



Open-Source Software in Metabolomics

Guest Editor:

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Message from the Guest Editor

Dear Colleagues,

Over the past 20 years, the field of metabolomics has expanded significantly, highlighting the need for open-source software for experimental design, analysis, visualization, database creation, and more. For this Special Issue, we encourage data scientists to share open-source software with the metabolomics community. We welcome all papers on open-source software, including open-source web tools, developed in any computer language, such as R, Python, MATLAB, JAVA, C++, etc. The software must be publicly and freely available to non-commercial users. We also welcome original research comparing the performances of existing open-source software and/or developing new methodologies for experimental design, analysis, visualization, database creation, and more, and review articles exploring existing open-source software in metabolomics. There is no restriction on paper length, but articles not including original research or review articles should ideally fall within approximately 2000 words.

Prof. Dr. Seongho Kim

Guest Editor





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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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