Modeling the Architecture of the Olfactory System *

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1 Modeling the Architecture of the Drosophila Olfactory System

The object of this paper is to present a model of the architecture of the olfactory system of the Drosophila.

1.1 Modeling the Architecture

Our initial model of the fly olfactory system (see Figure 1) consists of four cascaded building blocks (networks). Each block models a transduction, information representation or processing stage of odor information.

The first block represents the network of receptors and the dendritic arbor (cilia) of the OSNs. The input to this network is provided by odor molecules binding to the receptors. Each output of the receptor network is an analog waveform that models the dendritic current feeding the soma of exactly one of the olfactory sensory neurons.

The second block is the network of OSNs. The input to this network is identical to the output of the receptor network. Its output models the multidimensional spike train generated by the OSN assemblies.

The third block models the glomerular network. The glomerular network accepts as input the spike train generated by the OSNs and has as output the dendritic tree current feeding each of the somas of the PNs. Hence, the output of the glomerular network is modeled as an analog waveform. In addition to the direct axon/dendritic

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arbor connectivity, the circuit diagram of the glomerular network is characterized by the interconnectivity between glomeruli due to local interneurons and (possibly by) feedback. Feedback between the glomerular network and the network of PNs is shown by the red arrow in Figure 1.

The fourth building block models the network of projection neurons. The input to this network coincides with the output of the glomerular network whereas its output is modeled as a multidimensional spike train.

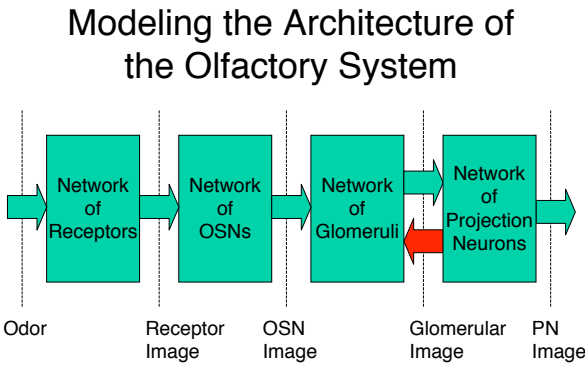

Figure 1: The Architecture of the Olfactory System

Information processing in the olfactory system begins with the mapping of an odor by the subset of odorant receptors that it activates. This odor receptor map (implemented as a network) creates a time dependent *receptor image* (or trajectory). Similarly, the three other networks in Figure 1 implement input/output maps. These maps create the *OSN image*, the *glomerular image* and the *PN image*, respectively. Whereas the OSN and the PN images (i.e., spike trains) can be readily recorded using whole-cell recording, the receptor image and the glomerular image are difficult to measure experimentally. Elucidating the nature of odor representation in the initial stages of the olfactory system, however, calls for understanding the main structural characteristics of all four images. We shall demonstrate in the next section how to recover the receptor and the glomerular image from the OSN and the PN image, respectively. This enables us to identify the wiring diagram of the glomerular network from neuron spiking data.

An olfactory system must solve the problem of odor detection, recognition and segmentation [12]. Segmentation is necessary because the odor environment often contains two or more odors. The system must be able to identify these objects separately and signal their presence to higher brain areas. Odor recognition must be concentration invariant over a broad range of odor concentrations [3].

In the language of communication theory odor recognition calls for finding good partitions of the multidimensional odor space, mapping odors into such partitions through a sequence of processing steps and identifying the partitions with the appropriate odors. Accordingly, we shall model the overall operation of the olfactory system of the Drosophila as a real-time odor detection system (in the sense of [15]). From a theoretical point of view, the detector is viewed as an instantiation of a hypothesis testing system. In its

simplest form, the null hypothesis or H_0 is "lack of odor" (only spontaneous activity is present). The alternative or H_1 is "odor plus spontaneous activity is present" (spontaneous activity is usually interpreted as noise). This basic model can be easily generalized to both the case of an arbitrary number of odors as well as the case of segmenting (or extracting) an odor from a mixture of odors.

What is a possible realization of the overall odor detection system beyond the four distinct networks depicted in Figure 1? Since the data available about the higher brain centers is scant, the following comments have only a suggestive value. Genetic experiments have determined that the precise spatial map in the antennal fly lobe is represented in the protocerebrum [18]. Therefore, the dimensionality of the higher order olfactory networks can be expected to be preserved, that is, it is the same as that of the networks in Figure 1. The functionality of the glomerular network is interpreted here as a spatial (non-linear) filter whose dimensionality (or cardinality) is given by the maximum number of taps (outputs corresponding to distinct glomeruli). For a single odor of given concentration, a number of taps "light up". These active taps give rise to a single "symbol" (odor representation in the antennal lobe). For a segmentation problem with two odors, a more complex pattern of activity will be discernible at these taps. This activity pattern typically exhibits "intersymbol interference". (The two patterns each corresponding to a single odor overlap, or interfere.) Up to the same number of taps characterize one or more olfactory networks residing in the higher brain centers. The role of these networks is to simply remove, to the extent possible, the intersymbol interference. Finally, the last decision step in the detection system is executed by a network of cardinal neurons (also labeled as taps) in a "voting network" that maps symbols into unique odor outcomes.

Neural decision models are also employed in other areas of (systems) neuroscience [13] where they are often associated with behavioral experiments. Our model, however, is markedly different from other computational models proposed for the olfactory system of a number of insects or mammals [5], [1], [2], [3]. The latter models use timing based computation of synchrony of oscillatory waves observed in the olfactory system of these organisms. To the best of our knowledge there is no clear indication in the published literature of oscillations in the olfactory system of the fly.

1.2 Relationship to Experimental Observations

The task of the olfactory system is to separate different odor representations through processing. Evolutionary tinkering [7], we believe, created an olfactory system in the fly that exploits through a small sequence of processing steps the distance between odors in the coding space and, thereby, makes accurate detection and segmentation decisions. In what follows we shall discuss methods for (i) evaluating the odor coding space and, (ii) extracting an input/output characterization of the antennal lobe of the fly. Referring to Figure 1, our model of the architecture of the olfactory system calls for

a complete characterization of the space of receptor images and the transfer function of the glomerular network. A combination of experimental and theoretical tools is used for this purpose.

By defining the odor coding space as the space spanned by receptor images, the most faithful representation of odors in the olfactory system is obtained. By further assuming that the set of dendritic currents is bandlimited (i.e., these currents have a bounded rate of change), the construction of the coding space and its investigation with tools of information theory becomes tractable.

In the experiemental literature, the input/output description of the olfactory lobe is typically given in terms of the activity patterns of OSNs and of PNs [18], [19], [17]. By assuming that the OSN and PN spike trains are essentially equivalent representations of their respective input image (i.e., dendritic tree currents), the input/output transfer function of the olfactory lobe is reduced to the transfer function of an *equivalent* glomerular network accepting the receptor image as input and the glomerular image as output.

The input to each glomerulus, however, is the sum of all activity patterns of the axons of the neurons expressing the same receptor. We postulate that this convergence can be modeled as a beamforming operation. In beamforming, a widely used strategy in array processing [8], the summation of multiple observations of the same phenomena leads to an increase in the signal-to-noise ratio. Operationally, the input to the equivalent glomerular network can be aggregated using an appropriate sum of receptor images. By reducing the dimensionality, input aggregation greatly simplifies the evaluation of the transfer function of the equivalent glomerular network. Working with the (receptor, glomerular) image pair instead of the (OSN, PN) image pair also adds an additional degree of "hardware independence". This is because spike trains generated by anatomically identical neurons might physiologically be substantially different. The receptor and glomerular images are largely insensitive to these differences.

In the next section we shall present our approach to modeling and characterization of the odor coding space and the input/output characterization of the glomerular network.

2 Functional Characterization of the Architecture

What are the limits of the olfactory system in the Drosophila? Is there a number of odors beyond which the system is not capable of recognizing odors with high probability? A back of the envelope calculation suggests that, for a given concentration, the number of recognizable odors could be anywhere between n and 2^n, where n is the number of glomeruli. For computing this rather rough estimate, we assumed that the time average of the neural activity is averaged on some small time interval. To investigate such questions, there is a need to go beyond empirical results and set up a formal mathematical model. The first step in the process calls for defining the odor coding

space. Once established, the coding space can be investigated with tools of information theory [4].

One simple way to define the odor coding space is to consider the space spanned by the set of OSN images. This approach has the advantage that, for given odor stimuli, the OSN spike trains can be readily measured in different flies. The disadvantage of this methodology, however, is that spiking neurons both within the same organism and among different sample organisms might vary. As a result the typical raster diagrams depicting the spike trains of the OSNs while qualitatively similar, display visible variations. What is the information the OSNs carry? Are variations in the timing and number of spikes among anatomically identical neurons in different sample organisms due to the underlying "hardware"? A satisfactory answer to these questions is needed in order to tackle the nature of the processing taking place in the antennal lobe.

2.1 The Odor Coding Space

We shall model the receptor image as a continuous bandlimited function

$$u^s = u^s(o, r, c, t), \tag{1}$$

where s denotes the olfactory sensory neuron, o denotes the odor, r the receptor, c the concentration and t the time variable. Thus, for a given odor receptor pair (o, r) and odor concentration c, a time function models the dendritic tree current feeding the soma of an OSN expressing the receptor r.

Each coordinate of the receptor image in Figure 1 is mapped by an OSN into a spike train. (t_k^s) denotes the sequence of spike times at the output of network of the olfactory sensory neurons. The set of these neurons is denoted by $\mathcal{S}$. The coding space is defined by $\mathcal{U} = \{u^s, s \in \mathcal{S} | u^s = u^s(o, r, c, t), o \in \mathcal{O}, r \in \mathcal{R}, c \in \mathcal{C}\}$, where $\mathcal{O}$ is the family of odors, $\mathcal{R}$ is the set of receptors and $\mathcal{C}$ is the concentration range. For example, $o = CO_2$ is an odor in the family $\mathcal{O}$ and $r =$OR22a is a member of the receptor set $\mathcal{R}$. For the fruit fly the number of detectable odors in not known. The set of receptors currently stands at 60. Thus, the coding space at the input to the OSN network is parametrized along three dimensions. One of the dimensions is given by the set of odors, one by the set of receptors and one by the concentration. Hence, the family $\mathcal{U}$ of continuous time bandlimited functions u introduced above represents the set of the odor space/time codes.

The above formalism can be used for reasoning about the nature of the odor code. A purely combinatorial space code would aggregate (abstract) information of the time component in u thus effectively providing information about the odor only through the activated receptors. Since receptors with the same identity uniquely map into the same glomerulus, the activation of the glomeruli could be used for odor recognition and segmentation. A purely time code on the other hand, would aggregate receptor information and map it into the time domain. Explicit knowledge about the activated

receptor would not be made available to higher processing centers. Without capacity constraints, a combined four dimensional (odor, receptor, concentration, time) code provides for the largest possible coding space. Information theory [4] teaches us that this space *can not be enlarged* by processing.

While taking measurements of the receptor image u appears to be at least for now a daunting task, algorithms for estimating the dendritic current based on information provided by the OSN spike trains have been developed. The OSN spike train can be readily recorded for various values of the triplet (o, r, c).

2.2 Estimating the Receptor Image

The characteristics of the spike train including, the odor response spectrum, the spontaneous firing rate, the signaling mode (excitatory or inhibitory) and the time constant of the response to stimuli (response termination) [6] must be reflected in the dendritic current as well.

An algorithm for perfect recovery of the stimulus of an integrate-and-fire neuron from reading the spiking times at its output was derived in [10] and [11]. This algorithm can readily be tailored for recovering the receptor image $u = u(o, r, c, t)$, $t \in \mathbb{R}$, based on the knowledge of the trigger (spike) times (t_k), $k \in \mathbb{Z}$. In order to simplify the notation in this section we dropped the superscript s specifying the olfactory sensory neuron and, $\mathbb{R}$ and $\mathbb{Z}$ denote the real numbers and the integers, respectively. The structure of a decoder implementing the perfect recovery algorithm is highly intuitive. Spikes are generated at times s_k, $s_k = (t_{k+1} + t_k)/2$, with weight c_k, $k \in \mathbb{Z}$, and then passed through an ideal low pass filter with unity gain for $\omega \in [-\Omega, \Omega]$ and zero otherwise, where Ω is the bandwidth of x. Thus, the output of the decoder is given by

$$u(o, r, c, t) = \sum_{k \in \mathbb{Z}} c_k(o, r, c) \cdot g(t - s_k), \tag{2}$$

where $g(t) = sin(\Omega t)/\pi t$ for all $t, t \in \mathbb{R}$. The c_k's, are the solution to a linear equation that will be discussed below. For describing the adaptation of our main theoretical result, the following notation will be used: $\mathbf{g} = [g(t - s_k)]$, $\mathbf{q} = [\int_{t_l}^{t_{l+1}} x(u) \exp(-\frac{t_{l+1}-u}{RC})\ du]$, $\mathbf{G} = [G_{lk}] = [\int_{t_l}^{t_{l+1}} g(u - s_k) \exp(-\frac{t_{l+1}-u}{RC})\ du]$ and finally, $r = RC \cdot \ln[1 - \frac{\delta - y(t_0)}{\delta - (b-a)R}] \cdot \frac{\Omega}{\pi}$, where $y(t_0)$ is the resting potential, δ is the threshold voltage, R and C are the parameters of the (leaky) integrate-and-fire model and, a and b are constants (see below).

Theorem 1 (Perfect Recovery Algorithm) *Let $u = u(o, r, c, t)$, $t \in \mathbb{R}$, be a bounded stimulus $|u(o, r, c, t)| \leq a < b$ bandlimited to $[-\Omega, \Omega]$. If $r < 1$, the stimulus u can be perfectly recovered from $(t_k)_{k \in \mathbb{Z}}$ as*

$$u(o, r, c, t) = \mathbf{g}^T \mathbf{G}^+ \mathbf{q}, \tag{3}$$

where $\mathbf{G}^+$ denotes the pseudo-inverse of $\mathbf{G}$.

We have shown [9] that this algorithm can be re-written in such a way as to become threshold insensitive. Therefore, the receptor image u does not depend on the value of the threshold voltage of the olfactory sensory neuron. This is rather obvious from an experimental standpoint. However, since direct measurements of the receptor image are not yet available, an estimate of the receptor image needs to be provided that does not dependent on the particular details of the cellular mechanism that generates spikes.

2.3 Beamforming: Characterizing the Aggregated Input to the Glomerular Network

Our working assumption in this subsection is that OSNs expressing the same receptor converge on the same glomerulus in order to increase the signal-to-noise ratio at the input to the olfactory lobe. This is akin to beamforming in array processing where observations in vector form correspond to multiple sensing devices [8]. The dimension of the observation vector is given by the number of neurons expressing the same receptor. Intuitively, beamforming of spiking neuron data would suggest that the activity pattern of neurons converging on the same glomerulus can be generated by an "ideal" equivalent neuron with improved signal-to-noise ratio.

2.4 Input/Output Characterization of the Glomerular Network

The interconnectivity between the glomeruli in the antennal lobe is determined by a set of local interneurons [14]. In order to understand how these interneurons affect the transfer of odor information between the input and output, the transfer function of the antennal lobe can be identified following an established methodology in system theory and spectral analysis [16]. The transfer function is simply the ratio between the Fourier spectrum of the glomerular and the receptor images. The transfer function provides key information regarding the functionality of the circuit diagram of the glomerular network. Note that the PN image and the OSN image can not be used for evaluating the transfer function because the neuron-induced non-linearities lead to unmanageable spectral components.

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