

Characterizing Vision with Persistent Homology

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The neural code is one of the largest and most perplexing frontiers in modern science. There is an increasing body of evidence that suggests that the brain uses a small set of the same neural computations in different configurations to create the neural responses we see in different functional areas of the brain [1]. The primary visual cortex (V1) is commonly held as an exemplar for general neural behavior, so we focus our efforts for this proposal on using the topological technique of persistent homology to characterize the response to natural and white noise stimuli in V1.

The traditional model is that V1 is composed of two different cell types, *simple* and *complex* [2]. Recent studies have cast doubt on this model, and there is no consensus in the literature about what makes a cell *simple*, or even if two classes exist at all [3–6]. *Simple* and *complex* cells in the primary visual cortex were originally described and classified according to the degree of segregation between their spatial ON and OFF subregions [2,7,8]. It was later shown that *simple* and *complex* cells could be quantitatively classified by their responses to moving sinusoidal gratings. However, this straightforward classification has been questioned in a variety of studies that show that the bimodality in the neural response to sinusoidal gratings could arise from nonlinearities in spike generation [6,9,10] or that *simple* and *complex* cells could be operating as low and high-gain limits of the same basic circuit [3–5].

Persistent homology is a powerful data analysis technique that allows researchers to calculate and then analyze the shape of a dataset based on the number of “holes” in the shape in a way that minimizes the impact of noise on the characterization. The power of this technique arises from the lack of a dependence on a coordinate plane; datasets collected from different animals, using different stimuli, or even from different areas of the brain can be readily compared without painstaking parameterization. Understanding V1 through persistent homology will open a wealth of data to this analysis.

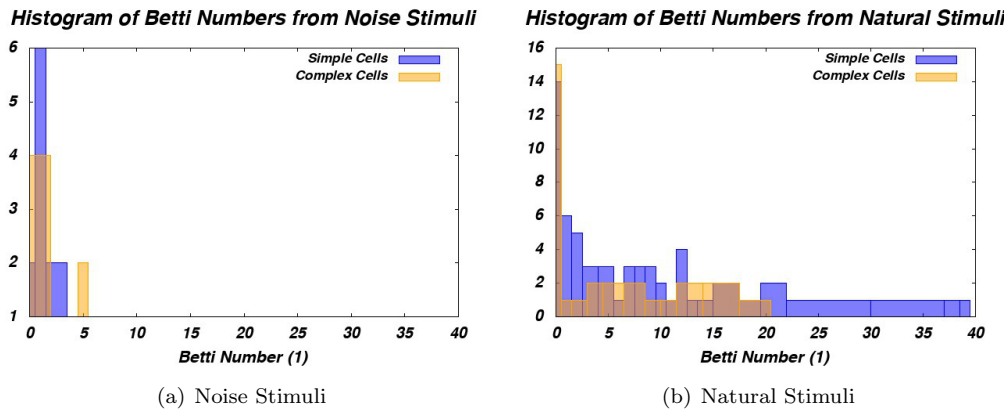


Figure 1: Betti numbers split between simple and complex cells. We see distinct differences between the responses of *simple* cells and *complex* cells to natural stimuli, but the effect is greatly reduced for white noise stimuli. This could indicate that the characterization of cells as *simple* or *complex* is stimulus-dependent.

Our spike trains are transformed into an abstract simplicial complex and the homology, represented by the Betti number, is calculated. Figure 1 shows the Betti number distributions for *simple* and *complex* cells with natural and noise stimuli. We see that the natural data has consistently greater complexity, as indicated by Betti number, than noise, which suggests that white noise stimuli are insufficient to fully probe the space of neural responses in V1. While the noise data is inconclusive, the natural data also show significantly higher Betti numbers for *simple* cells. This hints that either there exists an intrinsic difference or that the natural stimulus is eliciting a complex response from a subpopulation of cells, and suggests that *complex* cells are more invariant, and are thus more tightly integrated [11]. We hope these insights into the mechanics of information processing in vision will lead to a deeper understanding of a broad range of neural functions.

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