



Development and Application of Statistical Methods for Analyzing Metabolomics Data

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Message from the Guest Editors

In the last decade, the field of metabolomics has developed tremendously: it is now possible to routinely measure a wide range of metabolites for many specimens at reduced costs. This opens the door to many exciting experiments such as time resolved metabolomics, multi-sample and multi-species metabolomics, or cross-omics experiments, to name but a few. Data analysis is a crucial step to be able to extract meaningful information from the complex data thus acquired. Because of this, the rapid developments in powerful metabolomics experiments have to be matched with developments in statistical methodology for analysis of these experiments.

This Special Issue is dedicated to the development or application of statistical methods for analyzing metabolomics data. We invite researchers to submit their manuscripts outlining novel data processing and data analysis methods for metabolomics. However, the scope of this Special Issue is not limited to this topic, but also includes experimental design, data acquisition methods, and applied metabolomics studies in which data analysis played an especially attractive role





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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.

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