

## Special Issue

# Estimating Phylogenies from Large Genomic Datasets

### Message from the Guest Editors

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

Dr. Charles Bell

Department of Biological Sciences, University of New Orleans, New Orleans, LA 70148, USA

Dr. Stephen A. Smith

Department of Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, MI, USA

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### Deadline for manuscript submissions

closed (30 November 2017)

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## Genes

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*Genes*  
Editorial Office  
MDPI, Grosspeteranlage 5  
4052 Basel, Switzerland  
Tel: +41 61 683 77 34  
[genes@mdpi.com](mailto:genes@mdpi.com)

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### Message from the Editor-in-Chief

*Genes* is central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fast-moving 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. Why not consider *Genes* for your next genetics paper?

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### Editor-in-Chief

Prof. Dr. Selvarangan Ponnazhagan  
Department of Pathology, The University of Alabama at Birmingham,  
1825 University Blvd, SHEL 814, Birmingham, AL 35294-2182, USA

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