Introduction to the Special Issue on Biological Networks

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In this special issue on biological networks, we aim to interest the readership of *Internet Mathematics* in network theory applied to bioinformatics. Network biology is a new and emerging research area that is fast-growing, spurred by the collection of biological data representing connections or interactions of molecules in the cell. As such, it has the potential to have at least as profound an impact on our understanding of the cell as sequence data has had. However, the datasets are large, noisy and many graph theoretic problems are formally intractable (impossible to solve exactly in any time less than the age of the universe), and so heuristic approximations must be developed in an attempt to find approximate solutions. Furthermore, the tools developed to solve these problems must be made accessible to biological practitioners. In this direction, this issue contains papers on the many databases available, theoretical and algorithmic advances in analyzing these data, as well as papers on some specific biomedical applications, and two papers introducing software tools.

This issue presents six papers from some of the leading research groups in the area. Three papers present significant theoretical advances in techniques. Two of them (Elberfeld et al.; Crofts and Higham) look at directed graphs. First, Elberfeld et al. attack the "maximum graph orientation problem", in which, given a list of source-sink pairs of nodes, we attempt to add direction to an undirected graph in such a way as to maximize the number of pairs for which directed paths exist from the source to the sink. This has applications in the problem of learning biological pathways, but Elberfeld et al. show that the problem is NP-hard