

A CNN model framework and simulator for biological sensory systems

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Abstract – An abstract neuron model framework and simulator is proposed for qualitative spatio-temporal studies for biologic sensory systems. The proposed framework defines a huge number of layer-ordered simple base cells with neuromorphic relevant parameters [1]. The created models can be translated to hardware-level general multi-layer Cellular Neural/non-linear Neural Network (CNN) templates [2]. The framework is used to create a complete mammalian retina model. The definition of the model elements is based on retinal anatomy and electro-physiology measurements [1]. The developed model complexity is moderate, compared to a fully neuromorphic one [3] therefore chances of its implementation on a complex-cell CNN Universal Machine [4] chips [5] using multi-layer technology [6] and algorithmic programmability are good.

1 Introduction

This paper proposes a Cellular Neural/nonlinear Network (CNN) [2, 4] model framework and simulator (RefineC) for biologic sensory systems, especially for the vertebrate retina [7, 8]. It presents a pure CNN based complete mammalian functional retina model as an example. Through the years, starting with the early CNN models [9, 10] several simulators have been developed. The latest one is RefineC [11] (REceptive Field Network Calculus).

The development of the model components is based on neurobiologic measurements [1]. The modeling approach is neuromorphic in its spirit, relying on both morphological and electro-physiological information. However, the primary aim was to fit as close as possible the spatial and temporal output of the model to the data recorded from mammalian ganglion neurons. From an engineering point of view the presented model is a simple multi-layer CNN template, which consists of 3-layer coupled cell structures to pave the way for a complex-cell CNN-UM chip implementation [6, 12].

The retina, as a computational device, is a complex and sophisticated tool for preprocessing a video flow. It is anticipated that the results can be embedded into

several complex algorithms and applications targeting real-life applications, like object classification, recognition, tracking, and alarming.

The common neuronal modeling packages simulate networks of synaptically connected neurons [13], a few examples are Genesis, Saber, Spice, Swim, and NeuronC [14, 15]. The typical size of the network is about 10.000 neurons and each has about 20 compartments. Simulating biologic sensory system with several neuron-types require powerful workstations because of the huge number of variables that need to be computed [13]. The proposed simulation framework is simpler than previous ones because single neuron is composed from maximum three quasi-compartments thus only the most important parameters should be specified. The size of the simulated network is much bigger, nearly half million, because the size of the computed video is 1800 by 1350 μm , the distances between the photoreceptor cells are 10 μm and we model several neuron-layers. In a typical simulation project huge fraction of time spent on creating and modifying the model [15] therefore a good user interface is important. The simulator RefineC [11] has user-friendly graphical interface for creating, simulating, analyzing, tuning, and managing your high-level neuronal network models.

Chapter 2 describes the proposed abstract neuron model framework. Chapter 3 summarizes the results of the mammalian retina simulation.

2 Abstract neuron model framework

The basic blocks of the model framework are the abstract neurons. These neurons are simple but they can keep the qualitatively interesting features of the modeled biologic sensory system therefore we do not follow the classical compartment modeling approach [14] but use a lumped parameterized model [9].

The abstract neuron model defines different types of neurons with receptors using as few parameters as possible. These neurons are organized into separate layers. The parameters are the neuron time constant(s), the intra-layer spatial coupling, and the output function.

Subsequent layers supply the input of the next layer through synapses. The abstract neuron has receptors to implement these synapses. The three different type of receptors are plain, delayed and desensitizing.

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The modeling takes the following steps: First, the model structure is defined i.e. the neuron layers with receptors are created. Second, the model parameters are defined: the time constants, the coupling, the output function and the receptor properties. Third, the stimulus is selected, e.g. the same stimulus is used as in the measurement, and the simulation begins.

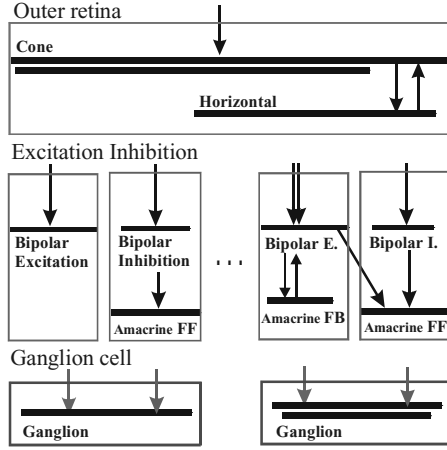


Figure 1. The processing structure of the mammalian CNN retina model. Horizontal lines represent abstract neuron layers (section 2.1) and vertical lines represent the receptors (section 2.2).

The middle abstraction-level models can be transformed into a low-level CNN multi-layer template. Each column-, surface- or array-ordered biological cells are modeled with CNN layers and the synapses (inter and intra layer, chemical and electrical, excitatory and inhibitory, as well) are assigned to a specific CNN template. The result contains several simple layers, where each layer has its own time-constant and feedback connection matrices. In the retina modeling the inter-layer connections are zero neighborhoods cell-to-cell links with linear or rectifier transfer functions and the intra-layer connections are linear nearest neighborhood links. These restrictions guarantee the hardware feasibility of the designed models in the near future on the CNN-UM platform [6, 12].

2.1 The abstract neuron

The parameters of the abstract neuron are the time constant(s) (τ), neuronal feedback (s), and the transmitter output function (f^o). The time constant is given in ms. If the neuron model is second-order the neuronal feedback is definable (eq. 2). The transmitter output function is the non-linear output of the neuron (voltage to transmitter release) (eq. 3).

The abstract neurons are organized into separate layers. The coupling (λ) is a layer property, it

describes the spatial direct coupling (electrical connections) between the neurons. The space-constant is one of the quantities supplied by the model so it is not an independent parameter but a measurable result.

The differential equations of the n^{th} abstract neuron are equations 1-3, where U refers to the receptors and \otimes to the convolution operator.

$$\tau_n^l \dot{X}_n^l = -sX_n^l + \left(\frac{\lambda}{D_n}\right) \begin{vmatrix} 1 & & \\ & 2 & \\ & & 1 \end{vmatrix} \otimes X_n^l + \sum_{\forall m \in Sy} U_m^r \quad (1)$$

$$\tau_n^j \dot{X}_n^j = -X_n^j + X_n^l \quad (2)$$

$$Y_n^l = f_n^o(X_n^l) \quad (3)$$

The resting potential is set to zero therefore the modeled voltage of the neuron (X^l) is not equal to the measured value. Modeled and measured values, however, can be compared after having applied a scaling factor.

2.2 Receptors

The connection between two neurons is called synapse. The synapses constitute the only couplings between the layers. The source neuron is the input of the synapse and the receptor is the receiver. Each abstract neuron has some receptors.

The lateral extension of the synapse depends on the physical area of the dendrite and the axon of the source neuron. The type of the synapse spatial organization could be gaussian (G) or pattern defined. It defines the spatial strength of the interaction. The gain (g) is the strength of the interaction and sigma (σ) is the spatial strength property of the connection. The receptor transfer curve (f^r) is the non-linear input of the neuron (transmitter concentrate to voltage).

Three different types of receptors are modeled: plain, continuous delayed (τ^d) and desensitivity. The differential equations of the m^{th} general receptor in the n^{th} abstract neuron layer are equations 4-6.

$$\tau_{nm}^r \dot{X}_{nm}^r = -X_{nm}^r + f_{nm}^r(G_{nm}^\sigma \otimes Y_m^l) \quad (4)$$

$$\tau_{nm}^d \dot{X}_{nm}^d = -X_{nm}^d + X_{nm}^r \quad (5)$$

$$U_m^r = g(X_{nm}^r - r X_{nm}^d) \quad (6)$$

The desensitivity synapse operates in a way that the effect of the synapse decreases over time as the synapse becomes less effective. The parameters describing the receptor are the speed of reaching the final stage (τ^r) and the ratio between the transient- and the sustained-part of the input at the steady state (r).

2.3 Transfer functions

Each abstract neuron and receptor has its own transfer function. The system has a well-defined steady state description: the state value of each abstract neuron is zero. The transfer function should have a zero crossing in the origin to ascertain this property. The transfer function is monotonic and continuous. Two groups of functions are defined: quasi-linear (eq. 7-9) and rectified (eq. 10-11).

$$\text{Linear: } f^L(x) = x \quad (7)$$

$$\text{Saturated: } f^{Ch}(x) = \frac{1}{2} (|x+1| - |x-1|) \quad (8)$$

$$\text{Bipolar: } f_s^B(x) = \frac{(1+e^s)(e^{sx}-1)}{(1+e^{sx})(e^s-1)} \quad (9)$$

$$\text{Rectifier: } f_c^R(x) = \frac{x-c+|c-x|}{2(1-c)} \quad (10)$$

$$\text{Convex: } f_s^{Cx}(x) = \frac{2(e^{sx}-1)}{(e^s-1)(1+e^{s(x-1)})} \quad (11)$$

3 Mammalian retina modeling

Recent studies [1] have revealed that the retina sends to the brain a parallel set of about a dozen different space-time spiking flows. The generated representations are carried to the brain by a feature-specific array of retinal output neurons. The input of the retina is the activation of the cone (photoreceptor) layer and the output is the ganglion cell spiking [8].

The retina has two main parts: the outer and the inner retina [3, 10] we model the latter with several blocks, therefore the mammalian retina model consists of the following parts: the outer retina model, the excitation pattern generators, the inhibitory subsystems, and the ganglion cell models [12]. On figure 1 the rectangles symbolize the blocks.

The outer retina model is the same for all the different blocks. It has two interacting cone and horizontal layers, which model the time- and space-behavior of the outer retina.

The inner retina is more complex. The retina has several types of ganglion cells. The two qualitatively different inputs of a ganglion cell are the excitation and the inhibition. The excitation comes from a bipolar cell; the inhibition derives through an amacrine cell. Each amacrine cell has connection at least to one bipolar cell. The input of the bipolar cells is the outer retina.

The inner retina model is divided into parts, each one representing a given type of ganglion cells and its input blocks: the excitatory subsystem and the inhibitory subsystem. In general we need some bipolar layers and a few amacrine feedback layers for

one excitatory block. Each inhibitory block has some amacrine feed-forward layers and a few bipolar layers. The ganglion blocks combine the outputs of the excitatory and inhibitory blocks.

All of the above mentioned layers are modeled with one abstract neuron layer. Figure 2 shows the comparison of the simulations and measurements [1]. The model qualitatively reproduces the inhibition, excitation and spiking patterns for the flashed square stimulus.

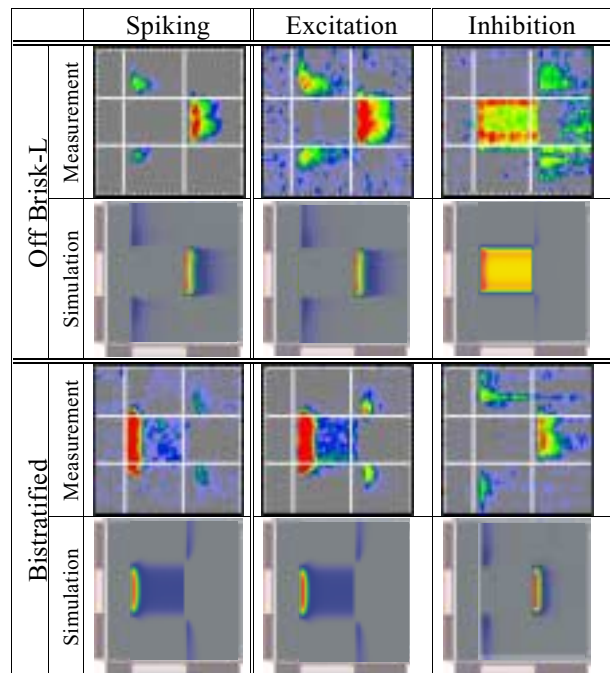


Figure 2. The measured and simulated space-time feature-specific arrays in two different cases of retinal outputs. The time runs horizontally and the middle row of the retina is the vertical axes. The first column of the table contains the biologic name of the modeled cell [1].

Figure 2 contains patterns of excitation and inhibition for different ganglions. Time runs horizontally, space is shown vertically. The patterns illustrate the temporal and spatial distributions of activity for a flashed square.

The following video-flow is projected to the retina. A white square against a gray background is presented at the first vertical white bar and "turned off" after the 2nd second. The dimension of the stimulus falls between the two horizontal bars. The spiking pattern is the output of the ganglion cell model, the excitation and inhibition are the bipolar and amacrine input of the ganglion layer, respectively.

4 Conclusions

The paper showed that the proposed modeling framework is a powerful and effective simulation platform for creating retinal and other sensory models with biologically relevant parameters. The presented model is developed for mimic the mammalian retina from photoreceptors to the ganglion cells, which is output of the retina. The presented whole mammalian retina model incorporates the abstract neuron model framework. The structure of the model is based on the morphology and the parameters determined by the flashed square measurements. The results of the model for the flashed square stimuli are very similar to the measurement of the rabbit retina for each excitation, inhibition and spiking patterns [1].

The multi-layer mammalian retina model can be iteratively decomposed in time and space to a sequence of a low-level, low-complexity, stored programmability, simple 3-layer units (Complex R-units) with different specified parameters [12]. These units can be represented as complex cells of a CNN Universal Machine [4, 6].

The proposed framework can be applied to create a low-complexity therefore hardware feasible neurobiologic models that can be implemented in the near future by sugar-cube or multi-chip technology. It could be incorporated into any sensory prosthetic device that is required to send biologically correct stimuli to the brain.

The developed simulator serves as a basic research tool, allowing us to manipulate parameters and to utilize the wisdom of biological design in a powerful adaptable silicon device. Some examples that could be directly inserted into image processing algorithms are static and dynamic trailing and leading edge and object corner detection in space and time, object level motion detection and tracking with size selectivity (beside local interactions), speed, size, direction, and intensity selective video-flow processing.

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