Lecture 10: Single-Cell RNA Sequencing
BIOINF3005/7160: Transcriptomics Applications

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Background

Introduction

- scRNA-Seq is the 'latest and greatest' transcriptomic technique
- Previously all our analysis involved multiple cells per sample
- All were combined during tissue extraction, library preparation etc.
- Most experiments have **highly** heterogeneous cell populations, e.g.

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  - Different regions of the brain contain highly specialised cells
  - The immune system is highly complex
  - Cancer samples have both infiltrating and tumour cells

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Introduction

- If a gene is increased 2-fold in expression:
  - Is this 2-fold in 100% of cells?
  - Or is it 4-fold in 50% of cells?
  - Or is it down 2-fold in 25% and up 8-fold in 25% and unchanged in 50%?
- Changes in gene expression can be highly specific to individual cell-types
- In general, determining heterogeneity of our samples is challenging

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- Reality is much trickier than this
- How do we characterise which cell is which cell-type?
- How do we capture as many transcripts from each cell as we can?
  - Missing values are a huge issue in scRNA-seq
- How do we compare within the same cell-types between experimental groups?
  - E.g., treated and untreated cell types may not be assigned to the same cluster/cell-type

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Workflow Outline
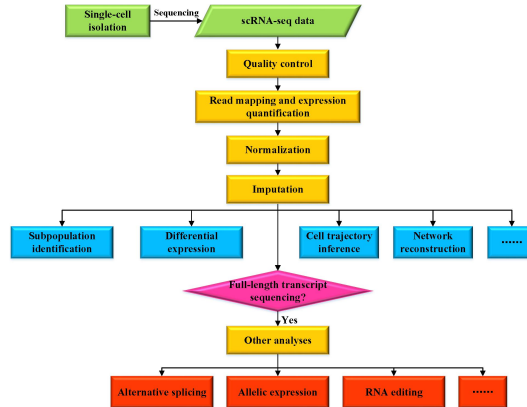
scRNA Protocols

Data Analysis

Spatial Transcriptomics