

Using Crowds to Design Biological Network Visualizations

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Biologists often perform experiments whose results generate large quantities of data, such as interactions between molecules in a cell, that are best represented as networks (graphs). To visualize these networks and communicate them in publications, biologists must manually position the nodes and edges of each network to reflect their real-world physical structure. This process does not scale well, and graph layout algorithms lack the biological underpinnings to offer a viable alternative. We present GraphCrowd, a crowdsourcing system that leverages human intelligence and creativity to design layouts of biological network visualizations. GraphCrowd provides design guidelines, abstractions, and editing tools to help novice workers perform like experts.

We evaluated GraphCrowd with two experiments. The first found that crowdsourced layouts of real biological networks were as good as or better than layouts designed by expert biologists, and significantly better than a popular graph drawing algorithm. A second experiment found that crowds provided quality ratings of network layouts that were similar to an expert biologist, suggesting that GraphCrowd can both create and identify high-quality layouts.

Our contributions include: 1) novel techniques for generating and evaluating scalable, high-quality biological network visualizations via novice crowdsourcing, 2) experiments providing empirical evidence of the benefits of these techniques compared to expert and algorithmic baselines, 3) implications for crowdsourcing complex design work, including other types of network visualizations, and 4) the GraphCrowd system itself, which we will release as open-source software.