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Exploring olfactory sensory networks: simulations and hardware emulation

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***Abstract*— Olfactory stimuli are represented in a high-dimensional space by neural networks of the olfactory system. A great deal of research in olfaction has focused on this representation within the first processing stage, the olfactory bulb (vertebrates) or antennal lobe (insects) glomeruli. In particular the mapping of chemical stimuli onto olfactory glomeruli and the relation of this mapping to perceptual qualities have been investigated. While a number of studies have illustrated the importance of inhibitory networks within the olfactory bulb or the antennal lobe for the shaping and processing of olfactory information, it is not clear how exactly these inhibitory networks are organized to provide filtering and contrast enhancement capabilities. In this work the aim is to study the topology of the proposed networks by using software simulations and hardware implementation. While we can study the dependence of the activity on each parameter of the theoretical models with the simulations, it is important to understand whether the models can be used in robotic applications for real-time odor recognition. We present the results of a linear simulation, a spiking simulation with I&F neurons and a real-time hardware emulation using neuromorphic VLSI chips. We used an input data set of neurophysiological recordings from olfactory receptive neurons of insects, especially Drosophila.**

I. Introduction

The insect olfactory system is an ideal model for the study of information processing in biological neural networks. In particular the fruit fly *Drosophila melanogaster* has proved to be a useful tool for the analysis and manipulation of information processing mechanisms.

The first olfactory relay in insects, the antennal lobe (AL), consists of a relatively small number (ca. 50 in *Drosophila*) of functionally distinct processing units or glomeruli. These units are zones of high synaptic convergence between the axons of one type of olfactory receptor neurons (ORN) and the dendrites of a few projection neurons (PN) projecting to higher brain areas [1]. The spatio-temporal activation pattern of the neurons in the glomeruli reliably reflects the identity of the odor presented to the insect [2]. This odor code is conserved between individuals. This is helpful for the systematic comparison and pooling of experimental results.

Furthermore, genetic and physiological tools have been developed to allow both monitoring and manipulation of specific parts of the olfactory processing stream by means of insertion of reporter proteins [3].

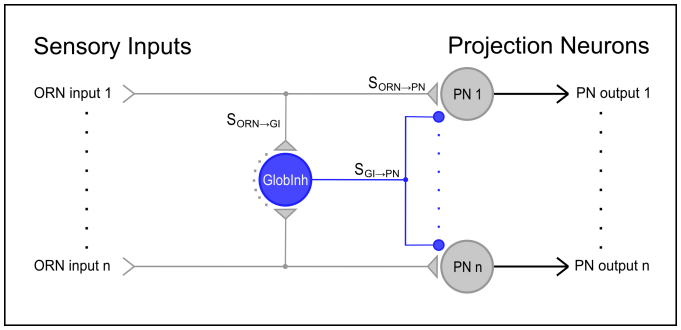

Fig. 1. Simplified model of the AL as used in all our simulations. Small triangles: excitatory connections. Small circles: inhibitory connections. Weights of excitatory and inhibitory connections (gray and blue pathways) are the only free parameters used to study the behavior of the network.

Glomeruli are interconnected with local interneurons (LN). These intra-AL connections have a significant influence on the processing of information in the AL [4], [5].

In this paper we show that we can use the same input data set and obtain comparable results with three different tools: a linear model, a spiking simulation and neuromorphic VLSI emulation. The linear model can provide a complete characterization of the parameter space, is simple in simulation and analysis but does not take into account the temporal dynamics observed in biology. The spiking simulation has the advantage of including the temporal dynamics in the model but it is computationally intensive especially for large network simulations. The neuromorphic VLSI emulation exhibits the advantages of the spiking simulation in a compact, low-power, real-time system. The network architecture under examination is based on a previous study by Silbering and Galizia [**?**].

II. Methods

LNs in the *Drosophila* AL are predominantly GABAergic [6] and densely connect glomeruli all across the AL [7], [8]. We modeled this with a global inhibitory neuron (blue neuron in Fig. 1) which is excited by all sensory neurons and inhibits

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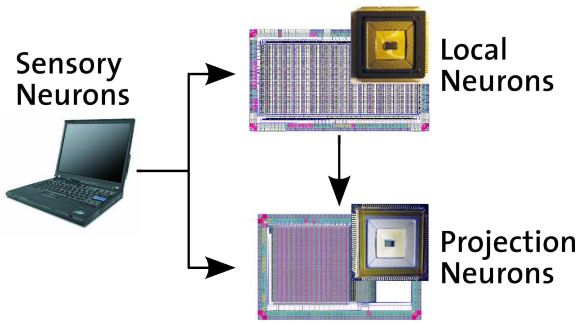

Fig. 2. Multi-chip system. LNs and PNs are allocated on two different chips. For each chip, the layout and a picture of the real chip is shown (chips size is $15mm^2$). Analog I&F neuron circuits and analog synaptic circuits are implemented in VLSI technology (128 neurons, 4096 synapses on LNs chip; 2048 neurons and 6144 on PNs chip). Input data matrix of Calcium concentrations is converted into Poisson spike trains and sent to the multi-chip network as digital events (AER protocol). The activity of all neurons can be monitored in real-time from the same computer from which we send the input trains.

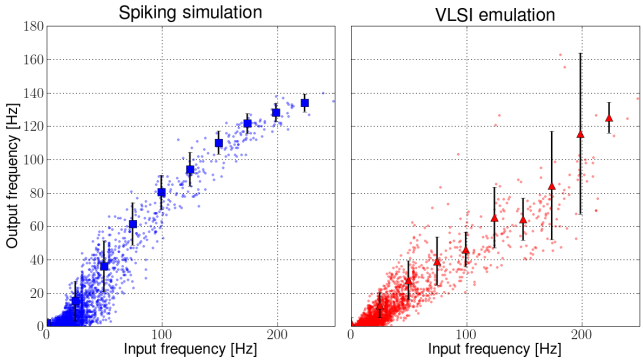

Fig. 3. FF-curves. The activity of PNs is plotted against the activity of input neurons. Small dots in the background represent all the input-output couples (single simulation run). Large squares/triangles in foreground are the average on each bin and vertical bars are the standard deviation. Raw data used to produce these plots as in center column of Fig.4.

all PNs.

Every ORN makes an excitatory synapse onto one PN only [9]. Multi-glomerular PNs do exist in *Drosophila* but have been shown to carry highly correlated signals [10].

As input to our network we used a subset of the DoOR odorant response database [11]. In this database each odorant is represented as an ORN activation vector of mean-rate activity. We excluded odorants with less than 7 data points and receptor neurons with less than 80 data points. The remaining input matrix contains data for 137 odorants in 23 glomeruli. The empty cells in the matrix (ca. 15%) were filled with estimations of the receptor neurons' spontaneous activity. All values in the input matrix were globally normalized.

A. Linear simulation

At present most data about *in vivo* activation of AL networks is from calcium imaging studies [12], [13]. This technique produces data with high spatial but relatively low temporal resolution. In order to simulate the *Drosophila* AL network in a fashion that is both close to the experimental results in resolution and simple in simulation and analysis we built a simulation based on linear algebraic techniques.

Each odor is represented as a vector of ORN activation values in n-dimensional space, where n is the number of glomeruli in the network (23). We subjected the odor vectors to a linear transformation of the form that modified each element in the input vector by the summed activity in the input.

The activity of a single PN can therefore be expressed by the following equation:

$$\rho_i^{PN} = \rho_i^{ORN} - \alpha \sum_k \rho_k^{ORN} \qquad (1)$$

where α scales the global feed-forward inhibition and the term ρ_k^{ORN} represents the activity of ORN k for the presented odor. This enabled us to explore the glomerulus-unspecific, global component of the AL network in the most generic terms.

B. Spiking simulation

The spiking simulation was implemented using the Python software package Brian [14] to simulate a population of 23 glomeruli as leaky integrate-and-fire (I&F) neurons with exponential inhibitory and excitatory synaptic currents. These ORNs are linked via a global inhibitory neuron to a population of 23 uniglomerular PNs (see Fig. 1). The input matrix described above was used to generate Poisson trains with corresponding mean firing rates to be used as input to the spiking network.

The parameters controlling the neural dynamics are global: all neurons in the network have the same refractory period, leak, etc. The synapses have near-instantaneous activation with an amplitude equal to the connection weight. Synaptic time constants are on the order of magnitude of $100\ ms$, while the refractory period is dimensioned as to limit the maximum firing rate to $250\ Hz$. The only two tuning parameters were the synaptic weights of the excitatory and inhibitory connections, which proved to be a good compromise between the number of available parameters and the variability of the network performance.

C. VLSI spiking emulation

During the last decade the neuromorphic engineering community has made substantial progress by developing the technology for constructing distributed multi-chip systems of sensors and neuronal processors that operate asynchronously and communicate using action-potential-like signals (or spikes) [15], [16]. The unique advantages of VLSI networks of spiking neurons permit the embodiment of this platforms on robotic devices, providing the circuits with realistic inputs which are affected by the interaction of the robot with the environment. In this context the robustness of the adopted model is a crucial requirement and can be easily tested. The experiment we describe in this section represents a preliminary step in this direction.

Thanks to the multi-chip setup flexibility we were able to emulate all the complexity of the modeled network in terms

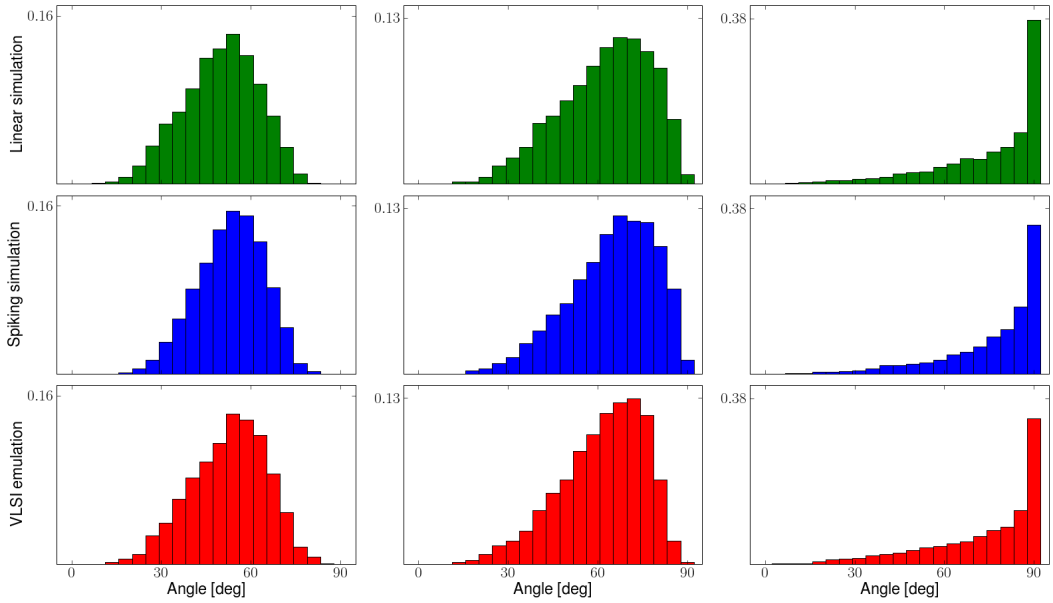

Fig. 4. Histogram of angles between activation vectors of odor pairs for the three simulations (rows) and for three values of inhibition strength (columns). Increasing inhibition strength (from left to right) produces a shift of the angle distribution towards the 90 degrees limit, therefore increasing odor discriminability.

of number of neurons, synapses and parameters. The VLSI spiking emulation was performed using a setup comprising two neuromorphic chips.

The global inhibitory neuron was implemented on a chip comprising 2048 I&F neurons and 6144 dynamic input synapses. The silicon neurons and synapses are implemented on a 15 mm^2 standard 0.35 μm four-metal CMOS technology chip. Each neuron can receive input current from one inhibitory and two excitatory AER[1] synapses with independent parameters (weights and time constants). A second chip was used for the projection neurons. The chip is composed of 128 I&F neurons, each one receiving inputs from 32 AER synapses (2 inhibitory, 2 excitatory and 28 excitatory plastic synapses). Only the non-plastic synapses were used in the network.

The leaky I&F circuit used in this chip [18] is compact and optimized for power consumption, it implements spike-frequency adaptation as well as a tunable refractory period and voltage threshold modulation. The silicon synapses are "Diff-Pair Integrator" circuits [19] and model the temporal dynamics of biological post-synaptic currents.

We can interface the chip to a workstation using dedicated boards and this allows us to stimulate the synapses on the chips, monitor the activity of the neurons [20], and map events from one neuron to a synapse belonging to a neuron on the same chip or on another chip. Therefore arbitrary connectivity patterns can be implemented.

[1]The Address Event Representation (AER) is one of the most common asynchronous communication protocols used in spiking neuromorphic chips [17]. In this representation, input and output signals are real-time digital events that carry analog information in their temporal relationship. Each event is represented by a binary word encoding the address of the sending node.

III. Results

In order to compare the behavior of the network in the three different approaches we focused on basic measurements relating the input activity at the level of the ORNs with the output of the AL network from PNs.

A. Network transfer function

Given the nature of the input vectors of mean-rate activities, i.e. without any temporal structure, we represent the activation dynamics of the network with the FF-curve, sometimes also referred to as the rate-based transfer function. Each point in the plot represents the input activity of one ORN to its glomerulus (x-axis) and the activity of the corresponding PN neuron (y-axis) that the ORN is directly exciting. The scatter plot of all the activities for all odors is shown in the background of Fig. 3 while the binned average of these values is shown in the foreground.

After a short non-linear range (below 25 Hz) the curves show linear dynamics in a wide range, which is comparable with values of activity typically found in *Drosophila* PNs [6]. Higher variability in the transfer function of VLSI neurons is due to device mismatch present in the hardware and not simulated in the software.

B. Odor pair separation

One hypothesis about the role of the AL in the olfactory processing stream is to increase odor discriminability. In the AL, all axons with the same receptor expression profile converge onto a single glomerulus [1], so that the array of activity values of each ORN for a given odor represents a vector in a multidimensional space. Intuitively, we can consider the Euclidean angle between pairs of vectors as a measure of odors proximity, thus the network should increase angles to improve

odor discriminability. This approach has the advantage over similar measures, like for example the Euclidean distance, of being concentration independent.

The table in Fig. 4 shows the distribution of angles (computed for all possible odor pairs) for the three simulations (rows) and for three values of inhibition strength (columns). When inhibition is disabled (left column) the PNs angle histogram is identical to the input (ORN) angle histogram for the linear simulation (top graph). Small variations due to the noise introduced by the Poisson statistic of the spike trains are observed in the spiking simulation; more noise is observed in the VLSI emulation because of device mismatch. When inhibition is enabled (center column) an average increase in angles between odors is observed in the three models. This network effect can be increased by increasing the strength of inhibition (right column).

These results show that inhibition could be used by the AL to increase angles between odor pairs and therefore improve odor discriminability. The three models show comparable results.

IV. Conclusions

We showed results from a linear simulation, a spiking simulation and a VLSI emulation of a simple model of the AL. The network behavior is consistent in the three representations and shows the ability of the model to increase the angle between odor pairs, therefore improving odor discriminability. The mean angle between activation vector for odor pairs increases with increasing inhibition strength as shown by the shift of the angle histograms toward the 90 degrees limit.

Our results show that even if the spatio-temporal activation of the AL has an important role in odor representation [21], the spatial activation alone can describe the influence of the sensory olfactory system on the discriminability of odor representations.

The spiking simulation and VLSI emulation are perfectly suited for studying the temporal dynamics of the network. This work lies the foundation for future studies in this direction.

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