

Model-Driven Data Integration of Metabolomic and Genomic Data in Microbiome Systems

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Message from the Guest Editors

Dear Colleagues,

Genome-scale metabolic models (GEMs) have emerged as important tools: (i) GEMs serve as a bridge between genomics and chemistry containing interconnected representation of both data types; (ii) GEMs have a distinct capacity to integrate numerous individual data points together into a broader representation of biological activity; and (iii) GEMs may be extended into broader models of entire microbial communities.

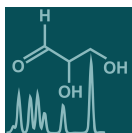
This Special Issue of Metabolomics is focused on genome-scale metabolic modeling, and how genome-scale metabolic models are used to integrate metabolomics and next generation sequencing data for analysis of isolate and microbiome-based systems. We are particularly interested in articles about: (i) improved annotation of metabolomic and genomic data by removing knowledge gaps in microbiome system chemistry; (ii) new metabolomics and genomic data integration techniques using GEMs in microbiome systems; and (iii) improved databases that support improved annotation of metabolomic data, model reconstruction, and model interoperability.

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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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