Coding and computation by neural ensembles in the primate retina

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— with J. Pillow (UT Austin), E. Simoncelli (NYU), E.J. Chichilnisky, J. Gauthier, J. Shlens (Salk), E. Lalor (TC Dublin), S. Koyama (CMU), Y. Ahmadian, J. Kulkarni, H. Liu, T. Machado, D. Pfau, X. Pitkow, M. Vidne (Columbia).

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The coming statistical neuroscience decade

Some notable recent developments:

- machine learning / statistics methods for extracting information from high-dimensional data in a computationally-tractable, systematic fashion
- computing (Moore's law, massive parallel computing)
- optical methods (eg two-photon, FLIM) and optogenetics (channelrhodopsin, viral tracers, "brainbow")
- high-density multielectrode recordings (Litke's 512-electrode retinal readout system; Shepard's 65,536-electrode active array)

Some exciting open challenges

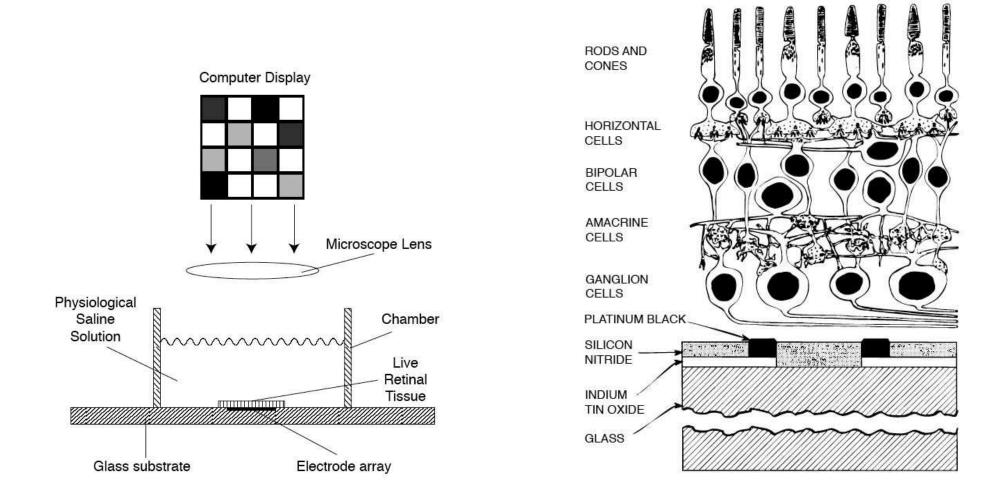
- inferring biophysical neuronal properties from noisy recordings
- reconstructing the full dendritic spatiotemporal voltage from noisy, subsampled observations
- estimating subthreshold voltage given superthreshold spike trains
- extracting spike timing from slow, noisy calcium imaging data
- reconstructing presynaptic conductance from postsynaptic voltage recordings
- inferring connectivity from large populations of spike trains
- decoding behaviorally-relevant information from spike trains
- optimal control of neural spike timing

— to solve these, we need to combine the two classical branches of computational neuroscience: dynamical systems and neural coding

Retinal ganglion neuronal data

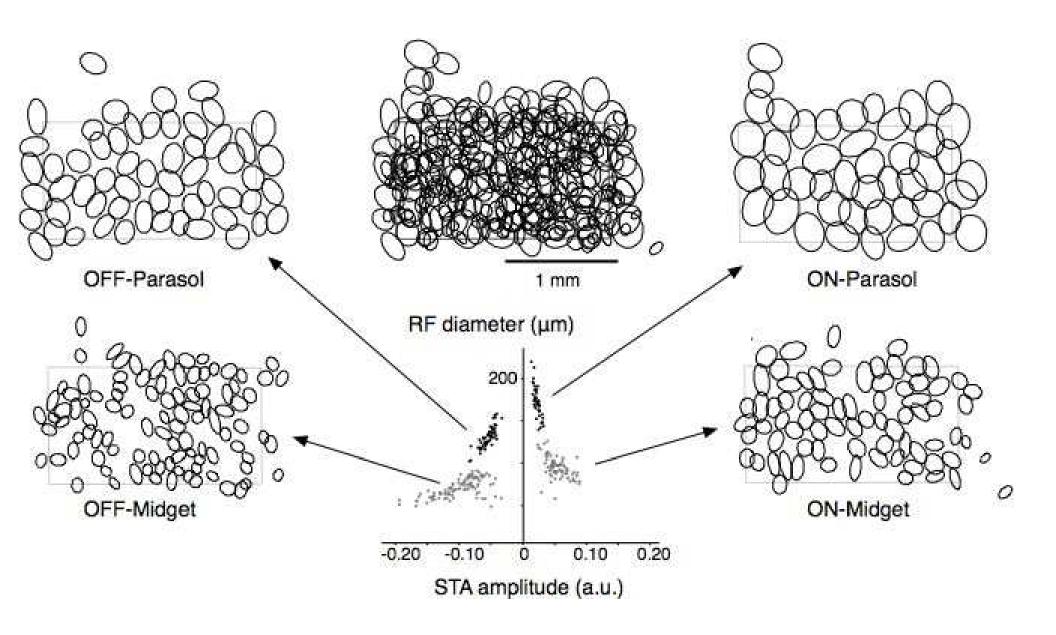
Preparation: dissociated macaque retina

— extracellularly-recorded responses of populations of RGCs

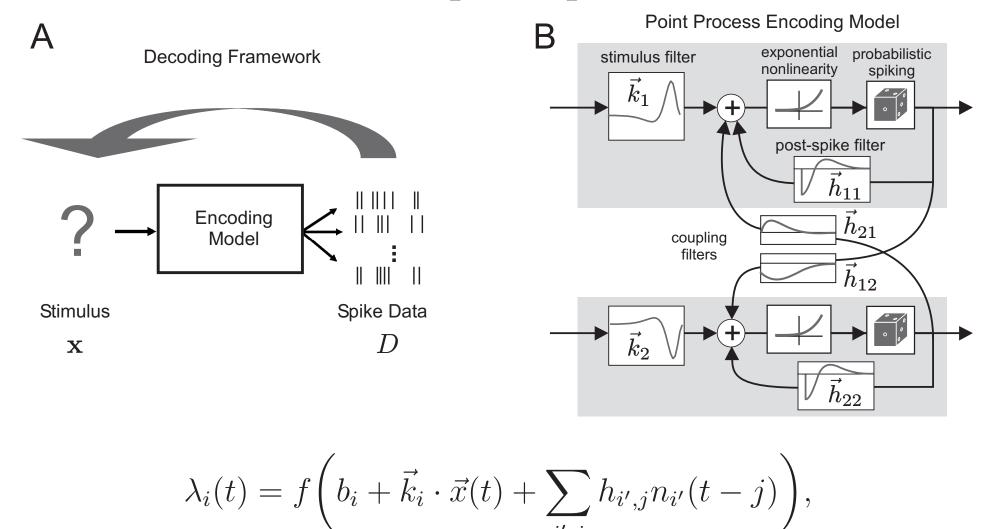


Stimulus: random spatiotemporal visual stimuli (Pillow et al., 2008)

Receptive fields tile visual space



Multineuronal point-process model

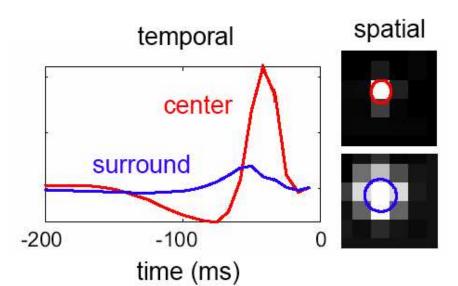


- likelihood is easy to compute and to maximize (concave optimization) (Paninski, 2004; Truccolo et al., 2005; Pillow et al., 2008)
- close connections to noisy integrate-and-fire model

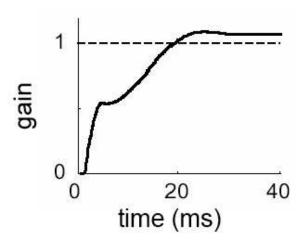
ON cells

OFF cells

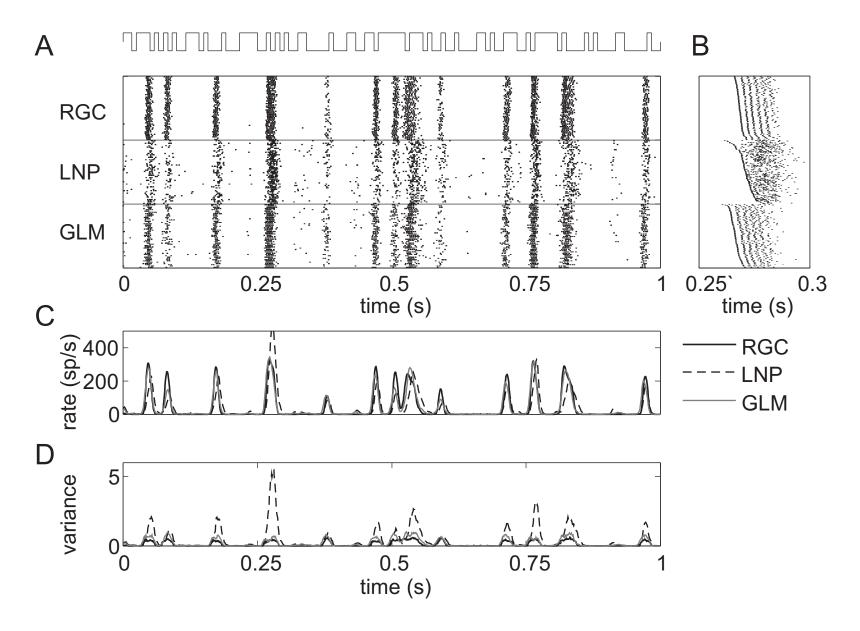
stimulus filter



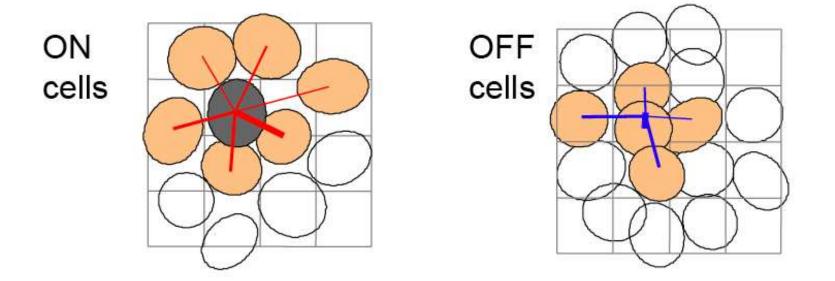
post-spike filter



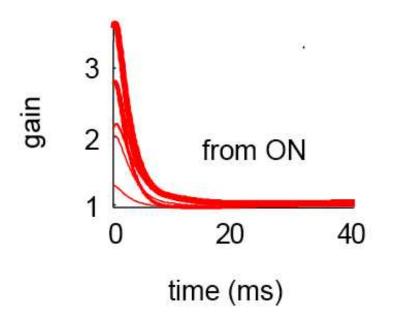
Predicting single-neuron responses

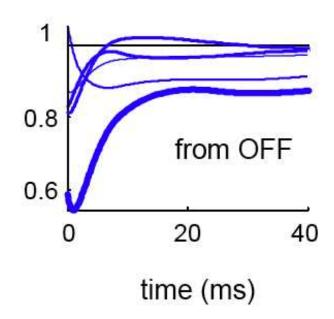


— model captures high precision of retinal responses.

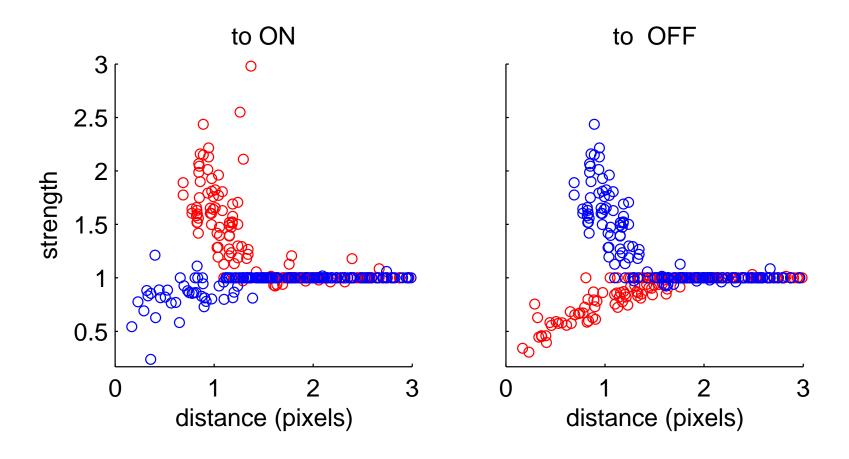


coupling filters

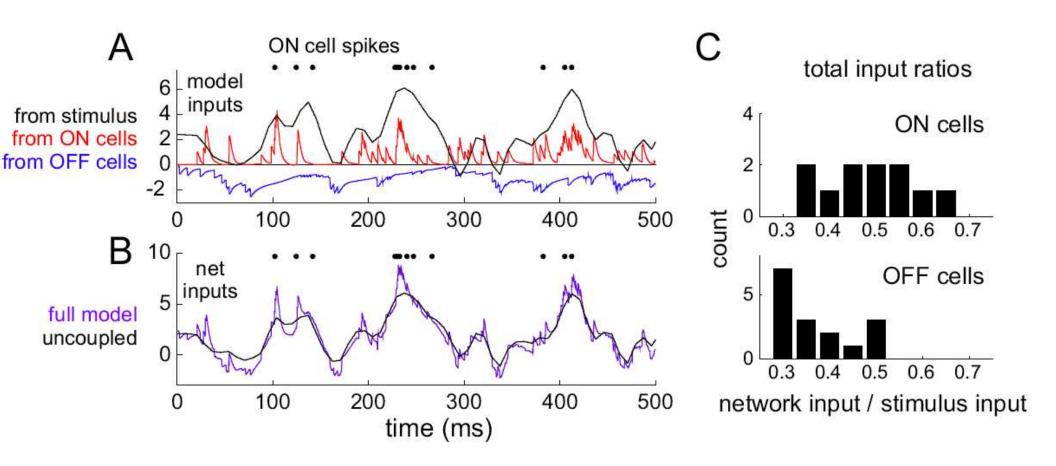




Nearest-neighbor effective connectivity

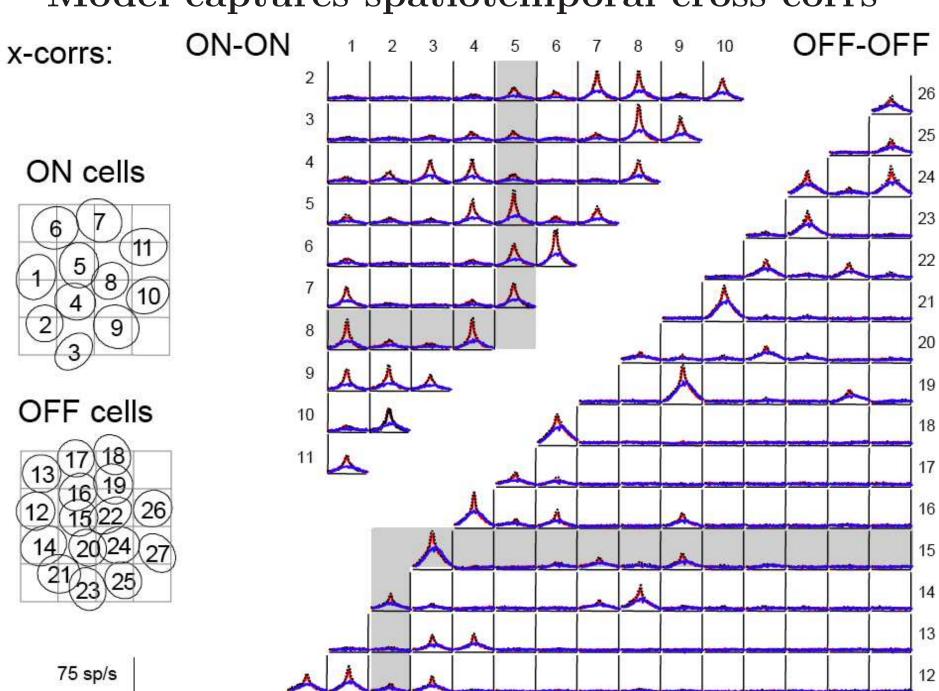


Network vs. stimulus drive



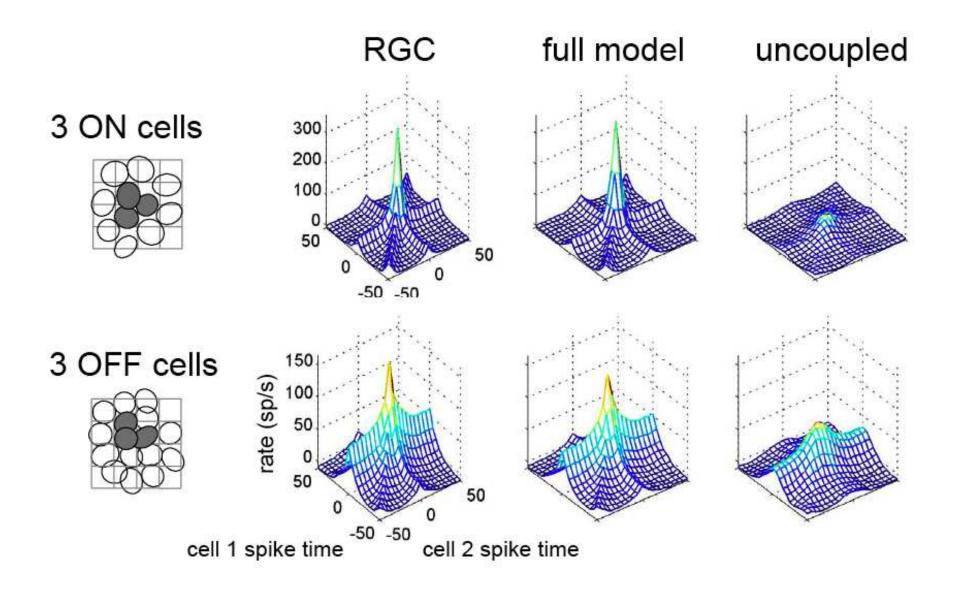
— Network effects are $\approx 50\%$ as strong as stimulus effects

Model captures spatiotemporal cross-corrs



50 ms

Triplet correlations



Optimal Bayesian decoding

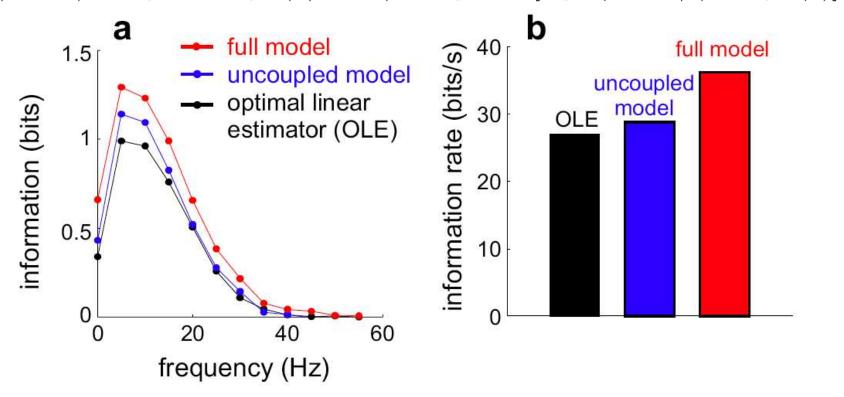
 $E(\vec{x}|spikes) \approx \arg\max_{\vec{x}} \log P(\vec{x}|spikes) = \arg\max_{\vec{x}} [\log P(spikes|\vec{x}) + \log P(\vec{x})]$

(Loading yashar-decode.mp4)

- Computational points:
 - $\log P(spikes|\vec{x})$ is concave in \vec{x} : concave optimization again.
 - Decoding can be done in linear time via standard Newton-Raphson methods, since Hessian of $\log P(\vec{x}|spikes)$ w.r.t. \vec{x} is banded (Pillow et al., 2009).

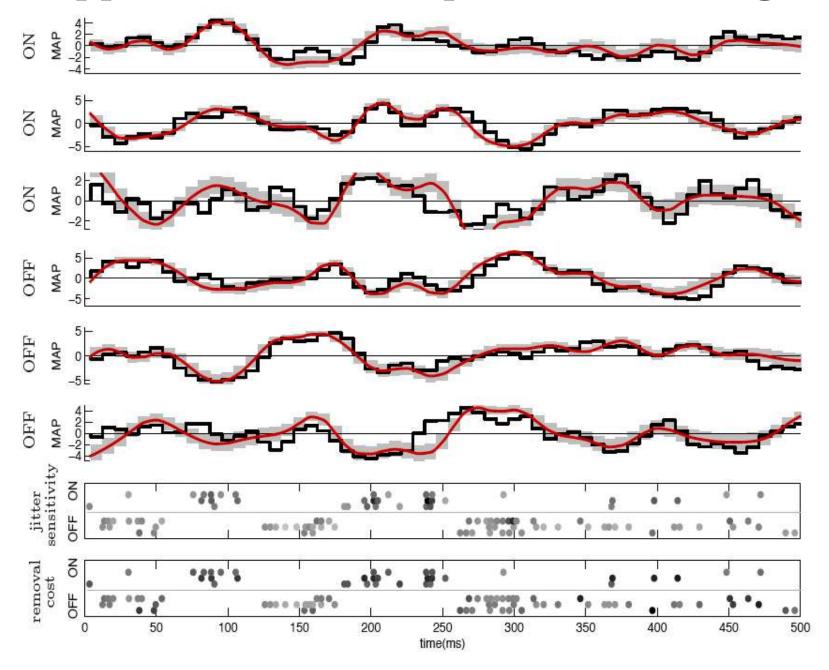
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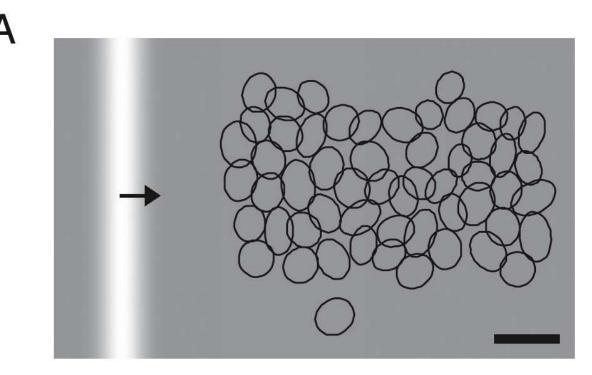
- Computational points:
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 - Decoding can be done in linear time via standard Newton-Raphson methods, since Hessian of $\log P(\vec{x}|spikes)$ w.r.t. \vec{x} is banded (Pillow et al., 2009).
- Biological point: paying attention to correlations improves decoding accuracy.

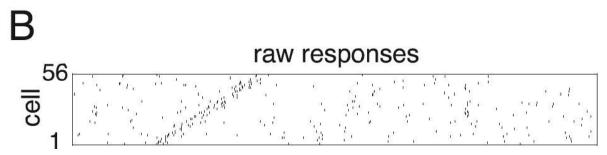
Application: how important is timing?



— Fast decoding methods let us look more closely (Ahmadian et al., 2010)

Application: optimal velocity decoding





Bayesian estimate requires us to integrate out unknown image I:

$$p(v|spikes) \propto p(v)p(spikes|v) = p(v) \int p(I)p(spikes|v,I)dI;$$

(Frechette et al., 2005; Lalor et al., 2009)

Application: image stabilization

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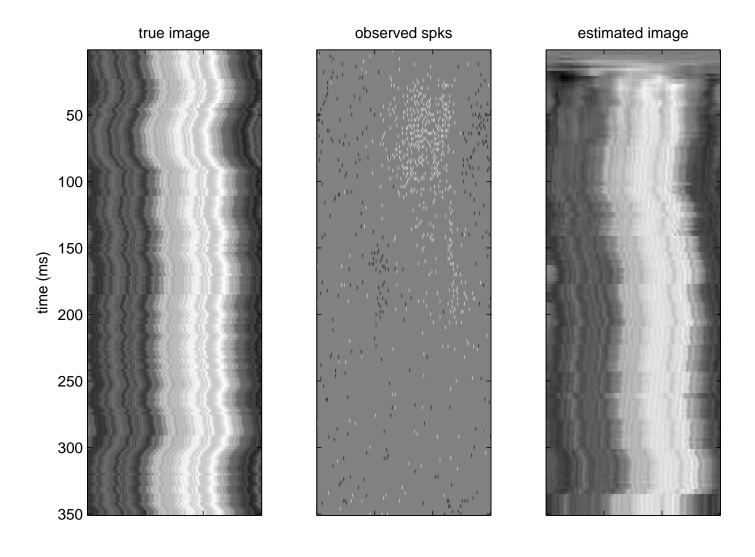
— from (Rossi and Roorda '09): quite a bit of motion in 1 sec.

Bayesian methods for image stabilization

Have to integrate out random eye movements:

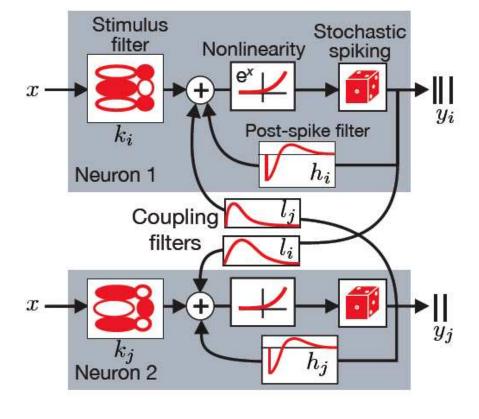
$$p(I|spikes) \propto p(I)p(spikes|I) = p(I) \int p(spikes|e, I)p(e)de;$$

e denotes eye path; integration by particle-filter methods.



Next steps: reconsidering the model

$$\lambda_i(t) = \exp\left(k_i \cdot x(t) + h_i \cdot y_i(t) + \sum_{i \neq j} l_{i,j} \cdot y_j(t)\right)$$



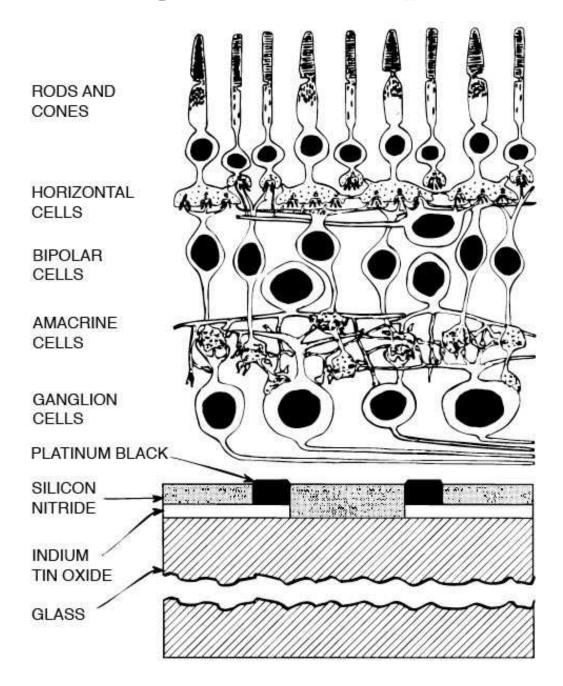
Pros:

- Tractable model-fitting and optimal decoding
- Captures response statistics

Cons:

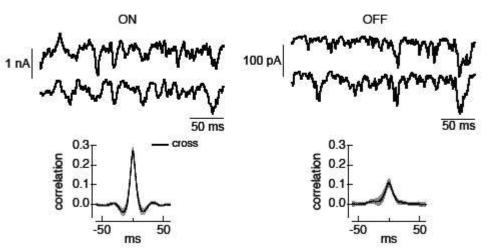
- Instantaneous coupling filters
- No explicit Common Input

Considering common input effects



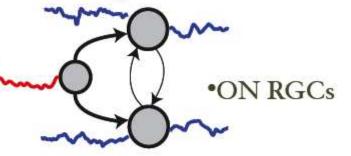
Intracellular findings:

 RGCs receive strongly correlated synaptic input in the absence of modulated light stimuli

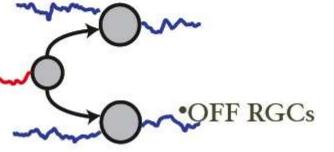


Khuc Trong & Rieke Nature Neuro 2008

• ON RGCs are weakly electrically coupled

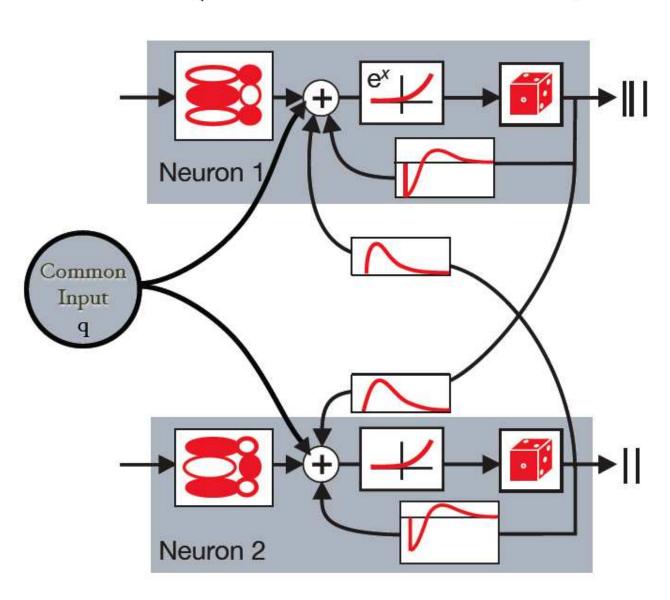


• No electrical coupling seen between OFF RGCs



Extension: including common input effects

$$\lambda_i(t) = \exp\left(k_i \cdot x(t) + h_i \cdot y_i(t) + \sum_{i \neq j} l_{i,j} \cdot y_j(t) + Lq(t)\right)$$



Direct state-space optimization methods

To fit parameters, optimize approximate marginal likelihood:

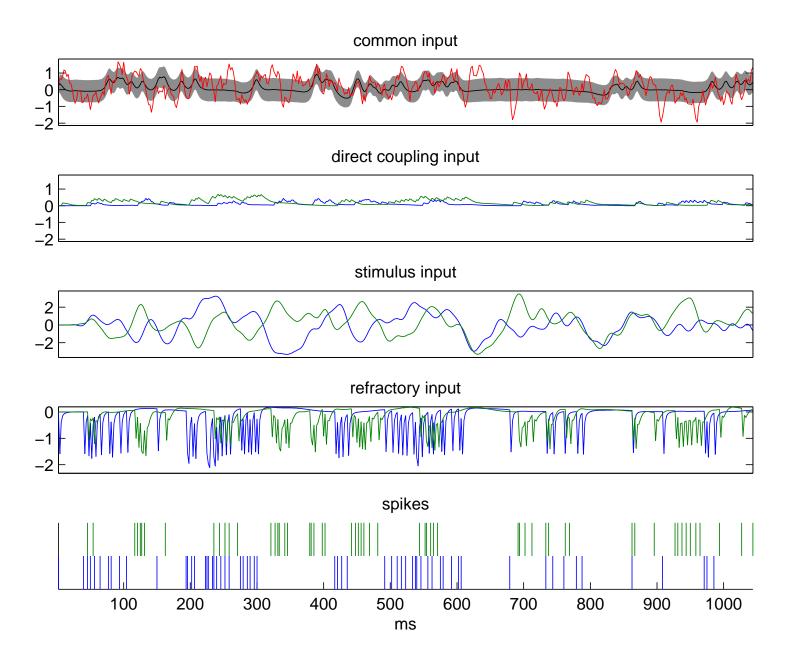
$$\log p(spikes|\theta) = \log \int p(Q|\theta)p(spikes|\theta,Q)dQ$$

$$\approx \log p(\hat{Q}_{\theta}|\theta) + \log p(spikes|\hat{Q}_{\theta}) - \frac{1}{2}\log|J_{\hat{Q}_{\theta}}|$$

$$\hat{Q}_{\theta} = \arg \max_{Q} \{\log p(Q|\theta) + \log p(spikes|Q)\}$$

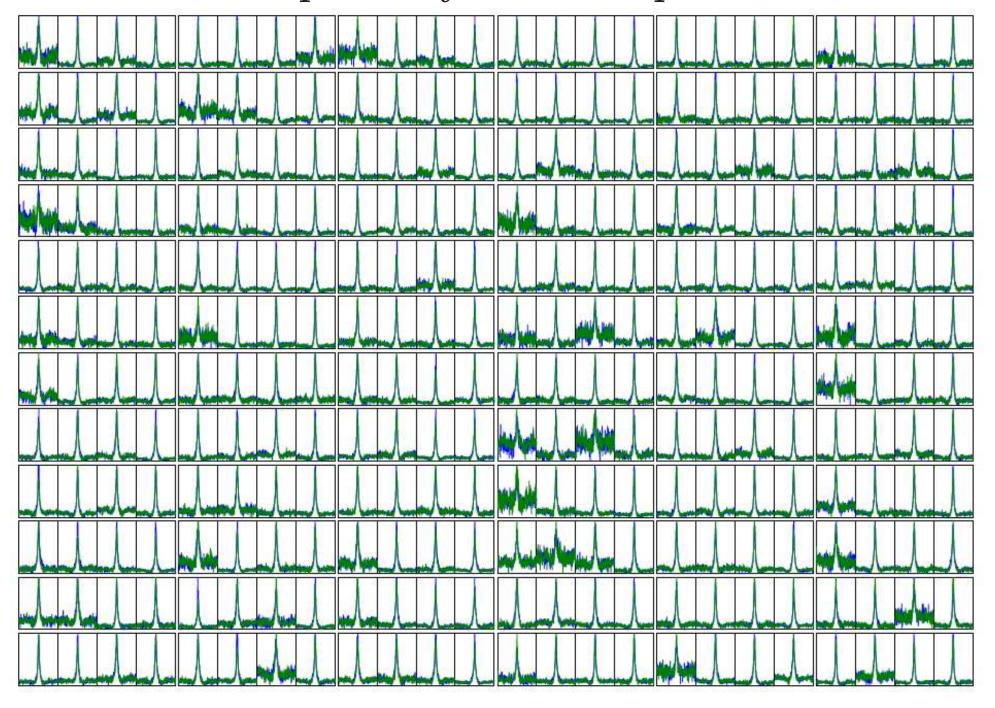
- Q is a very high-dimensional latent (unobserved) "common input" term. Taken to be a Gaussian process here with autocorrelation time ≈ 5 ms (Khuc-Trong and Rieke, 2008).
- correlation strength specified by one parameter per cell pair.
- all terms can be computed in O(T) via banded matrix methods (Paninski et al., 2010).

Inferred common input effects are strong

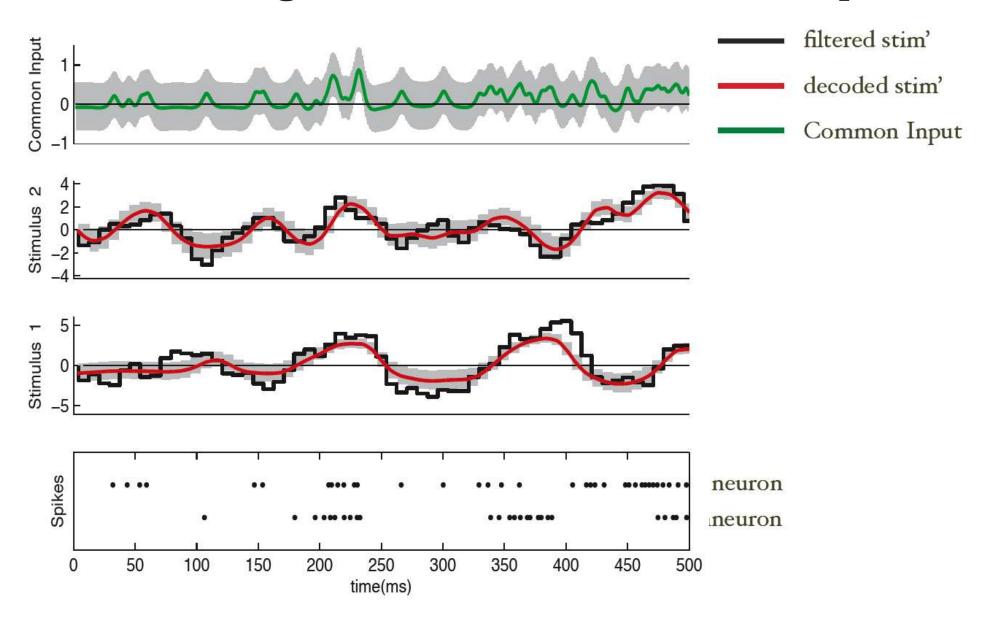


— note that inferred direct coupling effects are now relatively small.

Common-input-only model captures x-corrs

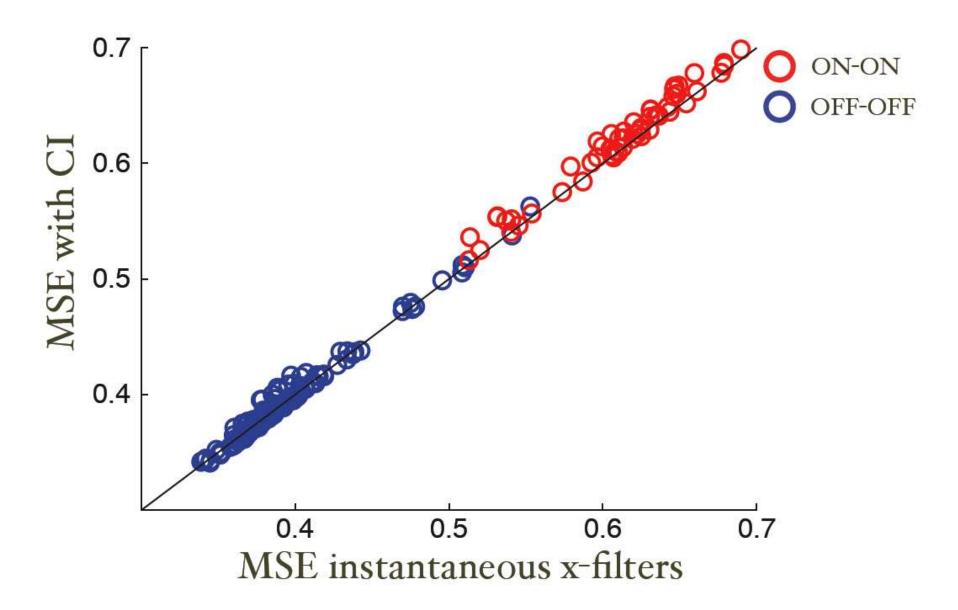


Decoding the stimulus and hidden input



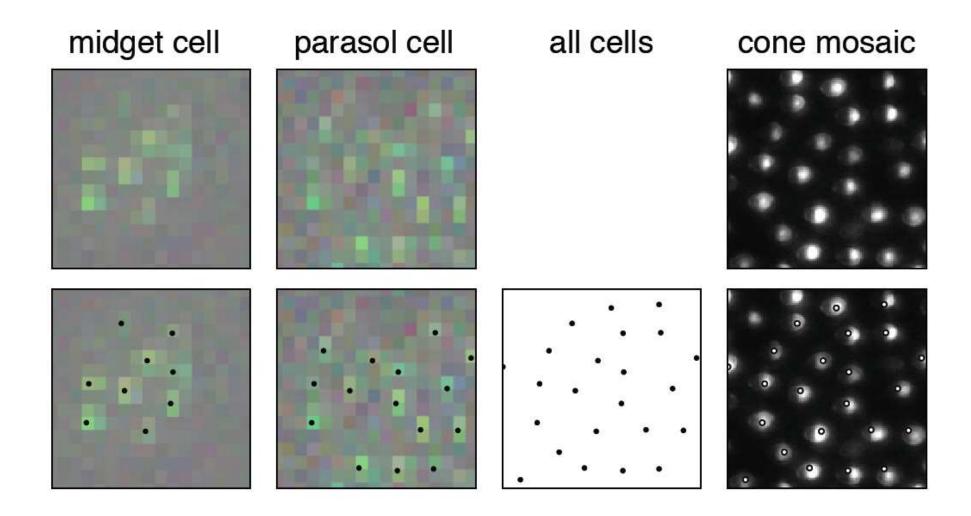
 $\arg\max_{\vec{x}} p(\vec{x}|y,\theta) = \arg\max_{\vec{x}} \int p(\vec{x},Q|y,\theta) dQ \approx \arg\max_{\vec{x},Q} p(\vec{x},Q|y,\theta)$

Models lead to similar decoding performance



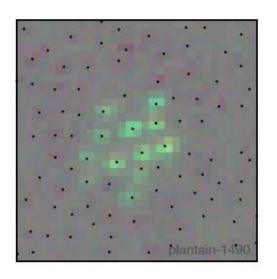
...but CI model is more robust to spike jitter and deletions (Vidne et al. 2010).

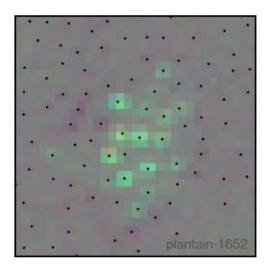
Next steps: inferring cones



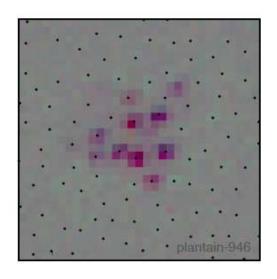
[—] cone locations and color identity can be inferred accurately with high spatial-resolution stimuli via maximum a posteriori estimates.

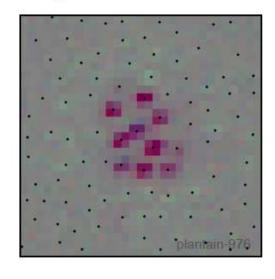
ON midget



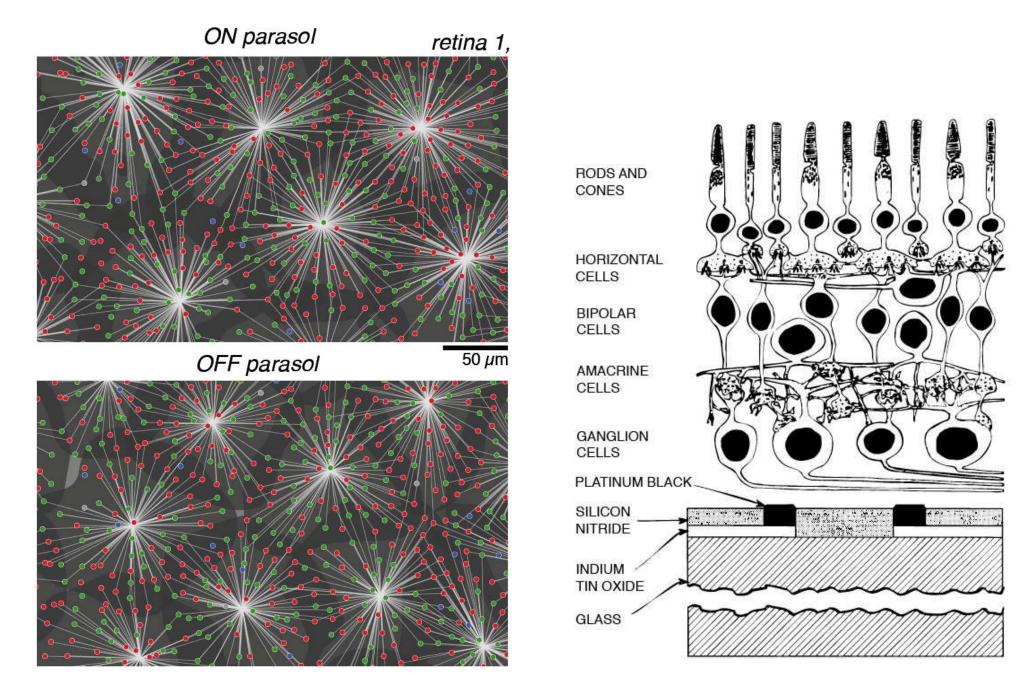


OFF midget





Next steps: inferring circuitry?



Conclusions

- GLM and state-space approaches provide flexible, powerful methods for answering key questions in neuroscience
- Close relationships between encoding and decoding (Paninski et al., 2007)
- Log-concavity, banded matrix methods make computations very tractable
- Experimental methods progressing rapidly; many new challenges and opportunities for breakthroughs based on statistical ideas

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