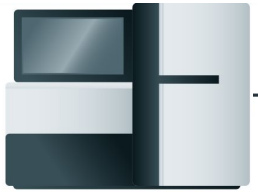
STA426 scRNA pipeline

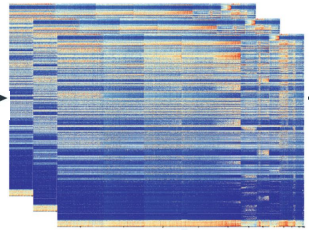
Anthony Sonrel, December 12

Single-cell RNA seq

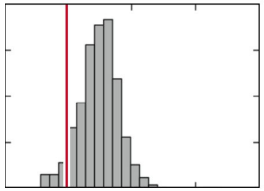
Sequencing



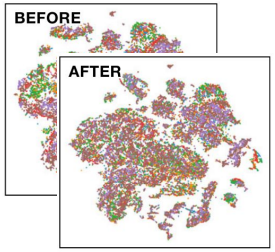
Count table



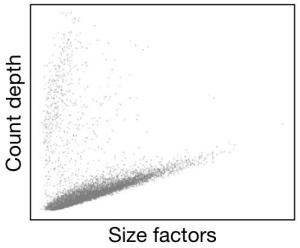
QC



Batch correction

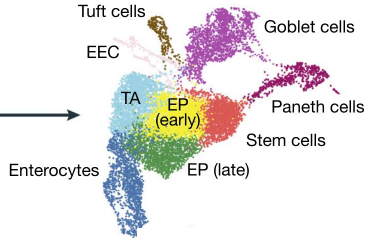


Normalization

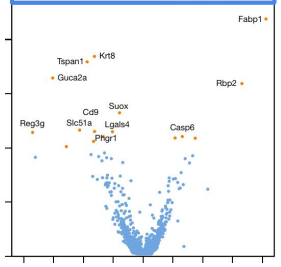


Clustering

Annotation



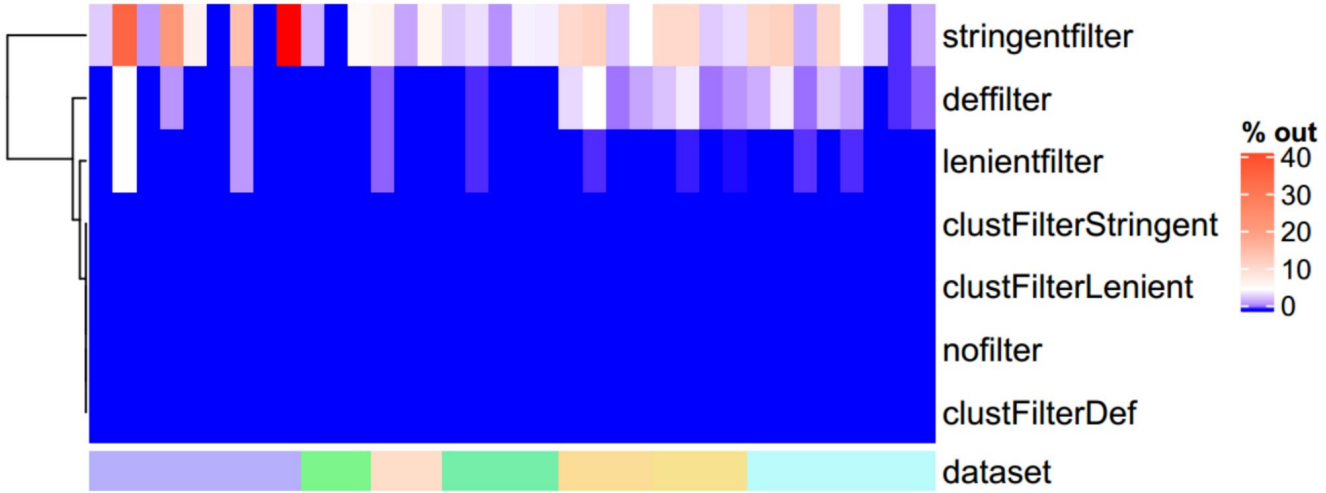
Differential expression



Adapted from
Luecken 2019, mol. syst. biol.

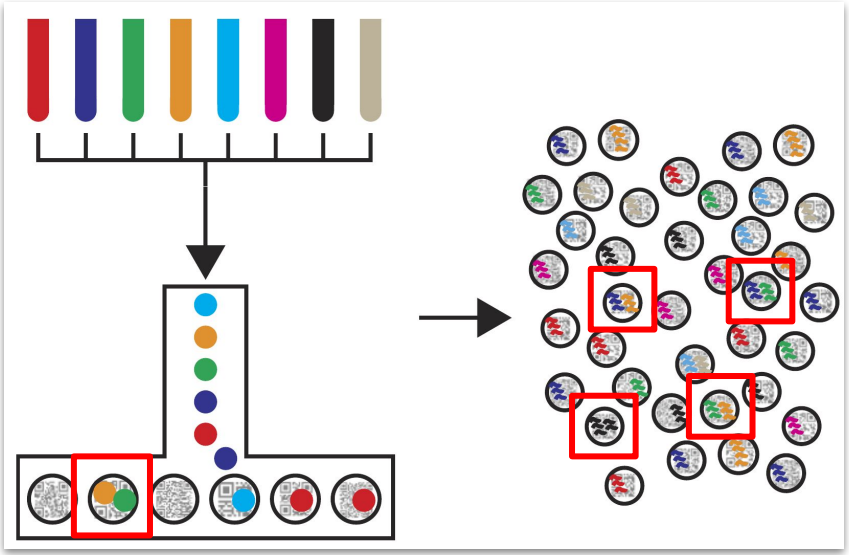
QC and filtering

- Stringent filters are heavily biased on some cell types
- Cluster-based filters typically remove nothing



Slide provided by
Pierre-Luc Germain

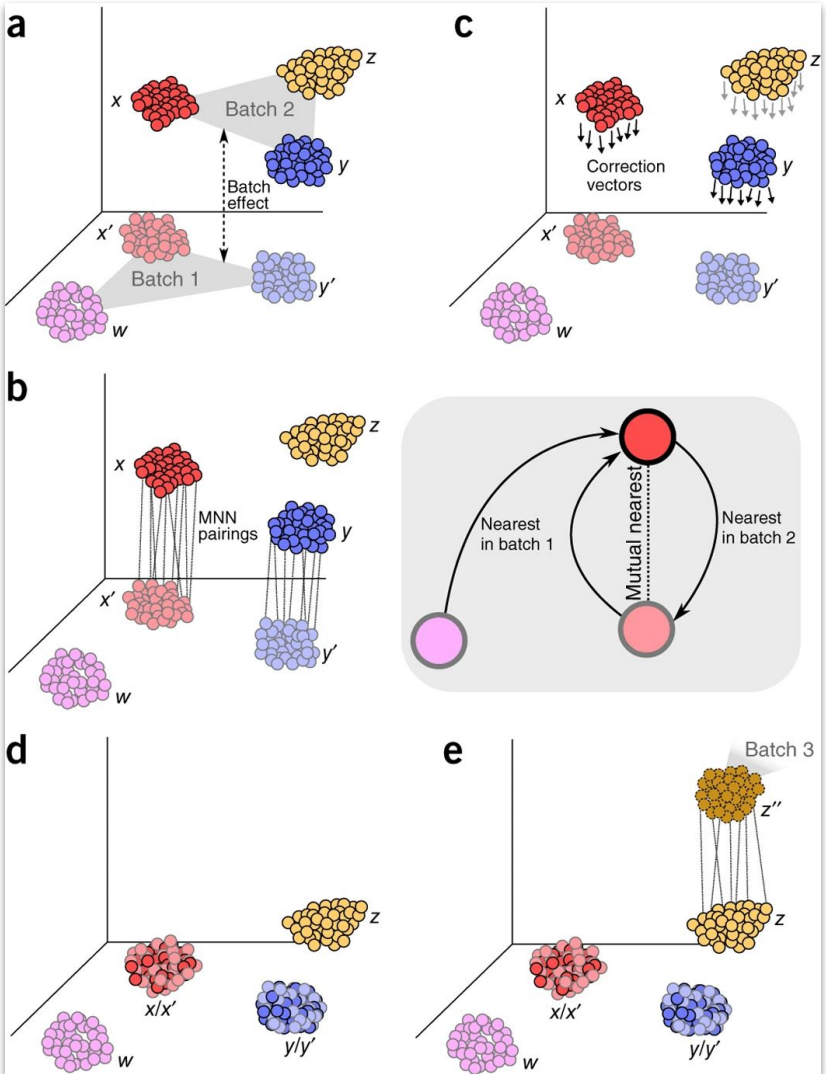
Doublets



- When >=2 cells get captured in the same droplet
- Detect droplets with 2n reads is not sufficient
- …and can be formed from 2 cells of the same (*homotypic*) or different (*heterotypic*) cell-types

Adapted from Kang et al. 2018, Nature Biotechnology

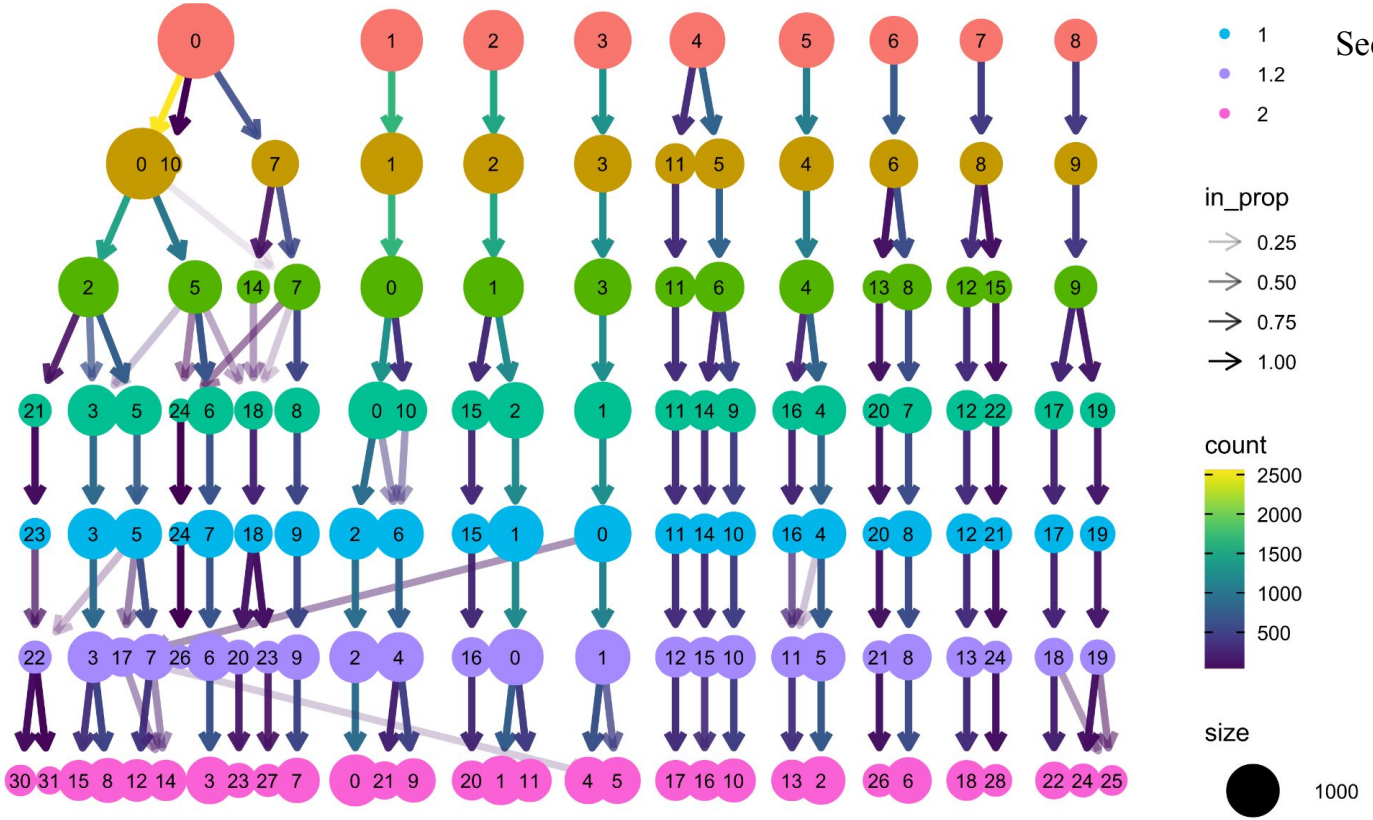
Batch correction



- Most batch effects can be seen as orthogonal effects in low dimension (A)
- Batch correction starts by identifying MNN pairs of cells (B)
- Batch correction ‘vectors’ are calculated from pairs (C)

Adapted from Haghverdi et al. 2018, Nature Biotechnology

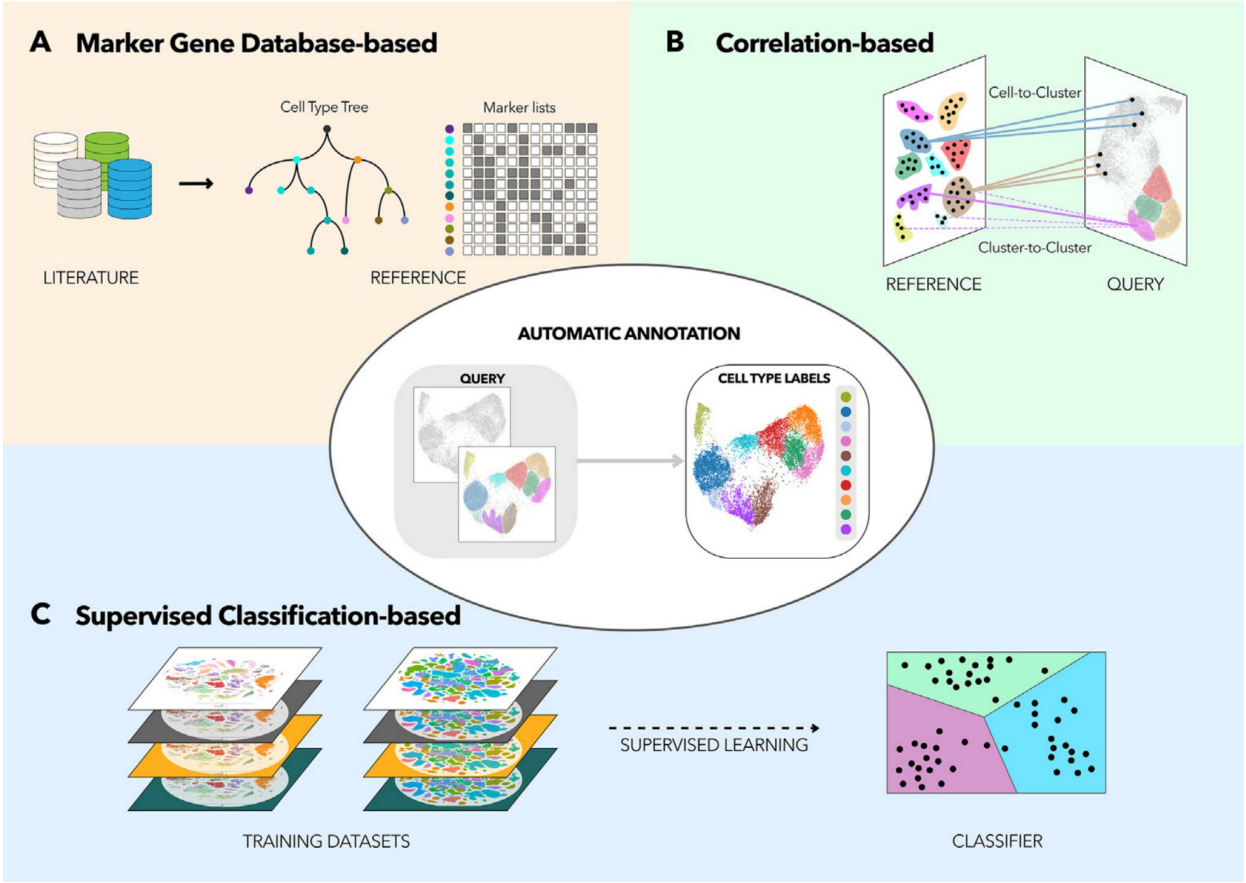
Clustering resolution



See also the clustree package

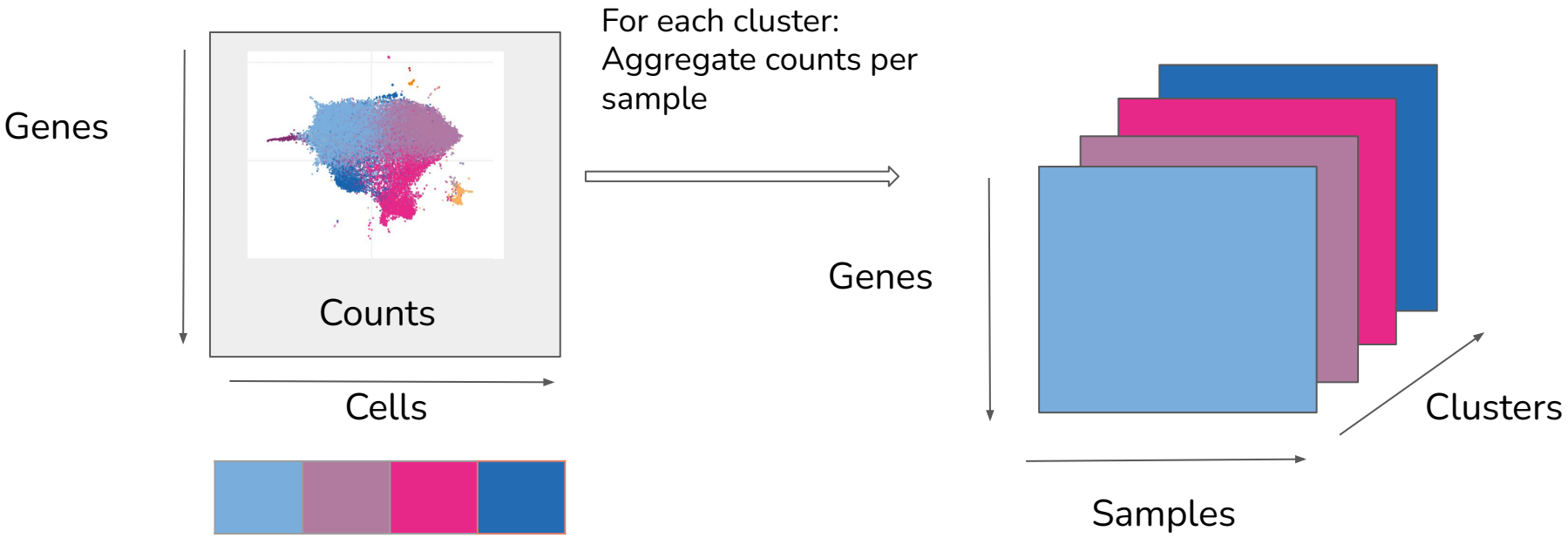
Slide provided by
Pierre-Luc Germain

Cell-type annotation



Pasquini 2021,
Comp. Struct. Biotech. Journal

Pseudobulk analysis



Thank you