

1. Pre-processing
 - a. Normalize
 - b. Log transformation
 - c. filter highly expressed genes (threshold=75%)
2. Pearson (No PCA) (p_dgms)
 - a. Bottleneck
 - i. 0-dim (p_dist_0)
 1. Average linkage
 2. Complete linkage
 - ii. 1-dim (p_dist_1)
 1. Average linkage
 2. Complete linkage
 - iii. Both-dim (Normalize, combine above) (p_dist_both)
 1. Average linkage
 2. Complete linkage
 - b. Persistence Image (change parameters to start=0.0, end=1.0; p-norm = 2-norm)
 - i. Padding (Max x&y size) (p_imgs_pad), (p_norms_pad)
 1. Average linkage
 2. Complete linkage
 - ii. Resize (10, 3) (p_imgs_resize), (p_norms_resize)
 1. Average linkage
 2. Complete linkage
3. Euclidean distance (With PCA, variance=0.99; UMAP, n_components=15) (e_dgms)
 - a. Bottleneck
 - i. 0-dim (e_dist_0)
 1. Average linkage
 2. Complete linkage
 - ii. 1-dim (e_dist_1)
 1. Average linkage
 2. Complete linkage
 - iii. Both-dim (Normalize, combine above) (e_dist_both)
 1. Average linkage
 2. Complete linkage
 - b. Persistence Image
 - i. Padding (Max x&y size) (e_imgs_pad), (e_norms_pad)
 1. Average linkage
 2. Complete linkage
 - ii. Resize (10, 3) (e_imgs_resize), (e_norms_resize)
 1. Average linkage
 2. Complete linkage
4. Consensus Hierarchical Clustering (Complete linkage)
 - a. Recluster the aggregate normalized distances.
 - i. Pearson
 1. both-dim + padding (p_dist_both) + (p_norms_pad)

- ii. Euclidean
 - 1. both-dim + padding (e_dist_both) + (e_norms_pad)
- iii. Bottleneck
 - 1. p-both-dim + e-both-dim (p_dist_both) + (e_dist_both)
- iv. Persistence image
 - 1. p-padding + e-padding (p_norms_pad) + (e_norms_pad)