Special Issue

Integrative Multi-Omics and Single-Cell Approaches to Study Complex Diseases

Message from the Guest Editors

In this Special Issue, we hope to bring together experts in genomics from multi-disciplinary backgrounds to share their collective expertise in a broad range of topics related to multi-omics data integration for various complex human diseases. We expect the themes to cover various topics, such as bulk and single-cell multi-omics and multi-modal data acquisition and analyses (e.g. single-cell RNA-seq and single-cell-ATAC-seq), other epigenomic profiling and proteomics methods, spatial transcriptomics, data harmonization and normalization methods, quantitative trait locus mapping methods, development of user-friendly pipelines for end-to-end analysis, web platforms for sharing and visualizing datasets, as well as challenges with computational scalability, cost, benchmarking and validation. We welcome applications to a broad range of cell/tissue and disease areas, involving either publicly available or custom datasets. We also welcome multiple manuscript formats, including original research articles, reviews or mini-reviews, opinions, hypotheses, or theories.

Guest Editors

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Deadline for manuscript submissions

closed (15 August 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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