A Probabilistic Model Predicting Retinal Ganglion Cell Responses to Natural Images

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Developing computational models that predict neurons' responses is important to reverse engineer our brain, cure neuronal diseases and build good prosthetic devices. Retinal Ganglion Cells (RGCs) form an ideal frame work to build such models upon because the retina, although physically separate from the brain, is anatomically defined and functions like a brain tissue and its RGCs respond directly to light stimuli. Existing computational models, like Linear-nonlinear-Poisson cascade model (LNP)[1], do a great job predicting the responses of Retinal Ganglion Cells (RGCs) to artificial images like Gaussian white noise, sinusoidal gratings and spot-annuli flashes of different intensities. However when challenged with predicting the responses of RGCs to the stimuli our visual system is evolutionary designed to encode, namely natural images, those models fail. The reason those models fail is because natural images hold special statistics like significant spatial correlations[2] and high kurtosis. Those special statistics generate a sparse response pattern making it hard for the models to predict, because their most likely outcome is zero. In addition, neurons responses are probabilistic, varying between trials and all existing models are deterministic, thus aiming to predict the absolute or average response. To overcome this difficulty we endeavored to develop a model that predicts RGC responses to images probabilistically.

In our experiments we presented long (either 10530 or 7020) and fast (30Hz) sequences of natural [3] and artificial (Gaussian white noise) images to *in vitro* retinas harvested from *Long Evans* rats. The RGC spiking responses were recorded using a multi electrode array system (Cerberus, Blackrock Microsystems, Salt Lake City, UT) and analyzed offline. In total we obtained the image-response relations of 108 RGCs and used those to develop the probabilistic model.

Our model contains elements arising from known retinal anatomy like a linear receptive field estimated with a Spike Triggered Average (STA) method [4], a normal distribution estimating the probabilities of the RGCs different pre-firing signals and a spike limiting function that accounts for the physiological refractory period of the cells. The model holds two free parameters: K*, the semi-saturation constant, controlling the RGC's sensitivity to spike saturation and A which represents the maximal firing rate of the cell. The model works well for different types of RGCs (ON, OFF and RGCs with a relatively long refractory period) and optimized with each stimuli type results in near perfect correlations (R^2=mean± standard error) for both natural (R^2=0.971±0.006) and artificial images (R^2=0.90±0.02). Evaluating the model fits with a stringent multinomial statistical test with randomization resulted in about a third of the cells having their model fits arising from the same statistical distribution as the data at a 5% significance level. In addition, our model helps explain the difference in the responses between natural and artificial images stimulation, where for each RGC the models' free parameters vary consistently, when optimized with either type of stimuli. However, we are still investigating the reason why the model predicts the responses to natural images slightly better than artificial once.

In conclusion, we believe that we have found a new model that is capable to better predict neuronal responses than existing models and we hope that our probabilistic approach will suggest a new direction in the field of computational neuroengineering.

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