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Autore	Christine Nardini
Titolo	Multi-omic Data Integration
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Descrizione fisica	1 online resource (135 p.)
Collana	Frontiers Research Topics
Soggetti	Genetics (non-medical)
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Sommario/riassunto	<p>Stable, predictive biomarkers and interpretable disease signatures are seen as a significant step towards personalized medicine. In this perspective, integration of multi-omic data coming from genomics, transcriptomics, glycomics, proteomics, metabolomics is a powerful strategy to reconstruct and analyse complex multi-dimensional interactions, enabling deeper mechanistic and medical insight. At the same time, there is a rising concern that much of such different omic data -although often publicly and freely available- lie in databases and repositories underutilised or not used at all. Issues coming from lack of standardisation and shared biological identities are also well-known. From these considerations, a novel, pressing request arises from the life sciences to design methodologies and approaches that allow for these data to be interpreted as a whole, i.e. as intertwined molecular signatures containing genes, proteins, mRNAs and miRNAs, able to capture inter-layers connections and complexity. Papers discuss data integration approaches and methods of several types and extents, their application in understanding the pathogenesis of specific diseases or in identifying candidate biomarkers to exploit the full benefit of multi-omic datasets and their intrinsic information content. Topics of interest include, but are not limited to:</p> <ul style="list-style-type: none"> • Methods for the integration of layered data, including, but not limited to, genomics, transcriptomics, glycomics, proteomics, metabolomics; • Application of multi-omic data integration approaches for diagnostic biomarker discovery in any field

of the life sciences; • Innovative approaches for the analysis and the visualization of multi-omic datasets; • Methods and applications for systematic measurements from single/undivided samples (comprising genomic, transcriptomic, proteomic, metabolomic measurements, among others); • Multi-scale approaches for integrated dynamic modelling and simulation; • Implementation of applications, computational resources and repositories devoted to data integration including, but not limited to, data warehousing, database federation, semantic integration, service-oriented and/or wiki integration; • Issues related to the definition and implementation of standards, shared identities and semantics, with particular focus on the integration problem. Research papers, reviews and short communications on all topics related to the above issues were welcomed.
