

# Statistical methods for understanding neural codes

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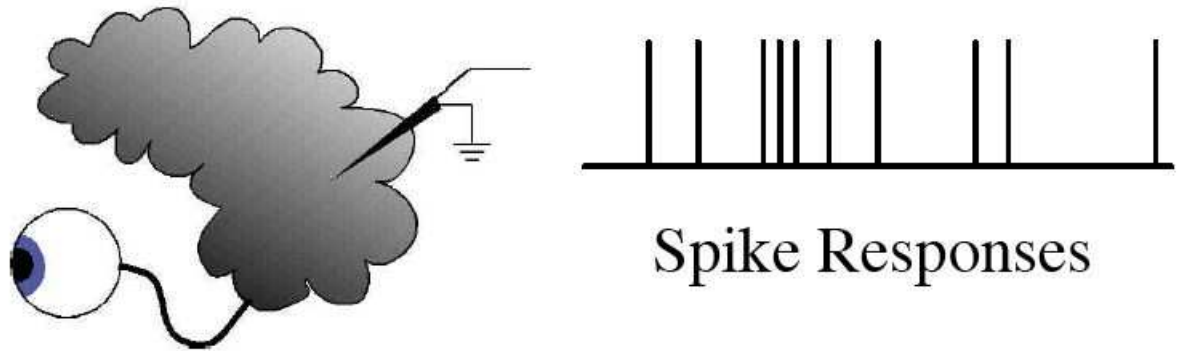
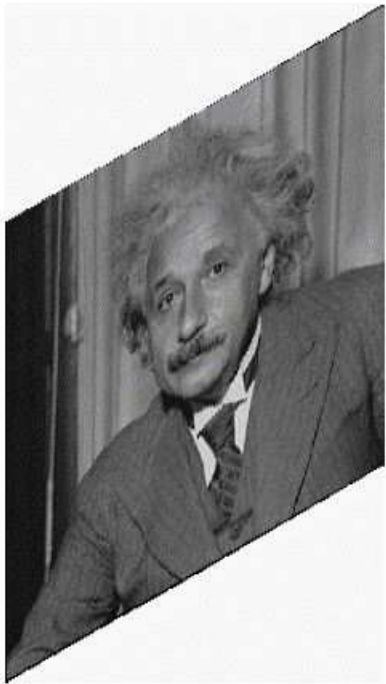
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# The neural code

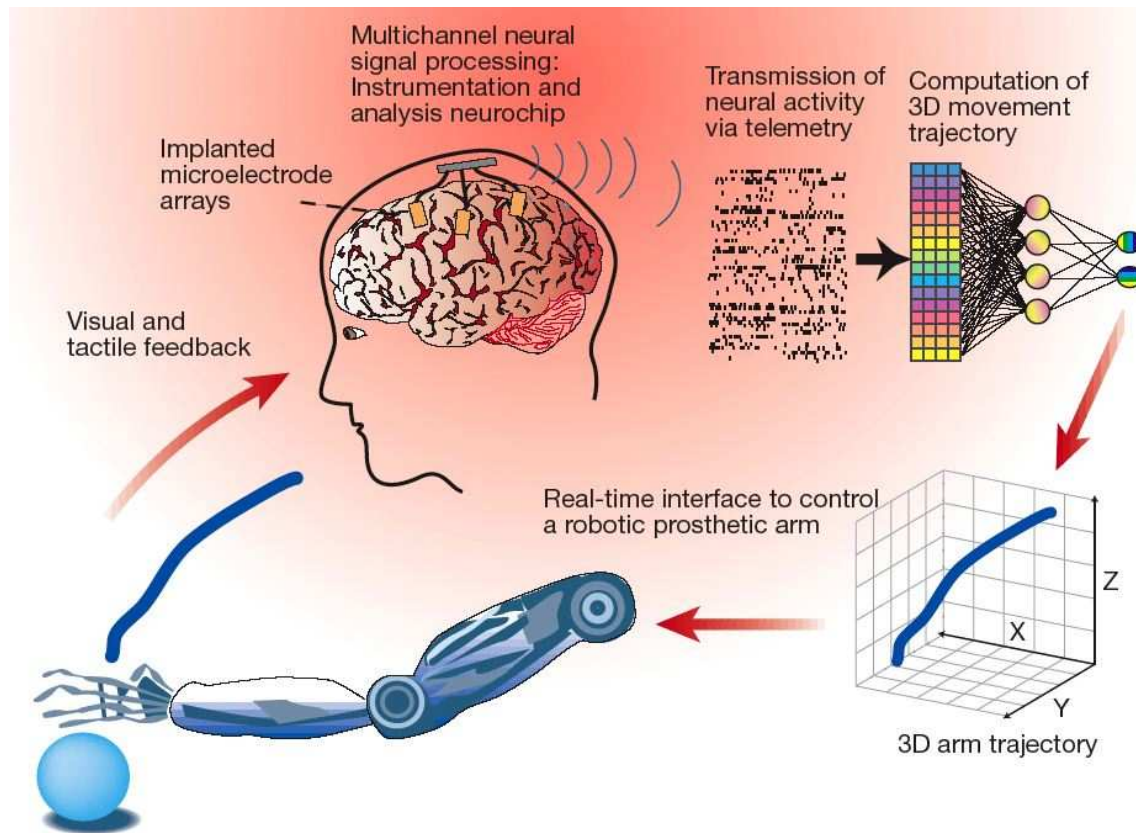


Input-output relationship between

- External observables  $x$  (sensory stimuli, motor responses...)
- Neural variables  $y$  (spike trains, population activity...)

Probabilistic formulation:  $p(y|x)$

# Example: neural prosthetic design



Nicolelis, Nature '01



Donoghue; Cyberkinetics, Inc. '04

(Paninski et al., 1999; Serruya et al., 2002; Shoham et al., 2005)

# Basic goal

...learning the neural code.

Fundamental question: how to estimate  $p(y|x)$  from experimental data?

General problem is too hard — not enough data, too many inputs  $x$  and spike trains  $y$

# Avoiding the curse of insufficient data

Many approaches to make problem tractable:

**1:** Estimate some functional  $f(p)$  instead

e.g., information-theoretic quantities (Nemenman et al., 2002; Paninski, 2003b)

**2:** Select stimuli as efficiently as possible

e.g., (Foldiak, 2001; Machens, 2002; Paninski, 2003a)

**3:** Fit a model with small number of parameters

# Part 1: Neural encoding models

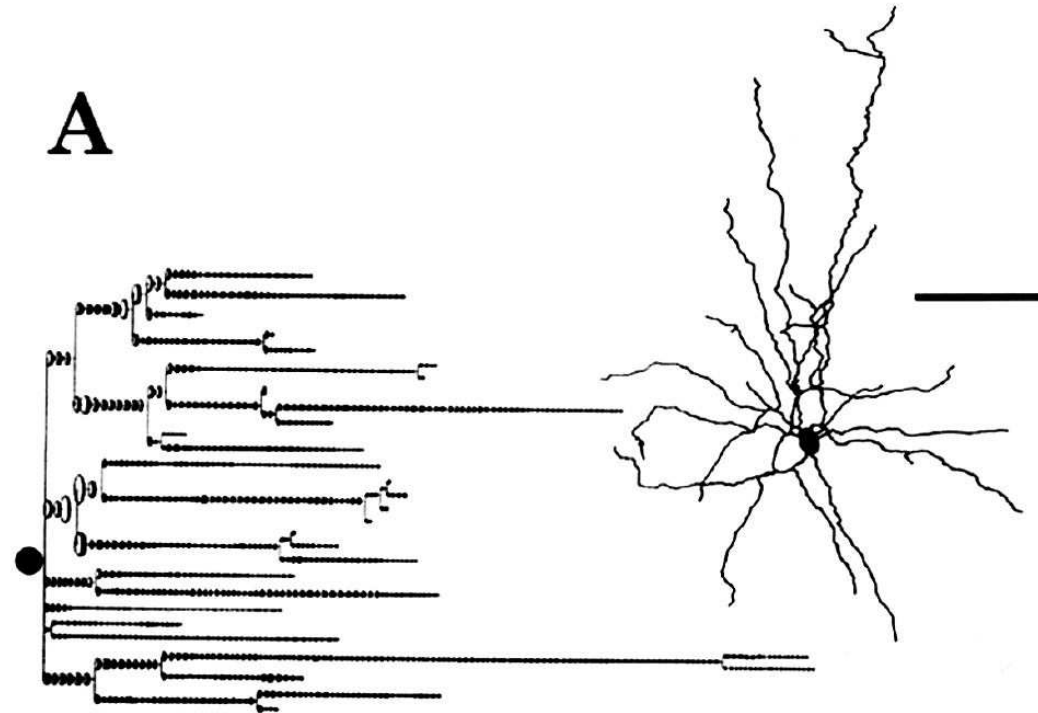
“Encoding model”:  $p_{\theta}(y|x)$ .

— Fit parameter  $\theta$  instead of full  $p(y|x)$

Main theme: want model to be flexible but not overly so

Flexibility vs. “fittability”

# Multiparameter HH-type model



Regional Conductances (mS/cm<sup>2</sup>)

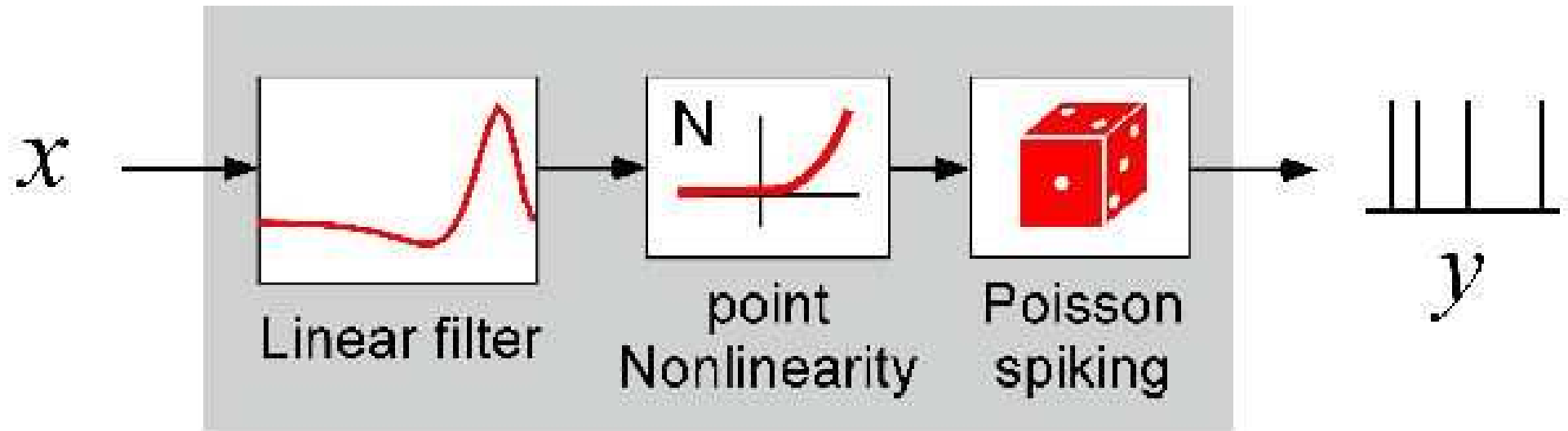
Model	Current	Dendrites	Soma	AH	NR	Axon
EC2.5 REAL	$I_{Ca}$	2.0	1.5	1.5	—	—
$j = 1$	$I_{K,Ca}$	0.001	0.065	0.065	0.065	0.065
SD* (real) = 21.9 $\mu\text{m}$	$I_{Na}$	25	80	100–150†	100	40–70‡
SD (EC2.5) = 20 $\mu\text{m}$	$I_K$	12	18	18	18	12–18‡
$\tau_{Ca} = 1.5$	$I_A$	36	54	54	54	—
$E_L = -60$ mV	Leak (Real)	0.008	0.008	0.008	0.008	0.008
$E_{Na} = 35$ mV	(EC2.5)	0.005	0.005	0.005	0.005	0.005

— highly biophysically plausible, flexible

— **but** very difficult to estimate parameters given spike times alone

(figure adapted from (Fohlmeister and Miller, 1997))

# Cascade (“LNP”) model



- easy to estimate: STA, STC (Simoncelli et al., 2004)
- **but** not biophysically plausible (fails to capture spike timing details: refractoriness, burstiness, adaptation, etc.)

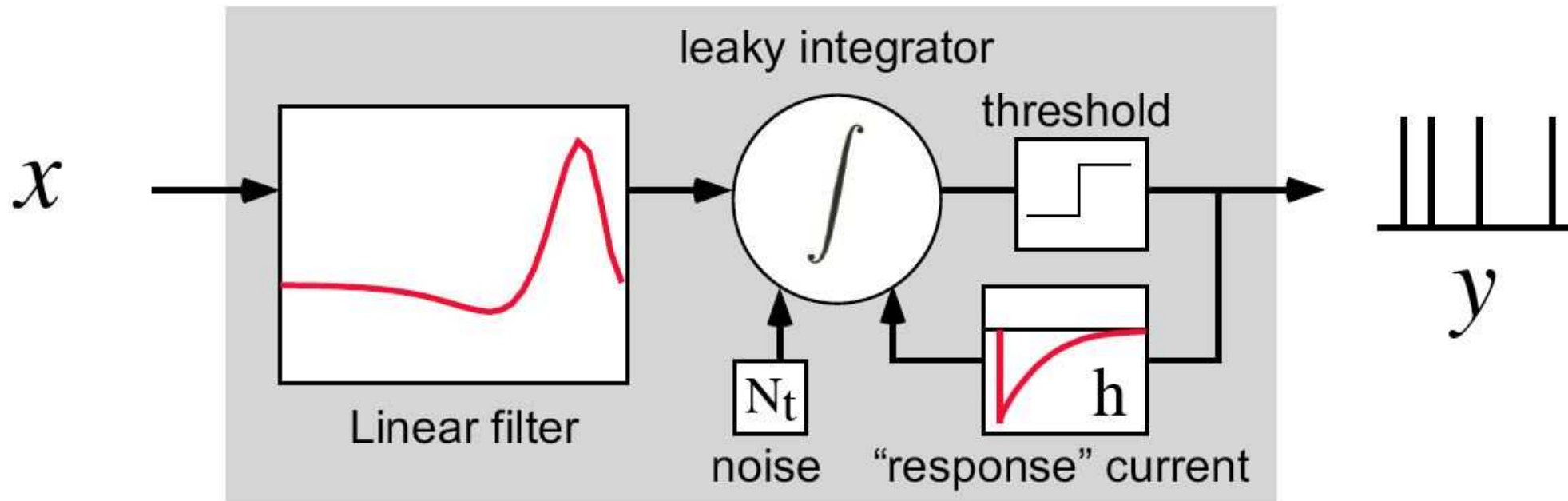


# Two key ideas

1. Use likelihood-based methods for fitting.
  - well-justified statistically
  - easy to incorporate prior knowledge, explicit noise models, etc.
  
2. Use models that are easy to fit via maximum likelihood
  - **concave** (downward-curving) functions have no non-global local maxima  $\implies$  concave functions are easy to maximize by gradient ascent.

Recurring theme: find flexible models whose loglikelihoods are guaranteed to be concave.

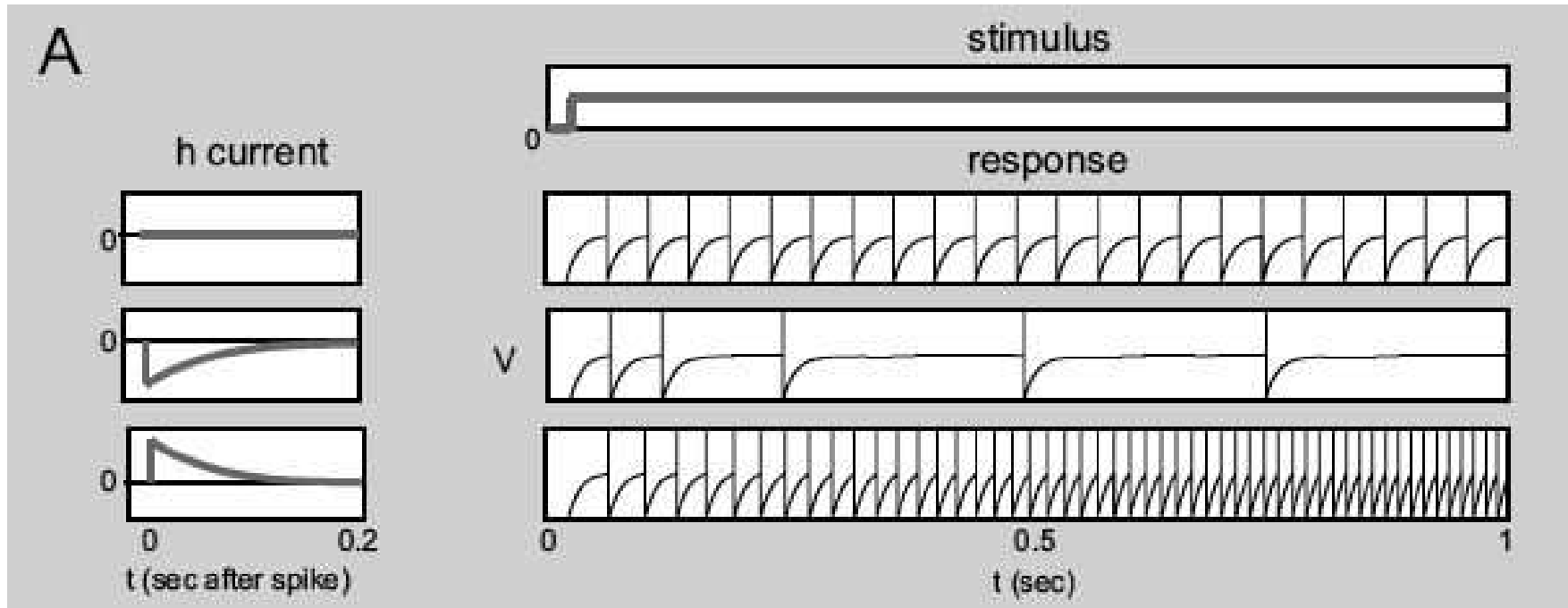
# Filtered integrate-and-fire model



$$dV(t) = \left( -g(t)V(t) + I_{DC} + \vec{k} \cdot \vec{x}(t) + \sum_{j=-\infty}^0 h(t - t_j) \right) dt + \sigma dN_t;$$

(Gerstner and Kistler, 2002; Paninski et al., 2004b)

# Model flexibility: Adaptation



# The estimation problem

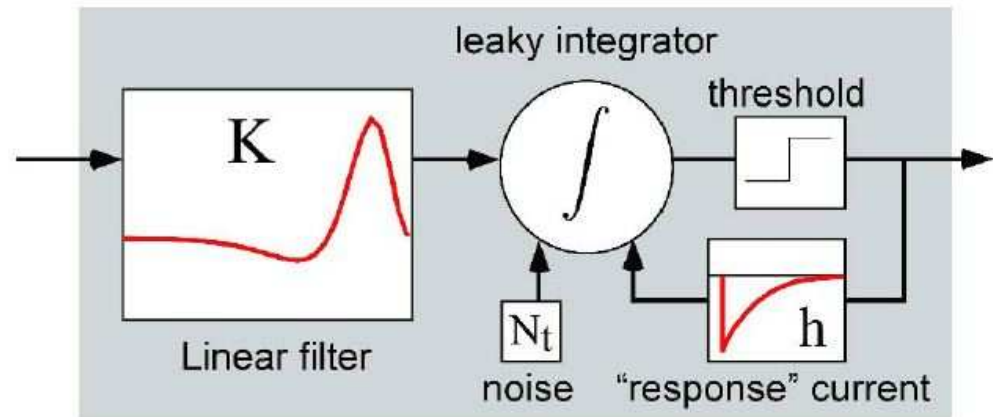
Learn the model parameters:

$\vec{K}$  = stimulus filter

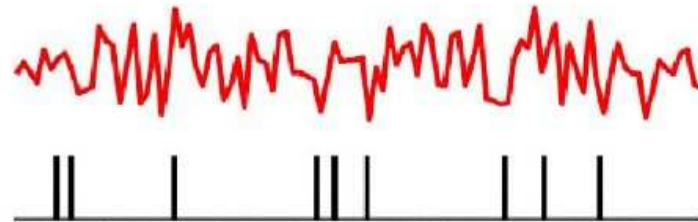
$g$  = leak conductance

$\sigma^2$  = noise variance

$\vec{h}$  = response current

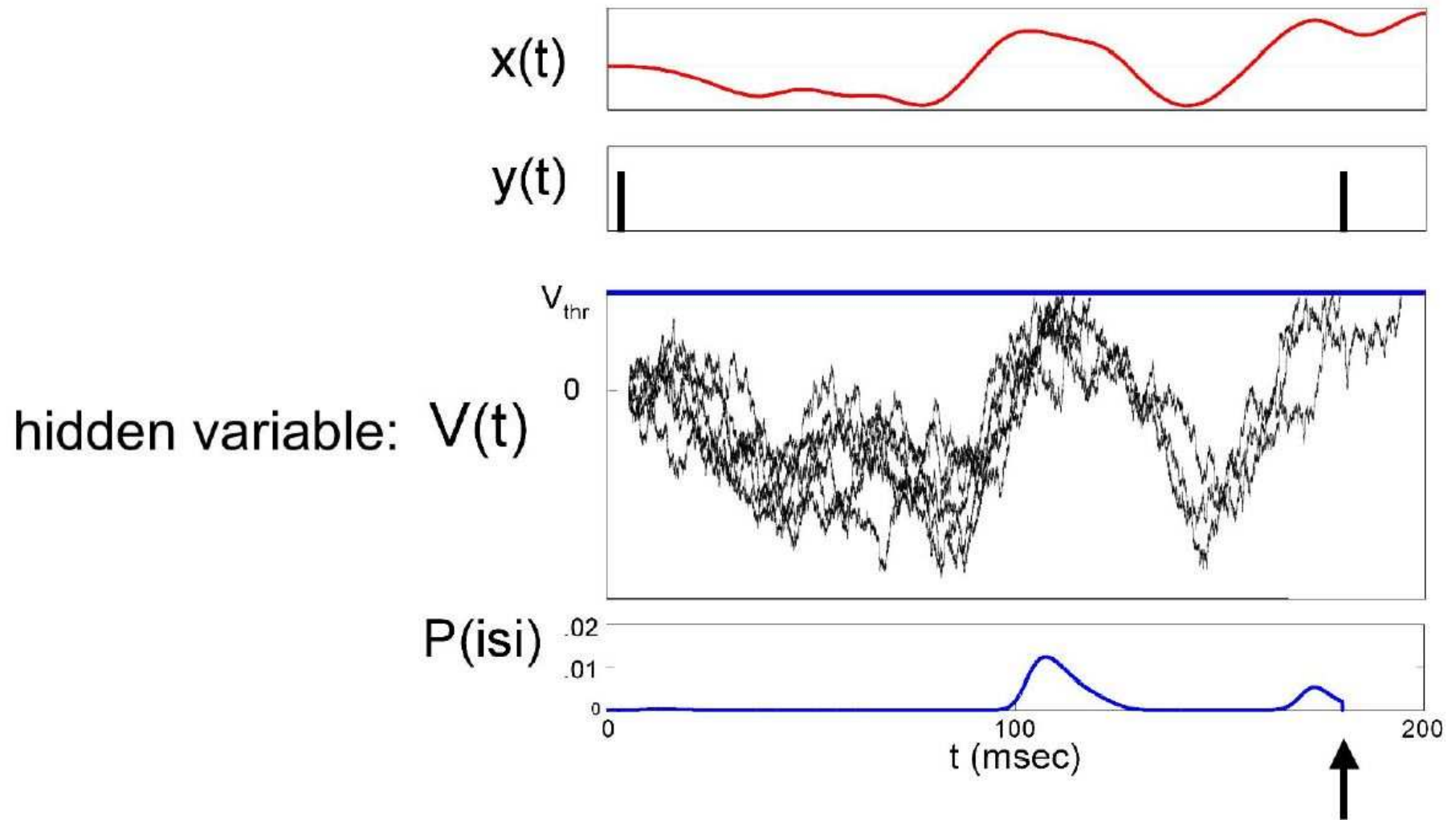


From: stimulus train  $x(t)$   
spike times  $t_i$



(Paninski et al., 2004b)

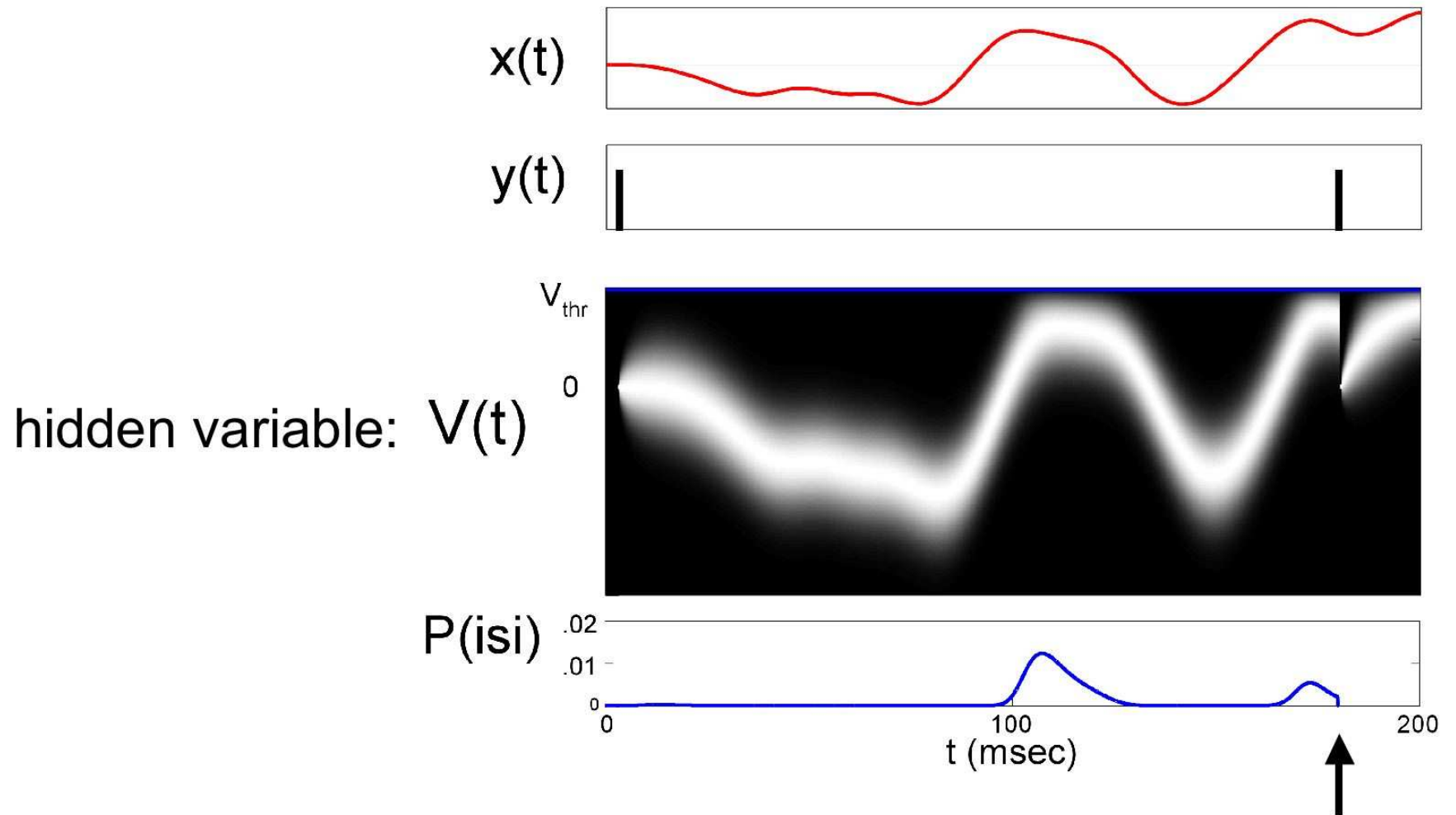
# First passage time likelihood



$P(\text{spike at } t_i) = \text{fraction of paths crossing threshold for first time at } t_i$

(computed numerically via Fokker-Planck or integral equation methods)

# Likelihood function



$P(\text{spike at } t_i) = \text{fraction of paths crossing threshold at } t_i$

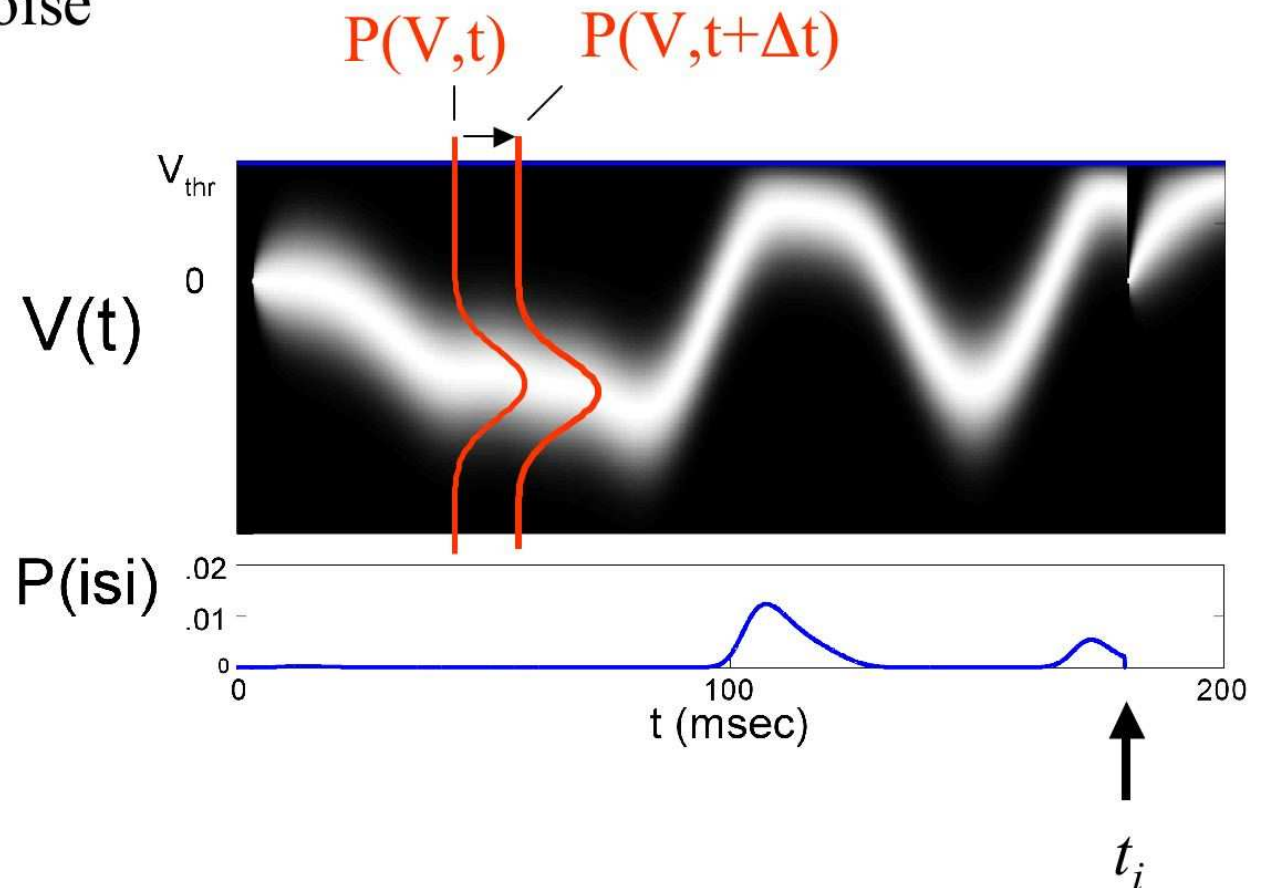
$t_i$

# Computing Likelihood

Diffusion Equation: 
$$\frac{\partial P(V,t)}{\partial t} = \frac{\sigma^2}{2} \frac{\partial^2 P}{\partial V^2} + g \frac{\partial [(V - V_0)P]}{\partial V},$$

- linear dynamics
- additive Gaussian noise

fast methods for solving  
linear PDE  
 $\Rightarrow$   
efficient procedure for  
computing likelihood

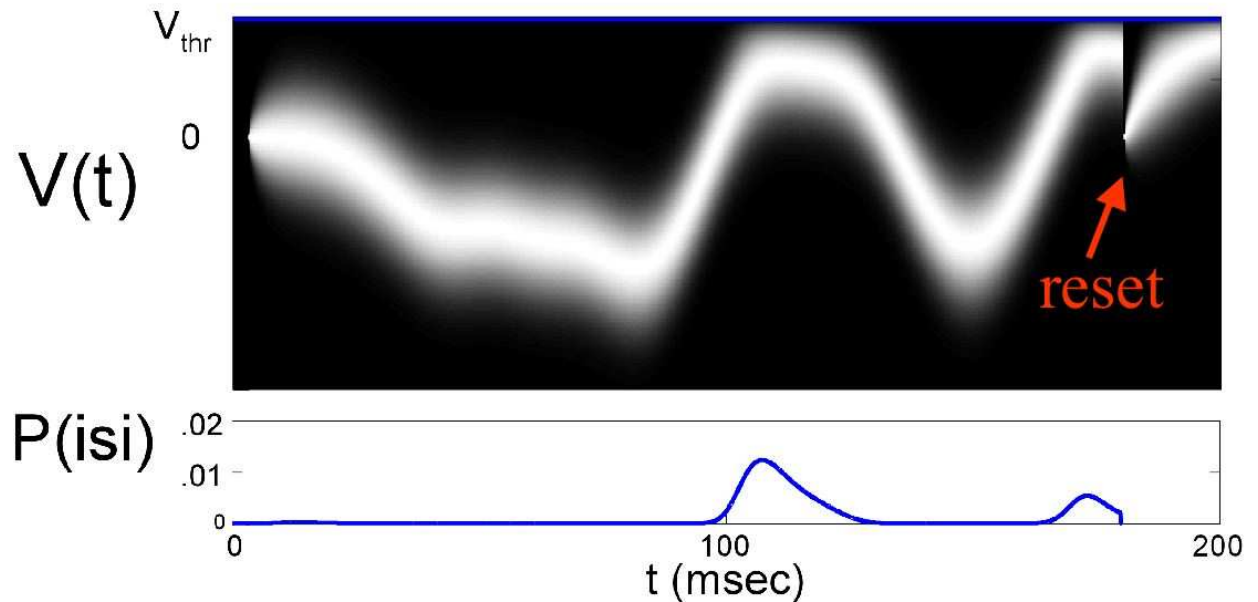


# Computing Likelihood

Diffusion Equation: 
$$\frac{\partial P(V, t)}{\partial t} = \frac{\sigma^2}{2} \frac{\partial^2 P}{\partial V^2} + g \frac{\partial [(V - V_0)P]}{\partial V},$$

- linear dynamics
- additive Gaussian noise

fast methods for solving  
linear PDE  
 $\Rightarrow$   
efficient procedure for  
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ISIs are conditionally independent  $\Rightarrow$  likelihood is product over ISIs



# Integral equation method

Let  $p(t) = P(\text{spike at time } t)$ .

Then  $p(t)$  solves Volterra integral equation  
(Plesser and Tanaka, 1997) (via “method of images”; goes back  
to Schrodinger):

$$G_{\theta}(V_{th}, t | V_{th}, 0) = \int_0^t G_{\theta}(V_{th}, t | V_{th}, s) p(s) ds$$

$G_{\theta}(y, t | x, s) =$  probability of  $V(t) = y$ , given  $V(s) = x$   
(analytically computable)

Lower-triangular linear system:  $O(d^2)$  (Paninski et al., 2005)

Can compute gradient  $p(t)$  w.r.t.  $\theta$  via matrix perturbation:  
efficient maximization

# Maximizing likelihood

Maximization seems difficult, even intractable:

- high-dimensional parameter space
- likelihood is a complex nonlinear function of parameters

**Main result:** The loglikelihood is concave in the parameters, no matter what data  $\{\vec{x}(t), t_i\}$  are observed.

$\implies$  no non-global local maxima

$\implies$  maximization easy by ascent techniques.

# Proof of log-concavity theorem

Based on probability integral representation of likelihood:

$$L(\theta) = \int 1(\mathbf{V} \in C) dG_{\vec{x}, \theta}(\mathbf{V})$$

$G_{\vec{x}, \theta}(\mathbf{V}) =$  OU-measure on voltage paths  $\mathbf{V}$

$C =$  set of voltage paths  $V(t)$  consistent with spike data:

$$V(t) \leq V_{th}; \quad V(t_i) = V_{th}; \quad V(t_i^+) = V_{reset}$$

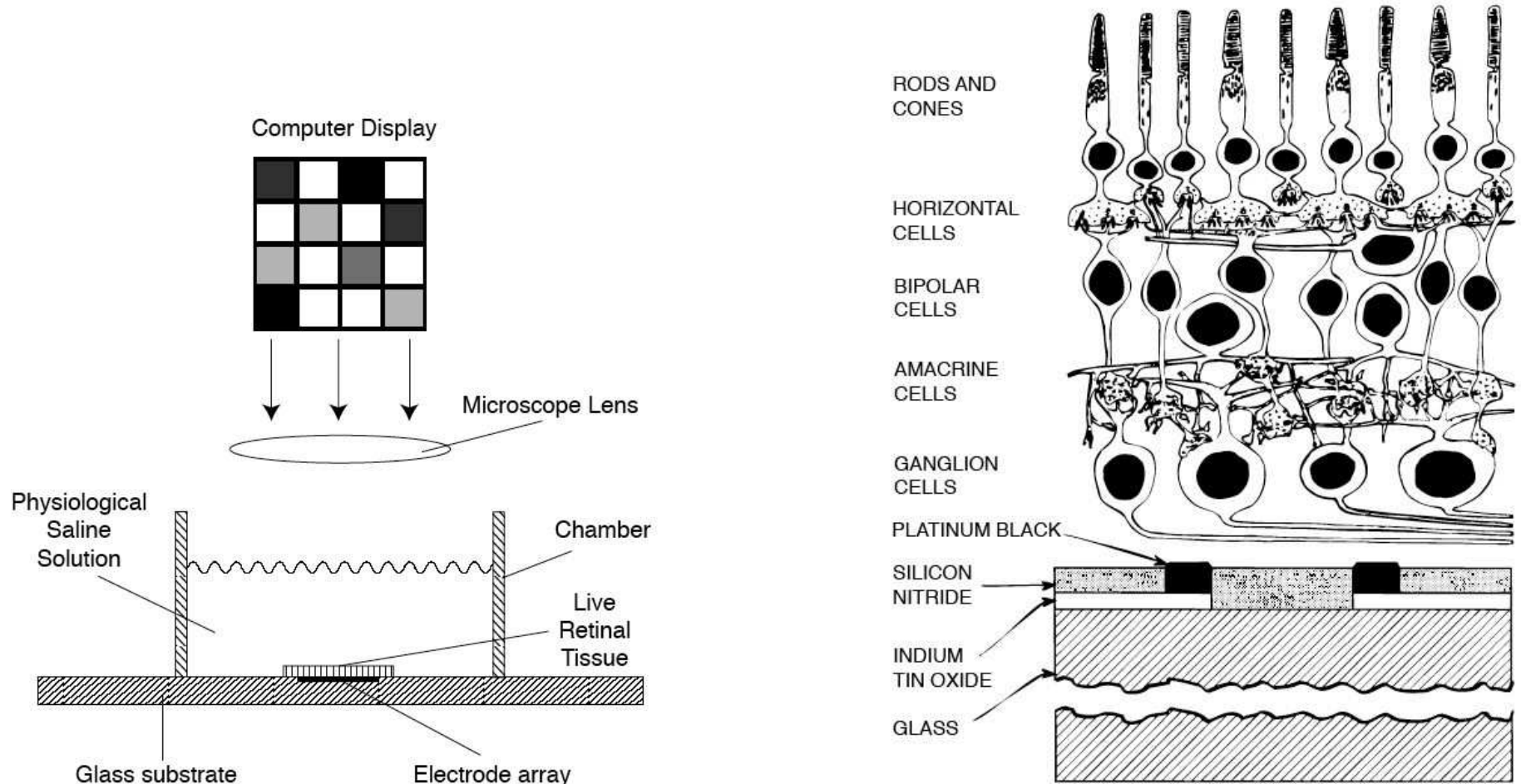
Now use fact that marginalizing preserves log-concavity (Prekopa, 1973): if  $f(\vec{x}, \vec{y})$  is jointly l.c., then so is

$$f_0(\vec{x}) \equiv \int f(\vec{x}, \vec{y}) d\vec{y}.$$

# Application: retinal ganglion cells

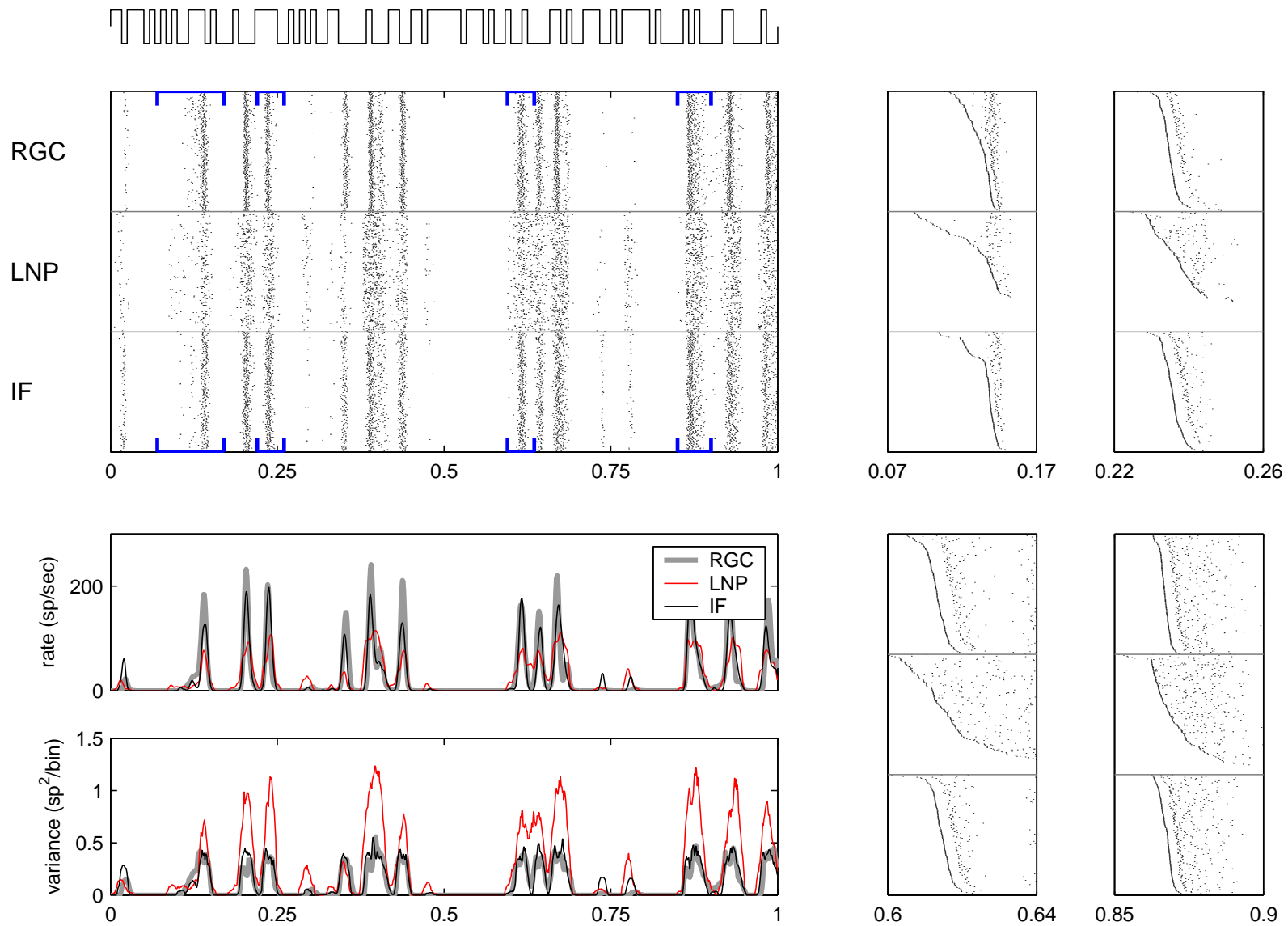
Preparation: dissociated salamander and macaque retina

— extracellularly-recorded responses of populations of RGCs



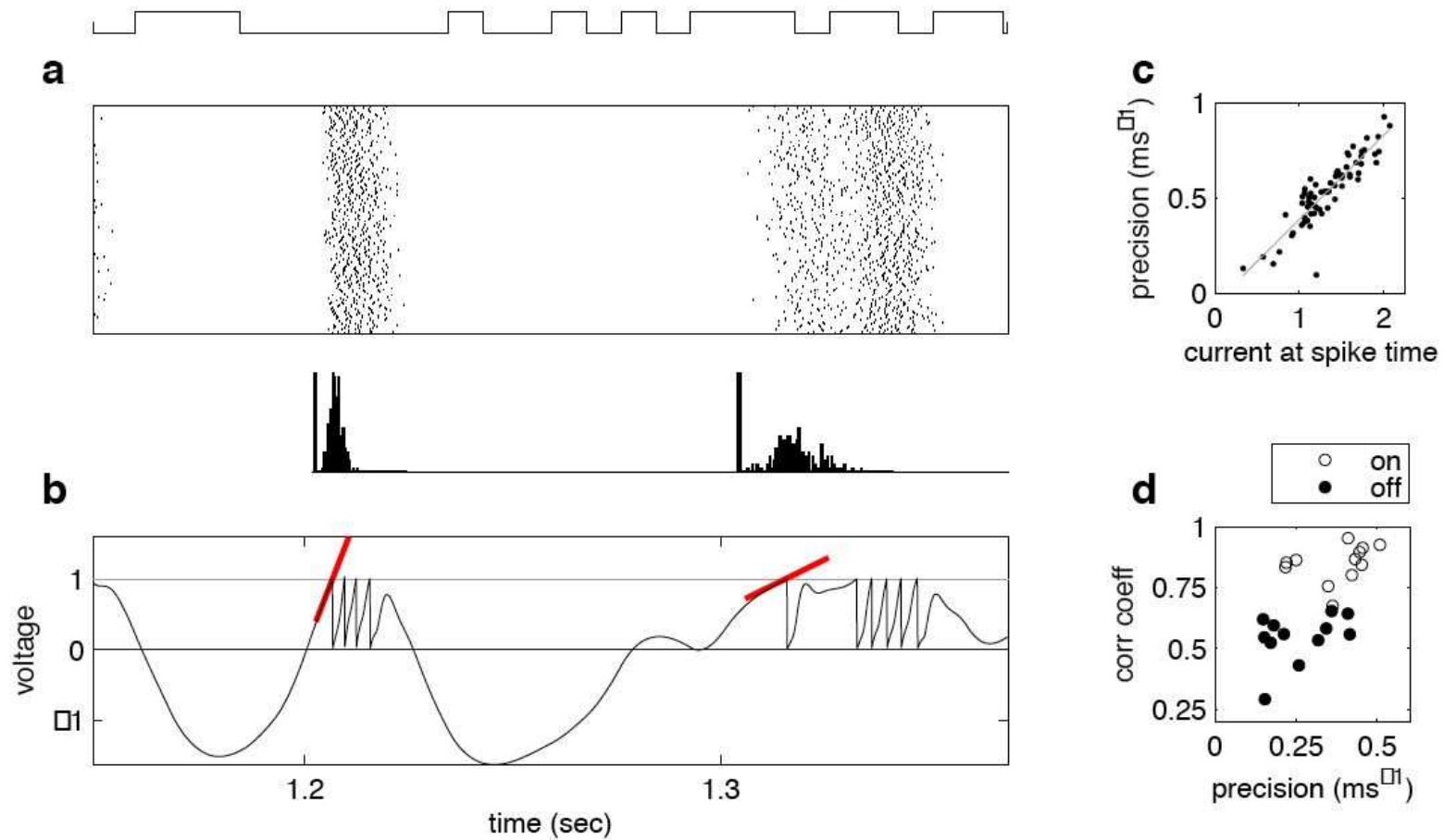
Stimulus: random “flicker” visual stimuli (Chander and Chichilnisky, 2001)

# Spike timing precision in retina



(Pillow et al., 2005)

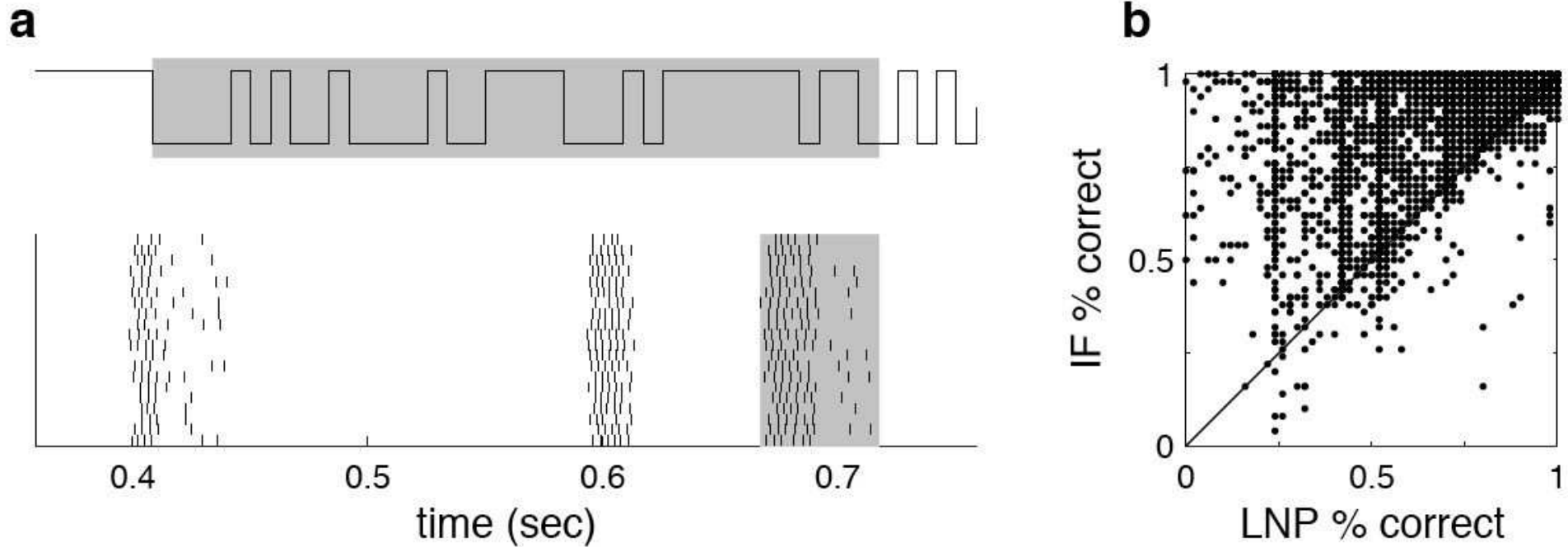
# Linking spike reliability and subthreshold noise



(Pillow et al., 2005)

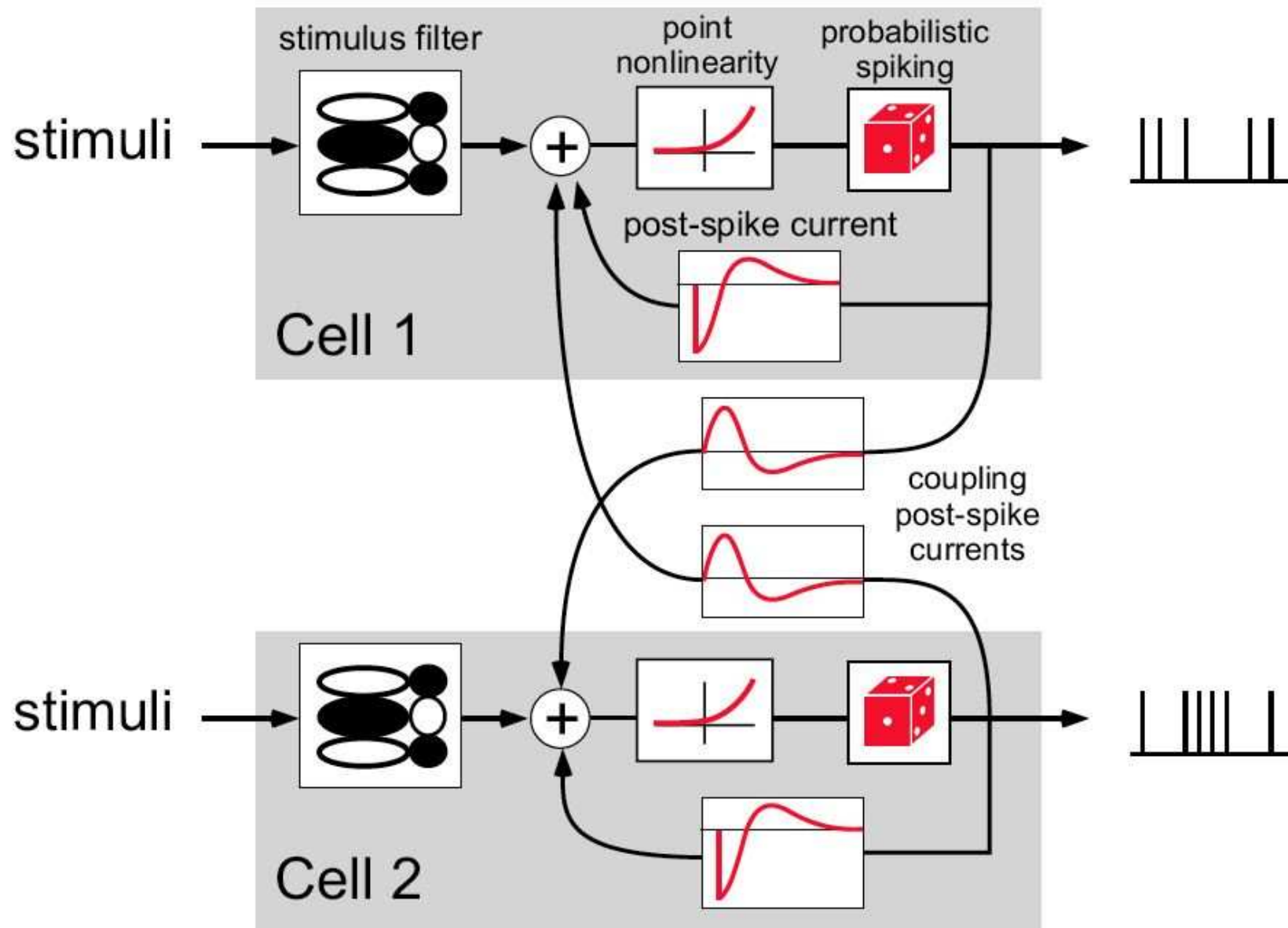
# Likelihood-based discrimination

Given spike data, optimal decoder chooses stimulus  $\vec{x}$  according to likelihood:  $p(\text{spikes}|\vec{x}_1)$  vs.  $p(\text{spikes}|\vec{x}_2)$ .



Using correct model is essential (Pillow et al., 2005)

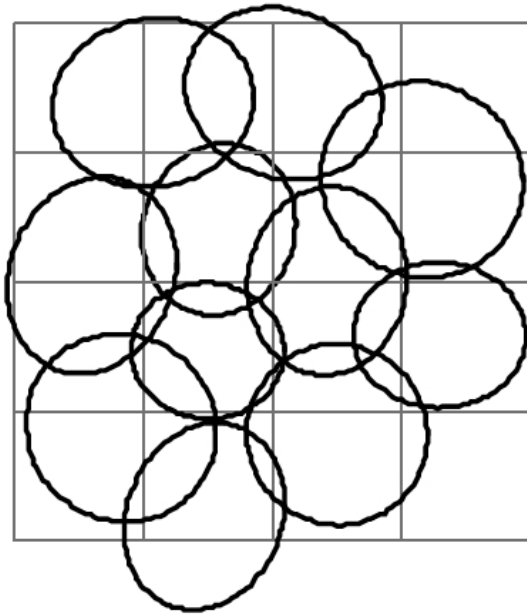
# Generalization: population responses



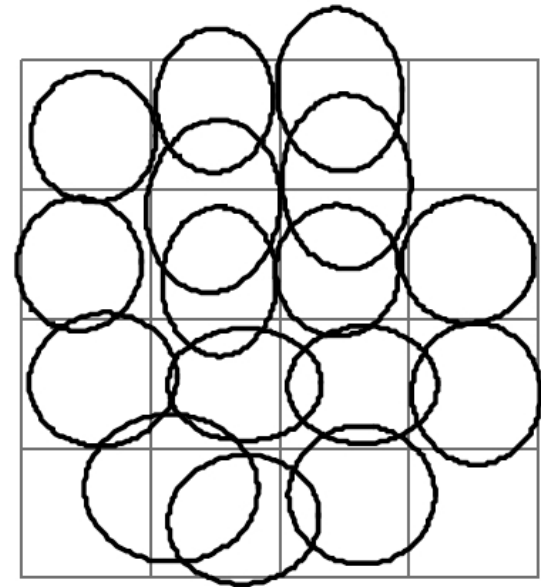


# Population retinal recordings

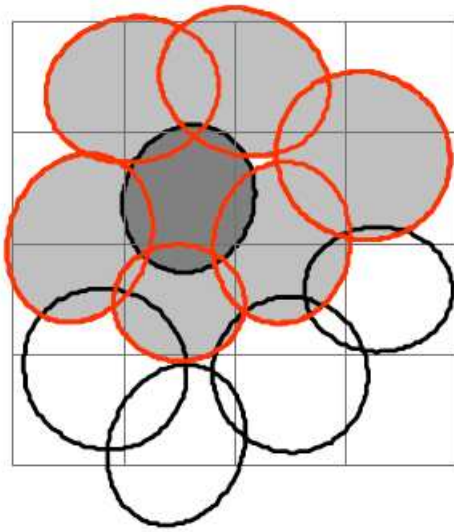
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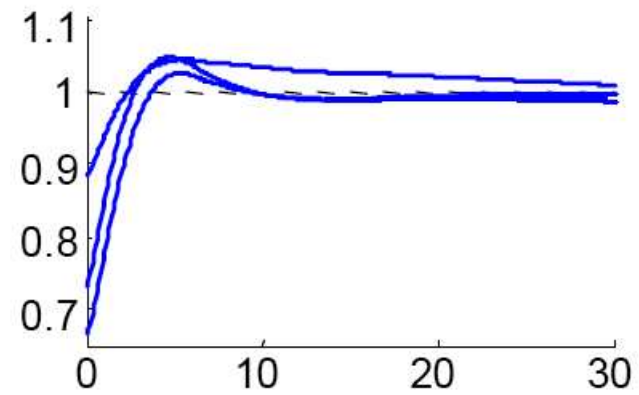
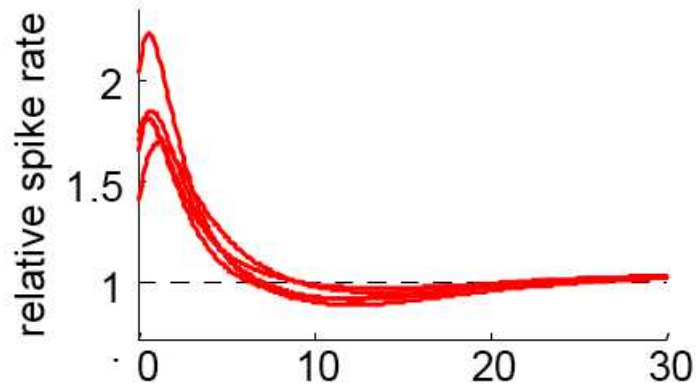
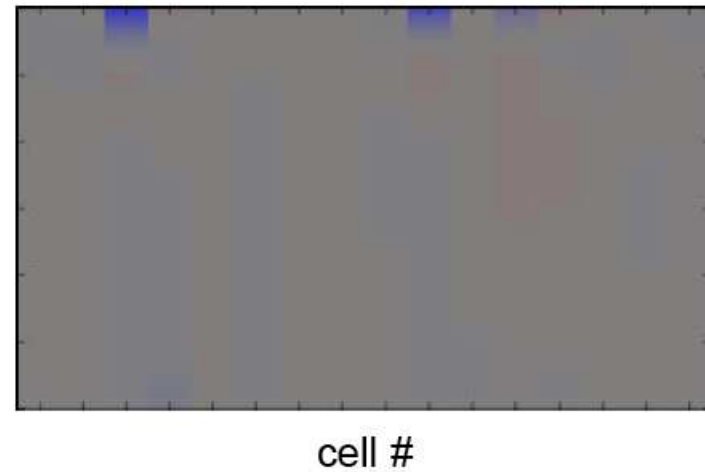
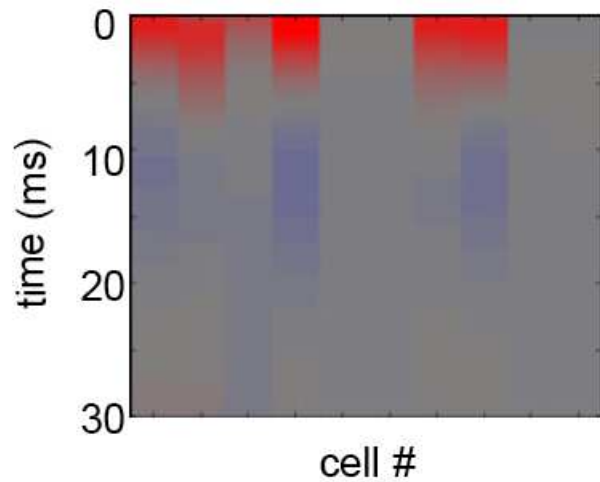
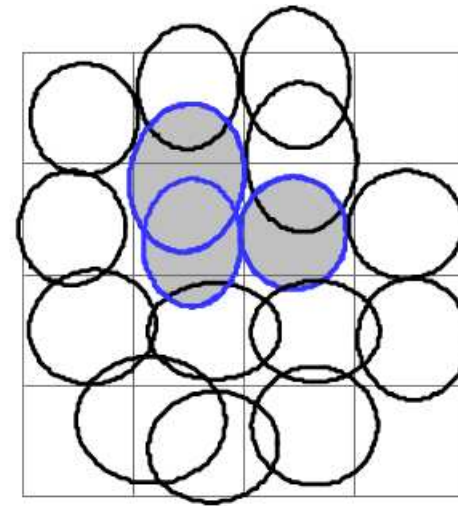
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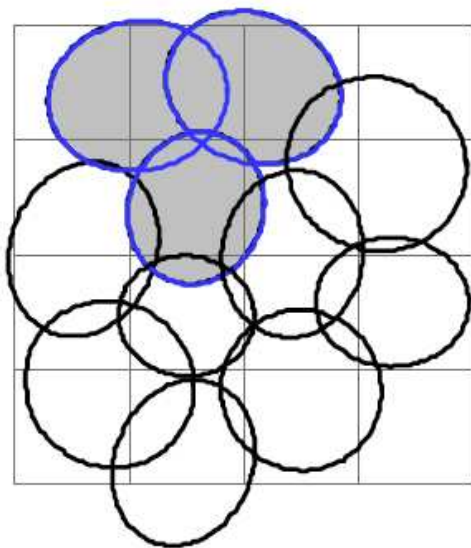
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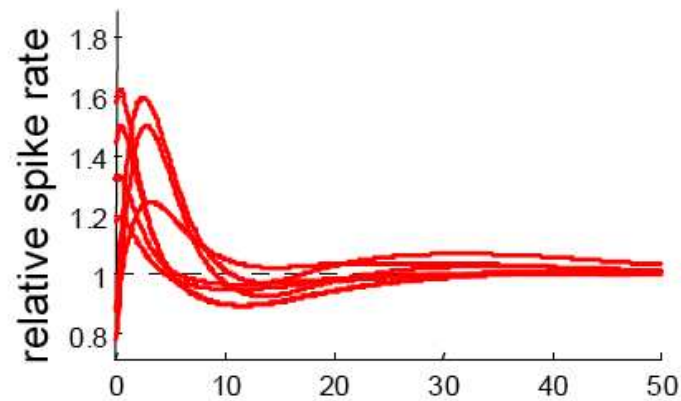
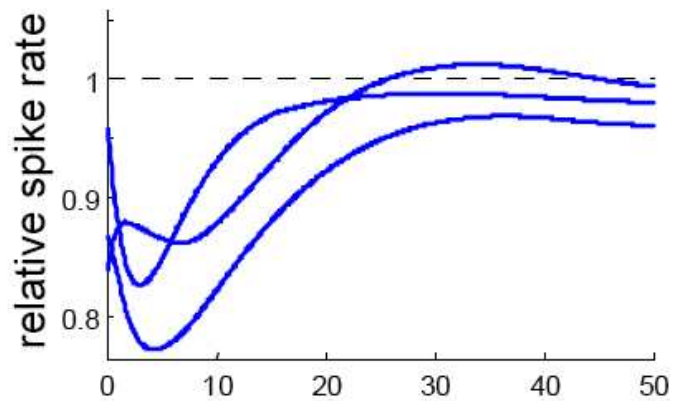
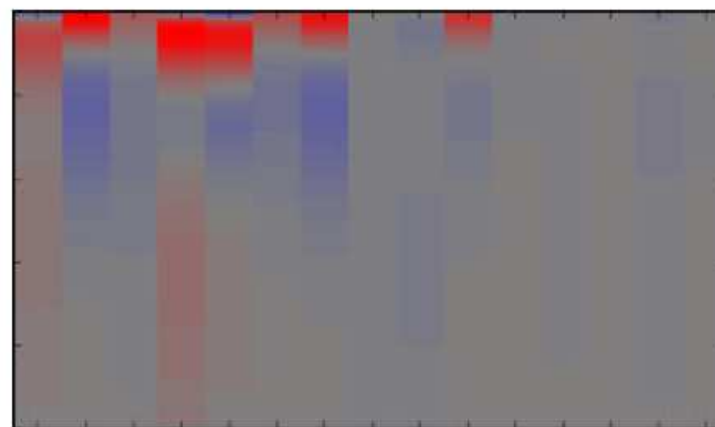
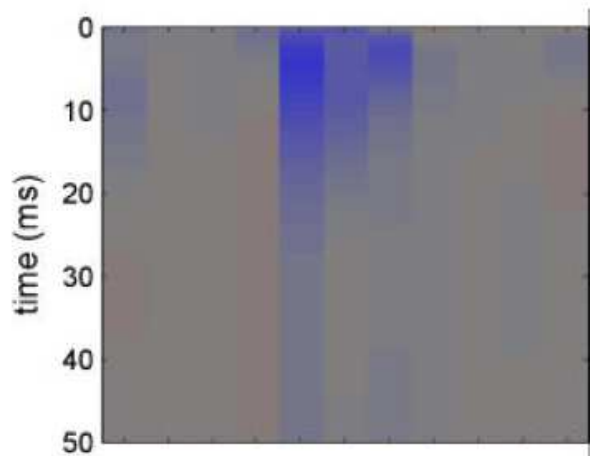
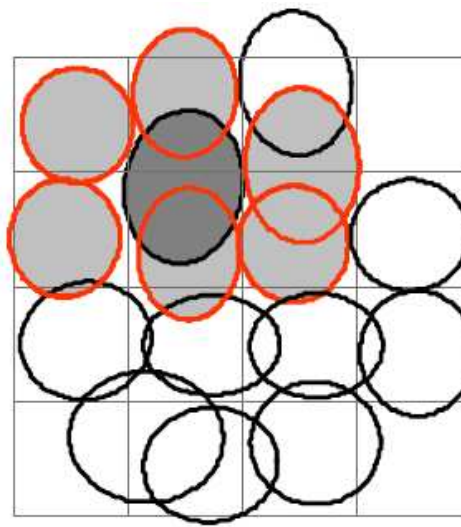
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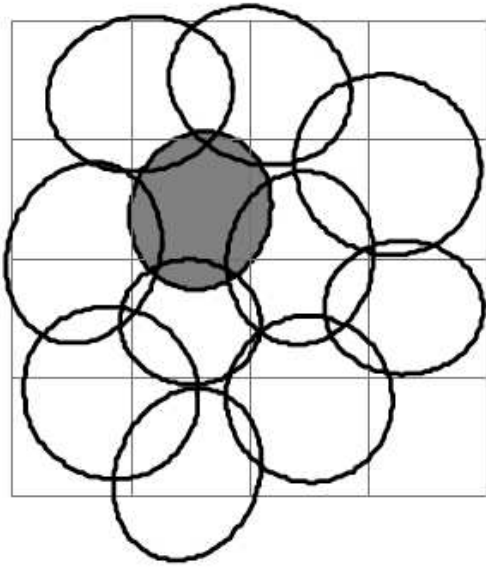
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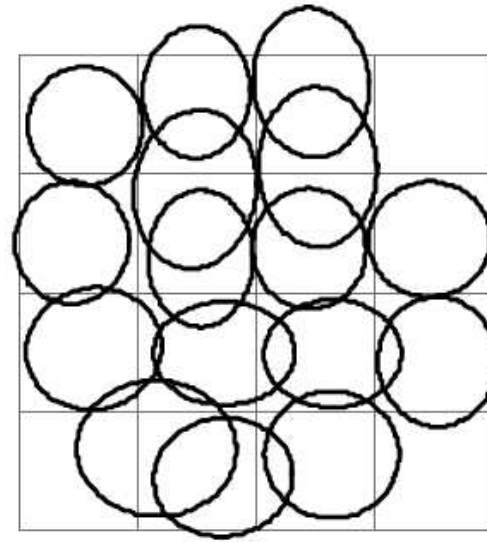
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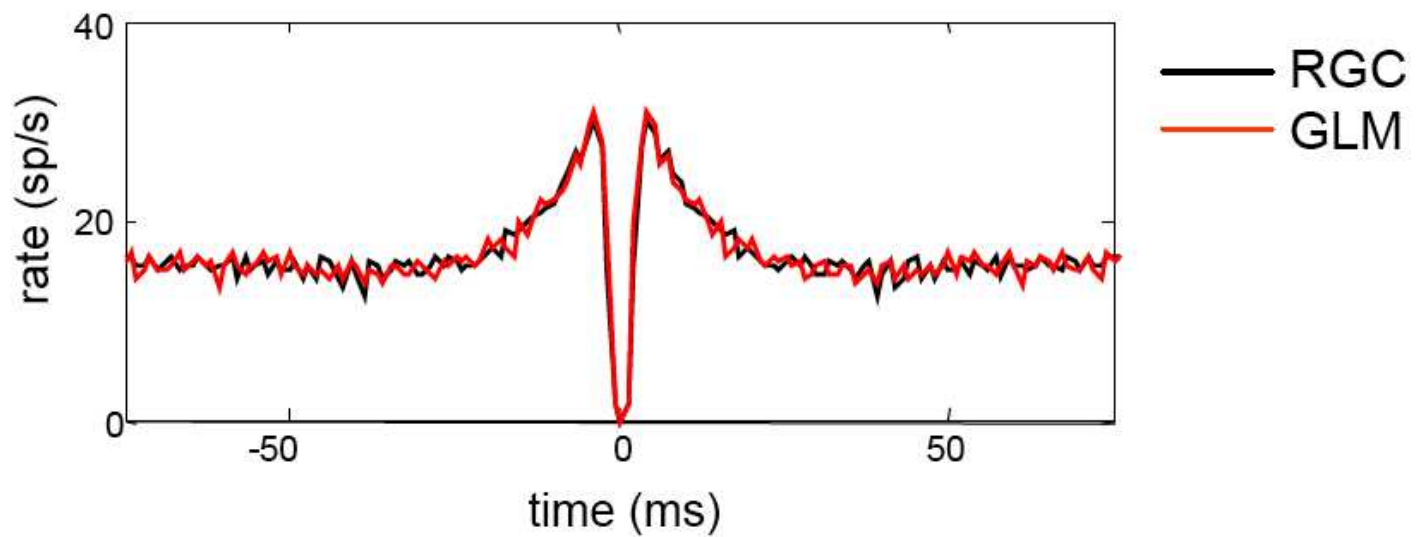
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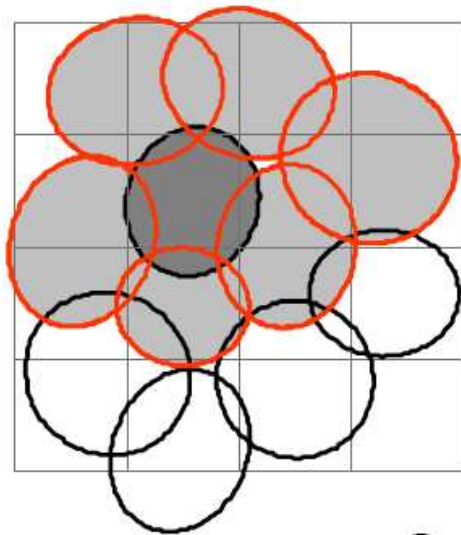
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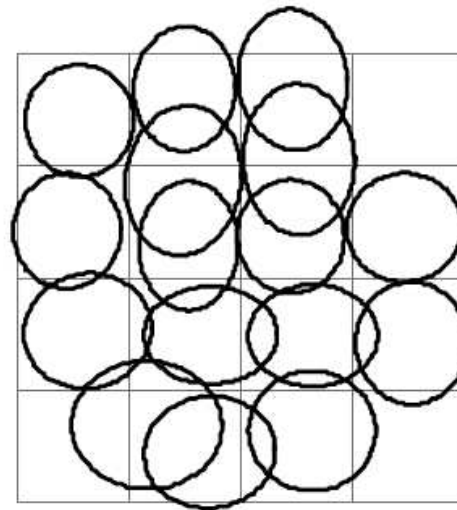
auto-correlation



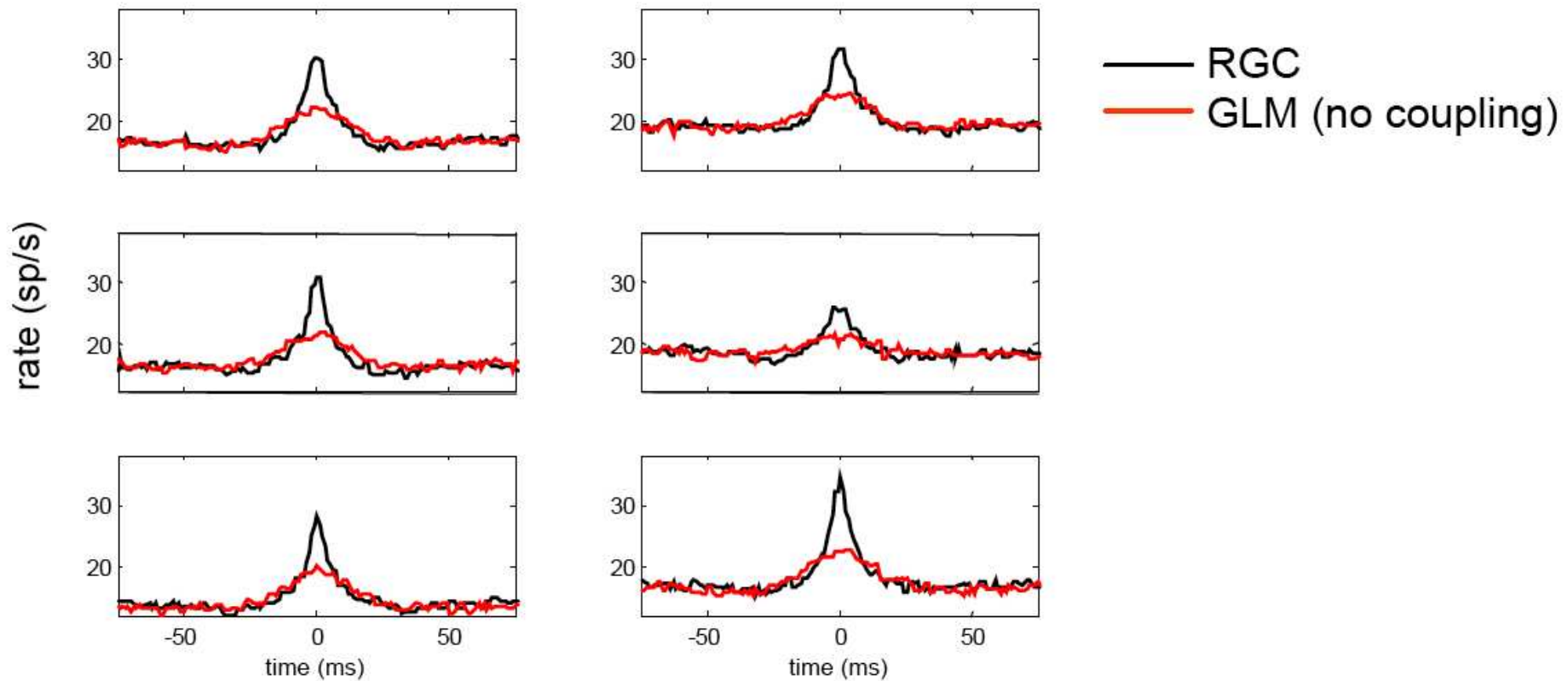
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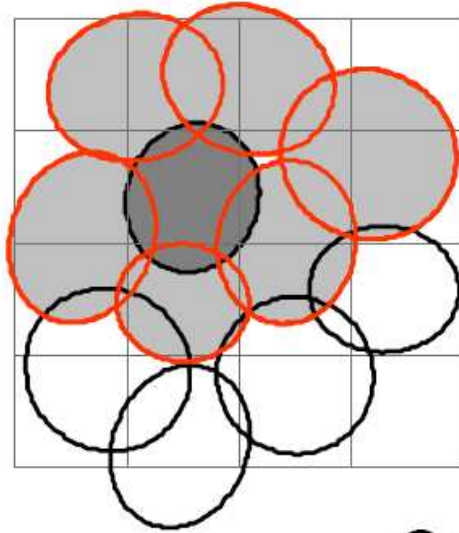
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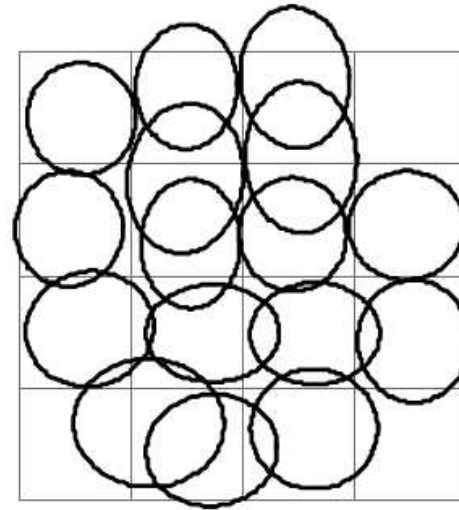
### Cross-Correlations



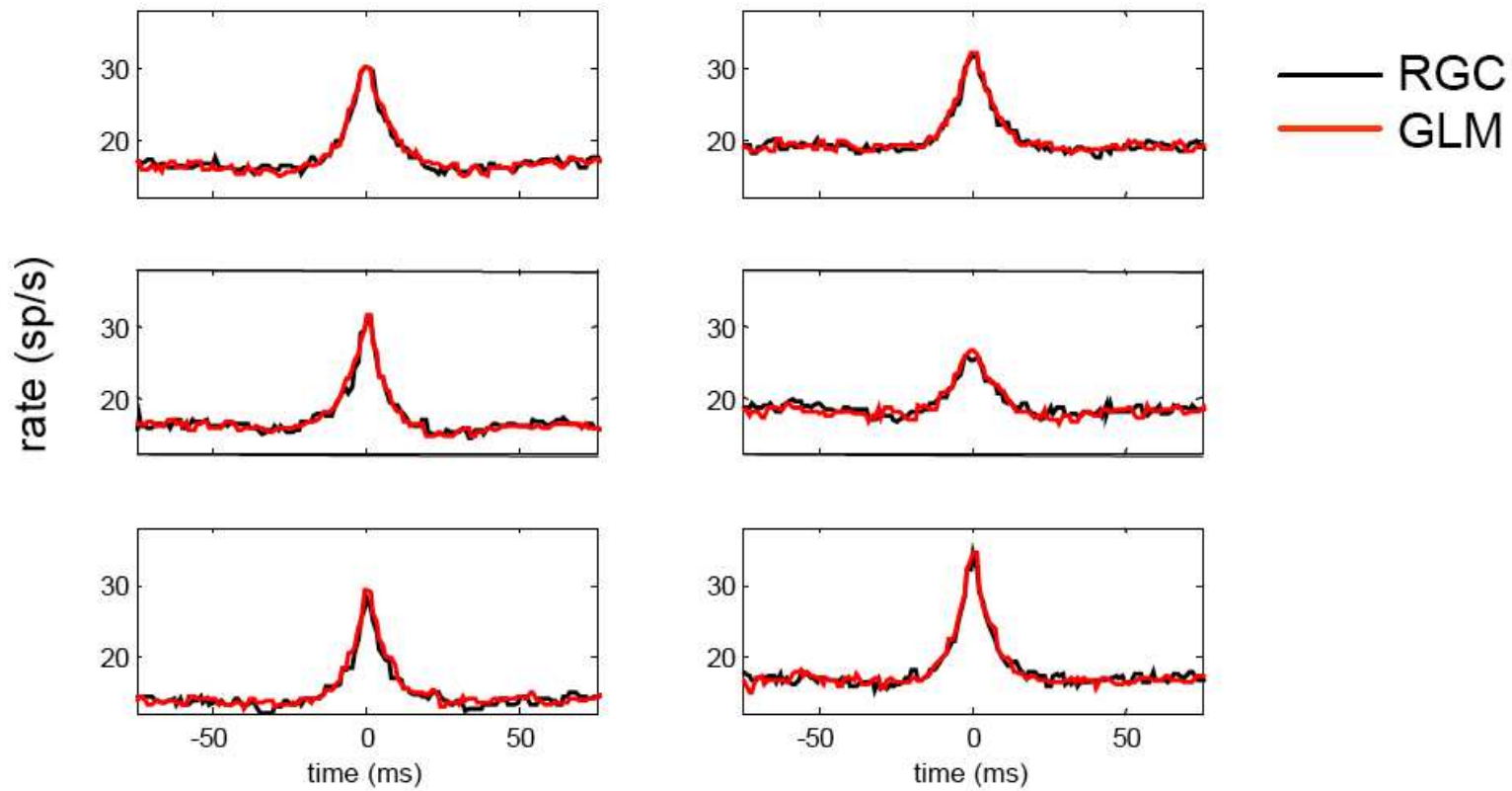
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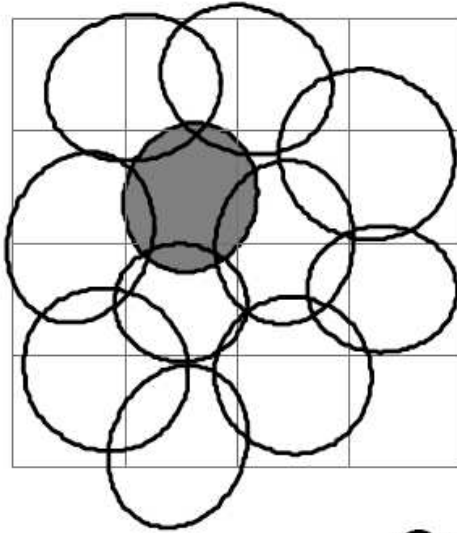
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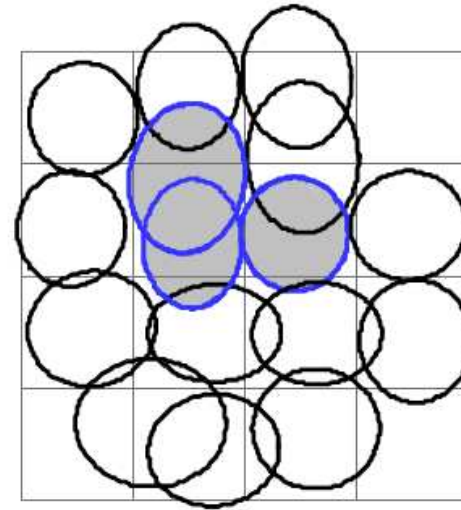
## Cross-Correlations



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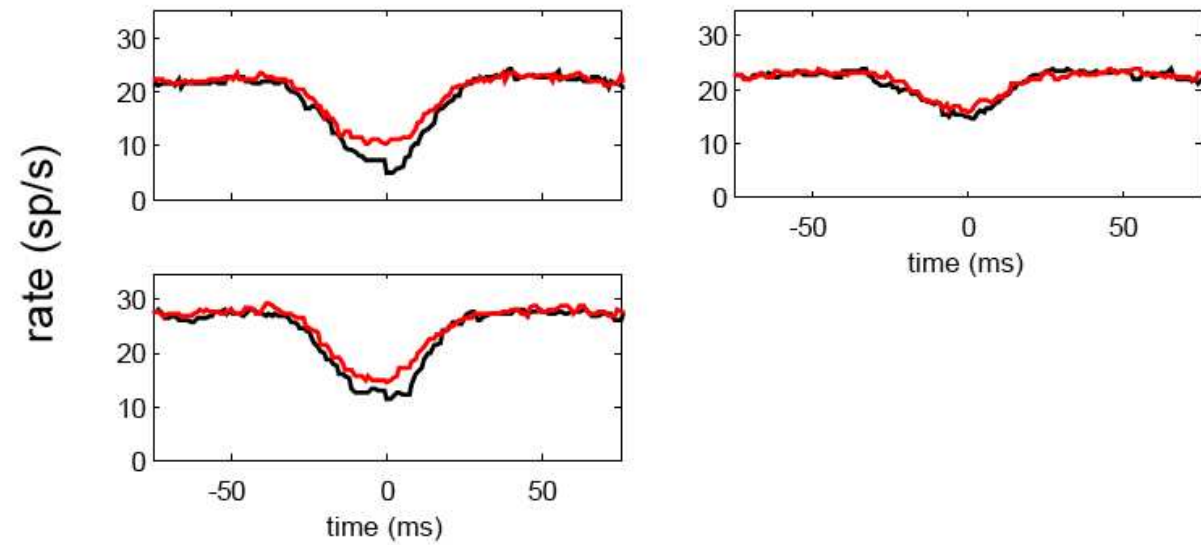


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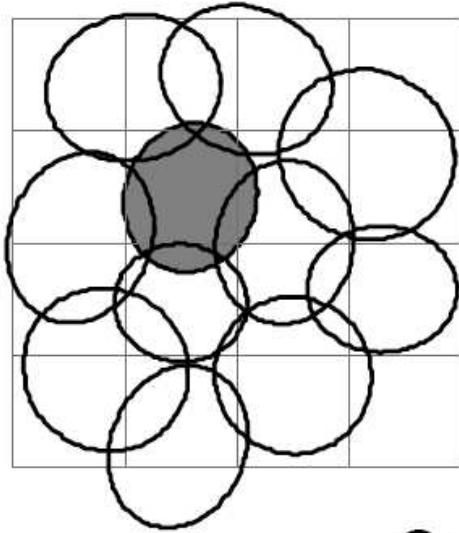


### Cross-Correlations

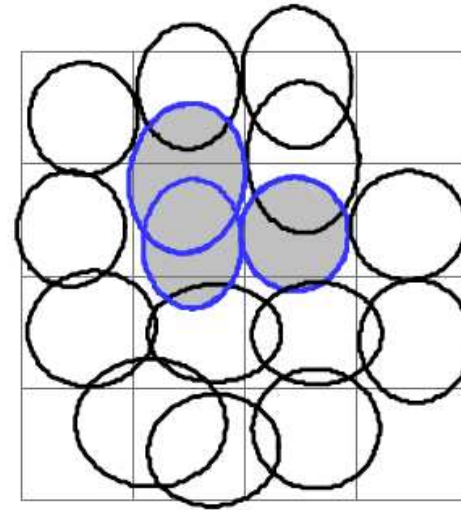
— RGC  
— GLM (no coupling)



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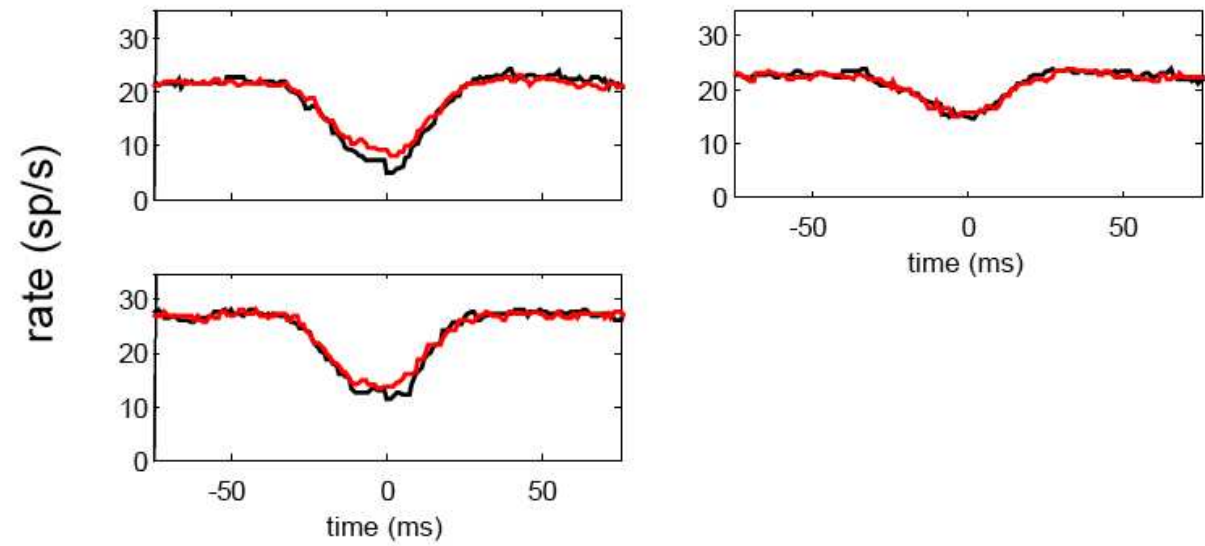


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### Cross-Correlations

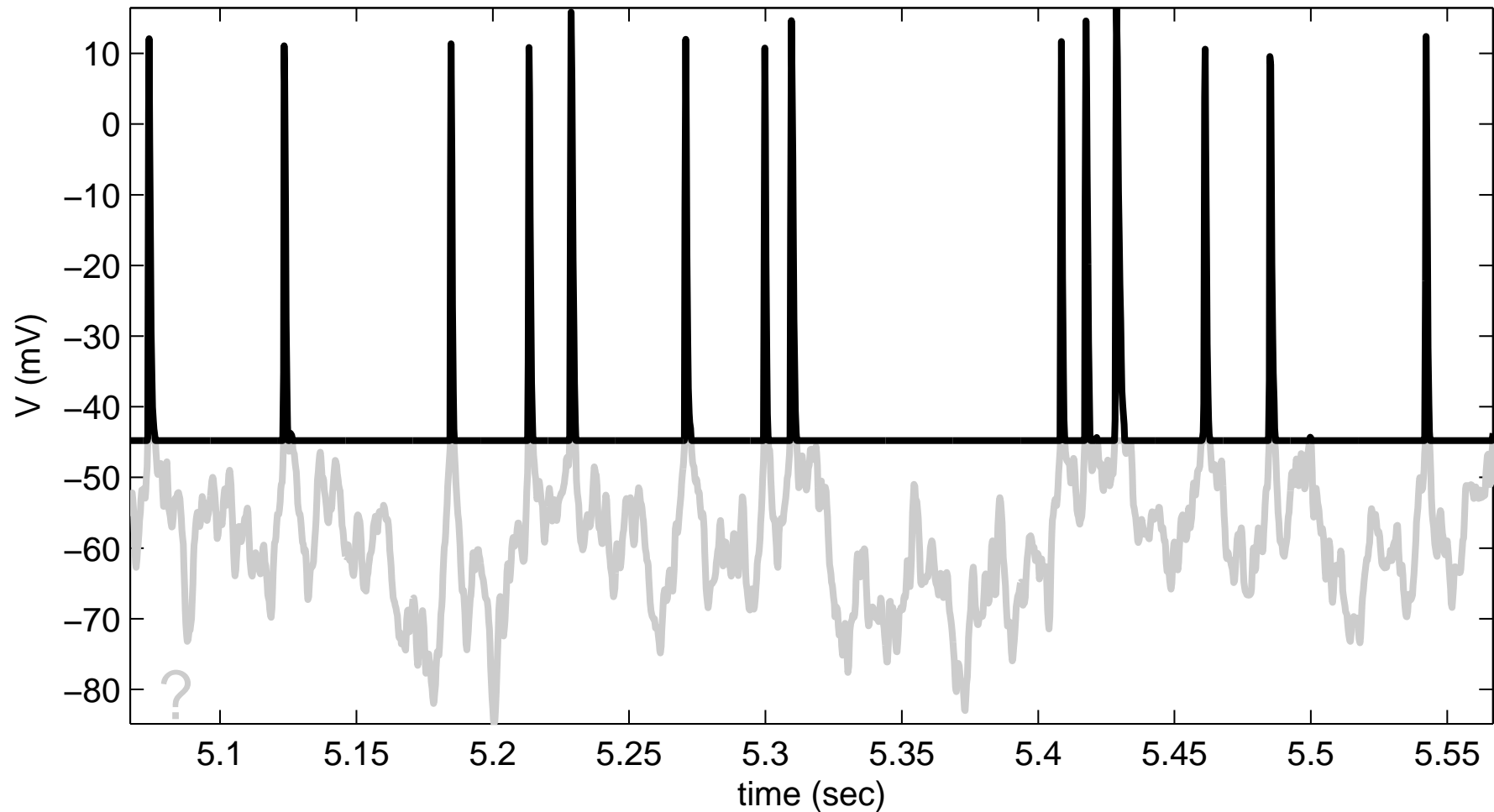
— RGC  
— GLM





# Part 2: Decoding subthreshold activity

Given extracellular spikes, what is most likely intracellular  $V(t)$ ?



# Computing $V_{ML}(t)$

Loglikelihood of  $V(t)$  (given LIF parameters, white noise  $N_t$ ):

$$L(\{V(t)\}_{0 \leq t \leq T}) = -\frac{1}{2\sigma^2} \int_0^T \left[ \dot{V}(t) - \left( -gV(t) + I(t) \right) \right]^2 dt$$

Constraints:

- Reset at  $t = 0$ :

$$V(0) = V_{reset}$$

- Spike at  $t = T$ :

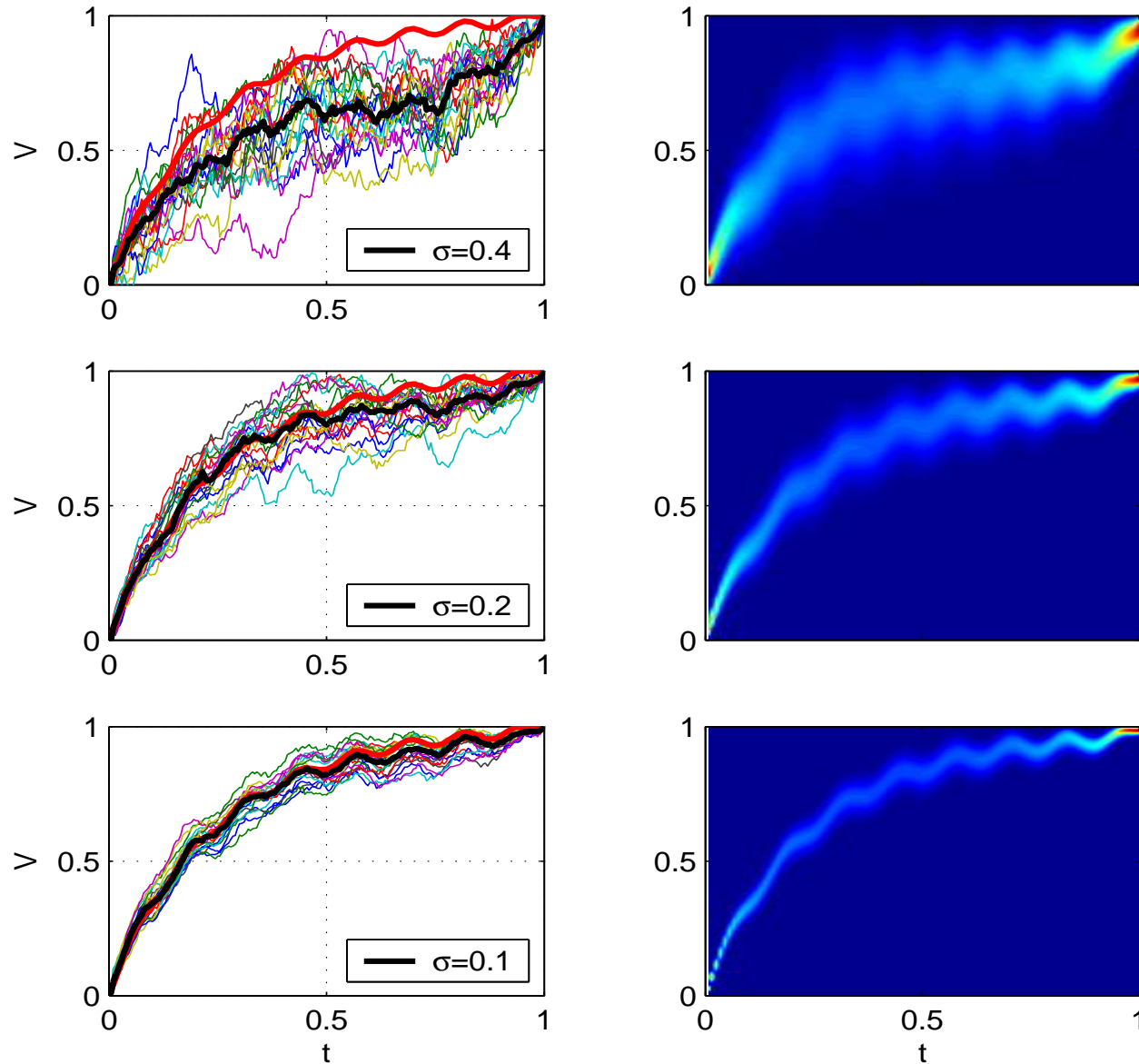
$$V(T) = V_{th}$$

- No spike for  $0 < t < T$ :

$$V(t) < V_{th}$$

Quadratic programming problem: optimize quadratic function under linear constraints. **Concave**: unique global optimum.

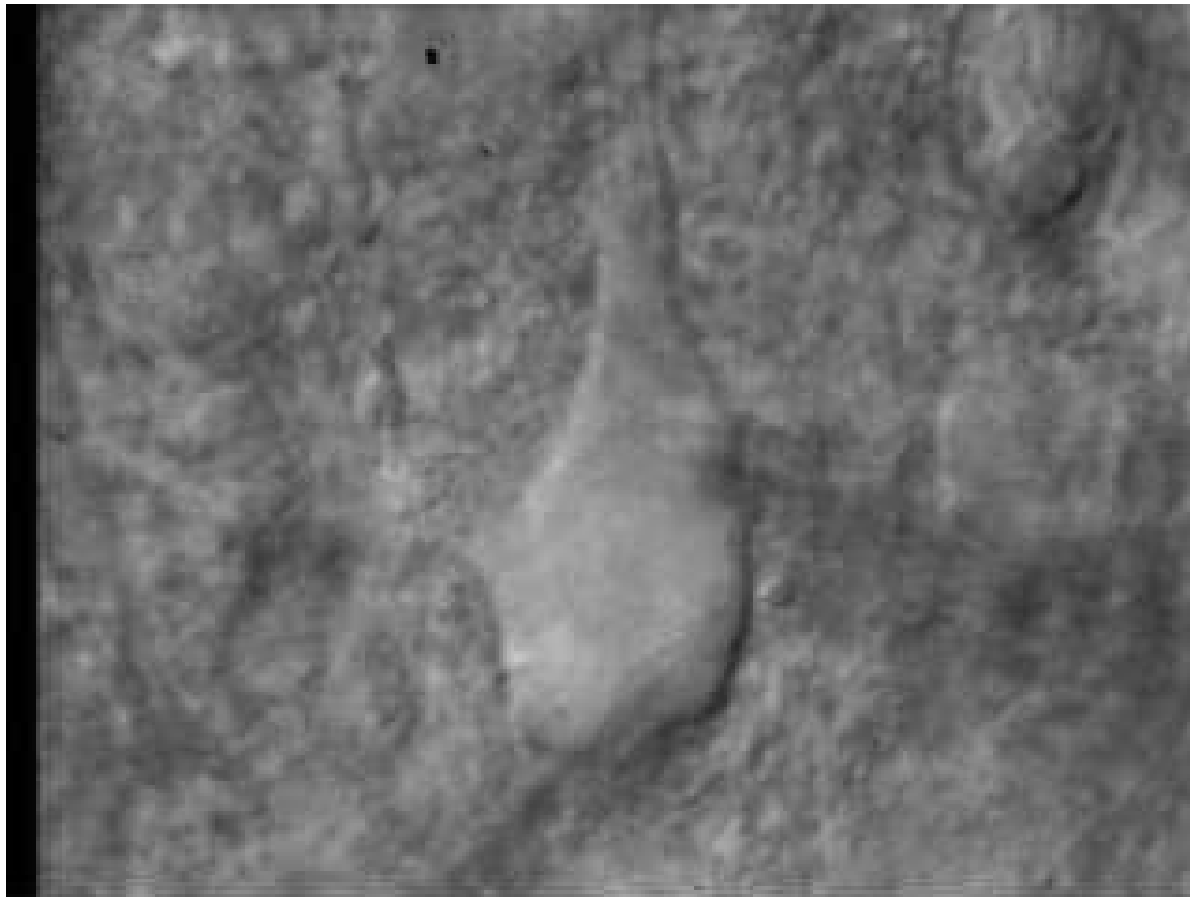
# Most likely vs. average $V(t)$



(Applications to spike-triggered average (Paninski, 2005a; Paninski, 2005b))

# Application: *in vitro* data

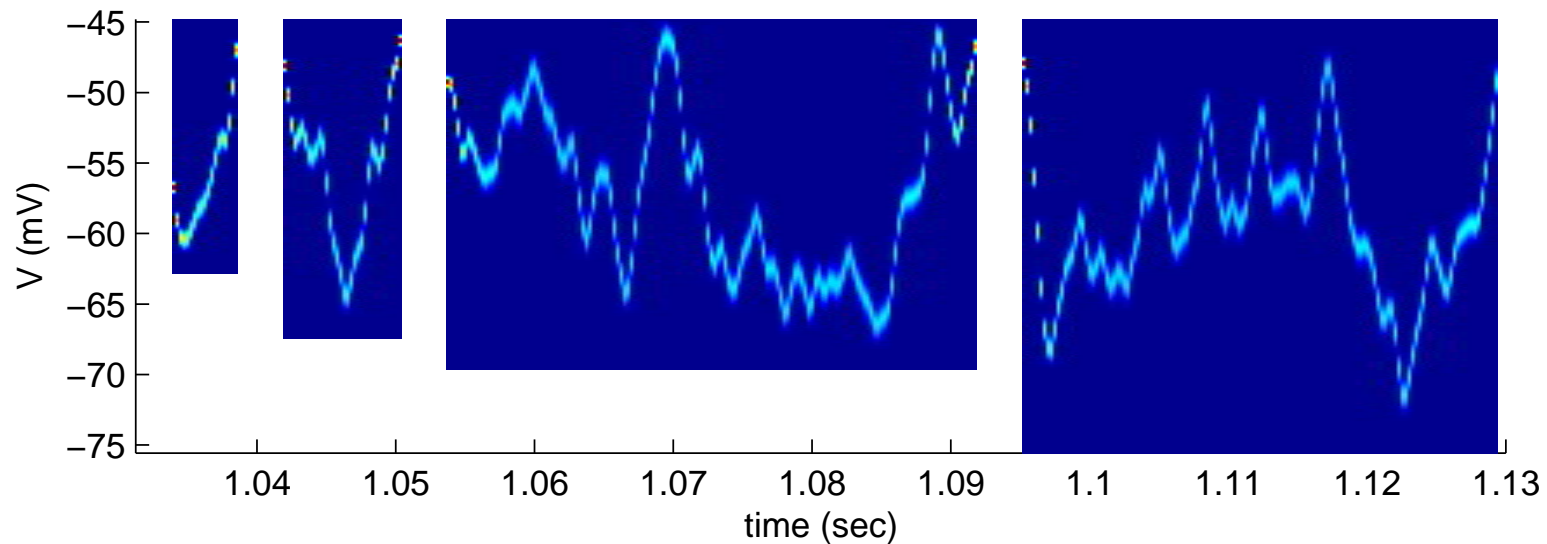
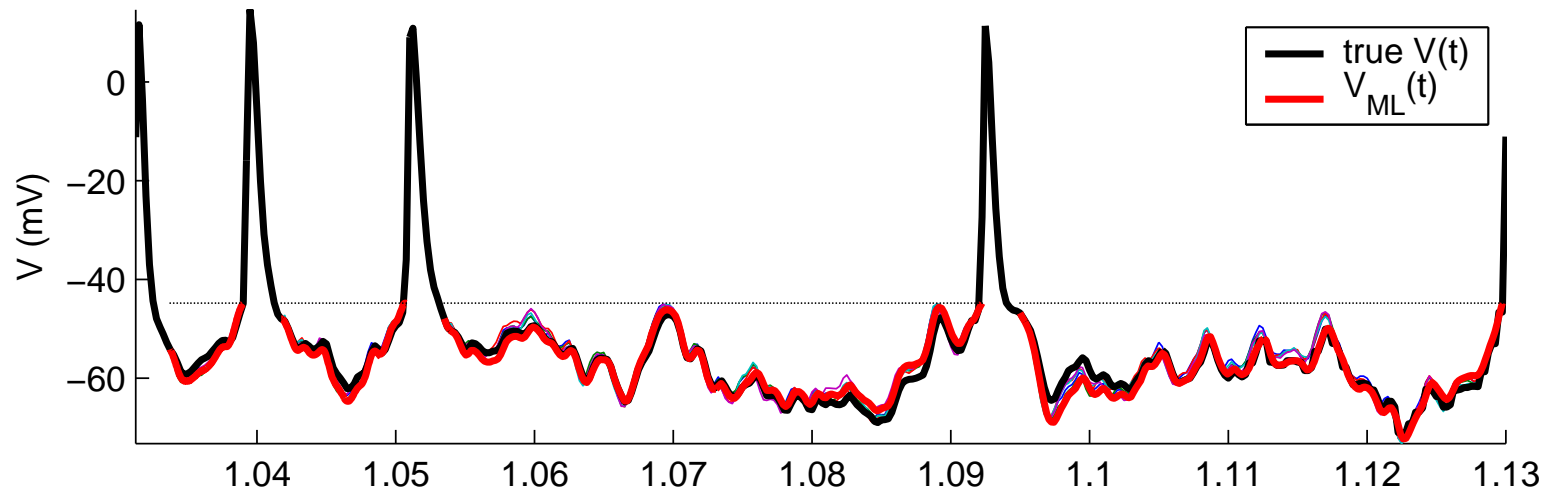
Recordings: rat sensorimotor cortical slice; dual-electrode whole-cell



Stimulus: Gaussian white noise current  $I(t)$

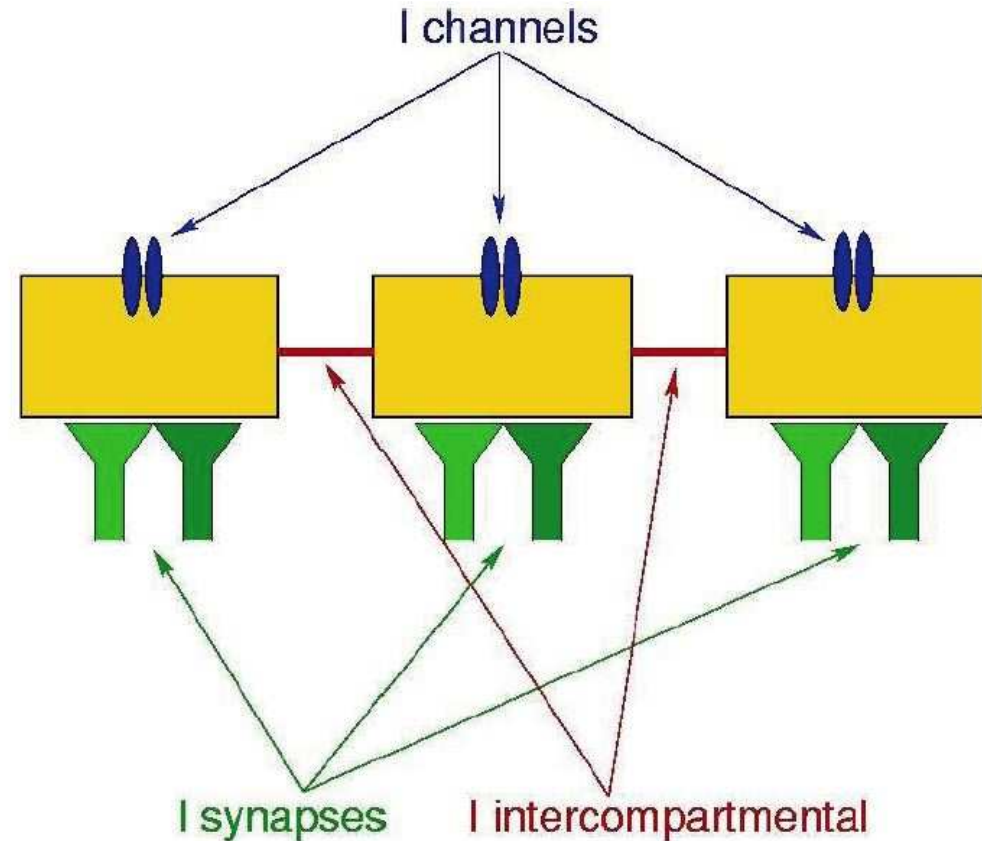
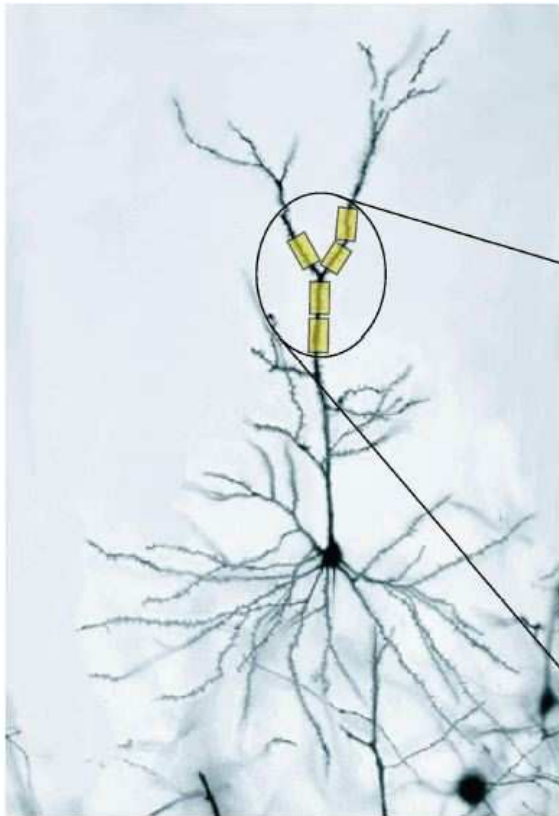
Analysis: fit IF model parameters  $\{g, \vec{k}, h(\cdot), V_{th}, \sigma\}$  by maximum likelihood (Paninski et al., 2003; Paninski et al., 2004a), then compute  $V_{ML}(t)$

# Application: *in vitro* data



$P(V(t)|\{t_i\}, \hat{\theta}_{ML}, \vec{x})$  computed via forward-backward hidden Markov model method (Paninski, 2005a).

# Part 3: Back to detailed models



Can we recover detailed biophysical properties?

- Active: membrane channel densities
- Passive: axial resistances, “leakiness” of membranes
- Dynamic: spatiotemporal synaptic input

# Conductance-based models

$$C \frac{dV_i}{dt} = I_i^{\text{channels}} + I_i^{\text{synapses}} + I_i^{\text{intercompartmental}}$$

$$I_i^{\text{channels}} = \sum_c \bar{g}_c g_c(t) (E_c - V_i(t))$$

$$I_i^{\text{synapses}} = \sum_s (\xi_s * k_s)(t) (E_s - V_i(t))$$

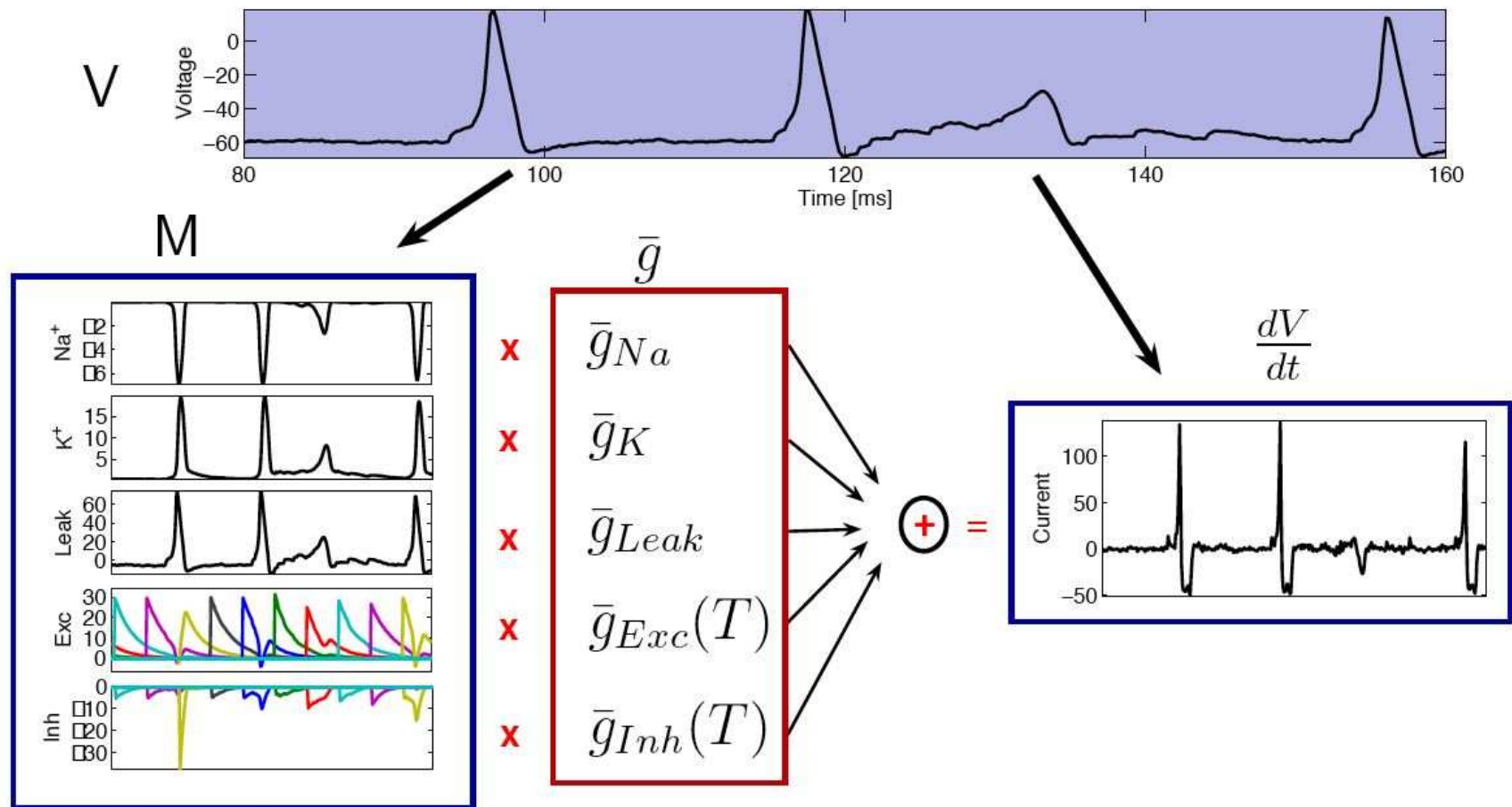
$$I_i^{\text{intercompartmental}} = \sum_a g_a \Delta V_a(t)$$

Key point: **if** we observe full  $V_i(t)$  + cell geometry, channel kinetics known + current noise is log-concave,

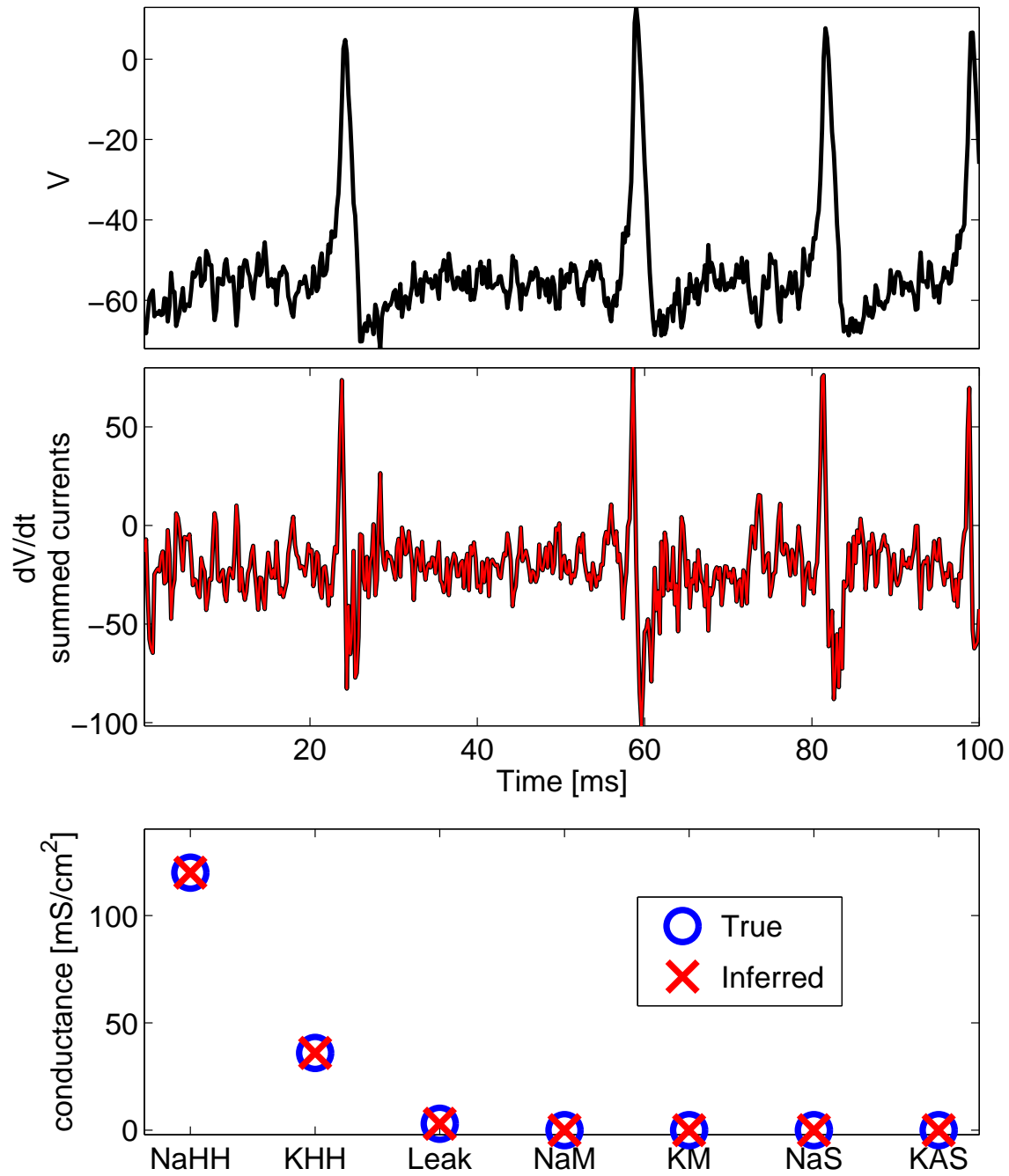
**then** loglikelihood of unknown parameters is concave.

Gaussian noise  $\implies$  standard nonnegative regression (albeit high-d).

# Estimating channel densities from $V(t)$

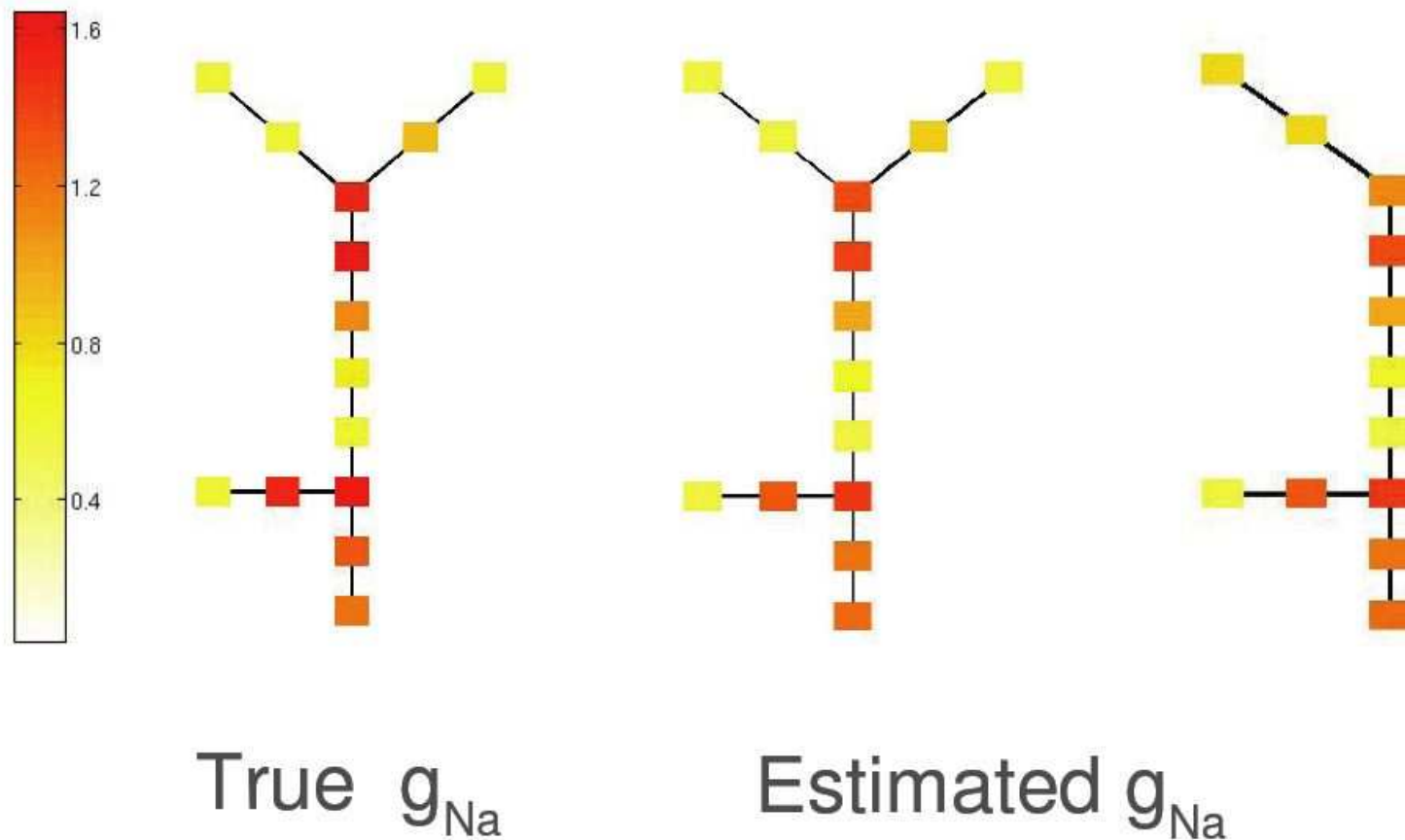




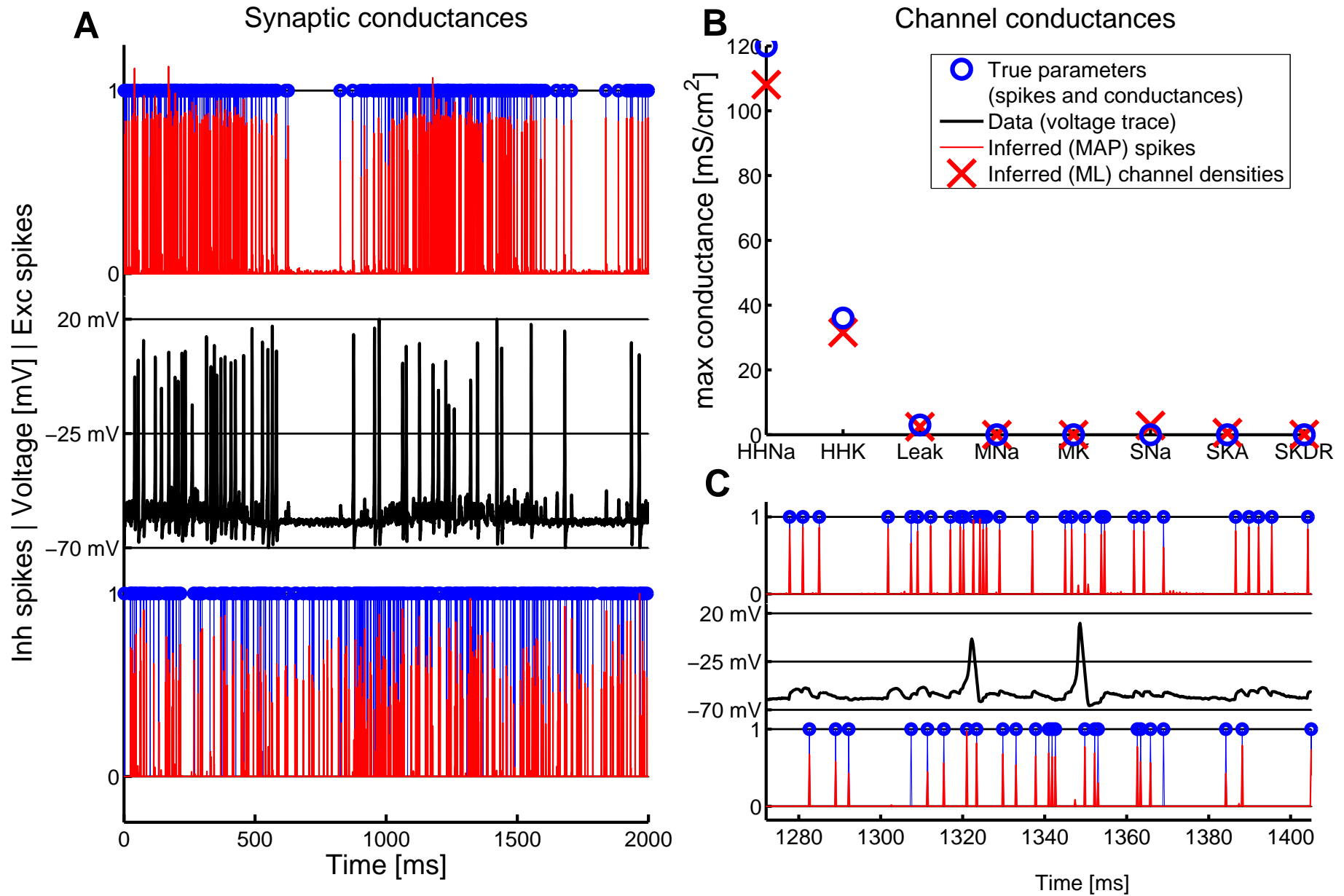


# Estimating non-homogeneous channel densities and axial resistances from spatiotemporal voltage recordings

$$I_i^{\text{channels}} = \sum_c \bar{g}_c g_c(t) (E_c - V_i(t))$$



# Estimating synaptic inputs given $V(t)$



# Collaborators

Theory and numerical methods

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Motor cortex physiology

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Retinal physiology

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Cortical *in vitro* physiology

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