

Package ‘chevreulShiny’

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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/>

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

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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	<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	<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	<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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