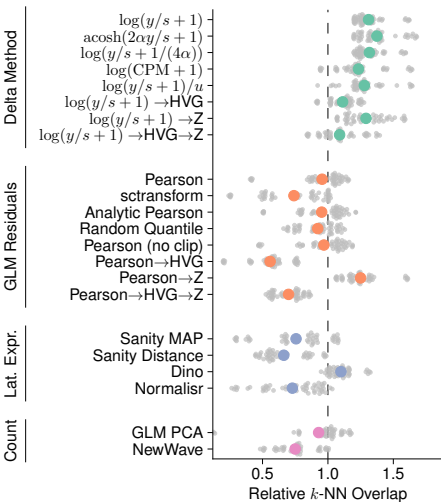


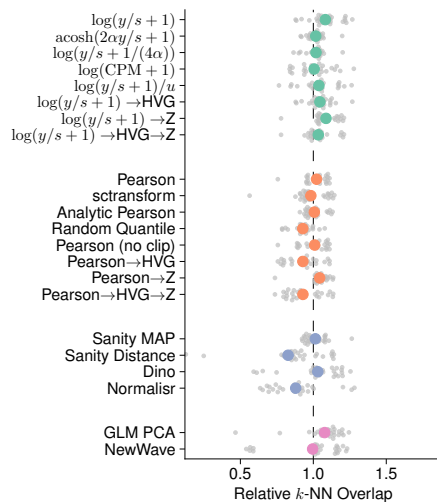
(A) Consistency

10X gene subset A vs. gene subset B



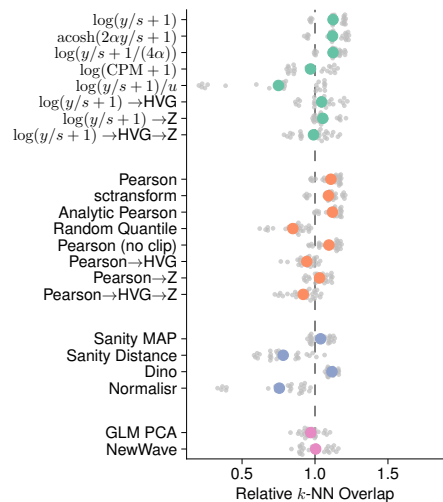
(B) Simulation

Ground truth vs. simulated counts



(C) Downsampling

Original vs. downsampled Smart-seq3 data



(D) k -NN overlap depends on #PCA-dimensions

