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Estimating Phylogenies from Large Genomic Datasets

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Message from the Guest Editors

Dear Colleagues,

With the explosion of new data from “next generation” sequencing technologies over the past decade, evolutionary biologists have been faced with a number of challenges in using this data for phylogenetic inference. The goal of this Special Issue is to provide a brief overview of recently proposed methods for phylogenetic inference, as well as novel techniques for the acquisition, curation, and implementation of large datasets. We are especially interested in a wide variety of studies (both theoretical and empirical), from overviews of recent software/techniques/pipelines that have been developed to infer phylogenies from large genomic datasets.

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Guest Editors



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Special Issue



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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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