

# Package ‘singIST’

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and a human condition

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*add\_missing\_psb\_rows* *Ensure all celltype-sample combinations are present in the pseudobulkmatrix*

**Description**

Ensure all celltype-sample combinations are present in the pseudobulkmatrix

**Usage**

`add_missing_psb_rows(mat, celltypes, sample_ids)`

**Arguments**

- `mat` A numeric matrix with rownames in the form “celltype\_sample”.
- `celltypes` Character vector of the celltypes you intend to include (in the exact order of `object@superpathway_info@celltypes`).
- `sample_ids` Character vector of all sample identifiers (in the order of `rownames(object@pseudobulk_lognorm)` split by “\_”).

**Value**

A numeric matrix with `length(celltypes) * length(sample_ids)` rows, in the canonical `paste(celltypes, sample_ids, sep = "_")` order, where newly added rows are filled with `NA_real_`.

asmbPLSDA.cv.kcv

*K-fold × Repeated Cross-Validation for asmbPLS-DA***Description**

Implements stratified K-fold cross-validation with repetitions, mirroring the structure of `asmbPLSDA.cv.loo` but using `K` `k` and `ncv` instead of LOO.

**Usage**

```
asmbPLSDA.cv.kcv(
  X.matrix,
  Y.matrix,
  PLS_term = 2,
  X.dim,
  quantile.comb.table,
  k = 4,
  ncv = 10,
  outcome.type = c("binary", "multiclass"),
  Method = NULL,
  measure = "B_accuracy",
  parallel = FALSE,
  expected.measure.increase = 0.005,
  center = TRUE,
  scale = TRUE,
  maxiter = 100
)
```

**Arguments**

<code>X.matrix</code>	Predictor matrix (n×p)
<code>Y.matrix</code>	Response one-hot matrix (n×q)
<code>PLS_term</code>	Integer: maximum number of PLS components
<code>X.dim</code>	Vector: feature counts per block
<code>quantile.comb.table</code>	Matrix (C×length(X.dim)): quantile combinations
<code>k</code>	Integer: number of CV k (K)
<code>ncv</code>	Integer: number of ncv
<code>outcome.type</code>	"binary" or "multiclass"
<code>Method</code>	Prediction method
<code>measure</code>	"B_accuracy", "accuracy", "precision", "recall", "F1"
<code>parallel</code>	Logical: TRUE to parallelize per-fold
<code>expected.measure.increase</code>	Numeric: min performance gain to add PLS

center	Logical: center predictors
scale	Logical: scale predictors
maxiter	Integer: max iterations for asmbPLSDA.fit

**Value**

A list with:

quantile_table_CV	Matrix (PLS_term $\times$ (blocks + metrics)) of optimal quantiles and CV metrics
optimal_nPLS	Integer: selected number of PLS components
splits	List of length (k*ncv) of train/validation splits

**Examples**

```
# example code
file <- system.file("extdata", "example_superpathway_input.rda",
package = "singIST")
load(file)
data <- example_superpathway_input
matrices <- matrixToBlock(data)
X.matrix <- matrices$block_predictor
Y.matrix <- matrices$matrix_response
X.dim <- matrices$block_dim
quantile.comb.table <- data$hyperparameters_info$quantile_comb_table
quantile.comb.table <- rbind(quantile.comb.table, c(0.1, 0.2)) # Add 2 cases
outcome.type <- data$hyperparameters_info$outcome_type
asmbPLSDA.cv.kcv(X.matrix, Y.matrix, PLS_term = 1,
X.dim,quantile.comb.table,Method = NULL, measure = "B_accuracy",
parallel = TRUE, outcome.type = outcome.type,
expected.measurement.increase = 0.005, center = TRUE, scale = TRUE,
maxiter = 100)
```

---

asmbPLSDA.cv.loo      *Leave-one-out Cross-validation*

---

**Description**

Leave-one-out Cross-validation

**Usage**

```
asmbPLSDA.cv.loo(
  X.matrix,
  Y.matrix,
  PLS_term = 1,
  X.dim,
  quantile.comb.table,
```

```

outcome.type = c("binary", "multiclass"),
Method = NULL,
measure = "B_accuracy",
parallel = FALSE,
expected.measure.increase = 0.005,
center = TRUE,
scale = TRUE,
maxiter = 100
)

```

### Arguments

X.matrix	Predictor block matrix from matrixToBlock
Y.matrix	Response matrix from matrixToBlock
PLS_term	An integer with the number of PLS components to use passed from hyperparameter list
X.dim	A list with the observed gene set size for each cell type from matrixToBlock
quantile.comb.table	A matrix with the quantile comb table passed from hyperparameters list object
outcome.type	A character indicating binary or multiclass passed from hyperparameters list object
Method	A parameter passed from fitOptimal
measure	A parameter passed from fitOptimal
parallel	A parameter passed from fitOptimal
expected.measure.increase	A parameter passed from fitOptimal
center	A parameter passed from fitOptimal
scale	A parameter passed from fitOptimal
maxiter	A parameter passed from fitOptimal

### Value

A list containing the optimal quantiles for each PLS component and the optimal number of PLS components.

### Examples

```

file <- system.file("extdata", "example_superpathway_input.rda",
package = "singIST")
load(file)
data <- example_superpathway_input
matrices <- matrixToBlock(data)
X.matrix <- matrices$block_predictor
Y.matrix <- matrices$matrix_response
X.dim <- matrices$block_dim
quantile.comb.table <- data$hyperparameters_info$quantile_comb_table

```

```

outcome.type <- data$hyperparameters_info$outcome_type
asmbPLSDA.cv.loo(X.matrix, Y.matrix, PLS_term = 1, X.dim, quantile.comb.table,
Method = NULL, measure = "B_accuracy", parallel = TRUE,
outcome.type = outcome.type, expected.measure.increase = 0.005,
center = TRUE, scale = TRUE, maxiter = 100)

```

---

biological\_link\_function

*Biological link function*


---

### Description

Maps the organism information in mapping organism list and superpathway fit model list to obtain the "singIST treated samples" with the simulated human. The biological link function involves the cell type mapping, orthology mapping and fold change computation.

### Usage

```

biological_link_function(
  object,
  model_object,
  object_gene_identifiers = "external_gene_name",
  model_species = "hsapiens",
  FC_list = NULL,
  ...
)

```

### Arguments

object	A mapping organism list with the disease model data
model_object	A superpathway fit model list with the fitted model
object_gene_identifiers	Annotation of gene identifiers used in object. By default external_gene_name. If NULL <a href="#">orthology_mapping</a> infers the gene identifiers of object, note this may add execution time.
model_species	Organism for which model_object has been trained. By default hsapiens.
FC_list	Optional parameter with list of matrices containing Fold Changes provided by the user. If such list is provided, logFC will not be computed via <a href="#">diff_expressed</a> and the list input will be used instead. The list length must match the number and order of human cell types modelled. Each element of the list must be a data.frame whose columns are: "p_value" p-value of test, "avg_log2FC" the log2FC provided, "pct.1" percent of cells where the gene is expressed in base class, "pct.2" percent of cells where the gene is expressed in target class, "p_val_adj" adjusted p-value. Rownames should contain the gene names. Note that log2FC provided should be comparable to log2FC computed in asmbPLSDA model. log2FC should be reported as descriptive point estimates of mean difference of log2 normalized expression values.
...	Other parameters to pass onto <a href="#">diff_expressed</a>

**Value**

A list with; ortholog gene sets as returned by [orthology\\_mapping](#); a list with the Fold Changes used; singIST treated samples as returned by [singIST\\_treat](#)

**Examples**

```
file <- system.file("extdata", "example_mapping_organism.rda",
package = "singIST")
load(file)
data_organism <- example_mapping_organism
file <- system.file("extdata", "example_superpathway_fit_model.rda",
package = "singIST")
load(file)
data_model <- example_superpathway_fit_model
biological_link_function(data_organism, data_model)
```

---

celltype_mapping	<i>Cell type mapping</i>
------------------	--------------------------

---

**Description**

For a given mapping organism list it updates the variable `celltype_cluster` so that each element of it is updated accordingly to the mapped cell types as indicated in `object$celltype_mapping`.

**Usage**

```
celltype_mapping(object)
```

**Arguments**

`object`            A mapping organism list

**Value**

A mapping organism list with the `object$counts` slot updated, for the variable `celltype_cluster` with the cell types according to the mapping defined in `object$celltype_mapping`.

**Examples**

```
file <- system.file("extdata", "example_mapping_organism.rda",
package = "singIST")
load(file)
data <- example_mapping_organism
new_object <- celltype_mapping(data)
new_object$counts$celltype_cluster
```

---

celltype_recap	<i>Derive cell type recapitulation</i>
----------------	--

---

### Description

Derive cell type recapitulation

### Usage

```
celltype_recap(model_object, data_original, data_singIST)
```

### Arguments

model_object	A superpathway fit model list passed from <a href="#">singISTrecapitulations</a>
data_original	A matrix with the cell type contributions as returned by <a href="#">derive_contributions</a> for the non-singIST treated samples, passed from <a href="#">singISTrecapitulations</a>
data_singIST	A matrix with the cell type contributions as returned by <a href="#">derive_contributions</a> for the singIST treated samples, passed from <a href="#">singISTrecapitulations</a>

### Value

A data.frame object with the variables: pathway name, celltype with the cell type name, recapitulation with the cell type recapitulation, and reference with the cell type reference recapitulation

### Examples

```
file <- system.file("extdata", "example_superpathway_fit_model.rda",
  package = "singIST")
load(file)
model <- example_superpathway_fit_model
file <- system.file("extdata", "example_mapping_organism.rda",
  package = "singIST")
load(file)
mapped <- example_mapping_organism

singIST_samples <- biological_link_function(mapped, model)$singIST_samples
original <- derive_contributions(model, singIST_samples)
derived <- derive_contributions(model, model$model_fit$predictor_block)
celltype_recap(model, original$celltype_contribution,
  derived$celltype_contribution)
```

---

check\_fit\_model      *Validate superpathway fit model*

---

### Description

Checks that all provided fields for a fitted asmbPLS-DA model meet the expected properties:

- superpathway\_input must be a valid superpathway\_input object (validated with check\_superpathway\_input()).
- hyperparameters\_fit must be valid hyperparameters (validated with check\_hyperparameters()).
- model\_fit and model\_validation must be lists.

### Usage

```
check_fit_model(
  superpathway_input,
  hyperparameters_fit,
  model_fit,
  model_validation
)
```

### Arguments

superpathway\_input      List. A superpathway object created by create\_superpathway().

hyperparameters\_fit      List. A hyperparameters object created by create\_hyperparameters().

model\_fit      List. Fitted model details.

model\_validation      List. Validation metrics of the fitted model.

### Value

TRUE if all checks pass; otherwise, an error is thrown.

---

check\_hyperparameters      *Validate asmbPLS-DA hyperparameters*

---

### Description

Checks that all provided hyperparameters meet the expected properties:

- quantile\_comb\_table must be a matrix with at least one row.
- outcome\_type must be "binary" or "multiclass".
- number\_PLS must be an integer  $\geq 0$ .
- folds\_CV and repetition\_CV must be integers  $\geq 0$  (or NULL).

**Usage**

```
check_hyperparameters(
  quantile_comb_table,
  outcome_type,
  number_PLS,
  folds_CV,
  repetition_CV
)
```

**Arguments**

quantile_comb_table	Matrix. Quantile (lambda) sparsity values for CV.
outcome_type	Character. Either "binary" or "multiclass".
number_PLS	Integer. Maximum number of PLS components.
folds_CV	Integer or NULL. Number of folds for CV (default 5).
repetition_CV	Integer or NULL. Number of repetitions for CV (default 10).

**Value**

TRUE if all checks pass; otherwise, an error is thrown.

**Examples**

```
quantile_comb_table <- base::as.matrix(RcppAlgos::permuteGeneral(seq(0.05,
0.95, by = 0.50)))
check_hyperparameters(quantile_comb_table, "binary", 3L, 1L, 1L)
```

---

check\_mapping\_organism

*Validate mapping organism input*

---

**Description**

Validates that all provided fields for a mapping organism meet expected properties:

- organism, target\_class, base\_class are scalar characters.
- celltype\_mapping is a list with non-empty names; each entry is a character vector (length 0 allowed).
- counts is a Seurat or SingleCellExperiment object with metadata columns: 'class' and 'celltype\_cluster'.
- target\_class and base\_class exist in meta\$class and are different (after normalization).
- all clusters referenced in celltype\_mapping exist in meta\$celltype\_cluster.

**Usage**

```
check_mapping_organism(
  organism,
  target_class,
  base_class,
  celltype_mapping,
  counts
)
```

**Arguments**

organism            Character(1). Scientific Latin name of the organism.

target\_class        Character(1). Name of the target class for this organism.

base\_class          Character(1). Name of the base class for this organism.

celltype\_mapping   List. Mapping of cell types (keys) to cluster names (character vectors).

counts              Seurat or SingleCellExperiment. Contains scRNA-seq counts and metadata.

**Value**

TRUE if all checks pass; otherwise an informative error is thrown.

**Examples**

```
# Seurat example
counts <- SeuratObject::pbmc_small
colnames(slot(counts, "meta.data"))[1] <- "donor"
colnames(slot(counts, "meta.data"))[6] <- "class"
colnames(slot(counts, "meta.data"))[7] <- "celltype_cluster"
celltype_mapping <- list("T-cell" = c("T"), "Dendritic Cell" = character(0))
check_mapping_organism("Mus musculus", "g1", "g2", celltype_mapping, counts)
```

---

check\_pathway

*Validate pathway fields*

---

**Description**

Checks that all provided fields for a pathway meet the expected properties.

**Usage**

```
check_pathway(standard_name, dbsource, collection, subcollection)
```

**Arguments**

standard_name	Character. Pathway standard name from MsigDB.
dbsource	Character. Database source (KEGG, PID, REACTOME, BIOCARTA, WIKIPATHWAYS).
collection	Character. MsigDB collection (c2 or m2).
subcollection	Character. MsigDB subcollection (CP).

**Value**

TRUE if all checks pass; otherwise, an error is thrown.

**Examples**

```
check_pathway(
  standard_name = "KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION",
  dbsource = "KEGG",
  collection = "c2",
  subcollection = "CP"
)
```

---

check\_superpathway      *Validate superpathway gene sets*

---

**Description**

Checks that all provided fields for a superpathway meet the expected properties:

- pathway\_info must be a valid pathway (validated with check\_pathway()).
- celltypes must be a character vector with at least 2 elements.
- gene\_sets\_celltype must be a list (or NULL) with same length as celltypes.

**Usage**

```
check_superpathway(pathway_info, celltypes, gene_sets_celltype)
```

**Arguments**

pathway_info	List. A pathway object created by create_pathway().
celltypes	Character vector. Each element represents a cell type.
gene_sets_celltype	List of character vectors. Each element corresponds to gene sets for each cell type. Can be NULL.

**Value**

TRUE if all checks pass; otherwise, an error is thrown.

**Examples**

```
my_pathway <- create_pathway("KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION",
  "KEGG", "c2", "CP")
check_superpathway(my_pathway, c("T-cell", "Dendritic Cell"), list(c("IL4",
  "IL5"), c("IL13")))
```

---

```
check_superpathway_input
```

*Check superpathway input for asmbPLS-DA*

---

**Description**

Checks the validity of the inputs. This version assumes that `superpathway_info` and `hyperparameters_info` are plain lists validated by `check_superpathway()` and `check_hyperparameters()`.

**Usage**

```
check_superpathway_input(
  superpathway_info,
  hyperparameters_info,
  pseudobulk_lognorm,
  sample_id,
  sample_class,
  base_class,
  target_class
)
```

**Arguments**

<code>superpathway_info</code>	A list representing a superpathway object.
<code>hyperparameters_info</code>	A list representing a hyperparameters object.
<code>pseudobulk_lognorm</code>	A pseudobulk matrix (rows: "Celltype_Sampleid", cols: genes in "HGNC" format or similar).
<code>sample_id</code>	A character vector of sample ids.
<code>sample_class</code>	A character vector with the class of each sample.
<code>base_class</code>	A character scalar indicating the base class.
<code>target_class</code>	A character scalar indicating the target class.

**Value**

Invisibly returns TRUE if all checks pass; otherwise errors.

**Examples**

```

# ---- Superpathway info (list) ----
my_pathway <- create_pathway("KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION",
"KEGG", "c2", "CP")
celltypes <- c("T-cell", "Dendritic Cell")

my_superpathway <- create_superpathway(my_pathway, celltypes, list(c("IL4",
"IL5"), c("IL13")))
# ---- Hyperparameters info (list) ----
quantile_comb_table <- base::as.matrix(
  RcppAlgos::permuteGeneral(seq(0.05, 0.95, by = 0.50)),
  ncol = length(celltypes)
)

my_hyperparameters <- create_hyperparameters(
  quantile_comb_table = quantile_comb_table,
  outcome_type = "binary",
  number_PLS = as.integer(3),
  folds_CV = as.integer(1),
  repetition_CV = as.integer(1)
)

# ---- Pseudobulk + labels ----
sample_id <- c("AD1", "AD2", "HC1", "HC2")
sample_class <- c("AD", "AD", "HC", "HC")
base_class <- "HC"
target_class <- "AD"

pseudobulk_lognorm <- matrix(
  rnorm(length(celltypes) * length(sample_id)),
  nrow = length(celltypes) * length(sample_id),
  ncol = length(celltypes)
)
rownames(pseudobulk_lognorm) <- as.vector(t(outer(
  celltypes, sample_id, function(x, y) paste(x, y, sep = "_")
)))

check_superpathway_input(
  superpathway_info = my_superpathway,
  hyperparameters_info = my_hyperparameters,
  pseudobulk_lognorm = pseudobulk_lognorm,
  sample_id = sample_id,
  sample_class = sample_class,
  base_class = base_class,
  target_class = target_class
)

```

**Description**

Computes CIP and GIP metrics from a superpathway fit model list for the target class

**Usage**

```
CIP_GIP(object)
```

**Arguments**

object            A superpathway fit model list

**Value**

A list with the CIP and GIP metrics for all cell types. The metrics are computed for the target class.

**Examples**

```
file <- system.file("extdata", "example_superpathway_fit_model.rda",
  package = "singIST")
load(file)
data <- example_superpathway_fit_model
CIP_GIP(data)
```

---

CIP\_GIP\_test

*Cell and Gene Importance Projections statistical significance*

---

**Description**

Computes Cell and Gene Importance Projection observed distribution from fitted asmbPLSDA, and its associated null distributions by permuting the block of predictor matrices. Returns a pvalue of the Mann-Whitney Wilcoxon between the observed and null distribution for each CIP and GIP.

**Usage**

```
CIP_GIP_test(
  object,
  npermut = 100,
  maxiter = 100,
  type = c("jackknife", "subsampling"),
  nsubsampling = 100,
  ...
)
```

**Arguments**

object	A superpathway fit model list
npermut	Number of permutations on response block matrices
maxiter	An integer indicating the maximum number of iterations. If NULL the default is 100.
type	Either jackknife or subsampling. If jackknife then the CIP and GIP observed distribution is generated by a jackknife procedure. If subsampling the CIP and GIP observed distribution is generated by subsampling the number of samples without replacement, each subsample is guaranteed to contain at least 2 samples per class. If a LOOCV was performed or one has small sample size it is recommended to select jackknife, otherwise select subsampling.
nsubsampling	Number of subsamples to generate CIP and GIP observed distributions. By default 100.
...	Other parameters to be passed onto <a href="#">wilcox_CIP_GIP</a>

**Value**

A list containing; observed distributions of CIP and GIP (variability\_param); its associated null distributions generated by permutations (NULL\_CIP\_GIP); the unadjusted pvalue of Mann-Whitney Wilcoxon for CIP distribution (CIP\_pvalue); and for GIP distribution (GIP\_pvalue).

**Examples**

```
file <- system.file("extdata", "example_superpathway_fit_model.rda",
  package = "singIST")
load(file)
data <- example_superpathway_fit_model
CIP_GIP_test(data, npermut = 3, type = "jackknife")
```

---

clean\_mfa\_data

*Clean a predictor matrix for multiblock MFA*


---

**Description**

Converts non-finite values to NA, removes any column that is 100% NA or has zero variance, and returns a logical mask of kept columns.

**Usage**

```
clean_mfa_data(X)
```

**Arguments**

X A numeric matrix or data.frame of predictors (samples × features).

**Value**

A list with components:

X\_clean Cleaned matrix (only kept columns).

keep\_cols Logical vector, TRUE for columns kept.

removed Integer indices of removed columns.

**Examples**

```
clean_mfa_data(matrix(matrix(c(0,0,0,NA, 1,2), ncol = 2, nrow = 3)))
```

---

create_fit_model	<i>Create superpathway fit model object</i>
------------------	---

---

**Description**

Creates a simple list representing a fitted asmbPLS-DA model, after validating its components.

**Usage**

```
create_fit_model(  
  superpathway_input,  
  hyperparameters_fit,  
  model_fit,  
  model_validation  
)
```

**Arguments**

superpathway\_input  
List. A superpathway object created by create\_superpathway().

hyperparameters\_fit  
List. A hyperparameters object created by create\_hyperparameters().

model\_fit  
List. Fitted model details.

model\_validation  
List. Validation metrics of the fitted model.

**Value**

A list with elements: superpathway\_input, hyperparameters\_fit, model\_fit, model\_validation.

**Examples**

```

my_pathway <- create_pathway("KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION",
"KEGG", "c2", "CP")

celltypes <- c("T-cell", "Dendritic Cell")

my_superpathway <- create_superpathway(my_pathway, celltypes,
list(c("IL4", "IL5"), c("IL13")))

my_hyperparameters <- create_hyperparameters(matrix(1:4, nrow = 2), "binary",
3L, 5L, 10L)

#' # ---- Pseudobulk + labels ----
sample_id <- c("AD1", "AD2", "HC1", "HC2")
sample_class <- c("AD", "AD", "HC", "HC")
base_class <- "HC"
target_class <- "AD"

pseudobulk_lognorm <- matrix(
  rnorm(length(celltypes) * length(sample_id)),
  nrow = length(celltypes) * length(sample_id),
  ncol = length(celltypes)
)
rownames(pseudobulk_lognorm) <- as.vector(t(outer(
  celltypes, sample_id, function(x, y) paste(x, y, sep = "_")
)))

my_superpathway_input <- create_superpathway_input(
  superpathway_info = my_superpathway,
  hyperparameters_info = my_hyperparameters,
  pseudobulk_lognorm = pseudobulk_lognorm,
  sample_id = sample_id,
  sample_class = sample_class,
  base_class = base_class,
  target_class = target_class
)
my_fit <- create_fit_model(my_superpathway_input, my_hyperparameters,
list(model = "fit"), list(accuracy = 0.95))

```

---

create\_hyperparameters

*Create asmbPLS-DA hyperparameters object*

---

**Description**

Creates a simple list representing hyperparameters for asmbPLS-DA, after validating them.

**Usage**

```
create_hyperparameters(
  quantile_comb_table,
  outcome_type,
  number_PLS,
  folds_CV = 5L,
  repetition_CV = 10L
)
```

**Arguments**

`quantile_comb_table` Matrix. Quantile (lambda) sparsity values for CV.

`outcome_type` Character. Either "binary" or "multiclass".

`number_PLS` Integer. Maximum number of PLS components.

`folds_CV` Integer or NULL. Number of folds for CV (default 5).

`repetition_CV` Integer or NULL. Number of repetitions for CV (default 10).

**Value**

A list with elements: `quantile_comb_table`, `outcome_type`, `number_PLS`, `folds_CV`, `repetition_CV`.

**Examples**

```
quantile_comb_table <- base::as.matrix(RcppAlgos::permuteGeneral(seq(0.05,
0.95, by = 0.50)))
my_hyperparameters <- create_hyperparameters(quantile_comb_table, "binary", 3L,
1L, 1L)
print(my_hyperparameters)
```

---

```
create_mapping_organism
```

*Create mapping organism object*

---

**Description**

Creates a simple S3 object (list with class "mapping.organism") after validating its components.

**Usage**

```
create_mapping_organism(
  organism,
  target_class,
  base_class,
  celltype_mapping,
  counts
)
```

**Arguments**

organism	Character(1). Scientific Latin name of the organism.
target_class	Character(1). Name of the target class for this organism.
base_class	Character(1). Name of the base class for this organism.
celltype_mapping	List. Mapping of cell types to clusters (character vectors).
counts	Seurat or SingleCellExperiment object with the scRNA-seq LogNormalized counts. This object should contain variables in slot(SeuratObject, meta.data) slot or slot(SingleCellExperimentObject, metadata); class indicating the class the sample belongs to; celltype_cluster indicating the cell type cluster (either character or numeric); donor indicating the sample ID.

**Value**

A list of class "mapping.organism" with elements:

- organism
- target\_class
- base\_class
- celltype\_mapping
- counts

**Examples**

```
counts <- SeuratObject::pbmc_small
colnames(slot(counts, "meta.data"))[1] <- "donor"
colnames(slot(counts, "meta.data"))[6] <- "class"
colnames(slot(counts, "meta.data"))[7] <- "celltype_cluster"
celltype_mapping <- list("T-cell" = c("T"), "Dendritic Cell" = character(0))
obj <- create_mapping_organism("Mus musculus", "g1", "g2", celltype_mapping,
counts)
```

---

create\_pathway      *Create pathway object*

---

**Description**

Creates a simple list representing a pathway, after validating its fields.

**Usage**

```
create_pathway(standard_name, dbsource, collection, subcollection)
```

**Arguments**

standard_name	Character. Pathway standard name from MsigDB.
dbsource	Character. Database source (KEGG, PID, REACTOME, BIOCARTA, WIKIPATHWAYS).
collection	Character. MsigDB collection (c2 or m2).
subcollection	Character. MsigDB subcollection (CP).

**Value**

A list with elements: standard\_name, dbsource, collection, subcollection.

**Examples**

```
my_pathway <- create_pathway(  
  standard_name = "KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION",  
  dbsource = "KEGG",  
  collection = "c2",  
  subcollection = "CP"  
)  
print(my_pathway)
```

---

create\_superpathway *Create superpathway gene sets object*

---

**Description**

Creates a simple list representing a superpathway, after validating its fields.

**Usage**

```
create_superpathway(pathway_info, celltypes, gene_sets_celltype)
```

**Arguments**

pathway_info	List. A pathway object created by create_pathway().
celltypes	Character vector. Each element represents a cell type.
gene_sets_celltype	List of character vectors. Each element corresponds to gene sets for each cell type. Can be NULL.

**Value**

A list with elements: pathway\_info, celltypes, gene\_sets\_celltype.

**Examples**

```
my_pathway <- create_pathway("KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION",
  "KEGG", "c2", "CP")
my_superpathway <- create_superpathway(my_pathway, c("T-cell",
  "Dendritic Cell"), list(c("IL4", "IL5"), c("IL13")))
print(my_superpathway)
```

---

```
create_superpathway_input
```

*Create superpathway input for asmbPLS-DA*

---

**Description**

Creates a plain list containing the fields for superpathway input object and validates the content with [check\\_superpathway\\_input](#).

**Usage**

```
create_superpathway_input(
  superpathway_info,
  hyperparameters_info,
  pseudobulk_lognorm,
  sample_id,
  sample_class,
  base_class,
  target_class
)
```

**Arguments**

superpathway_info	A list representing a superpathway object (formerly superpathway.gene.sets).
hyperparameters_info	A list representing a hyperparameters object (formerly hyperparameters).
pseudobulk_lognorm	A pseudobulk matrix.
sample_id	A character vector of sample ids.
sample_class	A character vector with the class of each sample.
base_class	A character scalar indicating the base class.
target_class	A character scalar indicating the target class.

**Value**

A list with elements:

- superpathway\_info
- hyperparameters\_info
- pseudobulk\_lognorm
- sample\_id
- sample\_class
- base\_class
- target\_class

**Examples**

```
# ---- Superpathway info (list) ----
my_pathway <- create_pathway("KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION",
"KEGG", "c2", "CP")
celltypes <- c("T-cell", "Dendritic Cell")

my_superpathway <- create_superpathway(my_pathway, celltypes, list(c("IL4",
"IL5"), c("IL13")))
# ---- Hyperparameters info (list) ----
quantile_comb_table <- base::as.matrix(
  RcppAlgos::permuteGeneral(seq(0.05, 0.95, by = 0.50)),
  ncol = length(celltypes)
)

my_hyperparameters <- create_hyperparameters(
  quantile_comb_table = quantile_comb_table,
  outcome_type = "binary",
  number_PLS = as.integer(3),
  folds_CV = as.integer(1),
  repetition_CV = as.integer(1)
)

# ---- Pseudobulk + labels ----
sample_id <- c("AD1", "AD2", "HC1", "HC2")
sample_class <- c("AD", "AD", "HC", "HC")
base_class <- "HC"
target_class <- "AD"

pseudobulk_lognorm <- matrix(
  rnorm(length(celltypes) * length(sample_id)),
  nrow = length(celltypes) * length(sample_id),
  ncol = length(celltypes)
)
rownames(pseudobulk_lognorm) <- as.vector(t(outer(
  celltypes, sample_id, function(x, y) paste(x, y, sep = "_")
)))

my_superpathway_input <- create_superpathway_input(
```

```
superpathway_info = my_superpathway,  
hyperparameters_info = my_hyperparameters,  
pseudobulk_lognorm = pseudobulk_lognorm,  
sample_id = sample_id,  
sample_class = sample_class,  
base_class = base_class,  
target_class = target_class  
)
```

---

derive\_contributions *Derive superpathway score, cell type contribution and gene contribution*

---

## Description

Computes the superpathway score, its cell type contribution and gene contribution for a block of predictor matrices for its later use to compute recapitulations

## Usage

```
derive_contributions(model_object, data)
```

## Arguments

model_object	A superpathway fit model list with the fitted asmbPLSDA
data	A matrix with the block of predictor matrices to compute score and contributions from

## Value

A list with the superpathway score for each sample, cell type and gene contributions to the former

## Examples

```
file <- system.file("extdata", "example_mapping_organism.rda",  
package = "singIST")  
load(file)  
mapped <- example_mapping_organism  
file <- system.file("extdata", "example_superpathway_fit_model.rda",  
package = "singIST")  
load(file)  
model <- example_superpathway_fit_model  
singIST_samples <- biological_link_function(mapped,  
model)$singIST_samples  
derive_contributions(model, singIST_samples)
```

---

derive_scores	<i>Compute predictor scores</i>
---------------	---------------------------------

---

### Description

Computes scores from the predictor to later derive the superpathway's score, cell type contribution and gene contributions, for the target class

### Usage

```
derive_scores(object, data, sample)
```

### Arguments

object	A superpathway fit model list passed from <a href="#">derive_contributions</a>
data	Block of predictor matrices to compute scores from
sample	Current sample from data to compute scores

### Value

A list containing the needed parameters to compute superpathway's score, cell type contributions and needed scores to compute gene contributions

### Examples

```
file <- system.file("extdata", "example_mapping_organism.rda",  
package = "singIST")  
load(file)  
mapped <- example_mapping_organism  
file <- system.file("extdata", "example_superpathway_fit_model.rda",  
package = "singIST")  
load(file)  
model <- example_superpathway_fit_model  
singIST_samples <- biological_link_function(mapped,  
model)$singIST_samples  
# Derive the scores for sample 2  
derive_scores(model, singIST_samples, 2)
```

---

diff_expressed	<i>Compute differentially expressed genes with FindMarkers/findMarkers and descriptive point estimates of log2FC</i>
----------------	--

---

## Description

Computes differentially expressed genes with `Seurat::FindMarkers`, for `Seurat` objects, or `scran::findMarkers`, for `SingleCellExperiment` objects, for the conditions indicated. Note that `Seurat::FindMarkers` will compute Wilcoxon Signed Rank Test by default, while `scran::findMarkers` will perform t-test by default instead. The reported logFC values are difference of means of log-normalized expression values with `Seurat::AggregateExpression` or `SingleCellExperiment::aggregateAcrossCells`. This logFC is consistent with the human log2FC computation by `asmbPLS-DA`.

## Usage

```
diff_expressed(
  object,
  condition_1 = c(),
  condition_2 = c(),
  logfc.treshold = 0.25,
  assay = "RNA",
  ...
)
```

## Arguments

<code>object</code>	A mapping organism list. If a <code>Seurat</code> object was provided, then <code>Idents(object)</code> assigned to variables with the conditions being tested is expected.
<code>condition_1</code>	A vector with the elements of the first factor to perform the hypothesis test. By default the mapped cell types <code>condition_1 = names(object\$celltype_mapping)</code>
<code>condition_2</code>	A vector with the elements of the second factor to perform the hypothesis test with. By default the class of the organism <code>condition_2 = c(object\$target_class), object\$base_c1</code>
<code>logfc.treshold</code>	Sets the minimum <code>FindMarkers</code> log-fold change (logFC) cutoff for identifying differentially expressed genes (DEGs). By default <code>logfc.treshold = 0.25</code> .
<code>assay</code>	Specific assay being used for analysis. By default <code>assay = RNA</code> .
<code>...</code>	Other parameters to pass onto <code>Seurat::FindMarkers()</code> or <code>scran::findMarkers</code> .

## Value

A list where each element is a `data.frame` for a cell type containing: `p_val` p-value of test, `avg_log2FC` descriptive point estimate of logFC, `pct.1` percentage of cells where the gene is detected in the base class, `pct.2` percentage of cells where the gene is detected in the target class, `p_val_adj` FDR.

**Examples**

```
# Set the identities
file <- system.file("extdata", "example_mapping_organism.rda",
package = "singIST")
load(file)
data_organism <- example_mapping_organism
data <- celltype_mapping(data_organism)
data$counts$test <- paste0(data$counts$celltype_cluster, "_",
data$counts$class)
SeuratObject::Idents(data$counts) <- "test"
diff_expressed(data)
```

fitOptimal

*Cross validation and fit of asmbPLSDA***Description**

Performs Cross Validation of the provided superpathway input, fits the optimal model and computes its validation metrics. The Cross Validation can either be Leave One-Out Cross Validation (LOOCV) or K-Fold Cross Validation (KCV). A LOOCV is performed if the number of folds was set to 1 or if the number of samples per class is less than 3 for any class. A K-Fold Cross Validation (KCV) is performed if the number of folds is greater or equal than 3 and the number of samples per class is always greater than the number of folds. If the number of samples is low for some of the classes LOOCV is recommended. If KCV is performed, missing values are automatically imputed in the K-CV process. The training set is imputed via `missMDA::imputeMFA()`, and `FactoMineR::MFA()` is trained on the imputed training set from which we extract the mean of each gene and the estimated loadings. We then estimate the validation set by projecting the samples onto MFA space of the training set. Gene whose variance is 0 are excluded from the imputation, if a gene has null variance and full of 0 values, the NA were imputed to 0.

**Usage**

```
fitOptimal(
  object,
  parallel = FALSE,
  measure = "B_accuracy",
  Method = NULL,
  expected_measure_increase = 0.005,
  maxiter = 100,
  global_significance_full = FALSE,
  CIP.GIP_significance_full = FALSE,
  npermut = 100,
  nbObsPermut = NULL,
  type = "jackknife",
  nsubsampling = 100,
  ...
)
```

**Arguments**

object	A superpathway input list to fit optimal asmbPLSDA.
parallel	A boolean indicating whether to parallelize (TRUE) for LOOCV on quantile combination or not (FALSE). Note this option is only available for LOOCV and not KCV. Default is FALSE.
measure	Accuracy measure to be used to select optimal asmbPLSDA model. Default is F1 measure. Options are: F1, accuracy, B_accuracy, precision and recall.
Method	Decision rule used for prediction. For binary outcome fixed_cutoff (default), Euclidean_distance_X, and Mahalanobis_distance_X. For categorical outcome with more than 2 levels, the methods include Max_Y (default), Euclidean_distance_X, Mahalanobis_distance_X, Euclidean_distance_Y, and PCA_Mahalanobis_distance_Y. If NULL the default method is used for the respective outcome binary.
expected_measure_increase	A double indicating the measure you expect to decrease by percent after including one more PLS component, this will affect the selection of optimal number of PLS components. If NULL the default is 0.005 (0.5%).
maxiter	An integer indicating the maximum number of iterations. If NULL the default is 100.
global_significance_full	A boolean indicating whether to return a list with information of each permutation for the global significance test of asmbPLSDA. By default FALSE. Note that if the number of permutations that is set is large, storing this information can be a burden on memory.
CIP.GIP_significance_full	A boolean indicating whether to return a list with the observed and null distributions of CIP and GIP or only the pvalue and adjusted pvalue. By default FALSE. Note that if the number of permutations that is set is large, storing this information can be a burden on memory.
npermut	Number of permutations for the tests. By default 100. Parameter passed onto <a href="#">permut_asmbplsda</a> and <a href="#">CIP_GIP_test</a> .
nbObsPermut	An integer indicating the number of samples to permute in each permutation. By default NULL. If NULL the number of samples to permute at each permutation is randomly chosen (for each permutation). Parameter passed onto <a href="#">permut_asmbplsda</a> .
type	Either jackknife or subsampling. If jackknife then the CIP and GIP observed distribution is generated by a jackknife procedure. If subsampling the CIP and GIP observed distribution is generated by subsampling the number of samples without replacement, each subsample is guaranteed to contain at least 2 samples per class. If a LOOCV was performed or one has small sample size it is recommended to select jackknife, otherwise select subsampling. Passed onto <a href="#">CIP_GIP_test</a> .
nsubsampling	Number of subsamples to generate CIP and GIP observed distributions. By default 100. Passed onto <a href="#">CIP_GIP_test</a> .
...	Other parameters to be passed onto <a href="#">wilcox_CIP_GIP</a> , wilcox test of GIP statistical tests

**Value**

A superpathway fit model list object with; a superpathway input list object used for CV and model fit; a hyperparameters list object with the hyperparameters used to fit the optimal model (includes optimal quantiles and PLS components from the CV step); a list with the fitted model information including: predictor and response matrices, observed gene sets, from matrixToBlock, and asmb-PLSDA output; a list with the validation metrics of fitted model.

**Examples**

```
# fitOptimal with jackknife for CIP/GIP statistics and 10 permutations
# for the global significance test of the optimal model
file <- system.file("extdata", "example_superpathway_input.rda",
  package = "singIST")
load(file)
data <- example_superpathway_input
fitOptimal(data, npermut = 10, type = "jackknife")
# fitOptimal with subsampling for CIP/GIP statistics with
# 10 subsamples and 50 permutations for the global significance test of the
# optimal model
fitOptimal(data, npermut = 50, type = "subsampling",
  nsubsampling = 10)
```

---

fit\_mfa\_imputer

*Fit a multiblock-MFA imputer on training data*


---

**Description**

Runs a full EM-based imputeMFA() on the training set then fits a pure MFA to extract the final means and loadings.

**Usage**

```
fit_mfa_imputer(X_train, group, ncp = 2, method = "Regularized")
```

**Arguments**

X_train	Numeric matrix (train samples $\times$ features), may contain NAs.
group	Integer vector of block sizes (must sum to ncol(X_train)).
ncp	Number of MFA components to use for imputation (default 2).
method	Method for imputeMFA(): "Regularized" or "EM".

**Value**

A list with components:

imputed Matrix X\_train with NAs filled.  
mu Numeric vector of column means (length = ncol).  
loadings Numeric matrix of loadings (ncol  $\times$  ncp).

**Examples**

```
fit_mfa_imputer(matrix(c(NA,runif(19))), nrow = 5, ncol = 4), c(2,2))
```

---

gene_contrib	<i>Derive gene contribution to cell type recapitulation</i>
--------------	---

---

**Description**

Derive gene contribution to cell type recapitulation

**Usage**

```
gene_contrib(model_object, data_original, data_singIST, cell_reference)
```

**Arguments**

**model\_object** A superpathway fit model list passed from [singISTrecapitulations](#)

**data\_original** A matrix with the gene contributions to superpathway's score as returned by [derive\\_contributions](#) for the non-singIST treated samples, passed from [singISTrecapitulations](#)

**data\_singIST** A matrix with the gene contributions to superpathway's score as returned by [derive\\_contributions](#) for the singIST treated samples, passed from [singISTrecapitulations](#)

**cell\_reference** A matrix with the cell type recapitulations as returned by [celltype\\_recap](#)

**Value**

A data.frame object with the variables: pathway name, celltype name, gene name, contribution  
gene contribution to cell type recapitulation

**Examples**

```
file <- system.file("extdata", "example_superpathway_fit_model.rda",
package = "singIST")
load(file)
model <- example_superpathway_fit_model
file <- system.file("extdata", "example_mapping_organism.rda",
package = "singIST")
load(file)
mapped <- example_mapping_organism

singIST_samples <- biological_link_function(mapped, model)$singIST_samples
original <- derive_contributions(model, singIST_samples)
derived <- derive_contributions(model, model$model_fit$predictor_block)
# Derive cell type reference
cell <- celltype_recap(model, original$celltype_contribution,
derived$celltype_contribution)
```

```
# Compute gene contributions
gene_contrib(model, original$gene_contribution, derived$gene_contribution,
cell)
```

---

 helpers

*Update block of predictor matrices in matrixToBlock()*


---

### Description

Fill up matrix with the corresponding expression values

get\_measure\_index() returns the index associated to each performance measure

Splits the predictor and response matrices into training and validation sets for leave-one-out cross-validation.

Function to train and validate asmbPLSDA excluding one observation parallelized for each quantile combination provided

Computes the prediction accuracy for different quantile combinations by fitting the asmbPLSDA model and making predictions.

Performs leave-one-out cross-validation (LOO-CV) in parallel.

Computes the performance measure selected between the training LOOCV samples and the validation LOOCV samples for all the quantile combination

For an optimal quantile combination and PLS component it computes its performance metrics between the training and validation sets

Selects the optimal number of PLS according to the performance measure

Iterates over all quantiles to generate the fitted asmbPLSDA for each and its associated predicted values

Creates a structured list to store permutation results.

Performs random permutations of the response matrix.

Calculates correlation, percentage change, and RV coefficient.

Selects sample indices for training and validation.

Fits the asmbPLS-DA model using permuted data.

Computes the p-value for the observed CV error against the null distribution of errors generated from permutation testing.

Calculates the 95% confidence interval for the null distribution of permutation errors.

Perform the jackknife resampling procedure for CIP/GIP calculations.

Perform the subsampling procedure for CIP/GIP calculations.

Generate null distributions of CIP and GIP using permutations.

Permute the X matrix to generate a null distribution.

Compute p-values by applying the Mann-Whitney test.

This helper function performs either Leave-One-Out Cross Validation (LOOCV) or K-Fold Cross Validation (KCV) on the given dataset and returns the optimal hyperparameters based on the specified accuracy measure.

This helper function computes various validation metrics, including global significance, CIP/GIP significance, and adjusted p-values for the fitted model based on cross-validation results.

For a given gene set it identifies the annotation of the genes, it does so if the genes have more than 50% match with a given annotation. Annotation must be either Ensembl, Entrez or Gene Symbols.

Retrieves one to one orthologs between from\_species and to\_species of [orthology\\_mapping](#)

Applies the biological link function conditions onto a predictor block matrix. The resulting gene expression of the predictor block are the cases defined in the biological link function.

Centers and scales each column of the predictor block matrices. The centering and scaling is according to the centroid and variance estimated in `fit_asmb`.

Given a block and the dimensions of all blocks it returns the indices of the genes belonging to that block within the predictor block matrix

Performs loading deflation for a given predictor block and PLS component

## Usage

```
update_block(
  celltype,
  observed_gene_sets,
  block_predictor = block_predictor,
  matrix = matrix
)

get_measure_index(measure)

get_train_val_sets(X.matrix, Y.matrix, validation_index)

quantile_computation(
  j,
  ...,
  results_CV_summary_n,
  F_matrix_validation_bind,
  X.matrix,
  Y.matrix,
  PLS_term = 1,
  X.dim,
  quantile.comb.table,
  outcome.type = c("binary", "multiclass"),
  quantile_table_CV,
  K,
  n_quantile_comb,
  Method = NULL,
  measure = "B_accuracy",
  expected.measure.increase = 0.005,
  center = TRUE,
```

```
    scale = TRUE,
    maxiter = 100
  )

  evaluate_quantile_combinations(
    j,
    results_CV_summary_n,
    F_matrix_validation_bind,
    E_matrix_training,
    F_matrix_training,
    E_matrix_validation,
    F_matrix_validation,
    quantile_table_CV,
    i,
    X.dim,
    quantile.comb.table,
    outcome.type,
    center,
    scale,
    maxiter,
    Method
  )

  execute_parallel_cv(
    K,
    results_CV_summary_n,
    F_matrix_validation_bind,
    X.matrix,
    Y.matrix,
    PLS_term,
    X.dim,
    quantile.comb.table,
    outcome.type,
    quantile_table_CV,
    Method,
    measure,
    expected.measure.increase,
    center,
    scale,
    maxiter,
    BPPARAM = BiocParallel::bpparam()
  )

  performance_measures(
    n_quantile_comb,
    results_CV_summary_n,
    F_matrix_validation_bind,
    outcome.type,
```

```
    measure_selected
  )

compute_final_measures(
  K,
  X.matrix,
  Y.matrix,
  i,
  X.dim,
  quantile_table_CV,
  outcome.type,
  center,
  scale,
  maxiter,
  Method
)

select_optimal_PLS(
  PLS_term,
  quantile_table_CV,
  X.dim,
  measure_selected,
  expected.measure.increase
)

execute_sequential_cv(
  K,
  n_quantile_comb,
  results_CV_summary_n,
  F_matrix_validation_bind,
  X.matrix,
  Y.matrix,
  PLS_term,
  X.dim,
  quantile_comb.table,
  outcome.type,
  quantile_table_CV,
  measure,
  expected.measure.increase,
  center,
  scale,
  maxiter,
  Method
)

initialize_results(npermut, q)

permute_Y_matrix(Y.matrix, nr, nbObsPermut, j)
```

```
compute_permutation_stats(res, Y.matrix, Ypermut, j, q, nr)

select_samples(object, nr, Nc)

fit_permuted_model(object, X_train, Y_train, maxiter)

evaluate_performance(
  res,
  Modelpermut,
  X_train,
  X_val,
  Y.matrix,
  s,
  measure,
  j,
  nr,
  Method,
  object
)

compute_pvalue(null_errors, CV_error)

compute_IC95(m)

jackknife_CIP_GIP(object, X.matrix, Y.matrix, K, maxiter, X.dim)

subsampling_CIP_GIP(
  object,
  X.matrix,
  Y.matrix,
  K,
  M,
  nsubsampling,
  maxiter,
  X.dim
)

generate_null_distributions(
  object,
  X.matrix,
  Y.matrix,
  npermut,
  K,
  X.dim,
  maxiter
)
```

```
permute_X_matrix(X.matrix, K, X.dim)

calculate_pvalues(variability, null_dist, test_func, ...)

perform_cv(
  object,
  model_block_matrices,
  nFC,
  measure,
  parallel,
  expected_measure_increase,
  maxiter,
  Method
)

compute_validation_metrics(
  output,
  optimal_hyperparameters,
  model_block_matrices,
  npermut,
  nbObsPermut,
  maxiter,
  global_significance_full,
  CIP.GIP_significance_full,
  type,
  nsubsampling,
  measure,
  Method
)

detect_gene_type(gene_set, mart)

retrieve_one2one_orthologs(
  annotation,
  gene_set,
  mart,
  from_species,
  to_species
)

FCtoExpression(model_object, b, samples, predictor_block, FC)

center_scale(data, fit_asmb)

get_indices(j, X.dim)

deflate_prediction(data, PLS, delta_cbind, fit_asmb)
```

**Arguments**

celltype	Cell types modelled
observed_gene_sets	Gene sets observed from your dataset
block_predictor	Block of predictor matrices to update
matrix	To iteratively update with block_predictor values
measure	The accuracy measure used for validation. Default is "F1".
X.matrix	Predictor matrix.
Y.matrix	Response matrix.
validation_index	Index of the validation sample.
j	Block to return indices for
...	Other parameters of test_func
results_CV_summary_n	Passed from <a href="#">asmbPLSDA.cv.loo</a>
F_matrix_validation_bind	Passed from <a href="#">asmbPLSDA.cv.loo</a>
PLS_term	Passed from <a href="#">asmbPLSDA.cv.loo</a>
X.dim	Vector with number of genes of each block
quantile_comb_table	Passed from <a href="#">asmbPLSDA.cv.loo</a>
outcome.type	Passed from <a href="#">asmbPLSDA.cv.loo</a>
quantile_table_CV	Passed from <a href="#">asmbPLSDA.cv.loo</a>
K	Number of samples.
n_quantile_comb	Passed from <a href="#">asmbPLSDA.cv.loo</a>
Method	The decision rule for prediction (e.g., "fixed_cutoff", "Euclidean_distance_X", etc.).
expected_measure_increase	Passed from <a href="#">asmbPLSDA.cv.loo</a>
center	Passed from <a href="#">asmbPLSDA.cv.loo</a>
scale	Passed from <a href="#">asmbPLSDA.cv.loo</a>
maxiter	The maximum number of iterations for validation tests. Default is 100.
E_matrix_training	Training predictor matrix.
F_matrix_training	Training response matrix.
E_matrix_validation	Validation predictor matrix.

F_matrix_validation	Validation response matrix
i	Passed from <a href="#">asmbPLSDA.cv.loo</a>
BPPARAM	A <code>BiocParallel::bpparam()</code> with parallelization options
measure_selected	Passed from <a href="#">asmbPLSDA.cv.loo</a>
npermut	The number of permutations for significance testing.
q	Number of classes.
nr	Number of samples
nbObsPermut	The number of samples to permute in each permutation. Default is NULL.
res	List of results to store statistics
Ypermut	Permuted response matrix.
object	A superpathway input list containing the data to be used for the cross-validation.
Nc	Number of samples to drop at each permutation.
X_train	Training predictor blocks
Y_train	Training response matrix.
Modelpermut	Permuted <code>asmbPLSDA</code> model
X_val	Validation predictor blocks
s	Validation samples
null_errors	A vector of errors from the null distribution (permuted errors).
CV_error	The observed cross-validation error.
m	A vector of errors from the null distribution (permuted errors).
M	Number of classes.
nsubsampling	The number of subsamples for CIP/GIP testing. Default is 100.
variability	A list of CIP or GIP values for observed distributions.
null_dist	A list of CIP or GIP values for null distributions.
test_func	The test function to use (typically Wilcoxon).
model_block_matrices	A list containing the model block matrices (predictor and response matrices).
nFC	The number of folds for K-fold cross-validation. If <code>nFC == 1</code> , LOOCV is performed.
parallel	A logical value indicating whether parallel computation should be used.
expected_measure_increase	Expected decrease in measure per additional PLS component. Default is 0.005.
output	The superpathway fit model list that contains the fitted model and validation information.
optimal_hyperparameters	The optimal hyperparameters obtained from cross-validation.
global_significance_full	Boolean flag indicating whether to return full global significance results.

CIP.GIP_significance_full	Boolean flag indicating whether to return full CIP/GIP significance results.
type	The procedure type for generating CIP/GIP distributions. Can be "jackknife" or "subsampling".
gene_set	A parameter passed from <a href="#">orthology_mapping</a>
mart	A parameter passed from <a href="#">orthology_mapping</a>
annotation	A parameter passed from <a href="#">orthology_mapping</a> , it indicates the annotation of the gene set provided
from_species	A parameter passed from <a href="#">orthology_mapping</a>
to_species	A parameter passed from <a href="#">orthology_mapping</a>
model_object	A superpathway fit model list
b	A parameter passed from <a href="#">singIST_treat</a> . The index of current iteration block.
samples	A parameter passed from <a href="#">singIST_treat</a> . The samples to modify its gene expression from predictor_block
predictor_block	A parameter passed from <a href="#">singIST_treat</a> . The predictor block of matrices from asmbPLSDA to modify its gene expression.
FC	A parameter passed from <a href="#">singIST_treat</a> . A data.frame with the Fold Changes, for a cell type, of each gene.
data	Matrix of predictor block to deflate
fit_asmb	asmbPLSDA fitted model
PLS	Numeric value indicating the PLS component
delta_cbind	Gene contributions (loadings) used to deflate the blocks

### Value

A list containing the training and validation sets:

E_matrix_validation	Validation predictor matrix
F_matrix_validation	Validation response matrix
E_matrix_training	Training predictor matrix
F_matrix_training	Training response matrix

A numeric vector containing predicted values for validation samples.

A list containing updated results\_CV\_summary\_n and F\_matrix\_validation\_bind matrices.

A vector with the performance measure of each quantile combination

Optimal quantile table for each PLS with all its performance measures

An integer with the optimal number of PLS



```

E_matrix_validation = E_valid,
F_matrix_validation = F_valid,
F_matrix_validation_bind =
F_matrix_validation_bind,
results_CV_summary_n =
results_CV_summary_n,
quantile_table_CV=quantile_table_CV,
i = 1, X.dim = c(5,5),
quantile.comb.table =quantile_table,
outcome.type = "binary",
center = TRUE,
scale = TRUE, maxiter = 100,
Method = NULL)

print(result)
set.seed(123)
K <- 5
X <- matrix(rnorm(50), nrow = 5, ncol = 10)
Y <- matrix(sample(0:1, 5, replace = TRUE), ncol = 1)
quantile_comb_table <- matrix(runif(10), nrow = 2, ncol = 10)
results_CV_summary_n <- matrix(0, nrow = 2, ncol = K)
F_matrix_validation_bind <- matrix(0, nrow = 2, ncol = K)
# Parallelization options
library(BiocParallel)
register(SnowParam(workers = 2, exportglobals = FALSE, progressbar = TRUE),
default = TRUE)
output <- execute_parallel_cv(K, results_CV_summary_n,
                             F_matrix_validation_bind, X, Y, PLS_term = 1,
                             X.dim = c(5,5),
                             quantile.comb.table = quantile_comb_table,
                             outcome.type = "binary",
                             quantile_table_CV = quantile_comb_table,
                             measure = "B_accuracy",
                             expected.measure.increase = 0.005,
                             center = TRUE, scale = TRUE, maxiter = 100,
                             Method = NULL)

register(SerialParam(), default = TRUE) # disable parallelization
str(output)
initialize_results(100, 3)
permute_Y_matrix(matrix(rnorm(100), 10, 10), nr = 10, nbObsPermut = 3, j = 2)
res <- initialize_results(100, 3)
compute_permutation_stats(res, matrix(rnorm(100), 10, 10),
matrix(rnorm(100), 10, 10), j = 2, q = 3, nr = 10)
null_errors <- c(0.3, 0.4, 0.35, 0.33)
CV_error <- 0.32
compute_pvalue(null_errors, CV_error)
null_errors <- c(0.3, 0.4, 0.35, 0.33)
compute_IC95(null_errors)
library(biomaRt)
gene_set <- c("IL13", "IL4", "IL5", "IL21")
mart <- biomaRt::useMart(biomart = "ensembl",
dataset = "hsapiens_gene_ensembl")
detect_gene_type(gene_set, mart)
annotation <- "external_gene_name"

```

```
gene_set <- c("IL13", "IL4", "IL5")
mart <- biomaRt::useMart(biomart = "ensembl", dataset = paste0("hsapiens",
"_gene_ensembl"))
retrieve_one2one_orthologs(annotation, gene_set, mart, "hsapiens",
"mmusculus")
X.dim <- c(30,40,60)
j <- 2
get_indices(j, X.dim)
```

---

matrixToBlock

*Build predictor and response blocks with superpathway input*

---

## Description

Builds the predictor block and matrix response for its fit in asmbPLS-DA

## Usage

```
matrixToBlock(object)
```

## Arguments

object            A superpathway input list object

## Value

A list containing the predictor block, response matrix, dimension of each block and observed gene sets with respect to gene\_sets\_celltype for the original pseudobulk\_lognorm matrix, for its use in asmbPLS-DA fit

## Examples

```
file <- system.file("extdata", "example_superpathway_input.rda",
package = "singIST")
load(file)
data <- example_superpathway_input
matrixToBlock(data)
```

---

multiple_check	<i>Check if parameter format is consistent</i>
----------------	--

---

### Description

For the wrapper functions [multiple\\_fitOptimal](#) and [multiple\\_singISTrecapitulations](#) one must pass multiple parameters. To check for the consistency of such parameters we use this function with the logic; if the parameter passed is NULL or its length is 1, it is assumed that the desired list of parameters is the repetition of such; if the parameter passed is a vector whose length is the number of objects that the wrappers iterate on, then the function returns a list whose elements are each of the vector elements; otherwise if the parameters are a vector whose length does not match with the number of objects to iterate on then the function stops

### Usage

```
multiple_check(parameter, objectLength)
```

### Arguments

parameter	The parameters passed from either <a href="#">multiple_fitOptimal</a> or <a href="#">multiple_singISTrecapitulations</a>
objectLength	The number of objects that the wrapper functions iterate on

### Value

A list with the repetition of the parameter

### Examples

```
# NULL parameter case
parameter <- NULL
objectLength <- 10
multiple_check(parameter, objectLength)

# Parameter equal for all elements
parameter <- FALSE
objectLength <- 5
multiple_check(parameter, objectLength)

# Parameter differing for all elements
parameter <- c(1, 6, 7, 8, 9)
objectLength <- 5
multiple_check(parameter, objectLength)
```

---

multiple\_fitOptimal *Multiple Cross validation and fit of asmbPLSDA*

---

### Description

Use [fitOptimal](#) for multiple superpathway input list objects. This wrapper is useful if one wants to assess multiple superpathways for analyses and needs to train its respective optimal models.

### Usage

```
multiple_fitOptimal(
  object = list(),
  parallel = c(FALSE),
  measure = c("B_accuracy"),
  expected_measure_increase = c(0.005),
  maxiter = c(100),
  global_significance_full = c(FALSE),
  CIP.GIP_significance_full = c(FALSE),
  npermut = c(100),
  nbObsPermut = c(NULL),
  type = c("jackknife"),
  nsubsampling = c(100),
  Method = c(NULL),
  ...
)
```

### Arguments

object	A list whose elements are superpathway input lists objects to use <a href="#">fitOptimal</a>
parallel	A vector whose elements are parallel parameters for each object as requested by <a href="#">fitOptimal</a>
measure	A vector whose elements are measure parameters for each object as requested by <a href="#">fitOptimal</a>
expected_measure_increase	A vector whose elements are expected_measure_increase parameters for each object as requested by <a href="#">fitOptimal</a>
maxiter	A vector whose elements are maxiter parameters for each object as requested by <a href="#">fitOptimal</a>
global_significance_full	A vector whose elements are global_significance_full parameters for each object as requested by <a href="#">fitOptimal</a>
CIP.GIP_significance_full	A vector whose elements are CIP.GIP_significance_full parameters for each object as requested by <a href="#">fitOptimal</a>

npermut	A vector whose elements are npermut parameters for each object as requested by <a href="#">fitOptimal</a>
nbObsPermut	A vector whose elements are nbObsPermut parameters for each object as requested by <a href="#">fitOptimal</a>
type	A vector whose elements are type parameters for each object as requested by <a href="#">fitOptimal</a>
nsubsampling	A vector whose elements are nsubsampling parameters for each object as requested by <a href="#">fitOptimal</a>
Method	A vector whose elements are Method parameters for each object as requested by <a href="#">fitOptimal</a>
...	Other parameters to be passed onto <a href="#">fitOptimal</a>

**Value**

A list of superpathway fit model list

**Examples**

```
file <- system.file("extdata", "example_superpathway_input.rda",
  package = "singIST")
load(file)
data <- example_superpathway_input
models <- list(data, data)
# Example with different options
multiple_model <- multiple_fitOptimal(models, type = c("jackknife",
  "subsampling"), nsubsampling = c(NULL, 10), npermut = c(10,15))
```

---

multiple\_singISTrecapitulations

*Compute singIST recapitulations for multiple superpathways*

---

**Description**

Use [singISTrecapitulations](#) for multiple superpathway fit model list against the same mapping organism list. This wrapper is useful if one wants to assess multiple superpathways against the same mapping organism list.

**Usage**

```
multiple_singISTrecapitulations(
  object,
  model_object = list(),
  model_species = list("hsapiens"),
  ...
)
```

**Arguments**

object	A mapping organism list
model_object	A list whose elements are superpathway fit model list
model_species	A list of characters indicating the organism of each model_object element. By default list("hsapiens") which assumes the same organism across all elements of model_object parameter
...	Other parameters to pass onto <a href="#">biological_link_function</a>

**Value**

A list with the row binded data.frame for each superpathway assessed for the superpathway and cell type recapitulations, and gene contributions to the former.

**Examples**

```
file <- system.file("extdata", "example_superpathway_input.rda",
package = "singIST")
load(file)
data_model <- example_superpathway_input
models <- list(data_model, data_model)
# Example with different options
multiple_model <- multiple_fitOptimal(models, type = c("jackknife",
"subsampling"), nsubsampling = c(NULL, 10), npermut = c(10,15))
file <- system.file("extdata", "example_mapping_organism.rda",
package = "singIST")
load(file)
data_organism <- example_mapping_organism
multiple_singISTrecapitulations(data_organism, multiple_model,
model_species = list("hsapiens", "hsapiens"))
```

---

orthology\_mapping      *Orthology mapping*

---

**Description**

Performs the one-to-one orthology mapping between the mapped disease model list to the reference (human) organism of the superpathway fit model list.

**Usage**

```
orthology_mapping(
  object,
  model_object,
  from_species,
  to_species = "mmusculus",
  annotation_to_species = "external_gene_name"
)
```

**Arguments**

object	A mapping organism list
model_object	A superpathway fit model list
from_species	A character indicating the reference organism for which the parameter model_fit has information from.
to_species	A character indicating the mapped organism for which the parameter object has information from. By default mmusculus.
annotation_to_species	A character indicating the gene identifier annotation used for the to_species. Note this should match with the gene names in object\$counts. By default external_gene_name. If NULL the annotation_to_species is inferred with <a href="#">detect_gene_type</a> , note this might take time.

**Value**

A list with the gene sets per cell type with the one-to-one orthology

**Examples**

```
# Case without stating the gene annotation of the mapping.organisms object
# note this will take longer to execute
file <- system.file("extdata", "example_mapping_organism.rda",
package = "singIST")
load(file)
data_organism <- example_mapping_organism
file <- system.file("extdata", "example_superpathway_fit_model.rda",
package = "singIST")
load(file)
data_model <- example_superpathway_fit_model
orthology_mapping(data_organism, data_model, "hsapiens",
annotation_to_species = NULL)
# Case assuming the gene annotation of the mapping.organism object is
# by default "external_gene_name" this is faster
orthology_mapping(data_organism, data_model, "hsapiens")
```

---

permut\_asmbplsda

*Permutation test for asmbPLSDA global significance for LOO*


---

**Description**

Performs permutation testing for asmbPLS-DA to evaluate model validity.

**Usage**

```
permut_asmbplsda(
  object,
  npermut = 100,
  nbObsPermut = NULL,
  Nc = 1,
  CV_error,
  measure = "B_accuracy",
  Method = NULL,
  maxiter = 100
)
```

**Arguments**

object	A superpathway fit model list.
npermut	Number of permutations (default: 100).
nbObsPermut	Number of samples to permute per iteration (default: NULL).
Nc	Number of samples dropped per permutation (default: 1).
CV_error	Cross-validation error of the fitted model.
measure	Accuracy measure ("F1", "accuracy", "B_accuracy", "precision", "recall", default: "B_accuracy").
Method	Decision rule for prediction (default: NULL).
maxiter	Maximum iterations (default: 100).

**Value**

A list with permutation statistics, p-value, and confidence intervals.

**Examples**

```
file <- system.file("extdata", "example_superpathway_fit_model.rda",
  package = "singIST")
load(file)
data <- example_superpathway_fit_model
permut_asmbplsda(data, npermut = 5, Nc = 1,
  CV_error = 1)
```

---

permut\_asmbplsda\_kcv *Permutation test for asmbPLS-DA global significance (LOO or KCV)*

---

**Description**

If `splits=NULL`, runs LOOCV-based permutation. Otherwise treats `splits` as a list of train/validate splits (e.g. from `make_splits_R()`) and does a fixed splits K-fold×repeats permutation test.

**Usage**

```

permut_asmbplsda_kcv(
  object,
  npermut = 100,
  splits = NULL,
  measure = "B_accuracy",
  nbObsPermut = NULL,
  Nc = 1,
  Method = NULL,
  maxiter = 100,
  CV_error = NULL,
  ...
)

```

**Arguments**

object	A superpathway fit model list
npermut	Number of permutations (default: 100)
splits	Optional list of splits; if NULL uses LOOCV branch
measure	Accuracy measure ("F1", "accuracy", "B_accuracy", "precision", "recall", default: "B_accuracy").
nbObsPermut	Number of samples to permute per iteration (default: NULL).
Nc	Number of samples dropped per permutation (default: 1 if LOOCV).
Method	Decision rule for prediction (default: NULL).
maxiter	Maximum iterations (default: 100).
CV_error	Error obtained from optimal model CV process
...	Other args passed to LOOCV or to evaluate_performance

**Value**

A list with null distribution, p-value, and (for KCV) splits

---

predict\_mfa\_imputer     *Impute new samples using a fitted MFA imputer*

---

**Description**

Projects each new sample into the latent space learned on training, then reconstructs its missing entries.

**Usage**

```
predict_mfa_imputer(X_new, mu, loadings)
```

**Arguments**

X_new	Numeric matrix (new samples × same features), may contain NAs.
mu	Numeric vector of column means (as returned by fit_mfa_imputer).
loadings	Numeric matrix of loadings (columns = components).

**Value**

Matrix X\_new with NAs replaced by reconstructed values.

---

pullGeneSet	<i>Pull Gene Set from MsigDB</i>
-------------	----------------------------------

---

**Description**

Retrieves the gene set associated with a pathway or superpathway from MsigDB.

**Usage**

```
pullGeneSet(object, gse = NULL, ...)
```

**Arguments**

object	List. A pathway (from create_pathway()) or superpathway (from create_superpathway()).
gse	Gene Set Collection from MsigDB. If NULL, loads default (human, ENTREZ + SYM IDs).
...	Additional arguments passed to msigdb::subsetCollection().

**Value**

A character vector with gene IDs for the specified pathway.

**Examples**

```
my_pathway <- create_pathway("KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION",
  "KEGG", "c2", "CP")
pullGeneSet(my_pathway)
```

---

```
render_multiple_outputs
```

*Render multiple singISTrecapitulation outputs*

---

### Description

Render output of [multiple\\_singISTrecapitulations](#) for multiple disease models and superpathways, the output is friendly for visualizing the results

### Usage

```
render_multiple_outputs(objects = list())
```

### Arguments

objects            A list as returned by [multiple\\_singISTrecapitulations](#)

### Value

A list with the row binded data.frame for each superpathway assessed for the superpathway and cell type recapitulations, gene contributions to the former, and fold changes. These row binds are performed for all disease models and superpathways.

---

```
restore_removed_columns
```

*Restore columns removed during MFA cleaning into the imputed matrix*

---

### Description

After cleaning and imputing a subset of predictors (removing any columns with zero variance or 100% missing), this function re-inserts those removed columns in their original order. For each re-inserted column, original non-missing values are kept and entries that were originally missing are set to zero.

### Usage

```
restore_removed_columns(X_imp_clean, X_raw, keep_cols)
```

### Arguments

X\_imp\_clean        Numeric matrix (n\_samples × p\_cleaned) of imputed values for the columns that were kept.

X\_raw              Numeric matrix or data.frame (n\_samples × p\_oril) of ginathe original predictor data before cleaning.

keep\_cols          Logical vector of length p\_original, where TRUE indicates the column was kept for imputation and FALSE indicates it was removed.

**Value**

A numeric matrix ( $n\_samples \times p\_original$ ) with all original columns in their original order. Columns where `keep_cols == TRUE` contain the values from `X_imp_clean`. Columns where `keep_cols == FALSE` contain the original non-NA values, and any entries that were originally NA are set to zero.

---

`Results_comparison_measure`*Compute performance metrics of predicted asmbPLSDA*

---

**Description**

Compute performance metrics of predicted asmbPLSDA

**Usage**

```
Results_comparison_measure(  
  Y_predict,  
  Y_true,  
  outcome.type = c("binary", "multiclass")  
)
```

**Arguments**

<code>Y_predict</code>	Predicted matrix from asmbPLSDA
<code>Y_true</code>	True class used to fit asmbPLSDA
<code>outcome.type</code>	Outcome type either "binary" or "multiclass"

**Value**

A vector with accuracy, balanced accuracy, precision, recall and F1 metric

**Examples**

```
Results_comparison_measure(c(1,0,1,0,1), c(0,0,1,1,1),  
  outcome.type = "binary")
```

---

setGeneSetsCelltype    *Set gene sets per cell type in a superpathway*

---

### Description

Updates the `gene_sets_celltype` element of a superpathway object, ensuring validity:

- The number of gene sets must match the number of cell types.

### Usage

```
setGeneSetsCelltype(object, value = NULL, ...)
```

### Arguments

<code>object</code>	List. A superpathway object created by <code>create_superpathway()</code> , or a pathway object created by <code>create_pathway()</code> .
<code>value</code>	List. A list of genes to incorporate in each cell type slot. By default <code>NULL</code> , only use if genes are to be introduced manually.
<code>...</code>	other parameters to pass onto <code>pullGeneSet()</code> .

### Value

The updated superpathway object (list).

### Examples

```
my_pathway <- create_pathway(  
  standard_name = "KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION",  
  dbsource = "KEGG",  
  collection = "c2",  
  subcollection = "CP"  
)  
  
my_superpathway <- create_superpathway(my_pathway, c("T-cell",  
  "Dendritic Cell"), list())  
  
my_superpathway <- setGeneSetsCelltype(my_superpathway, list(c("IL2"),  
  c("IL4")))
```

---

`singISTrecapitulations`*Compute singIST recapitulations*

---

**Description**

This method provides with all singIST recapitulations; superpathway recapitulations; cell type recapitulations; gene contributions to cell type recapitulations. The procedure encompasses the execution of the biological link function, the derivation of the predictor scores (superpathway, cell type and gene scores), and their use to compute the predicted recapitulations as a fraction of the reference recapitulation.

**Usage**

```
singISTrecapitulations(object, model_object, ...)
```

**Arguments**

<code>object</code>	A mapping organism list for which to calculate the recapitulations against the fitted superpathway model
<code>model_object</code>	A superpathway fit model list used to calculate the recapitulations
<code>...</code>	Other parameters to pass onto <a href="#">biological_link_function</a>

**Value**

A list with; a `data.frame` object with the superpathway recapitulation, containing variables pathway name, recapitulation, `p_val` with the global significance test of the fitted model as provided in `model_object`, and `target_organism` with the target class of the disease model as provided in `model_object`; a `data.frame` with the cell type recapitulation, containing variables pathway name, celltype, recapitulation, orthology with the percentage of observed one-to-one orthology coverage

- if all cell types have the same gene set this value is constant -, and `target_organism`; a `data.frame` object with the gene contributions to cell type recapitulation, containing variables pathway, celltype, gene name, contribution indicating the gene contribution to cell type recapitulation, and `target_organism`; orthologs a `data.frame` with the one-to-one orthology mapping for each cell type gene set.

**Examples**

```
file <- system.file("extdata", "example_mapping_organism.rda",
package = "singIST")
load(file)
data_organism <- example_mapping_organism
file <- system.file("extdata", "example_superpathway_fit_model.rda",
package = "singIST")
load(file)
data_model <- example_superpathway_fit_model
singISTrecapitulations(data_organism, data_model)
```

---

singIST\_treat                      *Derive singIST treated samples*

---

### Description

Derive singIST treated samples

### Usage

```
singIST_treat(object, model_object, orthologs, logFC)
```

### Arguments

object	A mapping organism list passed from <a href="#">biological_link_function</a> .
model_object	A superpathway fit model list passed from <a href="#">biological_link_function</a>
orthologs	A list of data.table objects, as returned by <a href="#">orthology_mapping</a> with the one-to-one orthologs of each gene set per cell type
logFC	A list of data.frame objects, as returned by <a href="#">diff_expressed</a> with the logFC for each gene and cell type.

### Value

A list object with the singIST treated samples predictor block matrix and a list of Fold Changes for each cell type used to compute the singIST treated samples.

### Examples

```
# Orthology mapping
file <- system.file("extdata", "example_mapping_organism.rda",
package = "singIST")
load(file)
data_organism <- example_mapping_organism
file <- system.file("extdata", "example_superpathway_fit_model.rda",
package = "singIST")
load(file)
data_model <- example_superpathway_fit_model
orthologs <- orthology_mapping(data_organism, data_model, "hsapiens")
# Set the identities
# Cell type mapping
data <- celltype_mapping(data_organism)
data$counts$test <- paste0(data$counts$celltype_cluster,
"_", data$counts$class)
SeuratObject::Idents(data$counts) <- "test"
logFC <- diff_expressed(data)
singIST_treat(data_organism, data_model, orthologs, logFC)
```

---

superpathway\_recap      *Derive superpathway recapitulation*

---

## Description

Derive superpathway recapitulation

## Usage

```
superpathway_recap(model_object, data_original, data_singIST)
```

## Arguments

`model_object`      A superpathway fit model list passed from [singISTrecapitulations](#)

`data_original`      A matrix with the superpathway's score as returned by [derive\\_contributions](#) for the non-singIST treated samples, passed from [singISTrecapitulations](#)

`data_singIST`      A matrix with the superpathway's score as returned by [derive\\_contributions](#) for the singIST treated samples, passed from [singISTrecapitulations](#)

## Value

An object data . frame with the variables: pathway name as indicated in `model_object`, recapitulation with the superpathway recapitulation

## Examples

```
file <- system.file("extdata", "example_superpathway_fit_model.rda",
package = "singIST")
load(file)
model <- example_superpathway_fit_model
file <- system.file("extdata", "example_mapping_organism.rda",
package = "singIST")
load(file)
mapped <- example_mapping_organism
singIST_samples <- biological_link_function(mapped,
model)$singIST_samples
original <- derive_contributions(model, singIST_samples)
derived <- derive_contributions(model,model$model_fit$predictor_block)
superpathway_recap(model, original$superpathway_score,
derived$superpathway_score)
```

---

update_group_sizes	<i>Update block-size vector after cleaning</i>
--------------------	--

---

**Description**

Given an original vector of block lengths and a mask of kept columns, recomputes the new block lengths.

**Usage**

```
update_group_sizes(group_orig, keep_cols)
```

**Arguments**

group_orig	Integer vector of original block sizes (sum group_orig = ncol before cleaning).
keep_cols	Logical vector of length sum(group_orig), TRUE for columns retained.

**Value**

Integer vector of same length as group\_orig with updated block sizes.

**Examples**

```
update_group_sizes(c(2,3), c(TRUE, TRUE, FALSE, TRUE, TRUE))
```

---

wilcox_CIP_GIP	<i>Mann-Whitney Wilcoxon test p-value</i>
----------------	---

---

**Description**

Mann-Whitney Wilcoxon test p-value

**Usage**

```
wilcox_CIP_GIP(ref_distr, null_distr, ...)
```

**Arguments**

ref_distr	A vector with the reference distribution
null_distr	A vector with the null distribution
...	Other parameters to be passed onto wilcox.test

**Value**

A pvalue with the Mann-Whitney Wilcoxon test with the "greater" as the alternative hypothesis

**Examples**

```
ref_distr <- rnorm(100, mean = 30, sd = 2)
null_distr <- rnorm(100, mean = 0, sd = 1)
wilcox_CIP_GIP(ref_distr, null_distr)
```

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