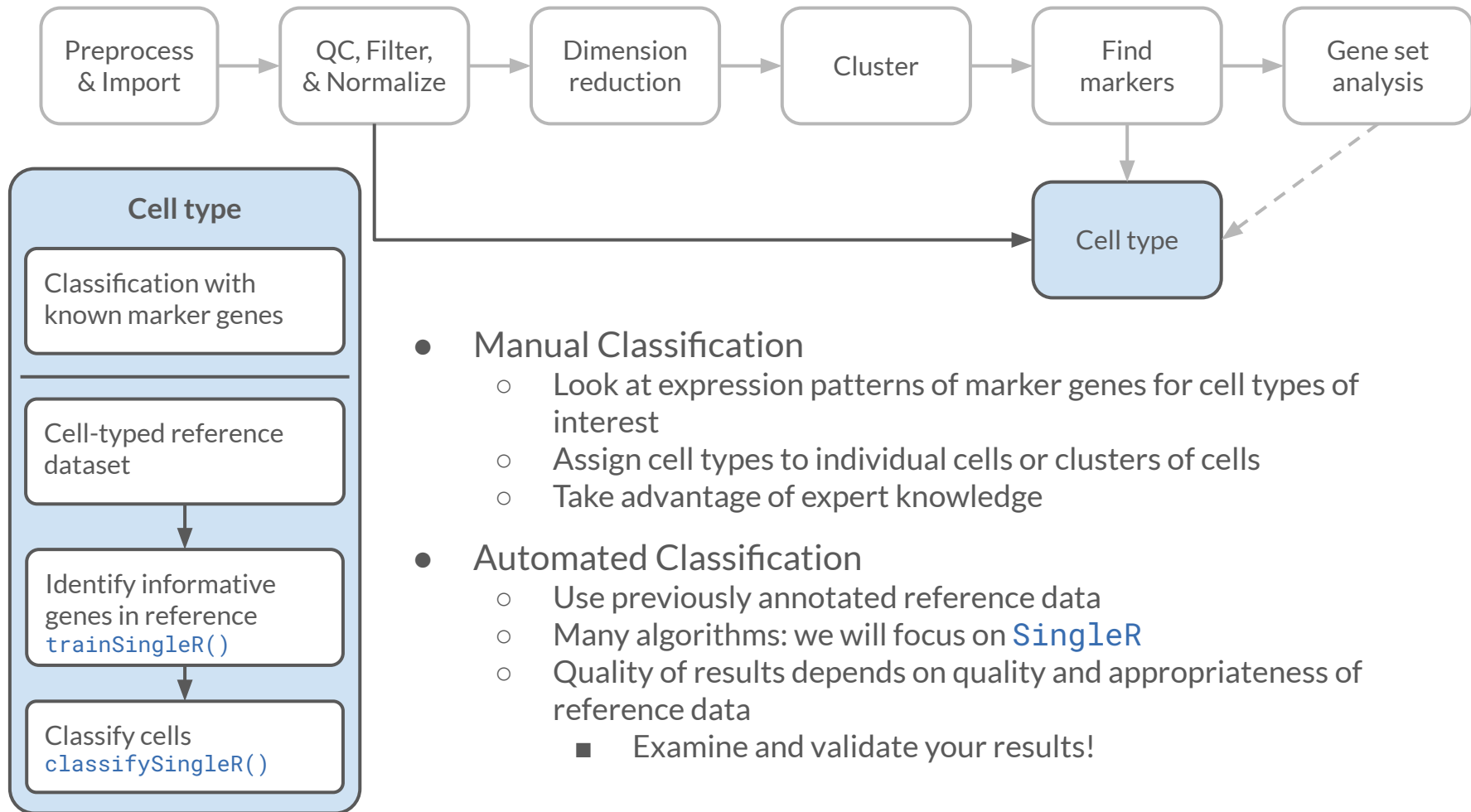




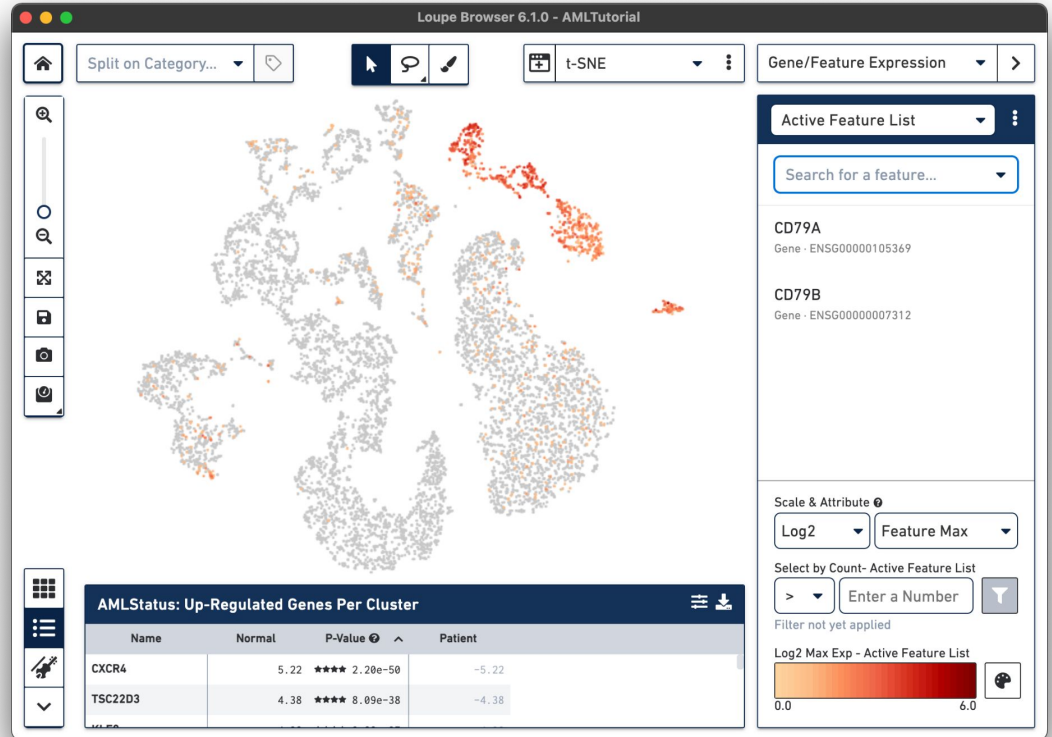
Annotating Cell Types from Single-cell Data

The Data Lab



Manual annotation

- Look at expression of known marker genes
- Label cells or clusters by expression thresholds
- Labor intensive, often requires expert knowledge



Where do you find marker genes?

- Literature and databases
 - commonly used marker genes and proteins
 - databases of marker genes
 - [C8 dataset from MSigDB](#) Cell type signature gene sets
 - [PanglaoDB](#)
 - [CellMarker](#)
- Within your data
 - differentially expressed genes among clusters

This is fine



Although labour-consuming and inevitably subjective and arbitrary, manual annotation must be mentioned here, because this primitive slash-and-burn mode of research is still being adopted by many laboratories and biotech companies...

– [Wang, Ding, and Zou 2020](#)

*The database of cell type markers was compiled by manual curation of thousands of published articles and abstracts, and by querying internet search engines with strings such as 'GENE1 is expressed in * cells'.*

– [Franzén, Gan, and Björkegren 2019](#)

Automated annotation tools

- Dozens of methods
 - A relatively recent review: [Li et al. \(2025\)](#)
- Marker-based
 - Use an input database of cell type marker genes
 - Assign cell types based on which genes are expressed in each cell
 - [CellAssign](#), [scTyper](#), [scType](#)
- Reference-based
 - Use a cell-type annotated gene expression reference dataset
 - Assign cell types based on the closest match in the reference
 - [SingleR](#), [Seurat/Azimuth](#), [scArches](#)
- “AI”-based methods
 - Train a foundation model based on large reference collections and use that for annotations
 - [SCimilarity](#), [scGPT](#), [scFoundation](#)
 - and/or use the literature via an LLM
 - [GPTCelltype](#), [scExtract](#), new methods every month...

Why focus on SingleR

- It works well and is well-integrated with the pipeline/tools we use
 - We have not rigorously evaluated others, YMMV!
- Flexible
 - Reference data can be bulk data RNA-seq, single-cell RNA-seq, even bulk microarrays
- Great documentation:
 - <http://bioconductor.org/books/release/SingleRBook/>

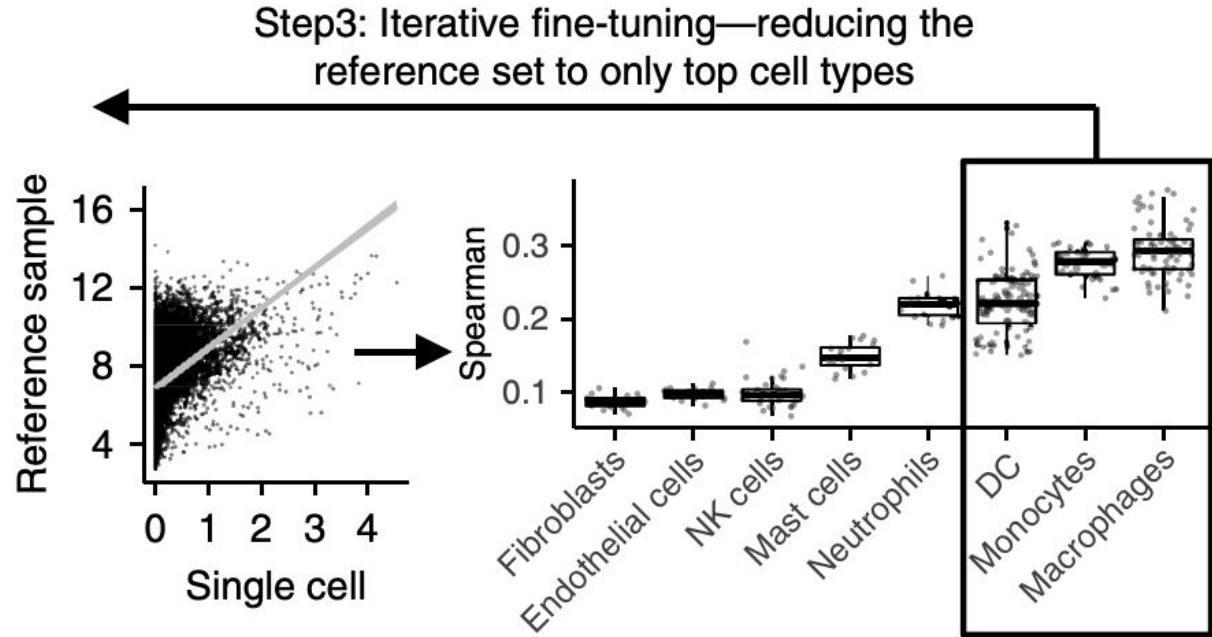
SingleR method

- “Train” on a labeled reference set
 - Identify most informative genes
 - differentially expressed among labels
 - method can vary depending on reference type
- Assign labels to query cells
 - For each cell (or group of cells), calculate the Spearman correlation to each reference sample
 - use only the markers identified previously
 - calculate label scores based on correlations to reference samples with each label
 - top label score is the assigned label
 - Optionally: fine tune labels
 - select top labels
 - repeat above, using only markers relevant to the top label groups

SingleR method

Step 1:
Identifying variable
genes among cell types
in the reference set

Step 2:
Correlating each
single-cell transcriptome
with each sample in the
reference set



Reference datasets

- Quality and appropriateness of the reference will strongly affect results
 - If your reference dataset does not have the cell types you are interested in, you won't find them!
 - Many methods will bias towards assigning labels, even if there is no good match
- Finding "good" reference data is one of the biggest challenges
 - Previous experiments, if you trust them
 - manual annotation isn't all bad!
 - Public data, if you can find it
 - `celldex` package: precompiled reference datasets ready for SingleR ([Usage guide](#))
 - [Azimuth](#) reference datasets
 - Be aware that most public datasets are of normal tissue!
 - If you are working with cancer cells, you may have trouble finding good references for automated annotation

Validating automatic annotations

“Don’t blindly trust the robots on this one.” –Ally

- Some methods provide diagnostic statistics and plots that may be useful
- Compare labels using different tools and references
- Visualize known markers to validate assignments

