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Record Nr.	UNINA9910557129603321
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Titolo	Computational Methods for the Analysis of Genomic Data and Biological Processes
Pubbl/distr/stampa	Basel, Switzerland, : MDPI - Multidisciplinary Digital Publishing Institute, 2021
Descrizione fisica	1 online resource (222 p.)
Soggetti	Biology, life sciences Research & information: general
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Sommario/riassunto	In recent decades, new technologies have made remarkable progress in helping to understand biological systems. Rapid advances in genomic profiling techniques such as microarrays or high-performance sequencing have brought new opportunities and challenges in the fields of computational biology and bioinformatics. Such genetic sequencing techniques allow large amounts of data to be produced, whose analysis and cross-integration could provide a complete view of organisms. As a result, it is necessary to develop new techniques and algorithms that carry out an analysis of these data with reliability and efficiency. This Special Issue collected the latest advances in the field of computational methods for the analysis of gene expression data, and, in particular, the modeling of biological processes. Here we present eleven works selected to be published in this Special Issue due to their interest, quality, and originality.