Special Issue

Bioinformatic Analysis of NGS Data

Message from the Guest Editors

With the fast advances in next generation sequencing (NGS) technologies, NGS and its associated bioinformatic analysis techniques have revolutionised omics disciplines over the past 15 years. There are two major paradigms in NGS technologies: short-read sequencing and long-read sequencing. Short-read sequencing, such as Illumina, offers cost-effective and high-accuracy data that have wide applications for research in genomics, transcriptomics, and epigenomics. By contrast, long-read sequencing, such as Oxford Nanopore and PacBio, is well-tailored for applications like de novo assembly and/or full-length sequencing for RNA, circular RNAs, extrachromosomal circular DNA elements, etc. This Special Issue in Genes will focus on the bioinformatic analysis of NGS data and the applications of NGS in various research areas. We welcome original articles, new methods and reviews covering any aspect of NGS data analysis.We look forward to receiving your contributions.

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Deadline for manuscript submissions

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Message from the Editor-in-Chief

Genes are central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fastmoving 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.
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Editor-in-Chief

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