

# Package ‘scviR’

July 4, 2025

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**Title** experimental interface from R to scvi-tools

**Version** 1.9.11

**Description** This package defines interfaces from R to scvi-tools. A vignette works through the totalVI tutorial for analyzing CITE-seq data. Another vignette compares outputs of Chapter 12 of the OSCA book with analogous outputs based on totalVI quantifications. Future work will address other components of scvi-tools, with a focus on building understanding of probabilistic methods based on variational autoencoders.

**License** Artistic-2.0

**Encoding** UTF-8

**Depends** R (>= 4.3), basilisk, shiny, SingleCellExperiment

**Imports** reticulate, BiocFileCache, utils, pheatmap,  
SummarizedExperiment, S4Vectors, limma, scater, stats,  
MatrixGenerics

**Suggests** knitr, testthat, reshape2, ggplot2, rhdf5, BiocStyle

**VignetteBuilder** knitr

**biocViews** Infrastructure, SingleCell, DataImport

**RoxygenNote** 7.3.2

**URL** <https://github.com/vjcitn/scviR>

**BugReports** <https://github.com/vjcitn/scviR/issues>

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|             |                                                                           |
|-------------|---------------------------------------------------------------------------|
| adtProfiles | <i>produce a heatmap from a specialized CITE-seq SingleCellExperiment</i> |
|-------------|---------------------------------------------------------------------------|

---

## Description

produce a heatmap from a specialized CITE-seq SingleCellExperiment

## Usage

```
adtProfiles(x, lb = -3, ub = 3, do_z = FALSE)
```

## Arguments

|      |                                                                                                         |
|------|---------------------------------------------------------------------------------------------------------|
| x    | SingleCellExperiment instance that has an 'se.averaged' component in its meta-data                      |
| lb   | numeric(1) lower bound on 'breaks' sequence for ComplexHeatmap::pheatmap, defaults to -3                |
| ub   | numeric(1) upper bound on 'breaks' sequence for ComplexHeatmap::pheatmap, defaults to 3                 |
| do_z | logical(1) if TRUE, divide the residuals by their standard deviation across clusters, defaults to false |

**Value**

ComplexHeatmap::pheatmap instance  
 side effect of pheatmap::pheatmap call

**Note**

See the OSCA book ch12.5.2 for the application.

**Examples**

```
ch12sce <- getCh12Sce()
adtProfiles(ch12sce)
adtProfiles(ch12sce, do_z = TRUE)
```

---

|          |                                   |
|----------|-----------------------------------|
| anndataR | <i>basic interface to anndata</i> |
|----------|-----------------------------------|

---

**Description**

basic interface to anndata

**Usage**

```
anndataR()
```

**Value**

basiliskRun result with import from reticulate, typically a Module

**Examples**

```
ad <- anndataR()
ad
ad$read
```

---

|         |                            |
|---------|----------------------------|
| bsklenv | <i>python declarations</i> |
|---------|----------------------------|

---

**Description**

python declarations

**Usage**

```
bsklenv
```

**Format**

An object of class BasiliskEnvironment of length 1.

---

```
cacheCiteSeq5k10kPbmcs
```

*grab scvi-tools-processed PBMC CITE-seq data in anndata format (gzipped) from Open Storage Network*

---

### Description

grab scvi-tools-processed PBMC CITE-seq data in anndata format (gzipped) from Open Storage Network

### Usage

```
cacheCiteSeq5k10kPbmcs()
```

### Value

invisibly, the path to the .h5ad file

### Note

Original h5ad files obtained using scvi-tools 0.18.0 `scvi.data.pbmcs_10x_cite_seq`, then processed according to steps in the scviR vignette, which follow the [scvi-tools tutorial](<https://colab.research.google.com/github/scvi-tools/tutorials/blob/0.18.0/totalVI.ipynb>) by Gayoso et al.

It may be advantageous to set `'options(timeout=3600)'` or to allow an even greater time for internet downloads, if working at a relatively slow network connection.

### Examples

```
h5path <- cacheCiteSeq5k10kPbmcs()
cmeta <- rhdf5::h5ls(h5path)
dim(cmeta)
head(cmeta, 17)
```

---

```
cacheCiteSeq5k10kTutvae
```

*Deprecated: grab scvi-tools VAE instance built on the PBMC datasets following the tutorial*

---

### Description

Deprecated: grab scvi-tools VAE instance built on the PBMC datasets following the tutorial

### Usage

```
cacheCiteSeq5k10kTutvae()
```

### Value

invisibly, the path to the .zip file holding the fitted VAE and associated data

**Note**

the serialized model is obsolete

VAE construction followed tutorial at <https://docs.scvi-tools.org/en/stable/tutorials/notebooks/totalVI.html>.

It may be advantageous to set `options(timeout=3600)` or to allow an even greater time for internet downloads, if working at a relatively slow network connection.

**Examples**

```
## Not run:
zpath <- cacheCiteSeq5k10kTutvae()
td <- tempdir()
utils::unzip(zpath, exdir = td)
vaedir <- paste0(td, "/vae2_ov")
scvi <- scviR()
adm <- anndataR()
hpath <- cacheCiteSeq5k10kPbmcs()
adata <- adm$read(hpath)
mod <- scvi$model$`_totalvi`$TOTALVI$load(vaedir, adata) #, use_gpu = FALSE)
mod

## End(Not run)
```

---

|                     |                                                                                             |
|---------------------|---------------------------------------------------------------------------------------------|
| cacheCiteSeqHDPdata | <i>retrieve and cache a 349-protein CITE-seq dataset as employed in scvi-tools tutorial</i> |
|---------------------|---------------------------------------------------------------------------------------------|

---

**Description**

retrieve and cache a 349-protein CITE-seq dataset as employed in scvi-tools tutorial

**Usage**

```
cacheCiteSeqHDPdata()
```

---

|                      |                                                                                                     |
|----------------------|-----------------------------------------------------------------------------------------------------|
| cacheCiteSeqHDPmodel | <i>grab scvi-tools muon-oriented VAE instance built on the PBMC datasets following the tutorial</i> |
|----------------------|-----------------------------------------------------------------------------------------------------|

---

**Description**

grab scvi-tools muon-oriented VAE instance built on the PBMC datasets following the tutorial

**Usage**

```
cacheCiteSeqHDPmodel()
```

**Value**

invisibly, the path to the .zip file holding the weights in pt format for the fitted VAE

**Note**

VAE construction followed tutorial at '<https://docs.scvi-tools.org/en/stable/tutorials/notebooks/totalVI.html>'.

We are using the scvi tutorial read early may 2025. The notebook uses "h5 format of single-cell multiomic data generated by Proteintech Genomics ... The data is from human resting PBMCs stained with the MultiPro® Human Discovery Panel (HDP) followed by processing using 10x Genomics Flex chemistry with Feature Barcoding Technology."

It may be advantageous to set 'options(timeout=3600)' or to allow an even greater time for internet downloads, if working at a relatively slow network connection.

**Examples**

```
zpath <- cacheCiteSeqHDPmodel()
td <- tempdir()
utils::unzip(zpath, exdir = td)
vaedir <- paste0(td, "/vae3_pt")
dir(vaedir)
```

---

|              |                                                                            |
|--------------|----------------------------------------------------------------------------|
| clusters.adt | <i>ADT-based cluster labels for 7472 cells in OSCA chapter 12 analysis</i> |
|--------------|----------------------------------------------------------------------------|

---

**Description**

ADT-based cluster labels for 7472 cells in OSCA chapter 12 analysis

**Usage**

```
clusters.adt
```

**Format**

```
factor
```

---

|              |                                                                             |
|--------------|-----------------------------------------------------------------------------|
| clusters.rna | <i>mRNA-based cluster labels for 7472 cells in OSCA chapter 12 analysis</i> |
|--------------|-----------------------------------------------------------------------------|

---

**Description**

mRNA-based cluster labels for 7472 cells in OSCA chapter 12 analysis

**Usage**

```
clusters.rna
```

**Format**

```
factor
```

---

|              |                                                                        |
|--------------|------------------------------------------------------------------------|
| exploreSubcl | <i>app to explore diversity in RNA-subclusters within ADT clusters</i> |
|--------------|------------------------------------------------------------------------|

---

**Description**

app to explore diversity in RNA-subclusters within ADT clusters

**Usage**

```
exploreSubcl(sce, inlist, adtcls)
```

**Arguments**

|        |                                                                                     |
|--------|-------------------------------------------------------------------------------------|
| sce    | a SingleCellExperiment with altExp with ADT quantification                          |
| inlist | list of SingleCellExperiments (SCEs) formed by <code>scrani::quickSubCluster</code> |
| adtcls | vector of ADT cluster assignments                                                   |

**Value**

shinyApp instance

**Note**

TSNE should already be available in `'altExp(sce)'`; follow OSCA book 12.5.2. If using example, set `'ask=FALSE'`.

**Examples**

```
sce <- getCh12Sce()
all.sce <- getCh12AllSce()
data(clusters.adt)
runApp(exploreSubcl(sce, all.sce, clusters.adt)) # trips up interactive pkgdown?)
```

---

|               |                                                                                           |
|---------------|-------------------------------------------------------------------------------------------|
| getCh12AllSce | <i>get list of cluster-specific SCE for 10k PBMC annotated as in OSCA book chapter 12</i> |
|---------------|-------------------------------------------------------------------------------------------|

---

**Description**

get list of cluster-specific SCE for 10k PBMC annotated as in OSCA book chapter 12

**Usage**

```
getCh12AllSce()
```

**Value**

SimpleList of SingleCellExperiment instances

**Note**

This is a list of SingleCellExperiment instances with data on a total of 7472 cells from a 10x CITE-seq experiment. An altExp component in each list element includes antibody-derived tag (ADT) counts on 17 proteins. The data are acquired and processed as described in ch 12 of the OSCA book, circa February 2023. List elements correspond to mRNA-based sub-clusters of ADT-based clusters.

**Examples**

```
ch12_allsce <- getCh12AllSce()
vapply(ch12_allsce, ncol, numeric(1))
```

---

getCh12Sce

---

*get SCE for 10k PBMC annotated as in OSCA book chapter 12*


---

**Description**

get SCE for 10k PBMC annotated as in OSCA book chapter 12

**Usage**

```
getCh12Sce(clear_cache = FALSE)
```

**Arguments**

clear\_cache      logical(1) will delete relevant entries in available cache before continuing, defaults to FALSE

**Value**

SingleCellExperiment instance

**Note**

This is a SingleCellExperiment instance with data on 7472 cells from a 10x CITE-seq experiment. An altExp component includes antibody-derived tag (ADT) counts on 17 proteins. The data are acquired and processed as described in ch 12 of the OSCA book, circa February 2023. A metadata element (se.averaged) includes the result of averaging protein abundance estimates within ADT-based clusters, as is done to give rise to Figure 12.8 of the OSCA book.

**Examples**

```
ch12sce <- getCh12Sce()
ch12sce
```



---

|                      |                                                                                        |
|----------------------|----------------------------------------------------------------------------------------|
| getCiteseq5k10kPbmcs | <i>helper to get the processed anndata for CITE-seq PBMCs from scvi-tools tutorial</i> |
|----------------------|----------------------------------------------------------------------------------------|

---

**Description**

helper to get the processed anndata for CITE-seq PBMCs from scvi-tools tutorial

**Usage**

```
getCiteseq5k10kPbmcs()
```

**Value**

python reference to anndata

**Note**

It may be advantageous to set 'options(timeout=3600)' or to allow an even greater time for internet downloads, if working at a relatively slow network connection.

**Examples**

```
getCiteseq5k10kPbmcs()
```

---

|                  |                                                                          |
|------------------|--------------------------------------------------------------------------|
| getCiteseqTutvae | <i>helper to get the tutorial VAE for PBMCs from scvi-tools tutorial</i> |
|------------------|--------------------------------------------------------------------------|

---

**Description**

helper to get the tutorial VAE for PBMCs from scvi-tools tutorial

**Usage**

```
getCiteseqTutvae(use_gpu = FALSE)
```

**Arguments**

|         |                                                         |
|---------|---------------------------------------------------------|
| use_gpu | logical(1), defaulting to FALSE, passed to TOTALVI.load |
|---------|---------------------------------------------------------|

**Value**

python reference to anndata

**Note**

March 2024 use\_gpu ignored

**Examples**

```
## Not run:
getCiteseqTutvae()

## End(Not run)
```

---

|                  |                                                                              |
|------------------|------------------------------------------------------------------------------|
| getPro5k10kAdata | <i>get an anndata reference to 5k10k protein after totalVI from tutorial</i> |
|------------------|------------------------------------------------------------------------------|

---

**Description**

get an anndata reference to 5k10k protein after totalVI from tutorial

**Usage**

```
getPro5k10kAdata()
```

**Value**

python reference to anndata

**Note**

It may be advantageous to set ‘options(timeout=3600)’ or to allow an even greater time for internet downloads, if working at a relatively slow network connection.

**Examples**

```
getPro5k10kAdata()
```

---

|            |                                                       |
|------------|-------------------------------------------------------|
| getSubclLM | <i>get lmFit for heterogeneity across subclusters</i> |
|------------|-------------------------------------------------------|

---

**Description**

get lmFit for heterogeneity across subclusters

**Usage**

```
getSubclLM(inlist, cname)
```

**Arguments**

|        |                                                                                   |
|--------|-----------------------------------------------------------------------------------|
| inlist | list of SingleCellExperiments (SCEs) formed by <code>scrn::quickSubCluster</code> |
| cname  | character(1) name of cluster SCE to assess                                        |

**Value**

limma::lmFit output

**Note**

It is assumed that 'logcounts' is an assay element, and that 'subcluster' is a colData element of each SCE in inlist

**Examples**

```
all.sce <- getCh12AllSce()
lm3 <- getSubclLM(all.sce, "3")
names(lm3)
```

---

getSubclusteringFeatures

*get lmFit F-stat based collection of n genes most varying in mean across subclusters*

---

**Description**

get lmFit F-stat based collection of n genes most varying in mean across subclusters

**Usage**

```
getSubclusteringFeatures(inlist, clname, n = 20)
```

**Arguments**

|        |                                                                                   |
|--------|-----------------------------------------------------------------------------------|
| inlist | list of SingleCellExperiments (SCEs) formed by <code>scrn::quickSubCluster</code> |
| clname | character(1) name of cluster SCE to assess                                        |
| n      | numeric(1) number to preserve                                                     |

**Value**

list with two elements, feat = rowData corresponding to variable genes, stats = topTable result

**Note**

Symbol will be taken from feat and placed in stats component if available

**Examples**

```
all.sce <- getCh12AllSce()
scl <- getSubclusteringFeatures(all.sce, "3", 10)
names(scl)
```

---

```
getTotalVI5k10kAdata
```

*get anndata reference to full totalVI processing of 5k10k data*

---

### Description

get anndata reference to full totalVI processing of 5k10k data

### Usage

```
getTotalVI5k10kAdata()
```

### Value

python reference to anndata

### Examples

```
full <- getTotalVI5k10kAdata()
full
```

---

```
getTotalVINormalized5k10k
```

*get matrices of normalized quantifications from full totalVI 5k10k from tutorial*

---

### Description

get matrices of normalized quantifications from full totalVI 5k10k from tutorial

### Usage

```
getTotalVINormalized5k10k()
```

### Value

list of matrices

### Examples

```
nm1ist <- getTotalVINormalized5k10k()
vapply(nm1ist, dim, numeric(2))
```

---

|         |                                  |
|---------|----------------------------------|
| MuDataR | <i>basic interface to MuData</i> |
|---------|----------------------------------|

---

**Description**

basic interface to MuData

**Usage**

```
MuDataR()
```

**Value**

basiliskRun result with import from reticulate, typically a Module

**Examples**

```
md <- MuDataR()
md
head(names(md))
```

---

|       |                                |
|-------|--------------------------------|
| muonR | <i>basic interface to muon</i> |
|-------|--------------------------------|

---

**Description**

basic interface to muon

**Usage**

```
muonR()
```

**Value**

basiliskRun result with import from reticulate, typically a Module

**Examples**

```
md <- muonR()
md
head(names(md))
```

---

|         |                                                                                         |
|---------|-----------------------------------------------------------------------------------------|
| pyHelp2 | <i>helper to get text from python help utility – may need handling through basilisk</i> |
|---------|-----------------------------------------------------------------------------------------|

---

**Description**

helper to get text from python help utility – may need handling through basilisk

**Usage**

```
pyHelp2(object)
```

**Arguments**

object            a reference to a python module typically with class 'python.builtin.module'

**Value**

character vector of lines from python help result

---

|              |                                                                                  |
|--------------|----------------------------------------------------------------------------------|
| scanpyHelper | <i>shiny app that helps access documentation on python-accessible components</i> |
|--------------|----------------------------------------------------------------------------------|

---

**Description**

shiny app that helps access documentation on python-accessible components

**Usage**

```
scanpyHelper()
```

**Value**

shinyApp instance

---

|         |                        |
|---------|------------------------|
| scanpyR | <i>basic interface</i> |
|---------|------------------------|

---

**Description**

basic interface

**Usage**

```
scanpyR()
```

**Value**

basiliskRun result with import from reticulate, typically a Module

**Examples**

```
sc <- scanpyR()
sc
sc$pp
```

---

|            |                                                                                  |
|------------|----------------------------------------------------------------------------------|
| scviHelper | <i>shiny app that helps access documentation on python-accessible components</i> |
|------------|----------------------------------------------------------------------------------|

---

**Description**

shiny app that helps access documentation on python-accessible components

**Usage**

```
scviHelper()
```

**Value**

shinyApp instance

---

`scviR`*basic interface*

---

**Description**

basic interface

**Usage**

```
scviR()
```

**Value**

basiliskRun result with import from reticulate, typically a Module

**Examples**

```
scvi <- scviR()
scvi
scvi$model
```



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