Special Issue

Bioinformatics and Population Genomics

Message from the Guest Editors

Studying genetic factors underlying phenotypic variation among populations has been the cornerstone of population genetics. In light of recent developments in sequencing technologies, the scope of these studies has dramatically changed, transforming it to an interdisciplinary field that integrates bioinformatic tools to analyze and manage large biological data. Both theoretical and computational methods are required to understand mechanisms producing and maintaining genetic diversity among populations. Population genetics studies can identify loci involved in adaptation or variants responsible for inbreeding depression. Moreover, these findings can be applied for wildlife conservation. This Special Issue aims to highlight recent discoveries and theoretical frameworks. We are interested in studies that describe the causes of adaptation as a result of domestication, invasion of non-native species, and climate change as well as disease susceptibility at the genome level by developing and applying novel bioinformatics tools.

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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?

Editor-in-Chief

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