Special Issue

Transcriptomics and Bioinformatics in Precision Medicine

Message from the Guest Editor

The mRNA transcriptome effectively shows the cellular context of active functions. Due to the significant information on individual cells and the relatively easy capturing process of gene expression, transcriptomics was explored from high-throughput genomic studies using microarray. Along with the advances of next-generation sequencing technology, three factors of cost-effectiveness (data creation), diverse analyses (interpretation), and easy usage (diagnosis) serve as a foundation for the accumulation of huge amount of RNA-seq data. Accordingly, transcriptomic studies became the essence of genomic studies, with diverse bioinformatics methodologies to better understand human disease and identify novel therapeutic targets. From transcriptomic data, scientists capture the expression profiles of genes, study alternative splicing, identify disease-specific transcripts, roles in the multi-omics landscape, and etc. In this Special Issue, authors are encouraged to submit original manuscripts describing diverse transcriptomics and bioinformatics studies applied to precision medicine. Also encouraged are papers describing reviews or comparisons of relevant bioinformatics methodologies.

Guest Editor

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Deadline for manuscript submissions

closed (10 January 2023)

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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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