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/`

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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, tidyr, tidyselect, utils, waiter, wiggleplotr

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Contents

`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

`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` *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` *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`

Examples

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

`grch38_tx2gene` *Human transcripts to genes*

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` *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` *Load Bigwigs*

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` *Make Bigwig Database*

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` *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 filename, 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`	ensembldb 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` *Read a database of chevreulShiny projects*

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` *Subset by new colData*

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` *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 transripts

Source

chevreuldata::human_gene_transcript_sce()

`unite_metadata` *Unite metadata*

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` *Update a database of chevreulShiny projects*

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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