

Omics Microbial Modeling And Technologies For Foodborne Pathogens

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This book provides comprehensive information on genetic analysis and multiple ""omics"" methods, microbial modeling, and other technologies used for the analysis of foodborne pathogens. Part I details the use of genomics and other omics technologies to study and classify foodborne bacteria, viruses, fungi and protozoa.

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There have been many recent efforts to model metabolic processes within microbial communities (Heinken and Thiele, 2015, Henry et al., 2009). However, the wealth of data available through multiple omics technologies remains underutilized in these models.

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Omics technologies provide the tools needed to look at the differences in DNA, RNA, proteins, and other cellular molecules between species and among individuals of a species. These types of molecular profiles can vary with cell or tissue exposure to chemicals or drugs and thus have potential use in toxicological assessments.

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omics microbial modeling and technologies for foodborne pathogens expands detection knowledge and classification of foodborne pathogens connects omics methods modeling data and food safety databases offers framework for risk assessment and rapid online surveillance and analysis the guide

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“Integrating microbial omics information to inform global climate change models is extremely challenging,” Zhou said. “The findings from this study have important implications for understanding and predicting the ecological consequences of climate warming.”

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Understanding microbial genes, their associated chemistries and functions would be valuable for engineering systemic metabolic pathways within the microbiota to manage human health and diseases. Given that there are many unknown gene metabolic functions and interactions, increasing efforts have been made to gain insights into the underlying functions of microbiota metabolism.

~~Meta?Omics? and Metabolic Modeling?Assisted Deciphering of ...~~

Metabolic network modeling of microbial communities. ... and novel algorithms for integrating omics data and engineering communities. As technologies and modeling frameworks improve, we expect that there will be corresponding advances in the fields of ecology, health science, and microbial community engineering. ...

~~Metabolic network modeling of microbial communities.~~

Here, we review state-of-the-art modeling approaches to evaluate their scope of prediction as in silico tools for microbiome design. We highlight the utility of advanced models for predicting context-dependent interactions, multi-omics data integration, and combined use of complementary modeling and computational tools for enhanced prediction and eventual facilitation of in silico microbiome ...

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To that end, we carried out the first pan-cancer, multi-omics comparative analysis of the relative performance of two proteomic technologies, targeted reverse phase protein array (RPPA) and global mass spectrometry (MS), in terms of their accuracy for predicting the sensitivity of cancer cells to both cytotoxic chemotherapeutics and molecularly targeted anticancer compounds.