Computational and AI Methods for Disease Gene Identification and Diagnosis

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Message from the Guest Editors

Dear Colleagues,

Over the past few decades, it has become clear that exceptional diversity and biodiversity are recurrent features in human evolution, leading advances in predictive, preventative and genomics medicine.

Rapid advances in multiomics techniques, computational data-driven health data science innovation and AI approaches are expected to revolutionize disease gene identification, early disease detection, prediction and diagnosis and strengthen whole-person health research in the next decade. These advances will lead to an improvement in the health of individuals and populations and enhance precision and patient-focused medicine, cost-effective therapeutic strategies and drug discovery, patient outcomes, counselling and delivery of care, as well as support policymakers.

This Special Issue will provide an update on the state of the art in computational data-driven and AI approaches for disease gene identification, risk prediction, risk-stratification and diagnosis as well as critical perspectives and novel insights in data-driven diagnosis. Given the broadness and complexity of these topics, we welcome contributions from experts in the field.

Special Issue

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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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