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Bioinformatics of Sequencing Data: A Machine Learning Approach

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Deadline for manuscript
submissions:

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Message from the Guest Editor

Over the past few years, the deluge of sequencing data prompted us to look for more efficient approaches to summarize and synthesize biological signals. Machine learning methods, diverse and flexible yet robust, provide answers in terms of the optimized processing of large amounts of data and uncovering underlying signals that are hidden (e.g., masked by noise) in traditional approaches.

This Special Issue is open for cutting-edge research spanning the wide range of bioinformatics interests, from purely algorithmic to tightly embedded in the particularities of a data modality. Bold applications of machine learning approaches are welcome. Applications of extracting the essence quantified by sequencing experiments to the interpretation of biological phenomena (e.g., detailing gene regulatory networks) are also invited.

This Special Issue will both underline recent developments in the field (research papers) and summarize the next set of data-processing challenges which may be tackled using machine learning methods (review papers). Case studies are also welcome but should specifically address limitations/shortcomings of current computational approaches.



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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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