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Type Package

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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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Contents

add_percent_mito . . . 3
annotate_cell_cycle . . . 4
append_to_project_db . . . 4
build_bigwig_db . . . 5
cc.genes.cyclone . . . 5
clustering_workflow . . . 6
convert_human_sce_to_mouse . . . 6
convert_symbols_by_species . . . 7
create_project_db . . . 7
ensembl_version . . . 8
find_all_markers . . . 8
genes_to_transcripts . . . 9
get_colData . . . 10
get_feature_types . . . 10
get_features . . . 11
get_sce_metadata . . . 11
get_transcripts_from_sce . . . 12
get_variable_features . . . 12
grch38 . . . 13
grch38_tx2gene . . . 14
human_to_mouse_homologs . . . 14
integrate . . . 15
integration_workflow . . . 15
load_bigwigs . . . 16
load_sce_from_proj . . . 17
load_sce_path . . . 17
make_bigwig_db . . . 18
merge_small_sces . . . 18
metadata_from_batch . . . 19
propagate_spreadsheet_changes . . . 19
query_experiment . . . 20
read_project_db . . . 20
record_experiment_data . . . 21
regress_cell_cycle . . . 22
reintegrate_sce . . . 22
retrieve_experiment . . . 23
save_sce . . . 23
sce_calcn . . . 24

sce_cluster 24
sce_de 25
sce_integrate 26
sce_preprocess 27
sce_process 28
sce_reduce_dimensions 29
set_colData 29
set_feature_type 30
small_example_dataset 30
splitByCol 31
stash_marker_features 31
subset_by_colData 32
tiny_sce 32
transcripts_to_genes 33
update_project_db 33

Index **35**

`add_percent_mito` *Annotate percent mitochondrial reads per cell*

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 *Annotate Cell Cycle*

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 *Create a database of chevreul projects*

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 *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
```

---

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 *Get cell metadata from a given object*

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_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_features *Get feature names*

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_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 *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

---

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 scran::findMarkers
experiment_name	arbitrary name to identify experiment
organism	either "human" or "mouse"
...	extra args passed to sce_integrate

Value

an integrated 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

load_sce_from_proj *Load SingleCellExperiment Files from a single project path*

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 load_sce_path

Value

a SingleCellExperiment object

load_sce_path *Read in Gene and Transcript SingleCellExperiment Objects*

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 *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

merge_small_sces *Merge Small SingleCellExperiment Objects*

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 *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

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` *Read a database of chevreul projects*

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 *Record Experiment Metadata*

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 *Regress SingleCellExperiment Object by Given Set of Genes*

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 *Reintegrate (filtered) SingleCellExperiment objects*

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 *Calculate Read Count Metrics for a object*

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 *Run Louvain Clustering at Multiple Resolutions*

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("bath") |>
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 * perplexity < 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 *Set cell metadata*

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 *Set Feature Types*

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

x	SingleCellExperiment object
f	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 transripts

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 *Update a database of chevreul 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

Index

∗ **datasets**
    cc.genes.cyclone, 5
    ensembl_version, 8
    grch38, 13
    grch38_tx2gene, 14
    human_to_mouse_homologs, 14
    small_example_dataset, 30
    tiny_sce, 32

add_percent_mito, 3
annotate_cell_cycle, 4
append_to_project_db, 4

build_bigwig_db, 5

cc.genes.cyclone, 5
clustering_workflow, 6
convert_human_sce_to_mouse, 6
convert_symbols_by_species, 7
create_project_db, 7

ensembl_version, 8

find_all_markers, 8

genes_to_transcripts, 9
get_colData, 10
get_feature_types, 10
get_features, 11
get_sce_metadata, 11
get_transcripts_from_sce, 12
get_variable_features, 12
grch38, 13
grch38_tx2gene, 14

human_to_mouse_homologs, 14

integrate, 15
integration_workflow, 15

load_bigwigs, 16
load_sce_from_proj, 17
load_sce_path, 17

make_bigwig_db, 18
merge_small_sces, 18
metadata_from_batch, 19

propagate_spreadsheet_changes, 19

query_experiment, 20

read_project_db, 20
record_experiment_data, 21
regress_cell_cycle, 22
reintegrate_sce, 22
retrieve_experiment, 23

save_sce, 23
sce_calcn, 24
sce_cluster, 24
sce_de, 25
sce_integrate, 26
sce_preprocess, 27
sce_process, 28
sce_reduce_dimensions, 29
set_colData, 29
set_feature_type, 30
small_example_dataset, 30
splitByCol, 31
stash_marker_features, 31
subset_by_colData, 32

tiny_sce, 32
transcripts_to_genes, 33

update_project_db, 33