Pencil

The rapid progress of protocols for sequencing single-cell transcriptomes over the past decade has been accompanied by equally impressive advances in the computational methods for analysis of such data. As capacity and accuracy of the experimental techniques grew, the emerging algorithm developments revealed increasingly complex facets of the underlying biology, from cell type composition to gene regulation to developmental dynamics. At the same time, rapid growth has forced continuous reevaluation of the underlying statistical models, experimental aims, and sheer volumes of data processing that are handled by these computational tools. Here, I review key computational steps of single-cell RNA sequencing (scRNA-seq) analysis, examine assumptions made by different approaches, and highlight successes, remaining ambiguities, and limitations that are important to keep in mind as scRNA-seq becomes a mainstream technique for studying biology.