

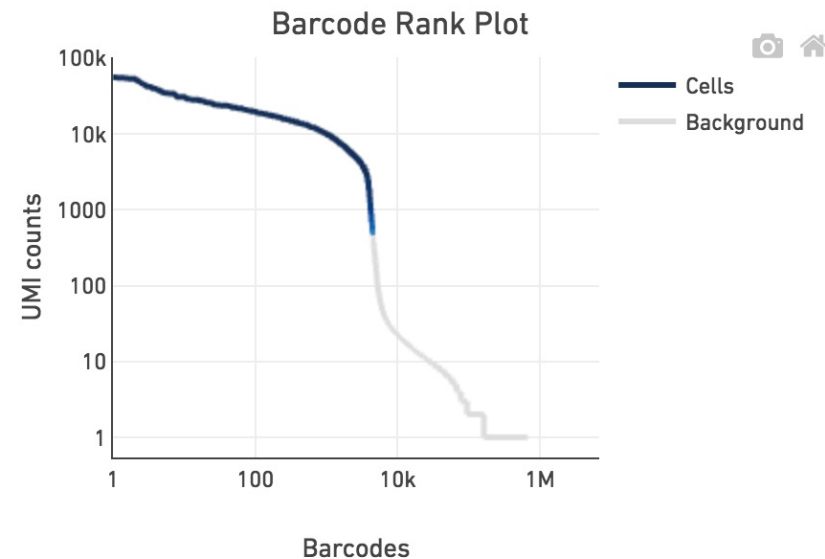
# Single cell transcriptomics

Quality control

# Cell calling

Dropouts: low #UMI/cell

## Cells ?



# Further cell filtering

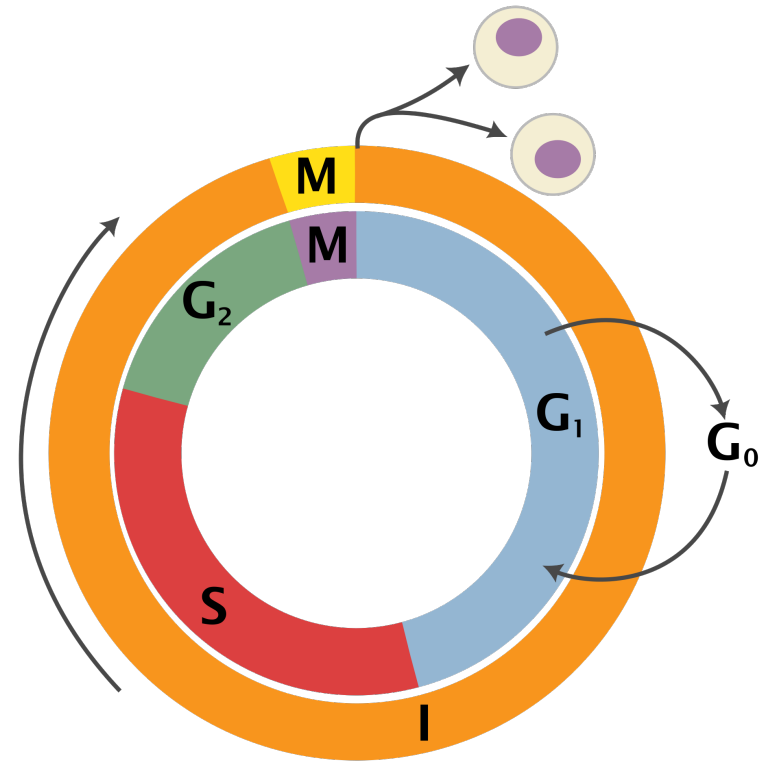
- Doublets: DoubletFinder
- % UMI in mitochondrial genes:
  - Points to dying/stressed cells
  - Filter by threshold (e.g. 20%)
- Number of detected genes/cell
  - High: possible doublet
  - Low: possible dropout

# Confounding variables

- % mitochondria
- % ribosomal genes
- % dissociation genes
- Library size
- Sex
- Age
- Cell cycle
- ..

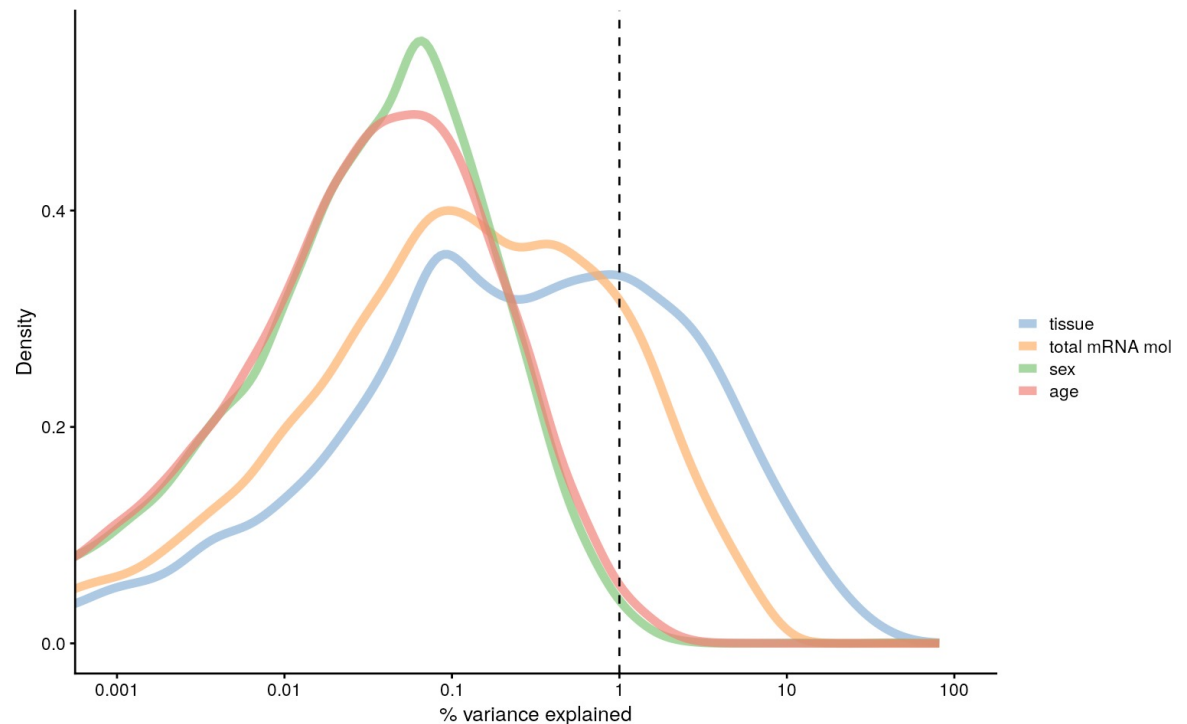
# Cell cycle

- Default clustering might be according to state
- Cycling state can be regressed out for clustering according to cell type



# Find explanatory variables

- With the package scater
- Plot variance explained per gene



# Regress out for clustering

- Regress out variables explaining a lot of variation
- At the scaling step -> affects PCA and therefore clustering/annotation
- **OR:** integrate data (day 2)