

# Package ‘chevreulProcess’

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**Type** Package

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**Version** 1.5.0

**Description** Tools for analyzing SingleCellExperiment objects as projects. for input into the chevreulShiny app downstream.  
Includes functions for analysis of single cell RNA sequencing data.  
Supported by NIH grants R01CA137124 and R01EY026661 to David Cobrinik.

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**URL** <https://github.com/whtns/chevreulProcess>,  
<https://whtns.github.io/chevreulProcess/>

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

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

---

## Description

Tools analyzing SingleCellExperiment objects as projects. for input into the Chevreul app downstream. Includes functions for analysis of single cell RNA sequencing 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/chevreulProcess>
- <https://whtns.github.io/chevreulProcess/>
- Report bugs at <https://github.com/cobriniklab/chevreulProcess/issues>

---

add_percent_mito	<i>Annotate percent mitochondrial reads per cell</i>
------------------	--

---

**Description**

Add a Percentage of Mitochondrial Read Count Categorical Variable to the Object (based on nCount\_RNA)

**Usage**

```
add_percent_mito(object, experiment = "gene")
```

**Arguments**

object	A object
experiment	gene

**Value**

a single cell object with cell metadata column containing mitochondrial percentage

---

annotate_cell_cycle	<i>Annotate Cell Cycle</i>
---------------------	----------------------------

---

**Description**

Annotate Cell Cycle for Gene and Transcript SingleCellExperiment Objects

**Usage**

```
annotate_cell_cycle(object)
```

**Arguments**

object	A SingleCellExperiment object
--------	-------------------------------

**Value**

a SingleCellExperiment object

---

append\_to\_project\_db    *Update a database of chevreul 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

---

build\_bigwig\_db        *Create a database of bigwigfiles*

---

**Description**

Create a sqlite database of bigwig files matching cell ids in objects

**Usage**

```
build_bigwig_db(bam_files, bigwig_db = "~/cache/chevreul/bw-files.db")
```

**Arguments**

bam_files	vector of paths to bam files
bigwig_db	bigwig database

**Value**

a path to a bigwig file sqlite database

---

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

---

clustering\_workflow      *Clustering Workflow*

---

### Description

Cluster and Reduce Dimensions of a object

### Usage

```
clustering_workflow(
  object,
  excluded_cells,
  resolution = seq(0.2, 1, by = 0.2),
  organism = "human",
  experiment_name = "default_experiment",
  ...
)
```

### Arguments

object	a SingleCellExperiment object
excluded_cells	named list of cells to exclude
resolution	resolution(s) to use for clustering cells
organism	Organism
experiment_name	name of the experiment
...	extra args passed to sce_process

**Value**

a clustered SingleCellExperiment object

---

convert\_human\_sce\_to\_mouse

*Convert SingleCellExperiment Objects from Human to Mouse*

---

**Description**

Convert SingleCellExperiment Objects from Human to Mouse

**Usage**

convert\_human\_sce\_to\_mouse(object, ...)

**Arguments**

object            Human SingleCellExperiment object  
...                to be passed to convert\_symbols\_by\_species

**Value**

a SingleCellExperiment object

---

convert\_symbols\_by\_species

*Convert gene symbols between mouse and human*

---

**Description**

Convert gene symbols between mouse and human

**Usage**

convert\_symbols\_by\_species(src\_genes, src\_species)

**Arguments**

src\_genes        Source gene symbol to be converted  
src\_species      Source species

**Value**

a SingleCellExperiment object

---

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

---

**Description**

Create a database containing chevreul 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

---

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
```

---

find\_all\_markers      *Find All Markers*

---

**Description**

Find all markers at a range of resolutions

**Usage**

```
find_all_markers(object, group_by = NULL, experiment = "gene", ...)
```

**Arguments**

object	An object.
group_by	A metadata variable to group by.
experiment	Assay to use, Default "gene".
...	extra args passed to stash_marker_features

**Value**

a SingleCellExperiment object containing marker genes

**Examples**

```
data("small_example_dataset")
find_all_markers(small_example_dataset, "gene_snn_res.1")
```

---

genes\_to\_transcripts      *Gene Symbols to Ensembl Transcript Ids*

---

**Description**

convert hgnc gene symbols to ensembl transcript ids

**Usage**

```
genes_to_transcripts(symbols)
```

**Arguments**

symbols	character vector of gene symbols
---------	----------------------------------

**Value**

a vector of transcripts

**Examples**

```
genes_to_transcripts("NRL")
```

---

get_colData	<i>Get cell metadata from a given object</i>
-------------	--

---

**Description**

Get cell metadata

**Usage**

```
get_colData(object)
```

**Arguments**

object            a SingleCellExperiment object

**Value**

dataframe containing object metadata

**Examples**

```
data(small_example_dataset)
get_colData(small_example_dataset)
```

---

get_features	<i>Get feature names</i>
--------------	--------------------------

---

**Description**

Get feature names

**Usage**

```
get_features(object, experiment = "gene")
```

**Arguments**

object            a SingleCellExperiment object  
experiment        "gene" or "transcript"

**Value**

variable features from a SingleCellExperiment object

**Examples**

```
data(small_example_dataset)
get_features(small_example_dataset)
```

---

`get_feature_types`      *Get Feature Types*

---

**Description**

Get Feature Types

**Usage**

```
get_feature_types(object)
```

**Arguments**

`object`              a SingleCellExperiment object

**Value**

vector of feature types in an object

**Examples**

```
data(small_example_dataset)
get_feature_types(small_example_dataset)
```

---

`get_sce_metadata`      *Get object metadata*

---

**Description**

Get object metadata

**Usage**

```
get_sce_metadata(object)
```

**Arguments**

`object`              a SingleCellExperiment object

**Value**

variable features from a SingleCellExperiment object

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

---

get\_variable\_features *Get variable features*

---

### **Description**

Get variable features

### **Usage**

```
get_variable_features(object, experiment = "gene")
```

### **Arguments**

object	a SingleCellExperiment object
experiment	"gene" or "transcript"

### **Value**

variable features from a SingleCellExperiment object

### **Examples**

```
data(small_example_dataset)  
get_variable_features(small_example_dataset)
```

---

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](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](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

---

integrate

*Batch Correct Multiple Single Cell Objects*

---

**Description**

Batch Correct Multiple Single Cell Objects

**Usage**

```
integrate(sce_list, organism = "human", ...)
```

**Arguments**

sce_list	List of two or more SingleCellExperiment objects
organism	human or mouse
...	extra args passed to sce_reduce_dimensions

**Value**

an integrated SingleCellExperiment object

---

integration\_workflow *Integration Workflow*

---

**Description**

Integrate multiple objects and save to file

**Usage**

```
integration_workflow(
  batches,
  excluded_cells = NULL,
  resolution = seq(0.2, 1, by = 0.2),
  experiment_name = "default_experiment",
  organism = "human",
  ...
)
```

**Arguments**

batches	objects for all batches provided as a list. If named, the resulting integrated object will be identified with corresponding values in 'batch' metadata
excluded_cells	named list of cells to exclude
resolution	value(s) to control the clustering resolution via <code>scanr::findMarkers</code>
experiment_name	arbitrary name to identify experiment
organism	either "human" or "mouse"
...	extra args passed to <code>sce_integrate</code>

**Value**

an integrated `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

---

load_sce_from_proj	<i>Load SingleCellExperiment Files from a single project path</i>
--------------------	---

---

**Description**

Load `SingleCellExperiment` Files from a single project path

**Usage**

```
load_sce_from_proj(proj_dir, ...)
```

**Arguments**

proj_dir	project directory
...	extra args passed to <code>load_sce_path</code>

**Value**

a SingleCellExperiment object

---

load_sce_path	<i>Read in Gene and Transcript SingleCellExperiment Objects</i>
---------------	---

---

**Description**

Read in Gene and Transcript SingleCellExperiment Objects

**Usage**

```
load_sce_path(proj_dir = getwd(), prefix = "unfiltered")
```

**Arguments**

proj_dir	path to project directory
prefix	default "unfiltered"

**Value**

a SingleCellExperiment object

---

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

---

merge_small_sces	<i>Merge Small SingleCellExperiment Objects</i>
------------------	---

---

**Description**

Merge Small SingleCellExperiment Objects

**Usage**

```
merge_small_sces(..., k.filter = 50)
```

**Arguments**

...	two or more singlecell objects
k.filter	minimum cell number for integration

**Value**

a SingleCellExperiment object

---

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

---

propagate\_spreadsheet\_changes  
*Propagate Metadata Changes*

---

**Description**

Propagate Metadata Changes

**Usage**

```
propagate_spreadsheet_changes(meta, object)
```

**Arguments**

meta	updated metadata
object	a SingleCellExperiment object

**Value**

a SingleCellExperiment object

**Examples**

```
data(small_example_dataset)
new_meta <- data.frame(row.names = colnames(small_example_dataset))
new_meta$example <- "example"

propagate_spreadsheet_changes(new_meta, small_example_dataset)
```

---

query\_experiment      *Query Experiment*

---

**Description**

Query Experiment

**Usage**

```
query_experiment(object, experiment)
```

**Arguments**

object	a SingleCellExperiment object
experiment	an experiment name

**Value**

logical scalar indicating if experiment is present in object

**Examples**

```
data(small_example_dataset)
query_experiment(small_example_dataset, "gene")
```

---

read_project_db	<i>Read a database of chevreul projects</i>
-----------------	---

---

**Description**

Reads database of chevreul 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

---

record_experiment_data	<i>Record Experiment Metadata</i>
------------------------	-----------------------------------

---

**Description**

Records miscellaneous data

**Usage**

```
record_experiment_data(
  object,
  experiment_name = "default_experiment",
  organism = "human"
)
```

**Arguments**

object	A object
experiment_name	name of the experiment
organism	human or mouse

**Value**

a SingleCellExperiment object

**Examples**

```
data(small_example_dataset)
record_experiment_data(small_example_dataset)
```

---

regress_cell_cycle	<i>Regress SingleCellExperiment Object by Given Set of Genes</i>
--------------------	--

---

**Description**

Regress SingleCellExperiment Object by Given Set of Genes

**Usage**

```
regress_cell_cycle(object)
```

**Arguments**

object	A object
--------	----------

**Value**

a SingleCellExperiment object with features regressed

---

reintegrate_sce	<i>Reintegrate (filtered) SingleCellExperiment objects</i>
-----------------	--

---

**Description**

This function takes a SCE object and performs the below steps

1. split by batch
2. integrate
3. run integration pipeline and save

**Usage**

```
reintegrate_sce(object, suffix = "", reduction = "PCA", ...)
```

**Arguments**

object	A SingleCellExperiment objects
suffix	to be appended to file saved in output dir
reduction	to use default is pca
...	extra args passed to sce_integrate

**Value**

a SingleCellExperiment object

---

retrieve\_experiment     *Retrieve Assay*

---

**Description**

Retrieve Assay

**Usage**

```
retrieve_experiment(object, experiment)
```

**Arguments**

object	a SingleCellExperiment object
experiment	an experiment name

**Value**

Main or alt experiment in a SingleCellExperiment object

---

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

---

sce_calcn	<i>Calculate Read Count Metrics for a object</i>
-----------	--

---

**Description**

Recalculate counts/features per cell for a object

**Usage**

```
sce_calcn(object)
```

**Arguments**

object	A SingleCellExperiment object
--------	-------------------------------

**Value**

a SingleCellExperiment object with nfeatures and ngenes stored in metadata

**Examples**

```
data(small_example_dataset)
sce_calcn(small_example_dataset)
```

---

sce_cluster	<i>Run Louvain Clustering at Multiple Resolutions</i>
-------------	---

---

**Description**

Run Louvain Clustering at Multiple Resolutions

**Usage**

```
sce_cluster(
  object = object,
  resolution = 0.6,
  custom_clust = NULL,
  reduction = "PCA",
  algorithm = 1,
  ...
)
```

**Arguments**

object	A SingleCellExperiment objects
resolution	Clustering resolution
custom_clust	custom cluster
reduction	Set dimensional reduction object
algorithm	1
...	extra args passed to single cell packages

**Value**

a SingleCellExperiment object with louvain clusters

**Examples**

```
data(small_example_dataset)
sce_cluster(small_example_dataset)
```

---

sce\_de

*Run Differential Expression*

---

**Description**

Run Differential Expression

**Usage**

```
sce_de(
  object,
  cluster1,
  cluster2,
  resolution = 0.2,
  diffex_scheme = "louvain",
  featureType = "gene",
  tests = c("t", "wilcox", "bimod")
)
```

**Arguments**

object	a SingleCellExperiment object
cluster1	cluster 1
cluster2	cluster 2
resolution	resolution
diffex_scheme	scheme for differential expression
featureType	gene or transcript
tests	t, wilcox, or bimod

**Value**

a dataframe with differential expression information

**Examples**

```
data("tiny_sce")
sce_de(tiny_sce,
  colnames(tiny_sce)[1:100],
  colnames(tiny_sce)[101:200],
  diffex_scheme = "custom")
```

---

sce\_integrate                      *Run SingleCellExperiment Integration*

---

## Description

Run batch correction, followed by:

1. stashing of batches in metadata 'batch'
2. clustering with resolution 0.2 to 2.0 in increments of 0.2
3. saving to <proj\_dir>/output/sce/sce.rds

## Usage

```
sce_integrate(
  sce_list,
  resolution = seq(0.2, 1, by = 0.2),
  suffix = "",
  organism = "human",
  batch_correct = TRUE,
  annotate_cell_cycle = FALSE,
  annotate_percent_mito = FALSE,
  reduction = "corrected",
  ...
)
```

## Arguments

sce_list	List of objects to be integrated
resolution	Range of resolution
suffix	a suffix to be appended to a file save in output dir
organism	Default "human"
batch_correct	whether to integrate by batch correction
annotate_cell_cycle	whether to score cell cycle phases
annotate_percent_mito	logical scalar whether to annotate mitochondrial percentage
reduction	pca, umap, or tsne
...	extra args passed to integrate

## Value

an integrated SingleCellExperiment object

## Examples

```
data("tiny_sce")
tiny_sce |>
splitByCol("batch") |>
sce_integrate(resolution = 0.2, batch_correct = FALSE)
```

---

sce\_preprocess      *Preprocess Single Cell Object*

---

### Description

Performs standard pre-processing workflow for scRNA-seq data

### Usage

```
sce_preprocess(
  object,
  scale = TRUE,
  normalize = TRUE,
  features = NULL,
  legacy_settings = FALSE,
  ...
)
```

### Arguments

object	Assay to use
scale	Perform linear transformation 'Scaling'
normalize	Perform normalization
features	Identify highly variable features
legacy_settings	Use legacy settings
...	extra args passed to scaling functions

### Value

a preprocessed SingleCellExperiment object

---

sce\_process      *Run SingleCellExperiment Pipeline*

---

### Description

This functions allows you to preprocess, cluster and reduce dimensions for one SingleCellExperiment object.

### Usage

```
sce_process(
  object,
  experiment = "gene",
  resolution = 0.6,
  reduction = "PCA",
  organism = "human",
  process = TRUE,
  ...
)
```

**Arguments**

object	A SingleCellExperiment object
experiment	Assay of interest in SingleCellExperiment object
resolution	Resolution for clustering cells. Default set to 0.6.
reduction	Dimensional reduction object
organism	Organism
process	whether to run dimensional reduction and clustering
...	extra parameters passed to internal functions

**Value**

a processed SingleCellExperiment object

**Examples**

```
data(tiny_sce)
sce_process(tiny_sce, process = FALSE)
```

---

sce\_reduce\_dimensions *Dimensional Reduction*

---

**Description**

Run PCA, TSNE and UMAP on a singlecell objects perplexity should not be bigger than  $3 * \text{perplexity} < \text{nrow}(X) - 1$ , see details for interpretation

**Usage**

```
sce_reduce_dimensions(object, experiment = "gene", ...)
```

**Arguments**

object	A SingleCellExperiment object
experiment	Experiment of interest to be processed
...	Extra parameters passed to sce_reduce_dimensions

**Value**

a SingleCellExperiment object with embeddings

---

set_colData	<i>Set cell metadata</i>
-------------	--------------------------

---

**Description**

Set cell metadata from a given object

**Usage**

```
set_colData(object, meta)
```

**Arguments**

object	a SingleCellExperiment object
meta	a dataframe containing object metadata

**Value**

a SingleCellExperiment object with new colData

**Examples**

```
data(small_example_dataset)
new_meta <- data.frame(row.names = colnames(small_example_dataset))
new_meta$example <- "example"
set_colData(small_example_dataset, new_meta)
```

---

set_feature_type	<i>Set Feature Types</i>
------------------	--------------------------

---

**Description**

Set Feature Types

**Usage**

```
set_feature_type(object, feature_type)
```

**Arguments**

object	a SingleCellExperiment object
feature_type	feature type

**Value**

a SingleCellExperiment object with assigned feature type

**Examples**

```
data(small_example_dataset)
set_feature_type(small_example_dataset, "transcript")
```

---

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`

---

`splitByCol` *Split SingleCellExperiment by colData variable*

---

**Description**

Split SingleCellExperiment by colData variable

**Usage**

```
splitByCol(x, f = "batch")
```

**Arguments**

<code>x</code>	SingleCellExperiment object
<code>f</code>	colData variable as a string

**Value**

a list of singlecellexperiments name by colData value

**Examples**

```
data(small_example_dataset)
splitByCol(small_example_dataset, "batch")
```

---

stash\_marker\_features *Stash Marker Genes in a SingleCellExperiment Object*

---

### Description

Marker Genes will be stored in object metadata as markers

### Usage

```
stash_marker_features(
  object,
  group_by,
  experiment = "gene",
  top_n = 200,
  p_val_cutoff = 0.5
)
```

### Arguments

object	A object
group_by	A metadata variable to group by
experiment	An experiment to use
top_n	Use top n genes, Default 200
p_val_cutoff	p value cut-off, Default value is "0.5"

### Value

a SingleCellExperiment object with marker genes

---

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 transcripts

**Source**

```
chevreuldata::human_gene_transcript_sce()
```

---

`transcripts_to_genes`*Ensembl Transcript Ids to Gene Symbols*

---

**Description**

Convert ensembl transcript ids to hgnc gene symbols

**Usage**

```
transcripts_to_genes(transcripts)
```

**Arguments**

```
transcripts    human transcripts
```

**Value**

a vector of gene symbols

**Examples**

```
NRL_transcripts_hs <-  
c("ENST00000359842", "ENST00000470566", "ENST00000465764")  
  
transcripts_to_genes(transcripts = NRL_transcripts_hs)
```

---

update_project_db	<i>Update a database of chevreul 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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