

Special Issue

Computational Methods for Biological Networks

Message from the Guest Editor

Biological networks are used to define relationships (edges) between biological entities (nodes). They are used to represent a variety of biological systems from the microscopic to the macroscopic and used to define dynamic relationships with time-varying networks representing molecular interactions, evolutionary changes, or space-varying networks, or predator–prey relationships in some particular region. Dynamic or space-varying networks are often simplified to be static and represent all possible relationships. Biological networks can have any number of nodes from a handful to tens of thousands or more; they can be directed or undirected. The diversity of biological networks gives rise to an equal diversity in the types of computational analyses that can be performed: one may model the dynamics of regulation in a handful of nodes in a small network using differential equations to look for steady states or cyclic behavior; or one may wish to transfer information between networks of similar but not identical types (e.g., genetic vs. protein interaction). In this issue, we welcome novel computational advances in any area of biological network analysis.

Guest Editor

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Message from the Editor-in-Chief

The journal *Mathematics* publishes high-quality, refereed papers that treat both pure and applied mathematics. The journal highlights articles devoted to the mathematical treatment of questions arising in physics, chemistry, biology, statistics, finance, computer science, engineering and sociology, particularly those that stress analytical/algebraic aspects and novel problems and their solutions. One of the missions of the journal is to serve mathematicians and scientists through the prompt publication of significant advances in any branch of science and technology, and to provide a forum for the discussion of new scientific developments.

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