

Special Issue

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

Message from the Guest Editors

In this Special Issue, we hope to bring together a diverse set of experts in genomics from multi-disciplinary backgrounds to share their collective expertise in a broad range of topics related to multi-omics profiling and 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., scRNA-seq, scATAC-seq, CITE-seq), other epigenomic, proteomic and spatial genomics in both healthy and diseased tissues/cells. We will highlight new statistical and machine learning approaches for -omics data harmonization, multi-ancestry analyses, quantitative trait locus mapping, GWAS variant prioritization, as well as web application development for end-to-end analyses, data sharing, visualization, annotation, target validation and precision medicine. 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

Dr. Clint L. Miller

Center for Public Health Genomics, Department of Public Health Sciences, University of Virginia, Charlottesville, VA 22908, USA

Prof. Dr. Xia Yang

Department of Integrative Biology and Physiology, University of California Los Angeles, Los Angeles, CA 90095, USA

Deadline for manuscript submissions

closed (5 December 2022)

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Editorial Office
MDPI, Grosspeteranlage 5
4052 Basel, Switzerland
Tel: +41 61 683 77 34
genes@mdpi.com

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About the Journal

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

Prof. Dr. Selvarangan Ponnazhagan
Department of Pathology, The University of Alabama at Birmingham,
1825 University Blvd, SHEL 814, Birmingham, AL 35294-2182, USA

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