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Metabolomics Data Analysis and Quality Assessment

Guest Editor:

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Message from the Guest Editor

Dear Colleagues,

In comparison to other major omics technologies, metabolomics analytical technologies create unique data and data quality issues in collected datasets. These unique data and data quality issues are not well recognized both inside and definitely outside of the metabolomics field. Detecting, understanding, and handling these issues is paramount to the successful extraction of useful information from metabolomics data analyses and the subsequent successful integration of this information with other omics datasets.

Therefore, this Special Issue is devoted to illuminating the unique data and data quality issues in metabolomics datasets and their impact on downstream data analyses. Appropriate topics include methodologies, software, and tools that can (i) qualitatively or quantitatively characterize either raw or intermediate metabolomics data and data quality, (ii) mitigate data quality issues in metabolomics data analyses, and/or (iii) evaluate the quality of metabolomics data analyses for general or specific use-cases. Additionally, review articles that cover these topics are welcomed, as well as case studies that illuminate unique analytical and data quality issues in metabolomics analytical technologies.

Prof. Hunter N. B. Moseley *Guest Editor*







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Editor-in-Chief

Prof. Dr. Peter Meikle Metabolomics Laboratory NHMRC, Baker Heart and Diabetes Institute, Melbourne, Victoria 3004, Australia

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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