

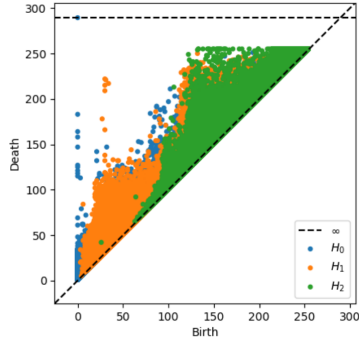
4 Analysis

The volumes of the eight samples' persistent homologies were analyzed in H_0, H_1, H_2 . Since the data is 3-dimensional only these three were of interest. H_0 generally determines the number of connected components, we expect H_0 to be 0 at a large enough filtration value. H_1 encodes “loopiness” of the sample, i.e. how many loops we find in the eye surface. H_2 encodes enclosed voids in the eye surface, i.e. how many empty spaces enclosed by the eye structure we find.

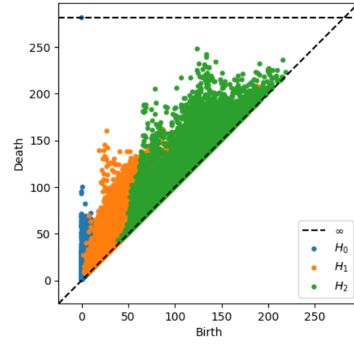
For the graph and heatmaps we have encoded the MorphoSource scan IDs according to the following scheme:

MorphoSource ID	Encoded ID
77967	0
60186	1
60185	2
77066	3
77974	4
77971	5
77973	6
77970	7

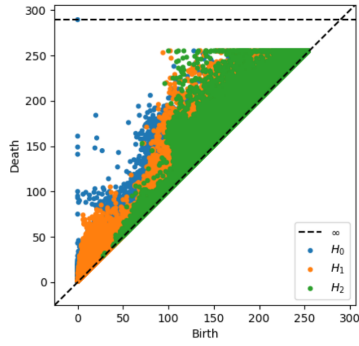
4 Analysis



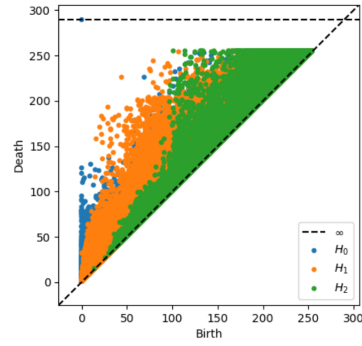
(a) 60185



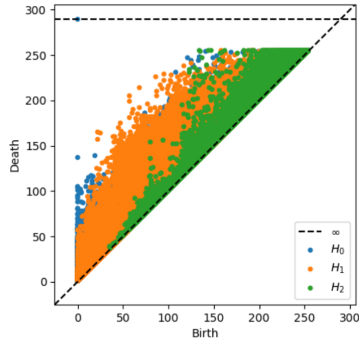
(b) 60186



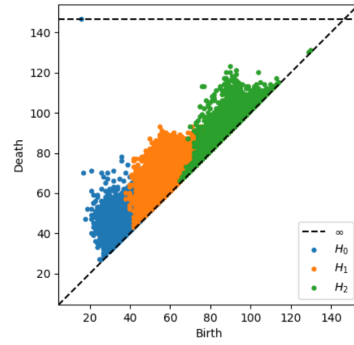
(c) 77066



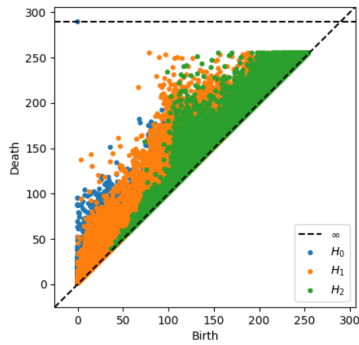
(d) 77967



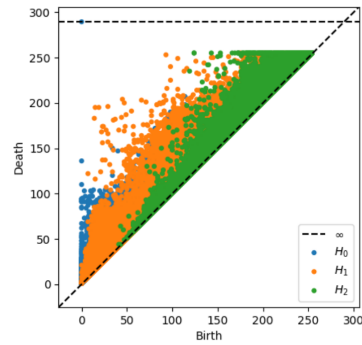
(e) 77970



(f) 77971



(g) 77973



(h) 77974

Figure 4.1: Persistence diagrams of the left eye of the eight bee samples.

4 Analysis

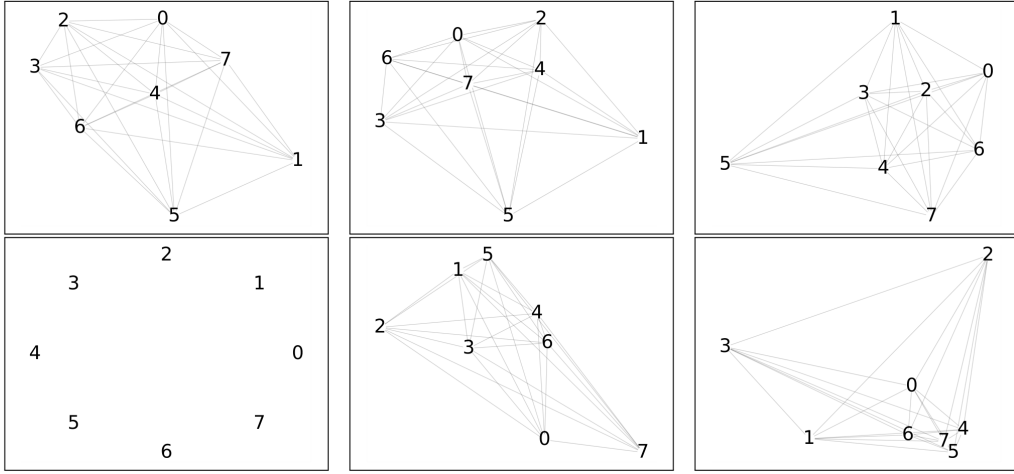


Figure 4.2: *Graphs that illustrates the pairwise bottleneck distance (top) and pairwise Wasserstein distance (bottom) between the persistence diagrams in H_0, H_1, H_2 (left, middle, right) of the bee eyes. Closer nodes indicate more similar persistence diagrams.*

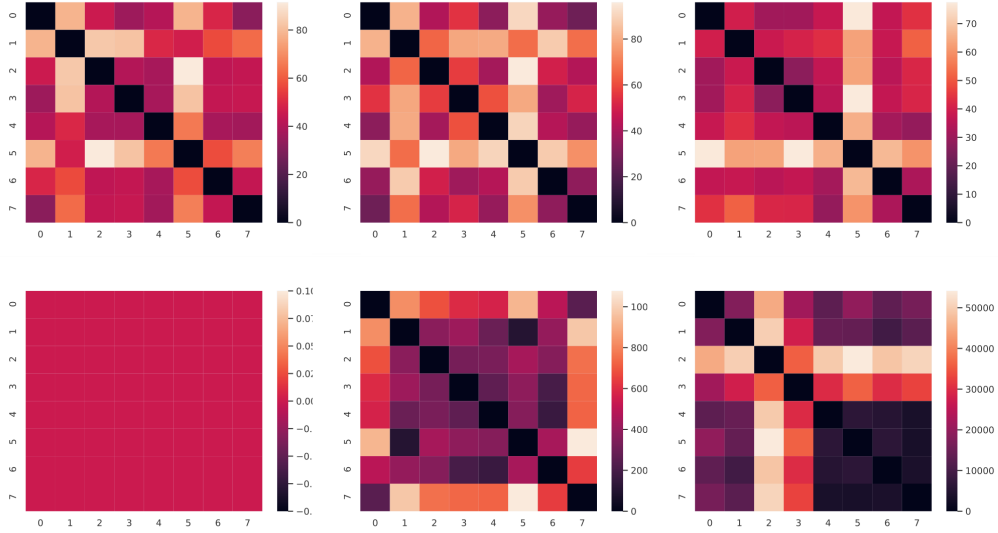


Figure 4.3: *Heatmaps that illustrates the pairwise bottleneck distance (top) and pairwise Wasserstein distance (bottom) between the persistence diagrams in H_0, H_1, H_2 (left, middle, right) of the bee eyes. Cooler colors indicate closer distance between persistence diagrams.*