Special Issue

Machine Learning in Cancer and Disease Genomics

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.

Guest Editors

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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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