
Leveraging multi-omic data for integrative exploratory and predictive analyses

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Résumé

The increased availability and affordability of high-throughput sequencing technologies in recent years have facilitated the use of multi-omic studies, expanding and enriching our understanding of complex systems across hierarchical biological levels. Integrative methods for these heterogeneous and multi-faceted omics data have shown promise for enhancing the interpretability of exploratory analyses, improving predictive power, and contributing to a holistic understanding of systems biology. However, such integrative analyses are accompanied by several major obstacles, including the potentially ambiguous relationships among omic levels, high dimensionality coupled with small sample sizes, technical artefacts due to batch effects, potentially incomplete or missing data... and the occasional difficulty in posing well-defined and answerable research questions of such data. In light of these challenges, in this talk I will discuss some of our recent methodological contributions to integrate multi-omic data for exploratory and predictive analyses.

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