Persistent Homology for Characterizing Stimuli Response in the Primary Visual Cortex

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Abstract

The neural code is one of the largest and most perplexing frontiers in modern science. Much of the difficulty of studying networks in the brain lies in the fact that biological datasets are often not directly comparable, restricting most analyses to a very small sample size. We use persistent homology to investigate a basic classification problem in the primary visual cortex (V1): how do we differentiate neural responses to natural scenes from neural response to a Gaussian noise or other synthetic image? Topological techniques are particularly suited to stimuli characterization because they are coordinate free, allowing for comparison across brains, and resilient to deformation, decreasing the influence of noise. We show promising results towards obtaining a classification based on the first-order Betti number of the V1 neural response.

1. Introduction

Classification of neural responses and determining the structure of information flow in the brain is a central problem in systems neuroscience. Sensory systems are particularly interesting because they are relatively easy to stimulate in a quantifiable manner and produce complex responses to simple stimuli (Werner et al., 2008). From olfaction to vision and audition, a growing number of experiments are examining the responses of sensory neurons to natural stimuli (Creutzfeldt & Nothdurft, 1978; Rieke et al., 1995; Baddeley et al., 1997; Stanley et al., 1999;

Theunissen et al., 2000; Vinje & Gallant, 2002; Weliky et al., 2003). Observing the full dynamic range of neural responses may require using stimulus ensembles that approximate those occurring in nature (Rieke et al., 1999; Simoncelli & Olshausen, 2001), and there are several attractive ramifications of a neural representation that has been evolutionarily tuned specifically for processing the types of natural scenes our ancestors were surrounded by. (Barlow, 1961; Bialek, 2002).

Currently, we lack a method for aggregating knowledge across datasets collected using different coordinate systems and stimuli because of issues of scaling or parameterization (Singh et al., 2008). Persistent homology is a powerful analysis technique that allows researchers to calculate and then analyze the shape of a dataset based on the number of "holes" in the shape. 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. Additionally, the topological characterization is consistent under deformation, making it very resistant to noise. We thus focus on using the topological technique of persistent homology to characterize the response to natural and white noise stimuli in V1 (Fournier et al., 2011; Sharpee et al., 2006). By using responses to natural stimuli, we hope to better understand coding behaviors that could inform research directions in other brain areas.

2. Background

Though prior efforts have used topology to better understand the neural code in the visual system (Singh et al., 2008), they have done so independently of the stimulus neurons receive. Many neurons

exhibit strongly nonlinear and adaptive responses that are are more complex than a combination of simple stimuli responses would predict; for example neurons have been shown to adapt to the distribution of sensory inputs, so that any characterization of these responses will depend on context (Smirnakis et al., 1997; Brenner et al., 2000; Fairhall et al., 2001). There is also evidence that neural response is strongly dependent on a variety of seemingly disjoint signals including eye movement (Martinez-Conde et al., 2013). The variability of neural responses decreases substantially when complex dynamical, rather than static, stimuli are used (Mainen & Sejnowski, 1995; van Steveninck et al., 1997; Kara et al., 2000; Liu et al., 2001; van Steveninck et al., 2001). All of these arguments point to the need for general tools to analyze the neural responses to complex, naturalistic inputs.

2.1. Vision and the Brain

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 (Carandini & Heeger, 2011). The primary visual cortex (V1) is a region of the brain that is relatively well studied and easy to probe in mammals, and studies have identified V1 as a key to understanding neural coding in the brain (Douglas & Martin, 1991). The traditional model is that V1 can be functionally characterized by two different cell types, *simple* and *complex* (Hubel & Wiesel, 1959). 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 only two classes exist at all (Debanne et al., 1998; Chance et al., 1999; Abbott & Chance, 2002; Priebe et al., 2004). If it is discovered that a feedback model better represents signal aggregation within V1 than the traditional feed-forward model, we have reason to seek feedback models for aggregate behavior in other brain regions (Douglas & Martin, 1991; Carandini & Heeger, 2011). Since the topological characteristics of a response are resistant to many forms of deformation, the persistent homology technique should be able to consistently separate classes of cells in V1, and eventually other brain areas, by their response to natural and noise stimuli.

3. Methods

While topology has traditionally only been used to analyze abstract and exotic mathematical constructs, the last decade has seen a signifi-

cant body of work emerge in topological data analysis (Mahadevan, 2005; Lum et al., 2013; Carlsson et al., 2008; Carlsson & Zomorodian, 2009; Zomorodian & Carlsson, 2005; Carlsson, 2009). The fundamental idea behind these analyses is that topology acts as a geometric tool for pattern recognition within a data set. A key premise in topology is that data is studied outside of a coordinate structure; as long as a distance function is definable within a space, the topology is calculable and comparable to that of the same data collected in a different coordinate space. Additionally, topological structures are immune to small deformations in shapes; the homology remains consistent. This tolerance allows more varied and noisier data to be classified according to an underlying structure.

Since datasets are a series of points and not a continuous surface, we approximate the shape using an *abstract simplicial complex*. A simplex is simply the n dimensional analog of a triangle. A simplicial complex is then essentially a polygonal mesh, or triangulation, over a surface in n dimensions; these models may be familiar from the wireframes used to render computer graphics. Whereas a simplicial complex is a geometric construct, an abstract simplicial complex is the combinatorial equivalent, which is useful when dealing with discrete, finite data. More rigorously, given a family Δ of finite subsets of a set S that contains all sets (including itself), Δ is a simplicial complex if for every set X in Δ, and every subset Y of X, Y is also a member of Δ. In matroid theory, which is part of the study of computer algorithms, these complexes are known as independence systems (Leiserson et al., 2001; Hatcher, 2000).

The complex we use for our analysis is a *Vietoris-Rips complex*, or simply Rips complex. This restricts our set to those abstract simplicial complexes that can be defined from a metric space M and threshold value ε such that the simplex for every finite set of points has diameter of at most ε. Using the Rips complex makes homology calculation viable for real datasets because the fully connected simplicial structure without a threshold would obscure any holes in the topology of the data. Betti numbers are a count of the persistent intervals when the nested family of simplicial complexes is plotted over a range of ε values.

Data: For this work, we used a previously published dataset of V1 responses to naturalistic movies and white noise stimuli in cats (Sharpee et al., 2006). The naturalistic movies were taken during a walk through a wooded area; sample stills from these movies are shown in Figure 2. The responses we have analyzed
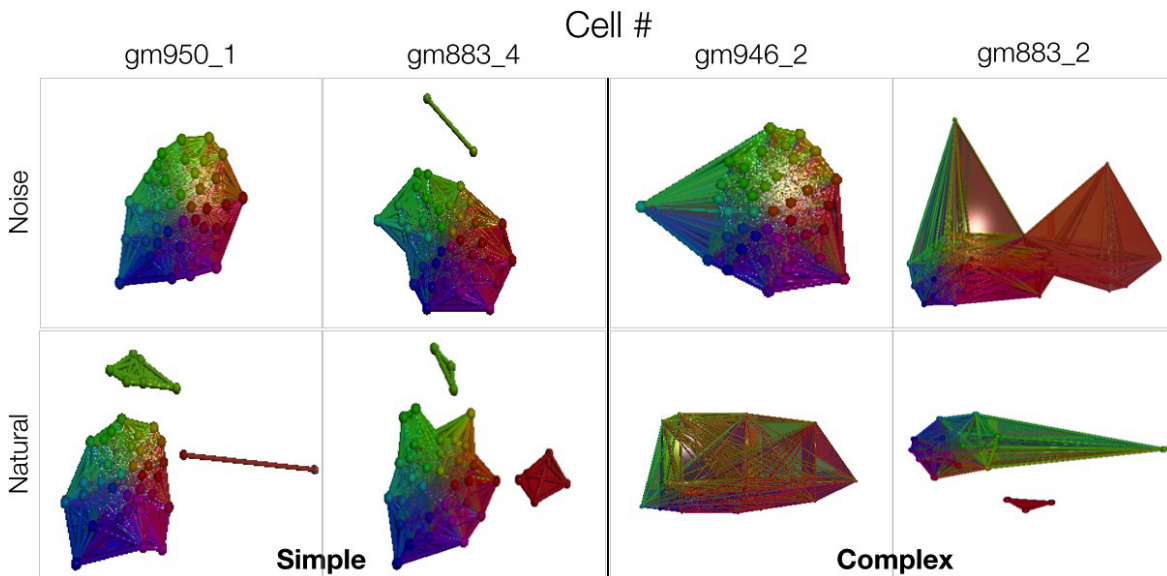
Figure 1. This figure shows the topology of two *simple* cells (left) and two *complex* cells (right) under noise (top) and natural (bottom) stimuli. Natural stimuli responses generally have a more componentized topology than responses to Gaussian noise in our V1 data.
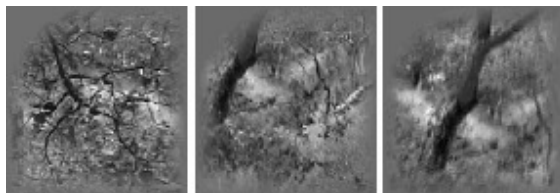

Figure 2. Sample scenes from the natural movies. Note: studies described in this paper were done without the Gaussian blur filter shown on the image edges.

thus far were collected for movies without the Gaussian blurred borders seen on the still frames in the stimulus frames. The statistical properties of this ensemble agree with previously published reports for natural stimuli (Ruderman, 1994; Simoncelli & Olshausen, 2001). One measure of the deviation from a Gaussian ensemble is the kurtosis of the distribution of light intensity values of individual pixels. The natural stimulus ensemble used in this study had a mean kurtosis value across pixels of 0.4 (range from 0.19 to 0.64) measured for the distribution of light intensity at single pixels across 50,000 frames. By comparison, one can expect to find kurtosis values less than 0.04 for a sequence of the same size taken from the uncorrelated Gaussian distribution (Press et al., 1992).

4. Analysis

Figure 1 shows a projection of the simplicial complexes for two *simple* neurons and two *complex* neurons under both natural and noise stimuli. Though several of the components appear sparse, we found that they were robust against the addition of random noise perturbations to the data. The complexes in this figure represent typical topologies found in our V1 responses. We observe that the complexes derived from responses to natural stimuli are disconnected relative to those from the noise stimuli. This is consistent with the notion that natural stimuli probe the response space more completely than Gaussian white noise would. Furthermore, we observe that complex cell responses generally have fewer components than simple cells when probed by natural stimuli. This suggests that complex cells have higher invariance and are thus more interconnected with other neurons in the visual cortex (Adelson & Bergen, 1985).

To obtain a numerical characterization, we measure the homology of the simplex and see if the homology stays constant, or persists, over a series of radii (ε). This method was used often in previous work by the CompTop lab (Dabaghian et al., 2012; Carlsson et al., 2005; Chan et al., 2013; Nicolau et al., 2011; Singh et al., 2008).

To compute the persistent homology, we derive Rips complexes for each cell using a range of ε values and then calculate the homology in each of n dimensions,
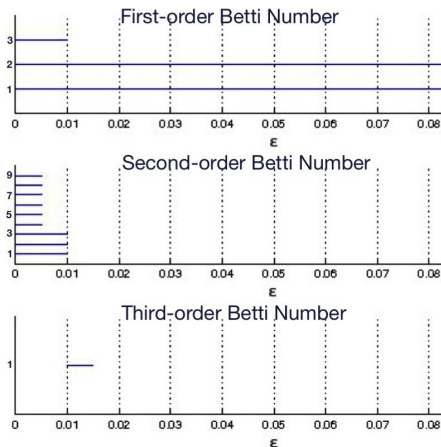
Figure 3. The "barcode" of a cell #883_4 given noise stimuli. Each set of lines corresponds to a dimension of the originating complex. The number of horizontal lines, which represent a series a Betti numbers in the space of nested simplicial complexes, is varied by ε on the x-axis

Figure 4. Histogram of the 1-Betti numbers derived from the entire database of V1 cat responses to both natural and noise stimuli. We see that the natural stimuli have consistently higher 1-Betti numbers, indicating greater topological complexity.

known as the *Betti numbers* for each cell. The ε range will vary from 0 (no connected components) to infinity (every point has an edge to every other point). For each ε value, the Betti interval represents the shape of the resulting Rips complex. Carlsson showed that at some point in the ε range, the number of holes per dimension will remain constant over a relatively long interval (Carlsson et al., 2009; 2005). The number of holes in every dimension are the Betti numbers of the dataset, with the holes in dimension i referred to as the i-Betti number. Figure 3 shows the homology for a simplex in dimensions 1, 2, and 3. Since the only lines that persist are 2 in dimension 1, the Betti number for the noise response of this cell is 2. Betti numbers will always be dimensionless non-negative integers. For each cell, we combined the spike trains for natural and noise stimuli into separate matrices and calculated the Betti numbers for each cell-stimuli pair using a witness stream (De Silva & Carlsson, 2004), which is essentially a filtered simplicial complex, to generate the underlying Rips complex. Using a witness stream is significantly more efficient than calculating the Rips complex directly because the witness stream selects landmark points and bases the simplex calculations around these points. Persistence intervals were selected by using the infinite filter function in Javaplex and then visually verified using barcode diagrams such as Figure 3. For this work, we set ν, the parameter that selects the nested family of complexes used, to 1 and the number of landmark points to 40 (out of 55 data points per instance). Figure 4 shows a histogram of Betti numbers across the entire neural response. We see that natural stimuli have consistently
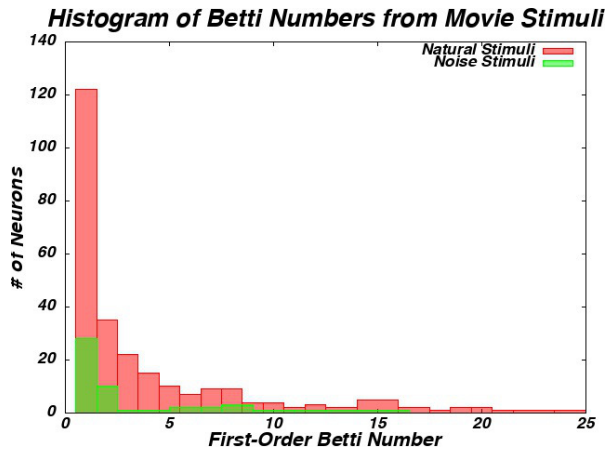
higher 1-Betti numbers, indicating that there are more distinct sections of neural response to natural versus noise stimuli.

5. Discussion

Nicolau *et al.* use a persistent homology technique very similar to the one we are developing to classify subgroups of breast cancer using gene expression data (Nicolau et al., 2011). We can subclass the space of V1 neural responses to both natural and noise stimuli into topological components and compare this classification to the labels derived from testing cells with a sinusoidal grating. We used an agglomerative clustering mechanism to select vertices for the simplicial complex to maintain scale invariance, and we will compare the results of the topological grouping to clustering done on the raw data.

Once a classification is obtained, we find features of the response using a number of feature selection techniques to better understand the role of each classified subtype if it does not match our current understanding of *simple* and *complex* groups (Sharpee et al., 2004; Yu & Liu, 2003). The same technique could then also be used on extrastriate data from macaques to validate both that the topological results are true in a different dataset and that they hold in different regions of the visual cortex.

Our next steps are to use more filter functions to obtain higher order Betti numbers as well as expand our model to characterize how quickly the topology of the neural response changes between cell types. We also

have preliminary results that show shifting topologies over time over a recording of natural stimuli response, and believe that there is a wealth of knowledge to be gained from this technique within sensory neuroscience.

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