

Package ‘chevreulShiny’

September 2, 2025

Type Package

Title Tools for managing SingleCellExperiment objects as projects

Version 1.1.2

Description Tools for managing SingleCellExperiment objects as projects.
Includes functions for analysis and visualization of single-cell data.
Also included is a shiny app for visualization of pre-processed scRNA data.
Supported by NIH grants R01CA137124 and R01EY026661 to David Cobrinik.

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URL <https://github.com/whtns/chevreulShiny>,
<https://whtns.github.io/chevreulShiny/>

Date 2024-03-24

BugReports <https://github.com/cobriniklab/chevreulShiny/issues>

Depends R (>= 4.5.0), SingleCellExperiment, shiny (>= 1.6.0),
shinydashboard, chevreulProcess, chevreulPlot

Imports alabaster.base, clustree, ComplexHeatmap, DataEditR (>= 0.0.9), DBI, dplyr, DT, EnhancedVolcano, fs, future, ggplot2, ggplotify, grDevices, methods, patchwork, plotly, purrr, rappdirs, readr, RSQLite, S4Vectors, scales, shinyFiles, shinyhelper, shinyjs, shinyWidgets, stats, stringr, tibble, tidy, tidyselect, utils, waiter, wigglyplotr

Suggests BiocStyle, knitr, RefManageR, rmarkdown, testthat (>= 3.0.0),
EnsDb.Mmusculus.v79, EnsDb.Hsapiens.v86

VignetteBuilder knitr

Encoding UTF-8

LazyData false

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.1

biocViews Coverage, RNASeq, Sequencing, Visualization, GeneExpression,
Transcription, SingleCell, Transcriptomics, Normalization,
Preprocessing, QualityControl, DimensionReduction, DataImport

Config/testthat/edition 3

git_url <https://git.bioconductor.org/packages/chevreulShiny>

git_branch devel

git_last_commit c77a2a9

git_last_commit_date 2025-06-04

Repository Bioconductor 3.22

Date/Publication 2025-09-02

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chevreulShiny-package *chevreulShiny: Tools for managing SingleCellExperiment objects as projects*

Description

Tools for managing SingleCellExperiment objects as projects. Includes functions for analysis and visualization of single-cell data. Also included is a shiny app for visualization of pre-processed scRNA data. Supported by NIH grants R01CA137124 and R01EY026661 to David Cobrinik.

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See Also

Useful links:

- <https://github.com/whtns/chevreulShiny>
- <https://whtns.github.io/chevreulShiny/>
- Report bugs at <https://github.com/cobriniklab/chevreulShiny/issues>

append_to_project_db *Update a database of chevreulShiny projects*

Description

Append projects to database

Usage

```
append_to_project_db(  
  new_project_path,  
  cache_location = "~/cache/chevreul",  
  sqlite_db = "single-cell-projects.db",  
  verbose = TRUE  
)
```

Arguments

new_project_path	new project path
cache_location	Path to cache "~/cache/chevreul"
sqlite_db	sqlite db
verbose	print messages

Value

a sqlite database with SingleCellExperiment objects

<code>cc.genes.cyclone</code>	<i>Cyclone cell cycle pairs by symbol</i>
-------------------------------	---

Description

cell cycle genes with paired expression represented by HGNC symbol

Usage

```
cc.genes.cyclone
```

Format

a list of dataframes with G1, G2, and S gene expression

G1 G1 gene symbols

G2 G2 gene symbols

S S gene symbols ...

Source

cyclone

<code>chevreulApp</code>	<i>Create a shiny app for a project on disk</i>
--------------------------	---

Description

Create a shiny app for a project on disk

Usage

```
chevreulApp(
  preset_project,
  appTitle = "chevreul",
  organism_type = "human",
  futureMb = 13000,
  db_name = "single-cell-projects.db"
)
```

Arguments

<code>preset_project</code>	A preloaded project to start the app with
<code>appTitle</code>	A title of the App
<code>organism_type</code>	human or mouse
<code>futureMb</code>	amount of Mb allocated to future package
<code>db_name</code>	sqlite database with list of saved SingleCellExperiment objects

Value

a shiny app

create_project_db	Create a database of chevreurShiny projects
-------------------	---

Description

Create a database containing chevreurShiny projects

Usage

```
create_project_db(  
  cache_location = "~/cache/chevreul",  
  sqlite_db = "single-cell-projects.db",  
  verbose = TRUE  
)
```

Arguments

cache_location	Path to cache "~/cache/chevreul"
sqlite_db	Database to be created
verbose	print messages

Value

a sqlite database with SingleCellExperiment objects

create_proj_matrix	Create a Table of single Cell Projects
--------------------	--

Description

Uses a list of projects to create a matrix of single cell projects

Usage

```
create_proj_matrix(proj_list)
```

Arguments

proj_list	List of projects
-----------	------------------

Value

a tibble of single cell projects

ensembl_version	<i>Ensembl version used for build</i>
-----------------	---------------------------------------

Description

Ensembl version used for build

Usage

ensembl_version

Format

An object of class character of length 1.

Source

<http://www.ensembl.org/>

Examples

```
# ensembl_version
```

get_transcripts_from_sce	<i>Get Transcripts in object</i>
--------------------------	----------------------------------

Description

Get transcript ids in objects for one or more gene of interest

Usage

```
get_transcripts_from_sce(object, gene)
```

Arguments

object	A SingleCellExperiment object
gene	Gene of interest

Value

transcripts constituting a gene of interest in a SingleCellExperiment object

grch38	<i>Human annotation data</i>
--------	------------------------------

Description

Human (*Homo sapiens*) annotations based on genome assembly GRCH38 from Ensembl.

Usage

```
grch38
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 76062 rows and 9 columns.

Details

Variables:

- `ensgene`
- `entrez`
- `symbol`
- `chr`
- `start`
- `end`
- `strand`
- `biotype`
- `description`

Source

http://ensembl.org/homo_sapiens

Examples

```
data("grch38")  
head(grch38)
```

grch38_tx2gene	<i>Human transcripts to genes</i>
----------------	-----------------------------------

Description

Lookup table for converting Human (*Homo sapiens*) Ensembl transcript IDs to gene IDs based on genome assembly GRCH38 from Ensembl.

Usage

```
grch38_tx2gene
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 277081 rows and 2 columns.

Details

Variables:

- `enstxp`
- `ensgene`

Source

http://ensembl.org/homo_sapiens

Examples

```
data(grch38_tx2gene)
head(grch38_tx2gene)
```

human_to_mouse_homologs	<i>Gene Homologs Between Human and Mouse</i>
-------------------------	--

Description

Homologs drawn from Biomart

Usage

```
human_to_mouse_homologs
```

Format

A data frame with 23188 rows and 2 columns

HGNC.symbol human gene symbols

MGI.symbol mouse gene symbols ...

Source

bioMart

list_plot_types	<i>Collate list of variables to be plotted</i>
-----------------	--

Description

Collate list of variables to be plotted

Usage

```
list_plot_types(object)
```

Arguments

object	a SingleCellExperiment object
--------	-------------------------------

Value

plot_types a list of category_vars or continuous_vars

Examples

```
data(small_example_dataset)
list_plot_types(small_example_dataset)
```

load_alabaster_from_proj	<i>Load SingleCellExperiment Files from a single project path</i>
--------------------------	---

Description

Load SingleCellExperiment Files from a single project path

Usage

```
load_alabaster_from_proj(proj_dir, ...)
```

Arguments

proj_dir	project directory
...	extra args passed to load_alabaster_path

Value

a SingleCellExperiment object

load_alabaster_path	<i>Read in Gene and Transcript SingleCellExperiment Objects</i>
---------------------	---

Description

Read in Gene and Transcript SingleCellExperiment Objects

Usage

```
load_alabaster_path(proj_dir = getwd(), prefix = "unfiltered")
```

Arguments

proj_dir	path to project directory
prefix	default "unfiltered"

Value

a SingleCellExperiment object

load_bigwigs	<i>Load Bigwigs</i>
--------------	---------------------

Description

Load a tibble of bigwig file paths by cell id

Usage

```
load_bigwigs(object, bigwig_db = "~/cache/chevreul/bw-files.db")
```

Arguments

object	A object
bigwig_db	Sqlite database of bigwig files

Value

a vector of bigwigs file paths

make_bigwig_db	<i>Make Bigwig Database</i>
----------------	-----------------------------

Description

Make Bigwig Database

Usage

```
make_bigwig_db(
  new_project = NULL,
  cache_location = "~/cache/chevreul/",
  sqlite_db = "bw-files.db"
)
```

Arguments

new_project	Project directory
cache_location	Path to cache "~/cache/chevreul"
sqlite_db	sqlite db containing bw files

Value

a sqlite database of bigwig files for cells in a SingleCellExperiment object

make_chevreul_clean_names	<i>Clean Vector of chevreulShiny Names</i>
---------------------------	--

Description

Cleans names of objects provided in a vector form

Usage

```
make_chevreul_clean_names(myvec)
```

Arguments

myvec	A vector of object names
-------	--------------------------

Value

a clean vector of object names

Examples

```
data(small_example_dataset)
make_chevreul_clean_names(colnames(
  get_colData(small_example_dataset)))
```

metadata_from_batch	<i>Retrieve Metadata from Batch</i>
---------------------	-------------------------------------

Description

Retrieve Metadata from Batch

Usage

```
metadata_from_batch(
  batch,
  projects_dir = "/dataVolume/storage/single_cell_projects",
  db_path = "single-cell-projects.db"
)
```

Arguments

batch	batch
projects_dir	path to project dir
db_path	path to .db file

Value

a tibble with cell level metadata from a SingleCellExperiment object

minimalChevreulApp	<i>Create a minimal chevreulShiny app using SingleCellExperiment input</i>
--------------------	--

Description

Create a minimal chevreulShiny app using SingleCellExperiment input

Usage

```
minimalChevreulApp(
  single_cell_sce = NULL,
  appTitle = NULL,
  organism_type = "human",
  futureMb = 13000,
  db_name = "single-cell-projects.db"
)
```

Arguments

single_cell_sce	a singlecell object
appTitle	a title for the app
organism_type	human or mouse
futureMb	the megabytes available for the future package
db_name	a database of bigwig files

Value

a minimal chevreulShiny app

Examples

```
if (interactive() ) {
  data("tiny_sce")
  minimalChevreulApp(tiny_sce)
}
```

plotly_settings	<i>Plotly settings</i>
-----------------	------------------------

Description

Change settings of a plotly plot

Usage

```
plotly_settings(plotly_plot, width = 600, height = 700)
```

Arguments

plotly_plot	A plotly plot
width	Default set to '600'
height	Default set to '700'

Value

a plotly plot with settings changed

plot_gene_coverage_by_var	<i>Plot BigWig Coverage for Genes of Interest by a Given Variable</i>
---------------------------	---

Description

Plot BigWig coverage for genes of interest colored by a given variable

Usage

```
plot_gene_coverage_by_var(
  genes_of_interest = "NRL",
  cell_metadata,
  bigwig_tbl,
  group_by = "batch",
  values_of_interest = NULL,
  organism = c("human", "mouse"),
  edb = NULL,
  heights = c(3, 1),
  scale_y = "log10",
  reverse_x = FALSE,
  start = NULL,
  end = NULL,
  summarize_transcripts = FALSE,
  ...
)
```

Arguments

<code>genes_of_interest</code>	Gene of interest
<code>cell_metadata</code>	a dataframe with cell metadata from object
<code>bigwig_tbl</code>	a tibble with colnames "name", "bigWig", and "sample_id" matching the file-name, absolute path, and sample name of each cell in the <code>cell_metadata</code>
<code>group_by</code>	Variable to color by
<code>values_of_interest</code>	values of interest
<code>organism</code>	human (default) or mouse
<code>edb</code>	ensembl db object
<code>heights</code>	The heights of each row in the grid of plot
<code>scale_y</code>	whether to scale coverage
<code>reverse_x</code>	whether to reverse x axis
<code>start</code>	start coordinates
<code>end</code>	end coordinates
<code>summarize_transcripts</code>	whether to summarize transcript counts
<code>...</code>	extra arguments passed to <code>plotCoverageFromEnsemblDb</code>

Value

a ggplot with coverage faceted by `group_by`

read_project_db	<i>Read a database of chevreulShiny projects</i>
-----------------	--

Description

Reads database of chevreulShiny projects to a data frame

Usage

```
read_project_db(  
  cache_location = "~/cache/chevreul",  
  sqlite_db = "single-cell-projects.db",  
  verbose = TRUE  
)
```

Arguments

cache_location	Path to cache "~/cache/chevreul"
sqlite_db	sqlite db
verbose	print messages

Value

a tibble with SingleCellExperiment objects

save_sce	<i>Save object to /output/sce/_sce.rds</i>
----------	--

Description

Save object to /output/sce/_sce.rds

Usage

```
save_sce(object, prefix = "unfiltered", proj_dir = getwd())
```

Arguments

object	a SingleCellExperiment object
prefix	a prefix for saving
proj_dir	path to a project directory

Value

a path to an rds file containing a SingleCellExperiment object

small_example_dataset	<i>Small example SingleCellExperiment</i>
-----------------------	---

Description

created with `scuttle::mockSCE`

Usage

```
small_example_dataset
```

Format

An SCE with 200 cells and 1000 genes

Source

`scuttle::mockSCE`

subset_by_colData	<i>Subset by new colData</i>
-------------------	------------------------------

Description

Subset the object using new `colData`

Usage

```
subset_by_colData(colData_path, object)
```

Arguments

<code>colData_path</code>	Path to new <code>colData</code>
<code>object</code>	A object

Value

a `SingleCellExperiment` object

tiny_sce*Tiny example SingleCellExperiment*

Description

subset to only NRL from `chevreuldata::human_gene_transcript_sce()`

Usage

```
tiny_sce
```

Format

An SCE with only expression of NRL gene and NRL transcripts

Source

```
chevreuldata::human_gene_transcript_sce()
```

unite_metadata*Unite metadata*

Description

Unite metadata

Usage

```
unite_metadata(object, group_bys)
```

Arguments

<code>object</code>	A <code>SingleCellExperiment</code> object
<code>group_bys</code>	A feature or variable to combine

Value

a `SingleCellExperiment` object with Idents formed from concatenation of `group_bys`

Examples

```
data(small_example_dataset)
unite_metadata(small_example_dataset, "Mutation_Status")
```

update_project_db	<i>Update a database of chevreulShiny projects</i>
-------------------	--

Description

Add new/update existing projects to the database by recursing fully

Usage

```
update_project_db(  
  projects_dir = NULL,  
  cache_location = "~/cache/chevreul",  
  sqlite_db = "single-cell-projects.db",  
  verbose = TRUE  
)
```

Arguments

projects_dir	The project directory to be updated
cache_location	Path to cache "~/cache/chevreul"
sqlite_db	sqlite db
verbose	print messages

Value

a sqlite database with SingleCellExperiment objects

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