Special Issue

Genome Assembly and Annotation in Biology

Message from the Guest Editors

Recent advances in sequencing technologies, the widespread availability of high-performance computing, and significant improvements in algorithms have greatly enhanced the accuracy and scalability of genome assembly and annotation. The generation and dissemination of high-quality genome assemblies provide essential foundational data for understanding genetic diversity, evolution, and biological function across a wide range of organisms. International databases, such as the INSDC, play a key role in aggregating and providing unrestricted access to such data. At the same time, reference resources for genome annotation continue to expand, accompanied by the rapid development of algorithms and pipelines. This Special Issue welcomes submissions presenting new methods, tools, and pipelines related to genome assembly and annotation. We also encourage the submission of high-quality case studies from both model and non-model organisms. By showcasing recent developments and practical applications, this issue aims to provide a platform for sharing knowledge that promotes reproducible, scalable, and biologically meaningful genomic analyses.

Guest Editors

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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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