Special Issue

Trends and Future Perspectives in Genome Annotation

Message from the Guest Editor

The current genomics era is now generating a plethora of biological data in the form of complete genome sequences. Once a new genome is available, the first step we need is the annotation of it, including both gene finding and functional annotation. Computational tools for sequence annotation have been developed during the last three decades, but now we need better tools for easy and fast annotation of complete genomes. This Special Issue welcomes articles of original research or reviews that present future perspectives for the annotation of complete genomes from either eukaryotic or prokaryotic organisms, in addition to viruses that usually show a high number of uncharacterized genes. Subjects can include structural annotation with new or updated gene finders, functional annotation with new algorithms or annotation sources, evaluation of methods and visualization of results from one or several genomes, as well as the comparison of annotations from different organisms, thus highlighting differences between annotations.

Guest Editor

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Deadline for manuscript submissions

closed (30 June 2021)

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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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