

## Download and load dataset

Let's use a 10x dataset from the 10x genomics website. You can download it to an anndata object with scanpy as follows:

```
library(anndata)
library(reticulate)
sc <- import("scanpy")
url <- "https://cf.10xgenomics.com/samples/cell-exp/6.0.0/SC3_v3_NextGem_DI_CellPlex_CSP_DTC_Sorted_30K_Squamous_Cell_Carcinoma/SC3_v3_NextGem_DI_CellPlex_CSP_DTC_Sorted_30K_Squamous_Cell_Carcinoma_count_sample_feature_bc_matrix.h5"
ad <- sc$read_10x_h5("dataset.h5", backup_url = url)
ad
## AnnData object with n_obs × n_vars = 5377 × 36601
## var: 'gene_ids', 'feature_types', 'genome'
```

## Preprocessing dataset

The resulting dataset is a wrapper for the Python class but behaves very much like an R object:

```
ad[1:5, 3:5]
## View of AnnData object with n_obs × n_vars = 5 × 3
## var: 'gene_ids', 'feature_types', 'genome'
dim(ad)
## [1] 5377 36601
```

You can still call scanpy functions on it, for example to perform preprocessing.

```
sc$pp$filter_cells(ad, min_genes = 200)
sc$pp$filter_genes(ad, min_cells = 3)
sc$pp$normalize_per_cell(ad)
sc$pp$log1p(ad)
```

## Analysing your dataset in R

You can seamlessly switch back to using your dataset with other R functions. For example, calculating the rowMeans of the expression matrix.

```
library(Matrix)
rowMeans(ad$X[1:10,])
## AAACCCAAGCGCGTTC-1 AAACCCAAGGCAATGC-1 AAACCCAGTATCTTCT-1
AAACCCAGTGACAACG-1
## 0.05451418 0.13627126 0.12637224 0.13958617
## AAACCCAGTTGAATCC-1 AAACCCATCGGCTTGG-1 AAACGAAAGAGAGCCT-1
AAACGAAAGCTTAAGA-1
## 0.05979424 0.11365747 0.05011727 0.14347849
## AAACGAAAGGCACGAT-1 AAACGAAAGGTAGCCA-1
## 0.12979302 0.12366312
```