Simplicial Homology and Burst-Synchronizing Neural Networks

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Abstract

Here we explore burst-synchronizing neural networks in the perspective of simplicial homology. We show that the algebraic and topological features of a biological neural network provide helpful information about which neurons are important in maintaining the synchrony of the network. Simulations are run over small homogeneous networks of about 35 neurons or less using the Hindmarsh-Rose model. Neurons are ablated sequentially and the synchrony of the network is measured. We find that neurons that are essential to the homology of the network are also essential to its ability to synchronize and neurons that do not contribute to the algebraic structure can be ablated with little change in the synchrony of the network.

1 Introduction

In this study we look at what algebraic topology can tell us about the behavior of neural networks that exhibit burst synchrony. Although our simulations closely model sections of the Pre-Bötzinger complex (PreBotC), we try to generalize our findings to any neural system that consists of neurons that produce a rhythmic bursting behavior. We focus on how the structure of a network can influence or even dictate its ability to synchronize. Tools from algebraic topology give can give us insight as to what features of a network that are not immediately apparent are crucial to how the system behaves. Previous studies (Gaiteri and Rubin 2011, Song 2016) have investigated network topology and its effect on neural systems, but few have approached network topology using simplicial homology in this way.

We use the Hindmarsh-Rose neuron model for our simulations because of its ability to exhibit complex dynamics while also being computationally simple. The parameters were chosen to have a neuron tonically spike when in isolation and then burst in synchrony when coupled to other neurons, as this closely models the rhythmic bursting behavior of the PreBotC. We create networks of about 35 neurons or less which are subnetworks of an Erdos-Renyi graph consisting of 330 neurons with a probability of connection of $p = 0.1$. This allows us to study more closely the topological features and how single-neuron interactions guide the emergent synchronized activity of the network.

In order to categorize the neurons that make up the network into ones that are essential to the topology and ones that are not ("essential" vs "extraneous" neurons), we construct topological and algebraic structure from the network's connectivity, and from there we use simplicial homology to determine when a neuron is essential or extraneous to the homology of the network.Then, to quantify the effect that topological features of a network have over its ability to synchronize, we simulate these bursting neural networks and systematically ablate neurons that are (or are not) essential to the topological structure and then measure how the synchrony of the network changes. We predict that neurons that contribute to the topology of the network will also contribute more to the synchronization than neurons that do not. So we will expect to see a greater drop in the synchronization measure after an essential neuron is ablated and little to no change in the synchronization measure when an extraneous neuron is ablated.

2 Model and Simulation Design

2.1 Neuron and Network Model

For this study we use the Hindmarsh-Rose neuron model. A system of three differential equations allow for enough complexity to exhibit a large range of behavior in neurons but it is also quite computationally simple. Each neuron has three state variables.

$$\dot{x} = y - ax^3 + bx^2 + I - z$$
$$\dot{y} = c - dx^2 - y$$
$$\dot{z} = r(s(x - x_{rest}) - z)$$

With this model, the membrane potential is represented by $x(t)$ which is usually the most observed variable while the movement of ions through fast channels such as sodium and potassium are accounted for by $y(t)$ and the movement of other ion through slow channels are accounted for by $z(t)$. We also use the parameters $a = 1, b = 3.3, I = 2, c = 1, d = 5, r = 0.001, s = 4, x_{rest} = -\frac{1+\sqrt{5}}{2}$.
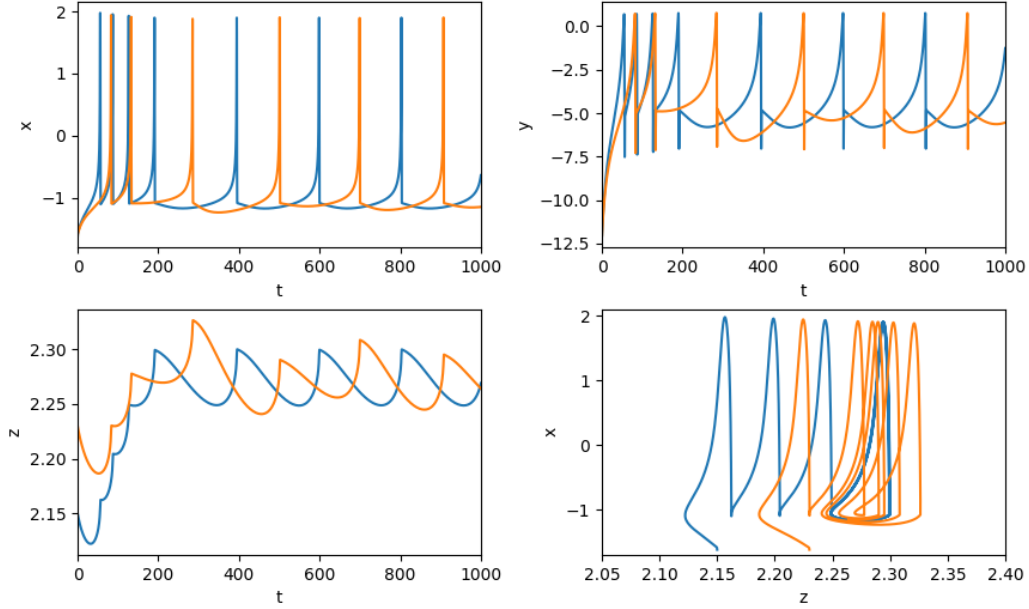

Figure 1: Two neurons spiking in isolation.

Since we are studying neural networks, we need to determine how to couple neurons together. We use a sigmoid curve to act as a threshold between the presynaptic and postsynaptic neurons giving the modified system of equations.

$$\dot{x}_{post} = y_{post} - ax_{post}^3 + bx_{post}^2 + I - z_{post} - gA_{i,j}(x_{post} - V_0)\sum \Gamma(x_{pre})$$
$$\dot{y}_{post} = c - dx_{post}^2 - y_{post}$$
$$\dot{z}_{post} = r(s(x_{post} - x_{rest}) - z_{post})$$

$$\Gamma(x) = \frac{1}{1 + e^{-\lambda(x-\theta)}}$$

So presynaptic neurons' action potentials greater than θ are summed at the postsynaptic neuron. The newly introduced coupling parameters have values $V_0 = 2, \lambda = 10, \theta = -0.6, g = 0.1$ and the term $A_{i,j}$ is the ith row and j^{th} column of the connection matrix that describes the network taking a value 1 if neuron i is connected to neuron j and 0 if not. The dynamics we observe with these parameters we attempted to model behavior similar to that of the pre-Bötzinger Complex because of its function in synchronizing rhythmic behavior but note that we are more generally studying networks that exhibit burst synchrony.
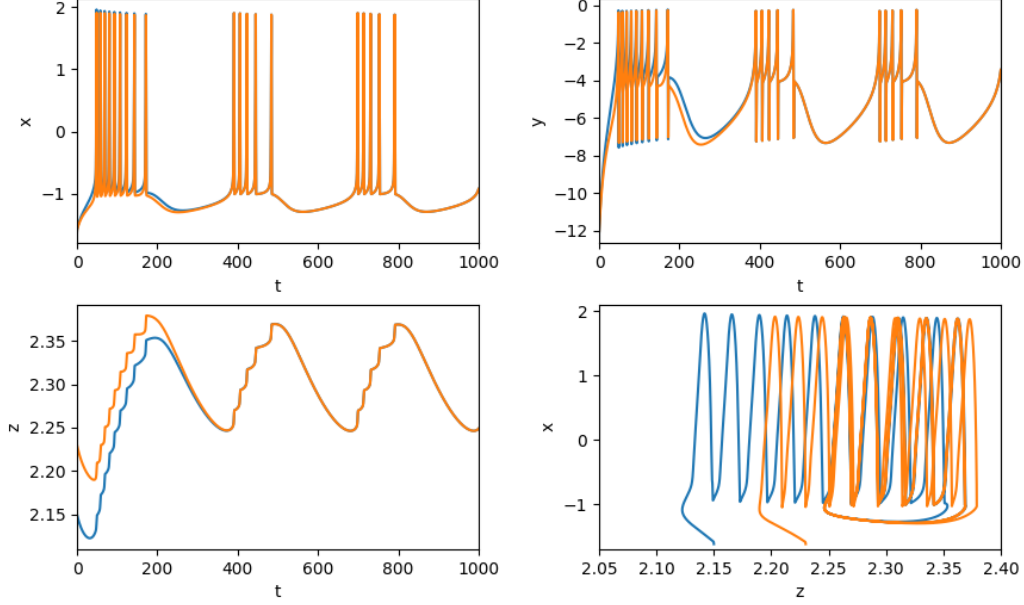

Figure 2: Two neurons bursting synchronously.

Our networks are homogeneous in that each neuron has the same parameters but we alter each neuron's initial conditions slightly to allow natural behavior to emerge. For these simulations, each neuron starts with the same initial state variables of $x_{init} = x_{rest}, y_{init} = 1 - 5x_{rest}^2, z_{init} = 1.7$ but before the simulation begins, each initial condition of each neuron is perturbed by some amount chosen from a normal distribution with $\mu = 0, \sigma = 0.5$.

2.2   Measuring Synchrony

The purpose of this study is to determine how the homology induced by the networks structure contributes to the system's ability to synchronize. For this, we need a way to measure the synchronization over a population of neurons

3   Introduction to Simplicial Homology

Definition 1. *A **simplex** is a generalization of a triangle or tetrahedron in higher dimensions. It is a $k-$dimensional polytope of $k + 1$ vertices*

In this paper, we will represent simplices (topologically) as sets. So an n-dimensional simplex will be denoted with the $n + 1$ vertices as $\{v_1, ..., v_{n+1}\}$, however, when we move to the perspective of algebra we will denote them as ordered tuples, $(v_1, ..., v_{n+1})$, which will help with computation.

Definition 2. *A **simplicial complex** is a set X of simplices that satisfy the following conditions*

   1. If $\sigma \in X$ and $\tau \subset \sigma$ then $\tau \subset X$;

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2. If $\sigma, \tau \in X$ and $\sigma \cap \tau \neq \emptyset$ then $\sigma \cap \tau \in X$

A simplicial complex can be thought of as a collection of simplices (points, line segments, triangles, tetrahedra, etc.) that intersect only at their faces.

(images from some paper saying what is allowed and visually explaining the two conditions)

For a simplicial complex, we can find topological invariants of that space such as holes of different dimensions if we look at the simplicial complex from an algebraic perspective. These following techniques and methods give us a nice way to travel between topology and algebra in a rigorous mathematical way.

Definition 3. *A **chain group** is a free abelian group generated by the simplices of a certain dimension in a simplicial complex. So for a simplicial complex K and a given dimension k, the respective chain group is defined to be $C_k = \langle \Delta_1, ..., \Delta_n \rangle$, where each Δ_i is a $k-$dimensional simplex in K so if $\sigma \in C_k$ then $\sigma = a_1 \Delta_1 + a_2 \Delta_2 + ... + a_n \Delta_n$ where each coefficient a_i is an element of some field $\mathbb{F}$. We call an element of a chain group a **chain**.*

So for example, take a simplicial complex

$$K = \{\{v_1\}, \{v_2\}, \{v_3\}, \{v_1, v_2\}, \{v_1, v_3\}, \{v_2, v_3\}, \{v_1, v_2, v_3\}\}$$

A filled-in two-dimensional triangle, we define

$$C_0 = \langle v_1, v_2, v_3 \rangle$$
$$C_1 = \langle (v_1, v_2), (v_1, v_3), (v_2, v_3) \rangle$$
$$C_2 = \langle (v_1, v_2, v_3) \rangle$$

And for all $n > 2$, $C_n = \{0\}$

This is the first step in obtaining algebraic structure from our topological structure through a simplicial complex. The next is to construct a way to travel between these different chain groups.

Definition 4. *For a simplicial complex K, and chain groups $C_0, ..., C_n$ we can define an function ∂_k called the **boundary operator**, a homomorphism that maps elements from C_k to elements in C_{k-1}*

$$\partial_k : C_k \to C_{k-1}$$

So for some $\sigma \in C_k$ where $\sigma = (v_0, ..., v_n)$ then

$$\partial_k(\sigma) = \sum_{i=1}^{k}(-1)^{i-1}(v_0, ..., v_{i-1}, v_{i+1}, ..., v_n),$$

Or algebraically as the alternating sum of the faces of the simplex. It can be observed that $\partial_k \circ \partial_{k+1} = 0$ which implies that $\text{Im}(\partial_{k+1}) \subseteq \ker(\partial_k)$

Now, with these chain groups that have homomorphisms between them, we can build what is called a chain complex.

Definition 5. *A **chain complex** is a sequence of chain groups connected by homomorphisms (boundary operators) such that $\partial_k \circ \partial_{k+1} = 0$ for all k*

$$\ldots \xrightarrow{\partial_3} C_2 \xrightarrow{\partial_2} C_1 \xrightarrow{\partial_1} C_0 \xrightarrow{\partial_0} C_{-1} \xrightarrow{\partial_{-1}} \ldots$$

For a simplicial complex with a finite maximum dimension n, $C_m = \{0\}$ for $m > n$ and $C_\ell = \{0\}$ for $\ell < 0$

When applying the boundary operator to the different chain groups of a simplicial complex, it can be seen that the chains in each chain group that map to 0 by ∂ are the chains that form cycles in the way we normally think about cycles on a graph, but again, can consist of elements of higher dimension that enclose a space.

So since $\mathrm{Im}(\partial_{k+1}) \subseteq \ker(\partial_k)$ we can take the quotient group

$$H_k := Z_k/B_k = \ker(\partial_k)/\mathrm{Im}(\partial_{k+1})$$

which is what we call the kth homology group.

Definition 6. *A **homology group** of dimension k, H_k, is the set of equivalence classes where two cycles are in the same equivalence class if they differ by a boundary, that is:*

$$For\ any\ \ [\gamma] \in H_k,\ if\ \ \sigma, \tau \in [\gamma]\ then\ \ \sigma - \tau = \partial(\beta)\ for\ some\ \ \beta \in C_{k+1}$$

Now, since each H_k is a group, the rank (number of generators) of H_k is what we call the kth Betti number of the simplicial complex.

Definition 7. Betti numbers *are positive integers associated with the homology groups of a given simplicial complex. The rank of the kth homology group, H_k, is called the kth Betti number or β_k. These Betti numbers tell give us how many "holes" of dimension k there are in a simplicial complex.*

And the homology of a simplicial complex is completely dependent on what elements are included as simplices, which can give rise to many different simplicial complexes even when starting with the same initial framework, as we will show in the next section. For example, take the two simplicial complexes

$K_1 = \{\{v_1\}, \{v_2\}, \{v_3\}, \{v_4\}, \{v_5\}, \{v_6\}, \{v_7\},$
$\{v_1, v_2\}, \{v_1, v_4\}, \{v_1, v_5\}, \{v_1, v_6\}, \{v_2, v_3\}, \{v_3, v_4\},$
$\{v_3, v_7\}, \{v_4, v_5\}, \{v_4, v_6\}, \{v_4, v_7\}, \{v_5, v_6\}, \{v_6, v_7\},$
$\{v_1, v_4, v_6\}, \{v_1, v_5, v_6\}, \{v_1, v_4, v_5\}, \{v_1, v_4, v_6\},$
$\{v_4, v_5, v_6\}, \{v_3, v_4, v_7\}\}$

$K_2 = \{\{v_1\}, \{v_2\}, \{v_3\}, \{v_4\}, \{v_5\}, \{v_6\}, \{v_7\},$
$\{v_1, v_2\}, \{v_1, v_4\}, \{v_1, v_5\}, \{v_1, v_6\}, \{v_2, v_3\}, \{v_3, v_4\},$
$\{v_3, v_7\}, \{v_4, v_5\}, \{v_4, v_6\}, \{v_4, v_7\}, \{v_5, v_6\}, \{v_6, v_7\},$
$\{v_1, v_4, v_6\}, \{v_1, v_5, v_6\}, \{v_1, v_4, v_5\}, \{v_1, v_4, v_6\},$
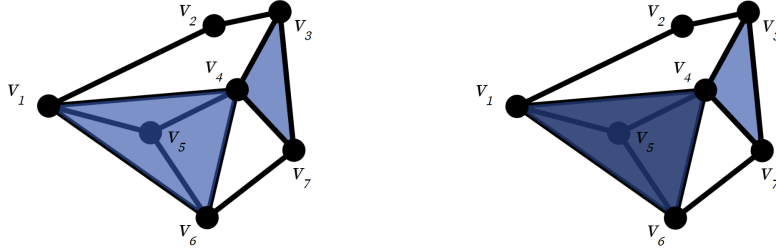$\{v_4, v_5, v_6\}, \{v_3, v_4, v_7\}, \{v_1, v_4, v_5, v_6\}\}$

Figure 3: K_1, shown on the left, and K_2, shown on the right

Which only differ by the simplex $\{v_1, v_4, v_5, v_6\}$ excluded in K_1 and included in K_2, meaning that K_1 has the Betti numbers: $\beta_0 = 1, \beta_1 = 2, \beta_2 = 1$ and K_2 has the Betti numbers: $\beta_0 = 1, \beta_1 = 2, \beta_2 = 0$. These two simplicial complexes have the same underlying graph (1-skeleton) but do in fact have different homology groups and thus are different simplicial complexes. In the next section we will introduce a way to construct a simplicial complex from a neural network, which again can be thought of as the 1-skeleton, with a careful choice of which cliques (complete subgraphs) of neurons to include as simplices and which to leave as topological holes.

3.1 Direct Cliques and Making Simplicial Complexes from Networks

Here we outline how to construct the algebraic object of a simplicial complex from the graph that realizes a network and still reflects the flow of information through synapses. This can be done using the **directed clique condition** proposed by Riemann et al (2017). To create a simplicial complex from a graph, we need to consider which complete subgraphs will be included as simplices and which will be left as topological "holes". It would be simple to make any clique a simplex but imposing a condition to limit only special cliques to be counted as simplices in the simplcial complex allows us to create a simplicial complex that reflects the flow of information in the network.
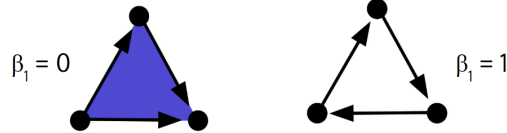

Figure 4: Left: a directed 3-clique, which would be included as a simplex and thus have $\beta_1 = 0$ and right: a 3-cycle which would not be included as a simplex and would be counted as a topological hole.

So given a network's connectivity matrix, which admits a 1-skeleton, we use this condition to construct a simplicial complex. From there, we analyze the topology of the complex and we have its Betti numbers. Then for each ablation, we check to see if the Betti numbers of the new simplicial complex are different than the previous Betti numbers. If the Betti numbers change then the ablated neuron was essential, if they remain the same after the ablation than the neuron was extraneous. Using the K_2 defined above, if we think about this as a simplicial complex that was built from a neural network where the 0-simplices are neurons, we can easily see that if neuron v_5 is removed, the homology of complex is not changed. This is because K_2 includes the simplex $\{v_1, v_4, v_5, v_6\}$ and thus v_5 is extraneous. Any other neuron, take v_2 for example, is essential because if it is removed, one of the 1-dimensional holes of the complex goes away and thus β_1 goes from 2 to 1.

4 Discussion

Simulations were run on Erdos-Renyi graphs with $n = 33$ and $p = 0.1$ giving an average degree of $np = 33 \cdot 0.1 = 3.3$.
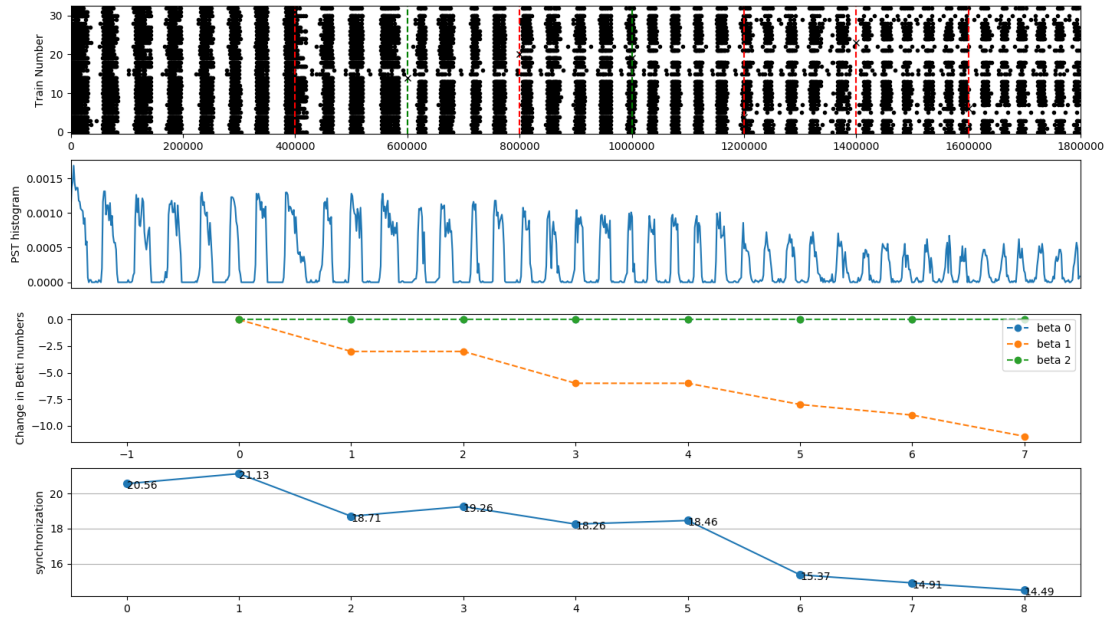
Figure 5: A simulation with 7 ablations, 2 of which preserve the homology (shown in green). We can see that these have little negative effect on the measured synchronization of the network while other ablations reduce the synchronization greatly.

References