

4.1 Brain network (work in progress)

(WIP) In this case analysis our main object of study will be two synthetic networks generated based on the striatum. One network consists of 50 001 vertices and the other network of 999 vertices. It has to be said that the smaller network suffers from being too small to give even the most central neurons all the neighbours it should have.

Definition 4.1.1. A directed clique is a directed graph $G = (V, E)$ such that every vertex has at least an outgoing or incoming edge to every other vertex in the graph.

Definition 4.1.2. Let $G=(V,E)$ be a directed graph. The directed flag complex $dFl(G)$ is defined to be the ordered simplicial complex whose k -simplices are all directed cliques with vertices v_0, \dots, v_k such that $\forall i : v_i \in V$ and $\forall i, j : i < j \implies (v_i, v_j) \in E$. The vertices v_0, v_k are called the source and the sink of a k -simplex.

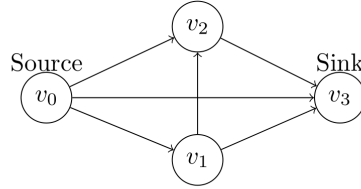


Figure 4.5: A 3-simplex in a directed flag complex.

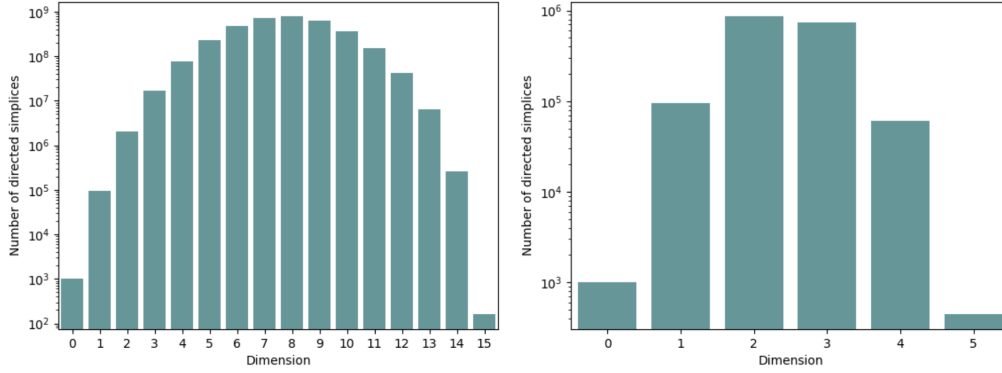


Figure 4.6: The number of simplices in each dimension for the directed flag complex generated by (a) synthetic network from Snudda, (b) random network generated with the same edge probability creation as the first network, both with 999 vertices.

In Figures 4.6 and 4.7 we see that the synthetic brain networks have much more higher order structure in terms of high dimensional simplices than a network generated solely

4 Analysis

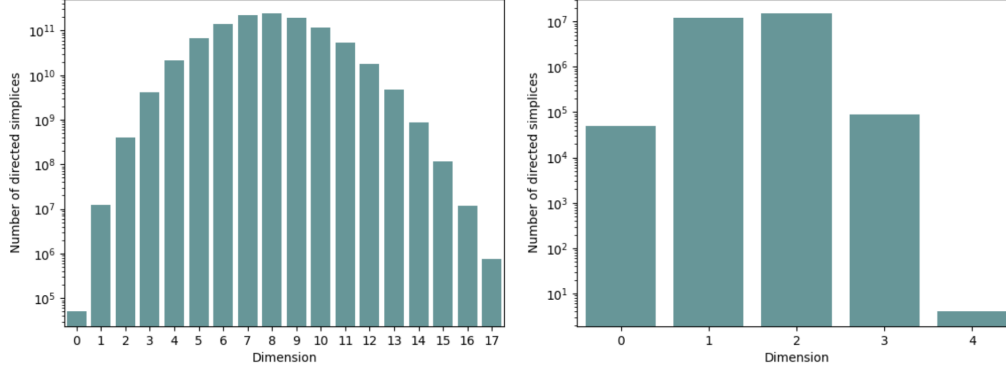


Figure 4.7: *The number of simplices in each dimension for the directed flag complex generated by (a) synthetic network from Snudda, (b) random network generated with the same edge probability creation as the first network, both with 50 001 vertices.*

based on edge connectivity. For instance, we see in 4.7 the presence of 17-dimensional cells in the synthetic network, which means directed cliques consisting of 18 participating neurons, whereas in the random network we see at most 4-dimensional cell.

In other to further investigate these higher order cells in the synthetic networks we can look at their persistent homology. However, a priori the directed brain network does not have any weights, and so it is not obvious what a filtration $f : V \rightarrow \mathbb{R}_+$ would look like. So we impose a metric space structure on the directed graph by giving the value of a directed edge between two vertices the Euclidean distance between the two neurons in the simulated model. This means that at low threshold values the filtration will only look at connections made by neurons very close to each other, but as the threshold increases we look at a larger and larger part of the network.

So what is a generator of a homology group in a brain network? It would have to be a k -simplex which is not the boundary of a $k + 1$ -simplex, which translated to the brain network means a clique of neurons that are in themselves an isolated source-sink network and not part of any other network.

Due to computational aspects it is not feasible to compute the persistent homology of the synthetic network with 50 001 vertices, so we restrict ourselves to a subnetwork of the full network consisting only of dSPN neurons as seen in Figure 4.8. We also look at a full synthetic network generated with only 999 vertices in Figure 4.9.

We see that the formation of higher order (> 5) homology generators mostly happens over small distances, which reaffirms the notion of the brain having a small-world structure.

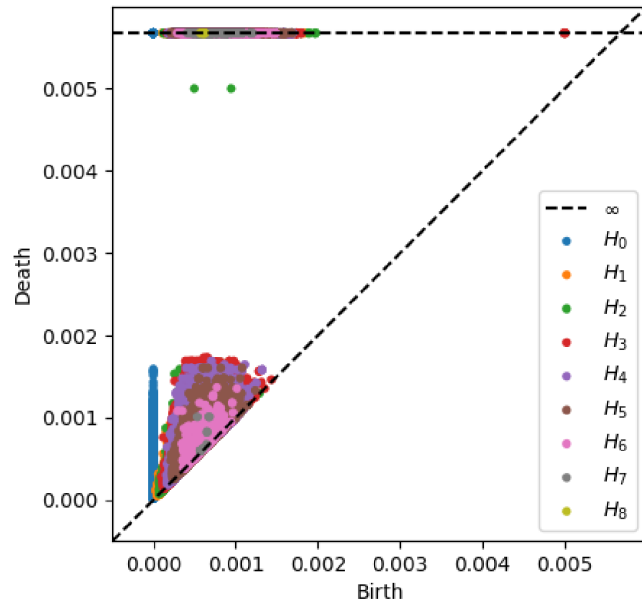


Figure 4.8: Persistence diagram of the subnetwork of dSPNs extracted from a synthetic network of 50 001 vertices.

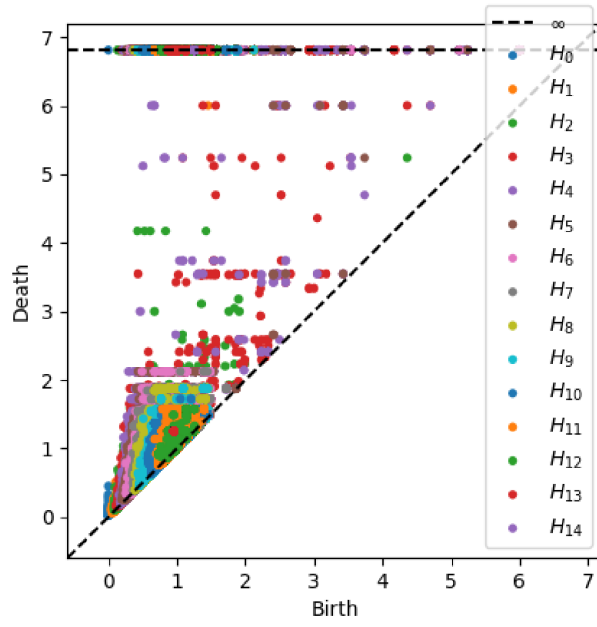


Figure 4.9: Persistence diagram of the entire synthetic network consisting of 999 vertices. (this is scaled 1000 larger than in actual data, generate new diagram)