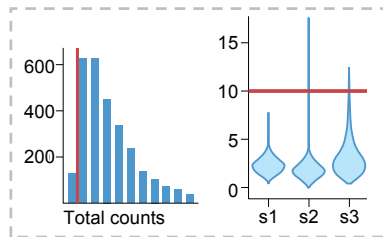


1. pre-processing

count matrix

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

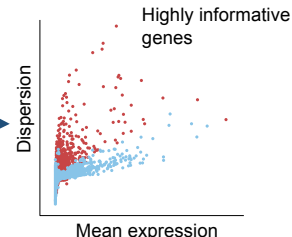
quality control



Normalization

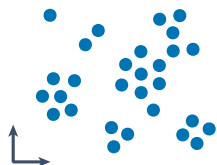
$n_{\text{filtered cells}}$	$m_{\text{filtered genes}}$
0	0.5 2 ...
0.6	0 0 ...
0.7	0 0 ...
...

Feature selection

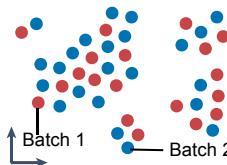


2. clustering

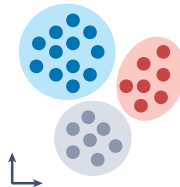
dimension reduction



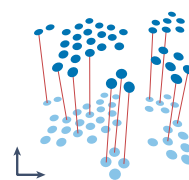
batch correction



clustering

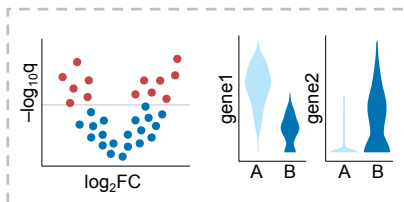


reference mapping

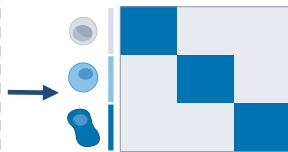


3. downstream

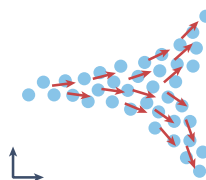
Differential expression



Cluster annotation



Trajectory inference



Gene set enrichment

