Package 'scKirby'

June 21, 2021

Type Package

Title Automated ingestion and conversion of various single-cell data formats.

Version 0.1.0

Description Automated ingestion and conversion of various single-cell data formats.

License MIT + file LICENSE

URL https://github.com/bschilder/scKirby

BugReports https://github.com/bschilder/scKirby/issues

Encoding UTF-8

LazyData true

Depends R (>= 3.6.0)

SystemRequirements Python (>= 3.7.0)

biocViews

Imports remotes,
   magrittr,
   BiocManager,
   dplyr,
   tibble,
   data.table,
   Matrix,
   SparseM,
   DescTools,
   reticulate,
   S4Vectors,
   Seurat,
   anndata,
   SummarizedExperiment,
   SingleCellExperiment,
   LoomExperiment,
   DelayedArray,
   BiocParallel,
   parallel,
   HDF5Array,
   rhdf5

Remotes github::mojaveazure/seurat-disk,
   github::mojaveazure/loomR,
   github::cellgeni/sceasy

VignetteBuilder knitr

RoxygenNote 7.1.1

R topics documented:

---

scKirby-package   *scKirby: Automated ingestion and conversion of various single-cell data formats.*

Description

Automated ingestion and conversion of various single-cell data formats.

Details

Automated ingestion and conversion of various single-cell data formats.

Author(s)

Brian M. Schilder

See Also

Useful links:

- https://github.com/bschilder/scKirby
- Report bugs at https://github.com/bschilder/scKirby/issues

---

anndata_to_sce   *Convert:* Anndata ==> SingleCellExperiment

Description

Convert: Anndata ==> SingleCellExperiment

Usage

```
anndata_to_sce(object, verbose = T)
```

Examples

```
library(scKirby)
data("example_anndata")
sce <- anndata_to_sce(example_anndata)
```

---

anndata_to_seurat   *Convert:* Anndata ==> Seurat

Description

Convert: Anndata ==> Seurat

Usage

```
anndata_to_seurat(object, save_dir = tempdir(), verbose = T)
```

Examples

```
library(scKirby)
seurat <- anndata_to_seurat(object=example_anndata())
```

EWCEctd_to_sce   *Convert:* EWCEctd ==> SingleCellExperiment

Description

Convert: EWCEctd ==> SingleCellExperiment

Usage

```
EWCEctd_to_sce(object, verbose = T)
```

Examples

```
library(scKirby)
data("example_ctd")
sce <- EWCEctd_to_sce(example_ctd)
```

EWCEctd_to_seurat   *Convert:* EWCEctd ==> Seurat

Description

Convert: EWCEctd ==> Seurat

Usage

```
EWCEctd_to_seurat(object, verbose = T)
```

Examples

```
library(scKirby)
data("example_ctd")
seurat <- EWCEctd_to_seurat(example_ctd)
```

EWCElist_to_sce   *Convert:* EWCElist ==> SingleCellExperiment

---

Description

Convert: EWCElist ==> SingleCellExperiment

Usage

```
EWCElist_to_sce(object, verbose = T)
```

Examples

```
library(scKirby)
data("example_EWCElist")
sce <- EWCElist_to_sce(example_EWCElist)
```

EWCElist_to_seurat   *Convert:* EWCElist ==> Seurat

Description

Convert: EWCElist ==> Seurat

Usage

```
EWCElist_to_seurat(object, verbose = T)
```

Examples

```
library(scKirby)
data("example_EWCElist")
seurat <- EWCElist_to_seurat(object=example_EWCElist)
```

example_anndata	*Example* anndata

Description

[anndata R package has a major bug currently.](#) Thus, add_filename must be kept False until this is fixed.

Usage

```
example_anndata(
  return_path = F,
  save_dir = tempdir(),
  backed = c("r", "r+"),
  overwrite = T,
  add_filename = F,
  verbose = T
)
```

Examples

```
## Not run:
#### Setup conda env ####
## Option 1: Point to where anndata is installed (or should be installed)
conda_dir <- dirname(dirname(reticulate::conda_list()[1,]$python))
reticulate::use_condaenv(condaenv = conda_dir)
reticulate::conda_install(conda = conda_dir, packages = "loompy", pip = T)
## Option 2: Just run anndata::install_anndata() and will install via miniconda
anndata::install_anndata(method = "conda", conda=conda_dir)

#### Usage ####
adata <- example_anndata()

## End(Not run)
```

example_ctd	*Example* CellTypeDataset

Description

Example CellTypeDataset

Usage

```
example_ctd
```

Format

An object of class list of length 2.

Examples

```
## Not run:
example_ctd <- ewceData::ctd()
### Remove dendrograms to reduce file size
example_ctd[[1]]$plotting <- NULL
example_ctd[[2]]$plotting <- NULL
usethis::use_data(example_ctd, overwrite = T)

## End(Not run)
```

---

example_EWCElist   *Example* EWCElist

Description

Example EWCElist

Usage

```
example_EWCElist
```

Format

An object of class list of length 2.

Examples

```
## Not run:
example_EWCElist <- ewceData::cortex_mrna()
usethis::use_data(example_EWCElist, overwrite = T)

## End(Not run)
```

---

example_loom   *Example* loom

Description

Example loom

Usage

```
example_loom(save_dir = tempdir())
```

---

example_sce   *Example* SingleCellExperiment

Description

A subsetted dataset containing 300 cells and 2026 genes from two batches of mouse ESC data.

Usage

```
example_sce
```

Format

A SingleCellExperiment object

Details

Copied from the R package **scMerge**.

Source

<https://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-2600/>

References

Kolodziejczyk et al.

Examples

```
## Not run:
if(!require(scMerge))BiocManager::install("scMerge")
data('example_sce', package = 'scMerge')
batch_names<-unique(example_sce$batch)
usethis::use_data(example_sce, overwrite = T)

## End(Not run)
```

---

example_seurat   *Example* Seurat

Description

Example Seurat

Usage

```
example_seurat
```

Format

An object of class Seurat with 230 rows and 80 columns.

Examples

```
## Not run:
library(Seurat)
data("pbmc_small")
example_seurat <- Seurat::UpdateSeuratObject(pbmc_small)
usethis::use_data(example_seurat, overwrite = T)

## End(Not run)
```

---

ingest_data   *Import and standardize scRNAseq data across different formats*

Description

Automatically infers data format of scRNAseq object, or a path to that object. It then uses the appropriate functions to import that data and convert it to a **SingleCellExperiment**, which is recognized by other **EWCE** functions.

Usage

```
ingest_data(
  obj,
  input_type = "guess",
  output_type = "SingleCellExperiment",
  custom_reader = NULL,
  save_dir = tempdir(),
  filename = "scKirby_output",
  save_output = T,
  overwrite = F,
  return_filepath = F,
  verbose = T,
  ...
)
```

Arguments

obj	Single-cell data object or path to saved single-cell data.
input_type	Format of obj. By default, the type will be inferred.
output_type	Format to convert obj to.
custom_reader	Custom function to read obj into R.
save_dir	Directory to save the converted obj.
filename	Name to save the converted obj.
save_output	Whether or not to save the converted obj.
overwrite	If a file of the same name exists, overwrite it.
return_filepath	
	If TRUE, a list with both the converted object and the saved file path will be returned (instead of just the converted object).
...	Additional arguments to be passed to scKirby::read_data().

Source

SeuratDisk anndata (R) anndata (python) loomR SingleCellExperiment DelayedArray workshop zellkonverter

Examples

```
## Not run:
library(SummarizedExperiment)
library(Seurat)
data("pbmc_small")
pbmc_small <- UpdateSeuratObject(pbmc_small)

#### Ingest expression matrix ####
sce <- ingest_data(obj=pbmc_small@assays$RNA@counts)

#### Ingest EWCElist ####
\dontrun{
### Example requires  data from \code{ewceData} package
cortex_mrna <- ewceData::cortex_mrna()
sce <- ingest_data(obj=cortex_mrna)
}

#### Ingest Seurat object in memory ####
sce <- ingest_data(obj=pbmc_small)

#### Ingest HDF5 SingleCellExperiment ####
sce <- HDF5Array::saveHDF5SummarizedExperiment(sce, dir = "~/Desktop/pbmc_small_h5", replace=T)
## Read in the sce object directly
sce <- ingest_data(obj=sce)
## Read it from disk
sce <- ingest_data(obj="~/Desktop/pbmc_small_h5")

#### Ingest AnnData ####
library(anndata)
## Can point to where anndata is installed (or should be installed)
## Can also just run anndata::install_anndata() and will install via miniconda
conda_dir <- dirname(dirname(reticulate::conda_list()[1,]$python))
reticulate::use_condaenv(condaenv = conda_dir)
reticulate::conda_install(conda = conda_dir, packages = "loompy", pip = T)
anndata::install_anndata(method = "conda", conda=conda_dir)

# Convert Seurat object to AnnData for example data
adata <- anndata::AnnData(X = t(GetAssay(pbmc_small)@counts), obs = pbmc_small@meta.data, var = GetAssay(pbmc_
## In memory
sce <- ingest_data(obj=adata)
## On disk
adata$write_h5ad(filename = "Desktop/pbmc_small.h5ad")
sce <- ingest_data(obj = "Desktop/pbmc_small.h5ad")


#### Ingest H5Seurat ####
library(SeuratDisk)
SaveH5Seurat(pbmc_small, filename = "~/Desktop/pbmc_small.h5Seurat", overwrite = T)
sce <- ingest_data(obj="~/Desktop/pbmc_small.h5Seurat")

#### Ingest loom (from loomR) ####
```

```
library(loomR)
loom <- loomR::create(data=adata, filename = "~/Desktop/pbmc_small.loom", overwrite = T)
## In memory
sce <- ingest_data(obj=loom)
## From disk
sce <- ingest_data(obj="~/Desktop/pbmc_small.loom")

## End(Not run)
```

---

loadRData   *loadRData*

Description

Load processed data using a function that assigns it to a specific variable (so you don't have to guess what the loaded variable name is).

Usage

```
loadRData(fileName)
```

---

loom_to_sce   *Convert:* loom ==> SingleCellExperiment

Description

Convert: loom ==> SingleCellExperiment

Usage

```
loom_to_sce(object, verbose = T, ...)
```

Examples

```
library(scKirby)
sce <- loom_to_sce(object=example_loom())
```

---

loom_to_seurat   *Convert:* loom ==> Seurat

Description

Convert: loom ==> Seurat

Usage

```
loom_to_seurat(object, verbose = T)
```

Examples

```
library(scKirby)
loom <- example_loom()
sce <- loom_to_seurat(loom)
```

---

matrix_to_sce   *Convert:* `matrix ==> SingleCellExperiment`

Description

Convert: `matrix ==> SingleCellExperiment`

Usage

```
matrix_to_sce(object, verbose = T)
```

Examples

```
library(scKirby)
data("example_seurat")
sce <- matrix_to_sce(example_seurat@assays$RNA@counts)
```

---

matrix_to_seurat   *Convert:* `matrix ==> Seurat`

Description

Convert: `matrix ==> Seurat`

Usage

```
matrix_to_seurat(object, verbose = T)
```

Examples

```
library(scKirby)
data("example_seurat")
sce <- matrix_to_seurat(object=example_seurat@assays$RNA@counts)
```

---

sce_cbind   *Combine several* `SingleCellExperiment` *objects from different batches/experiments*

Description

Combine several `SingleCellExperiment` objects from different batches/experiments. Extracted from the scMerge package.

Usage

```
sce_cbind(
  sce_list,
  method = "intersect",
  cut_off_batch = 0.01,
  cut_off_overall = 0.01,
  exprs = c("counts", "logcounts"),
  colData_names = NULL,
  batch_names = NULL
)
```

Arguments

sce_list	A list contains the `SingleCellExperiment` Object from each batch
method	A string indicates the method of combining the gene expression matrix, either union or intersect. Default to intersect. union only supports matrix class.
cut_off_batch	A numeric vector indicating the cut-off for the proportion of a gene is expressed within each batch
cut_off_overall	A numeric vector indicating the cut-off for the proportion of a gene is expressed overall data
exprs	A string vector indicating the expression matrices to be combined. The first assay named will be used to determine the proportion of zeros
colData_names	A string vector indicating the `colData` that are combined
batch_names	A string vector indicating the batch names for the output sce object

Value

A `SingleCellExperiment` object with the list of SCE objects combined.

Author(s)

Yingxin Lin

Examples

```
library(scKirby)
data("example_sce")
batch_names<-unique(example_sce$batch)
sce_list<-list(example_sce[,example_sce$batch=='batch2'],
               example_sce[,example_sce$batch=='batch3'])
sce_combine<-sce_cbind(sce_list,batch_names=batch_names)
```

---

sce_to_seurat *Convert:* SingleCellExperiment ==> Seurat

Description

Convert: SingleCellExperiment ==> Seurat

Usage

```
sce_to_seurat(object, verbose = T)
```

Examples

```
library(scKirby)
data("example_sce")
seurat <- sce_to_seurat(example_sce)
```

---

seurat_to_sce *Convert:* Seurat ==> SingleCellExperiment

Description

Convert: Seurat ==> SingleCellExperiment

Usage

```
seurat_to_sce(object, verbose = T)
```

Examples

```
library(scKirby)
data("example_seurat")
sce <- seurat_to_sce(example_seurat)
```

Index