

# Single cell transcriptomics

Analysis tools & QC

cells ->

genes ->

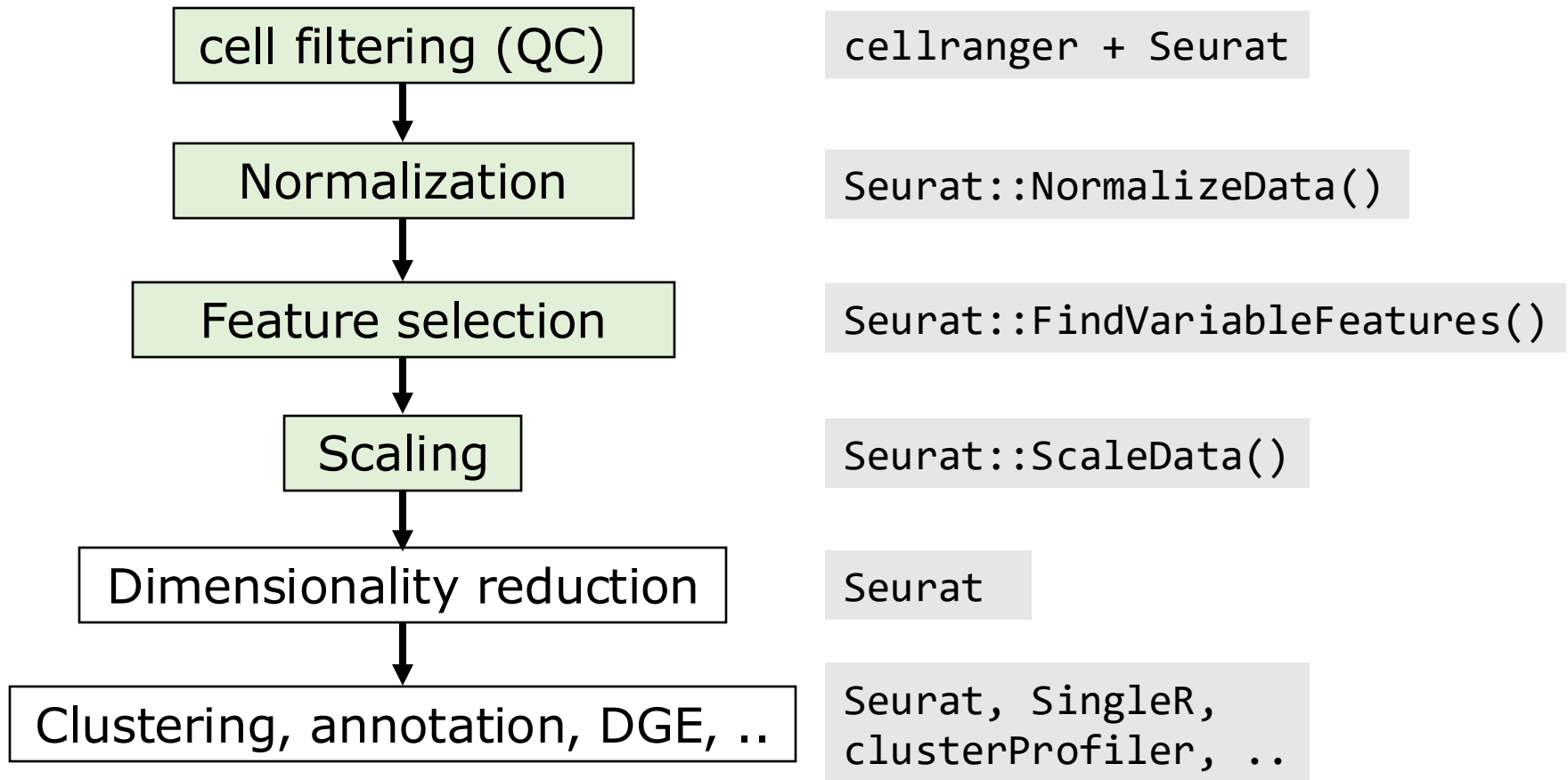
	ATAC-1	CCG-1	GCGA-1
RPL22	5	13	3
PARK7	0	9	3
ENO1	1	35	0
PLA2G2A	0	0	0
CAMK2N1	0	6	0
CDC42	0	8	1
C1QA	0	0	25
C1QC	0	0	25
C1QB	0	0	29
ID3	0	35	0
RPL11	18	29	16
CLIC4	0	4	0

# Frequently used analysis tools

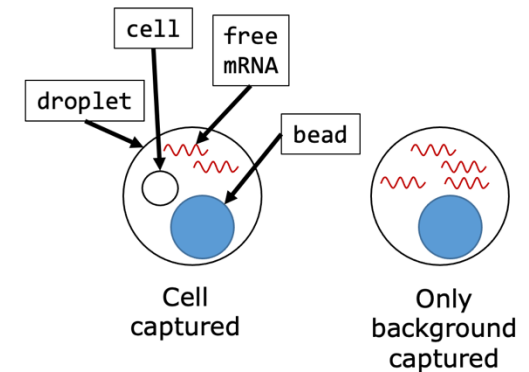
- Major tools perform (at least) the following:
  - QC
  - normalization & scaling
  - dimensionality reduction
- scanpy (python)
- scater + scran (R, Bioconductor)
- monocle3 (R, beta on github)
- Seurat (R, CRAN)



# Analysis overview



# Cell filtering



- Cellranger:
  - cell calling (filter against low #UMI)
- Manually (e.g. with Seurat):
  - #UMI: high -> possible doublet
  - #detected genes
  - % mitochondrial UMI: dying cells
  - % ribosomal UMI
  - % globin UMI
  - Relationships between variables

# Cell filtering

Often it makes sense to look at relationships

