Special Issue

Phylogenetic Methods in the Genomic Era: Challenges in Multiple Sequence Alignment and Phylogenetics for Genome-Scale Data

Message from the Guest Editors

Genome sequencing projects have become routine due to the drastically lower cost of sequencing. There are also grand-scale genome sequencing projects dedicating a systematic approach to targeting well-recognized taxonomic groups: B10K, Genome 10K... These mega sequencing projects are changing the analytical, posing new challenges to phylogeneticists and algorithmists for developing better ways to accommodate big data. Essentially, the tool development for phylogenetics and multiple sequence alignment (MSA) has been stimulated by the ever-rapidly-growing genomic data. Researchers have begun addressing some aspects of the challenges from a wide variety of angles. To name a few ex. (Lemoine et al. 2018), (Morel et al. 2019), (Chatzou et al. 2018), or (Sievers and Higgins 2018). To highlight the importance of this exciting moment for phylogenetic method development and evolutionary data inference in facing the big data era, this Special Issue welcomes contributions of methods and metrics addressing challenges from sequence alignment to tree reconstruction in phylogenomics.

Guest Editors

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Deadline for manuscript submissions

closed (10 January 2022)

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Message from the Editor-in-Chief

Genes are central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fastmoving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised.
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Editor-in-Chief

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