

Manuscript Title

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Abstract

Recently developed technologies to generate single-cell genomic data have made a revolutionary impact in the field of biology. Multi-omics assays offer even greater opportunities to understand cellular states and biological processes. However, the problem of integrating different -omics data with very different dimensionality and statistical properties remains quite challenging. A growing body of computational tools are being developed for this task, leveraging ideas ranging from machine translation to the theory of networks and representing a new frontier on the interface of biology and data science. Our goal in this review paper is to provide a comprehensive, up-to-date survey of computational techniques for the integration of multi-omics and alignment of multiple modalities of genomics data in the single cell research field.

References
