Package 'chevreulShiny'

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Title 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.

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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

---

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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