

# Package ‘chevreulShiny’

April 30, 2025

**Type** Package

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

**Version** 1.0.0

**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/>

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

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## Contents

|                                     |    |
|-------------------------------------|----|
| chevreulShiny-package . . . . .     | 3  |
| append_to_project_db . . . . .      | 3  |
| cc.genes.cyclone . . . . .          | 4  |
| chevreulApp . . . . .               | 5  |
| create_project_db . . . . .         | 5  |
| create_proj_matrix . . . . .        | 6  |
| ensembl_version . . . . .           | 6  |
| get_transcripts_from_sce . . . . .  | 7  |
| grch38 . . . . .                    | 7  |
| grch38_tx2gene . . . . .            | 8  |
| human_to_mouse_homologs . . . . .   | 9  |
| list_plot_types . . . . .           | 9  |
| load_alabaster_from_proj . . . . .  | 10 |
| load_alabaster_path . . . . .       | 10 |
| load_bigwigs . . . . .              | 11 |
| make_bigwig_db . . . . .            | 11 |
| make_chevreul_clean_names . . . . . | 12 |
| metadata_from_batch . . . . .       | 12 |
| minimalChevreulApp . . . . .        | 13 |
| plotly_settings . . . . .           | 14 |
| plot_gene_coverage_by_var . . . . . | 14 |
| read_project_db . . . . .           | 15 |
| save_sce . . . . .                  | 16 |
| small_example_dataset . . . . .     | 16 |
| subset_by_colData . . . . .         | 17 |
| tiny_sce . . . . .                  | 17 |
| unite_metadata . . . . .            | 18 |
| update_project_db . . . . .         | 18 |

**Index**

**20**

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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 | <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

---

|             |                                          |
|-------------|------------------------------------------|
| chevreulApp | Create a shiny app for a project on disk |
|-------------|------------------------------------------|

---

**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 | Create a database of chevreulShiny projects |
|-------------------|---------------------------------------------|

---

**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 | <i>Create a Table of single Cell Projects</i> |
|--------------------|-----------------------------------------------|

---

**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
```

*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)
```

---

|                             |                                   |
|-----------------------------|-----------------------------------|
| <code>grch38_tx2gene</code> | <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 | Create a minimal chevreulShiny app using SingleCellExperiment input |
|--------------------|---------------------------------------------------------------------|

---

**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**

|                       |                                                                                                                                                   |
|-----------------------|---------------------------------------------------------------------------------------------------------------------------------------------------|
| 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 db 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 plotCoverageFromEnsemblDb                                                                                               |

**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 | Save object to /output/sce/_sce.rds |
|----------|-------------------------------------|

---

**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 | Small example SingleCellExperiment |
|-----------------------|------------------------------------|

---

**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**

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

**Value**

a sqlite database with SingleCellExperiment objects

# Index

- \* **datasets**
  - cc.genes.cyclone, [4](#)
  - ensembl\_version, [6](#)
  - grch38, [7](#)
  - grch38\_tx2gene, [8](#)
  - human\_to\_mouse\_homologs, [9](#)
  - small\_example\_dataset, [16](#)
  - tiny\_sce, [17](#)
- \* **internal**
  - chevreulShiny-package, [3](#)
- append\_to\_project\_db, [3](#)
- cc.genes.cyclone, [4](#)
- chevreulApp, [5](#)
- chevreulShiny (chevreulShiny-package), [3](#)
- chevreulShiny-package, [3](#)
- create\_proj\_matrix, [6](#)
- create\_project\_db, [5](#)
- ensembl\_version, [6](#)
- get\_transcripts\_from\_sce, [7](#)
- grch38, [7](#)
- grch38\_tx2gene, [8](#)
- human\_to\_mouse\_homologs, [9](#)
- list\_plot\_types, [9](#)
- load\_alabaster\_from\_proj, [10](#)
- load\_alabaster\_path, [10](#)
- load\_bigwigs, [11](#)
- make\_bigwig\_db, [11](#)
- make\_chevreul\_clean\_names, [12](#)
- metadata\_from\_batch, [12](#)
- minimalChevreulApp, [13](#)
- plot\_gene\_coverage\_by\_var, [14](#)
- plotly\_settings, [14](#)
- read\_project\_db, [15](#)
- save\_sce, [16](#)
- small\_example\_dataset, [16](#)
- subset\_by\_colData, [17](#)
- tiny\_sce, [17](#)
- unite\_metadata, [18](#)
- update\_project\_db, [18](#)