Special Issue

Metabolic Networks

Message from the Guest Editor

Thanks to last year’s technological and methodological developments, metabolomics now allows us to detect and identify tens to hundreds of metabolites constituting metabolic fingerprints of environmental or genetic stresses. These metabolic profiles provide highly valuable information on the physiological status of cells, tissues or organisms. The current challenge lies in putting back these lists of metabolites in the context of genome scale metabolic networks. In fact, metabolic networks aim at gathering all the metabolic reactions which can occur in a given organism, hence allowing us to decipher the cascade of reactions connecting metabolites identified in metabolomics. This Special Issue is devoted to reviewing the current practical aspects of metabolomic data analysis in the context of metabolic networks, starting from network reconstruction, metabolite mapping (with a special challenge in identifier mappings), then discussing state-of-the-art and new network computational analysis methods (graphs, constraint-based modelling) and emphasising the need for new visualisation paradigms to deal with these large networks.

Guest Editor

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About the Journal

Message from the Editor-in-Chief

The metabolome is the result of the combined effects of genetic and environmental influences on metabolic processes. Metabolomic studies can provide a global view of metabolism and thereby improve our understanding of the underlying biology. Advances in metabolomic technologies have shown utility for elucidating mechanisms which underlie fundamental biological processes including disease pathology. *Metabolites* is proud to be part of the development of metabolomics and we look forward to working with many of you to publish high quality metabolomic studies.

Editor-in-Chief

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