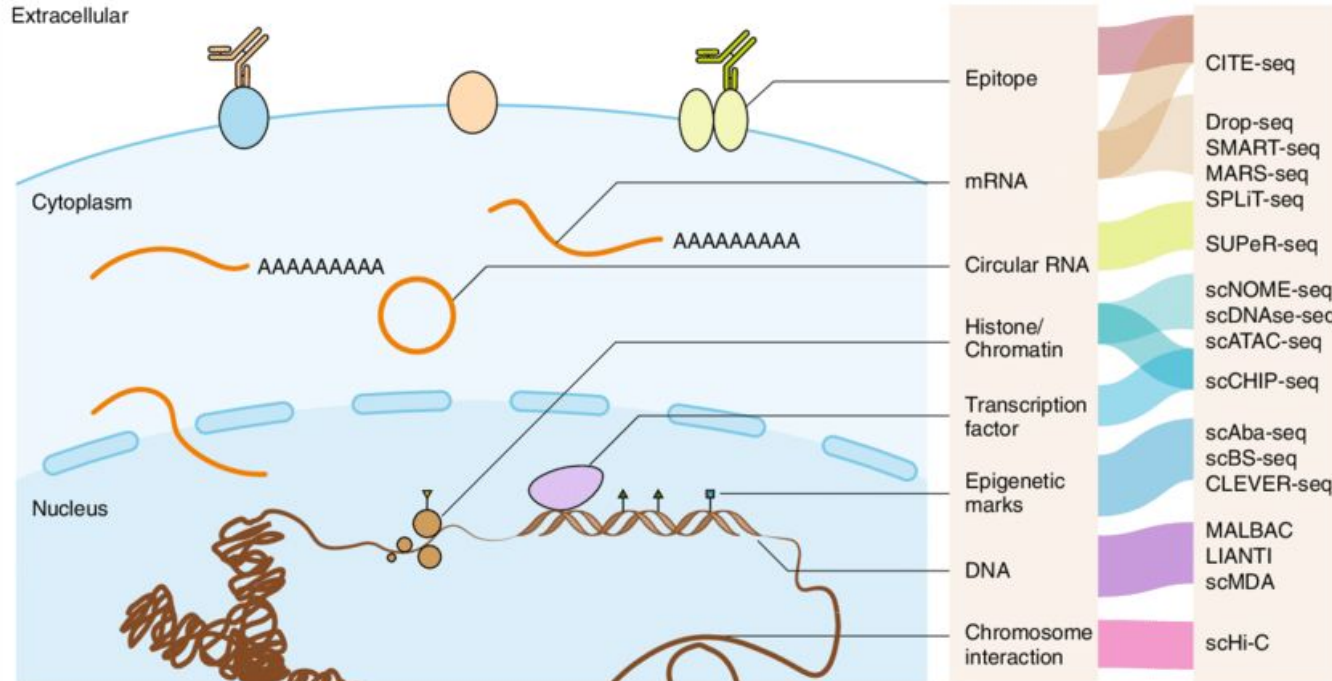


CPSC 547 project:

# An atlas exploring single-cell transcriptomics

Kieran Maheden & Brett Kiyota

# Single-cell sequencing technologies

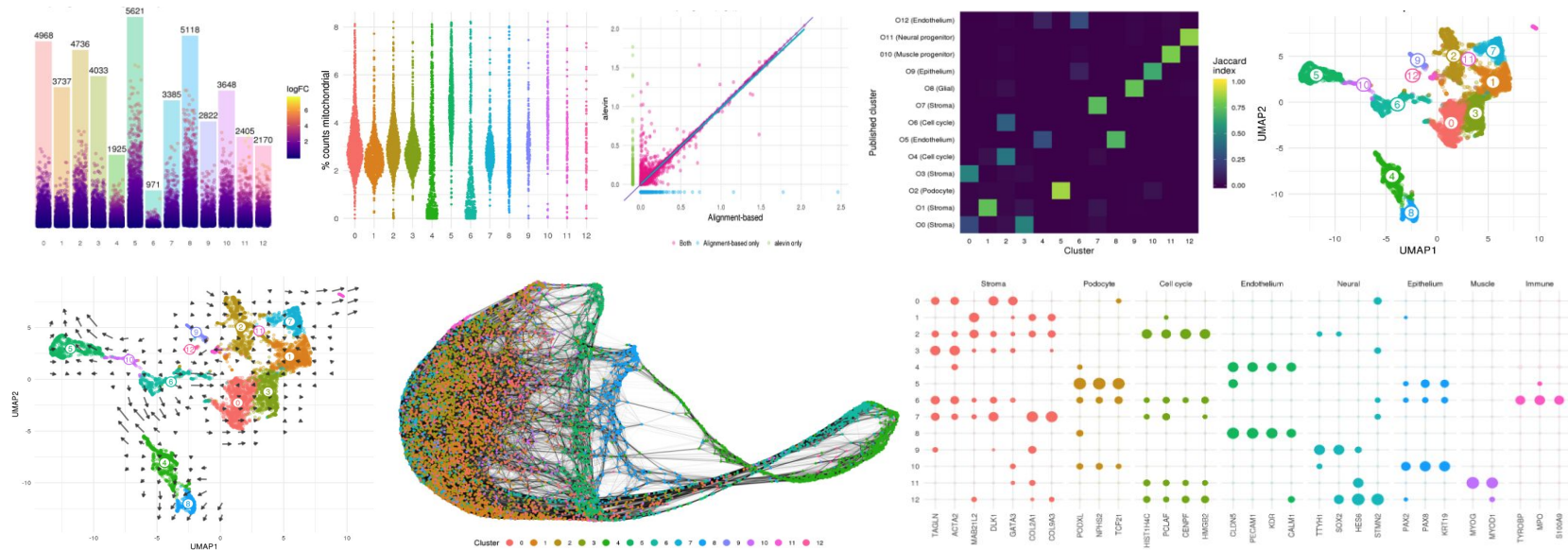


Cells can be characterized at many different levels of abstraction.

At each level, there are many viable approaches to quantify such information

# scRNA-seq: high-dimensional datasets

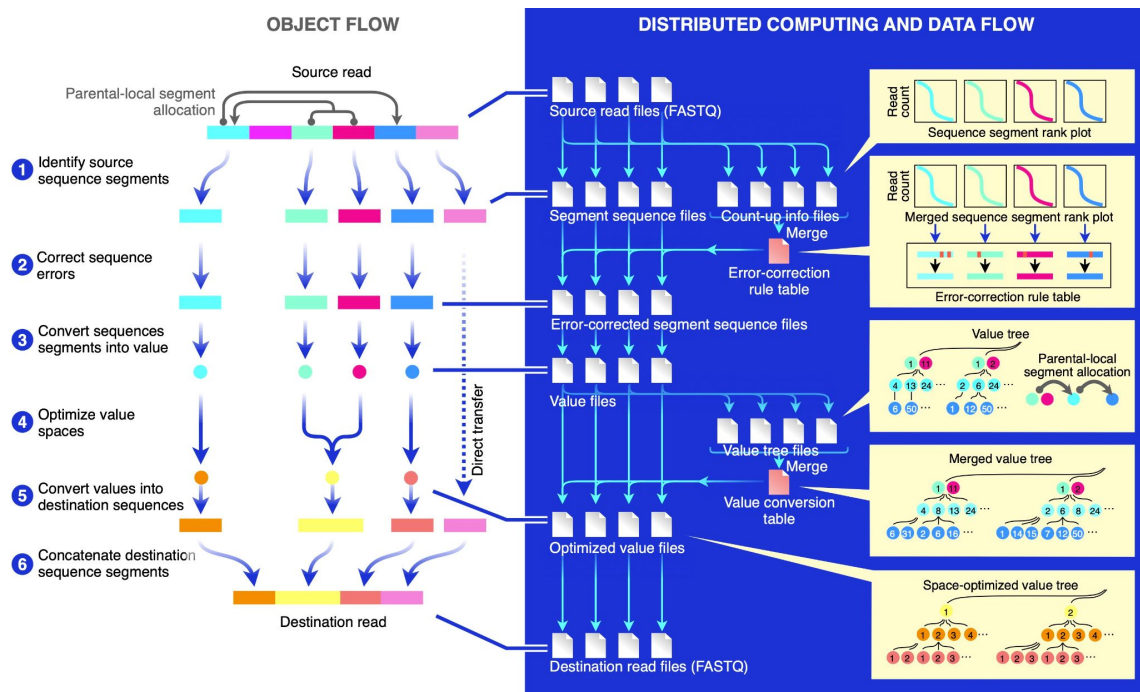
Visualization is an essential tool that guides the workflow of analysis



Adapted from <https://lazappi.github.io/phd-thesis/5-analysis.html>

# Software can translate sequencing data across technology platforms

## INTERSTELLAR



<https://github.com/yachielab/Interstellar>

Translatability of sequencing data across technologies facilitates creation of datasets that are rich in size and information.

# Proposed project

1. Construct a dataset from various scRNA-seq technologies (using a software to translate them all into a common format for analysis).
2. Create a tissue-specific atlas that involves visualizing different aspects of data throughout the analysis workflow.
3. Write a combination survey/analysis paper.

Example:

