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.

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

Deadline for manuscript submissions

closed (30 November 2017)

GCAT
TACG
GCAT

Genes

an Open Access Journal by MDPI

**Impact Factor 2.8
CiteScore 5.5
Indexed in PubMed**

mdpi.com/journal/
genes

About the Journal

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?

Editor-in-Chief

Prof. Dr. Selvarangan Ponnazhagan
Experimental Cancer Therapeutics, The University of Alabama at Birmingham, 1825 University Blvd., SHEL 814, Birmingham, AL 35294–2182, USA

Author Benefits

Open Access:
free for readers, with article processing charges (APC) paid by authors or their institutions.

High Visibility:
indexed within Scopus, SCIE (Web of Science), PubMed, MEDLINE, PMC, Embase, PubAg, and other databases.

Journal Rank:
JCR - Q2 (Genetics and Heredity) / CiteScore - Q2 (Genetics (clinical))

MDPI