### **Persistent Homology Guided Force-Directed Graph Layouts**

Ashley Suh, Mustafa Hajij, Bei Wang, Carlos Scheidegger & Paul Rosen Presented by Javier Castillo-Arnemann

1. Embed a weighted undirected graph in metric space by inducing a

3. PH features can be used either to contract the nodes that created the

feature, or to repulse the graph into two subsets, depending on user

2. Extract Persistence Homology (PH) features of the metric space

structure and sort them based on persistence.

#### Background

- Graphs/networks are commonly used to encode relationships among entities, used for data exploration.
- · Used to model social networks, digital networks, biological interactions, etc.
- · Their abstractness makes them difficult to analyze.
- A good graph vis should present structure quickly and clearly, and support further investigation of the data.

1. Embed an undirected graph in metric space by inducing a distance

o The inverse of the edge weight is the distance, and the shortest path between two nodes

### Background

· Force-directed/spring-mass layouts are the most popular graph layout for interactive applications.

 Good at showing topological structures in sparse graphs, but as graphs get bigger unrelated structures overlap.



### Approach

- 2. Extract Persistence Homology (PH) features of the metric space structure and sort them based on persistence.
- · The persistence homology of the graph can be calculated by finding its Minimum Spanning Tree (MST) Subset of edges that connects every node without cycles and minimizing the edge

weights

## Comparison

Fig. 2

- Comparing the PH of the traditional force-directed source layout and the user-selected target layout.
- PH calculated on Euclidean distance between the nodes, not topological distance.



#### Approach

- What? Improve force-directed graph layout visualization.
- Why? Identify, compare and separate important topological structures.
- How? Use persistence homology features to enable interactive manipulation of the graph layout, visually separating PH features.



#### Approach

2. Extract Persistence Homology (PH) features of the metric space structure and sort them based on persistence.

- Every node corresponds to a point in the
- metric space. Consider the set of balls centered at every point with a diameter t (metric space resolution)



The lifetime of a component is its persistence (0, 1/w).







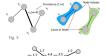
# Approach

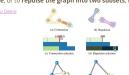
Approach

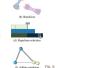
input.

distance between all nodes.

- 2. Extract Persistence Homology (PH) features of the metric space structure and sort them based on persistence.
- Every PH feature is associated with:
- Persistence measure 1/w
- Cause of death // and //
- Subsets of nodes V., and V., the sets of connected nodes after removing the feature from the MST.
- Subset ratio |V | : |V |, measures the centrality of the feature within the MST.







If the graph is unweighted, the Jaccard

index, edge centrality or other measures

can be computed and used as weights.

# Discussion

#### Strengths:

- Real-time selection of the PH features instead of choosing number of clusters heforehand
- Combination of repulsive and attractive forces allows better separation than either force alone
- Can be extended to other force-directed lavouts.
- Performance comparable to traditional force-directed layouts.

- - Performance with unweighted graphs. Can this approach be used with other
    - community detection/network clustering methods instead of PH features? What happens when the number of PH

Weaknesses:

features is too high to make the barcode impractical?

Shallow explanation of the modifications to

the force-directed algorithm.

Extra computations for weights?

Fig. 4





# Approach

Fig. 2

Approach

between all nodes.

is the distance between them.

The rest of the algorithm operates in this metric space.

3. PH features can be used either to contract the nodes that created the feature, or to repulse the graph into two subsets, depending on user input.