Special Issue

Computational Genomics and Bioinformatics in Microbiology

Message from the Guest Editor

Through continued advancements in high-throughput technology, the raw experimental data extracted from genomes of microorganisms continue to grow at an increasing rate. As viruses, archaea, bacteria, fungi and unicellular protozoa together are the main contributors to the Earth’s total biomass, its climate, and the known spectrum of human, animal and plant diseases, we must rise to this data challenge through scalable computational methods that help to uncover the intrinsic and contextual meaning of their genomes. At the same time, these data allow us to explore microbial genomes at unprecedented resolutions and precisions in terms of evolutionary time, structural organisation and their functional elements. Many of these data are already in public data repositories waiting to be (re-)analysed with novel computational and bioinformatics methods. With this preamble, this *Special Issue* invites research contributions in comparative, structural, and functional genomics that, from fine-grained details to large-scale organization, use computational methods to microbial genomics data.

Guest Editor

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