An atlas exploring single-cell transcriptomics

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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

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

INTERSTELLAR

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

https://www.nature.com/articles/s41586-020-2496-1