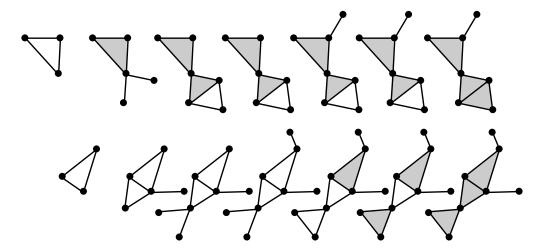
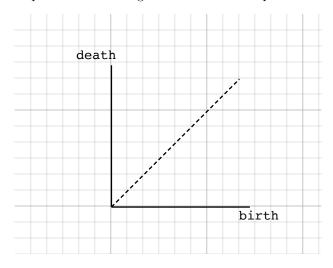
TDA Breakout: Day 4 Worksheet

Exercise. Consider the filtered simplicial complexes shown below. Each row shows a different filtered simplicial complex. Assume that the time steps are all spaced equally, the leftmost figures each occurring at time 1 and the rightmost occurring at time 7.



Plot the degree-1 persistence diagram for each filtered simplicial complex on the same axes below (use different colors or X's and O's to distinguish them visually). Remember that the degree-1 persistence diagram should track "births" and "deaths" of loops in each filtered simplicial complex. Assume the grid lines are 1 unit apart.



Now compute the bottleneck distance between the persistence diagrams. For your convenience, a precise definition of bottleneck distance is included below.

Appendix: Definition of Bottleneck Distance

Let D and D' be persistence diagrams. The bottleneck distance between them is given by

$$d_b(D, D') = \min_{\phi: A \to A'} \max \left\{ \max_{p \in A} c_m(p, \phi(p)), \max_{p \in D \setminus A} c_u(p), \max_{p' \in D' \setminus A'} c_u(p') \right\},$$

where the minimum is over partial matchings; i.e., bijections $\phi: A \to A'$ where $A \subset D$ and $A' \subset D'$. We use the matching cost between points p = (b, d) and p' = (b', d') given by

$$c_m(p, p') = \max\{|b - b'|, |d - d'|\}.$$

Another way to write this is

$$c_m(p, p') = ||p - p'||_{\infty},$$

where $\|\cdot\|_{\infty}$ is the ℓ_{∞} -norm, defined on an aribtrary vector in \mathbb{R}^2 by

$$||(x,y)||_{\infty} = \max\{|x|,|y|\}.$$

We also use a cost for each unmatched point p = (b, d) given by

$$c_u(p) = \frac{d-b}{2}.$$

This is just the ℓ_{∞} distance from p to the diagonal line y = x.