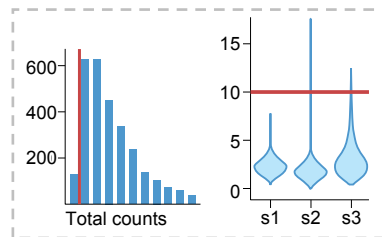


# 1. pre-processing

count matrix

$n_{\text{raw}} \text{ cells}$	$m_{\text{raw}} \text{ genes}$	
0	5	2 ...
10	0	0 ...
15	0	0 ...
...	...	...

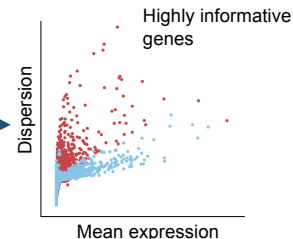
quality control



Normalization

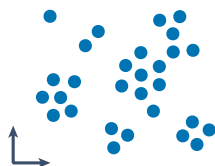
$n_{\text{filtered}} \text{ cells}$	$m_{\text{filtered}} \text{ genes}$	
0	0.5	2 ...
0.6	0	0 ...
0.7	0	0 ...
...	...	...

Feature selection

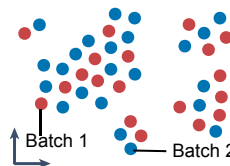


# 2. clustering

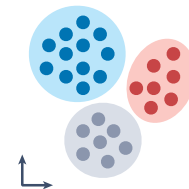
dimension reduction



batch correction

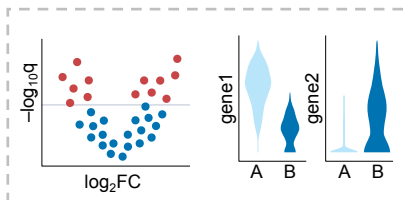


clustering

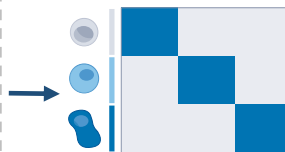


# 3. downstream

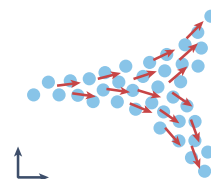
Differential expression



Cluster annotation



Trajectory inference



Gene set enrichment

