

Mining and Visualizing Connection Pathways in Large Information Networks

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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?

Algorithm

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

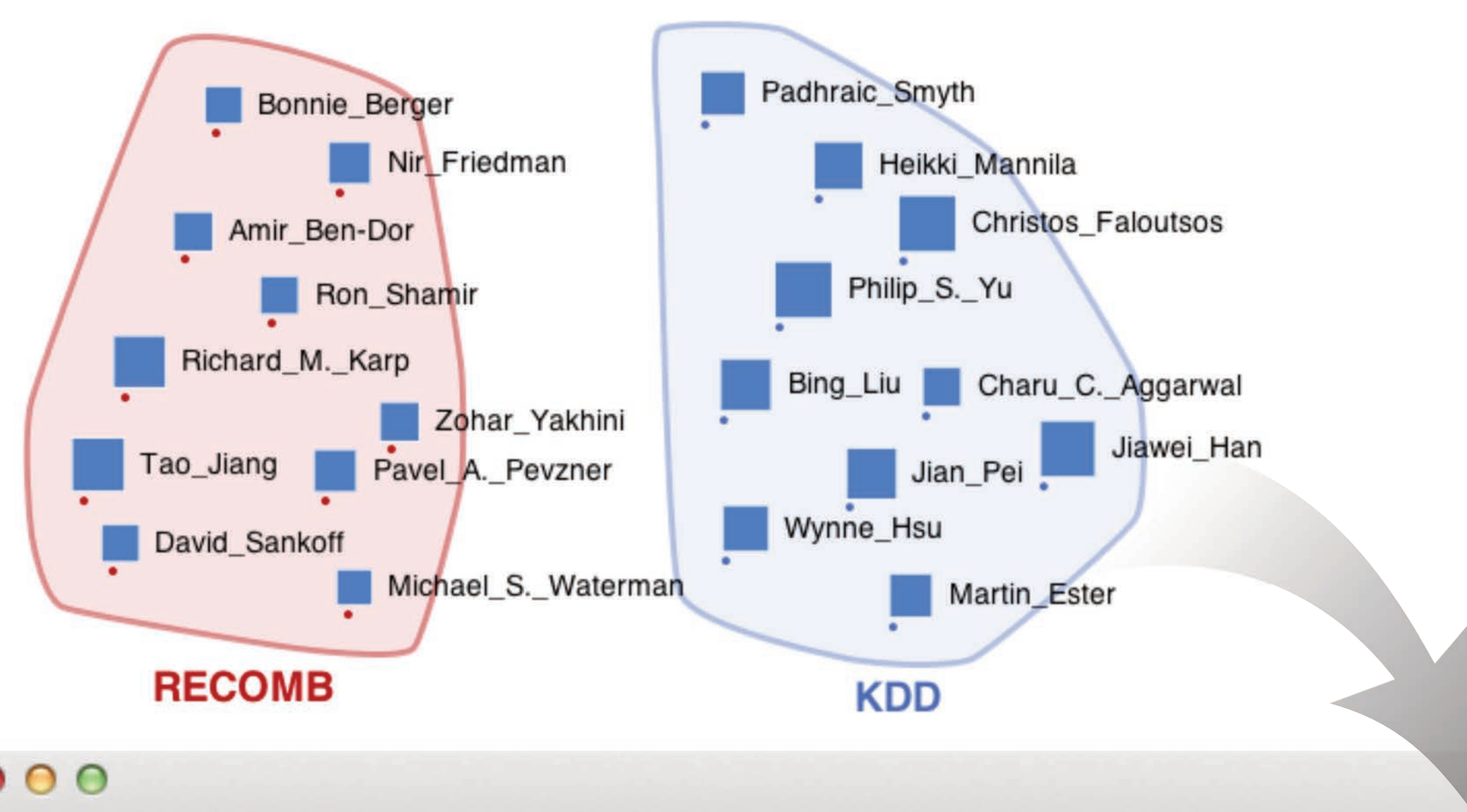
1 Search. Select.
Find nodes and drag them into the view.

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.



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

