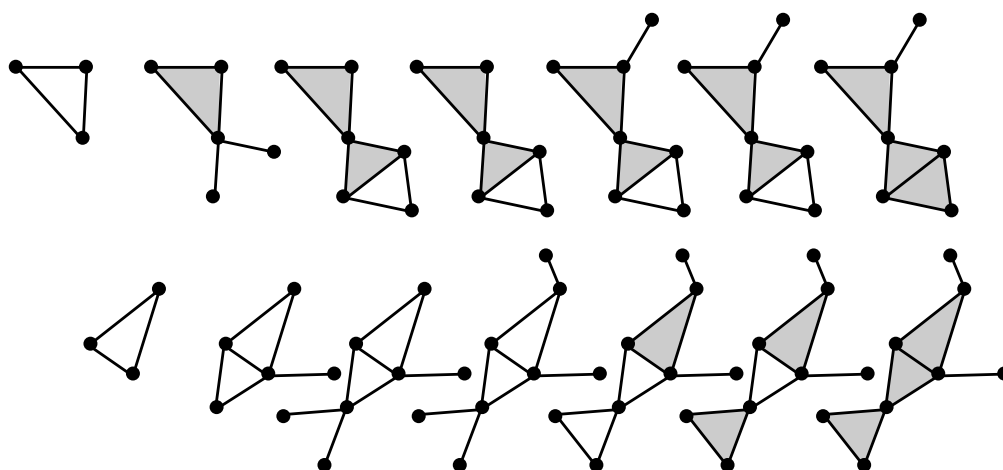# TDA Breakout: Day 4 Worksheet

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 occuring at time 1 and the rightmost occuring 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.
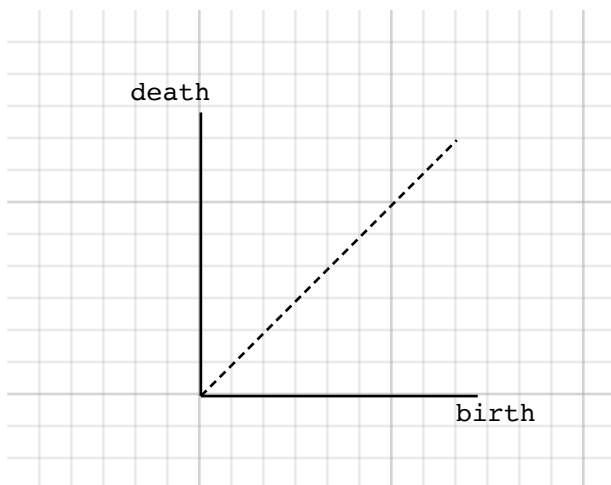
Now compute the bottleneck distance between the persistence diagrams. For your convenience, a precise definition of bottleneck distance is included below.

1 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 $\ell_i nfty$ distance from p to the diagonal line $y = x$.