

Stimulus/response characteristics of cricket cercal sensory interneurons

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February 8, 2002

Abstract

We characterize the neural coding schemes of several sensory interneurons in the cricket cercal system. To do so, we derive high-quality approximations of each cell’s coding scheme by quantizing its neural responses into a small reproduction set, and minimizing an information-based distortion function. During the experiment, the sensory stimulus world presented to the animal is modified to contain a richer set of relevant features, as those features are discovered. The method produces a “dictionary” of equivalence classes, in which classes of stimulus features correspond to classes of spike-pattern “codewords”. The dictionary for several cell types is consistent across animals.

One of the steps toward understanding the neural basis of an animal’s behavior is characterizing the code with which its nervous system represents information. We recently used tools from Information Theory [2] to achieve two goals towards characterizing the neural coding scheme of a simple sensory system. We demonstrated that in the context of information theory, a coding scheme is an almost deterministic relation between clusters of stimulus/response pairs. We also developed a method to find high quality approximations of such a coding scheme. To do this, we quantized the neural responses to a small reproduction set and minimized an information-based distortion function to optimize the quantization.

To use the method in cases involving complex, high dimensional input stimuli, we model the stimulus/response relation [4]. We use several classes of models that provide upper bounds to the information distortion, used in the optimization problem [3]. In general, a smaller value of the cost function indicates a better model. All models we used were variants of Gaussian Mixture Models (GMM) [1]. The differences pertained to the number of parameters used - richer models provided a better bound to the cost function, but needed more data for robust estimates. We demonstrated their applicability by investigating coding properties of several identified neurons in the cricket cercal sensory system [4, 3].

In this work we present a more consistent effort to characterize the stimulus/response properties of identified cercal interneurons. We present results for a larger set of distinct cells. We also analyze anatomically identified cells across different animals, and demonstrate similarities in their response characteristics.

During the course of the physiological recording, the system is initially stimulated with air current stimuli drawn from a band-limited (5-500Hz) Gaussian white noise

(GWN) source [5]. This broad, non-specific stimulus allows us to coarsely explore a large portion of the input space, and provides sufficient stimulation for a coarse (small reproduction space [2]) model of the system.

After the initial model is in place, we modify the stimulus generation in two ways. First, we present more samples from the stimulus classes associated with certain neural activity, to increase the frequency of occurrence of neural responses for that stimulus class. This allows us to sample a more relevant part of stimulus space more finely, and refine the stimulus/response model, thus lowering the distortion and increasing the informativeness of the reproduction. In effect, we are modifying the original GWN source to a Gaussian Mixture White Noise (GMWN) source, with a mixture of components determined by the analysis. In principle this approach will be effective until we explore the stimulus space in sufficient detail, after which further refinements of the stimulus will not produce refinements of the response model.

Second, we modify the variability along certain stimulus directions. Since most of the GMMs project parts of the stimulus to a smaller space, reducing the variability in the discarded subspace does not significantly affect the model. We test the hypothesis that it does not significantly affect the sensory system either. Modifying the variability in the retained subspace does, however, modify the properties of the model. In this case, we modify it in a way that will provide a tighter bound in the subsequent analysis, which indicates that we have built a better model. We also modify the variability in directions orthogonal to the ones already presented. The intent of this step is analogous to the initial GWN stimulation: to present parts of stimulus space which the sensory system has not yet perceived.

Here we present most of the aspects of this analytical technique as applied to one cell. Results for additional cells and more detailed analysis will be presented at the conferences.

References

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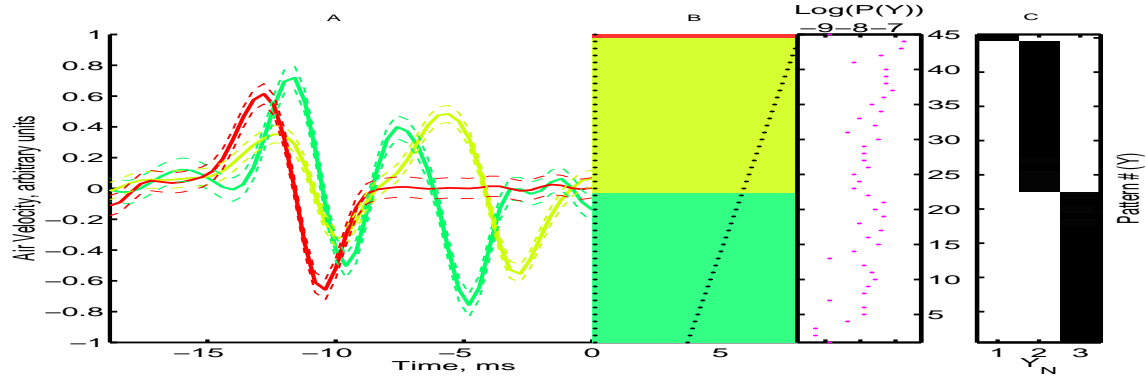


Figure 1: Results from the analysis of responses to initial GWN stimulation. Panel B) shows a raster plot of the set of unique spike patterns observed in a window of size 10ms. Each dot represents a spike. Patterns are ordered according to interspike interval. In this experiment, all but one were doublets. The patterns were clustered according to the methods described in [2, 4] into 3 classes, color-coded as red, yellow and green. To the right of panel B) are shown the probabilities (relative frequencies) of pattern occurrence. The quantizer that lead to this clustering is the conditional probability, shown in panel C). The class conditioned averages to each class in B) are show in A), color-coded according to class membership. From this analysis we adopted the working hypothesis that each spike responds to one full “sine wave” in the stimulus, and subsequent spikes represent linear superposition of the preferred stimulus.

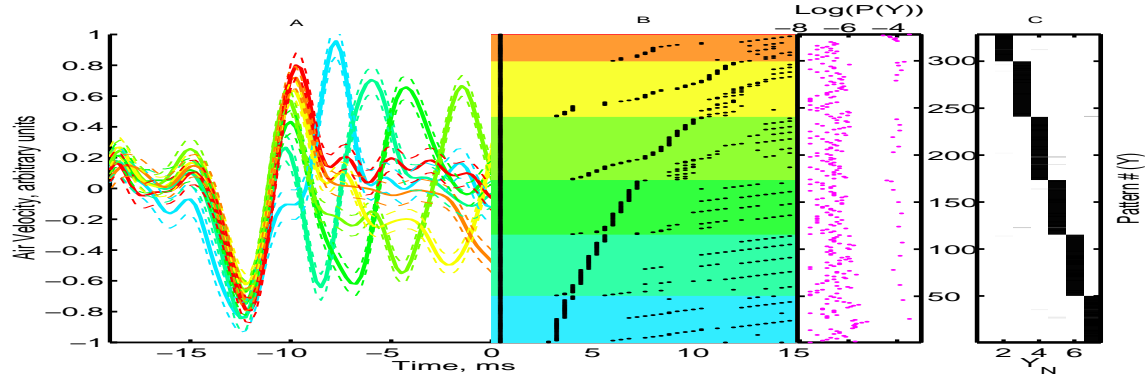


Figure 2: Results from the analysis of responses of the same cell in a different animal to stimulus, modified to reflect the results from Figure 1. The modified stimulus elicited responses with about twice the number of spikes within the same period. Patterns in B) were ordered according to class membership first. Members of the same class were ordered in ISI. The set of unique spike patterns B) was much richer than the one in Figure 1, containing many triplets, and a few quadruplets. The increased amount of data allowed us to refine the reproduction to 7 classes. The clustering seems related predominantly to the first interspike interval, and almost completely disregard the number of spikes, that is, doublets and triplets that have the same first ISI are clustered together. In some cases this does not seem to hold (e.g., the lower half of the light-green class). This can be due to one of two reasons - either we misclassify these low probability events (which is possible under any classification scheme), or the cell responds incorrectly (e.g., these spike patterns are correctly classified if we assume that the second spike in these triplet patterns was misfired).