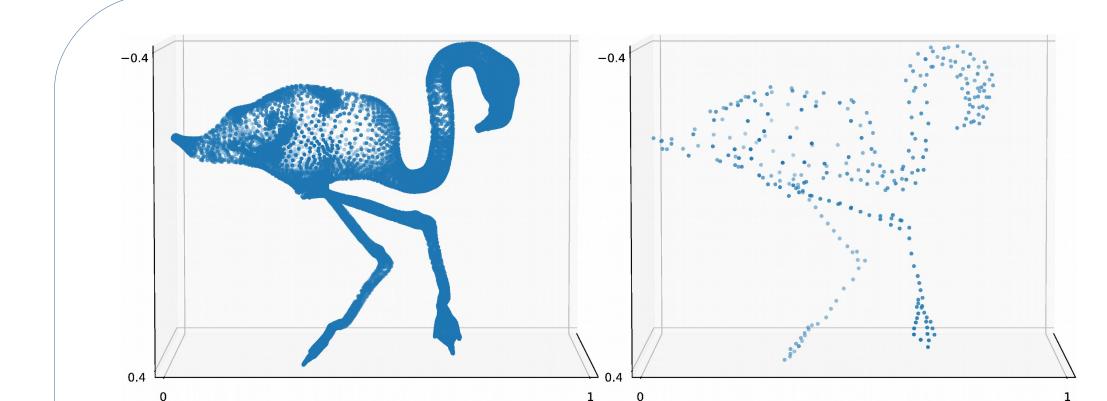
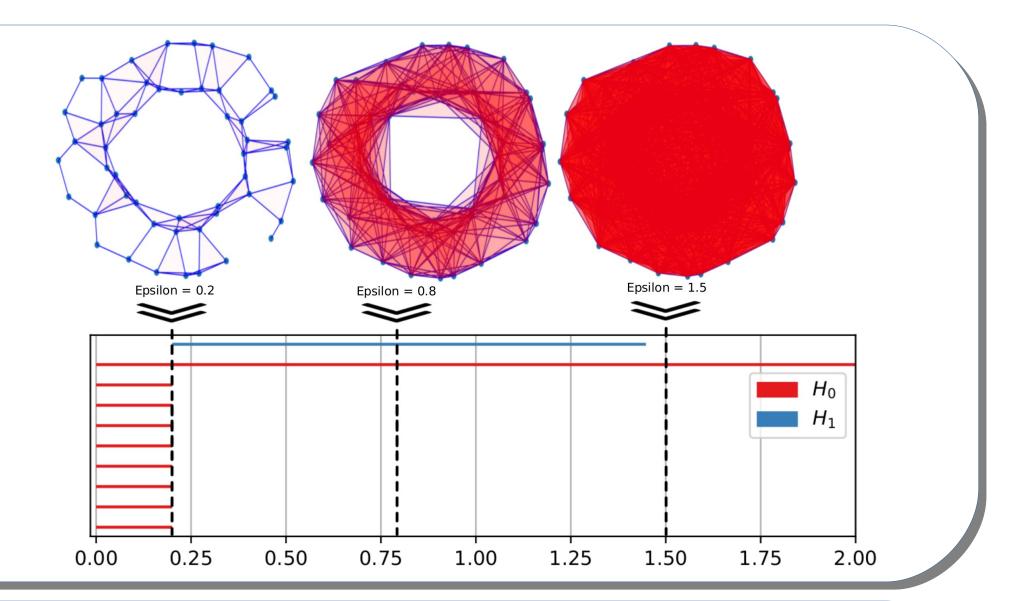


III:Small: Partitioning Big Data for High Performance Computation of Persistent Homology PI: Philip A. Wilsey Institution: University of Cincinnati

Topological Data Analysis/ Persistent Homology

- **Exponential Complexity** (time & space)
- Limited to ~10K points in R^3 (64GB RAM)
- Data reduction & Partitioning
- Use cluster centroids (samples)
- Use clusters $+\delta$ as partitions
- Parallelism and concurrency





Data Sampling and Partitioning

- Witness complex
- Random Sampling

Data reduction: $27K \rightarrow 300$ points Utilizing k-means++

Output Analysis

- Quantitative Analysis
 - Persistence Interval Comparison:
 - Bottleneck, Wasserstein, Heat Kernel Distances
 - Performance:
 - Runtime, Memory use, Scalability
 - Data Sampling & Partitioning:
 - Persistent Homology preserving sampling
 - Persistence interval preservation
 - Topological feature preservation

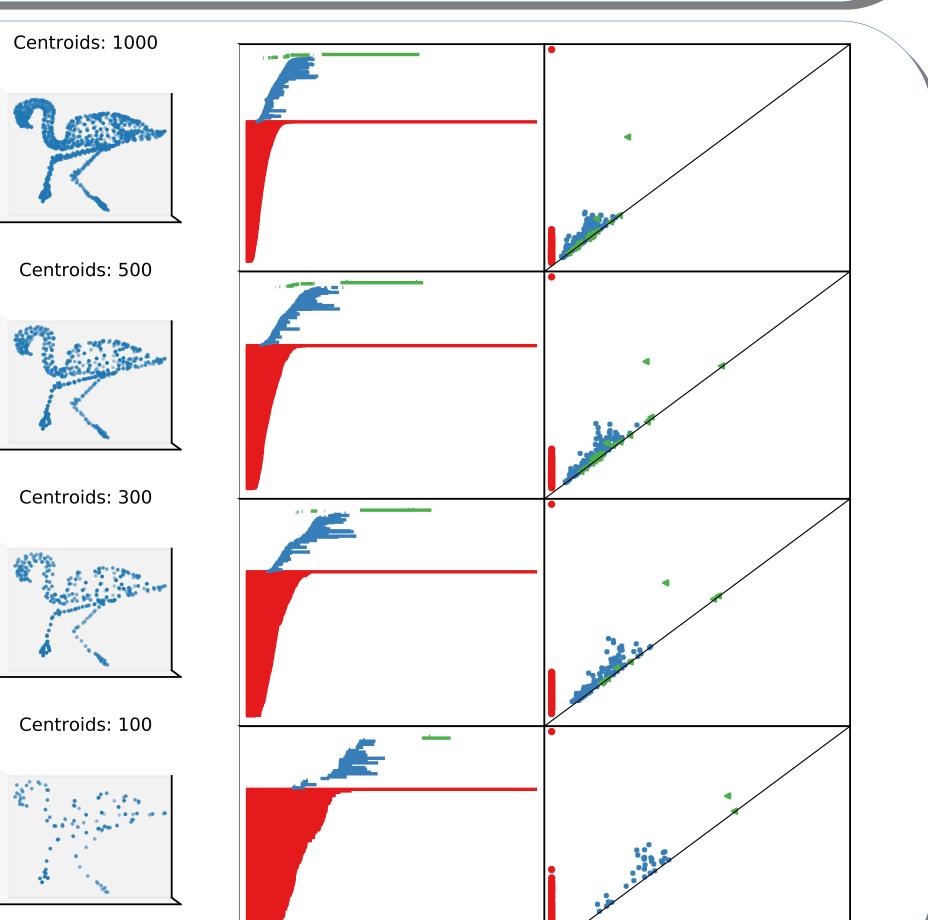
Qualitative Analysis

- Barcodes
- Persistence Diagrams
- Landscape Diagrams
- Persistence Images

Clustering (enables upscaling)

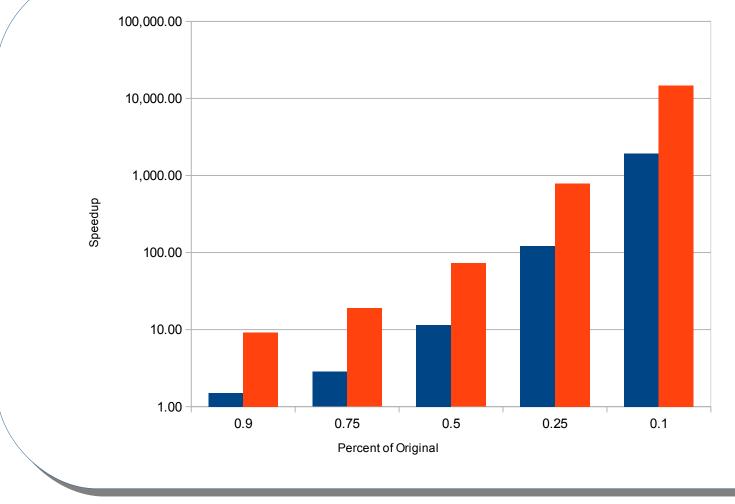
- Density-based: DBScan
- Grid-based (distance-independent)
- Partition-based: k-Means++
- Hierarchical-based: Agglomerative

• 3-4 orders of magnitude perf gains



• Feature Boundary Extraction

Two Circles Two Moons



Data Reduction performance Improvements

- Reduced input points results in:
 - Reduced Memory Footprint
 - Faster CPU and Wall Time
 - Approximations of large features with bounded error
 - Upscaling to improve boundary identification of topological feature

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