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Title: Diffusion-Based Methods for Biological Network Analysis

Abstract: Biological networks are powerful resources for the discovery of genes and genetic modules that drive disease. Similar to in the social networks analysis domain, diffusion-based low-dimensional network embedding methods have proved quite powerful for biological networks. In particular, these methods have been highly successful in creating coherent local neighborhoods that correlate to gene function, enabling the downstream use of the entire machine learning toolbox to perform multiple inference tasks on these networks. We highlight the recent success of diffusion-based methods in biological networks for gene function prediction, link prediction, and for disease module prediction. We also discuss structural ways in which some types of biological networks seem to be organized differently than social networks, and show the advantage of customizing methods for particular types of biological network data. Finally, the biological domain offers unique additional sources of principled structured data organization (such as evolution), that can be leveraged to improve inference, resulting in some interesting open problems in multiplex network inference.