Towards retina-like Bayer filtering with spikes

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Introduction

We consider the problem of demosaicking within the spike domain. A retina-like network [5] is simulated using Brian2 [3] and the PyRho optogenetics library [2] in order to produce an RGB-channelled image.

Spiking Neuronal Models

We make use of a leaky integrate-and-fire (LIF) neurons to describe the membrane potential dynamics of an individual neuron:

$$C_m \frac{dV}{dt} = -g_L(V - E_L) + I_{syn}(t)$$

where C_m is the membrane capacitance, g_L is the leak conductance, E_L is the resting potential, $I_{syn}(t)$ is the synaptic current, and V is the membrane potential. The LIF neuron fires an action potential when its membrane potential reaches a threshold value V_{th}, which can be expressed as:

$$V_{th} = V_{rest} + \Delta V$$

where V_{rest} is the resting membrane potential and ΔV is the threshold potential. When the membrane potential reaches the threshold value, the neuron "spikes" and its membrane potential is reset to a hyperpolarized value V_{reset}, which is typically more negative than the resting potential:

$$V \leftarrow V_{reset}$$

These equations describe the basic behavior of a single LIF neuron which may be grouped together as a neural population with each neuron representing a pixel.

Retina-like Bayer filtering

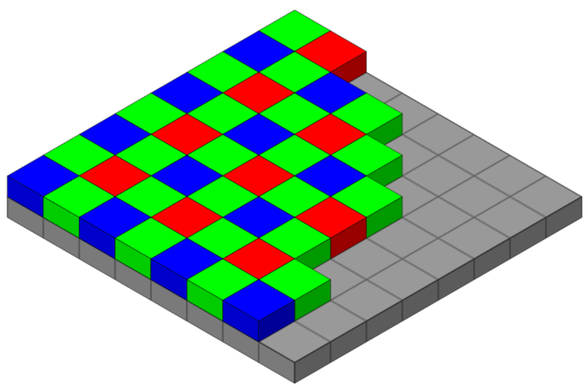

Figure 1. Bayer filter [1] samples different .RAW pixel values for a colour value to estimate RGB channel values for the entire image

We take as input a mosaicked $H \times W$ image of continuous values and output to a population of $H \times W \times 3$ spiking neurons representing a spike-encoded interpolation of the RGB values. In order to convert continuous values into spiking inputs, we first apply an input encoding population responsible for using each value as the rate parameter for a Poisson distribution of spikes. The model thus consists of two populations: one for encoding the .RAW values to an appropriate spiking neuron rate, and another for the interpolated value of all channels.

Optogenetics for biological plausibility

Opsins are proteins present in biological retinal cells (i.e. cones and rods) that produce an electrical response (i.e. action potential) when exposed to certain frequencies of light. For the RGB output neural population, we make use of [2] to model different opsins responsive to different wavelengths of light corresponding to RGB wavelengths. In this way, we retain the traditional Bayer filtering pattern but the spiking activity of each neuron is driven by an opsin model [4].

Spike-timing dependent plasticity learning

In order to learn the weights between input encoding population and interpolated RGB population, we apply spike-timing dependent plasticity (STDP) [6].

$$\Delta w_{ij} = \begin{cases} A_+ e^{-\frac{\Delta t}{\tau_+}} & \text{if } \Delta t \leq 0 \\ -A_- e^{-\frac{\Delta t}{\tau_-}} & \text{if } \Delta t > 0 \end{cases}$$

Here, Δw_{ij} is the change in the synaptic weight between neurons i and j, and Δt is the time difference between the pre-synaptic spike (t_{pre}) and the post-synaptic spike (t_{post}). The parameters A_+ and A_- control the magnitude of the weight change for pre-before-post and post-before-pre pairings, respectively, and τ_+ and τ_- control the time constants of the weight change. STDP is a biologically-inspired learning rule that allows neural networks to adapt to changing input patterns by strengthening or weakening the connections between neurons based on the temporal order of their spiking activity.

Comparison of spike encoded interpolations

In order to compare the spike encoded Bayer filtering, we compare the spike trains of our output network to the spiking activities of a $H \times W \times 3$ neural population where the spike rate of each neuron is determined by using the traditional Bayer filter interpolation as a rate parameter to the Poisson distribution. We make use of the Elephant [7] library in order to compute statistics and metrics between our retina-network RGB spiking output and the output of the "ground truth" interpolated values used as spiking rate. There are many ways to compare two sets of spike trains and so we explore the different metrics available:

Spike Train Comparison Method	Value
Victor-Purpura distance	2.08
van Rossum distance	1.09
ISI-distance	0.06
Spike time tiling coefficient (STTC)	0.24
Event synchronization (ES)	0.41
Modulation index (MI)	0.45
Kreuz metric	0.25

Table 1. Spike train comparison methods in Elephant. Values were determined by an average over 10 runs for a sample .RAW image

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