Statistical Methods for Multi-Omics Data

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Abstract

Recent advances in statistical methods play a vital role in multi-omics data analysis to integrate information from different omics layers to gain a more comprehensive understanding of biological processes. These methods address the challenge of analyzing high-dimensional data with many variables and relatively few samples, often while accounting for multiple testing adjustments in a heterogeneous framework. Some of recent works help to find combinations of variables from different omics layers that maximize correlation, helping to identify shared signals and relationships explore associations between different omics layers, identifying features in one layer that are related to features in other layers and shared factors influencing different omics data relationships. The machine learning based statistical algorithms help to model the relationships between different omics layers, predict outcomes, and identify predictive biomarkers. This paper presents some recent developments to leverage multi-omics data to gain deeper insights into complex biological systems, identify novel biomarkers, and develop targeted therapies.