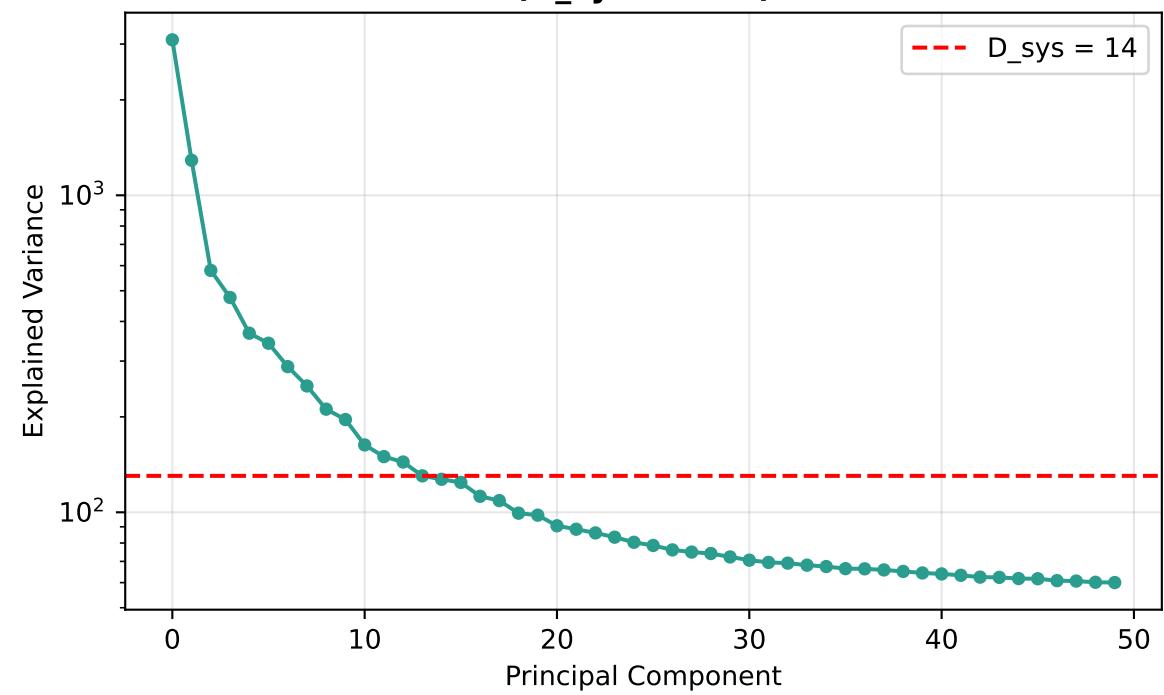
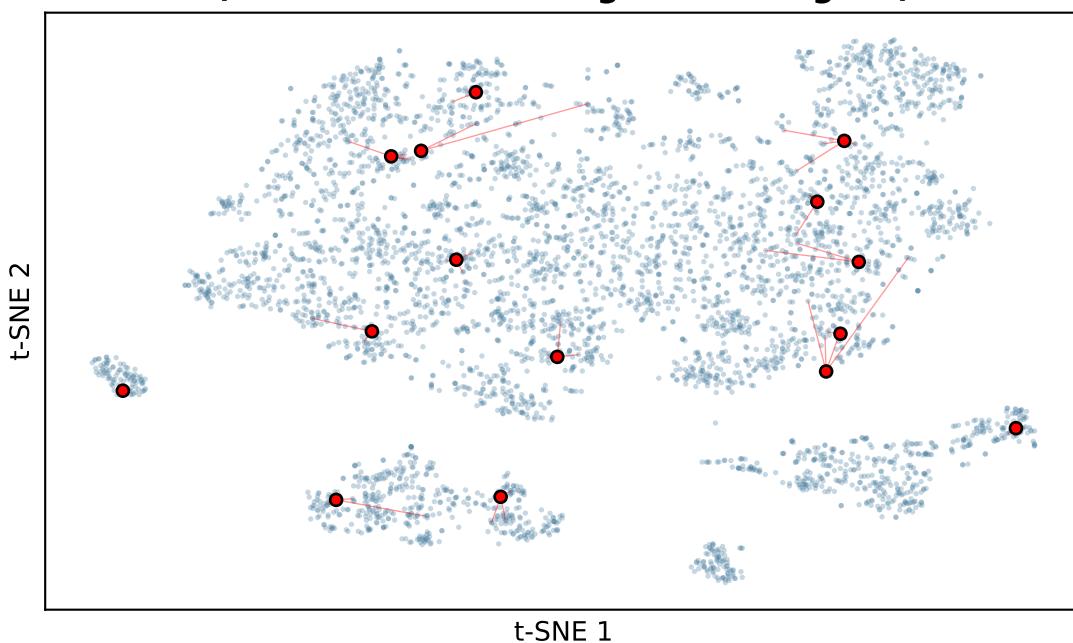


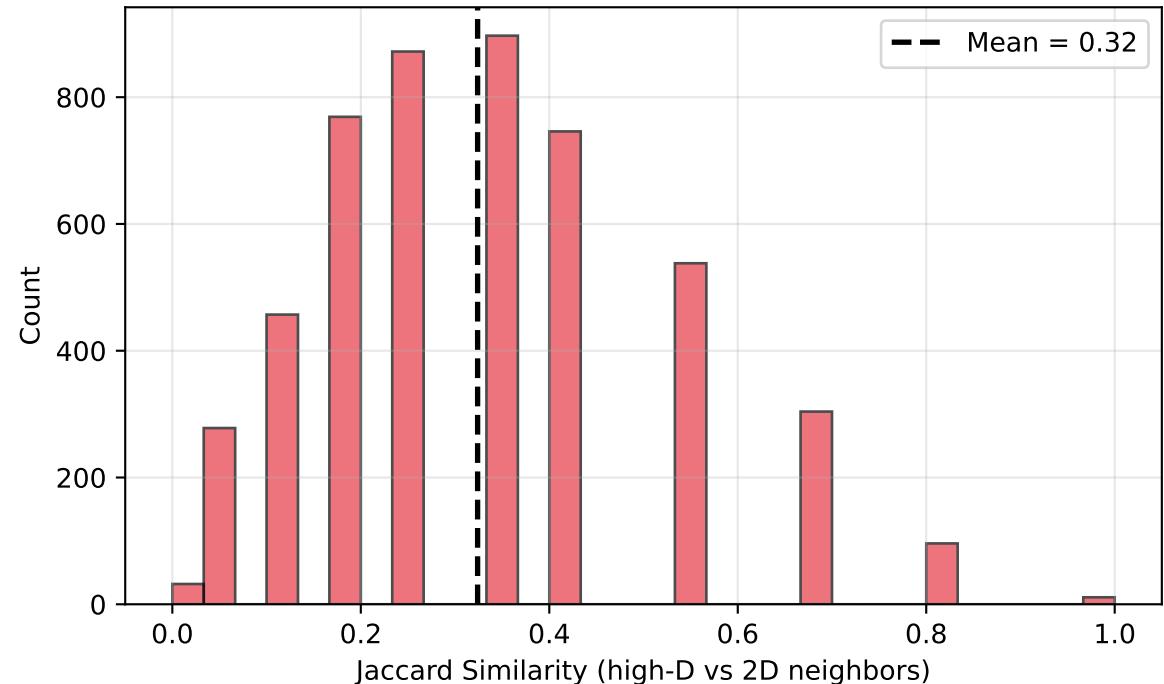
A. Eigenvalue Spectrum ($D_{sys} = 13.6$)



B. The Shadow Lie (red lines = TRUE neighbors in high-D)



C. Neighbor Preservation (Aliasing = 67.6%)



D. The Epistemological Point

TOPOLOGICAL ALIASING IN scRNA-seq

Dataset: GSE120575 (Sade-Feldman)
Cells: 16,291
Genes: 55,738 → 39,254 (filtered)

SYSTEM (D_{sys}):
Participation Ratio = 13.6
→ The gene expression manifold has ~14 effective dimensions

SHADOW (D_{obs}):
t-SNE dimension = 2
→ We project to a 2D visualization

ALIASING:
Rate = 67.6%
→ 68% of high-D neighbors are "lost" in the 2D projection

COVERAGE:
 $2.17e-06$ of 3^{20} cells occupied
→ The data covers a vanishing fraction of the high-D space

IMPLICATION:

When $D_{sys} \gg D_{obs}$, the 2D "shadow" introduces systematic distortions. Clusters that appear close may be far apart in reality, and vice versa.

This is topological aliasing applied to real biological data.