

# Package ‘EWCE’

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**Type** Package

**Title** Expression Weighted Celltype Enrichment

**Version** 1.21.0

**Description** Used to determine which cell types are enriched within gene lists. The package provides tools for testing enrichments within simple gene lists (such as human disease associated genes) and those resulting from differential expression studies. The package does not depend upon any particular Single Cell Transcriptome dataset and user defined datasets can be loaded in and used in the analyses.

**URL** <https://github.com/NathanSkene/EWCE>

**BugReports** <https://github.com/NathanSkene/EWCE/issues>

**License** GPL-3

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EWCE-package	<i>EWCE: Expression Weighted Celltype Enrichment</i>
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## Description

Used to determine which cell types are enriched within gene lists. The package provides tools for testing enrichments within simple gene lists (such as human disease associated genes) and those resulting from differential expression studies. The package does not depend upon any particular Single Cell Transcriptome dataset and user defined datasets can be loaded in and used in the analyses.

## Details

EWCE: Expression Weighted Celltype Enrichment

Used to determine which cell types are enriched within gene lists. The package provides tools for testing enrichments within simple gene lists (such as human disease associated genes) and those resulting from differential expression studies.

The package does not depend upon any particular Single Cell Transcriptome dataset and user defined datasets can be loaded in and used in the analyses.

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## See Also

Useful links:

- <https://github.com/NathanSkene/EWCE>
- Report bugs at <https://github.com/NathanSkene/EWCE/issues>

---

`add_res_to_merging_list`*Add to results to merging list*

---

### Description

`add_res_to_merging_list` adds EWCE results to a list for merging analysis.

### Usage

```
add_res_to_merging_list(full_res, existing_results = NULL)
```

### Arguments

`full_res` Results list generated using [bootstrap\\_enrichment\\_test](#) or [ewce\\_expression\\_data](#) functions. Multiple results tables can be merged into one results table, as long as the 'list' column is set to distinguish them.

`existing_results` Output of previous rounds from adding results to list. Leave empty if this is the first item in the list.

### Value

Merged results list.

### Examples

```
# Load the single cell data
ctd <- ewceData::ctd()

# Load the data
tt_alzh <- ewceData::tt_alzh()
# tt_alzh_BA36 <- ewceData::tt_alzh_BA36()
# Use 3 bootstrap lists for speed, for publishable analysis use >10000
reps <- 3
# Use 5 up/down regulated genes (thresh) for speed, default is 250
thresh <- 5
# Run EWCE analysis
# tt_results <- ewce_expression_data(
#   sct_data = ctd, tt = tt_alzh, annotLevel = 1, thresh = thresh,
#   reps = reps, ttSpecies = "human", sctSpecies = "mouse"
# )
# tt_results_36 <- ewce_expression_data(
#   sct_data = ctd, tt = tt_alzh_BA36, annotLevel = 1, thresh = thresh,
#   reps = reps, ttSpecies = "human", sctSpecies = "mouse"
# )

# Fill a list with the results
results <- add_res_to_merging_list(tt_alzh)
# results <- add_res_to_merging_list(tt_alzh_BA36, results)
```

---

assign_cores	<i>Assign cores</i>
--------------	---------------------

---

**Description**

Assign cores automatically for parallel processing, while reserving some.

**Usage**

```
assign_cores(worker_cores = 0.9, verbose = TRUE)
```

**Arguments**

worker_cores	Number (>1) or proportion (<1) of worker cores to use.
verbose	Print messages.

**Value**

List of core allocations.

---

bin_columns_into_quantiles	bin_columns_into_quantiles
----------------------------	----------------------------

---

**Description**

bin\_columns\_into\_quantiles is an internal function used to convert a vector of specificity into a vector of specificity quantiles. This function can be iterated across a matrix using [apply](#) to create a matrix of specificity quantiles.

**Usage**

```
bin_columns_into_quantiles(
  vec,
  numberOfBins = 40,
  defaultBin = as.integer(numberOfBins/2)
)
```

**Arguments**

vec	The vector of gene of specificity values.
numberOfBins	Number of quantile bins to use (40 is recommended).
defaultBin	Which bin to assign when there's only one non-zero quantile. In situations where there's only one non-zero quantile, <a href="#">cut</a> throws an error. Avoid these situations by using a default quantile.

**Value**

A vector with same length as vec but with columns storing quantiles instead of specificity.

**Examples**

```
ctd <- ewceData::ctd()
ctd[[1]]$specificity_quantiles <- apply(ctd[[1]]$specificity, 2,
  FUN = bin_columns_into_quantiles)
```

---

```
bin_specificity_into_quantiles
      bin_specificity_into_quantiles
```

---

**Description**

bin\_specificity\_into\_quantiles is an internal function used to convert add '\$specificity\_quantiles' to a ctd

**Usage**

```
bin_specificity_into_quantiles(
  ctdIN,
  numberOfBins,
  matrix_name = "specificity_quantiles",
  as_sparse = TRUE,
  verbose = TRUE
)
```

**Arguments**

ctdIN	A single annotLevel of a ctd, i.e. ctd[[1]] (the function is intended to be used via apply).
numberOfBins	Number of quantile 'bins' to use (40 is recommended).
matrix_name	Name of the specificity matrix to create (default: "specificity_quantiles").
as_sparse	Convert to sparseMatrix.
verbose	Print messages.

**Value**

A ctd with "specificity\_quantiles" matrix in each level (or whatever matrix\_name was set to.).

**Examples**

```
ctd <- ewceData::ctd()
ctd <- lapply(ctd, EWCE::bin_specificity_into_quantiles, numberOfBins = 40)
print(ctd[[1]]$specificity_quantiles[1:3, ])
```

---

bootstrap\_enrichment\_test

*Bootstrap cell type enrichment test*


---

## Description

bootstrap\_enrichment\_test takes a genelist and a single cell type transcriptome dataset and determines the probability of enrichment and fold changes for each cell type.

## Usage

```
bootstrap_enrichment_test(
  sct_data = NULL,
  hits = NULL,
  bg = NULL,
  genelistSpecies = NULL,
  sctSpecies = NULL,
  sctSpecies_origin = sctSpecies,
  output_species = "human",
  method = "homologene",
  reps = 100,
  no_cores = 1,
  annotLevel = 1,
  geneSizeControl = FALSE,
  controlledCT = NULL,
  mtc_method = "BH",
  sort_results = TRUE,
  standardise_sct_data = TRUE,
  standardise_hits = FALSE,
  verbose = TRUE,
  localHub = FALSE,
  store_gene_data = TRUE
)
```

## Arguments

sct_data	List generated using <a href="#">generate_celltype_data</a> .
hits	List of gene symbols containing the target gene list. Will automatically be converted to human gene symbols if geneSizeControl=TRUE.
bg	List of gene symbols containing the background gene list (including hit genes). If bg=NULL, an appropriate gene background will be created automatically.
genelistSpecies	Species that hits genes came from (no longer limited to just "mouse" and "human"). See <a href="#">list_species</a> for all available species.
sctSpecies	Species that sct_data is currently formatted as (no longer limited to just "mouse" and "human"). See <a href="#">list_species</a> for all available species.
sctSpecies_origin	Species that the sct_data originally came from, regardless of its current gene format (e.g. it was previously converted from mouse to human gene orthologs). This is used for computing an appropriate background.

output_species	Species to convert sct_data and hits to (Default: "human"). See <a href="#">list_species</a> for all available species.
method	R package to use for gene mapping: "gproufiler" Slower but more species and genes. "homologene" Faster but fewer species and genes. "babelgene" Faster but fewer species and genes. Also gives consensus scores for each gene mapping based on a several different data sources.
reps	Number of random gene lists to generate (Default: 100, but should be >=10,000 for publication-quality results).
no_cores	Number of cores to parallelise bootstrapping reps over.
annotLevel	An integer indicating which level of sct_data to analyse (Default: 1).
geneSizeControl	Whether you want to control for GC content and transcript length. Recommended if the gene list originates from genetic studies (Default: FALSE). If set to TRUE, then hits must be from humans.
controlledCT	[Optional] If not NULL, and instead is the name of a cell type, then the bootstrapping controls for expression within that cell type.
mtc_method	Multiple-testing correction method (passed to <a href="#">p.adjust</a> ).
sort_results	Sort enrichment results from smallest to largest p-values.
standardise_sct_data	Should sct_data be standardised? if TRUE: <ul style="list-style-type: none"> <li>• When sctSpecies!=output_species the sct_data will be checked for object formatting and the genes will be converted to the orthologs of the output_species with <a href="#">standardise_ctd</a> (which calls <a href="#">map_genes</a> internally).</li> <li>• When sctSpecies==output_species, the sct_data will be checked for object formatting with <a href="#">standardise_ctd</a>, but the gene names will remain untouched.</li> </ul>
standardise_hits	Should hits be standardised? If TRUE: <ul style="list-style-type: none"> <li>• When geneListSpecies!=output_species, the genes will be converted to the orthologs of the output_species with <a href="#">convert_orthologs</a>.</li> <li>• When geneListSpecies==output_species, the genes will be standardised with <a href="#">map_genes</a>.</li> </ul> If FALSE, hits will be passed on to subsequent steps as-is.
verbose	Print messages.
localHub	If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.
store_gene_data	Store sampled gene data for every bootstrap iteration. When the number of bootstrap reps is very high (>=100k) and/or the number of genes in hits is very high, you may want to set store_gene_data=FALSE to avoid using excessive amounts of CPU memory.

**Value**

A list containing three elements:

- `hit.cells`: vector containing the summed proportion of expression in each cell type for the target list.
- `gene_data`: `data.table` showing the number of time each gene appeared in the bootstrap sample.
- `bootstrap_data`: matrix in which each row represents the summed proportion of expression in each cell type for one of the random lists
- `controlledCT`: the controlled cell type (if applicable)

**Examples**

```
# Load the single cell data
sct_data <- ewceData::ctd()
# Set the parameters for the analysis
# Use 3 bootstrap lists for speed, for publishable analysis use >=10,000
reps <- 3
# Load gene list from Alzheimer's disease GWAS
hits <- ewceData::example_genelist()

# Bootstrap significance test, no control for transcript length or GC content
full_results <- EWCE::bootstrap_enrichment_test(
  sct_data = sct_data,
  hits = hits,
  reps = reps,
  annotLevel = 1,
  sctSpecies = "mouse",
  genelistSpecies = "human")
```

---

bootstrap\_plot

*Bootstrap plot*


---

**Description**

Plot bootstrap enrichment results. Support function for [generate\\_bootstrap\\_plots](#).

**Usage**

```
bootstrap_plot(
  gene_data,
  exp_mats = NULL,
  save_dir = file.path(tempdir(), "BootstrapPlots"),
  listFileName,
  signif_ct = NULL,
  hit_thresh = 25,
  facets = "CellType",
  scales = "free_x",
  show_plot = TRUE,
  verbose = TRUE
)
```

**Arguments**

gene_data	Output from <a href="#">compute_gene_scores</a> .
exp_mats	Output of <a href="#">generate_bootstrap_plots_exp_mats</a> .
save_dir	Directory to save plots to.
listFileName	listFileName
signif_ct	Significant celltypes to include the plots.
facets	<b>[Deprecated]</b> Please use rows and cols instead.
scales	Are scales shared across all facets (the default, "fixed"), or do they vary across rows ("free_x"), columns ("free_y"), or both rows and columns ("free")?
show_plot	Print the plot.

**Value**

Null output.

---

bootstrap\_plots\_for\_transcriptome  
*Bootstrap plot*

---

**Description**

Plot results of [generate\\_bootstrap\\_plots\\_for\\_transcriptome](#).

**Usage**

```
bootstrap_plots_for_transcriptome(  
  dat,  
  tag,  
  listFileName,  
  cc,  
  showGNameThresh,  
  graph_theme,  
  maxX,  
  save_dir = file.path(tempdir(), paste0("BootstrapPlots", "_for_transcriptome")),  
  height = 3.5,  
  width = 3.5,  
  show_plot = TRUE  
)
```

**Value**

Null result.

---

```
calculate_meanexp_for_level
    calculate_meanexp_for_level
```

---

**Description**

calculate\_meanexp\_for\_level

**Usage**

```
calculate_meanexp_for_level(
  ctd_oneLevel,
  expMatrix,
  as_sparse = TRUE,
  verbose = TRUE
)
```

**Value**

One level of a CellTypeDataset.

---

```
calculate_specificity_for_level
    Calculate specificity for one CTD level
```

---

**Description**

Calculate specificity for one CellTypeDataset (CTD) level.

**Usage**

```
calculate_specificity_for_level(
  ctd_oneLevel,
  matrix_name = "mean_exp",
  as_sparse = TRUE,
  verbose = TRUE
)
```

**Arguments**

ctd_oneLevel	One level from a CTD.
matrix_name	Name of the matrix to extract.
as_sparse	Whether to convert exp to sparse matrix
verbose	Print messages.

**Value**

One CTD level.

---

cell_list_dist	<i>cell_list_dist</i>
----------------	-----------------------

---

**Description**

specificity is generated in the main\_CellTypeAnalysis\_Preperation.r file

**Usage**

```
cell_list_dist(hits, sct_data, annotLevel)
```

**Arguments**

hits	List of gene symbols containing the target gene list.
sct_data	List generated using <a href="#">generate_celltype_data</a> .
annotLevel	An integer indicating which level of sct_data to analyse ( <i>Default: 1</i> ).

**Value**

The summed specificity of each celltype across a set of hits.

---

check_annotLevels	<i>check_annotLevels</i> First, check the number of annotations equals the number of columns in the expression data.
-------------------	--

---

**Description**

check\_annotLevels

First, check the number of annotations equals the number of columns in the expression data.

**Usage**

```
check_annotLevels(annotLevels, exp)
```

**Arguments**

exp	exp (#fix).
-----	-------------

**Value**

Null output.

---

```
check_args_for_bootstrap_plot_generation
    check_args_for_bootstrap_plot_generation
```

---

### Description

Check the input arguments of the [generate\\_bootstrap\\_plots\\_for\\_transcriptome](#).

### Usage

```
check_args_for_bootstrap_plot_generation(
    sct_data,
    tt,
    thresh,
    annotLevel,
    reps,
    full_results,
    listFileName,
    showGNameThresh,
    sortBy
)
```

### Arguments

sct_data	List generated using <a href="#">generate_celltype_data</a> .
tt	Differential expression table. Can be output of <a href="#">topTable</a> function. Minimum requirement is that one column stores a metric of increased/decreased expression (i.e. log fold change, t-statistic for differential expression etc) and another contains gene symbols.
thresh	The number of up- and down- regulated genes to be included in each analysis (Default: 250).
annotLevel	An integer indicating which level of sct_data to analyse (Default: 1).
reps	Number of random gene lists to generate (Default: 100, but should be >=10,000 for publication-quality results).
full_results	The full output of <a href="#">ewce_expression_data</a> for the same gene list.
listFileName	String used as the root for files saved using this function.
showGNameThresh	Integer. If a gene has over X percent of it's expression proportion in a cell type, then list the gene name.
sortBy	Column name of metric in tt which should be used to sort up- from down-regulated genes (Default: "t").

### Value

Null output.

---

check\_bootstrap\_args    *check\_bootstrap\_args*

---

### Description

Check the input arguments of the [bootstrap\\_enrichment\\_test](#).

### Usage

```
check_bootstrap_args(
  sct_data,
  hits,
  annotLevel,
  reps,
  controlledCT = NULL,
  fix_celltypes = TRUE
)
```

### Arguments

sct_data	List generated using <a href="#">generate_celltype_data</a> .
hits	List of gene symbols containing the target gene list. Will automatically be converted to human gene symbols if geneSizeControl=TRUE.
annotLevel	An integer indicating which level of sct_data to analyse ( <i>Default: 1</i> ).
reps	Number of random gene lists to generate ( <i>Default: 100</i> , but should be $\geq 10,000$ for publication-quality results).
controlledCT	[Optional] If not NULL, and instead is the name of a cell type, then the bootstrapping controls for expression within that cell type.

### Value

Null output.

---

check\_controlled\_args    *check\_controlled\_args*

---

### Description

Check the input arguments of the [controlled\\_geneset\\_enrichment](#).

### Usage

```
check_controlled_args(
  bg,
  sct_data,
  annotLevel,
  disease_genes,
  hits,
```

```

    functional_genes,
    funcGenes,
    combinedGenes
)

```

### Arguments

bg	List of gene symbols containing the background gene list (including hit genes). If bg=NULL, an appropriate gene background will be created automatically.
sct_data	List generated using <a href="#">generate_celltype_data</a> .
annotLevel	An integer indicating which level of sct_data to analyse ( <i>Default: 1</i> ).
disease_genes	Array of gene symbols containing the disease gene list. Does not have to be disease genes. Must be from same species as the single cell transcriptome dataset.
hits	Hit genes.
functional_genes	Array of gene symbols containing the functional gene list. The enrichment of this gene set within the disease_genes is tested. Must be from same species as the single cell transcriptome dataset.
funcGenes	functional_genes that are within combinedGenes.
combinedGenes	sct_data genes that are in the background bg.

### Value

Null output.

---

```

check_ewce_expression_data_args
      check_ewce_expression_data_args

```

---

### Description

Check the input arguments of the [ewce\\_expression\\_data](#).

### Usage

```
check_ewce_expression_data_args(sortBy, tt, thresh)
```

### Arguments

sortBy	Column name of metric in tt which should be used to sort up- from down-regulated genes (Default: "t").
tt	Differential expression table. Can be output of <a href="#">topTable</a> function. Minimum requirement is that one column stores a metric of increased/decreased expression (i.e. log fold change, t-statistic for differential expression etc) and another contains gene symbols.
thresh	The number of up- and down- regulated genes to be included in each analysis (Default: 250).

### Value

Null output.

---

```
check_ewce_genelist_inputs
      check_ewce_genelist_inputs
```

---

## Description

check\_ewce\_genelist\_inputs Is used to check that hits and bg gene lists passed to EWCE are setup correctly. Checks they are the appropriate length. Checks all hits are in bg. Checks the species match and if not reduces to 1:1 orthologs.

## Usage

```
check_ewce_genelist_inputs(
  sct_data,
  hits,
  bg = NULL,
  genelistSpecies = NULL,
  sctSpecies = NULL,
  sctSpecies_origin = sctSpecies,
  output_species = "human",
  method = "homologene",
  geneSizeControl = FALSE,
  standardise_sct_data = TRUE,
  standardise_hits = FALSE,
  min_genes = 4,
  verbose = TRUE
)
```

## Arguments

sct_data	List generated using <a href="#">generate_celltype_data</a> .
hits	List of gene symbols containing the target gene list. Will automatically be converted to human gene symbols if geneSizeControl=TRUE.
bg	List of gene symbols containing the background gene list (including hit genes). If bg=NULL, an appropriate gene background will be created automatically.
genelistSpecies	Species that hits genes came from (no longer limited to just "mouse" and "human"). See <a href="#">list_species</a> for all available species.
sctSpecies	Species that sct_data is currently formatted as (no longer limited to just "mouse" and "human"). See <a href="#">list_species</a> for all available species.
sctSpecies_origin	Species that the sct_data originally came from, regardless of its current gene format (e.g. it was previously converted from mouse to human gene orthologs). This is used for computing an appropriate background.
output_species	Species to convert sct_data and hits to (Default: "human"). See <a href="#">list_species</a> for all available species.
method	R package to use for gene mapping: "gprofiler" Slower but more species and genes.

"homologene" Faster but fewer species and genes.

"babelgene" Faster but fewer species and genes. Also gives consensus scores for each gene mapping based on a several different data sources.

geneSizeControl

Whether you want to control for GC content and transcript length. Recommended if the gene list originates from genetic studies (*Default: FALSE*). If set to TRUE, then hits must be from humans.

standardise\_sct\_data

Should sct\_data be standardised? if TRUE:

- When sctSpecies!=output\_species the sct\_data will be checked for object formatting and the genes will be converted to the orthologs of the output\_species with [standardise\\_ctd](#) (which calls [map\\_genes](#) internally).
- When sctSpecies==output\_species, the sct\_data will be checked for object formatting with [standardise\\_ctd](#), but the gene names will remain untouched.

standardise\_hits

Should hits be standardised? If TRUE:

- When genelistSpecies!=output\_species, the genes will be converted to the orthologs of the output\_species with [convert\\_orthologs](#).
- When genelistSpecies==output\_species, the genes will be standardised with [map\\_genes](#).

If FALSE, hits will be passed on to subsequent steps as-is.

min\_genes

Minimum number of genes in a gene list to test.

verbose

Print messages.

## Value

A list containing

- hits: Array of MGI/HGNC gene symbols containing the target gene list.
- bg: Array of MGI/HGNC gene symbols containing the background gene list.

## Examples

```
ctd <- ewceData::ctd()
example_genelist <- ewceData::example_genelist()

# Called from "bootstrap_enrichment_test()" and "generate_bootstrap_plots()"
checkedLists <- EWCE::check_ewce_genelist_inputs(
  sct_data = ctd,
  hits = example_genelist,
  sctSpecies = "mouse",
  genelistSpecies = "human"
)
```

---

```
check_full_results    check_full_results
```

---

**Description**

Check full results generated by [bootstrap\\_enrichment\\_test](#).

**Usage**

```
check_full_results(full_results, sct_data)
```

**Arguments**

full_results	The full output of <a href="#">bootstrap_enrichment_test</a> for the same gene list.
sct_data	List generated using <a href="#">generate_celltype_data</a> .

**Value**

Null output.

---

```
check_generate_controlled_bootstrap_geneset
      generate_controlled_bootstrap_geneset
```

---

**Description**

Check input arguments to [generate\\_controlled\\_bootstrap\\_geneset](#).

**Usage**

```
check_generate_controlled_bootstrap_geneset(
  controlledCT,
  annotLevel,
  sct_data,
  hits
)
```

**Arguments**

controlledCT	[Optional] If not NULL, and instead is the name of a cell type, then the bootstrapping controls for expression within that cell type.
annotLevel	An integer indicating which level of sct_data to analyse ( <i>Default: 1</i> ).
sct_data	List generated using <a href="#">generate_celltype_data</a> .
hits	List of gene symbols containing the target gene list. Will automatically be converted to human gene symbols if geneSizeControl=TRUE.

**Value**

Null output.

---

check_group_name	<i>Check group name</i>
------------------	-------------------------

---

**Description**

Ensure groupName argument is provided to [generate\\_celltype\\_data](#).

**Usage**

```
check_group_name(groupName)
```

**Arguments**

groupName	A human readable name for referring to the dataset being used.
-----------	--

**Value**

Null output.

---

check_nas	<i>Check NAs</i>
-----------	------------------

---

**Description**

Check for any NAs in an expression matrix.

**Usage**

```
check_nas(exp)
```

**Arguments**

exp	Expression matrix.
-----	--------------------

**Value**

Null output.

---

check_numeric	<i>Check numeric</i>
---------------	----------------------

---

**Description**

Ensure that a matrix is numeric. If not, it will be converted to numeric.

**Usage**

```
check_numeric(exp)
```

**Arguments**

exp	Input matrix.
-----	---------------

**Value**

Numeric expression matrix.

---

check_percent_hits	<i>Get percentage of target cell type hits</i>
--------------------	--

---

**Description**

After you run [bootstrap\\_enrichment\\_test](#), check what percentage of significantly enriched cell types match an expected cell type.

**Usage**

```
check_percent_hits(
  full_results,
  target_celltype,
  mtc_method = "bonferroni",
  q_threshold = 0.05,
  verbose = TRUE
)
```

**Arguments**

full_results	bootstrap_enrichment_test results.
target_celltype	Substring to search to matching cell types (case-insensitive).
mtc_method	Multiple-testing correction method.
q_threshold	Corrected significance threshold.
verbose	Print messages.

**Value**

Report list.

**Examples**

```
## Bootstrap significance test,
## no control for transcript length or GC content
## Use pre-computed results to speed up example
full_results <- EWCE::example_bootstrap_results()

report <- EWCE::check_percent_hits(
  full_results = full_results,
  target_celltype = "microglia"
)
```

---

check_sce	<i>Check SingleCellExperiment</i>
-----------	-----------------------------------

---

**Description**

Check whether exp is a SingleCellExperiment (SCE) object and extract the relevant components.

**Usage**

```
check_sce(exp, verbose = TRUE)
```

**Value**

List of extracted SCE components.

---

check_species	<i>Check species</i>
---------------	----------------------

---

**Description**

If species arguments are NULL, set default species.

**Usage**

```
check_species(
  genelistSpecies = NULL,
  sctSpecies = NULL,
  sctSpecies_origin = NULL,
  sctSpecies_origin_default = "mouse",
  verbose = TRUE
)
```

**Arguments**

genelistSpecies	Species that hits genes came from (no longer limited to just "mouse" and "human"). See <a href="#">list_species</a> for all available species.
sctSpecies	Species that sct_data is currently formatted as (no longer limited to just "mouse" and "human"). See <a href="#">list_species</a> for all available species.
sctSpecies_origin	Species that the sct_data originally came from, regardless of its current gene format (e.g. it was previously converted from mouse to human gene orthologs). This is used for computing an appropriate background.
sctSpecies_origin_default	Default value for sctSpecies_origin.
verbose	Print messages.

**Value**

List of corrected species names.

---

compute\_gene\_counts    *Compute gene counts*

---

**Description**

Counts the number of times each gene appeared in the randomly sampled gene lists.

**Usage**

```
compute_gene_counts(bootstrap_list, verbose = TRUE)
```

**Arguments**

bootstrap_list	The output of <code>get_summed_proportions_iterate</code> .
verbose	Print messages.

**Value**

[data.table](#)

---

compute\_gene\_scores     *Compute gene counts*

---

## Description

Aggregate gene-level scores across all bootstrap iterations.

- boot: Mean specificity of all genes within a given cell type.
- hit: Mean specificity of a hit gene within a given cell type.

## Usage

```
compute_gene_scores(  
  sct_data,  
  annotLevel,  
  bootstrap_list = NULL,  
  hits,  
  combinedGenes,  
  reps = NULL,  
  exp_mats = NULL,  
  return_hit_exp = FALSE,  
  verbose = TRUE  
)
```

## Arguments

sct_data	List generated using <a href="#">generate_celltype_data</a> .
annotLevel	An integer indicating which level of sct_data to analyse ( <i>Default: 1</i> ).
bootstrap_list	The output of <code>get_summed_proportions_iterate</code> .
hits	list of gene names. The target gene set.
reps	Number of random gene lists to generate ( <i>Default: 100</i> , but should be $\geq 10,000$ for publication-quality results).
return_hit_exp	Return the expression of each hit gene.
verbose	Print messages.

## Value

[data.table](#)

---

controlled\_geneset\_enrichment  
*Celltype controlled geneset enrichment*

---

## Description

controlled\_geneset\_enrichment tests whether a functional gene set is still enriched in a disease gene set after controlling for the disease gene set's enrichment in a particular cell type (the 'controlledCT')

## Usage

```
controlled_geneset_enrichment(  
  disease_genes,  
  functional_genes,  
  bg = NULL,  
  sct_data,  
  sctSpecies = NULL,  
  output_species = "human",  
  disease_genes_species = NULL,  
  functional_genes_species = NULL,  
  method = "homologene",  
  annotLevel,  
  reps = 100,  
  controlledCT,  
  use_intersect = FALSE,  
  verbose = TRUE  
)
```

## Arguments

**disease\_genes** Array of gene symbols containing the disease gene list. Does not have to be disease genes. Must be from same species as the single cell transcriptome dataset.

**functional\_genes** Array of gene symbols containing the functional gene list. The enrichment of this gene set within the disease\_genes is tested. Must be from same species as the single cell transcriptome dataset.

**bg** List of gene symbols containing the background gene list (including hit genes). If bg=NULL, an appropriate gene background will be created automatically.

**sct\_data** List generated using [generate\\_celltype\\_data](#).

**sctSpecies** Species that sct\_data is currently formatted as (no longer limited to just "mouse" and "human"). See [list\\_species](#) for all available species.

**output\_species** Species to convert sct\_data and hits to (Default: "human"). See [list\\_species](#) for all available species.

**disease\_genes\_species** Species of the disease\_genes gene set.

**functional\_genes\_species** Species of the functional\_genes gene set.

**method** R package to use for gene mapping:

	"gprofiler" Slower but more species and genes.
	"homologene" Faster but fewer species and genes.
	"babelgene" Faster but fewer species and genes. Also gives consensus scores for each gene mapping based on a several different data sources.
annotLevel	An integer indicating which level of sct_data to analyse ( <i>Default: 1</i> ).
reps	Number of random gene lists to generate ( <i>Default: 100</i> , but should be $\geq 10,000$ for publication-quality results).
controlledCT	[Optional] If not NULL, and instead is the name of a cell type, then the bootstrapping controls for expression within that cell type.
use_intersect	When species1 and species2 are both different from output_species, this argument will determine whether to use the intersect (TRUE) or union (FALSE) of all genes from species1 and species2.
verbose	Print messages.

### Value

A list containing three data frames:

- `p_controlled` The probability that functional\_genes are enriched in disease\_genes while controlling for the level of specificity in controlledCT
- `z_controlled` The z-score that functional\_genes are enriched in disease\_genes while controlling for the level of specificity in controlledCT
- `p_uncontrolled` The probability that functional\_genes are enriched in disease\_genes WITHOUT controlling for the level of specificity in controlledCT
- `z_uncontrolled` The z-score that functional\_genes are enriched in disease\_genes WITHOUT controlling for the level of specificity in controlledCT
- `reps=reps`
- `controlledCT`
- `actualOverlap=actual` The number of genes that overlap between functional and disease gene sets

### Examples

```
# See the vignette for more detailed explanations
# Gene set enrichment analysis controlling for cell type expression
# set seed for bootstrap reproducibility
set.seed(12345678)
## load merged dataset from vignette
ctd <- ewceData::ctd()
schiz_genes <- ewceData::schiz_genes()
hpsd_genes <- ewceData::hpsd_genes()
# Use 3 bootstrap lists for speed, for publishable analysis use >10000
reps <- 3

res_hpsd_schiz <- EWCE::controlled_geneset_enrichment(
  disease_genes = schiz_genes,
  functional_genes = hpsd_genes,
  sct_data = ctd,
  annotLevel = 1,
  reps = reps,
  controlledCT = "pyramidal CA1"
)
```

---

```
convert_new_ewce_to_old
      convert_new_ewce_to_old
```

---

**Description**

convert\_new\_ewce\_to\_old Used to get an old style EWCE ctd file from a new one

**Usage**

```
convert_new_ewce_to_old(ctd, lvl)
```

**Arguments**

ctd	A cell type data structure containing "mean_exp" and "specificity".
lvl	The annotation level to extract.

**Value**

CellTypeData in the old data structure style.

---

```
convert_old_ewce_to_new
      convert_old_ewce_to_new
```

---

**Description**

convert\_old\_ewce\_to\_new Used to get a new style EWCE ctd file (mean\_exp/specificity) from old ones (all\_scts).

**Usage**

```
convert_old_ewce_to_new(level1 = NA, level2 = NA, celltype_data = NA)
```

**Arguments**

level1	File path to old level1 of EWCE ctd.
level2	File path to old level2 of EWCE ctd.
celltype_data	The ctd to be converted.

**Details**

If you've already loaded it and want to pass it as a celltype\_data structure, then don't set level1 or level2.

**Value**

CellTypeData in the new data structure style.

---

`create_background_multilist`*Create background gene list for multiple species*

---

### Description

Create background gene list for the intersection/union between multiple species (`gene_list1_species`, `gene_list2_species`, and `sctSpecies`), and then filter the gene lists to only include genes within the background.

### Usage

```
create_background_multilist(  
  gene_list1,  
  gene_list2,  
  gene_list1_species,  
  gene_list2_species,  
  output_species = "human",  
  bg = NULL,  
  use_intersect = FALSE,  
  method = "homologene",  
  verbose = TRUE  
)
```

### Arguments

- |                             |  |
|-----------------------------|--|
| <code>output_species</code> | Species to convert all genes from <code>species1</code> and <code>species2</code> to first. Default="human", but can be to either any species supported by <b>orthogene</b> , including <code>species1</code> or <code>species2</code> .   |
| <code>bg</code>             | User supplied background list that will be returned to the user after removing duplicate genes.  |
| <code>use_intersect</code>  | When <code>species1</code> and <code>species2</code> are both different from <code>output_species</code> , this argument will determine whether to use the intersect (TRUE) or union (FALSE) of all genes from <code>species1</code> and <code>species2</code> .                             |
| <code>method</code>         | R package to use for gene mapping:<br><br>"gprofiler" Slower but more species and genes.<br>"homologene" Faster but fewer species and genes.<br>"babelgene" Faster but fewer species and genes. Also gives consensus scores for each gene mapping based on a several different data sources. |
| <code>verbose</code>        | Print messages.  |

### Value

Background and gene list.

---

```
create_list_network  create_list_network
```

---

**Description**

Support function for prepare\_genesize\_control\_network.

**Usage**

```
create_list_network(data_byGene2, hits_NEW, reps = 10000, no_cores = 1)
```

**Value**

List network

---

```
ctd_to_sce          CellTypeDataset to SingleCellExperiment
```

---

**Description**

Copied from [scKirby](#), which is not yet on CRAN or Bioconductor.

**Usage**

```
ctd_to_sce(object, as_sparse = TRUE, as_DelayedArray = FALSE, verbose = TRUE)
```

**Arguments**

object	CellTypeDataset object.
as_sparse	Store SingleCellExperiment matrices as sparse.
as_DelayedArray	Store SingleCellExperiment matrices as DelayedArray.
verbose	Print messages.

**Value**

SingleCellExperiment

**Examples**

```
ctd <- ewceData::ctd()
sce <- EWCE::ctd_to_sce(ctd)
```

---

delayedarray\_normalize

*Efficiently normalize a DelayedArray*

---

### Description

The following is a matrix normalization procedure that takes advantage of functions designed to be more efficient for DelayedArray objects.

### Usage

```
delayedarray_normalize(  
  exp,  
  log_norm = TRUE,  
  min_max = TRUE,  
  plot_hists = FALSE,  
  no_cores = 1  
)
```

### Arguments

exp	Input matrix (e.g. gene expression).
log_norm	Whether to first log-normalise exp with <a href="#">log1p</a> .
min_max	Whether to min/max-normalise exp.
no_cores	Number of cores to parallelise across.

### Value

Normalised matrix.

---

drop\_nonexpressed\_cells

*Drop cells with zero gene counts*

---

### Description

Remove columns (cells) in which (gene) counts sum to zero.

### Usage

```
drop_nonexpressed_cells(exp, annotLevels, verbose = TRUE)
```

### Arguments

exp	Gene expression matrix.
annotLevels	Cell-wise annotations to be subset if some cells are dropped.
verbose	Print messages.

### Value

List of filtered exp and annotLevels.

---

 drop\_nonexpressed\_genes

*Drop genes with zero counts*


---

### Description

Remove rows (genes) in which counts sum to zero.

### Usage

```
drop_nonexpressed_genes(exp, verbose = TRUE)
```

### Arguments

exp	Gene expression matrix.
verbose	Print messages.

### Value

List of filtered exp.

---

drop\_uninformative\_genes

*Drop uninformative genes*


---

### Description

drop\_uninformative\_genes drops uninformative genes in order to reduce compute time and noise in subsequent steps. It achieves this through several steps, each of which are optional:

- Drop non-1:1 orthologs:  
Removes genes that don't have 1:1 orthologs with the output\_species ("human" by default).
- Drop non-varying genes:  
Removes genes that don't vary across cells based on variance deciles.
- Drop non-differentially expressed genes (DEGs):  
Removes genes that are not significantly differentially expressed across cell-types (multiple DEG methods available).

### Usage

```
drop_uninformative_genes(
  exp,
  level2annot,
  mtc_method = "BH",
  adj_pval_thresh = 1e-05,
  convert_orths = FALSE,
  input_species = NULL,
  output_species = "human",
  non121_strategy = "drop_both_species",
```

```

method = "homologene",
as_sparse = TRUE,
as_DelayedArray = FALSE,
return_sce = FALSE,
no_cores = 1,
verbose = TRUE,
...
)

```

## Arguments

exp	Expression matrix with gene names as rownames.
level2annot	Array of cell types, with each sequentially corresponding a column in the expression matrix.
mtc_method	Multiple-testing correction method used by DGE step. See <a href="#">p.adjust</a> for more details.
adj_pval_thresh	Minimum differential expression significance that a gene must demonstrate across level2annot (i.e. cell types).
convert_orths	If input_species!=output_species and convert_orths=TRUE, will drop genes without 1:1 output_species orthologs and then convert exp gene names to those of output_species.
input_species	Which species the gene names in exp come from. See <a href="#">list_species</a> for all available species.
output_species	Which species' genes names to convert exp to. See <a href="#">list_species</a> for all available species.
non121_strategy	How to handle genes that don't have 1:1 mappings between input_species:output_species. Options include:  "drop_both_species" or "dbs" or 1 Drop genes that have duplicate mappings in either the input_species or output_species ( <i>DEFAULT</i> ). "drop_input_species" or "dis" or 2 Only drop genes that have duplicate mappings in the input_species. "drop_output_species" or "dos" or 3 Only drop genes that have duplicate mappings in the output_species. "keep_both_species" or "kbs" or 4 Keep all genes regardless of whether they have duplicate mappings in either species. "keep_popular" or "kp" or 5 Return only the most "popular" interspecies ortholog mappings. This procedure tends to yield a greater number of returned genes but at the cost of many of them not being true biological 1:1 orthologs. "sum", "mean", "median", "min" or "max" When gene_df is a matrix and gene_output="rowname" these options will aggregate many-to-one gene mappings (input_species-to-output_species) after dropping any duplicate genes in the output_species.
method	R package to use for gene mapping: "gprofiler" Slower but more species and genes. "homologene" Faster but fewer species and genes.

"babelgene" Faster but fewer species and genes. Also gives consensus scores for each gene mapping based on a several different data sources.

as\_sparse Convert exp to sparse matrix.

as\_DelayedArray Convert exp to DelayedArray for scalable processing.

return\_sce Whether to return the filtered results as an expression matrix or a **SingleCellExperiment**.

no\_cores Number of cores to parallelise across. Set to NULL to automatically optimise.

verbose Print messages. #' @inheritParams orthogene::convert\_orthologs

... Arguments passed on to [orthogene::convert\\_orthologs](#)

gene\_df Data object containing the genes (see gene\_input for options on how the genes can be stored within the object).  
Can be one of the following formats:

- matrix A sparse or dense matrix.
- data.frame A data.frame, data.table. or tibble.
- list A list or character vector.

Genes, transcripts, proteins, SNPs, or genomic ranges can be provided in any format (HGNC, Ensembl, RefSeq, UniProt, etc.) and will be automatically converted to gene symbols unless specified otherwise with the ... arguments.

*Note:* If you set method="homologene", you must either supply genes in gene symbol format (e.g. "Sox2") OR set standardise\_genes=TRUE.

gene\_input Which aspect of gene\_df to get gene names from:

- "rownames" From row names of data.frame/matrix.
- "colnames" From column names of data.frame/matrix.
- <column name> From a column in gene\_df, e.g. "gene\_names".

gene\_output How to return genes. Options include:

- "rownames" As row names of gene\_df.
- "colnames" As column names of gene\_df.
- "columns" As new columns "input\_gene", "ortholog\_gene" (and "input\_gene\_standard" if standardise\_genes=TRUE) in gene\_df.
- "dict" As a dictionary (named list) where the names are input\_gene and the values are ortholog\_gene.
- "dict\_rev" As a reversed dictionary (named list) where the names are ortholog\_gene and the values are input\_gene.

standardise\_genes If TRUE AND gene\_output="columns", a new column "input\_gene\_standard" will be added to gene\_df containing standardised HGNC symbols identified by [gorth](#).

drop\_norths Drop genes that don't have an ortholog in the output\_species.

agg\_fun Aggregation function passed to [aggregate\\_mapped\\_genes](#). Set to NULL to skip aggregation step (default).

mthreshold Maximum number of ortholog names per gene to show. Passed to [gorth](#). Only used when method="gprofiler" (*DEFAULT*: Inf).

sort\_rows Sort gene\_df rows alphanumerically.

`gene_map` A [data.frame](#) that maps the current gene names to new gene names. This function's behaviour will adapt to different situations as follows:

`gene_map=<data.frame>` When a `data.frame` containing the gene key:value columns (specified by `input_col` and `output_col`, respectively) is provided, this will be used to perform aggregation/expansion.

`gene_map=NULL and input_species!=output_species` A `gene_map` is automatically generated by [map\\_orthologs](#) to perform inter-species gene aggregation/expansion.

`gene_map=NULL and input_species==output_species` A `gene_map` is automatically generated by [map\\_genes](#) to perform within-species gene symbol standardization and aggregation/expansion.

`input_col` Column name within `gene_map` with gene names matching the row names of `X`.

`output_col` Column name within `gene_map` with gene names that you wish you map the row names of `X` onto.

### Value

`exp` Expression matrix with gene names as row names.

### Examples

```
cortex_mrna <- ewceData::cortex_mrna()
# Use only a subset of genes to keep the example quick
cortex_mrna$exp <- cortex_mrna$exp[1:300, ]

## Convert orthologs at the same time
exp2_orth <- drop_uninformative_genes(
  exp = cortex_mrna$exp,
  level2annot = cortex_mrna$annot$level2class,
  input_species = "mouse"
)
```

---

dt\_to\_df

*Convert a data.table to a data.frame.*

---

### Description

Converts a `data.table` to a `data.frame` by setting the first column as the rownames.

### Usage

```
dt_to_df(exp)
```

### Value

[data.frame](#)

---

ewce\_expression\_data *Bootstrap cell type enrichment test for transcriptome data*


---

## Description

ewce\_expression\_data takes a differential gene expression (DGE) results table and determines the probability of cell type enrichment in the up- and down- regulated genes.

## Usage

```
ewce_expression_data(
  sct_data,
  annotLevel = 1,
  tt,
  sortBy = "t",
  thresh = 250,
  reps = 100,
  ttSpecies = NULL,
  sctSpecies = NULL,
  output_species = NULL,
  bg = NULL,
  method = "homologene",
  verbose = TRUE,
  localHub = FALSE
)
```

## Arguments

sct_data	List generated using <a href="#">generate_celltype_data</a> .
annotLevel	An integer indicating which level of sct_data to analyse ( <i>Default: 1</i> ).
tt	Differential expression table. Can be output of <a href="#">topTable</a> function. Minimum requirement is that one column stores a metric of increased/decreased expression (i.e. log fold change, t-statistic for differential expression etc) and another contains gene symbols.
sortBy	Column name of metric in tt which should be used to sort up- from down-regulated genes ( <i>Default: "t"</i> ).
thresh	The number of up- and down- regulated genes to be included in each analysis ( <i>Default: 250</i> ).
reps	Number of random gene lists to generate ( <i>Default: 100</i> , but should be $\geq 10,000$ for publication-quality results).
ttSpecies	The species the differential expression table was generated from.
sctSpecies	Species that sct_data is currently formatted as (no longer limited to just "mouse" and "human"). See <a href="#">list_species</a> for all available species.
output_species	Species to convert sct_data and hits to ( <i>Default: "human"</i> ). See <a href="#">list_species</a> for all available species.
bg	List of gene symbols containing the background gene list (including hit genes). If bg=NULL, an appropriate gene background will be created automatically.
method	R package to use for gene mapping:

	"gprofiler" Slower but more species and genes.
	"homologene" Faster but fewer species and genes.
	"babelgene" Faster but fewer species and genes. Also gives consensus scores for each gene mapping based on a several different data sources.
verbose	Print messages.
localHub	If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.

## Value

A list containing five data frames:

- `results`: dataframe in which each row gives the statistics (p-value, fold change and number of standard deviations from the mean) associated with the enrichment of the stated cell type in the gene list. An additional column `*Direction*` stores whether it the result is from the up or downregulated set.
- `hit.cells.up`: vector containing the summed proportion of expression in each cell type for the target list.
- `hit.cells.down`: vector containing the summed proportion of expression in each cell type for the target list.
- `bootstrap_data.up`: matrix in which each row represents the summed proportion of expression in each cell type for one of the random lists.
- `bootstrap_data.down`: matrix in which each row represents the summed proportion of expression in each cell type for one of the random lists.

## Examples

```
# Load the single cell data
ctd <- ewceData::ctd()

# Set the parameters for the analysis
# Use 3 bootstrap lists for speed, for publishable analysis use >10000
reps <- 3
# Use 5 up/down regulated genes (thresh) for speed, default is 250
thresh <- 5
annotLevel <- 1 # <- Use cell level annotations (i.e. Interneurons)

# Load the top table
tt_alzh <- ewceData::tt_alzh()

tt_results <- EWCE::ewce_expression_data(
  sct_data = ctd,
  tt = tt_alzh,
  annotLevel = 1,
  thresh = thresh,
  reps = reps,
  ttSpecies = "human",
  sctSpecies = "mouse"
)
```

---

ewce_plot	<i>Plot EWCE results</i>
-----------	--------------------------

---

### Description

ewce\_plot generates plots of EWCE enrichment results

### Usage

```
ewce_plot(
  total_res,
  mtc_method = "bonferroni",
  q_threshold = 0.05,
  ctd = NULL,
  annotLevel = 1,
  heights = c(0.3, 1),
  make_dendro = FALSE,
  verbose = TRUE
)
```

### Arguments

total_res	Results data.frame generated using <a href="#">bootstrap_enrichment_test</a> or <a href="#">ewce_expression_data</a> functions. Multiple results tables can be merged into one results table, as long as the 'list' column is set to distinguish them. Multiple testing correction is then applied across all merged results.
mtc_method	Method to be used for multiple testing correction. Argument is passed to <a href="#">p.adjust</a> (DEFAULT: "bonferroni").
q_threshold	Corrected significance threshold.
ctd	CellTypeDataset object. Should be provided so that the dendrogram can be taken from it and added to plots.
annotLevel	An integer indicating which level of ctd to analyse ( <i>Default: 1</i> ).
heights	The relative heights row in the grid. Will get repeated to match the dimensions of the grid. Passed to <a href="#">wrap_plots</a> .
make_dendro	Add a dendrogram (requires ctd).
verbose	Print messages.

### Value

A named list containing versions of the [ggplot](#) with and without the dendrogram. Note that cell type order on the x-axis is based on hierarchical clustering for both plots if `make_dendro = TRUE`.

### Examples

```
## Bootstrap significance test,
## no control for transcript length or GC content
## Use pre-computed results to speed up example
total_res <- EWCE::example_bootstrap_results()$results
plt <- ewce_plot(total_res = total_res)
```

---

example\_bootstrap\_results

*Example bootstrap enrichment results*

---

## Description

Example cell type enrichment results produced by [bootstrap\\_enrichment\\_test](#).

## Usage

```
example_bootstrap_results(verbose = TRUE, localHub = FALSE)
```

## Arguments

verbose	Print messages.
localHub	If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.

## Value

List with 3 items.

## Source

```
# Load the single cell data
ctd <- ewceData::ctd()
# Set the parameters for the analysis
# Use 3 bootstrap lists for speed, for publishable analysis use >=10,000
reps <- 3
# Load gene list from Alzheimer's disease GWAS
example_genelist <- ewceData::example_genelist()
# Bootstrap significance test, no control for transcript length or GC content
full_results <- EWCE::bootstrap_enrichment_test( sct_data = ctd, hits = example_genelist, reps =
reps, annotLevel = 1, sctSpecies = "mouse", genelistSpecies = "human" )
bootstrap_results <- full_results
save(bootstrap_results,file = "inst/extdata/bootstrap_results.rda")
```

## Examples

```
full_results <- example_bootstrap_results()
```

---

`example_transcriptome_results`*Example bootstrap celltype enrichment test for transcriptome data*

---

**Description**

Example celltype enrichment results produced by [ewce\\_expression\\_data](#).

**Usage**

```
example_transcriptome_results(verbose = TRUE, localHub = FALSE)
```

**Arguments**

<code>verbose</code>	Print messages.
<code>localHub</code>	If working offline, add argument <code>localHub=TRUE</code> to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.

**Value**

List with 5 items.

**Source**

```
## Load the single cell data
ctd <- ewceData::ctd()
## Set the parameters for the analysis
## Use 3 bootstrap lists for speed, for publishable analysis use >10,000
reps <- 3
annotLevel <- 1 # <- Use cell level annotations (i.e. Interneurons)
## Use 5 up/down regulated genes (thresh) for speed, default is 250
thresh <- 5
## Load the top table
tt_alzh <- ewceData::tt_alzh()
tt_results <- EWCE::ewce_expression_data( sct_data = ctd, tt = tt_alzh, annotLevel = 1, thresh =
thresh, reps = reps, ttSpecies = "human", sctSpecies = "mouse" )
save(tt_results, file = "inst/extdata/tt_results.rda")
```

**Examples**

```
tt_results <- EWCE::example_transcriptome_results()
```

---

extract_matrix	<i>Extract a matrix from a CellTypeDataset</i>
----------------	--

---

## Description

Extracts a particular matrix (e.g., mean\_exp, specificity) from a CellTypeDataset object.

## Usage

```
extract_matrix(
  ctd,
  dataset,
  level = 1,
  input_species = NULL,
  output_species = "human",
  metric = "specificity",
  non121_strategy = "drop_both_species",
  method = "homologene",
  numberOfBins = 40,
  remove_unlabeled_clusters = FALSE,
  force_new_quantiles = FALSE,
  as_sparse = TRUE,
  as_DelayedArray = FALSE,
  rename_columns = TRUE,
  make_columns_unique = FALSE,
  verbose = TRUE,
  ...
)
```

## Arguments

ctd	Input CellTypeData.
dataset	CellTypeData. name.
level	CTD level to extract from.
input_species	Which species the gene names in exp come from. See <a href="#">list_species</a> for all available species.
output_species	Which species' genes names to convert exp to. See <a href="#">list_species</a> for all available species.
metric	Name of the matrix to extract.
non121_strategy	How to handle genes that don't have 1:1 mappings between input_species:output_species. Options include: <ul style="list-style-type: none"> <li>"drop_both_species" or "dbs" or 1 Drop genes that have duplicate mappings in either the input_species or output_species (<i>DEFAULT</i>).</li> <li>"drop_input_species" or "dis" or 2 Only drop genes that have duplicate mappings in the input_species.</li> <li>"drop_output_species" or "dos" or 3 Only drop genes that have duplicate mappings in the output_species.</li> </ul>

	"keep_both_species" or "kbs" or 4	Keep all genes regardless of whether they have duplicate mappings in either species.
	"keep_popular" or "kp" or 5	Return only the most "popular" interspecies ortholog mappings. This procedure tends to yield a greater number of returned genes but at the cost of many of them not being true biological 1:1 orthologs.
	"sum", "mean", "median", "min" or "max"	When gene_df is a matrix and gene_output="rowname" these options will aggregate many-to-one gene mappings (input_species-to-output_species) after dropping any duplicate genes in the output_species.
method	R package to use for gene mapping:	
	"gprofiler"	Slower but more species and genes.
	"homologene"	Faster but fewer species and genes.
	"babelgene"	Faster but fewer species and genes. Also gives consensus scores for each gene mapping based on a several different data sources.
numberOfBins		Number of non-zero quantile bins.
remove_unlabeled_clusters		Remove any samples that have numeric column names.
force_new_quantiles		By default, quantile computation is skipped if they have already been computed. Set =TRUE to override this and generate new quantiles.
as_sparse		Convert to sparse matrix.
as_DelayedArray		Convert to DelayedArray.
rename_columns		Remove replace_chars from column names.
make_columns_unique		Rename each columns with the prefix dataset.species.celltype.
verbose		Print messages. Set verbose=2 if you want to print all messages from internal functions as well.
...		Arguments passed on to <a href="#">orthogene::convert_orthologs</a>
gene_df		Data object containing the genes (see gene_input for options on how the genes can be stored within the object). Can be one of the following formats:
	matrix	A sparse or dense matrix.
	data.frame	A data.frame, data.table. or tibble.
	list	A list or character vector.
		Genes, transcripts, proteins, SNPs, or genomic ranges can be provided in any format (HGNC, Ensembl, RefSeq, UniProt, etc.) and will be automatically converted to gene symbols unless specified otherwise with the ... arguments.
		<i>Note:</i> If you set method="homologene", you must either supply genes in gene symbol format (e.g. "Sox2") OR set standardise_genes=TRUE.
gene_input		Which aspect of gene_df to get gene names from:
	"rownames"	From row names of data.frame/matrix.
	"colnames"	From column names of data.frame/matrix.
	<column name>	From a column in gene_df, e.g. "gene_names".

gene\_output How to return genes. Options include:

- "rownames" As row names of gene\_df.
- "colnames" As column names of gene\_df.
- "columns" As new columns "input\_gene", "ortholog\_gene" (and "input\_gene\_standard" if standardise\_genes=TRUE) in gene\_df.
- "dict" As a dictionary (named list) where the names are input\_gene and the values are ortholog\_gene.
- "dict\_rev" As a reversed dictionary (named list) where the names are ortholog\_gene and the values are input\_gene.
- standardise\_genes If TRUE AND gene\_output="columns", a new column "input\_gene\_standard" will be added to gene\_df containing standardised HGNC symbols identified by [gorth](#).
- drop\_nonorths Drop genes that don't have an ortholog in the output\_species.
- agg\_fun Aggregation function passed to [aggregate\\_mapped\\_genes](#). Set to NULL to skip aggregation step (default).
- mthreshold Maximum number of ortholog names per gene to show. Passed to [gorth](#). Only used when method="gprofiler" (*DEFAULT*: Inf).
- sort\_rows Sort gene\_df rows alphanumerically.
- gene\_map A [data.frame](#) that maps the current gene names to new gene names. This function's behaviour will adapt to different situations as follows:
  - gene\_map=<data.frame> When a data.frame containing the gene key:value columns (specified by input\_col and output\_col, respectively) is provided, this will be used to perform aggregation/expansion.
  - gene\_map=NULL **and** input\_species!=output\_species A gene\_map is automatically generated by [map\\_orthologs](#) to perform inter-species gene aggregation/expansion.
  - gene\_map=NULL **and** input\_species==output\_species A gene\_map is automatically generated by [map\\_genes](#) to perform within-species gene symbol standardization and aggregation/expansion.
- input\_col Column name within gene\_map with gene names matching the row names of X.
- output\_col Column name within gene\_map with gene names that you wish you map the row names of X onto.

## Value

(specificity) matrix.

---

filter\_ctd\_genes

*Filter genes in a CellTypeDataset*

---

## Description

Removes rows from each matrix within a CellTypeDataset (CTD) that are not within gene\_subset.

## Usage

```
filter_ctd_genes(ctd, gene_subset)
```

**Arguments**

ctd                    CellTypeDataset.  
 gene\_subset        Genes to subset to.

**Value**

Filtered CellTypeDataset.

**Examples**

```
ctd <- ewceData::ctd()
ctd <- standardise_ctd(ctd, input_species="mouse")
gene_subset <- rownames(ctd[[1]]$mean_exp)[1:100]
ctd_subset <- EWCE::filter_ctd_genes(ctd = ctd, gene_subset = gene_subset)
```

---

filter\_genes\_without\_1to1\_homolog  
*filter\_genes\_without\_1to1\_homolog*

---

**Description**

Deprecated function. Please use [filter\\_nonorthologs](#) instead.

**Usage**

```
filter_genes_without_1to1_homolog(
  filenames,
  input_species = "mouse",
  convert_nonhuman_genes = TRUE,
  annot_levels = NULL,
  suffix = "_orthologs",
  verbose = TRUE
)
```

**Arguments**

filenames            List of file names for sct\_data saved as *.rda* files.  
 input\_species        Which species the gene names in exp come from.  
 convert\_nonhuman\_genes    Whether to convert the exp row names to human gene names.  
 annot\_levels        [Optional] Names of each annotation level.  
 suffix                Suffix to add to the file name (right before *.rda*).  
 verbose              Print messages.

**Details**

**Note:** This function replaces the original filter\_genes\_without\_1to1\_homolog function. filter\_genes\_without\_1to1\_homolog is now a wrapper for filter\_nonorthologs.

**Value**

List of the filtered CellTypeData file names.

**Examples**

```
# Load the single cell data
ctd <- ewceData::ctd()
tmp <- tempfile()
save(ctd, file = tmp)
fNames_ALLCELLS_orths <- EWCE::filter_nonorthologs(filenamees = tmp)
```

---

filter_nonorthologs	<i>Filter non-orthologs</i>
---------------------	-----------------------------

---

**Description**

filter\_nonorthologs Takes the filenames of CellTypeData files, loads them, drops any genes which don't have a 1:1 orthologs with humans, and then convert the gene to human orthologs. The new files are then saved to disk, appending '\_orthologs' to the file name.

**Usage**

```
filter_nonorthologs(
  filenames,
  input_species = NULL,
  convert_nonhuman_genes = TRUE,
  annot_levels = NULL,
  suffix = "_orthologs",
  method = "homologene",
  non121_strategy = "drop_both_species",
  verbose = TRUE,
  ...
)
```

**Arguments**

filenames	List of file names for sct_data saved as <i>.rda</i> files.
input_species	Which species the gene names in exp come from.
convert_nonhuman_genes	Whether to convert the exp row names to human gene names.
annot_levels	[Optional] Names of each annotation level.
suffix	Suffix to add to the file name (right before <i>.rda</i> ).
method	R package to use for gene mapping: "gprofiler" Slower but more species and genes. "homologene" Faster but fewer species and genes. "babelgene" Faster but fewer species and genes. Also gives consensus scores for each gene mapping based on a several different data sources.

non121\_strategy

How to handle genes that don't have 1:1 mappings between input\_species:output\_species. Options include:

"drop\_both\_species" or "dbs" or 1 Drop genes that have duplicate mappings in either the input\_species or output\_species (*DEFAULT*).

"drop\_input\_species" or "dis" or 2 Only drop genes that have duplicate mappings in the input\_species.

"drop\_output\_species" or "dos" or 3 Only drop genes that have duplicate mappings in the output\_species.

"keep\_both\_species" or "kbs" or 4 Keep all genes regardless of whether they have duplicate mappings in either species.

"keep\_popular" or "kp" or 5 Return only the most "popular" interspecies ortholog mappings. This procedure tends to yield a greater number of returned genes but at the cost of many of them not being true biological 1:1 orthologs.

"sum", "mean", "median", "min" or "max" When gene\_df is a matrix and gene\_output="rowname" these options will aggregate many-to-one gene mappings (input\_species-to-output\_species) after dropping any duplicate genes in the output\_species.

verbose

Print messages.

...

Arguments passed on to [orthogene::convert\\_orthologs](#)

gene\_df Data object containing the genes (see gene\_input for options on how the genes can be stored within the object).

Can be one of the following formats:

matrix A sparse or dense matrix.

data.frame A data.frame, data.table. or tibble.

list A list or character vector.

Genes, transcripts, proteins, SNPs, or genomic ranges can be provided in any format (HGNC, Ensembl, RefSeq, UniProt, etc.) and will be automatically converted to gene symbols unless specified otherwise with the ... arguments.

*Note:* If you set method="homologene", you must either supply genes in gene symbol format (e.g. "Sox2") OR set standardise\_genes=TRUE.

gene\_input Which aspect of gene\_df to get gene names from:

"rownames" From row names of data.frame/matrix.

"colnames" From column names of data.frame/matrix.

<column name> From a column in gene\_df, e.g. "gene\_names".

gene\_output How to return genes. Options include:

"rownames" As row names of gene\_df.

"colnames" As column names of gene\_df.

"columns" As new columns "input\_gene", "ortholog\_gene" (and "input\_gene\_standard" if standardise\_genes=TRUE) in gene\_df.

"dict" As a dictionary (named list) where the names are input\_gene and the values are ortholog\_gene.

"dict\_rev" As a reversed dictionary (named list) where the names are ortholog\_gene and the values are input\_gene.

`standardise_genes` If TRUE AND `gene_output="columns"`, a new column "input\_gene\_standard" will be added to `gene_df` containing standardised HGNC symbols identified by [gorth](#).

`output_species` Name of the output species (e.g. "human","chicken"). Use [map\\_species](#) to return a full list of available species.

`drop_nonorths` Drop genes that don't have an ortholog in the `output_species`.

`agg_fun` Aggregation function passed to [aggregate\\_mapped\\_genes](#). Set to NULL to skip aggregation step (default).

`mthreshold` Maximum number of ortholog names per gene to show. Passed to [gorth](#). Only used when `method="gprofiler"` (*DEFAULT*: Inf).

`as_sparse` Convert `gene_df` to a sparse matrix. Only works if `gene_df` is one of the following classes:

- `matrix`
- `Matrix`
- `data.frame`
- `data.table`
- `tibble`

If `gene_df` is a sparse matrix to begin with, it will be returned as a sparse matrix (so long as `gene_output= "rownames" or "colnames"`).

`as_DelayedArray` Convert aggregated matrix to [DelayedArray](#).

`sort_rows` Sort `gene_df` rows alphanumerically.

`gene_map` A [data.frame](#) that maps the current gene names to new gene names. This function's behaviour will adapt to different situations as follows:

`gene_map=<data.frame>` When a `data.frame` containing the gene key:value columns (specified by `input_col` and `output_col`, respectively) is provided, this will be used to perform aggregation/expansion.

`gene_map=NULL and input_species!=output_species` A `gene_map` is automatically generated by [map\\_orthologs](#) to perform inter-species gene aggregation/expansion.

`gene_map=NULL and input_species==output_species` A `gene_map` is automatically generated by [map\\_genes](#) to perform within-species gene symbol standardization and aggregation/expansion.

`input_col` Column name within `gene_map` with gene names matching the row names of X.

`output_col` Column name within `gene_map` with gene names that you wish you map the row names of X onto.

## Details

**Note:** This function replaces the original `filter_genes_without_1to1_homolog` function. `filter_genes_without_1` is now a wrapper for `filter_nonorthologs`.

## Value

List of the filtered `CellTypeData` file names.

## Examples

```
# Load the single cell data
```

```
ctd <- ewceData::ctd()
tmp <- tempfile()
save(ctd, file = tmp)
fNames_ALLCELLS_orths <- EWCE::filter_nonorthologs(filenamees = tmp)
```

---

filter\_variance\_quantiles  
*Filter variance quantiles*

---

### Description

Remove rows in exp that do not vary substantially across rows.

### Usage

```
filter_variance_quantiles(
  exp,
  log10_norm = TRUE,
  n_quantiles = 10,
  min_variance_quantile = as.integer(n_quantiles/2),
  verbose = TRUE
)
```

### Arguments

exp	Gene expression matrix.
log10_norm	Log10-normalise exp before computing variance.
n_quantiles	Number of quantile bins to use. Defaults to deciles (n_quantiles=10).
min_variance_quantile	The minimum variance quantile to keep values from.
verbose	Print messages.

### Value

Filtered exp.

---

fix\_bad\_hgnc\_symbols *fix\_bad\_hgnc\_symbols*

---

### Description

Given an expression matrix, wherein the rows are supposed to be HGNC symbols, find those symbols which are not official HGNC symbols, then correct them if possible. Return the expression matrix with corrected symbols.

**Usage**

```
fix_bad_hgnc_symbols(
  exp,
  dropNonHGNC = FALSE,
  as_sparse = TRUE,
  verbose = TRUE,
  localHub = FALSE
)
```

**Arguments**

exp	An expression matrix where the rows are HGNC symbols or a SingleCellExperiment (SCE) or other Ranged Summarized Experiment (SE) type object.
dropNonHGNC	Boolean. Should symbols not recognised as HGNC symbols be dropped?
as_sparse	Convert exp to sparse matrix.
verbose	Print messages.
localHub	If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.

**Value**

Returns the expression matrix with the rownames corrected and rows representing the same gene merged. If a SingleCellExperiment (SCE) or other Ranged Summarized Experiment (SE) type object was inputted this will be returned with the corrected expression matrix under counts.

**Examples**

```
# create example expression matrix, could be part of a exp, annot list obj
exp <- matrix(data = runif(70), ncol = 10)
# Add HGNC gene names but add with an error:
# MARCH8 is a HGNC symbol which if opened in excel will convert to Mar-08
rownames(exp) <-
  c("MT-TF", "MT-RNR1", "MT-TV", "MT-RNR2", "MT-TL1", "MT-ND1", "Mar-08")
exp <- fix_bad_hgnc_symbols(exp)
# fix_bad_hgnc_symbols warns the user of this possible issue
```

---

fix_bad_mgi_symbols	<i>fix_bad_mgi_symbols - Given an expression matrix, wherein the rows are supposed to be MGI symbols, find those symbols which are not official MGI symbols, then check in the MGI synonm database for whether they match to a proper MGI symbol. Where a symbol is found to be an aliases for a gene that is already in the dataset, the combined reads are summed together.</i>
---------------------	---

---

**Description**

Also checks whether any gene names contain "Sep", "Mar" or "Feb". These should be checked for any suggestion that excel has corrupted the gene names.

**Usage**

```
fix_bad_mgi_symbols(
  exp,
  mrk_file_path = NULL,
  printAllBadSymbols = FALSE,
  as_sparse = TRUE,
  verbose = TRUE,
  localHub = FALSE
)
```

**Arguments**

exp	An expression matrix where the rows are MGI symbols, or a SingleCellExperiment (SCE) or other Ranged Summarized Experiment (SE) type object.
mrk_file_path	Path to the MRK_List2 file which can be downloaded from <a href="http://www.informatics.jax.org/downloads/reports">www.informatics.jax.org/downloads/reports</a>
printAllBadSymbols	Output to console all the bad gene symbols
as_sparse	Convert exp to sparse matrix.
verbose	Print messages.
localHub	If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.

**Value**

Returns the expression matrix with the rownames corrected and rows representing the same gene merged. If no corrections are necessary, input expression matrix is returned. If a SingleCellExperiment (SCE) or other Ranged Summarized Experiment (SE) type object was inputted this will be returned with the corrected expression matrix under counts.

**Examples**

```
# Load the single cell data
cortex_mrna <- ewceData::cortex_mrna()
# take a subset for speed
cortex_mrna$exp <- cortex_mrna$exp[1:50, 1:5]
cortex_mrna$exp <- fix_bad_mgi_symbols(cortex_mrna$exp)
```

---

fix\_celltype\_names      *Fix celltype names*

---

**Description**

Make sure celltypes don't contain characters that could interfere with downstream analyses. For example, the R package **MAGMA.Celltyping** cannot have spaces in celltype names because spaces are used as a delimiter in later steps.

**Usage**

```
fix_celltype_names(  
  celltypes,  
  replace_chars = "[ - ] | [ . ] | [ / ] | [ \\ ]",  
  make_unique = TRUE  
)
```

**Arguments**

`celltypes` Character vector of celltype names.

`replace_chars` Regex string of characters to replace with "\_" when renaming columns.

`make_unique` Make all entries unique.

**Value**

Fixed celltype names.

**Examples**

```
ct <- c("microglia", "astrocytes", "Pyramidal SS")  
ct_fixed <- fix_celltype_names(celltypes = ct)
```

---

fix\_celltype\_names\_full\_results

*Fix celltype name in full results*

---

**Description**

Aligns celltype names in full results generated by [bootstrap\\_enrichment\\_test](#) with the standardised CellTypeDataset (CTD) produced by [standardise\\_ctd](#).

**Usage**

```
fix_celltype_names_full_results(full_results, verbose = TRUE)
```

**Arguments**

`full_results` Cell-type enrichment results generated by [bootstrap\\_enrichment\\_test](#).

`verbose` Print messages.

**Value**

Fixed full results.

---

 generate\_bootstrap\_plots

*Generate bootstrap plots*


---

## Description

generate\_bootstrap\_plots takes a gene list and a single cell type transcriptome dataset and generates plots which show how the expression of the genes in the list compares to those in randomly generated gene lists.

## Usage

```
generate_bootstrap_plots(
  sct_data = NULL,
  hits = NULL,
  bg = NULL,
  genelistSpecies = NULL,
  sctSpecies = NULL,
  output_species = "human",
  method = "homologene",
  reps = 100,
  annotLevel = 1,
  geneSizeControl = FALSE,
  full_results = NULL,
  listFileName = paste0("_level", annotLevel),
  adj_pval_thresh = 0.05,
  facets = "CellType",
  scales = "free_x",
  save_dir = file.path(tempdir(), "BootstrapPlots"),
  show_plot = TRUE,
  verbose = TRUE
)
```

## Arguments

sct_data	List generated using <a href="#">generate_celltype_data</a> .
hits	List of gene symbols containing the target gene list. Will automatically be converted to human gene symbols if geneSizeControl=TRUE.
bg	List of gene symbols containing the background gene list (including hit genes). If bg=NULL, an appropriate gene background will be created automatically.
genelistSpecies	Species that hits genes came from (no longer limited to just "mouse" and "human"). See <a href="#">list_species</a> for all available species.
sctSpecies	Species that sct_data is currently formatted as (no longer limited to just "mouse" and "human"). See <a href="#">list_species</a> for all available species.
output_species	Species to convert sct_data and hits to (Default: "human"). See <a href="#">list_species</a> for all available species.
method	R package to use for gene mapping: "gprofiler" Slower but more species and genes.

	"homologene" Faster but fewer species and genes.
	"babelgene" Faster but fewer species and genes. Also gives consensus scores for each gene mapping based on a several different data sources.
reps	Number of random gene lists to generate ( <i>Default: 100</i> , but should be $\geq 10,000$ for publication-quality results).
annotLevel	An integer indicating which level of sct_data to analyse ( <i>Default: 1</i> ).
geneSizeControl	Whether you want to control for GC content and transcript length. Recommended if the gene list originates from genetic studies ( <i>Default: FALSE</i> ). If set to TRUE, then hits must be from humans.
full_results	The full output of <a href="#">bootstrap_enrichment_test</a> for the same gene list.
listFileName	String used as the root for files saved using this function.
adj_pval_thresh	Adjusted p-value threshold of celltypes to include in plots.
facets	<b>[Deprecated]</b> Please use rows and cols instead.
scales	Are scales shared across all facets (the default, "fixed"), or do they vary across rows ("free_x"), columns ("free_y"), or both rows and columns ("free")?
save_dir	Directory where the BootstrapPlots folder should be saved, default is a temp directory.
show_plot	Print the plot.
verbose	Print messages.

## Value

Saves a set of pdf files containing graphs and returns the file where they are saved. These will be saved with the file name adjusted using the value of listFileName. The files are saved into the 'BootstrapPlot' folder. Files start with one of the following:

- qqplot\_noText: sorts the gene list according to how enriched it is in the relevant cell type. Plots the value in the target list against the mean value in the bootstrapped lists.
- qqplot\_wtGSym: as above but labels the gene symbols for the highest expressed genes.
- bootDists: rather than just showing the mean of the bootstrapped lists, a boxplot shows the distribution of values
- bootDists\_LOG: shows the bootstrapped distributions with the y-axis shown on a log scale

## Examples

```
## Load the single cell data
sct_data <- ewceData::ctd()

## Set the parameters for the analysis
## Use 5 bootstrap lists for speed, for publishable analysis use >10000
reps <- 5

## Load the gene list and get human orthologs
hits <- ewceData::example_genelist()

## Bootstrap significance test,
## no control for transcript length or GC content
## Use pre-computed results to speed up example
```

```

full_results <- EWCE::example_bootstrap_results()

### Skip this for example purposes
# full_results <- EWCE::bootstrap_enrichment_test(
#   sct_data = sct_data,
#   hits = hits,
#   reps = reps,
#   annotLevel = 1,
#   sctSpecies = "mouse",
#   genelistSpecies = "human"
# )

output <- EWCE::generate_bootstrap_plots(
  sct_data = sct_data,
  hits = hits,
  reps = reps,
  full_results = full_results,
  sctSpecies = "mouse",
  genelistSpecies = "human",
  annotLevel = 1
)

```

---

```

generate_bootstrap_plots_for_transcriptome
  Generate bootstrap plots

```

---

## Description

Takes a gene list and a single cell type transcriptome dataset and generates plots which show how the expression of the genes in the list compares to those in randomly generated gene lists.

## Usage

```

generate_bootstrap_plots_for_transcriptome(
  sct_data,
  tt,
  bg = NULL,
  thresh = 250,
  annotLevel = 1,
  reps = 100,
  full_results = NA,
  listFileName = "",
  showGNameThresh = 25,
  ttSpecies = NULL,
  sctSpecies = NULL,
  output_species = NULL,
  sortBy = "t",
  sig_only = TRUE,
  sig_col = "q",
  sig_thresh = 0.05,
  celltype_col = "CellType",
  plot_types = c("bootstrap", "bootstrap_distributions", "log_bootstrap_distributions"),
  save_dir = file.path(tempdir(), "BootstrapPlots"),

```

```

method = "homologene",
verbose = TRUE
)

```

### Arguments

sct_data	List generated using <a href="#">generate_celltype_data</a> .
tt	Differential expression table. Can be output of <a href="#">topTable</a> function. Minimum requirement is that one column stores a metric of increased/decreased expression (i.e. log fold change, t-statistic for differential expression etc) and another contains gene symbols.
bg	List of gene symbols containing the background gene list (including hit genes). If bg=NULL, an appropriate gene background will be created automatically.
thresh	The number of up- and down- regulated genes to be included in each analysis (Default: 250).
annotLevel	An integer indicating which level of sct_data to analyse (Default: 1).
reps	Number of random gene lists to generate (Default: 100, but should be >=10,000 for publication-quality results).
full_results	The full output of <a href="#">ewce_expression_data</a> for the same gene list.
listFileName	String used as the root for files saved using this function.
showGNameThresh	Integer. If a gene has over X percent of it's expression proportion in a cell type, then list the gene name.
ttSpecies	The species the differential expression table was generated from.
sctSpecies	Species that sct_data is currently formatted as (no longer limited to just "mouse" and "human"). See <a href="#">list_species</a> for all available species.
output_species	Species to convert sct_data and hits to (Default: "human"). See <a href="#">list_species</a> for all available species.
sortBy	Column name of metric in tt which should be used to sort up- from down-regulated genes (Default: "t").
sig_only	Should plots only be generated for cells which have significant changes?
sig_col	Column name in tt that contains the significance values.
sig_thresh	Threshold by which to filter tt by sig_col.
celltype_col	Column within tt that contains celltype names.
plot_types	Plot types to generate.
save_dir	Directory where the BootstrapPlots folder should be saved, default is a temp directory.
method	R package to use for gene mapping: "gprouf" Slower but more species and genes. "homologene" Faster but fewer species and genes. "babelgene" Faster but fewer species and genes. Also gives consensus scores for each gene mapping based on a several different data sources.
verbose	Print messages.

**Value**

Saves a set of PDF files containing graphs. Then returns a nested list with each plot and the path where it was saved to. Files start with one of the following:

- qqplot\_noText: sorts the gene list according to how enriched it is in the relevant cell type. Plots the value in the target list against the mean value in the bootstrapped lists.
- qqplot\_wtGSym: as above but labels the gene symbols for the highest expressed genes.
- bootDists: rather than just showing the mean of the bootstrapped lists, a boxplot shows the distribution of values
- bootDists\_LOG: shows the bootstrapped distributions with the y-axis shown on a log scale

**Examples**

```
## Load the single cell data
ctd <- ewceData::ctd()

## Set the parameters for the analysis
## Use 3 bootstrap lists for speed, for publishable analysis use >10,000
reps <- 3
annotLevel <- 1 # <- Use cell level annotations (i.e. Interneurons)
## Use 5 up/down regulated genes (thresh) for speed, default is 250
thresh <- 5

## Load the top table
tt_alzh <- ewceData::tt_alzh()

## See ?example_transcriptome_results for full code to produce tt_results
tt_results <- EWCE::example_transcriptome_results()

## Bootstrap significance test,
## no control for transcript length or GC content
savePath <- EWCE::generate_bootstrap_plots_for_transcriptome(
  sct_data = ctd,
  tt = tt_alzh,
  thresh = thresh,
  annotLevel = 1,
  full_results = tt_results,
  listFileName = "examples",
  reps = reps,
  ttSpecies = "human",
  sctSpecies = "mouse",
  # Only do one plot type for demo purposes
  plot_types = "bootstrap"
)
```

---

generate\_celltype\_data

*Generate CellTypeData (CTD) file*

---

**Description**

generate\_celltype\_data takes gene expression data and cell type annotations and creates Cell-TypeData (CTD) files which contain matrices of mean expression and specificity per cell type.

**Usage**

```

generate_celltype_data(
  exp,
  annotLevels,
  groupName,
  no_cores = 1,
  savePath = tempdir(),
  file_prefix = "ctd",
  as_sparse = TRUE,
  as_DelayedArray = FALSE,
  normSpec = FALSE,
  convert_orths = FALSE,
  input_species = "mouse",
  output_species = "human",
  non121_strategy = "drop_both_species",
  method = "homologene",
  force_new_file = TRUE,
  specificity_quantiles = TRUE,
  numberOfBins = 40,
  dendrograms = TRUE,
  return_ctd = FALSE,
  verbose = TRUE,
  ...
)

```

**Arguments**

exp	Numerical matrix with row for each gene and column for each cell. Row names are gene symbols. Column names are cell IDs which can be cross referenced against the annot data frame.
annotLevels	List with arrays of strings containing the cell type names associated with each column in exp.
groupName	A human readable name for referring to the dataset being used.
no_cores	Number of cores that should be used to speedup the computation. <i>NOTE:</i> Use no_cores=1 when using this package in windows system.
savePath	Directory where the CTD file should be saved.
file_prefix	Prefix to add to saved CTD file name.
as_sparse	Convert exp to a sparse Matrix.
as_DelayedArray	Convert exp to DelayedArray.
normSpec	Boolean indicating whether specificity data should be transformed to a normal distribution by cell type, giving equivalent scores across all cell types.
convert_orths	If input_species!=output_species and convert_orths=TRUE, will drop genes without 1:1 output_species orthologs and then convert exp gene names to those of output_species.
input_species	The species that the exp dataset comes from. See <a href="#">list_species</a> for all available species.
output_species	Species to convert exp to (Default: "human"). See <a href="#">list_species</a> for all available species.

non121\_strategy

How to handle genes that don't have 1:1 mappings between input\_species:output\_species. Options include:

"drop\_both\_species" or "dbs" or 1 Drop genes that have duplicate mappings in either the input\_species or output\_species (*DEFAULT*).

"drop\_input\_species" or "dis" or 2 Only drop genes that have duplicate mappings in the input\_species.

"drop\_output\_species" or "dos" or 3 Only drop genes that have duplicate mappings in the output\_species.

"keep\_both\_species" or "kbs" or 4 Keep all genes regardless of whether they have duplicate mappings in either species.

"keep\_popular" or "kp" or 5 Return only the most "popular" interspecies ortholog mappings. This procedure tends to yield a greater number of returned genes but at the cost of many of them not being true biological 1:1 orthologs.

"sum", "mean", "median", "min" or "max" When gene\_df is a matrix and gene\_output="rowname" these options will aggregate many-to-one gene mappings (input\_species-to-output\_species) after dropping any duplicate genes in the output\_species.

method

R package to use for gene mapping:

"gprofiler" Slower but more species and genes.

"homologene" Faster but fewer species and genes.

"babelgene" Faster but fewer species and genes. Also gives consensus scores for each gene mapping based on a several different data sources.

force\_new\_file If a file of the same name as the one being created already exists, overwrite it.

specificity\_quantiles

Compute specificity quantiles. Recommended to set to TRUE.

numberOfBins

Number of quantile 'bins' to use (40 is recommended).

dendrograms

Add dendrogram plots

return\_ctd

Return the CTD object in a list along with the file name, instead of just the file name.

verbose

Print messages.

...

Arguments passed on to [orthogene::convert\\_orthologs](#)

gene\_df Data object containing the genes (see gene\_input for options on how the genes can be stored within the object).

Can be one of the following formats:

matrix A sparse or dense matrix.

data.frame A data.frame, data.table. or tibble.

list A list or character vector.

Genes, transcripts, proteins, SNPs, or genomic ranges can be provided in any format (HGNC, Ensembl, RefSeq, UniProt, etc.) and will be automatically converted to gene symbols unless specified otherwise with the ... arguments.

*Note:* If you set method="homologene", you must either supply genes in gene symbol format (e.g. "Sox2") OR set standardise\_genes=TRUE.

gene\_input Which aspect of gene\_df to get gene names from:

"rownames" From row names of data.frame/matrix.  
 "colnames" From column names of data.frame/matrix.  
 <column name> From a column in gene\_df, e.g. "gene\_names".  
 gene\_output How to return genes. Options include:

"rownames" As row names of gene\_df.  
 "colnames" As column names of gene\_df.  
 "columns" As new columns "input\_gene", "ortholog\_gene" (and "input\_gene\_standard" if standardise\_genes=TRUE) in gene\_df.  
 "dict" As a dictionary (named list) where the names are input\_gene and the values are ortholog\_gene.  
 "dict\_rev" As a reversed dictionary (named list) where the names are ortholog\_gene and the values are input\_gene.

standardise\_genes If TRUE AND gene\_output="columns", a new column "input\_gene\_standard" will be added to gene\_df containing standardised HGNC symbols identified by [gorth](#).

drop\_nonorths Drop genes that don't have an ortholog in the output\_species.

agg\_fun Aggregation function passed to [aggregate\\_mapped\\_genes](#). Set to NULL to skip aggregation step (default).

mthreshold Maximum number of ortholog names per gene to show. Passed to [gorth](#). Only used when method="gprofiler" (DEFAULT: Inf).

sort\_rows Sort gene\_df rows alphanumerically.

gene\_map A [data.frame](#) that maps the current gene names to new gene names. This function's behaviour will adapt to different situations as follows:

gene\_map=<data.frame> When a data.frame containing the gene key:value columns (specified by input\_col and output\_col, respectively) is provided, this will be used to perform aggregation/expansion.

gene\_map=NULL **and** input\_species!=output\_species A gene\_map is automatically generated by [map\\_orthologs](#) to perform inter-species gene aggregation/expansion.

gene\_map=NULL **and** input\_species==output\_species A gene\_map is automatically generated by [map\\_genes](#) to perform within-species gene symbol standardization and aggregation/expansion.

input\_col Column name within gene\_map with gene names matching the row names of X.

output\_col Column name within gene\_map with gene names that you wish you map the row names of X onto.

## Value

File names for the saved CellTypeData (CTD) files.

## Examples

```
# Load the single cell data
cortex_mrna <- ewceData::cortex_mrna()
# Use only a subset to keep the example quick
expData <- cortex_mrna$exp[1:100, ]
l1 <- cortex_mrna$annot$level1class
l2 <- cortex_mrna$annot$level2class
annotLevels <- list(l1 = l1, l2 = l2)
```

```
fNames_ALLCELLS <- EWCE::generate_celltype_data(
  exp = expData,
  annotLevels = annotLevels,
  groupName = "allKImouse"
)
```

---

```
generate_controlled_bootstrap_geneset
  generate_controlled_bootstrap_geneset
```

---

### Description

Used to generate cell type-controlled bootstrapped gene sets.

### Usage

```
generate_controlled_bootstrap_geneset(
  hits,
  sct_data,
  annotLevel,
  reps,
  controlledCT = FALSE,
  verbose = TRUE
)
```

### Arguments

hits	List of gene symbols containing the target gene list. Will automatically be converted to human gene symbols if <code>geneSizeControl=TRUE</code> .
sct_data	List generated using <a href="#">generate_celltype_data</a> .
annotLevel	An integer indicating which level of <code>sct_data</code> to analyse ( <i>Default: 1</i> ).
reps	Number of random gene lists to generate ( <i>Default: 100</i> , but should be $\geq 10,000$ for publication-quality results).
controlledCT	[Optional] If not NULL, and instead is the name of a cell type, then the bootstrapping controls for expression within that cell type.
verbose	Print messages.

### Details

See [controlled\\_geneset\\_enrichment](#) for examples.

### Value

Matrix of genes (such that `nrows=length(hits)` and `ncols=reps`), where each column is a gene list.

---

get_celltype_table	<i>get_celltype_table</i>
--------------------	---------------------------

---

### Description

get\_celltype\_table Generates a table that can be used for supplementary tables of publications. The table lists how many cells are associated with each cell type, the level of annotation, and the dataset from which it was generated.

### Usage

```
get_celltype_table(annot)
```

### Arguments

annot	An annotation dataframe, which columns named 'level1class', 'level2class' and 'dataset_name'
-------	--

### Value

A dataframe with columns 'name', 'level', 'freq' and 'dataset\_name'

### Examples

```
# See PrepLDSC.Rmd for origin of merged_ALLCELLS$annot
cortex_mrna <- ewceData::cortex_mrna()
cortex_mrna$annot$dataset_name <- "cortex_mrna"
celltype_table <- EWCE::get_celltype_table(cortex_mrna$annot)
```

---

get_ctd_levels	<i>Get the names of CellTypeDataset levels</i>
----------------	--

---

### Description

Returns the level names of a CellTypeDataset. If none are available, will instead return a vector of numbers (one number per level).

### Usage

```
get_ctd_levels(ctd, max_only = FALSE)
```

### Arguments

ctd	CellTypeDataset.
max_only	Only return the level with the greatest depth (e.g. "level3" in c("level1", "level2", "level3")).

### Value

List of levels in ctd.

---

get\_ctd\_matrix\_names    *Get CTD matrix names*

---

### Description

Find the names of all data matrices in a CellTypeDataset.

### Usage

```
get_ctd_matrix_names(  
  ctd = NULL,  
  matrices = c("mean_exp", "median_exp", "specificity", "median_specificity",  
              "specificity_quantiles"),  
  verbose = TRUE  
)
```

### Arguments

ctd	CellTypeDataset. If set to NULL (default), will simply return all possible matrix names.
matrices	Matrix names to search for.
verbose	Print messages.

### Value

List of matrix names.

---

get\_exp\_data\_for\_bootstrapped\_genes  
*get\_exp\_data\_for\_bootstrapped\_genes*

---

### Description

Support function for [generate\\_bootstrap\\_plots\\_for\\_transcriptome](#).

### Usage

```
get_exp_data_for_bootstrapped_genes(  
  results,  
  signif_res,  
  sct_data,  
  hits,  
  combinedGenes,  
  annotLevel,  
  nReps = 100,  
  as_sparse = TRUE,  
  verbose = TRUE  
)
```

**Arguments**

results	Results for a single direction from full_results\$joint_results.
signif_res	Significant cell types to generate bootstrap expression data for.
sct_data	List generated using <a href="#">generate_celltype_data</a> .
hits	Gene hits.
combinedGenes	Combined list of genes from sct_data, hits, and background bg.
annotLevel	An integer indicating which level of sct_data to analyse ( <i>Default: 1</i> ).
nReps	Number of bootstrap replicates.
as_sparse	Convert returned matrices to sparse matrices.
verbose	Print messages.

**Value**

exp\_mats

---

get_sig_results	<i>Extract significant results</i>
-----------------	------------------------------------

---

**Description**

Extract significant results from output of [bootstrap\\_enrichment\\_test](#).

**Usage**

```
get_sig_results(
  full_results,
  mtc_method = "BH",
  q_threshold = 0.05,
  verbose = TRUE
)
```

**Arguments**

full_results	Output of <a href="#">bootstrap_enrichment_test</a> .
mtc_method	Multiple-testing correction method (passed to <a href="#">p.adjust</a> ).
q_threshold	Maximum multiple-testing-corrected p-value to include.
verbose	Print messages.

**Value**

Filtered enrichment results table.

---

get\_summed\_proportions

*Get summed proportions*


---

### Description

get\_summed\_proportions Given the target gene set, randomly sample gene lists of equal length, obtain the specificity of these and then obtain the mean specificity in each sampled list (and the target list).

### Usage

```
get_summed_proportions(
  hits,
  sct_data,
  annotLevel,
  reps,
  no_cores = 1,
  geneSizeControl,
  controlledCT = NULL,
  control_network = NULL,
  store_gene_data = TRUE,
  verbose = TRUE
)
```

### Arguments

hits	list of gene names. The target gene set.
sct_data	List generated using <a href="#">generate_celltype_data</a> .
annotLevel	An integer indicating which level of sct_data to analyse ( <i>Default: 1</i> ).
reps	Number of random gene lists to generate ( <i>Default: 100</i> , but should be $\geq 10,000$ for publication-quality results).
no_cores	Number of cores to parallelise bootstrapping reps over.
geneSizeControl	Whether you want to control for GC content and transcript length. Recommended if the gene list originates from genetic studies ( <i>Default: FALSE</i> ). If set to TRUE, then hits must be from humans.
controlledCT	[Optional] If not NULL, and instead is the name of a cell type, then the bootstrapping controls for expression within that cell type.
control_network	If geneSizeControl=TRUE, then must provide the control network.
store_gene_data	Store sampled gene data for every bootstrap iteration. When the number of bootstrap reps is very high ( $\geq 100k$ ) and/or the number of genes in hits is very high, you may want to set store_gene_data=FALSE to avoid using excessive amounts of CPU memory.
verbose	Print messages.

**Details**

See [bootstrap\\_enrichment\\_test](#) for examples.

**Value**

A list containing three elements:

- `hit.cells`: vector containing the summed proportion of expression in each cell type for the target list.
- `gene_data`: `data.table` showing the number of time each gene appeared in the bootstrap sample.
- `bootstrap_data`: matrix in which each row represents the summed proportion of expression in each cell type for one of the random lists
- `controlledCT`: the controlled cell type (if applicable)

---

<code>is_32bit</code>	<i>Checks whether OS is a 32-bit Windows</i>
-----------------------	--

---

**Description**

Helper function to avoid duplicate test runs on Windows OS.

**Usage**

```
is_32bit()
```

**Value**

Null

---

<code>is_celltypedataset</code>	<i>Check whether object is a CellTypeDataset</i>
---------------------------------	--

---

**Description**

Check whether an object is a CellTypeDataset.

**Usage**

```
is_celltypedataset(ctd)
```

**Arguments**

`ctd`                      Object.

**Value**

boolean

---

is\_ctd\_standardised     *Check whether a CellTypeDataset is standardised*

---

**Description**

Check whether a CellTypeDataset was previously standardised using [standardise\\_ctd](#).

**Usage**

```
is_ctd_standardised(ctd)
```

**Arguments**

ctd                    CellTypeDataset.

**Value**

Whether the ctd is standardised.

---

is\_delayed\_array        *Assess whether an object is a DelayedArray.*

---

**Description**

Assess whether an object is a DelayedArray or one of its derived object types.

**Usage**

```
is_delayed_array(X)
```

**Arguments**

X                      Object.

**Value**

boolean

---

is_matrix	<i>Assess whether an object is a Matrix</i>
-----------	---

---

**Description**

Assess whether an object is a Matrix or one of its derived object types.

**Usage**

```
is_matrix(X)
```

**Arguments**

X            Object.

**Value**

boolean

---

is_sparse_matrix	<i>Assess whether an object is a sparse matrix</i>
------------------	--

---

**Description**

Assess whether an object is a sparse matrix or one of its derived object types.

**Usage**

```
is_sparse_matrix(X)
```

**Arguments**

X            Object.

**Value**

boolean

---

list_species	<i>List all species</i>
--------------	-------------------------

---

**Description**

List all species that EWCE can convert genes from/to. Wrapper function for [map\\_species](#).

**Usage**

```
list_species(verbose = TRUE)
```

**Arguments**

verbose          Print messages.

**Value**

List of species EWCE can input/output genes as.

**Examples**

```
list_species()
```

---

load_rdata	load_rdata
------------	------------

---

**Description**

Load processed data (*.rda* format) using a function that assigns it to a specific variable (so you don't have to guess what the loaded variable name is).

**Usage**

```
load_rdata(fileName)
```

**Arguments**

fileName          Name of the file to load.

**Value**

Data object.

**Examples**

```
tmp <- tempfile()
save(mtcars, file = tmp)
mtcars2 <- load_rdata(tmp)
```

---

max_ctd_depth	<i>Get max CTD depth</i>
---------------	--------------------------

---

**Description**

Get the maximum level depth from a list of CellTypeDataset objects.

**Usage**

```
max_ctd_depth(CTD_list)
```

**Arguments**

CTD_list	A list of CellTypeDataset objects.
----------	------------------------------------

**Value**

integer

---

merged_ewce	<i>Multiple EWCE results from multiple studies</i>
-------------	--

---

**Description**

merged\_ewce combines enrichment results from multiple studies targetting the same scientific problem

**Usage**

```
merged_ewce(results, reps = 100)
```

**Arguments**

results	a list of EWCE results generated using <a href="#">add_res_to_merging_list</a> .
reps	Number of random gene lists to generate (Default=100 but should be >=10,000 for publication-quality results).

**Value**

dataframe in which each row gives the statistics (p-value, fold change and number of standard deviations from the mean) associated with the enrichment of the stated cell type in the gene list.

**Examples**

```

# Load the single cell data
ctd <- ewceData::ctd()

# Use 3 bootstrap lists for speed, for publishable analysis use >10000
reps <- 3
# Use 5 up/down regulated genes (thresh) for speed, default is 250
thresh <- 5

# Load the data
tt_alzh_BA36 <- ewceData::tt_alzh_BA36()
tt_alzh_BA44 <- ewceData::tt_alzh_BA44()

# Run EWCE analysis
tt_results_36 <- EWCE::ewce_expression_data(
  sct_data = ctd,
  tt = tt_alzh_BA36,
  thresh = thresh,
  annotLevel = 1,
  reps = reps,
  ttSpecies = "human",
  sctSpecies = "mouse"
)
tt_results_44 <- EWCE::ewce_expression_data(
  sct_data = ctd,
  tt = tt_alzh_BA44,
  thresh = thresh,
  annotLevel = 1,
  reps = reps,
  ttSpecies = "human",
  sctSpecies = "mouse"
)

# Fill a list with the results
results <- EWCE::add_res_to_merging_list(tt_results_36)
results <- EWCE::add_res_to_merging_list(tt_results_44, results)

# Perform the merged analysis
# For publication reps should be higher
merged_res <- EWCE::merged_ewce(
  results = results,
  reps = 2
)
print(merged_res)

```

merge\_ctd

*Merge multiple CellTypeDataset references***Description**

Import CellTypeDataset (CTD) references from a remote repository, standardize each, and then merge into one CTD. Optionally, can return these as a merged [SingleCellExperiment](#).

**Usage**

```
merge_ctd(
  CTD_list,
  save_dir = tempdir(),
  standardise_CTD = FALSE,
  as_SCE = FALSE,
  gene_union = TRUE,
  merge_levels = seq(1, 5),
  save_split_SCE = FALSE,
  save_split_CTD = FALSE,
  save_merged_SCE = TRUE,
  force_new_quantiles = FALSE,
  numberOfBins = 40,
  as_sparse = TRUE,
  as_DelayedArray = FALSE,
  verbose = TRUE,
  ...
)
```

**Arguments**

CTD_list	(Named) list of CellTypeDatasets.
save_dir	The directory to save merged files in.
standardise_CTD	Whether to run <code>standardise_ctd</code> .
as_SCE	If TRUE (default), returns the merged results as a named list of <a href="#">SingleCellExperiments</a> . If FALSE, returns as a CTD object.
gene_union	Whether to take the gene union or intersection when merging matrices (mean_exp, specificity, etc.).
merge_levels	Which CTD levels you want to merge. Can be a single value (e.g. <code>merge_levels=5</code> ) or a list c(e.g. <code>merge_levels=c(1:5)</code> ). If some CTD don't have the same number of levels, the maximum level depth available in that CTD will be used instead.
save_split_SCE	Whether to save individual SCE files in the subdirectory <code>standardized_CTD_SCE</code> .
save_split_CTD	Whether to save individual CTD files in the subdirectory <code>standardized_CTD</code> .
save_merged_SCE	Save the final merged SCE object, or simply to return it.
force_new_quantiles	If specificity quantiles matrix already exists, create a new one.
numberOfBins	Number of bins to compute specificity quantiles with.
as_sparse	Convert matrices to sparse matrix.
as_DelayedArray	Convert matrices to DelayedArray.
verbose	Print messages.
...	Additional arguments to be passed to <code>standardise_ctd</code> .

**Value**

List of CellTypeDatasets or SingleCellExperiments.

**Examples**

```
## Let's pretend these are different CTD datasets
ctd1 <- ewceData::ctd()
ctd2 <- ctd1
CTD_list <- list(ctd1, ctd2)
CTD_merged <- EWCE::merge_ctd(CTD_list = CTD_list)
```

merge\_sce

*Merge multiple SingleCellExperiment objects***Description**

Merge several SingleCellExperiment (SCE) objects from different batches/experiments. Extracted from the [scMerge](#) package.

**Usage**

```
merge_sce(
  sce_list,
  method = "intersect",
  cut_off_batch = 0.01,
  cut_off_overall = 0.01,
  use_assays = NULL,
  colData_names = NULL,
  batch_names = NULL,
  verbose = TRUE
)
```

**Arguments**

sce_list	A list contains the SingleCellExperiment Object from each batch.
method	A string indicates the method of combining the gene expression matrix, either union or intersect. Default to intersect. union only supports matrix class.
cut_off_batch	A numeric vector indicating the cut-off for the proportion of a gene is expressed within each batch.
cut_off_overall	A numeric vector indicating the cut-off for the proportion of a gene is expressed overall data.
use_assays	A string vector indicating the expression matrices to be combined. The first assay named will be used to determine the proportion of zeros.
colData_names	A string vector indicating the colData that are combined.
batch_names	A string vector indicating the batch names for the output SCE object.
verbose	Print messages.

**Value**

A SingleCellExperiment object with the list of SCE objects combined.

**Author(s)**

Yingxin Lin (modified by Brian Schilder)

**Source**

[scMerge](#).

**Examples**

```
ctd <- ewceData::ctd()
sce_list <- EWCE::ctd_to_sce(object = ctd)
sce_combine <- merge_sce(sce_list = sce_list)
```

---

merge_sce_list	<i>Merge of list of SingleCellExperiment objects</i>
----------------	--

---

**Description**

Merge of list of CellTypeDatasets stored as [SingleCellExperiment](#) objects into one [SingleCellExperiment](#) object.

**Usage**

```
merge_sce_list(
  SCE_lists = NULL,
  parent_folder = NULL,
  pattern = ".rds$",
  merge_levels = seq(1, 5),
  gene_union = TRUE,
  as_sparse = TRUE,
  as_DelayedArray = TRUE,
  verbose = TRUE
)
```

**Arguments**

SCE_lists	A list of <a href="#">SingleCellExperiment</a> objects.
parent_folder	Can supply the path to a folder instead of SCE_lists. Any <a href="#">SingleCellExperiment</a> objects matching pattern will be imported.
merge_levels	CellTypeDataset levels to merge.

**Value**

[SingleCellExperiment](#)

---

merge_two_expfiles	<i>Merge two exp files</i>
--------------------	----------------------------

---

### Description

merge\_two\_expfiles Used to combine two single cell type datasets.

### Usage

```
merge_two_expfiles(
  exp1,
  exp2,
  annot1,
  annot2,
  name1 = "",
  name2 = "",
  as_sparse = TRUE,
  as_DelayedArray = FALSE,
  verbose = TRUE
)
```

### Arguments

exp1	Numerical expression matrix for dataset1 with row for each gene and column for each cell. Row names are gene symbols. Column names are cell IDs which can be cross referenced against the annot data frame.
exp2	Numerical expression matrix for dataset2 with row for each gene and column for each cell. Row names are gene symbols. Column names are cell IDs which can be cross referenced against the annot data frame.
annot1	Annotation data frame for dataset1 which contains three columns at least: cell_id, level1class and level2class
annot2	Annotation data frame for dataset2 which contains three columns at least: cell_id, level1class and level2class
name1	Name used to refer to dataset 1. Leave blank if it's already a merged dataset.
name2	Name used to refer to dataset 2. Leave blank if it's already a merged dataset.
as_sparse	Convert the merged exp to a sparse matrix.
as_DelayedArray	Convert the merged exp to a DelayedArray.
verbose	Print messages.

### Value

List containing merged exp and annot.

**Examples**

```

cortex_mrna <- ewceData::cortex_mrna()
exp1 <- cortex_mrna$exp[, 1:50]
exp2 <- cortex_mrna$exp[, 51:100]
annot1 <- cortex_mrna$annot[1:50, ]
annot2 <- cortex_mrna$annot[51:100, ]
merged_res <- EWCE::merge_two_expfiles(
  exp1 = exp1,
  exp2 = exp2,
  annot1 = annot1,
  annot2 = annot2,
  name1 = "dataset1",
  name2 = "dataset2"
)

```

---

messenger	<i>Print messages</i>
-----------	-----------------------

---

**Description**

Print messages with option to silence.

**Usage**

```
messenger(..., v = TRUE)
```

**Arguments**

...	Message input.
v	Whether to print messages.

**Value**

Null output.

---

message_parallel	<i>Print messages</i>
------------------	-----------------------

---

**Description**

Print messages even from within parallelised functions.

**Usage**

```
message_parallel(...)
```

**Arguments**

...	Message input.
-----	----------------

**Value**

Null output.

---

myScalesComma	myScalesComma
---------------	---------------

---

**Description**

Adjusts **ggplot2** label display. See [comma](#) for details. Support function for [plot\\_log\\_bootstrap\\_distributions](#).

**Usage**

```
myScalesComma(x)
```

**Value**

Numeric vector

---

plot_ctd	<i>Plot CellTypeData metrics</i>
----------	----------------------------------

---

**Description**

Plot *CellTypeData* metrics such as mean\_exp, specificity and/or specificity\_quantiles.

**Usage**

```
plot_ctd(ctd, genes, level = 1, metric = "specificity", show_plot = TRUE)
```

**Arguments**

ctd	CellTypeDataset.
genes	Which genes in ctd to plot.
level	Annotation level in ctd to plot.
metric	Which metric in the ctd to plot: <ul style="list-style-type: none"> <li>• "mean_exp"</li> <li>• "specificity"</li> <li>• "specificity_quantiles"</li> </ul>
show_plot	Whether to print the plot or simply return it.

**Value**

ggplot object.

**Examples**

```
ctd <- ewceData::ctd()
plt <- EWCE::plot_ctd(ctd, genes = c("ApoE", "Gfap", "Gapdh"))
```

plot\_log\_bootstrap\_distributions

*Plot log bootstrap distributions*

---

### Description

Plot results of [generate\\_bootstrap\\_plots\\_for\\_transcriptome](#).

### Usage

```
plot_log_bootstrap_distributions(  
  dat,  
  exp_mats,  
  cc,  
  hit_exp,  
  tag,  
  listFileName,  
  graph_theme,  
  save_dir = file.path(tempdir(), paste0("BootstrapPlots", "_for_transcriptome")),  
  height = 3.5,  
  width = 3.5  
)
```

### Value

Null result.

---

plot\_with\_bootstrap\_distributions

*Plot with bootstrap distributions*

---

### Description

Plot results of [generate\\_bootstrap\\_plots\\_for\\_transcriptome](#).

### Usage

```
plot_with_bootstrap_distributions(  
  exp_mats,  
  cc,  
  hit_exp,  
  tag,  
  listFileName,  
  graph_theme,  
  save_dir = file.path(tempdir(), paste0("BootstrapPlots", "_for_transcriptome")),  
  height = 3.5,  
  width = 3.5  
)
```

**Value**

Null result.

---

prep.dendro	<i>prep.dendro</i>
-------------	--------------------

---

**Description**

prep\_dendro adds a dendrogram to a CellTypeDataset (CTD).

**Usage**

```
prep.dendro(ctdIN)
```

**Arguments**

ctdIN	A single annotLevel of a ctd, i.e. ctd[[1]] (the function is intended to be used via apply).
-------	--

**Value**

A CellTypeDataset with dendrogram plotting info added.

---

prepare_genesize_control_network	<i>Prepare genesize control network</i>
----------------------------------	---

---

**Description**

prepare\_genesize\_control\_network takes a gene list and finds semi-randomly selected gene lists which are matched for gene length and GC content.

**Usage**

```
prepare_genesize_control_network(
  hits,
  bg = NULL,
  reps = 10000,
  no_cores = 1,
  sctSpecies = NULL,
  genelistSpecies = NULL,
  verbose = TRUE,
  localHub = FALSE
)
```

**Arguments**

hits	List of gene symbols containing the target gene list. Will automatically be converted to human gene symbols if geneSizeControl=TRUE.
bg	List of gene symbols containing the background gene list (including hit genes). If bg=NULL, an appropriate gene background will be created automatically.
reps	Number of gene lists to sample.
no_cores	Number of cores to parallelise bootstrapping reps over.
sctSpecies	Species that sct_data is currently formatted as (no longer limited to just "mouse" and "human"). See <a href="#">list_species</a> for all available species.
genelistSpecies	Species that hits genes came from (no longer limited to just "mouse" and "human"). See <a href="#">list_species</a> for all available species.
verbose	Print messages.
localHub	If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.

**Value**

A list containing three data frames:

- hits: Array of HGNC symbols containing the hit genes. May be slightly reduced if gene length / GC content could not be found for all genes.
- list\_network: The control gene lists as a data frame of HGNC symbols

---

```
prepare_tt
```

*Prepare differential gene expression table*

---

**Description**

Prepare differential gene expression table for [generate\\_bootstrap\\_plots\\_for\\_transcriptome](#) or [ewce\\_expression\\_data](#).

**Usage**

```
prepare_tt(
  tt,
  tt_genecol = NULL,
  ttSpecies,
  output_species,
  method = "homologene",
  verbose = TRUE
)
```

**Arguments**

tt	Differential expression table. Can be output of <a href="#">topTable</a> function. Minimum requirement is that one column stores a metric of increased/decreased expression (i.e. log fold change, t-statistic for differential expression etc) and another contains gene symbols.
ttSpecies	The species the differential expression table was generated from.
output_species	Species to convert sct_data and hits to (Default: "human"). See <a href="#">list_species</a> for all available species.
method	R package to use for gene mapping: "gproufiter" Slower but more species and genes. "homologene" Faster but fewer species and genes. "babelgene" Faster but fewer species and genes. Also gives consensus scores for each gene mapping based on a several different data sources.
verbose	Print messages.

**Value**

List of 3 items

---

prep_dendro	<i>Prepare dendrogram</i>
-------------	---------------------------

---

**Description**

prep\_dendro adds a dendrogram to a CellTypeDataset (CTD).

**Usage**

```
prep_dendro(ctdIN, expand = c(0, 0.66))
```

**Arguments**

ctdIN	A single annotLevel of a ctd, i.e. ctd[[1]] (the function is intended to be used via apply).
-------	--

**Value**

A CellTypeDataset with dendrogram plotting info added.

---

report_dge	<i>Report DGE</i>
------------	-------------------

---

**Description**

Report differential gene expression (DGE) results

**Usage**

```
report_dge(exp, keep_genes, adj_pval_thresh = 0.05, verbose = TRUE)
```

**Arguments**

exp	Gene expression matrix.
keep_genes	Genes kept after DGE.
adj_pval_thresh	Minimum differential expression significance that a gene must demonstrate across level2annot (i.e. cell types).
verbose	Print messages. #' @inheritParams orthogene::convert_orthologs

**Value**

Null output.

---

report_results	<i>Report cell type enrichment results</i>
----------------	--

---

**Description**

Report cell type enrichment results generated by [bootstrap\\_enrichment\\_test](#).

**Usage**

```
report_results(results, sig_thresh = 0.05, verbose = TRUE)
```

**Value**

NULL output.

---

run\_deseq2

*Run DGE: DESeq2*


---

**Description**

Run Differential Gene Expression with **DESeq2**.

**Usage**

```
run_deseq2(exp, level2annot, test = "LRT", no_cores = 1, verbose = TRUE, ...)
```

**Arguments**

exp	Expression matrix with gene names as rownames.
level2annot	Array of cell types, with each sequentially corresponding a column in the expression matrix.
test	either "Wald" or "LRT", which will then use either Wald significance tests (defined by <code>nbinomWaldTest</code> ), or the likelihood ratio test on the difference in deviance between a full and reduced model formula (defined by <code>nbinomLRT</code> )
no_cores	Number of cores to parallelise across. Set to NULL to automatically optimise.
verbose	Print messages. #' @inheritParams orthogene::convert_orthologs
...	Additional arguments to be passed to <code>gorth</code> or <code>homologene</code> .

*NOTE:* To return only the most "popular" interspecies ortholog mappings, supply `mthreshold=1` here AND set `method="gprofiler"` above. This procedure tends to yield a greater number of returned genes but at the cost of many of them not being true biological 1:1 orthologs.

For more details, please see [here](#).

**Value**

DESeq results

---

run\_limma

*Run DGE: limma*


---

**Description**

Run Differential Gene Expression with **limma**.

**Usage**

```
run_limma(exp, level2annot, mtc_method = "BH", verbose = TRUE, ...)
```

**Arguments**

exp	Expression matrix with gene names as rownames.
level2annot	Array of cell types, with each sequentially corresponding a column in the expression matrix.
mtc_method	Multiple-testing correction method used by DGE step. See <a href="#">p.adjust</a> for more details.
verbose	Print messages. #' @inheritParams orthogene::convert_orthologs
...	Additional arguments to be passed to <a href="#">gorth</a> or <a href="#">homologene</a> .

*NOTE:* To return only the most "popular" interspecies ortholog mappings, supply `mtthreshold=1` here AND set `method="gprofiler"` above. This procedure tends to yield a greater number of returned genes but at the cost of many of them not being true biological 1:1 orthologs.

For more details, please see [here](#).

**Value**

limma results.

---

run\_mast

*Run DGE: MAST*

---

**Description**

Run Differential Gene Expression with **MAST**.

**Usage**

```
run_mast(exp, level2annot, test = "LRT", mtc_method = "BH", no_cores = 1, ...)
```

**Arguments**

exp	Expression matrix with gene names as rownames.
level2annot	Array of cell types, with each sequentially corresponding a column in the expression matrix.
mtc_method	Multiple-testing correction method used by DGE step. See <a href="#">p.adjust</a> for more details.
no_cores	Number of cores to parallelise DGE across.
...	Additional arguments to be passed to <a href="#">gorth</a> or <a href="#">homologene</a> .

*NOTE:* To return only the most "popular" interspecies ortholog mappings, supply `mtthreshold=1` here AND set `method="gprofiler"` above. This procedure tends to yield a greater number of returned genes but at the cost of many of them not being true biological 1:1 orthologs.

For more details, please see [here](#).

**Value**

MAST results

**Source**

[MAST tutorial](#)

---

sce_lists_apply	<i>sce_lists_apply</i>
-----------------	------------------------

---

**Description**

Support function for `EWCE::merge_sce_list`.

**Usage**

```
sce_lists_apply(  
  SCE_lists,  
  return_genes = FALSE,  
  level = 2,  
  as_matrix = FALSE,  
  as_DelayedArray = FALSE  
)
```

**Value**

List of `SingleCellExperiments`.

---

sce_merged_apply	<i>sce_merged_apply</i>
------------------	-------------------------

---

**Description**

Merge a list of `SingleCellExperiments`.

**Usage**

```
sce_merged_apply(SCE_merged, as_sparse = TRUE, as_DelayedArray = FALSE)
```

**Value**

Merged `SingleCellExperiment`.

---

sct\_normalize                      *Normalize expression matrix*

---

### Description

Normalize expression matrix by accounting for library size. Uses **sctransform**.

### Usage

```
sct_normalize(exp, as_sparse = TRUE, verbose = TRUE)
```

### Arguments

exp	Gene x cell expression matrix.
as_sparse	Convert exp to sparse matrix.
verbose	Print messages.

### Value

Normalised expression matrix.

### Examples

```
cortex_mrna <- ewceData::cortex_mrna()
exp_sct_normed <- EWCE::sct_normalize(exp = cortex_mrna$exp[1:300, ])
```

---

standardise\_ctd                      *Convert a CellTypeDataset into standardized format*

---

### Description

This function will take a CTD, drop all genes without 1:1 orthologs with the output\_species ("human" by default), convert the remaining genes to gene symbols, assign names to each level, and convert all matrices to sparse matrices and/or DelayedArray.

### Usage

```
standardise_ctd(
  ctd,
  dataset,
  input_species = NULL,
  output_species = "human",
  sctSpecies_origin = input_species,
  non121_strategy = "drop_both_species",
  method = "homologene",
  force_new_quantiles = TRUE,
  force_standardise = FALSE,
  remove_unlabeled_clusters = FALSE,
  numberOfBins = 40,
```

```

    keep_annot = TRUE,
    keep_plots = TRUE,
    as_sparse = TRUE,
    as_DelayedArray = FALSE,
    rename_columns = TRUE,
    make_columns_unique = FALSE,
    verbose = TRUE,
    ...
)

```

## Arguments

ctd	Input CellTypeData.
dataset	CellTypeData. name.
input_species	Which species the gene names in exp come from. See <a href="#">list_species</a> for all available species.
output_species	Which species' genes names to convert exp to. See <a href="#">list_species</a> for all available species.
sctSpecies_origin	Species that the sct_data originally came from, regardless of its current gene format (e.g. it was previously converted from mouse to human gene orthologs). This is used for computing an appropriate background.
non121_strategy	How to handle genes that don't have 1:1 mappings between input_species:output_species. Options include: <ul style="list-style-type: none"> <li>"drop_both_species" or "dbs" or 1 Drop genes that have duplicate mappings in either the input_species or output_species (<i>DEFAULT</i>).</li> <li>"drop_input_species" or "dis" or 2 Only drop genes that have duplicate mappings in the input_species.</li> <li>"drop_output_species" or "dos" or 3 Only drop genes that have duplicate mappings in the output_species.</li> <li>"keep_both_species" or "kbs" or 4 Keep all genes regardless of whether they have duplicate mappings in either species.</li> <li>"keep_popular" or "kp" or 5 Return only the most "popular" interspecies ortholog mappings. This procedure tends to yield a greater number of returned genes but at the cost of many of them not being true biological 1:1 orthologs.</li> <li>"sum", "mean", "median", "min" or "max" When gene_df is a matrix and gene_output="rowname" these options will aggregate many-to-one gene mappings (input_species-to-output_species) after dropping any duplicate genes in the output_species.</li> </ul>
method	R package to use for gene mapping: <ul style="list-style-type: none"> <li>"gprofiler" Slower but more species and genes.</li> <li>"homologene" Faster but fewer species and genes.</li> <li>"babelgene" Faster but fewer species and genes. Also gives consensus scores for each gene mapping based on a several different data sources.</li> </ul>
force_new_quantiles	By default, quantile computation is skipped if they have already been computed. Set =TRUE to override this and generate new quantiles.

**force\_standardise** If ctd has already been standardised, whether to rerun standardisation anyway (Default: FALSE).

**remove\_unlabeled\_clusters** Remove any samples that have numeric column names.

**numberOfBins** Number of non-zero quantile bins.

**keep\_annot** Keep the column annotation data if provided.

**keep\_plots** Keep the dendrograms if provided.

**as\_sparse** Convert to sparse matrix.

**as\_DelayedArray** Convert to DelayedArray.

**rename\_columns** Remove replace\_chars from column names.

**make\_columns\_unique** Rename each columns with the prefix `dataset.species.celltype`.

**verbose** Print messages. Set `verbose=2` if you want to print all messages from internal functions as well.

**...** Arguments passed on to [orthogene::convert\\_orthologs](#)

**gene\_df** Data object containing the genes (see `gene_input` for options on how the genes can be stored within the object).  
 Can be one of the following formats:

- `matrix` A sparse or dense matrix.
- `data.frame` A `data.frame`, `data.table`, or `tibble`.
- `list` A list or character vector.

Genes, transcripts, proteins, SNPs, or genomic ranges can be provided in any format (HGNC, Ensembl, RefSeq, UniProt, etc.) and will be automatically converted to gene symbols unless specified otherwise with the ... arguments.

*Note:* If you set `method="homologene"`, you must either supply genes in gene symbol format (e.g. "Sox2") OR set `standardise_genes=TRUE`.

**gene\_input** Which aspect of `gene_df` to get gene names from:

- `"rownames"` From row names of `data.frame/matrix`.
- `"colnames"` From column names of `data.frame/matrix`.
- `<column name>` From a column in `gene_df`, e.g. `"gene_names"`.

**gene\_output** How to return genes. Options include:

- `"rownames"` As row names of `gene_df`.
- `"colnames"` As column names of `gene_df`.
- `"columns"` As new columns `"input_gene"`, `"ortholog_gene"` (and `"input_gene_standard"` if `standardise_genes=TRUE`) in `gene_df`.
- `"dict"` As a dictionary (named list) where the names are `input_gene` and the values are `ortholog_gene`.
- `"dict_rev"` As a reversed dictionary (named list) where the names are `ortholog_gene` and the values are `input_gene`.

**standardise\_genes** If TRUE AND `gene_output="columns"`, a new column `"input_gene_standard"` will be added to `gene_df` containing standardised HGNC symbols identified by [gorth](#).

**drop\_nonorths** Drop genes that don't have an ortholog in the output\_species.  
**agg\_fun** Aggregation function passed to [aggregate\\_mapped\\_genes](#). Set to NULL to skip aggregation step (default).  
**mthreshold** Maximum number of ortholog names per gene to show. Passed to [gorth](#). Only used when method="gprofiler" (*DEFAULT*: Inf).  
**sort\_rows** Sort gene\_df rows alphanumerically.  
**gene\_map** A [data.frame](#) that maps the current gene names to new gene names. This function's behaviour will adapt to different situations as follows:  
**gene\_map=<data.frame>** When a data.frame containing the gene key:value columns (specified by **input\_col** and **output\_col**, respectively) is provided, this will be used to perform aggregation/expansion.  
**gene\_map=NULL and input\_species!=output\_species** A gene\_map is automatically generated by [map\\_orthologs](#) to perform inter-species gene aggregation/expansion.  
**gene\_map=NULL and input\_species==output\_species** A gene\_map is automatically generated by [map\\_genes](#) to perform within-species gene symbol standardization and aggregation/expansion.  
**input\_col** Column name within gene\_map with gene names matching the row names of X.  
**output\_col** Column name within gene\_map with gene names that you wish you map the row names of X onto.

### Value

Standardised CellTypeDataset.

### Examples

```

ctd <- ewceData::ctd()
ctd_std <- EWCE::standardise_ctd(
  ctd = ctd,
  input_species = "mouse",
  dataset = "Zeisel2016"
)
  
```

---

theme\_graph

*Get graph theme*

---

### Description

Get graph theme for plots created by [generate\\_bootstrap\\_plots\\_for\\_transcriptome](#).

### Usage

```
theme_graph()
```

### Value

ggplot2 graph theme.

---

to_dataframe	<i>Convert object to data.frame</i>
--------------	-------------------------------------

---

**Description**

Convert a variety of object types to data.frame format.

**Usage**

```
to_dataframe(X, verbose = TRUE)
```

**Arguments**

X	Object.
verbose	Print messages.

**Value**

[data.frame](#).

---

to_delayed_array	<i>Convert object to DelayedArray</i>
------------------	---------------------------------------

---

**Description**

Convert a variety of object types to [DelayedArray](#) format.

**Usage**

```
to_delayed_array(exp, as_DelayedArray = TRUE, verbose = TRUE)
```

**Arguments**

exp	Object.
as_DelayedArray	Whether to convert exp to <a href="#">DelayedArray</a> .
verbose	Print messages.

**Value**

[DelayedArray](#).

---

to_sparse_matrix	<i>Convert object to sparse matrix</i>
------------------	--

---

**Description**

Convert a variety of object types to sparse matrix format.

**Usage**

```
to_sparse_matrix(exp, as_sparse = TRUE, verbose = TRUE)
```

**Arguments**

exp	Object.
as_sparse	Whether to convert exp to sparse matrix
verbose	Print messages.

**Value**

Sparse matrix.

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