**Dot2Dot** is an efficient framework that groups selected nodes in a graph and finds simple connection pathways among nodes within each group.

**Problem**
How to make sense of selected nodes in a large graph (e.g., anomalies, infected people, activated genes)?

How are they connected? Are they close by or segregated? How many groups do they form? Are there simple paths to connect nodes in a group? Who are good connectors?

**Idea of encoding:** We seek to find easy to “describe” paths between selected nodes, based on the Minimum Description Length principle, so that each node-2-node path needs few bits to describe, e.g., avoid high-degree nodes, unless need to visit many of its spokes.

**Problem hardness:** We show this is an NP-hard problem (reduction from the Steiner Tree Problem).

**Fast heuristic methods:** Our algorithm is based on building k-level trees iteratively, where intermediate nodes decrease encoding cost, details are in [1].

**Interactive Visualization**
Dot2Dot showing connection pathways among authors from DBLP coauthorship graph (300K nodes, 1M edges).
- **Blue square:** selected nodes
- **Orange circle:** connectors
- **Thick orange edge:** simple path found by Dot2Dot

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1. **Search. Select.**
   - Find nodes and drag them into the view.

2. **Select nodes. Go.**
   - Turn your nodes of interest into squares. Dot2Dot will find simple paths among them.
   - You can also group nodes visually.

3. **Visualize. Interact.**
   - Dot2Dot visualizes paths among marked nodes.
   - You can interact with them: add or delete nodes, mark or unmark them, see their neighbors, and more.

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