

Special Issue on Network Structure and Biological Function: Reconstruction, Modelling, and Statistical Approaches

Call for Papers

We are particularly interested in contributions, which elucidate the relationship between structure or dynamics of biological networks and biological function. This relationship may be observed on different scales, for example, on a global scale, or on the level of subnetworks or motifs.

Several levels exist on which to relate biological function to network structure. Given molecular biological interactions, networks may be analysed with respect to their structural and dynamical patterns, which are associated with phenotypes of interest. On the other hand, experimental profiles (e.g., time series, disturbances) can be used to reverse engineer network structures based on a model of the underlying functional network.

Is it possible to detect the interesting features with the current methods? And how is our picture of the relationship between network structure and biological function affected by the choice of methods?

Perspectives both from simulation approaches as well as the evaluation of experimental data and combinations thereof are welcome and will be integrated within this special issue.

Authors should follow the EURASIP Journal on Bioinformatics and Systems Biology manuscript format described at the journal site <http://www.hindawi.com/journals/bsb/>. Prospective authors should submit an electronic copy of their complete manuscript through the journal Manuscript Tracking System at <http://mts.hindawi.com/>, according to the following timetable:

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