Machine Learning in Cancer and Disease Genomics

Guest Editors:

Prof. Dr. Piero Fariselli
Department of Medical Sciences,
University of Torino, 10126
Torino, Italy

Dr. Giovanni Birolo
Department of Medical Sciences,
University of Torino, 10126
Torino, Italy

Deadline for manuscript
submissions:
25 March 2025

Message from the Guest Editors

We aim to highlight the pivotal role that advanced computational techniques play in the understanding and treatment of complex diseases. Machine learning algorithms have shown great potential in identifying patterns and making predictions from vast and complex genomic data, thus contributing significantly to personalized medicine and targeted therapies. Machine learning (also known as artificial intelligence) has revolutionized various fields by providing powerful tools to analyze large datasets and uncover hidden patterns. In the context of genomics, these techniques are crucial for making sense of the massive amounts of data encoded in the human genome.

This Special Issue seeks to cover a wide range of topics, including, but not limited to, the development of new machine learning methods for the analysis of genomic data, focusing on applications to cancer and other complex diseases, the integration of multi-omics data, machine learning for biomarker discovery, genome interpretation, and prediction of the effects of genomic variation on disease phenotypes or on DNA/RNA and proteins.

Special Issue

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

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.

Why not consider *Genes* for your next genetics paper?

Author Benefits

Open Access: free for readers, with article processing charges (APC) paid by authors or their institutions.
High Visibility: indexed within Scopus, SCIE (Web of Science), PubMed, MEDLINE, PMC, Embase, PubAg, and other databases.
Journal Rank: JCR - Q2 (*Genetics and Heredity*) / CiteScore - Q2 (*Genetics (clinical)*)

Contact Us