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Integration of Omics Data with Machine Learning and Literature Mining: An Accurate and Fast Approach in Drug Repurposing and Comprehensive Systems Biology

Guest Editors:

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Deadline for manuscript submissions:
closed (15 January 2023)

Message from the Guest Editors

The development and widespread use of next-generation sequencing (NGS) technologies founded the era of big data in biology and medicine. In particular, it led to an accumulation of datasets that opened up a vast number of possible applications for data-driven methodologies. However, NGS-based studies usually utilized small sample sizes, and thus many research results gave low reproducibility rates in followed studies. Hence, the meta-analysis of available data from several studies was soon identified as the appropriate technique to obtain adequate sample sizes and optimal strength for the detection of genetic associations.

Also, data-driven NGS research areas have tailored data mining technologies such as machine learning. A machine learning model can incorporate prior knowledge from different omics data. Subsequently, the models can identify hidden knowledge, patterns, and relationships in an enormous amount of NGS information.

The combination of machine learning and meta-analysis in the analysis of multiple NGS experiments simultaneously may open up a new avenue to use publicly available data to better uncover key molecular factors and underlying mechanisms in omics studies.

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