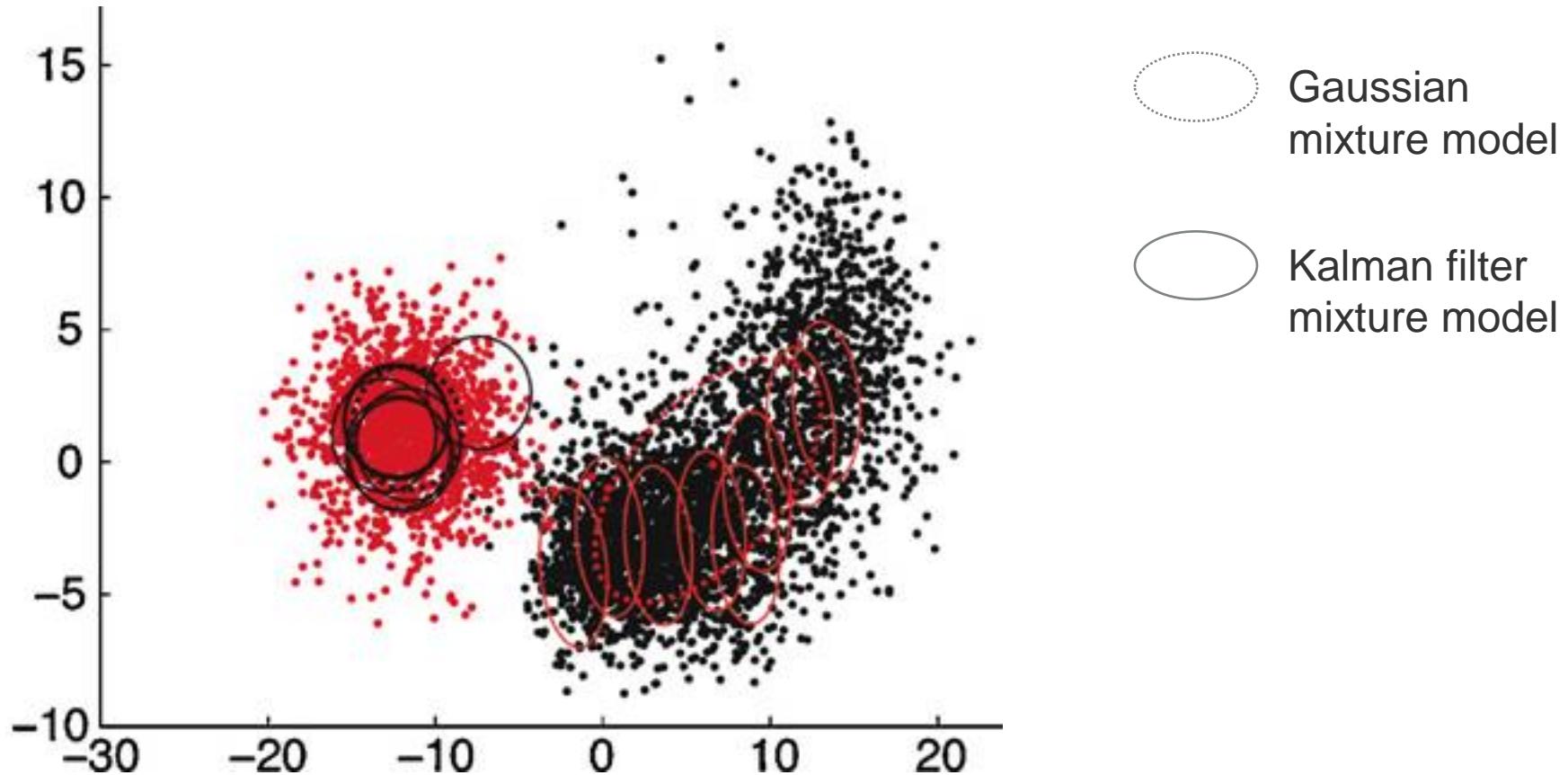
- Take a standard Gaussian mixture model
- Let cluster means μ_j drift over time

$$\mu_j^{t+1} = \mu_j^t + \epsilon_j^t, \quad \epsilon_j^t \sim \mathcal{N}(0, C_j)$$

- Update of μ in M step via standard forward-backward Kalman recursion



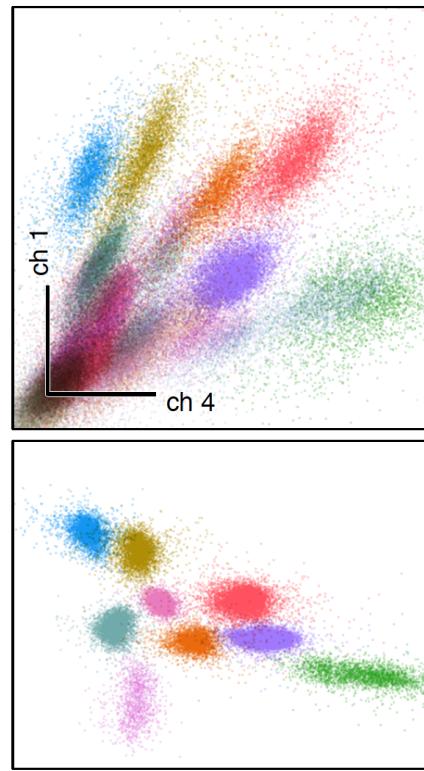
Kalman filter mixture model



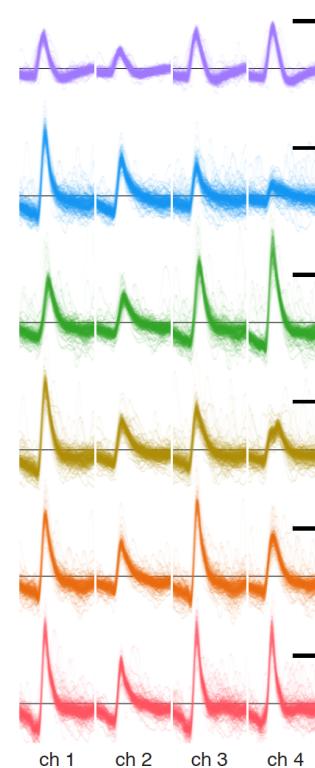


Drifting mixture of t-distributions

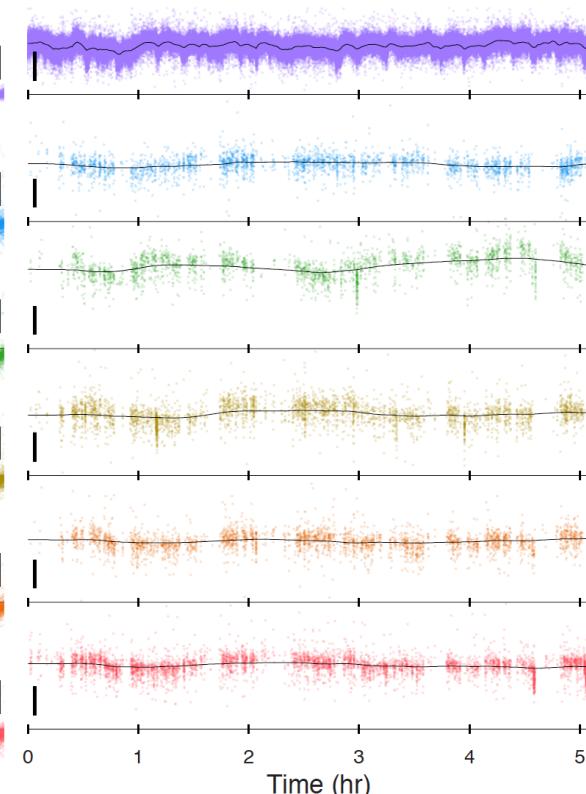
A Feature space scatterplots



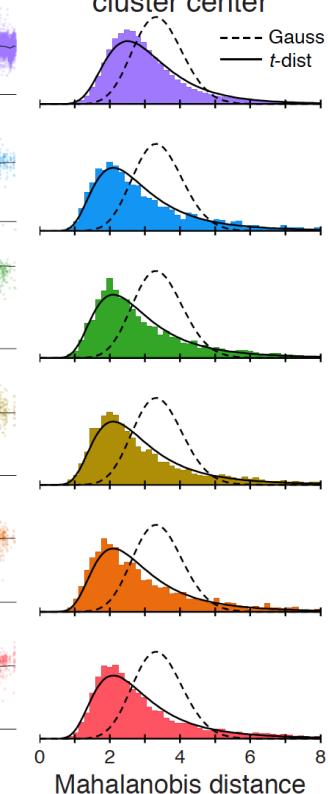
B Spike waveforms



C Cluster location over time



D Deviation from cluster center

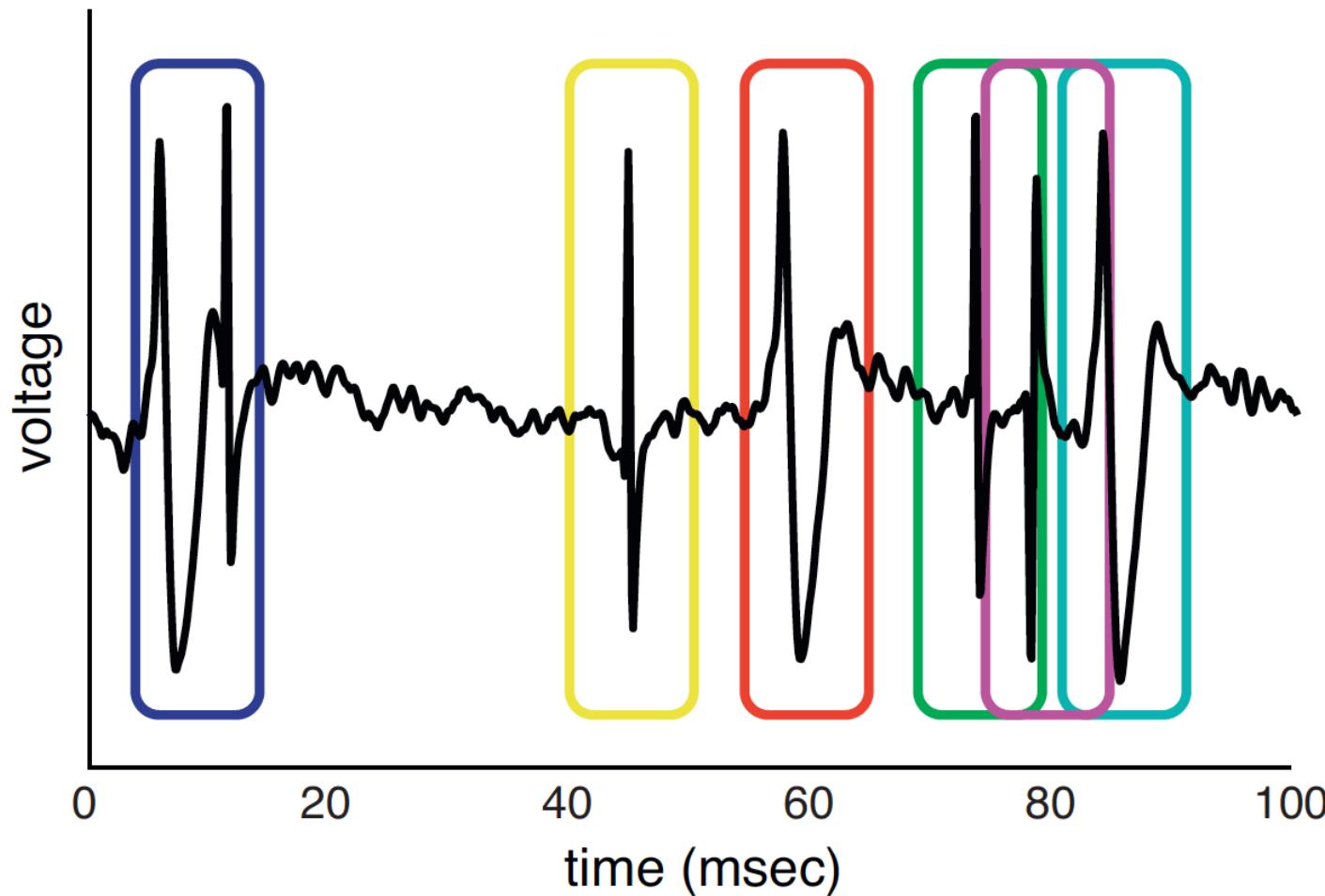


Drifting mixture of t distributions

- Ecker et al. (2014): State dependence of noise correlations in macaque primary visual cortex. *Neuron*.
- Shan, Lubenov, Siapas (2017): Model-based spike sorting with a mixture of drifting t-distributions. *bioRxiv*.
- Code: <https://github.com/aecker/moksm>



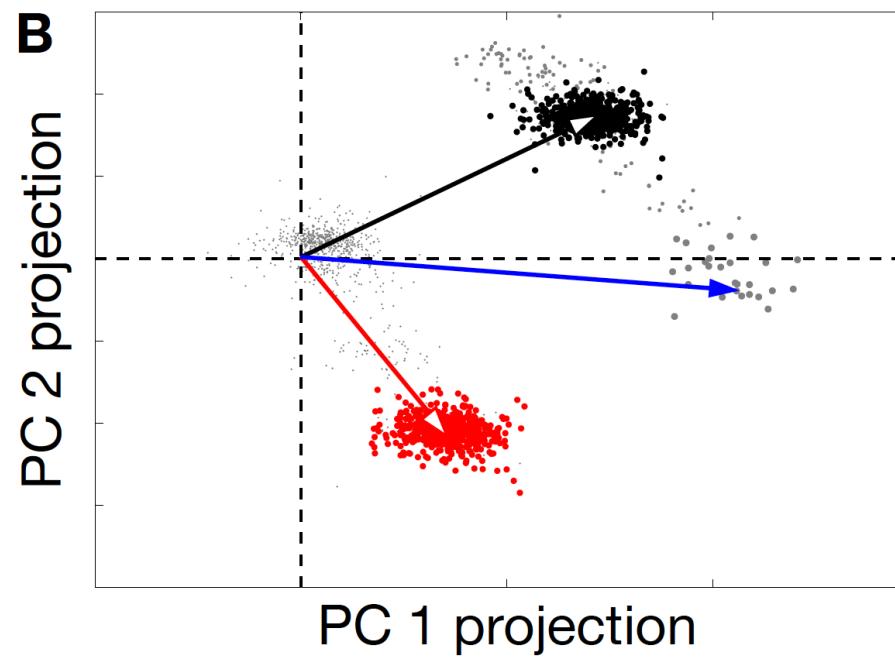
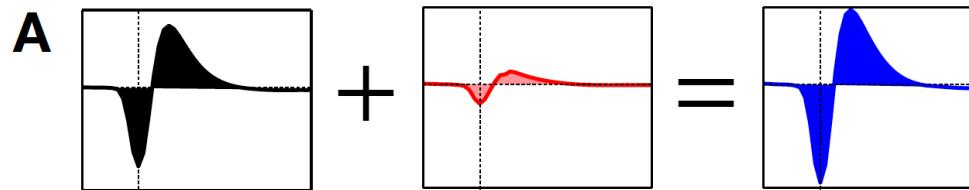
Problem: Synchronous spikes





Problem: Synchronous spikes

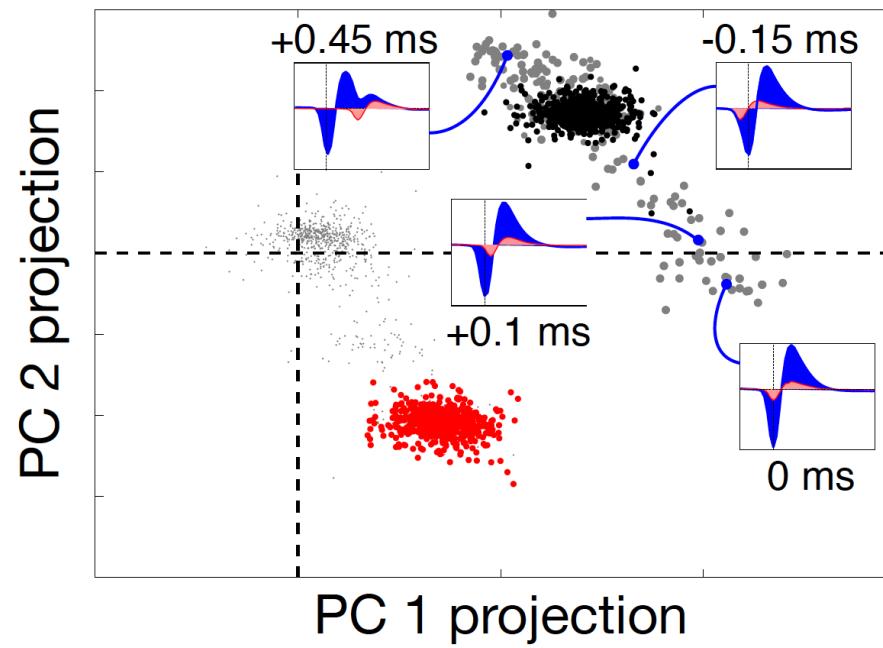
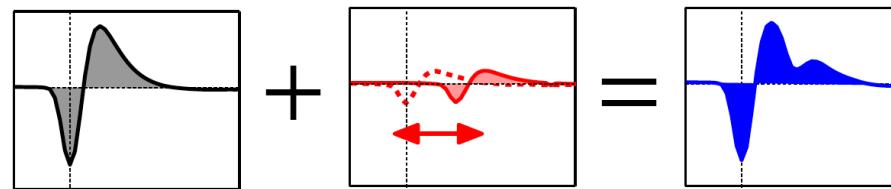
synchronous spiking





Problem: Synchronous spikes

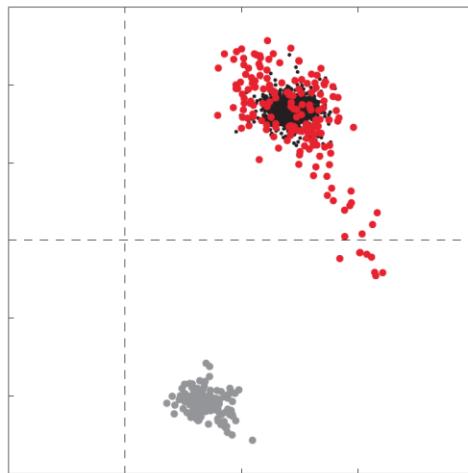
superposition for various time shifts



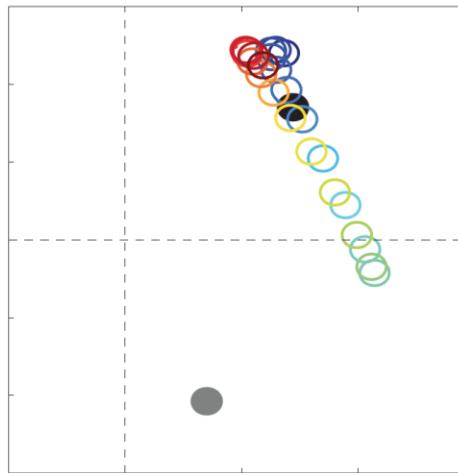
Pillow et al. 2013



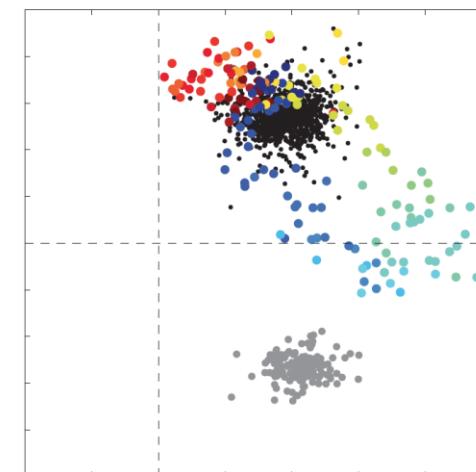
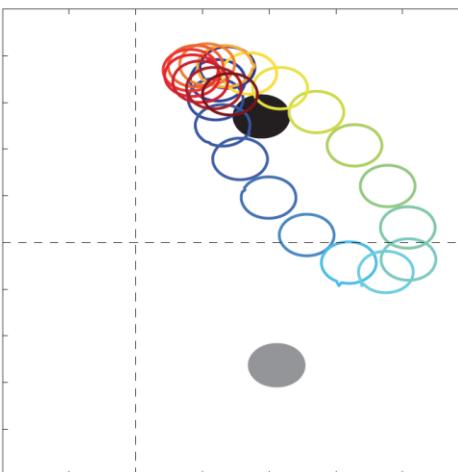
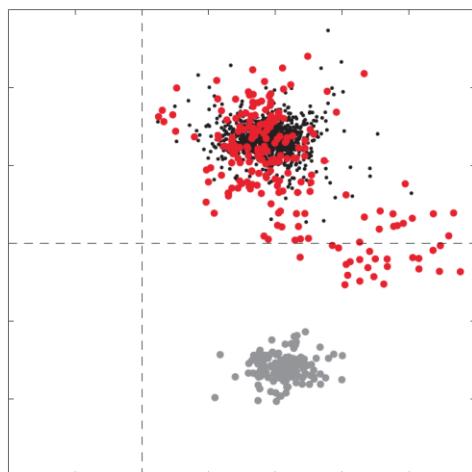
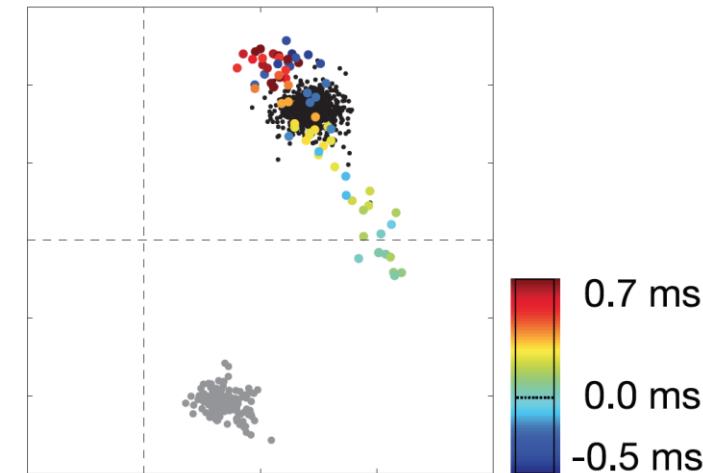
additional
spikes identified



predicted positions
of overlapping spikes

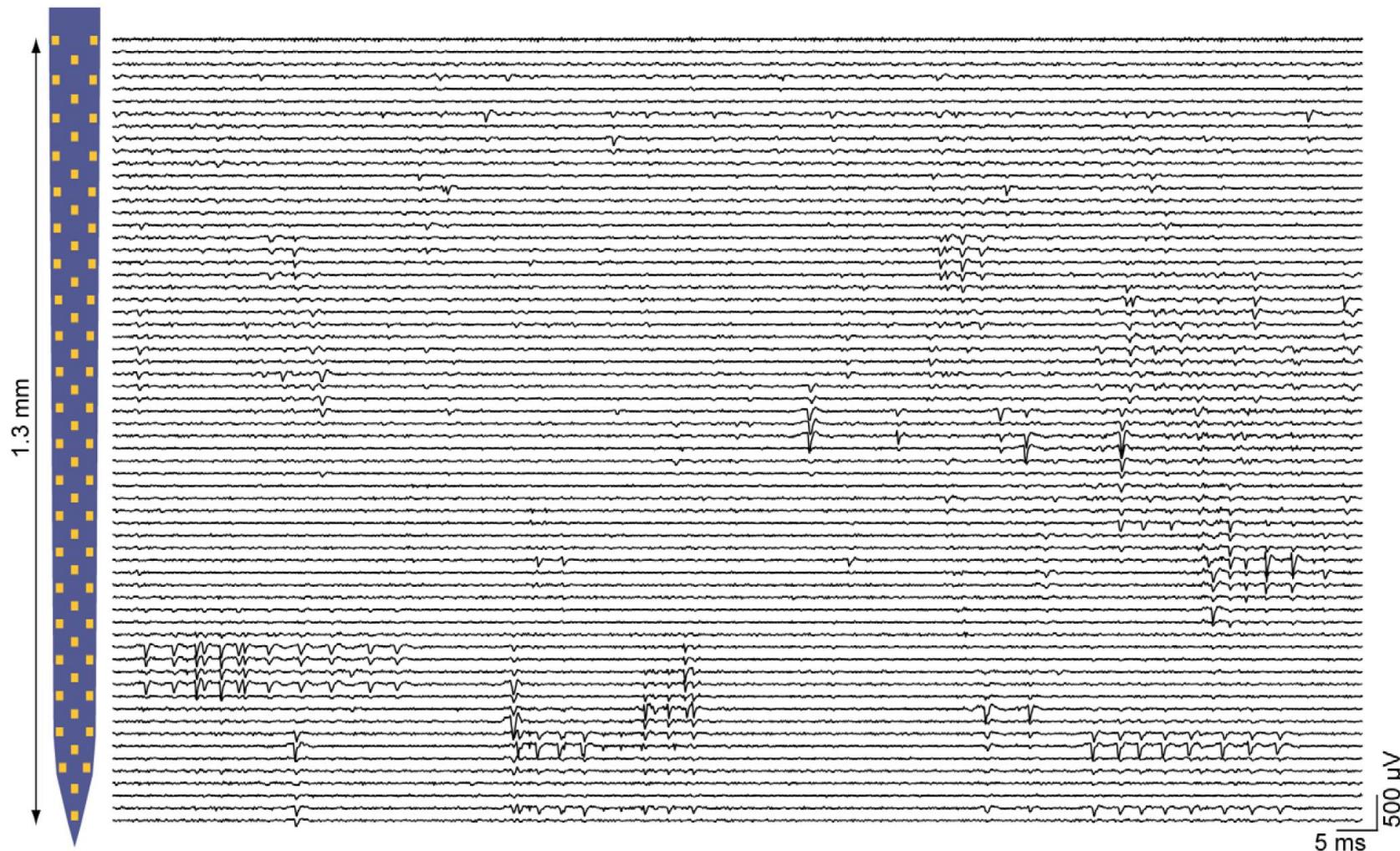


observed
overlapping spikes

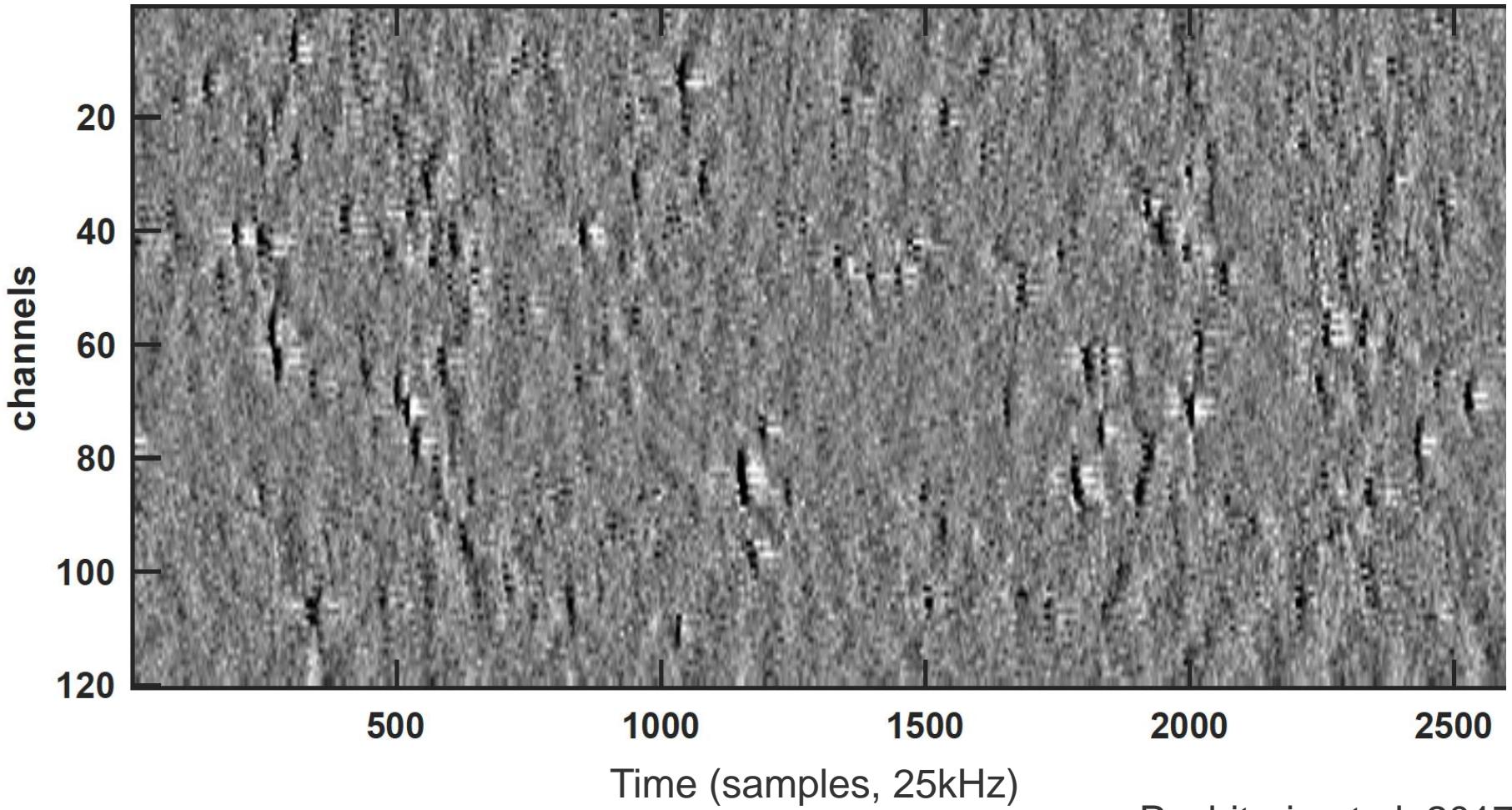




Multi-channel silicon probes



Multi-channel silicon probes



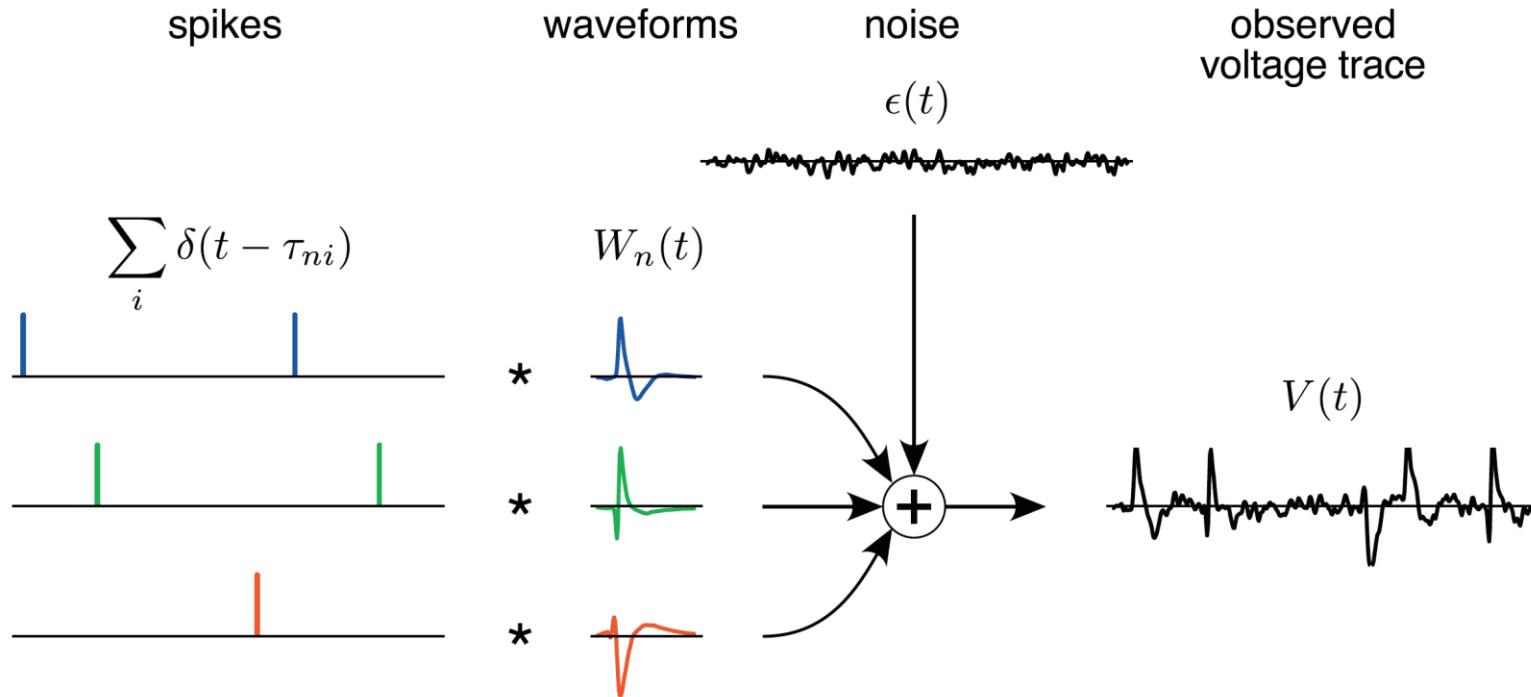
Pachitariu et al. 2017



Generative model

$$V(t) = \sum_n X_n(t) * W_n + \epsilon(t)$$

$$\epsilon \sim \mathcal{N}(0, \Lambda) \quad X_n \sim \text{Bernoulli}(p_n)$$



Pillow et al. 2013, Ekanadham et al. 2014

Generative model

$$V(t) = \sum_n X_n(t) * W_n + \epsilon(t)$$

Solve by alternating:

- Given spike times $X(t)$: estimate waveforms by linear regression
- Given waveforms W : determine spike times by template matching
→ Binary pursuit

Binary Pursuit

Generative model:

$$V(t) = \sum_n X_n(t) * W_n + \epsilon(t) \quad \begin{aligned} \epsilon &\sim \mathcal{N}(0, \Lambda) \\ X_n &\sim \text{Bernoulli}(p_n) \end{aligned}$$

Loss function:

$$L(\mathbf{X}, \mathbf{W}) = \left[\frac{1}{2} (\mathbf{V} - \mathbf{W} \circledast \mathbf{X})^T \Lambda^{-1} (\mathbf{V} - \mathbf{W} * \mathbf{X}) \right] + \gamma^T \mathbf{X},$$

Change in loss function after adding (deleting) spike i to (from) \mathbf{X}

$$\Delta \tilde{L}_i = \mathbf{V}^T \mathbf{w}_i - \mathbf{w}_i^T M_w^{i,i} \mathbf{X}^{i,i} - \gamma_i - \frac{1}{2} \mathbf{w}_i^T \mathbf{w}_i,$$

Greedy algorithm

Repeat until $\Delta L_i < 0$ everywhere:

1. Flip X_i for the bin i for which $(1 - 2X)\Delta L_i$ is largest
2. Update ΔL_i

Binary Pursuit

Initialize by traditional clustering. Then repeat until convergence:

1. Estimate waveforms W by linear regression given voltage data V and current spike train estimate X
2. Compute the residuals $R = V - W * X$ and estimate noise covariance $\Lambda = \text{cov}(R)$
3. Whiten by the square root of the inverse covariance:

$$\tilde{V} = \Lambda^{-0.5} V \quad \tilde{W} = \Lambda^{-0.5} W$$

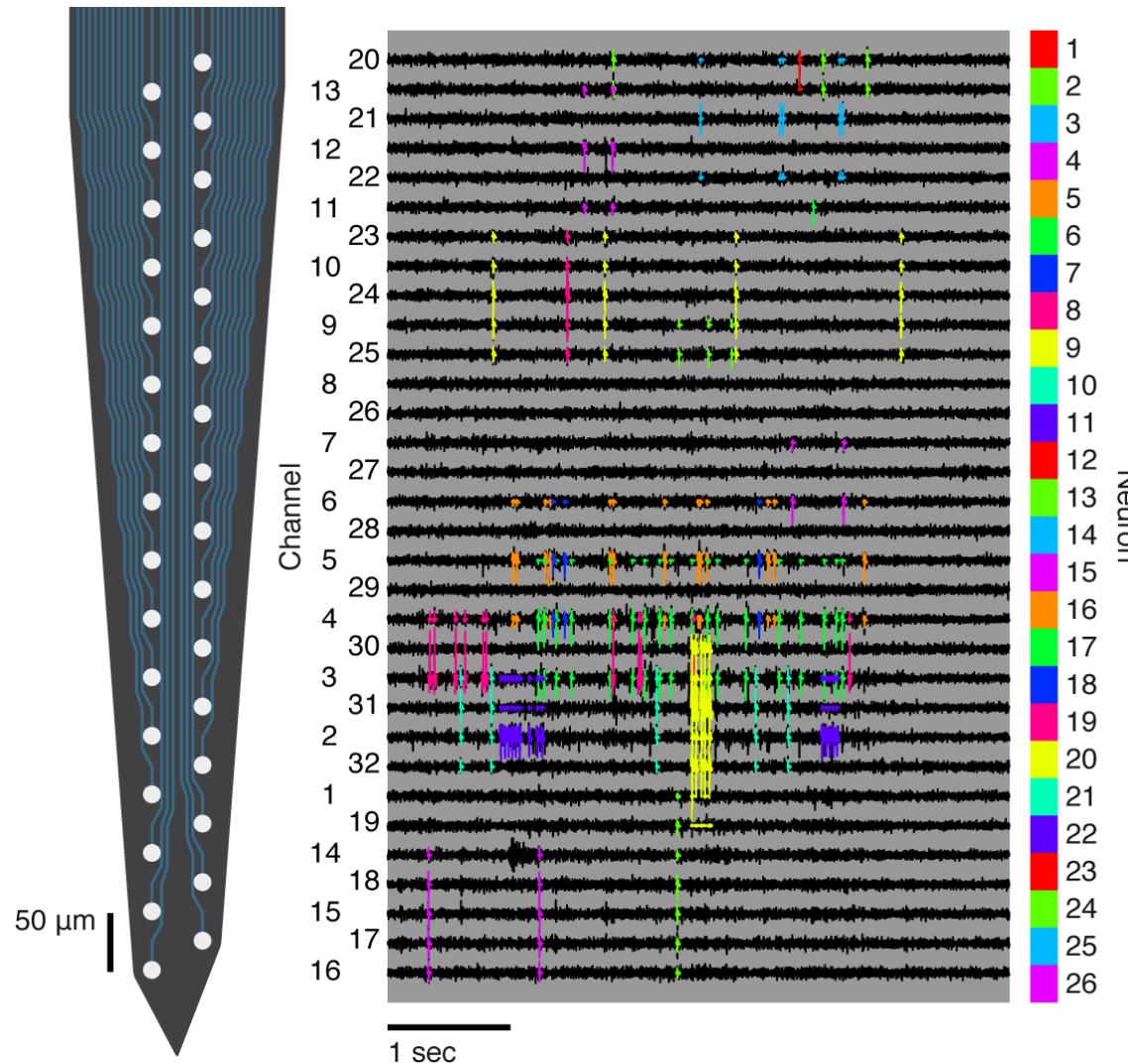
4. Estimate prior spike probabilities for each neuron:

$$\hat{p}_j = \frac{1}{N} \sum_t X_{jt}$$

5. Estimate spike trains X via binary pursuit given \tilde{V}, \tilde{W} and \hat{p}_j



Results: binary Pursuit

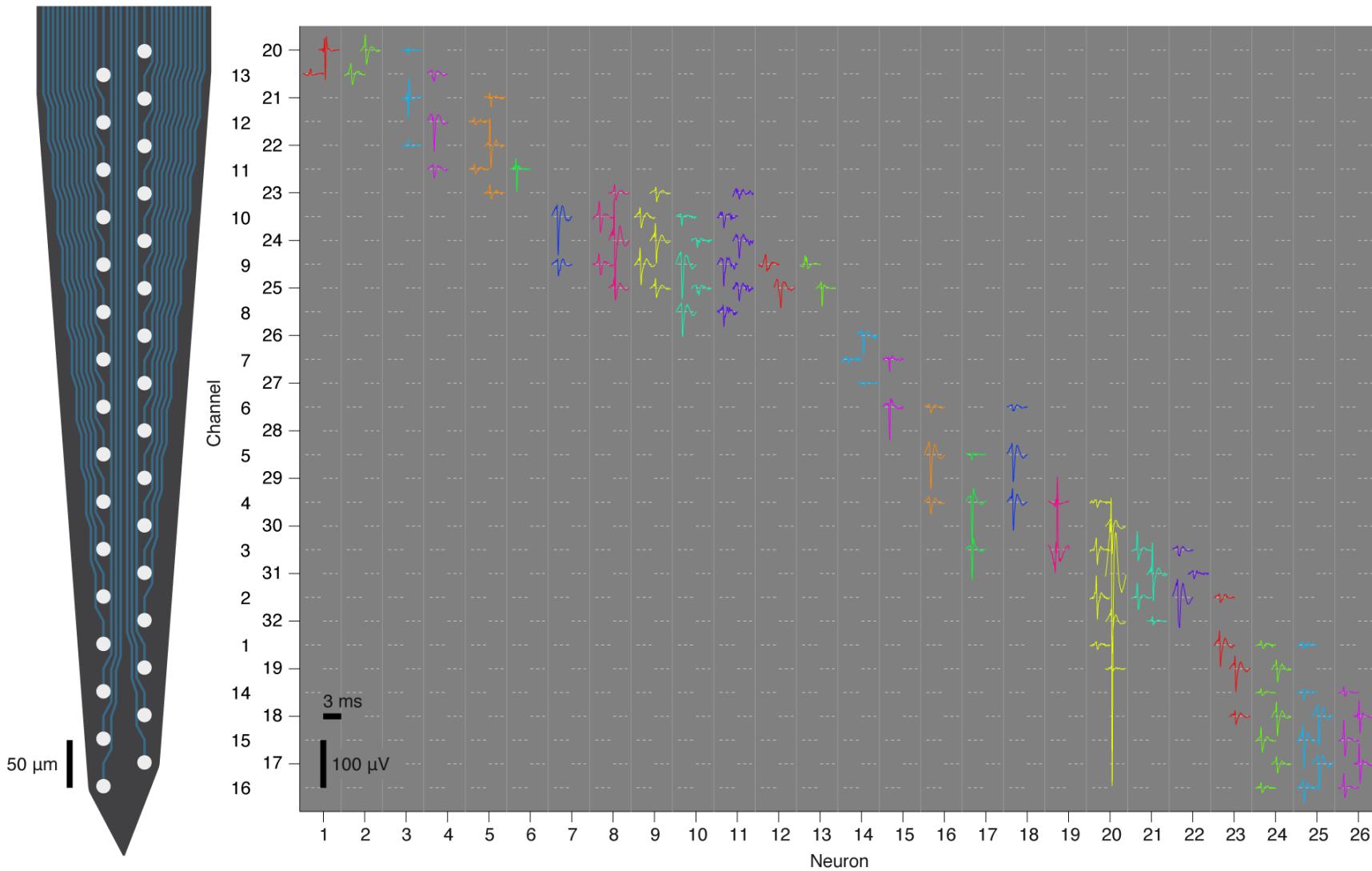


Denfield, Ecker,
Tolias, unpublished



Results: Binary Pursuit

V1x32-Poly2





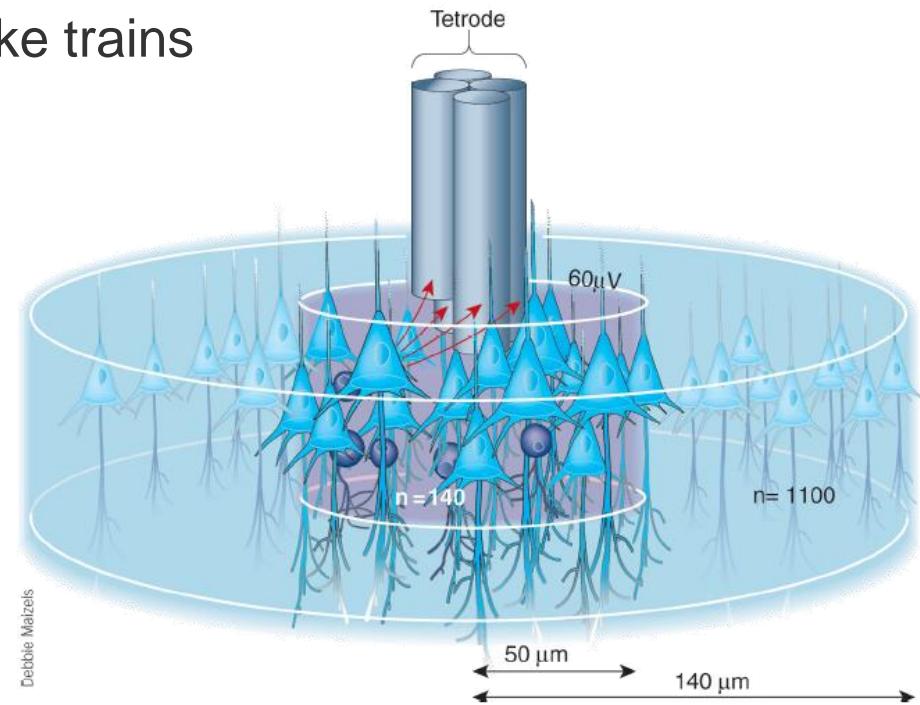
Interpreting clustering results

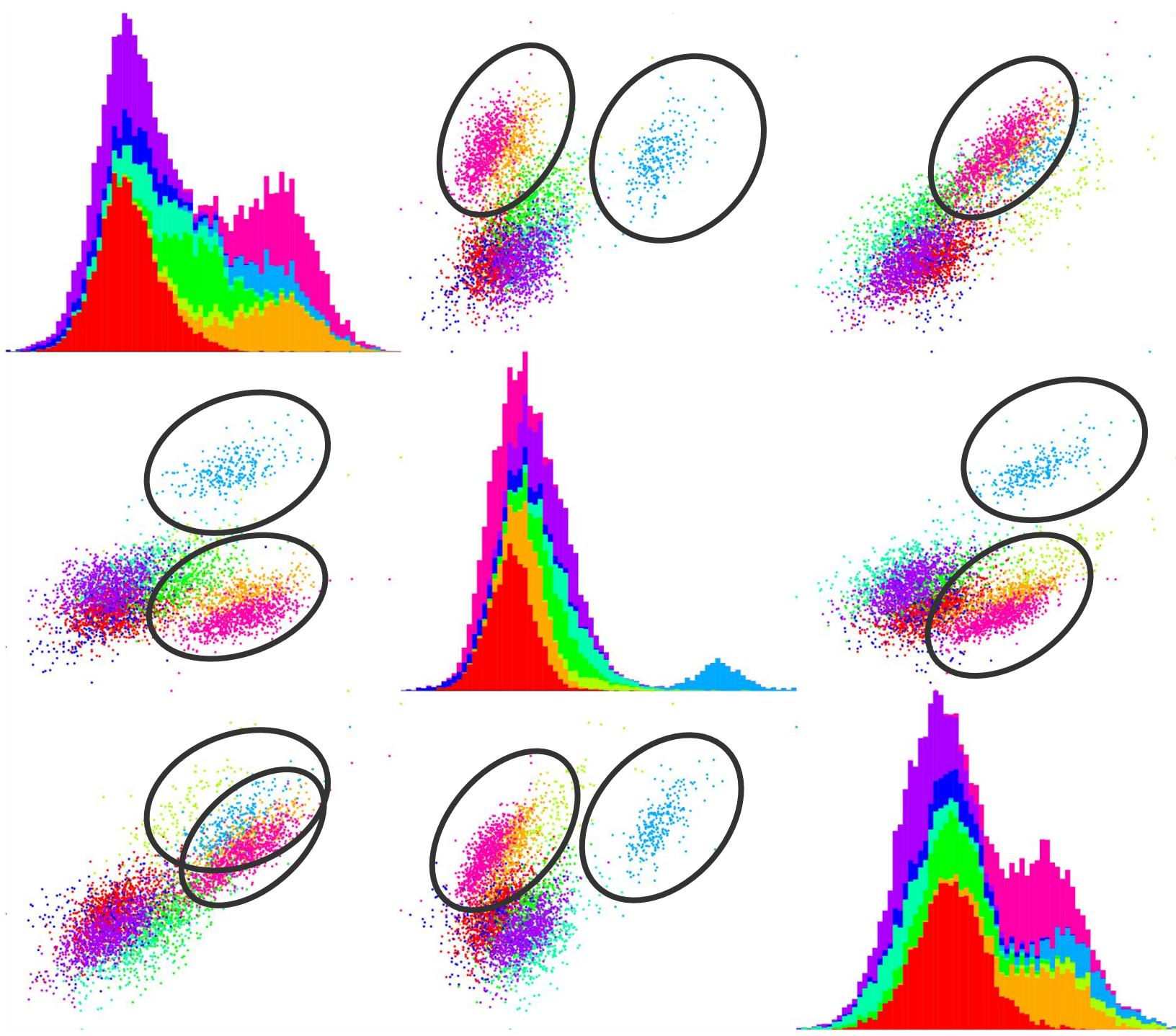
Not all clusters represent the spikes of a single neuron

- **Single unit:** a cluster with one neuron's spikes
- **Multi unit:** a cluster with multiple neurons' spikes

Tools for evaluating clustering:

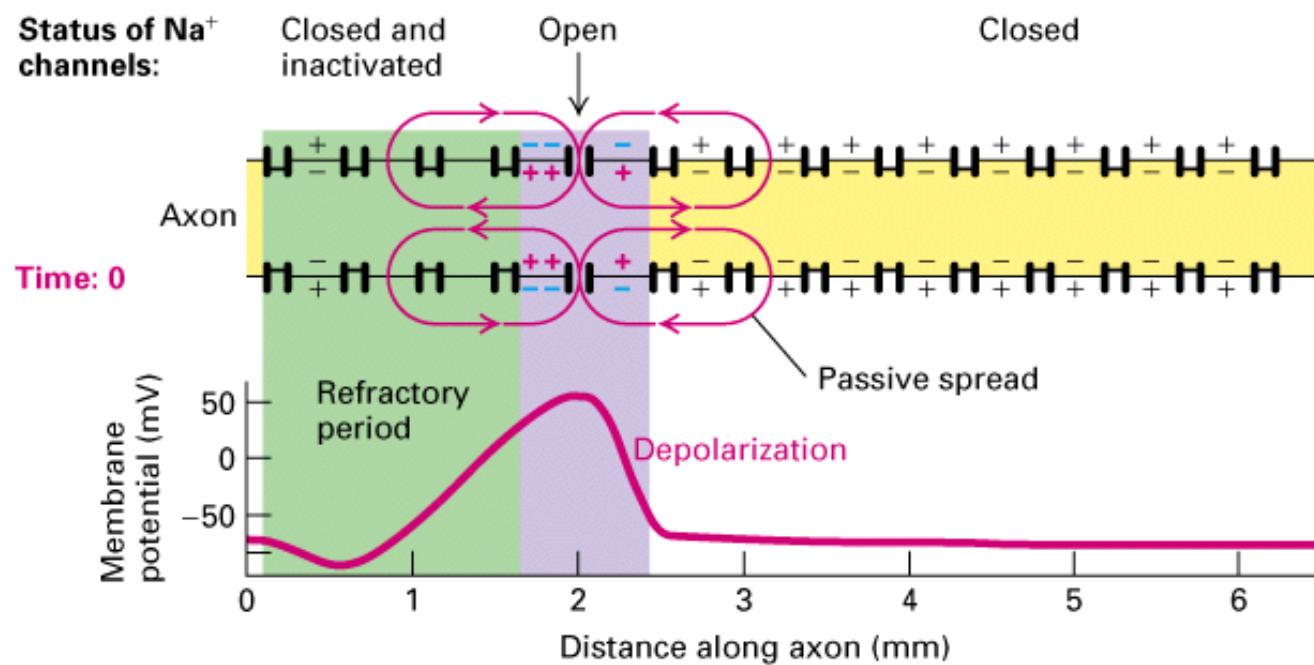
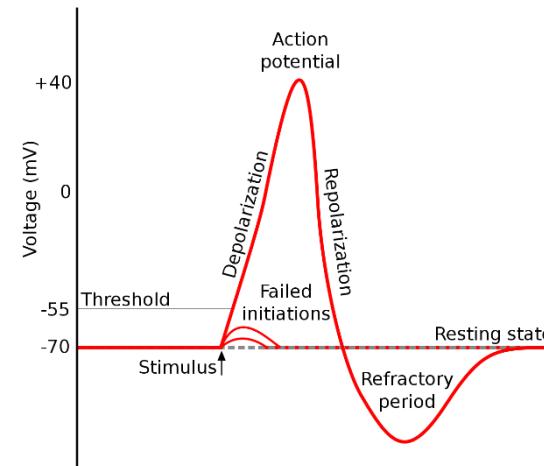
- Temporal structure of the spike trains
→ refractory period
- Quantify cluster separation







Refractory Period





Correlogram

Cross correlation function

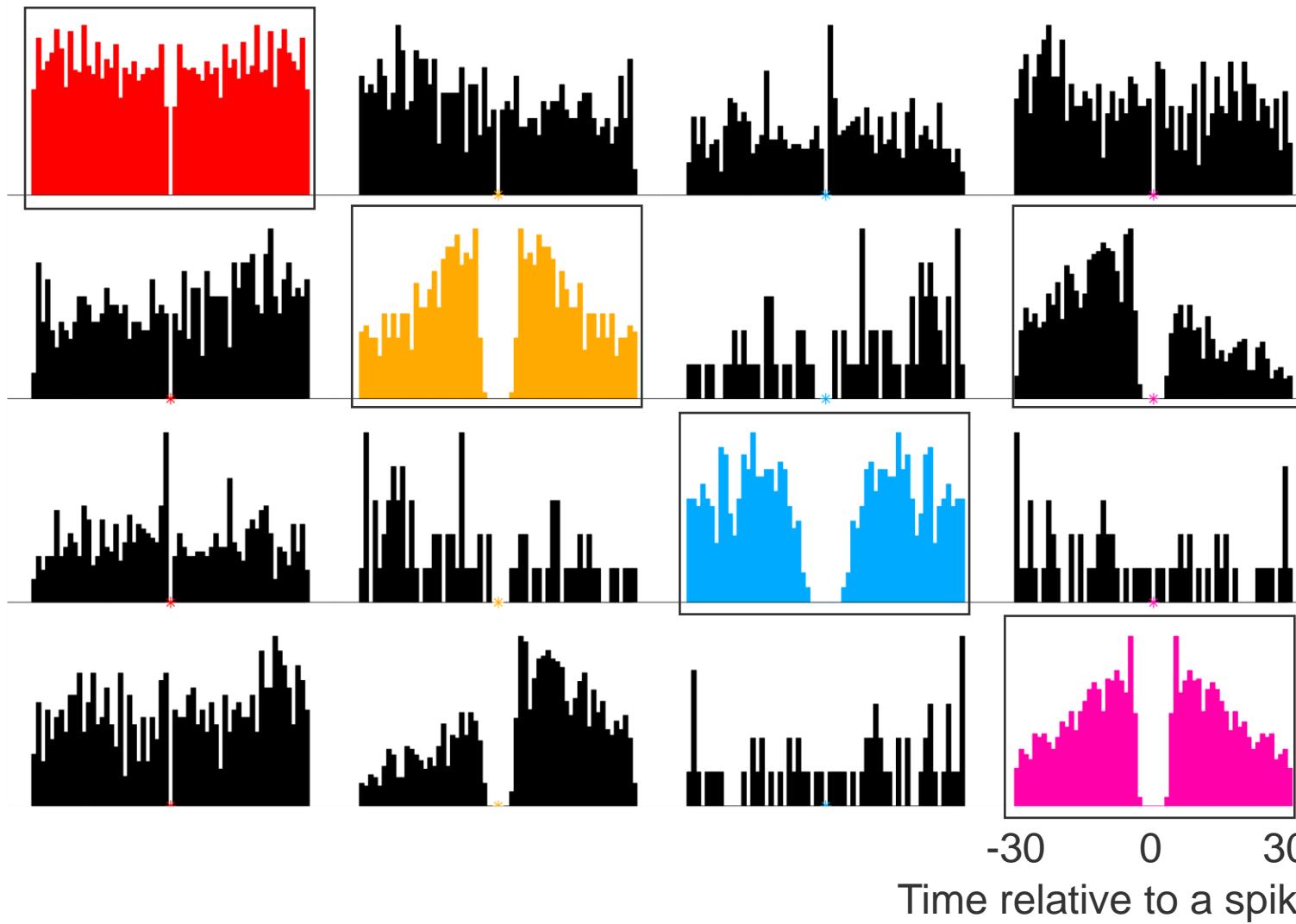
$$R_{uv}(\tau) = \int u(t)v(t - \tau)dt$$

Histogram of $\tau = t_i - t_j$ for all spike times t_i and t_j



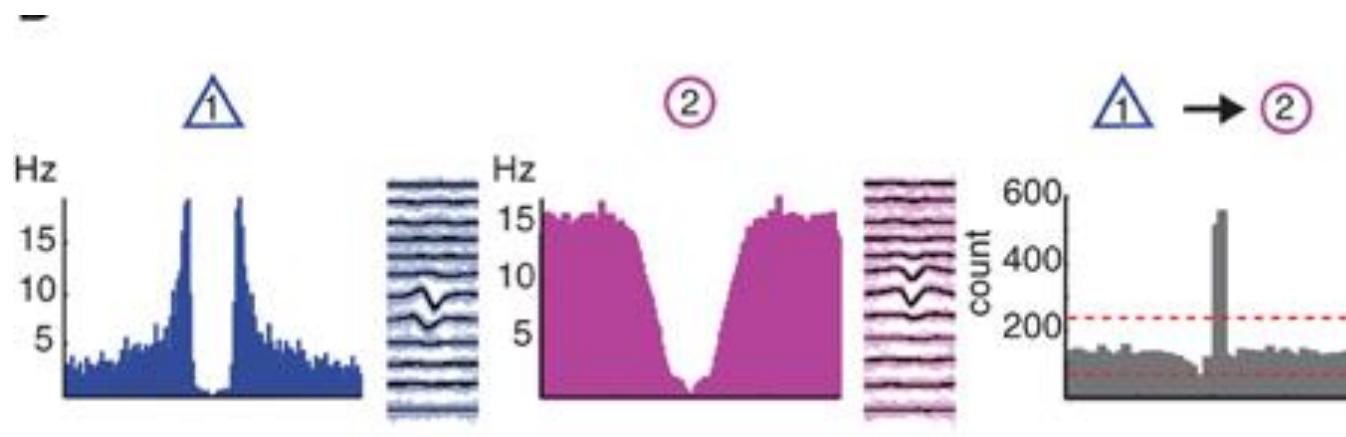


Cross-/Auto-Correlograms



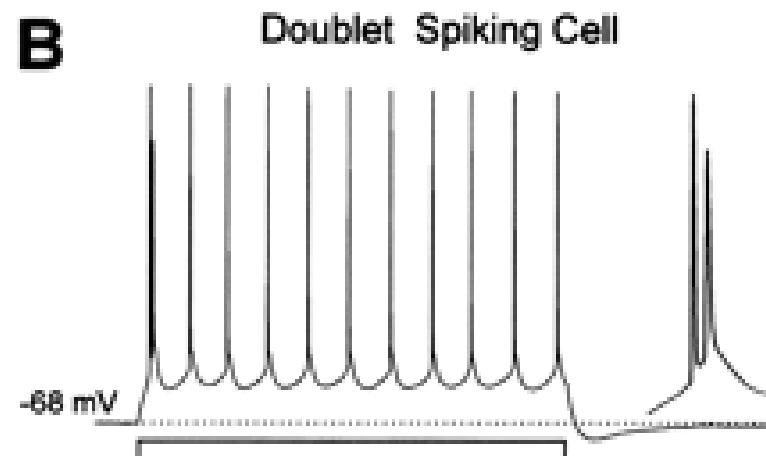
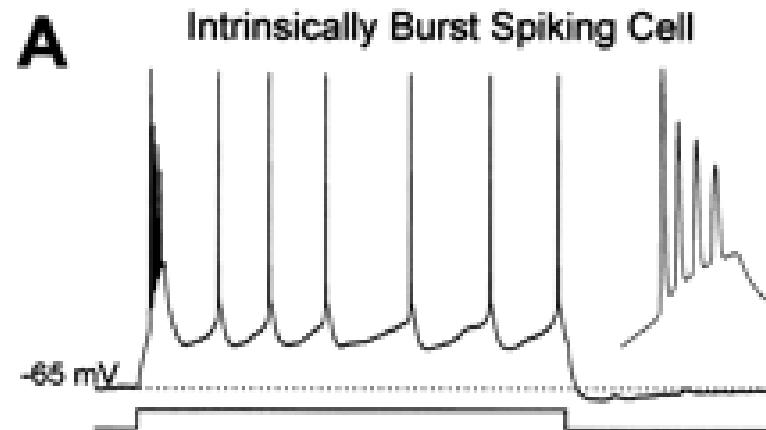


Coupled neurons



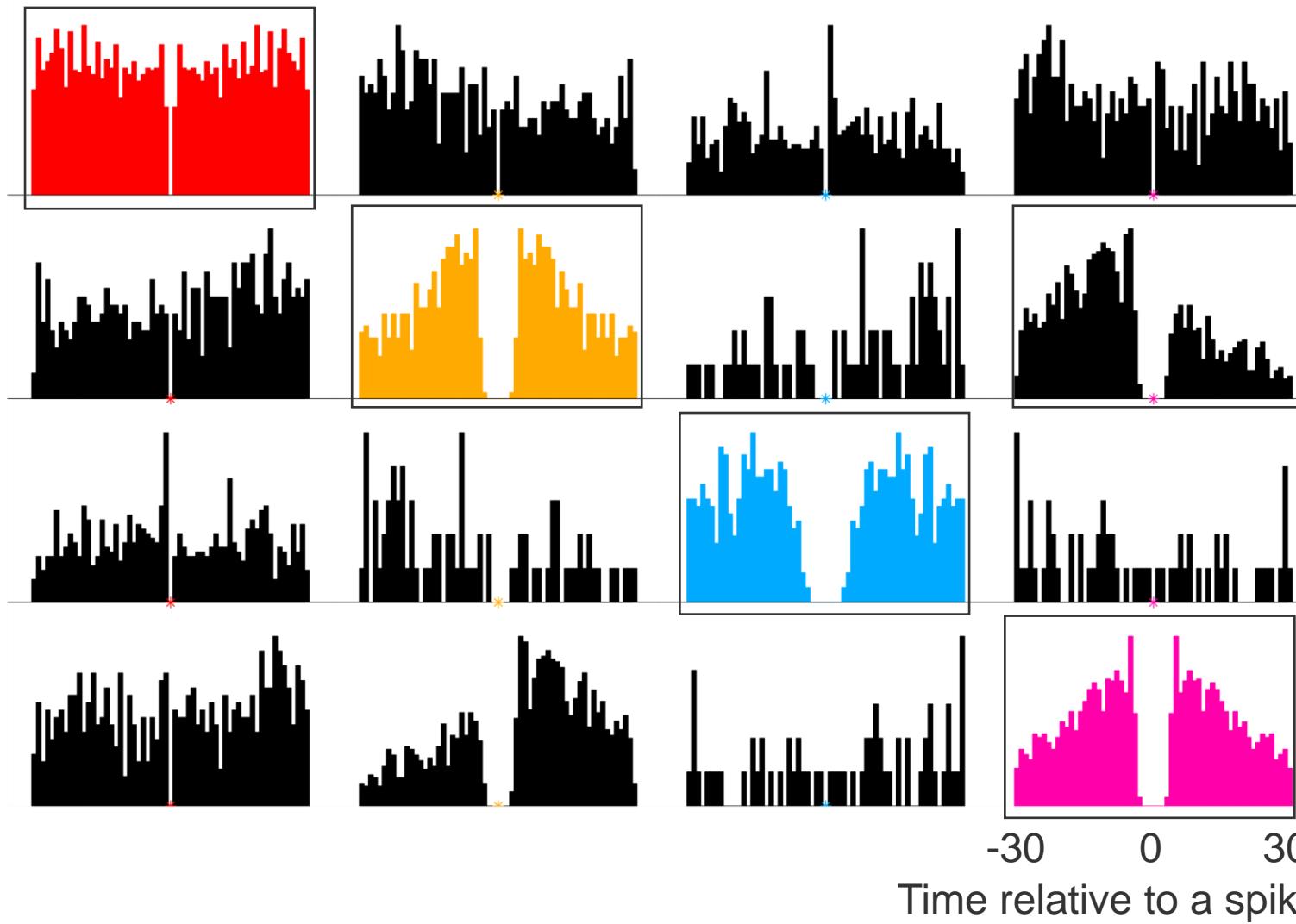


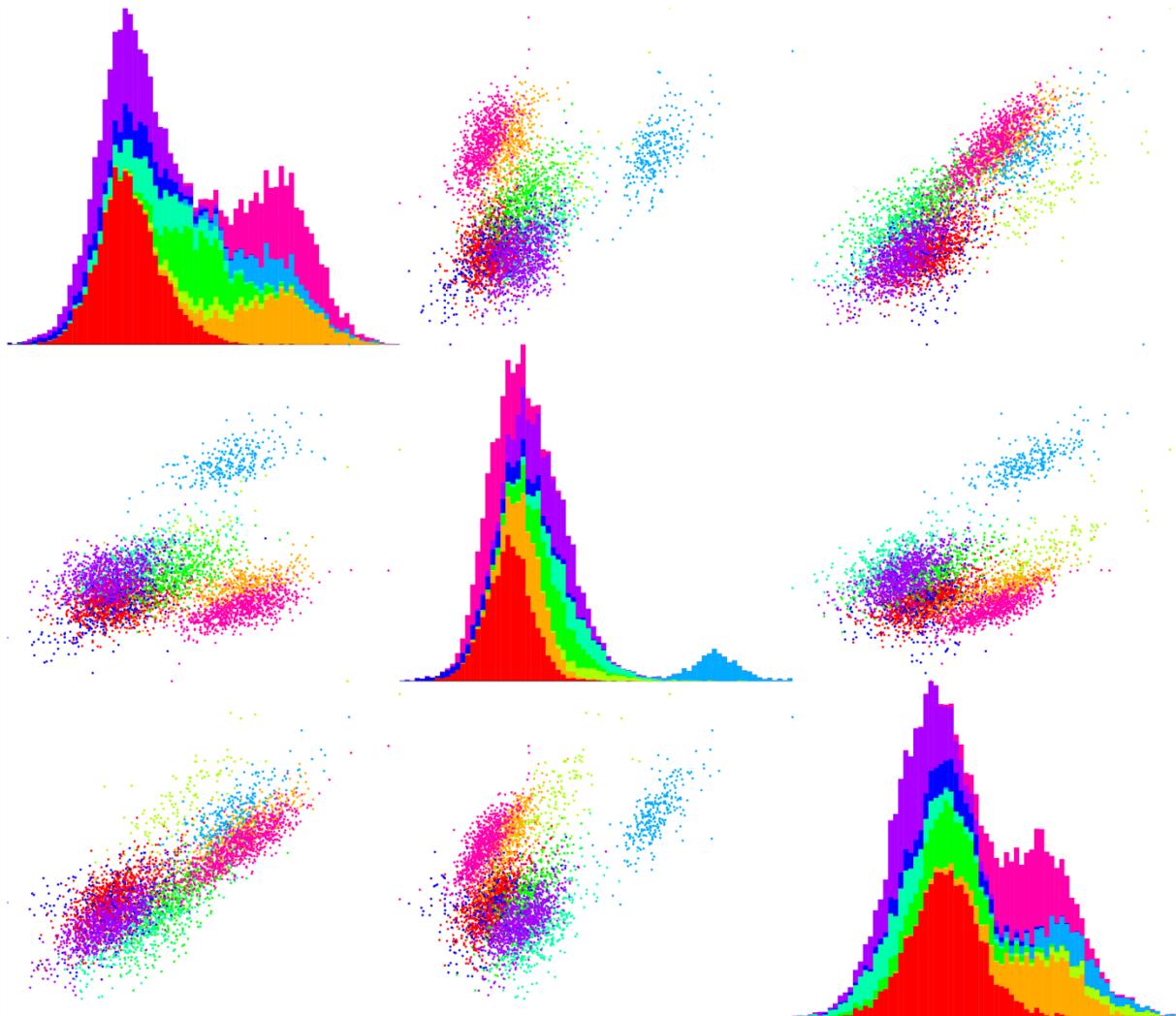
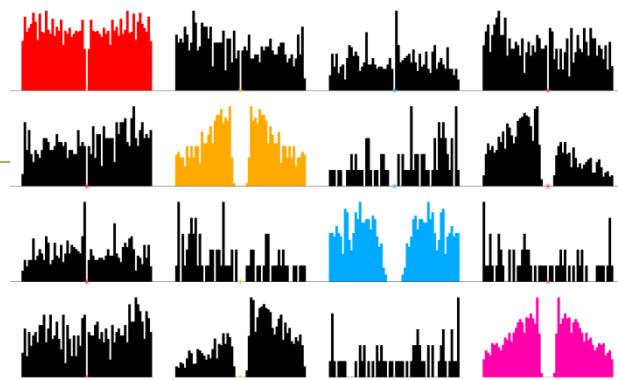
Bursting neuron with spike amplitude adaptation





Cross-/Auto-Correlograms



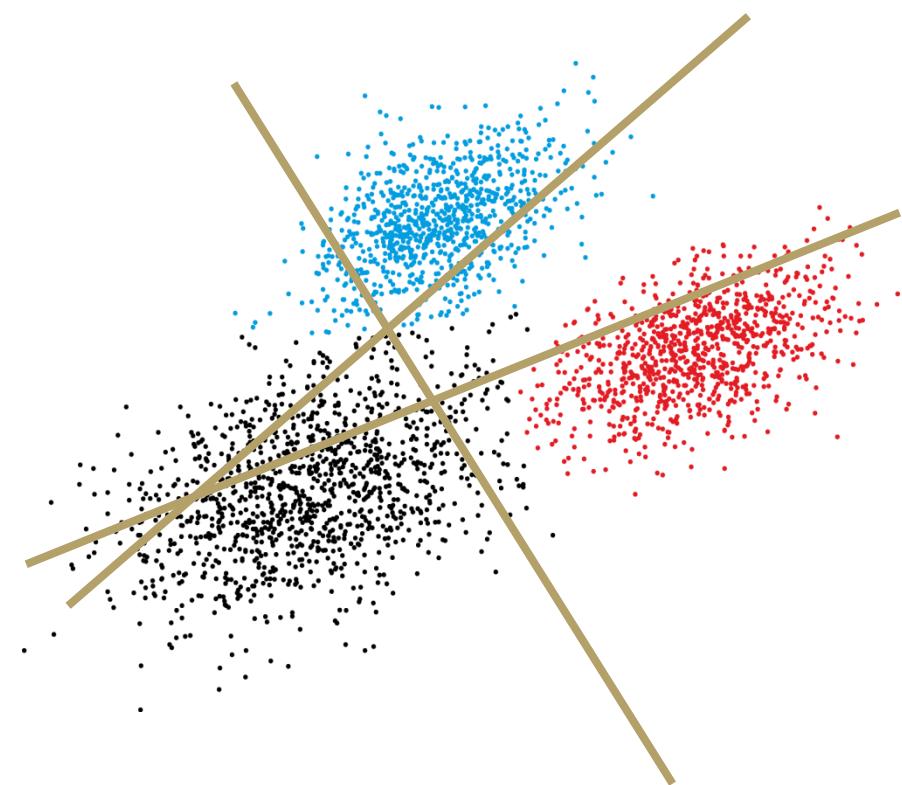
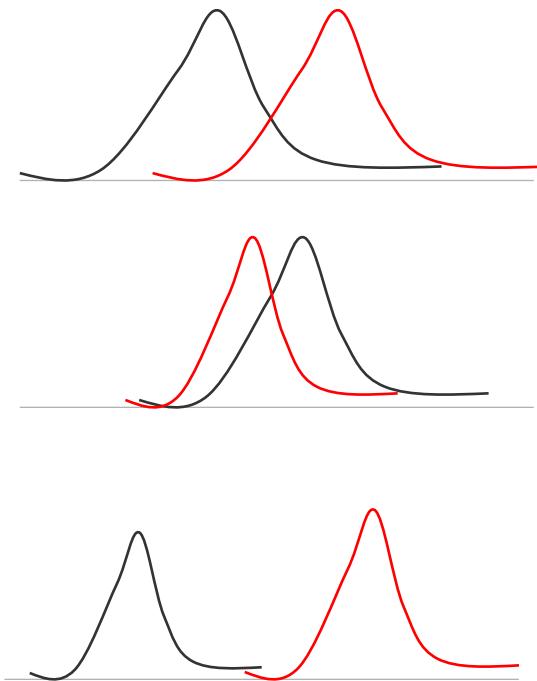




Pairwise cluster separation

Tool for visual inspection

Project clusters onto one dimension





Linear discriminant analysis

$$y = w^T x, \quad C_1: y \geq -w_0$$

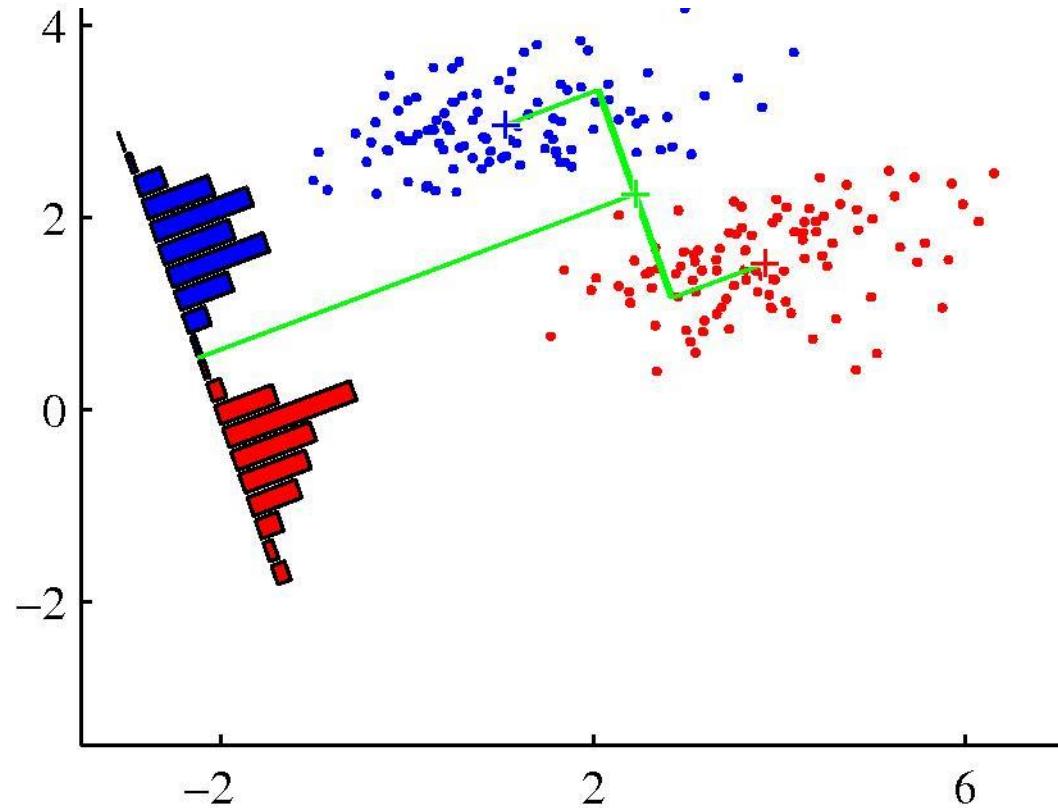
$$J(w) = \frac{w^T S_B w}{w^T S_W w}$$

$$(w^T S_B w) S_W w = (w^T S_W w) S_B w$$

$$w = \Sigma_w^{-1} (m_2 - m_1)$$

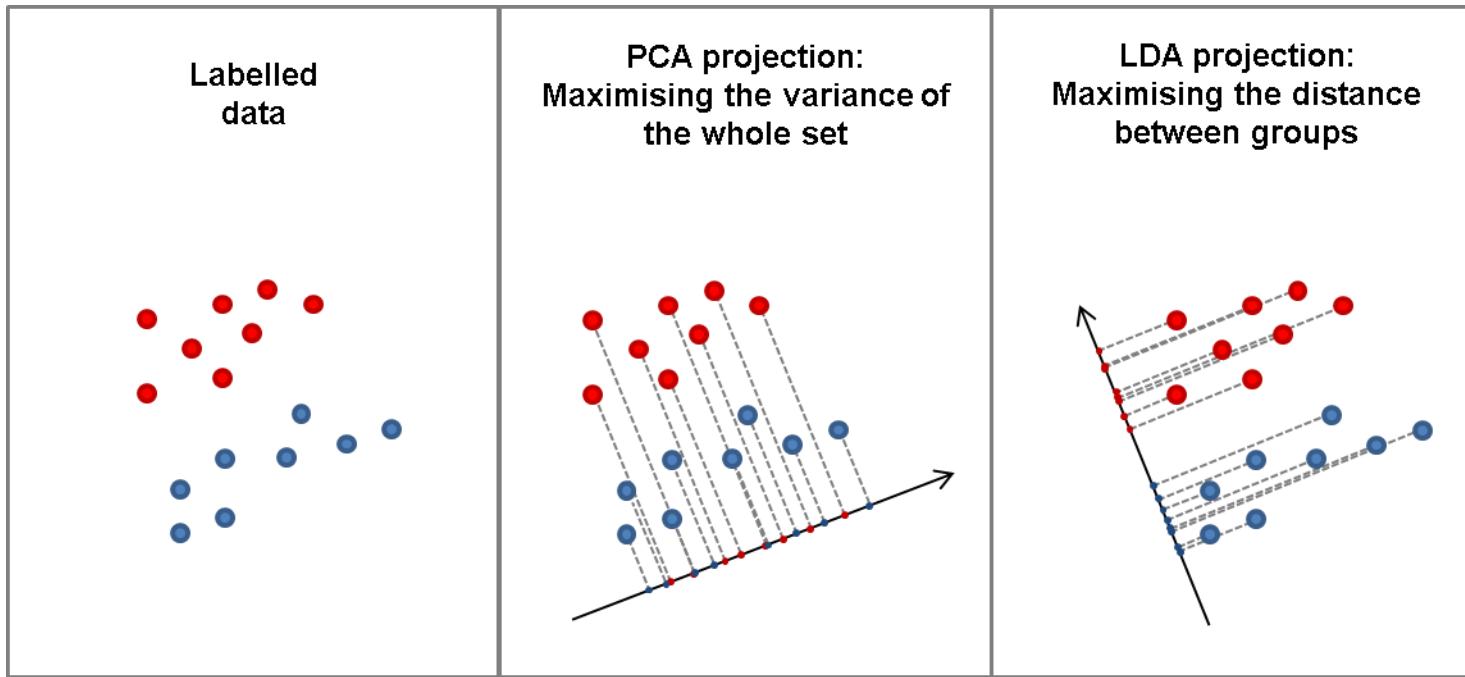


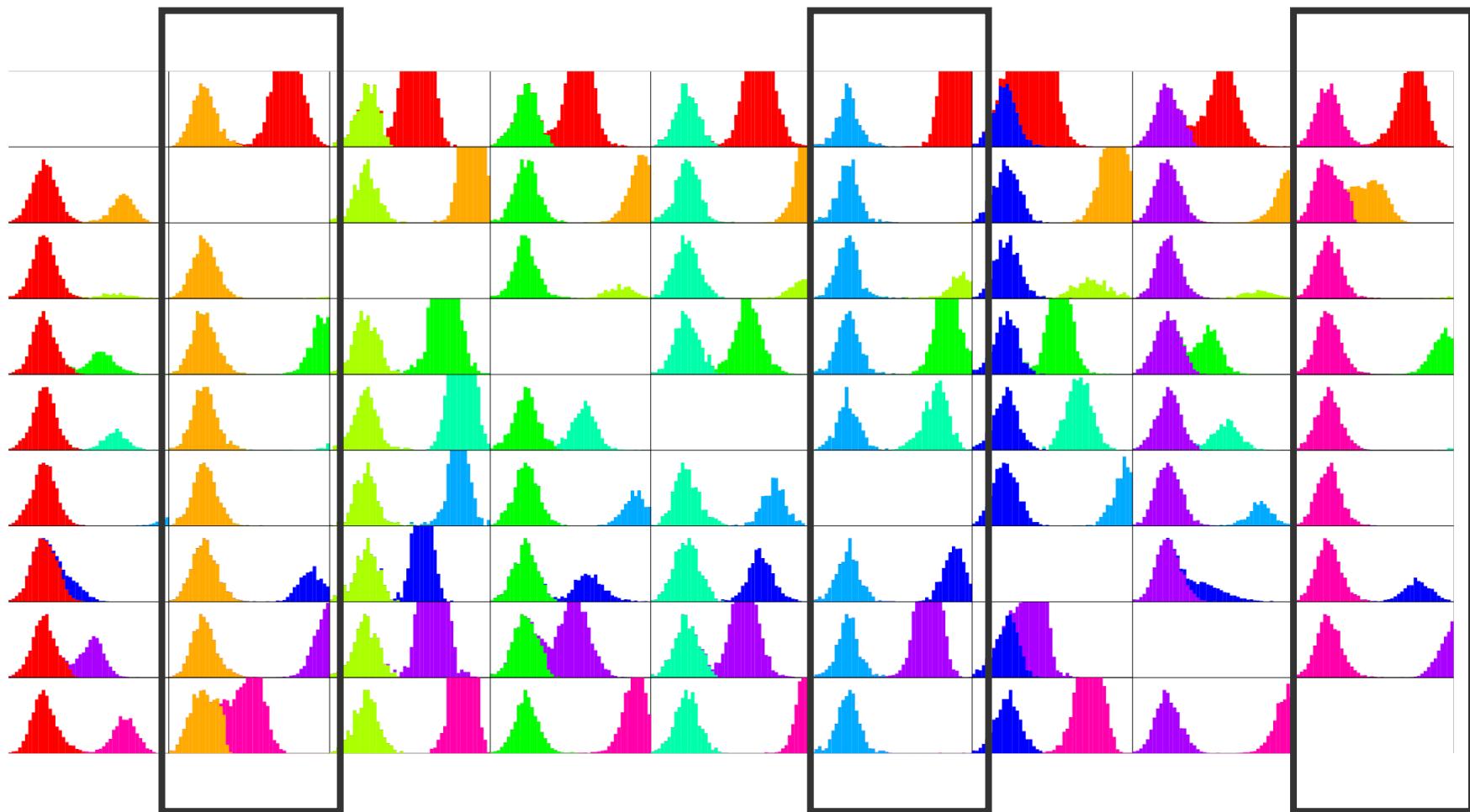
Linear Discriminant Analysis





Difference between LDA and PCA

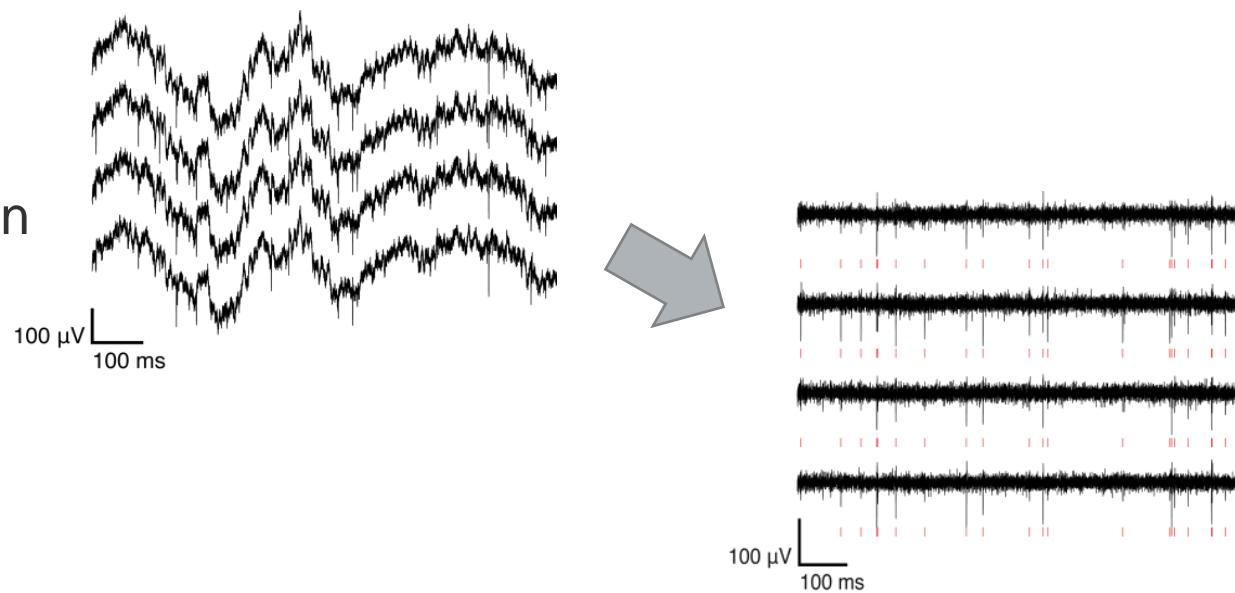






Spike sorting

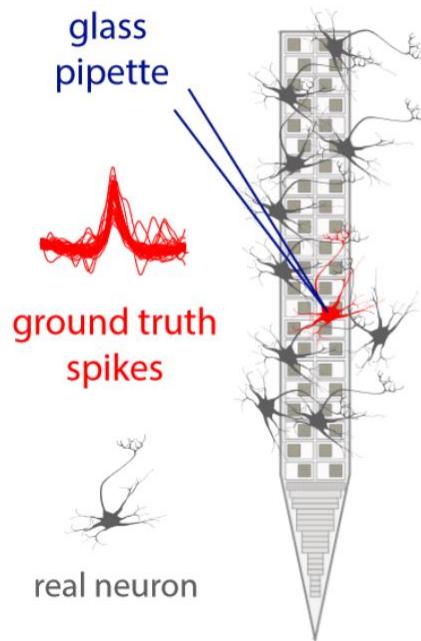
- Raw data
- Spike detection
- Feature extraction
- Clustering
- Verification



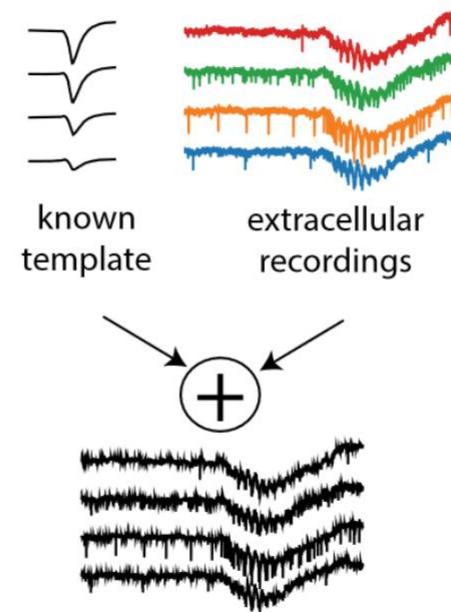


Benchmarking spike sorting algorithms

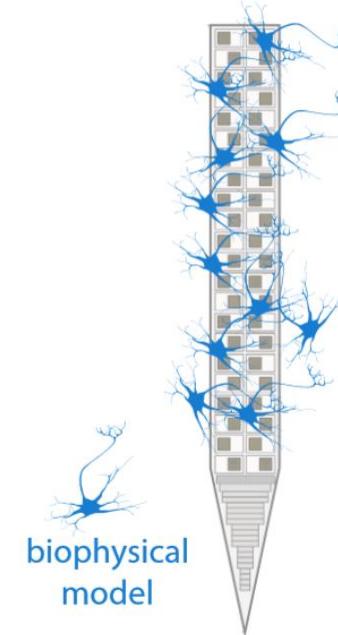
1. paired recordings
(in vivo or in vitro)



2. artificial cells + real recordings
(hybrid)

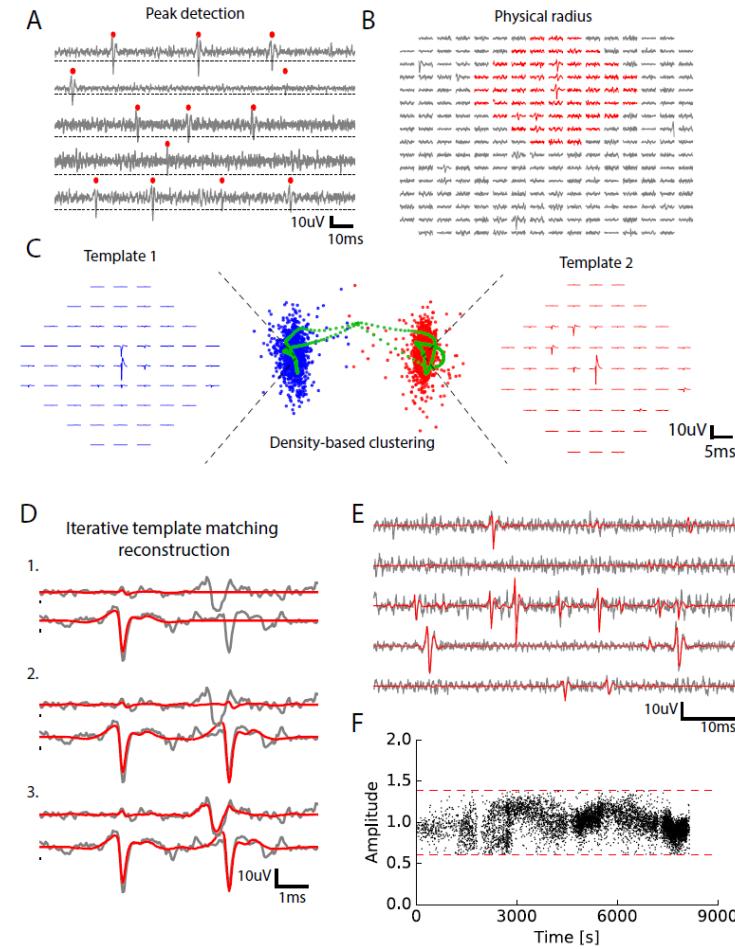


3. biophysically detailed
(synthetic)





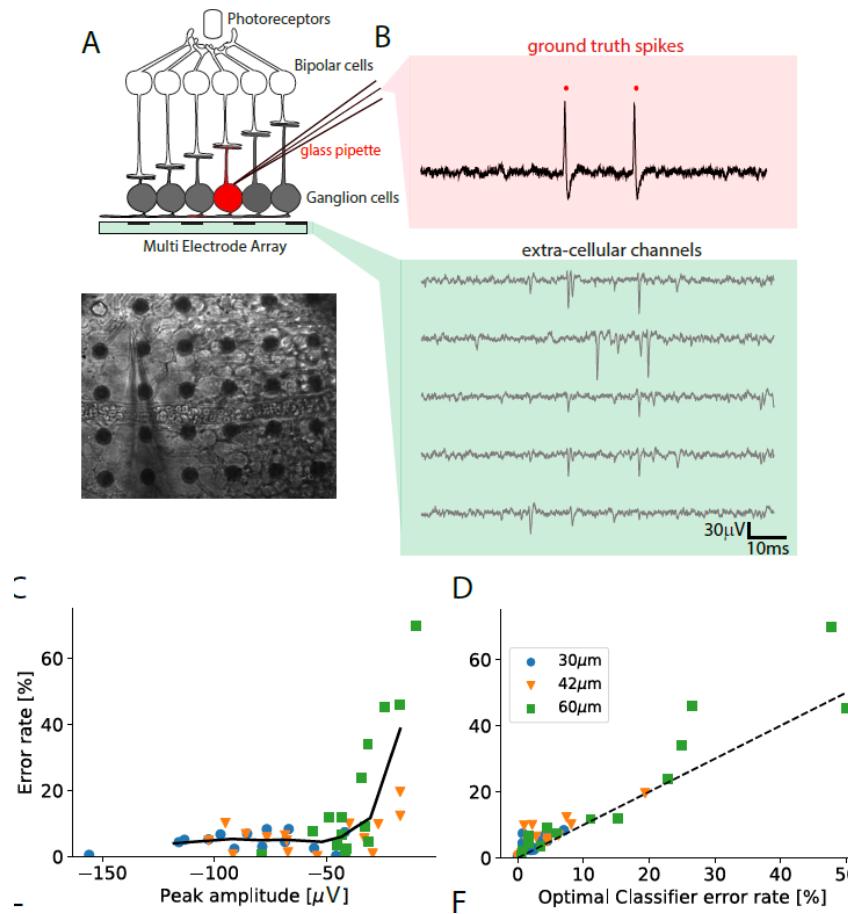
Ground truth verification



$$s(t) = \sum_{ij} a_{ij} w_j(t - t_i) + b_{ij} v_j(t - t_i) + e(t)$$

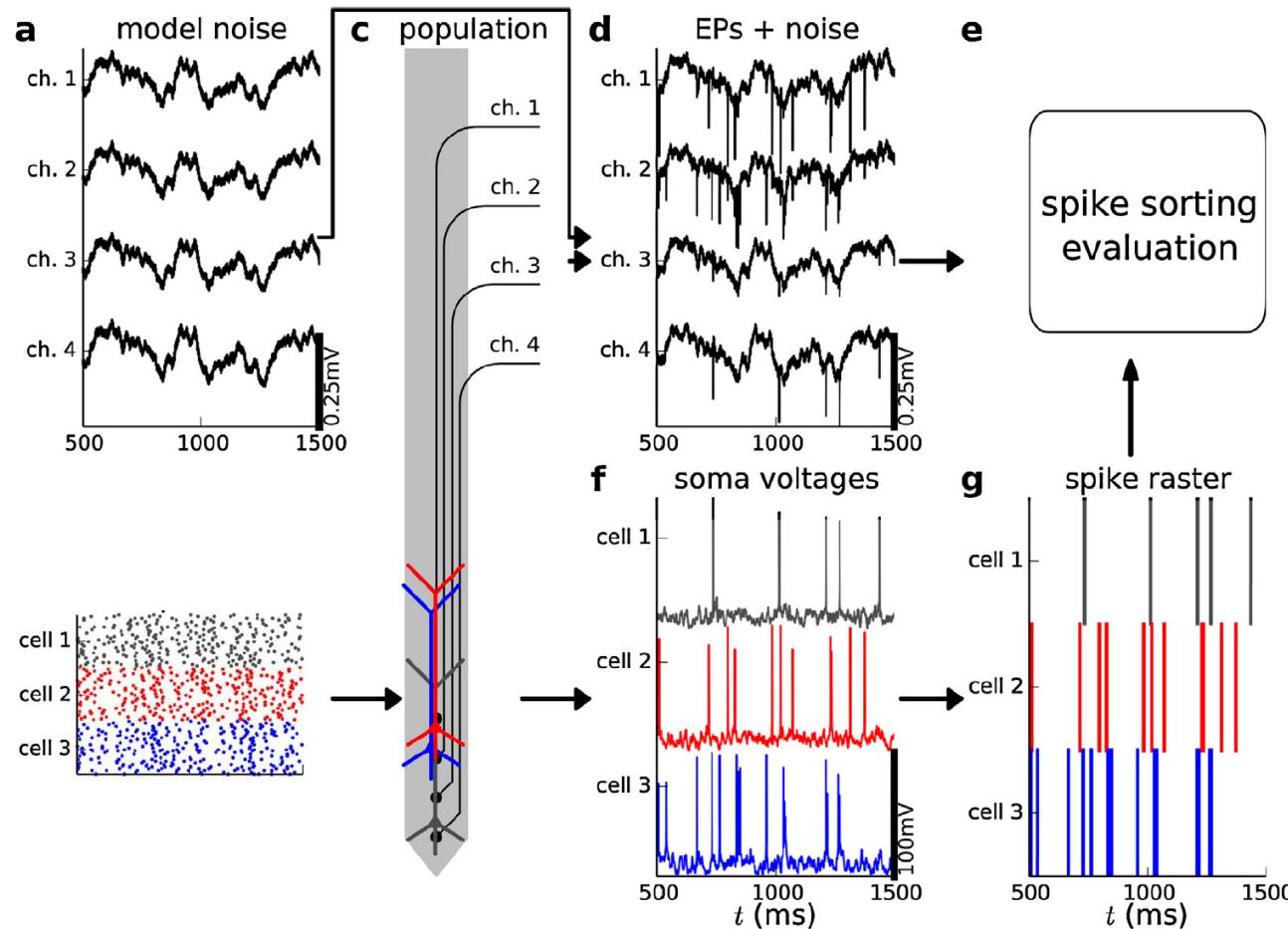


Verification: Patch-clamp data





Verification: synthetic data



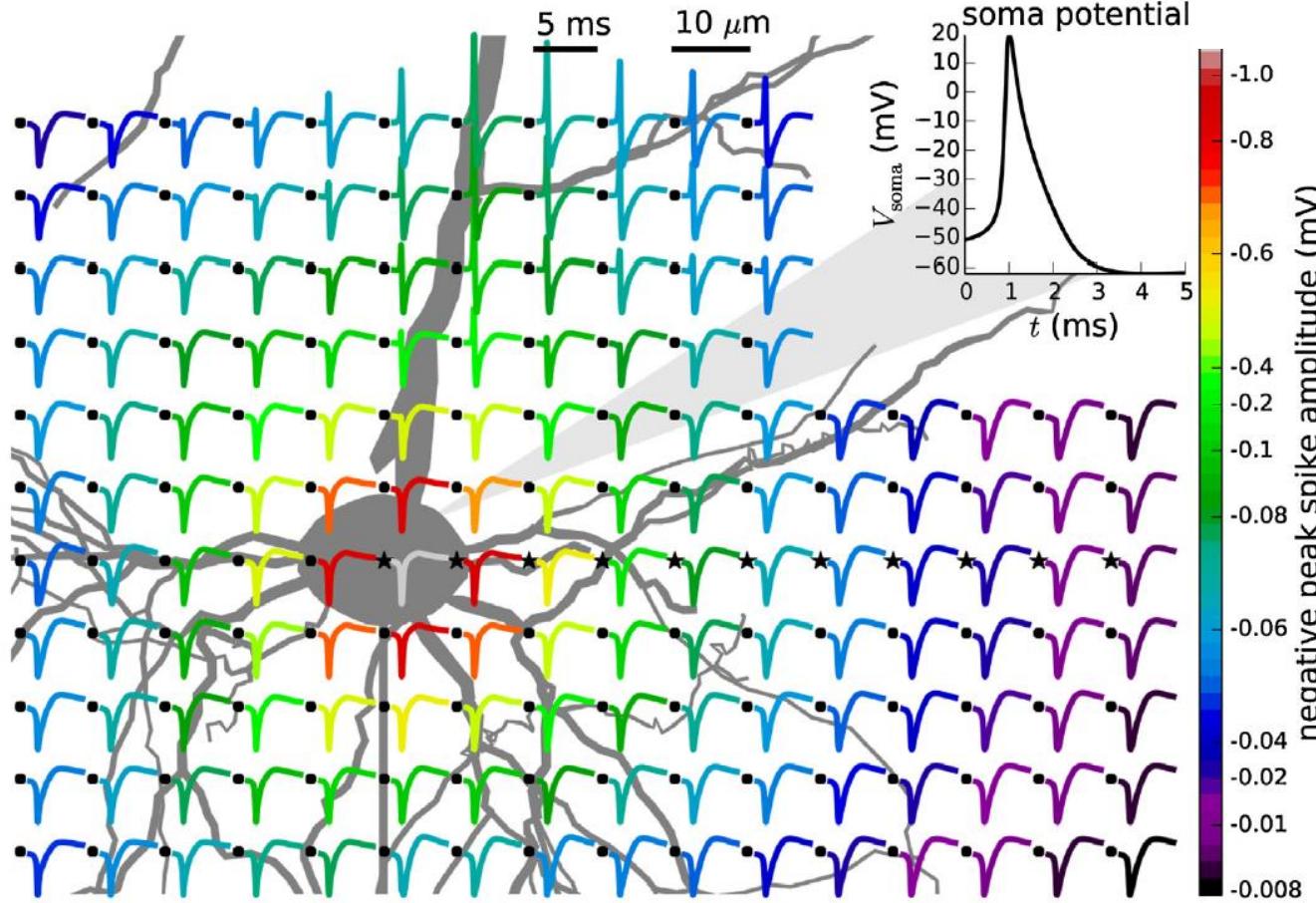


Verification: synthetic data



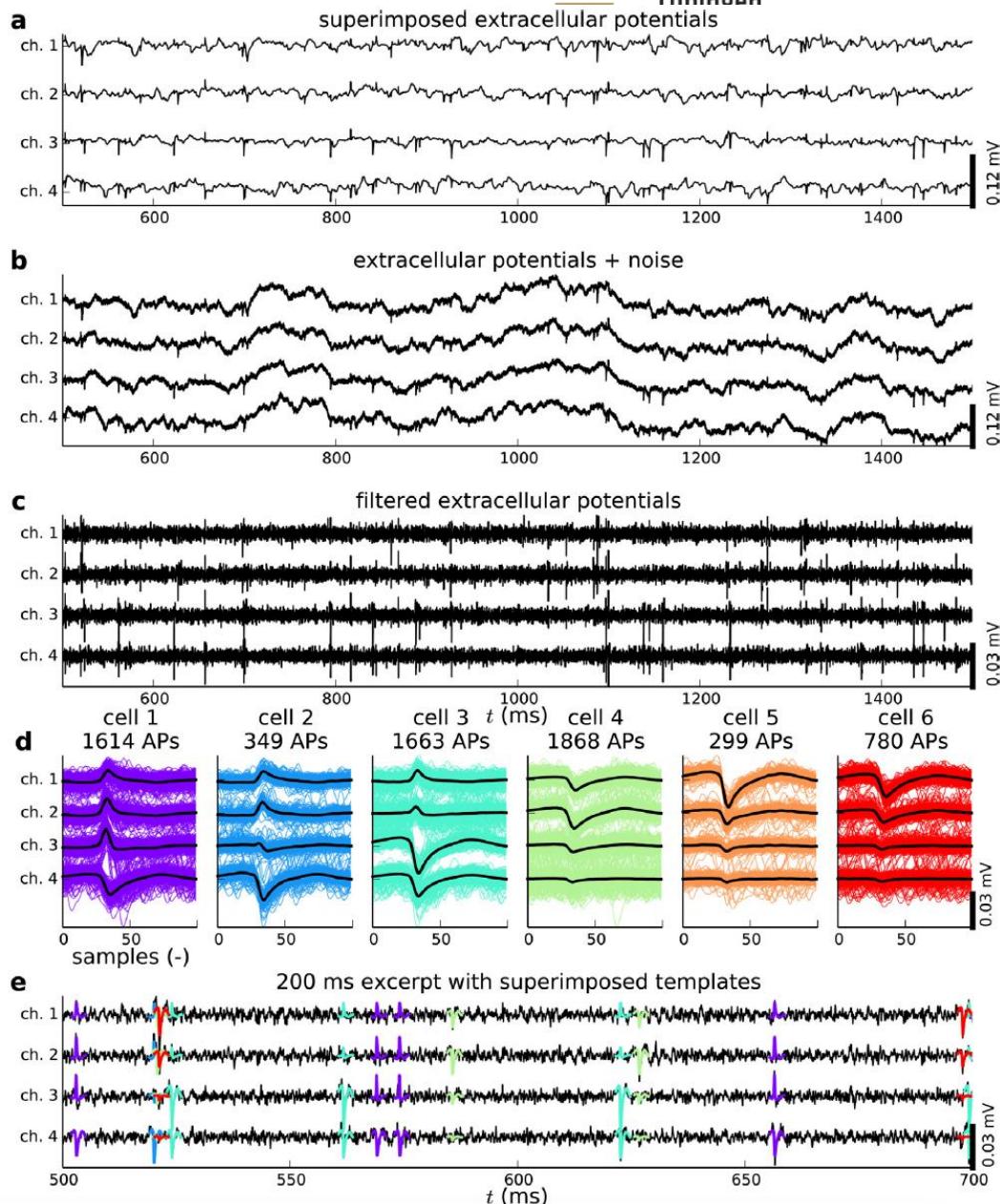


Verification: synthetic data



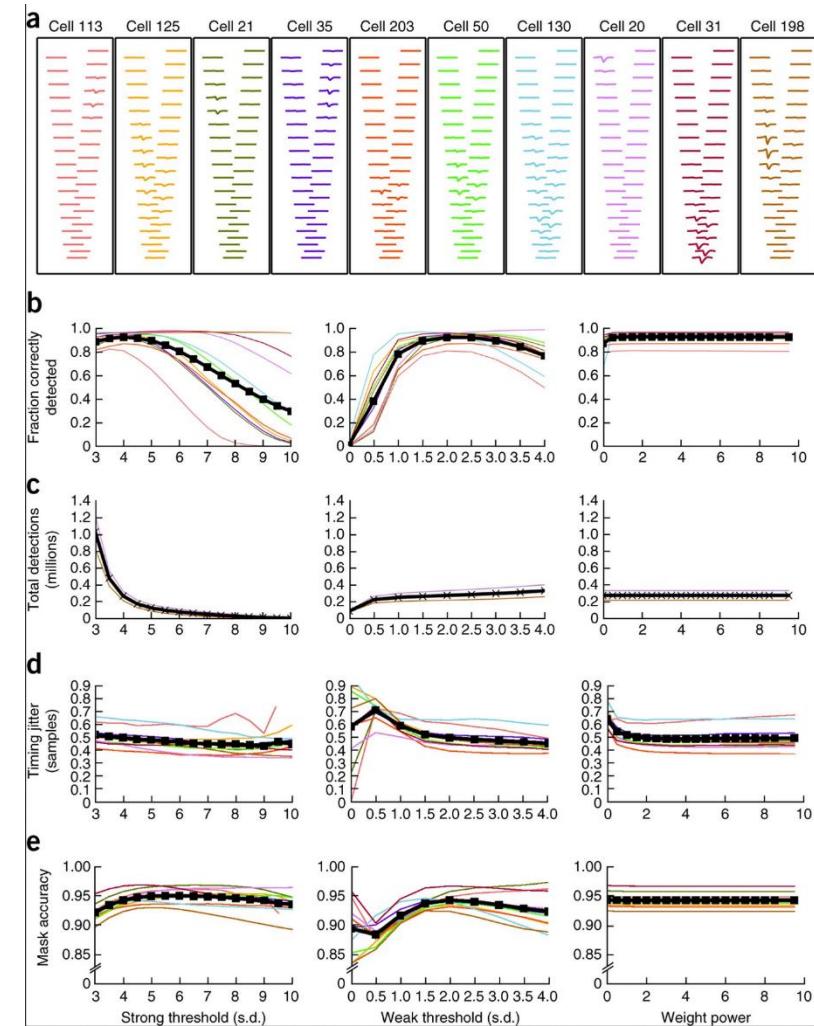
Verification: synthetic data

[http://spike.g-node.org/
spike_eval/benchmark/detail/10/](http://spike.g-node.org/spike_eval/benchmark/detail/10/)



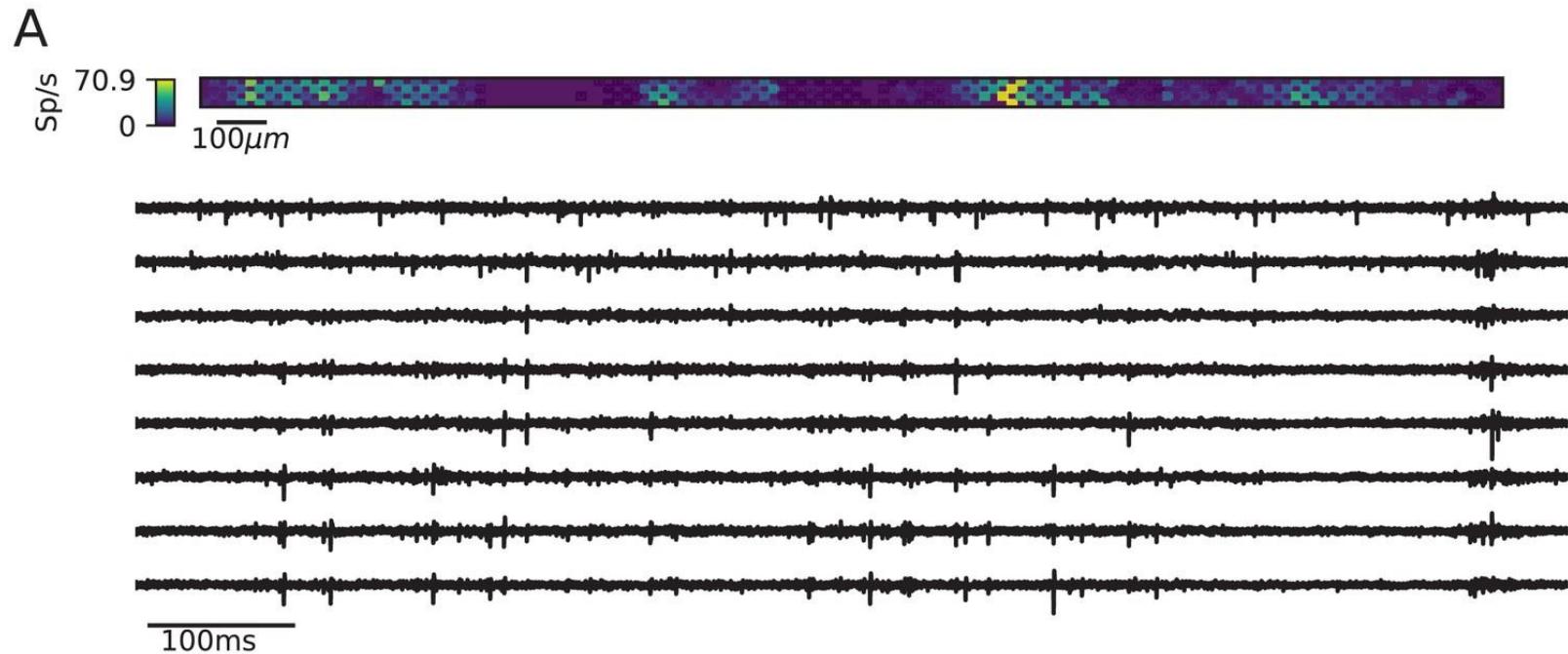
Hybrid data

- Problem: synthetic data not realistic enough! (especially noise properties)
- Use spike templates of “donor cells” and add to “acceptor” recording at known times!
- Simulate amplitude variability & drift



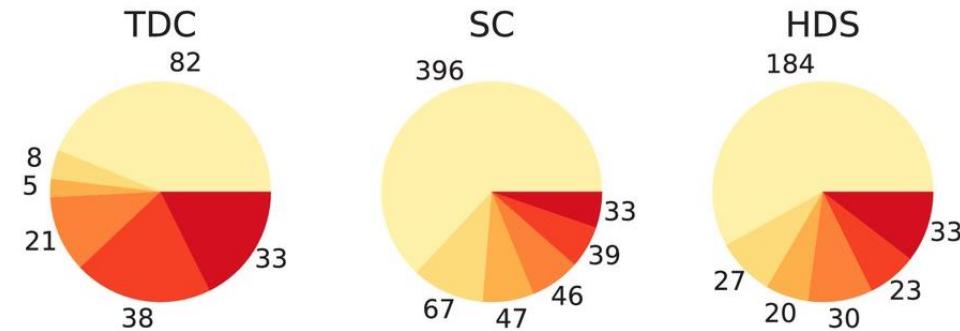
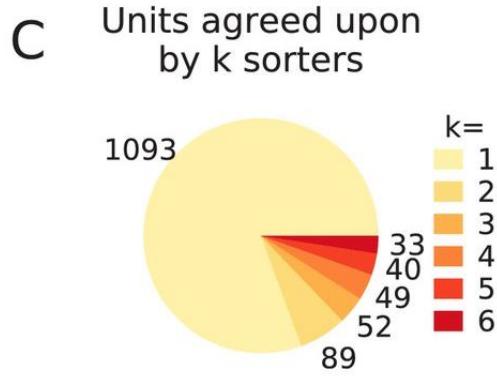
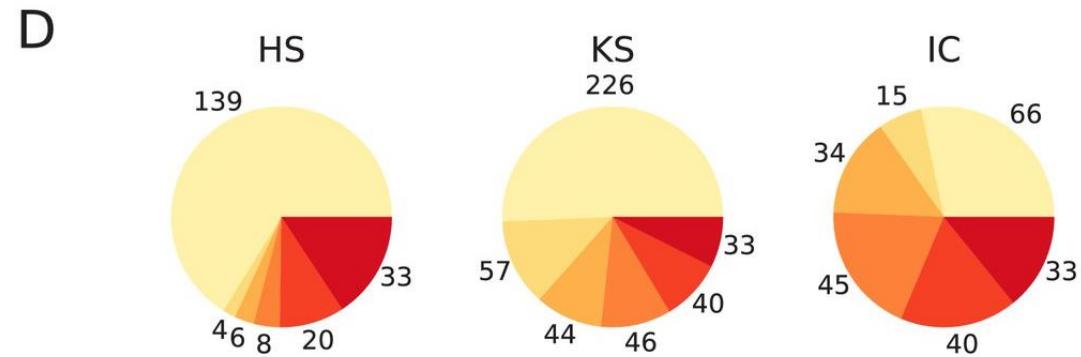
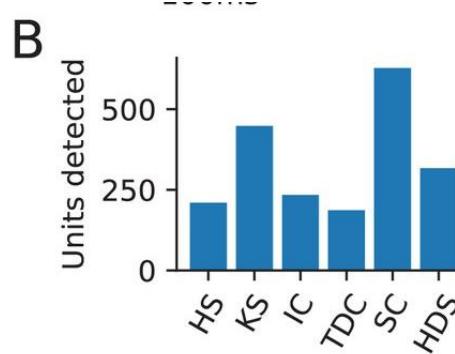


Comparison of different spike sorters



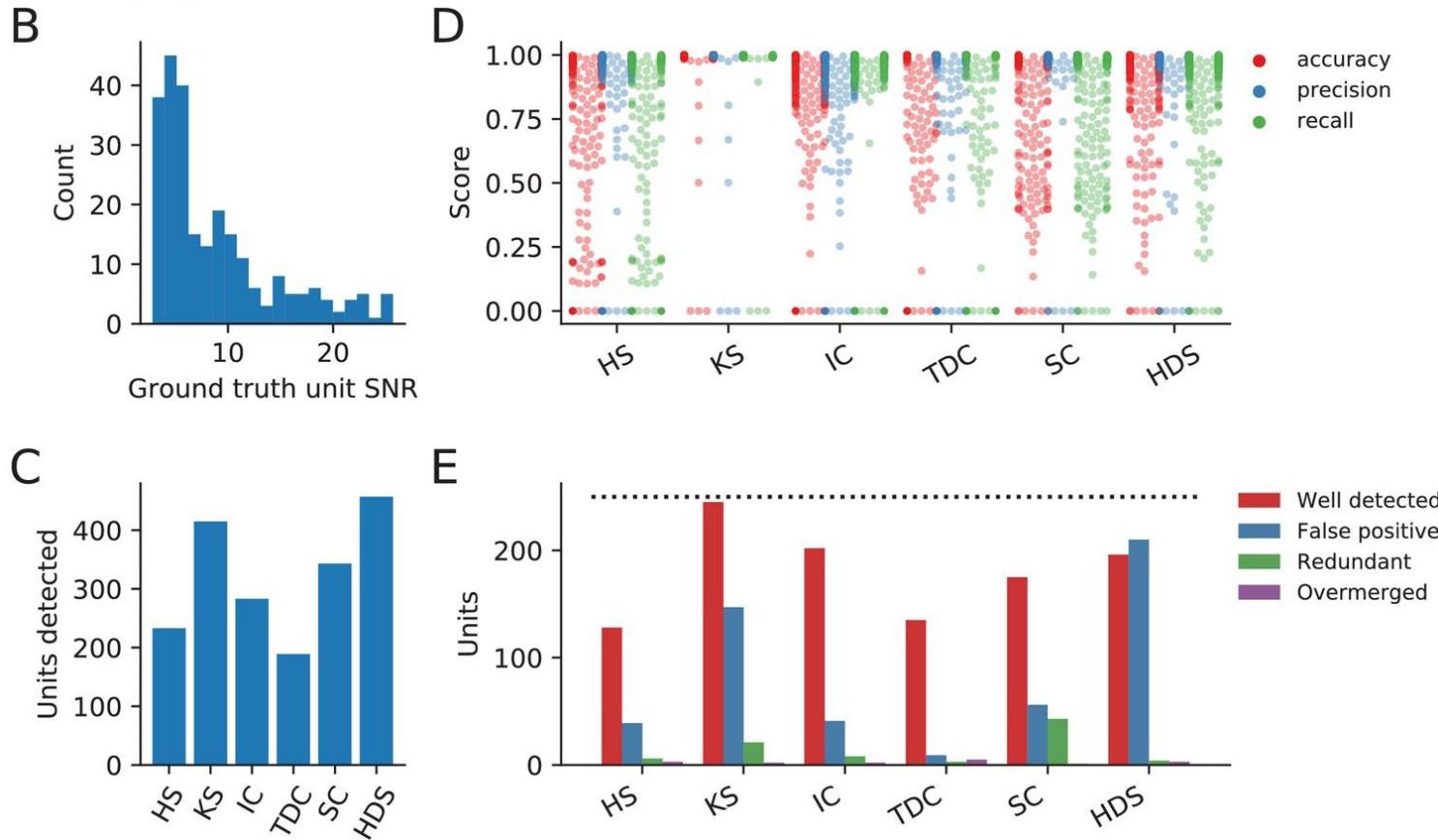


Comparison of different spike sorters





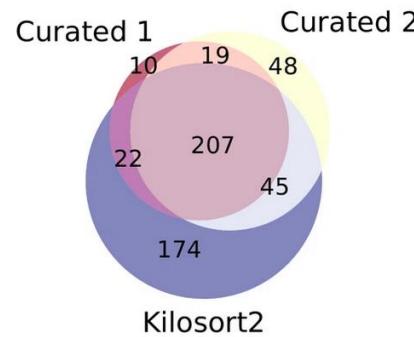
Comparison of different spike sorters





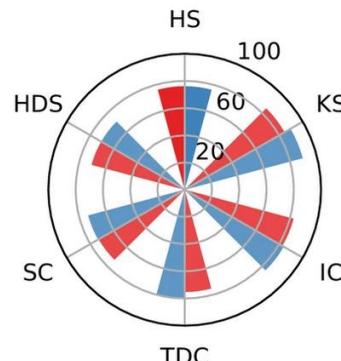
Comparison of different spike sorters

A



C

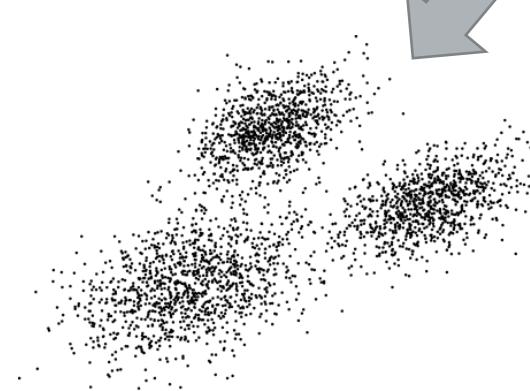
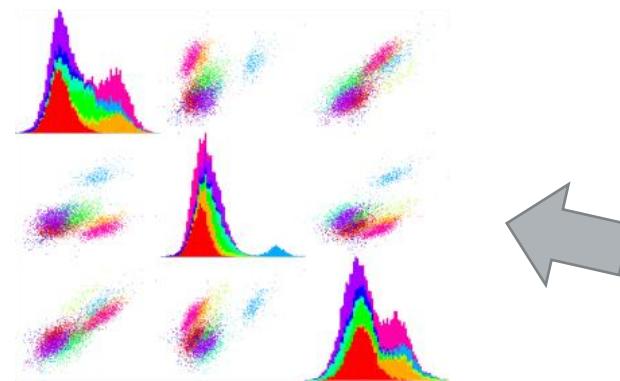
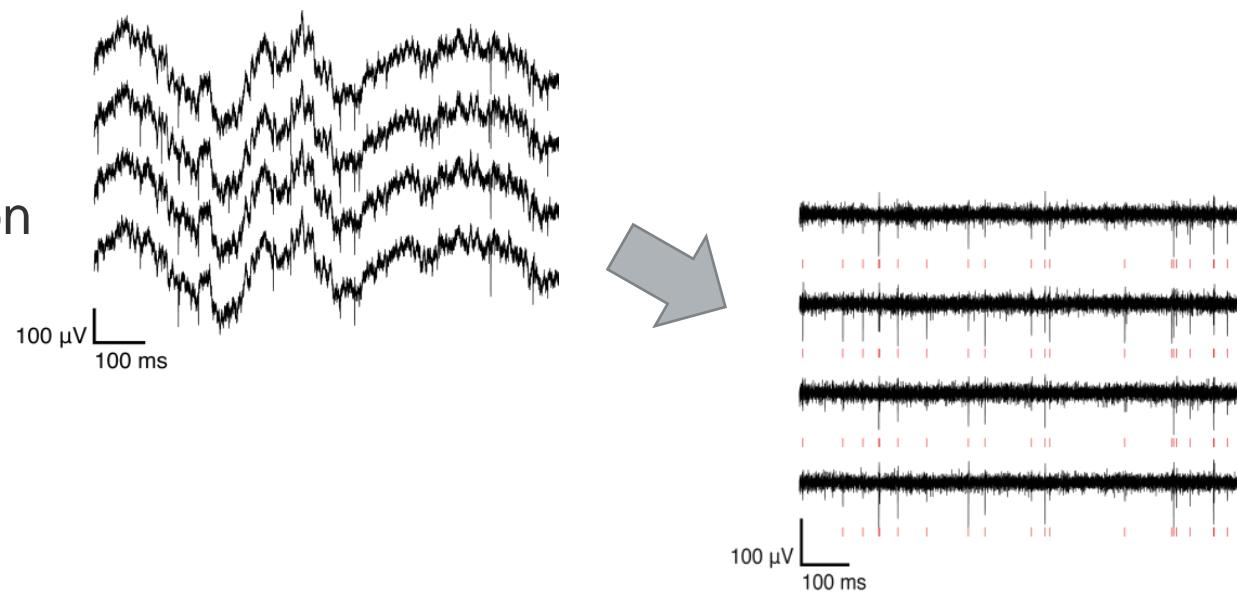
Percent consensus units
with match in curated sets





Spike sorting

- Raw data
- Spike detection
- Feature extraction
- Clustering
- Verification



See Buccino et al. Review on Illias