Gene regulatory network inference in the era of single-cell multi-omics.

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Abstract

The interplay between chromatin, transcription factors and genes generates complex regulatory circuits that can be represented as gene regulatory networks (GRNs). The study of GRNs is useful to understand how cellular identity is established, maintained and disrupted in disease. GRNs can be inferred from experimental data – historically, bulk omics data – and/or from the literature. The advent of single-cell multi-omics technologies has led to the development of novel computational methods that leverage genomic, transcriptomic and chromatin accessibility information to infer GRNs at an unprecedented resolution. Here, we review the key principles of inferring GRNs that encompass transcription factor-gene interactions from transcriptomics and chromatin accessibility data. We focus on the comparison and classification of methods that use single-cell multimodal data. We highlight challenges in GRN inference, in particular with respect to benchmarking, and potential further developments using additional data modalities.