



A Bio-inspired Extension of the Convolutional Neural Network Models for Neuronal Modeling



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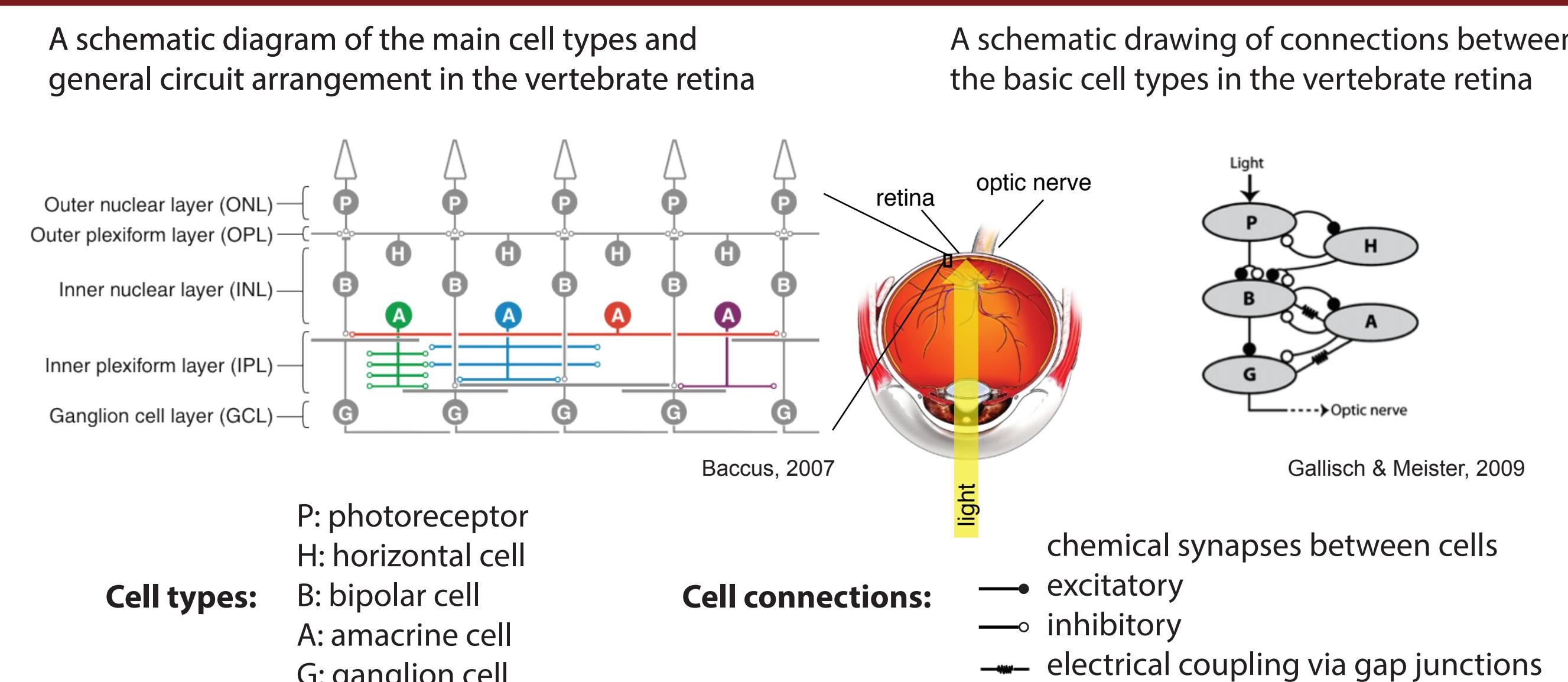


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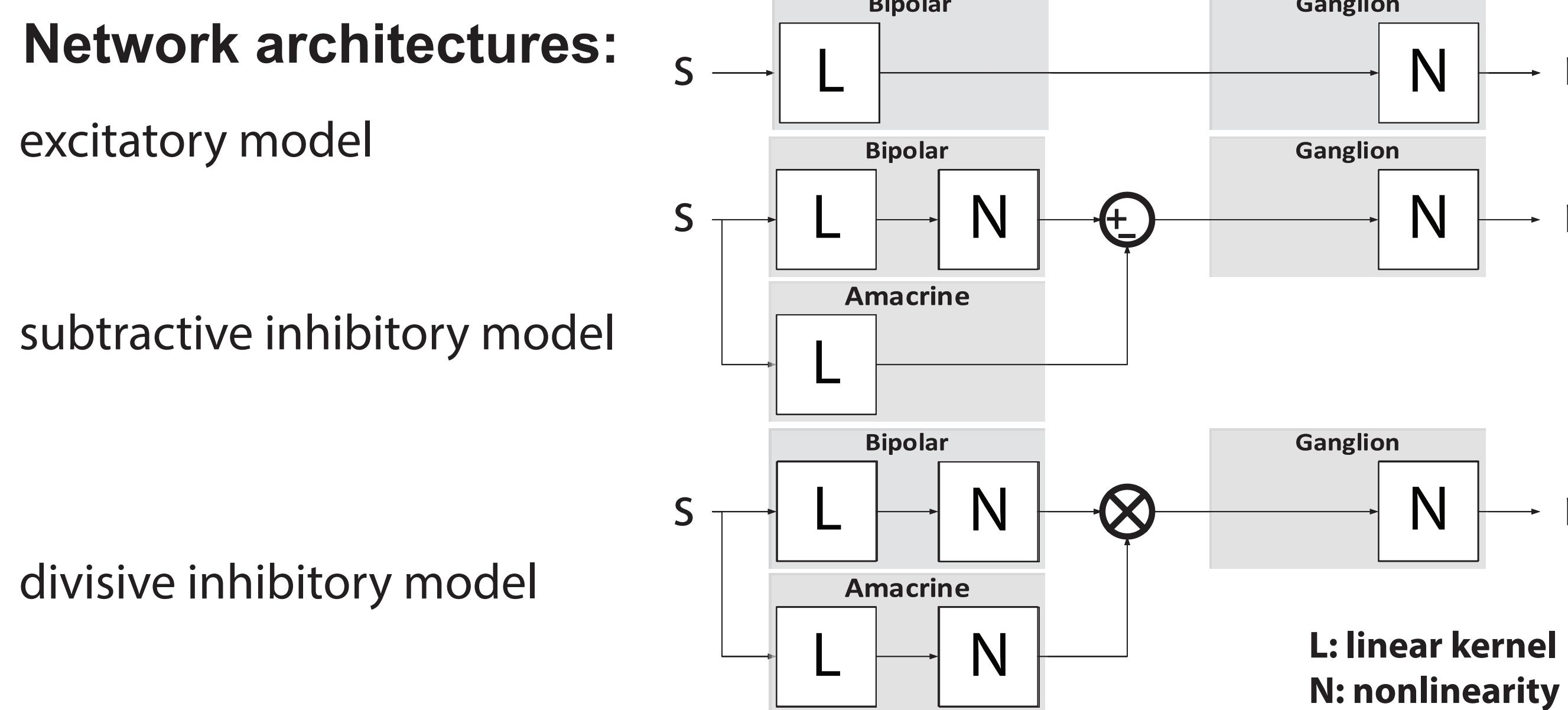
Background

Understanding many of the complex visual functions in the vertebrate retina requires characterizing various types of interactions between its excitatory and inhibitory neural pathways. Although quite successful in predicting retinal responses to simple synthetic visual stimuli, existing computational models are not sufficient to characterize retinal responses to more complex visual stimuli whose processing involves various types of excitatory and inhibitory interactions. In this study, we develop a computational model in the convolutional neural network framework in order to incorporate both excitatory and inhibitory computations generating retinal responses. This model framework provides a powerful tool for understanding how complex computations at the integration of excitatory and inhibitory pathways lead to the retina's complex visual functions. This capability can in turn advance existing retinal prosthetic devices to be able to implement more naturalistic processing of real-world visual scenes.

Introduction: retinal circuitry



Method: Directed Acyclic Graph (DAG)



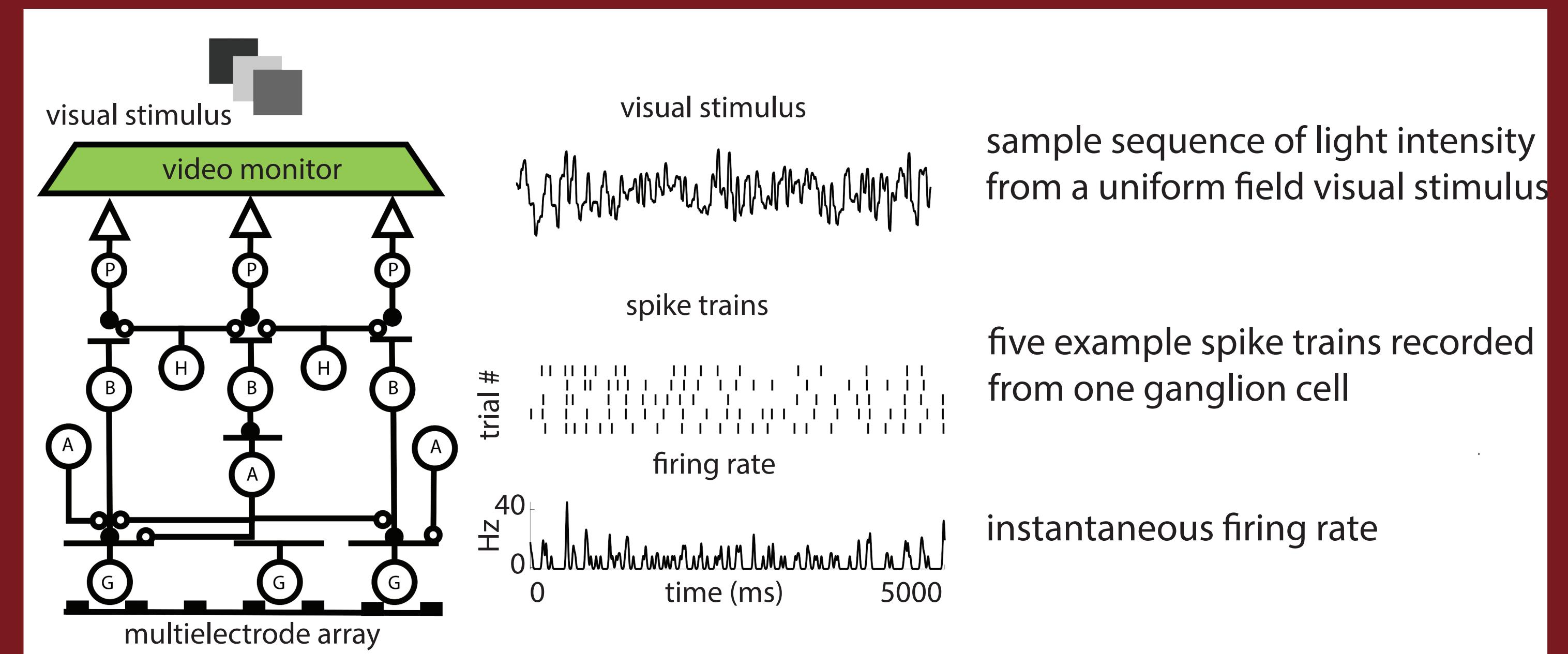
Model: parameterization

The linear kernels are represented by a sequence of weight values $\{k(n), n = 1, \dots, 25\}$, which are used to filter their input $x(t)$ as, $r(t) = \sum k(n)x(t-n)$, where $r(t)$ denotes the output of the filter at time t .

A rectifying nonlinearity is used to represent activations along excitatory pathways as, $F(u) = \max(0, u+b)$, where b represents the bias parameter.

A log-sigmoid function is used to represent the nonlinearity along inhibitory pathways as, $F(u) = 1 / (1 + \exp(-(u+b)))$ where b denotes the bias parameter.

Data: experiment



Data: simulation

network input:
white Gaussian noise sequences with zero mean and unit variance

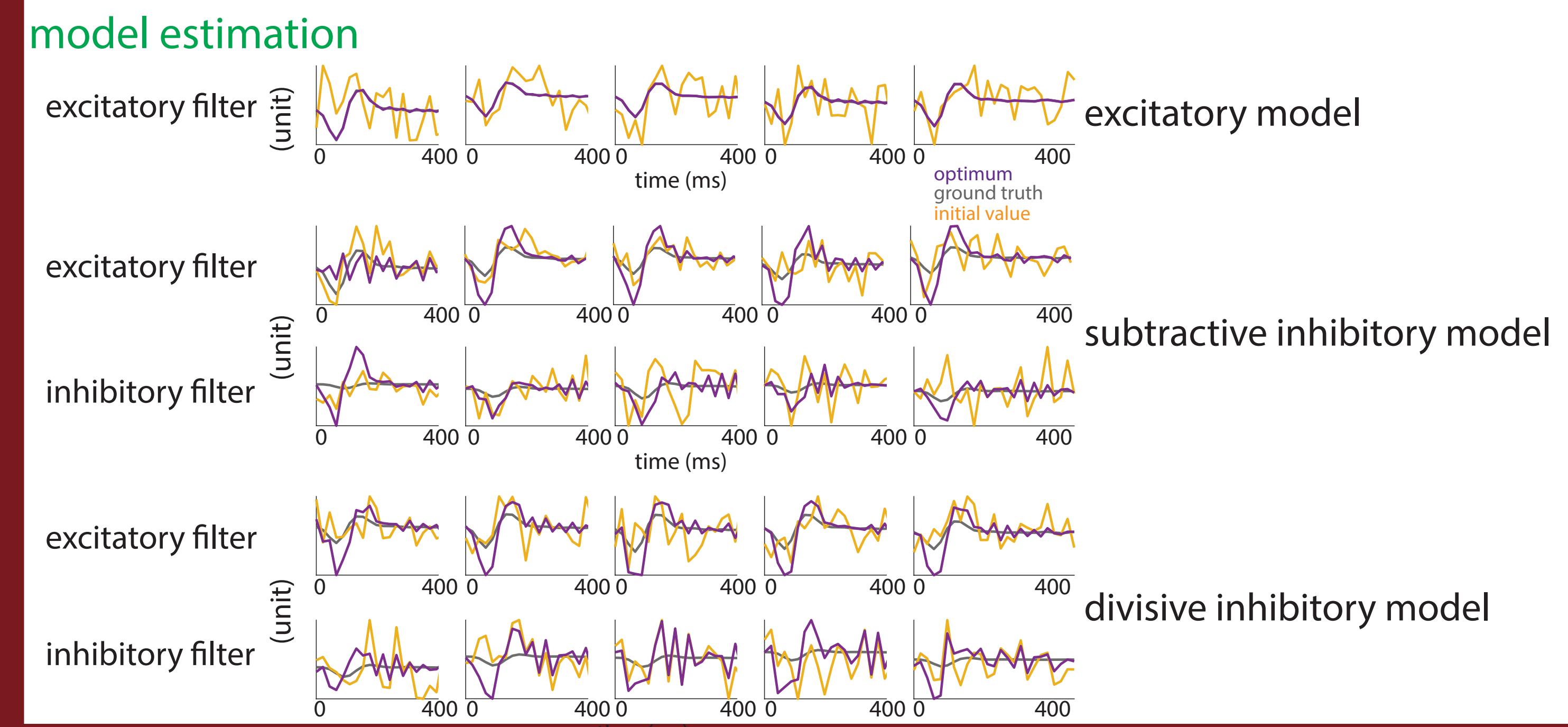
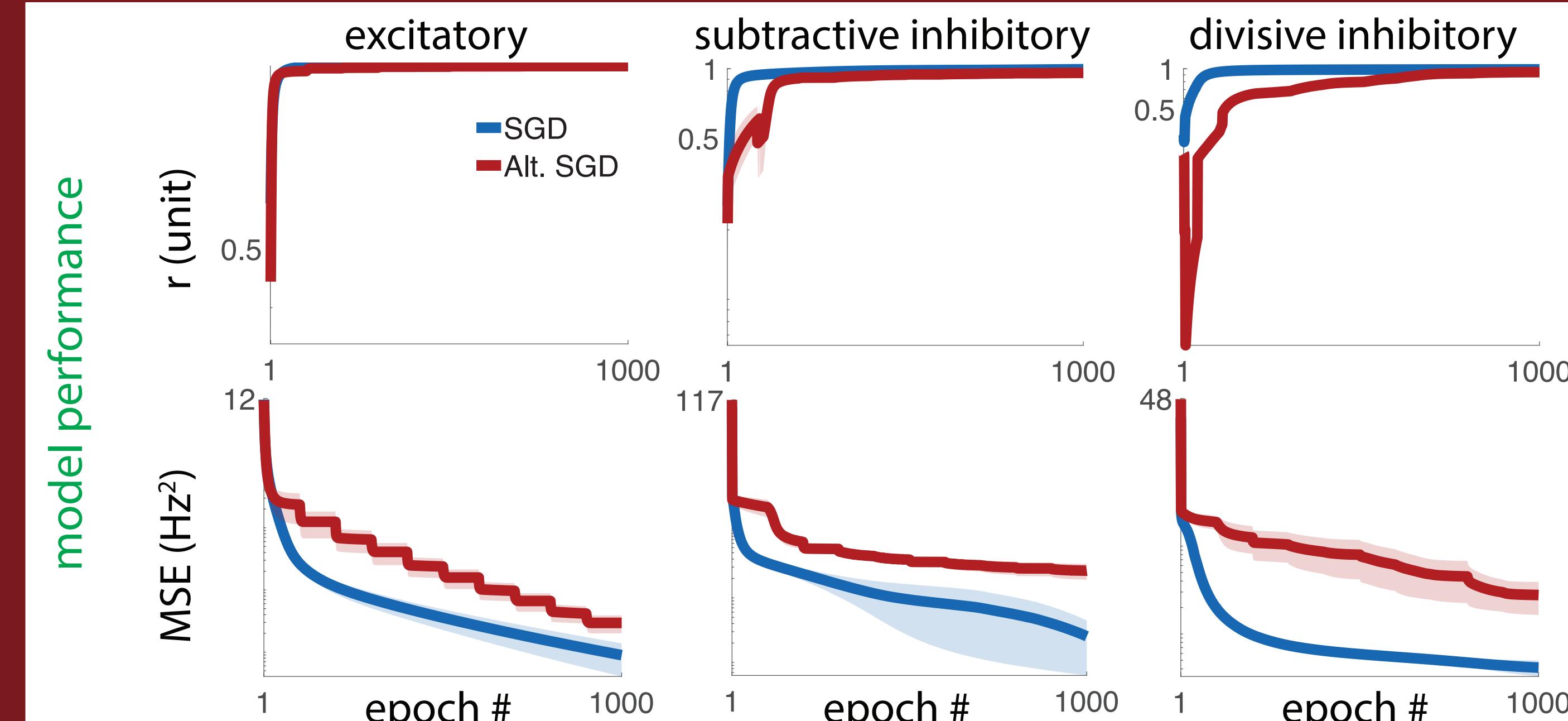
network output:
firing rate output of the networks, with preset parameters, were used as the regression labels

These input-output data were used to estimate the simulated network parameters.

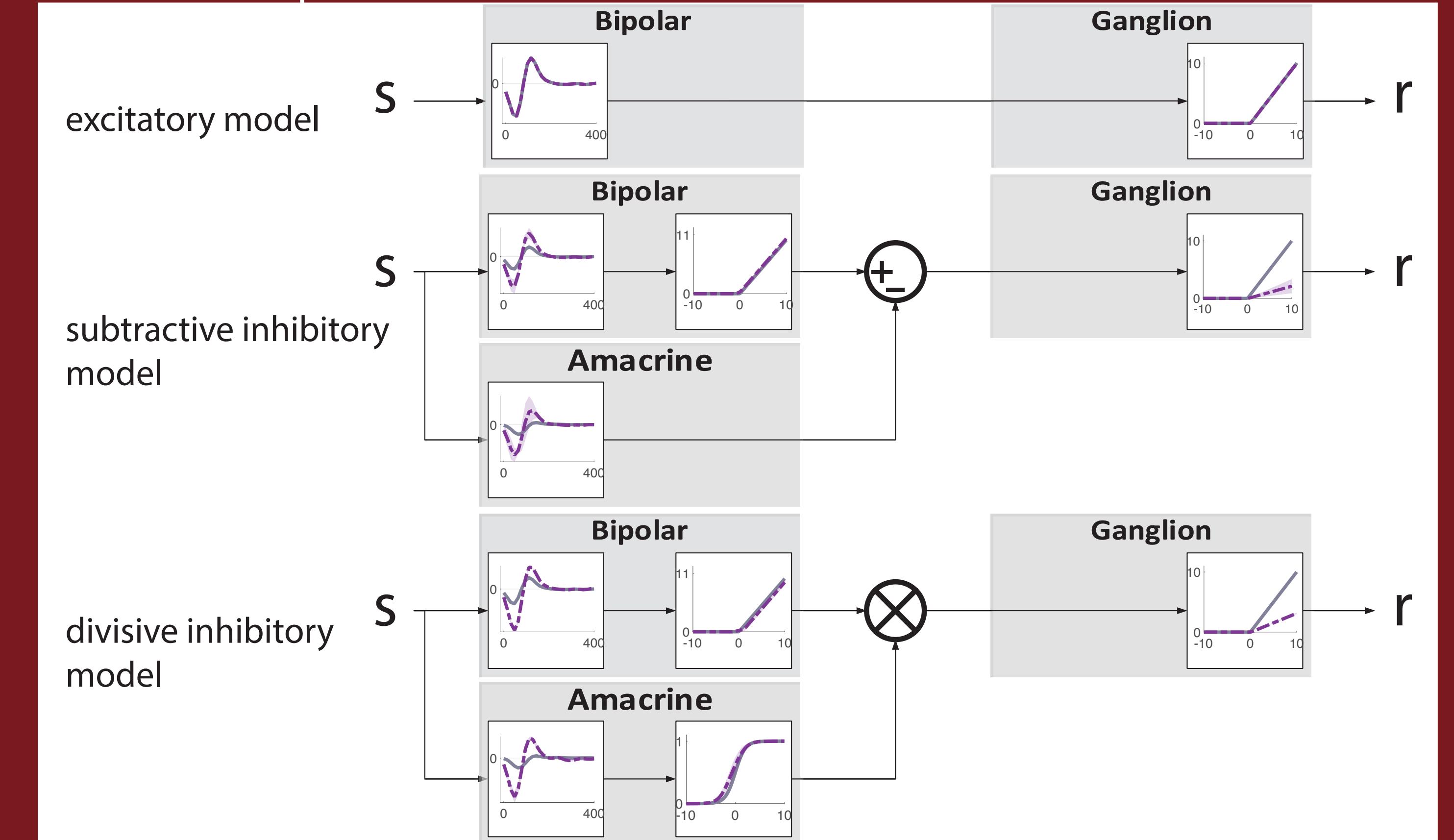
The simulation parameters are chosen to produce output signals with the statistics of real spiking output of the retinal ganglion cells in response to the same visual input.

Results:

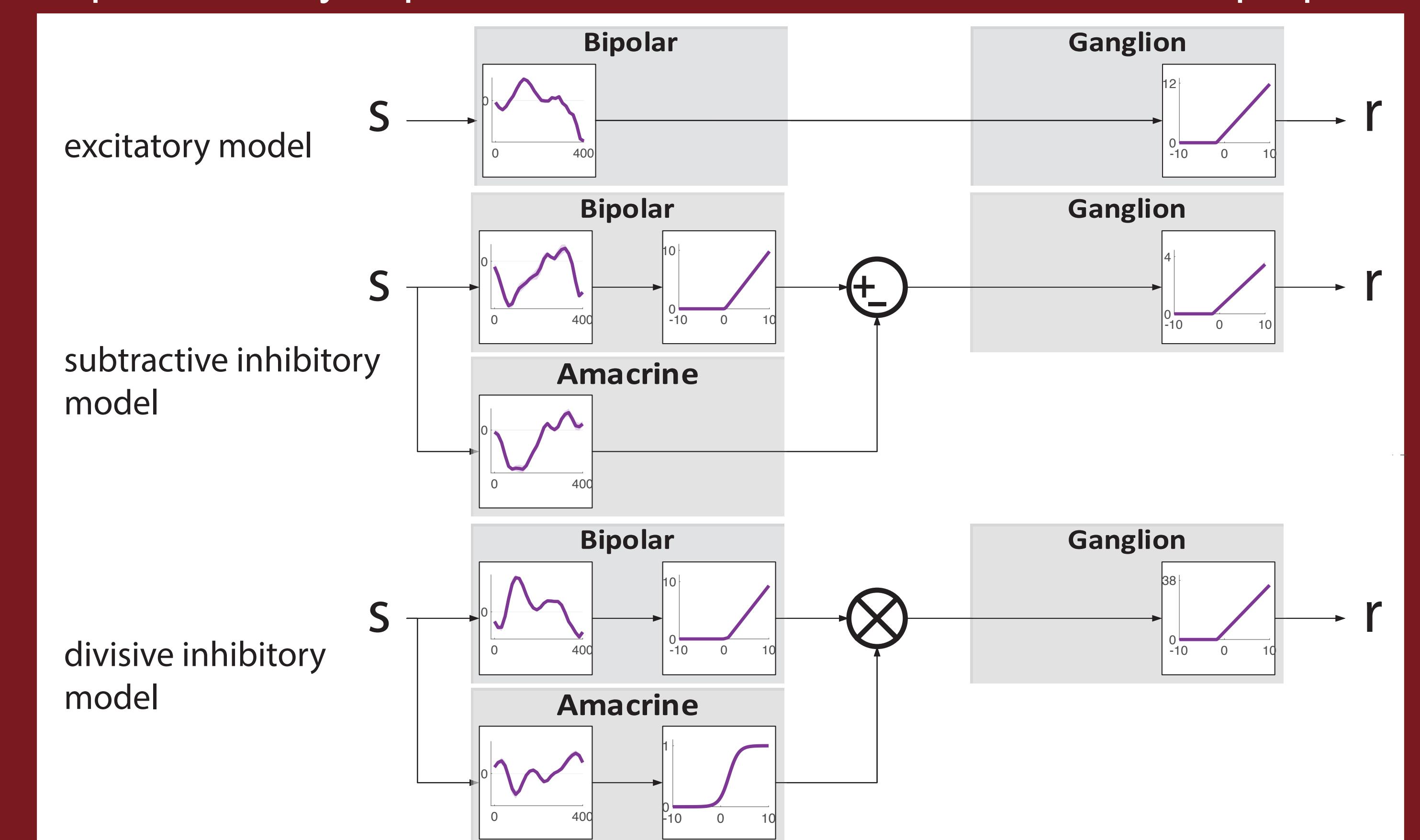
DAG architectures accurately capture the input-output relationship on simulated data



The new learning algorithm provides robust optimum solutions for the network components



The model applied to real ganglion cell responses measured experimentally captures the neuron's linear and nonlinear properties



Summary

This study develops a convolutional neural network-based computational model of the retina that can predict the responses of retinal ganglion cells driven by both excitatory and inhibitory computations.

The computationally robust learning algorithm developed in this study provides stable optimal solutions across different initializations and datasets.

The model successfully predicts the spiking rate of retinal ganglion cells.

The recovered model parameters represent the linear and nonlinear processing across different layers in the retina.

References

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