

# Package ‘chevreulShiny’

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**Type** Package

**Title** Tools for managing SingleCellExperiment objects as projects

**Version** 0.99.29

**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, wiggleplotr

**Suggests** BiocStyle, knitr, RefManageR, rmarkdown, testthat (>= 3.0.0),  
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Bhavana Bhat [aut]**Maintainer** Kevin Stachelek <[kevin.stachelek@gmail.com](mailto:kevin.stachelek@gmail.com)>**Contents**

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

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## 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.

## Author(s)

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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

---

cc.genes.cyclone      *Cyclone cell cycle pairs by symbol*

---

**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

---

chevreulApp	<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**

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

**Value**

a shiny app

---

create_project_db	<i>Create a database of chevreulShiny projects</i>
-------------------	--

---

**Description**

Create a database containing chevreulShiny 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 *Ensembl version used for build*

---

**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  
    Get Transcripts in object
```

---

### 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    Human annotation data
```

---

### 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](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](http://ensembl.org/homo_sapiens)

**Examples**

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

---

human\_to\_mouse\_homologs

*Gene Homologs Between Human and Mouse*

---

**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

*Collate list of variables to be plotted*

---

**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
```

*Load SingleCellExperiment Files from a single project path*

---

**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 Read in Gene and Transcript SingleCellExperiment Objects
```

---

**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

*Clean Vector of chevreulShiny Names*

---

### **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

*Retrieve Metadata from Batch*

---

### **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      *Plotly settings*

---

**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  
*Plot BigWig Coverage for Genes of Interest by a Given Variable*

---

**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**

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

**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**

colData_path	Path to new colData
object	A object

**Value**

a SingleCellExperiment object

---

tiny_sce	<i>Tiny example SingleCellExperiment</i>
----------	--

---

**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	<i>Unite metadata</i>
----------------	-----------------------

---

**Description**

Unite metadata

**Usage**

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

**Arguments**

object	A SingleCellExperiment object
group_bys	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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