

# Package ‘cosmosR’

December 18, 2024

**Type** Package

**Title** COSMOS (Causal Oriented Search of Multi-Omic Space)

**Version** 1.15.0

**Description** COSMOS (Causal Oriented Search of Multi-Omic Space) is a method that integrates phosphoproteomics, transcriptomics, and metabolomics data sets based on prior knowledge of signaling, metabolic, and gene regulatory networks. It estimated the activities of transcription factors and kinases and finds a network-level causal reasoning. Thereby, COSMOS provides mechanistic hypotheses for experimental observations across mult-omics datasets.

**URL** <https://github.com/saezlab/COSMOSR>

**BugReports** <https://github.com/saezlab/COSMOSR/issues>

**Depends** R (>= 4.1)

**License** GPL-3

**Encoding** UTF-8

**LazyData** false

**RoxygenNote** 7.2.3

**VignetteBuilder** knitr

**Imports** CARNIVAL, dorothea, dplyr, GSEABase, igraph, progress, purrr, rlang, stringr, utils, visNetwork, decoupleR

**Suggests** testthat, knitr, rmarkdown, piano, ggplot2

**biocViews** CellBiology, Pathways, Network, Proteomics, Metabolomics, Transcriptomics, GeneSignaling

**git\_url** <https://git.bioconductor.org/packages/cosmosR>

**git\_branch** devel

**git\_last\_commit** 7c6afd6

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.21

**Date/Publication** 2024-12-18

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---

compress\_same\_children

*Compress Network by Merging Nodes with Identical Children*

---

## Description

This function compresses a network by merging nodes that have the same children. The input network is represented as a data frame with three columns: source, target, and sign of interaction. The function returns a list containing the compressed network, node signatures, and duplicated signatures.

**Usage**

```
compress_same_children(df, sig_input, metab_input)
```

**Arguments**

**df** A data frame representing the network with three columns: source, target, and sign of interaction.

**sig\_input** A list of input node signatures to be considered for the merging process.

**metab\_input** A list of input metabolic signatures to be considered for the merging process.

**Value**

A list containing the following elements:

**compressed\_network**  
A data frame representing the compressed network.

**node\_signatures**  
A list of signatures of nodes in the network after the merging process.

**duplicated\_signatures**  
A list of duplicated signatures in the network after the merging process.

**Examples**

```
# Create a sample network
df <- data.frame(source = c("A", "A", "B", "B"),
                 target = c("C", "D", "C", "D"),
                 sign_of_interaction = c(1, 1, 1, 1))

# Define input node and metabolic signatures
sig_input <- list()
metab_input <- list()

# Compress the network
result <- compress_same_children(df, sig_input, metab_input)
compressed_network <- result$compressed_network
```

---

cosmos\_data

*Create Cosmos Data*

---

**Description**

An S3 class that combines the required data into a comprehensive list. Use the [preprocess\\_COSMOS\\_signaling\\_to\\_metabolism](#) or [preprocess\\_COSMOS\\_metabolism\\_to\\_signaling](#) to create an instance.

**Usage**

```

cosmos_data(
  meta_network,
  tf_regulon = NULL,
  signaling_data,
  metabolic_data,
  expression_data,
  verbose = TRUE
)

```

**Arguments**

meta_network	Prior knowledge network (PKN). By default COSMOS use a PKN derived from Omnipath, STITCHdb and Recon3D. See details on the data <a href="#">meta_network</a> .
tf_regulon	Collection of transcription factor - target interactions. A default collection from dorothea can be obtained by the <a href="#">load_tf_regulon_dorothea</a> function.
signaling_data	Numerical vector, where names are signaling nodes in the PKN and values are from {1, 0, -1}. Continuous data will be discretized using the <a href="#">sign</a> function.
metabolic_data	Numerical vector, where names are metabolic nodes in the PKN and values are continuous values that represents log2 fold change or t-values from a differential analysis. These values are compared to the simulation results (simulated nodes can take value -1, 0 or 1).
expression_data	Numerical vector that represents the results of a differential gene expression analysis. Names are gene names using EntrezID starting with an X and values are log fold change or t-values. Genes with NA values are considered none expressed and they will be removed from the TF-gene expression interactions.
verbose	(default: TRUE) Reports details about the <a href="#">cosmos_data</a> object.

**Value**

cosmos data class instance.

---

decompress\_solution\_network

*Decompress Solution Network*

---

**Description**

This function decompresses a solution network by mapping node signatures back to their original identifiers. The input is a formatted solution network, a meta network, node signatures, and duplicated parents. The function returns a list containing the decompressed solution network and attribute table.

**Usage**

```
decompress_solution_network(
  formatted_res,
  meta_network,
  node_signatures,
  duplicated_parents
)
```

**Arguments**

`formatted_res` A list containing the solution network and attribute table.

`meta_network` A data frame representing the meta network.

`node_signatures` A list of node signatures.

`duplicated_parents` A list of duplicated parents from the compression process.

**Value**

A list containing the following elements:

`SIF` A data frame representing the decompressed solution network.

`ATT` A data frame containing the attributes of the decompressed solution network.

**Examples**

```
# Create a sample formatted_res
formatted_res <- list(
  SIF = data.frame(source = c("parent_of_D1", "D"),
                  target = c("D", "F"),
                  interaction = c(1, 1),
                  Weight = c(1, 1)),
  ATT = data.frame(Nodes = c("parent_of_D1", "D", "F"),
                  NodeType = c("", "", ""),
                  ZeroAct = c(0, 0, 0),
                  UpAct = c(1, 1, 1),
                  DownAct = c(0, 0, 0),
                  AvgAct = c(1, 1, 1),
                  measured = c(0, 0, 0),
                  Activity = c(1, 1, 1))
)

# Create a sample meta_network
meta_network <- data.frame(source = c("A", "B", "D"),
                          target = c("D", "D", "F"),
                          interaction_type = c(1, 1, 1))

# Define node_signatures and duplicated_parents
node_signatures <- list("A" = "parent_of_D1", "B" = "parent_of_D1", "D" = "parent_F1")
duplicated_parents <- c("A" = "parent_of_D1", "B" = "parent_of_D1")
```

```
# Decompress the solution network
result <- decompress_solution_network(formatted_res, meta_network, node_signatures, duplicated_parents)
decompressed_network <- result[[1]]
attribute_table <- result[[2]]
```

---

decoupleRnival

*DecoupleRnival*

---

## Description

Iteratively propagate downstream input activity through a signed directed network using the weighted mean enrichment score from decoupleR package

## Usage

```
decoupleRnival(
  upstream_input = NULL,
  downstream_input,
  meta_network,
  n_layers,
  n_perm = 1000,
  downstream_cutoff = 0
)
```

## Arguments

**upstream\_input** A named vector with up\_stream nodes and their corresponding activity.

**downstream\_input** A named vector with down\_stream nodes and their corresponding activity.

**meta\_network** A network data frame containing signed directed prior knowledge of molecular interactions.

**n\_layers** The number of layers that will be propagated upstream.

**n\_perm** The number of permutations to use in decoupleR's algorithm.

**downstream\_cutoff** If downstream measurements should be included above a given threshold

## Value

A data frame containing the score of the nodes upstream of the downstream input based on the iterative propagation

## Examples

```
# Example input data
upstream_input <- c("A" = 1, "B" = -1, "C" = 0.5)
downstream_input <- c("D" = 2, "E" = -1.5)
meta_network <- data.frame(
  source = c("A", "A", "B", "C", "C", "D", "E"),
  target = c("B", "C", "D", "E", "D", "B", "A"),
  sign = c(1, -1, -1, 1, -1, -1, 1)
)

# Run the function with the example input data
result <- decoupleRnival(upstream_input, downstream_input, meta_network, n_layers = 2, n_perm = 100)

# View the results
print(result)
```

---

default\_CARNIVAL\_options

*Setting Default CARNIVAL Options*

---

## Description

Returns the default CARNIVAL options as a list. You can modify the elements of the list and then use it as an argument in [run\\_COSMOS\\_metabolism\\_to\\_signaling](#) or [run\\_COSMOS\\_signaling\\_to\\_metabolism](#). If you choose CPLEX or CBC, you must modify then the solverPath field and point to the CPLEX/CBC executable (See Details).

## Usage

```
default_CARNIVAL_options(solver = NULL)
```

## Arguments

solver	one of 'cplex' (recommended, but require 3rd party tool), 'cbc' (also require 3rd party tool) or 'lpSolve' (only for small networks)
--------	--

## Details

COSMOS is dependent on CARNIVAL for exhibiting the signalling pathway optimisation. CARNIVAL requires the interactive version of IBM Cplex, Gurobi or CBC-COIN solver as the network optimiser. The IBM ILOG Cplex is freely available through Academic Initiative [here](#). Gurobi license is also free for academics, request a license following instructions [here](#). The CBC solver is open source and freely available for any user, but has a significantly lower performance than CPLEX or Gurobi. Obtain CBC executable directly usable for cosmos [here](#). Alternatively for small networks, users can rely on the freely available [lpSolve R-package](#), which is automatically installed with the package.

**Value**

returns a list with all possible options implemented in CARNIVAL. see the documentation on [runCARNIVAL](#).

**Examples**

```
# load and change default options:
my_options = default_CARNIVAL_options(solver = "cplex")

my_options$solverPath = "/Applications/CPLEX_Studio128/cplex/bin/x86-64_osx/cplex"
my_options$threads = 2
my_options$timelimit = 3600*15
```

---

```
display_node_neighborhood
      display_node_neighborhood
```

---

**Description**

display input and measurements within n steps of a given set of nodes

**Usage**

```
display_node_neighborhood(central_node, sif, att, n = 100)
```

**Arguments**

<code>central_node</code>	character or character vector; node ID(s) around which a network will be branched out until measurements and input are reached
<code>sif</code>	df; COSMOS network solution in sif format like the first list element returned by the <code>format_cosmos_res</code> function
<code>att</code>	df; attributes of the nodes of the COSMOS network solution like the second list element returned by the <code>format_cosmos_res</code> function
<code>n</code>	numeric; maximum number of steps in the network to look for inputs and measurements

**Value**

a visnetwork object



## Examples

```
CARNIVAL_options <- cosmosR::default_CARNIVAL_options("lpSolve")
data(toy_network)
data(toy_signaling_input)
data(toy_metabolic_input)
data(toy_RNA)
test_for <- preprocess_COSMOS_signaling_to_metabolism(meta_network = toy_network,
signaling_data = toy_signaling_input,
metabolic_data = toy_metabolic_input,
diff_expression_data = toy_RNA,
maximum_network_depth = 15,
remove_unexpressed_nodes = TRUE,
CARNIVAL_options = CARNIVAL_options
)
test_result_for <- run_COSMOS_signaling_to_metabolism(data = test_for,
CARNIVAL_options = CARNIVAL_options)
test_result_for <- format_COSMOS_res(test_result_for)
network_plot <- display_node_neighborhood(central_node = 'MYC',
sif = test_result_for[[1]],
att = test_result_for[[2]],
n = 7)
network_plot
```

---

extract\_nodes\_for\_ORA *Extract COSMOS nodes for ORA analysis*

---

## Description

Function to extract the nodes that appear in the COSMOS output network and the background genes (all genes present in the prior knowledge network)

## Usage

```
extract_nodes_for_ORA(sif, att)
```

## Arguments

<code>sif</code>	df; COSMOS network solution in sif format like the first list element returned by the <code>format_cosmos_res</code> function
<code>att</code>	df; attributes of the nodes of the COMSOS network solution like the second list element returned by the <code>format_cosmos_res</code> function

## Value

List with 2 objects: the success and the background genes

**Examples**

```

CARNIVAL_options <- cosmosR::default_CARNIVAL_options("lpSolve")
data(toy_network)
data(toy_signaling_input)
data(toy_metabolic_input)
data(toy_RNA)
test_for <- preprocess_COSMOS_signaling_to_metabolism(meta_network = toy_network,
signaling_data = toy_signaling_input,
metabolic_data = toy_metabolic_input,
diff_expression_data = toy_RNA,
maximum_network_depth = 15,
remove_unexpressed_nodes = TRUE,
CARNIVAL_options = CARNIVAL_options
)
test_result_for <- run_COSMOS_signaling_to_metabolism(data = test_for,
CARNIVAL_options = CARNIVAL_options)
test_result_for <- format_COSMOS_res(test_result_for)
extracted_nodes <- extract_nodes_for_ORA(
sif = test_result_for[[1]],
att = test_result_for[[2]]
)

```

---

```

filter_incoherent_TF_target
      filter_incoherent_TF_target

```

---

**Description**

Filters incoherent target genes from a regulatory network based on a decoupling analysis of upstream and downstream gene expression.

**Usage**

```

filter_incoherent_TF_target(
  decoupleRnival_res,
  TF_reg_net,
  meta_network,
  RNA_input
)

```

**Arguments**

<code>decoupleRnival_res</code>	A data frame resulting from the <code>decoupleRnival</code> function.
<code>TF_reg_net</code>	A data frame containing prior knowledge of transcription factor (TF) regulatory interactions.
<code>meta_network</code>	A network data frame containing signed directed prior knowledge of molecular interactions.
<code>RNA_input</code>	A named vector containing differential gene expression data.

**Value**

A network data frame containing the genes that are not incoherently regulated by TFs.

**Examples**

```
# Example input data
upstream_input <- c("A" = 1, "B" = -1, "C" = 0.5)
downstream_input <- c("D" = 2, "E" = -1.5)
meta_network <- data.frame(
  source = c("A", "A", "B", "C", "C", "D", "E"),
  target = c("B", "D", "D", "E", "D", "B", "A"),
  interaction = c(-1, 1, -1, 1, -1, -1, 1)
)
RNA_input <- c("A" = 1, "B" = -1, "C" = 5, "D" = -0.7, "E" = -0.3)

TF_reg_net <- data.frame(
  source = c("B"),
  target = c("D"),
  mor = c(-1)
)

# Run the decoupleRnival function to get the upstream influence scores
upstream_scores <- decoupleRnival(upstream_input, downstream_input, meta_network, n_layers = 2, n_perm = 100)

filtered_network <- filter_incoherent_TF_target(upstream_scores, TF_reg_net, meta_network, RNA_input)

print(filtered_network)
```

---

```
format_COSMOS_res      format_COSMOS_res
```

---

**Description**

formats the network with readable names

**Usage**

```
format_COSMOS_res(cosmos_res, metab_mapping = NULL)
```

**Arguments**

cosmos_res	results of COSMOS run
metab_mapping	a named vector with HMDB Ids as names and desired metabolite names as values.

**Value**

list with network and attribute tables.

---

gmt_to_dataframe	<i>Convert gmt file to data frame</i>
------------------	---------------------------------------

---

**Description**

This function is designed to convert a gmt file (gene set file from MSigDB) into a two column data frame where the first column corresponds to omic features (genes) and the second column to associated terms (pathway the gene belongs to). One gene can belong to several pathways.

**Usage**

```
gmt_to_dataframe(gmtfile)
```

**Arguments**

gmtfile            a full path name of the gmt file to be converted

**Value**

a two column data frame where the first column corresponds to omic features and the second column to associated terms (pathways).

---

HMDB_mapper_vec	<i>Toy Input Transcription Data Set</i>
-----------------	---

---

**Description**

This exemplary transcription data are the specific deregulated gene expression of the 786-O cell line from the NCI60 dataset.

**Usage**

```
data(HMDB_mapper_vec)
```

**Format**

An object of class “character” containing the marching between HMDB metabolite IDs and there corresponding metabolite names.

**Source**

<https://bioconductor.org/packages/release/data/annotation/html/metaboliteIDmapping.html>

**Examples**

```
data(HMDB_mapper_vec)
```

---

```
load_tf_regulon_dorothea
  load transcription factor regulon
```

---

**Description**

load the transcription factors from DOROTHEA package and converts gene symbols to EntrezID using org.Hs.eg.db

**Usage**

```
load_tf_regulon_dorothea(confidence = c("A", "B", "C"))
```

**Arguments**

confidence strong vector (by default: c("A","B","C")). Subset of {A, B, C, D, E}. See the ‘dorothea’ for the meaning of confidence levels. package for further details.

**Value**

returns a PKN of a form of a data table. Each row is an interaction. Columns names are:

- ‘tf’ transcription factor - ‘confidence’ class of confidence - ‘target’ target gene - ‘sign’ indicates if interaction is up (1) or down-regulation (-1).

**Examples**

```
load_tf_regulon_dorothea()
```

---

```
meta_network      Meta Prior Knowledge Network
```

---

**Description**

Comprehensive Prior Knowledge Network (PKN), which combines signaling and metabolic interaction networks. The network was constructed using the Recon3D and STITCH metabolic networks as well as the signaling network from OmniPath.

**Usage**

```
data(meta_network)
```

## Format

An object of class “tibble” with 117065 rows (interactions) and three variables:

source Source node, either metabolite or protein

interaction Type of interaction, 1 = Activation, -1 = Inhibition

target Target node, either metabolite or protein A detailed description of the identifier formatting can be found under [https://metapkn.omnipathdb.org/00\\_README.txt](https://metapkn.omnipathdb.org/00_README.txt).

## Source

The network is available in Omnipath: [https://metapkn.omnipathdb.org/metapkn\\_\\_20200122.txt](https://metapkn.omnipathdb.org/metapkn__20200122.txt), the scripts used for the build of the network are available under [https://github.com/saezlab/Meta\\_PKN](https://github.com/saezlab/Meta_PKN).

## References

Dugourd, A., Kuppe, C. and Sciacovelli, M. et. al. (2021) *Molecular Systems Biology*. **17**, e9730.

## Examples

```
data(meta_network)
```

---

```
meta_network_cleanup meta_network_cleanup
```

---

## Description

This function cleans up a meta network data frame by removing self-interactions, calculating the mean interaction values for duplicated source-target pairs, and keeping only interactions with values of 1 or -1.

## Usage

```
meta_network_cleanup(meta_network)
```

## Arguments

meta\_network A data frame with columns 'source', 'interaction', and 'target'.

## Value

A cleaned up meta network data frame.

**Examples**

```
# Create a meta network data frame
example_meta_network <- data.frame(
  source = c("A", "B", "C", "D", "A", "B", "C", "D", "A"),
  interaction = c(1, 1, 1, -1, 1, -1, 1, -1, 1),
  target = c("B", "C", "D", "A", "C", "D", "A", "B", "B")
)

# Clean up the example meta network
cleaned_meta_network <- meta_network_cleanup(example_meta_network)
print(cleaned_meta_network)
```

---

```
prepare_metab_inputs  add metabolic compartment and metab__ prefix to metabolite IDs
```

---

**Description**

This function adds metabolic compartments to the metabolic identifiers provided by the user.

**Usage**

```
prepare_metab_inputs(metab_input, compartment_codes)
```

**Arguments**

`metab_input` a named vector with metabolic statistics as inputs and metabolite identifiers as names

`compartment_codes` a character vector, the desired compartment codes to be added. Possible values are "r", "c", "e", "x", "m", "l", "n" and "g"

**Value**

a named vector with the compartment code and prefixed added to the names

---

```
preprocess_COSMOS_metabolism_to_signaling
  Preprocess COSMOS Inputs For Metabolism to Signaling
```

---

**Description**

Runs checks on the input data and simplifies the prior knowledge network. Simplification includes the removal of (1) nodes that are not reachable from signaling nodes and (2) interactions between transcription factors and target genes if the target gene does not respond or the response is contradictory with the change in the transcription factor activity. Optionally, further TF activities are estimated via network optimization via CARNIVAL and the interactions between TF and genes are filtered again.

**Usage**

```
preprocess_COSMOS_metabolism_to_signaling(
  meta_network = meta_network,
  tf_regulon = load_tf_regulon_dorothea(),
  signaling_data,
  metabolic_data,
  diff_expression_data = NULL,
  diff_exp_threshold = 1,
  maximum_network_depth = 8,
  expressed_genes = NULL,
  remove_unexpressed_nodes = TRUE,
  filter_tf_gene_interaction_by_optimization = TRUE,
  CARNIVAL_options = default_CARNIVAL_options("lpSolve")
)
```

**Arguments**

meta_network	prior knowledge network (PKN). A PKN released with COSMOS and derived from Omnipath, STITCHdb and Recon3D can be used. See details on the data <a href="#">meta_network</a> .
tf_regulon	collection of transcription factor - target interactions. A default collection from dorothea can be obtained by the <a href="#">load_tf_regulon_dorothea</a> function.
signaling_data	numerical vector, where names are signaling nodes in the PKN and values are from {1, 0, -1}. Continuous data will be discretized using the <a href="#">sign</a> function.
metabolic_data	numerical vector, where names are metabolic nodes in the PKN and values are continuous values that represents log2 fold change or t-values from a differential analysis. These values are compared to the simulation results (simulated nodes can take value -1, 0 or 1)
diff_expression_data	(optional) numerical vector that represents the results of a differential gene expression analysis. Names are gene names using gene symbols and values are log fold change or t-values. We use the “diff_exp_threshold” parameter to decide which genes changed significantly. Genes with NA values are considered none expressed and they will be removed from the TF-gene expression interactions.
diff_exp_threshold	threshold parameter (default 1) used to binarize the values of “diff_expression_data”.
maximum_network_depth	integer > 0 (default: 8). Nodes that are further than “maximum_network_depth” steps from the signaling nodes on the directed graph of the PKN are considered non-reachable and are removed.
expressed_genes	character vector. Names of nodes that are expressed. By default we consider all the nodes that appear in diff_expression_data with a numeric value (i.e. nodes with NA are removed)
remove_unexpressed_nodes	if TRUE (default) removes nodes from the PKN that are not expressed, see input “expressed_genes”.



`filter_tf_gene_interaction_by_optimization`  
 (default:TRUE), if TRUE then runs a network optimization that estimates TF activity not included in the inputs and checks the consistency between the estimated activity and change in gene expression. Removes interactions where TF and gene expression are inconsistent

`CARNIVAL_options`  
 list that controls the options of CARNIVAL. See details in [default\\_CARNIVAL\\_options](#).

### Value

`cosmos_data` object with the following fields:

`meta_network` Filtered PKN

`tf_regulon` TF - target regulatory network

`signaling_data_bin` Binarised signaling data

`metabolic_data` Metabolomics data

`diff_expression_data_bin` Binarized gene expression data

`optimized_network` Initial optimized network if `filter_tf_gene_interaction_by_optimization` is TRUE

### See Also

[meta\\_network](#) for meta PKN, [load\\_tf\\_regulon\\_dorothea](#) for tf regulon, [runCARNIVAL](#).

### Examples

```
data(toy_network)
data(toy_signaling_input)
data(toy_metabolic_input)
data(toy_RNA)
test_back <- preprocess_COSMOS_metabolism_to_signaling(
  meta_network = toy_network,
  signaling_data = toy_signaling_input,
  metabolic_data = toy_metabolic_input,
  diff_expression_data = toy_RNA,
  maximum_network_depth = 15,
  remove_unexpressed_nodes = TRUE,
  CARNIVAL_options = default_CARNIVAL_options("lpSolve")
)
```

## Description

Runs checks on the input data and simplifies the prior knowledge network. Simplification includes the removal of (1) nodes that are not reachable from signaling nodes and (2) interactions between transcription factors and target genes if the target gene does not respond or the response is contradictory with the change in the transcription factor activity. Optionally, further TF activities are estimated via network optimization via CARNIVAL and the interactions between TF and genes are filtered again.

## Usage

```
preprocess_COSMOS_signaling_to_metabolism(
  meta_network = meta_network,
  tf_regulon = load_tf_regulon_dorothea(),
  signaling_data,
  metabolic_data,
  diff_expression_data = NULL,
  diff_exp_threshold = 1,
  maximum_network_depth = 8,
  expressed_genes = NULL,
  remove_unexpressed_nodes = TRUE,
  filter_tf_gene_interaction_by_optimization = TRUE,
  CARNIVAL_options = default_CARNIVAL_options("lpSolve")
)
```

## Arguments

<code>meta_network</code>	prior knowledge network (PKN). A PKN released with COSMOS and derived from Omnipath, STITCHdb and Recon3D can be used. See details on the data <a href="#">meta_network</a> .
<code>tf_regulon</code>	collection of transcription factor - target interactions. A default collection from dorothea can be obtained by the <code>load_tf_regulon_dorothea</code> function.
<code>signaling_data</code>	numerical vector, where names are signaling nodes in the PKN and values are from {1, 0, -1}. Continuous data will be discretized using the <code>sign</code> function.
<code>metabolic_data</code>	numerical vector, where names are metabolic nodes in the PKN and values are continuous values that represents log2 fold change or t-values from a differential analysis. These values are compared to the simulation results (simulated nodes can take value -1, 0 or 1)
<code>diff_expression_data</code>	(optional) numerical vector that represents the results of a differential gene expression analysis. Names are gene names using gene symbols and values are log fold change or t-values. We use the “ <code>diff_exp_threshold</code> ” parameter to decide which genes changed significantly. Genes with NA values are considered none expressed and they will be removed from the TF-gene expression interactions.
<code>diff_exp_threshold</code>	threshold parameter (default 1) used to binarize the values of “ <code>diff_expression_data</code> ”.

`maximum_network_depth`  
integer > 0 (default: 8). Nodes that are further than “`maximum_network_depth`” steps from the signaling nodes on the directed graph of the PKN are considered non-reachable and are removed.

`expressed_genes`  
character vector. Names of nodes that are expressed. By default we consider all the nodes that appear in `diff_expression_data` with a numeric value (i.e. nodes with NA are removed)

`remove_unexpressed_nodes`  
if TRUE (default) removes nodes from the PKN that are not expressed, see input “`expressed_genes`”.

`filter_tf_gene_interaction_by_optimization`  
(default:TRUE), if TRUE then runs a network optimization that estimates TF activity not included in the inputs and checks the consistency between the estimated activity and change in gene expression. Removes interactions where TF and gene expression are inconsistent

`CARNIVAL_options`  
list that controls the options of CARNIVAL. See details in [default\\_CARNIVAL\\_options](#).

**Value**

`cosmos_data` object with the following fields:

`meta_network` Filtered PKN

`tf_regulon` TF - target regulatory network

`signaling_data_bin` Binarised signaling data

`metabolic_data` Metabolomics data

`diff_expression_data_bin` Binarized gene expression data

`optimized_network` Initial optimized network if `filter_tf_gene_interaction_by_optimization` is TRUE

**See Also**

[meta\\_network](#) for meta PKN, [load\\_tf\\_regulon\\_dorothea](#) for tf regulon, [runCARNIVAL](#).

**Examples**

```
data(toy_network)
data(toy_signaling_input)
data(toy_metabolic_input)
data(toy_RNA)
test_for <- preprocess_COSMOS_signaling_to_metabolism(meta_network = toy_network,
  signaling_data = toy_signaling_input,
  metabolic_data = toy_metabolic_input,
  diff_expression_data = toy_RNA,
  maximum_network_depth = 15,
  remove_unexpressed_nodes = TRUE,
  CARNIVAL_options = default_CARNIVAL_options("lpSolve"))
```

---

```
print.cosmos_data      Print Cosmos Data Summary Print a summary of cosmos data.
```

---

**Description**

Print Cosmos Data Summary Print a summary of cosmos data.

**Usage**

```
## S3 method for class 'cosmos_data'  
print(x, ...)
```

**Arguments**

x                    [cosmos\\_data](#) object. Use the [preprocess\\_COSMOS\\_signaling\\_to\\_metabolism](#) or [preprocess\\_COSMOS\\_metabolism\\_to\\_signaling](#) functions to create one.

...                  Further print arguments passed to or from other methods.

**Value**

input (invisible)

**See Also**

[print, cosmos\\_data](#)

---

```
reduce_solution_network  
                          reduce_solution_network
```

---

**Description**

Reduces a solution network based on a decoupling analysis of upstream and downstream gene expression, by filtering out edges that do not meet a consistency threshold, and limiting the network to a certain number of steps from upstream input nodes.

**Usage**

```
reduce_solution_network(  
  decoupleRnival_res,  
  meta_network,  
  cutoff,  
  upstream_input,  
  RNA_input = NULL,  
  n_steps = 10  
)
```

**Arguments**

decoupleRnival_res	A data frame resulting from the decoupleRnival function.
meta_network	A network data frame containing signed directed prior knowledge of molecular interactions.
cutoff	The consistency threshold for filtering edges from the solution network.
upstream_input	A named vector with up_stream nodes and their corresponding activity.
RNA_input	A named vector containing differential gene expression data.
n_steps	The maximum number of steps from upstream input nodes to include in the solution network.

**Value**

A list containing the solution network (SIF) and an attribute table (ATT) with gene expression data.

**Examples**

```
# Example input data
upstream_input <- c("A" = 1, "B" = -1, "C" = 0.5)
downstream_input <- c("D" = 2, "E" = -1.5)
meta_network <- data.frame(
  source = c("A", "A", "B", "C", "C", "D", "E"),
  target = c("B", "D", "D", "E", "D", "B", "A"),
  interaction = c(-1, 1, -1, 1, -1, -1, 1)
)
RNA_input <- c("A" = 1, "B" = -1, "C" = 5, "D" = 0.7, "E" = -0.3)

# Run the decoupleRnival function to get the upstream influence scores
upstream_scores <- decoupleRnival(upstream_input, downstream_input, meta_network, n_layers = 2, n_perm = 100)

# Reduce the solution network based on the upstream influence scores
reduced_network <- reduce_solution_network(upstream_scores, meta_network, 0.4, upstream_input, RNA_input, 3)

# View the resulting solution network and attribute table
print(reduced_network$SIF)
print(reduced_network$ATT)
```

---

```
run_COSMOS_metabolism_to_signaling
      run COSMOS metabolism to signaling
```

---

**Description**

Runs COSMOS from metabolism to signaling. This function uses CARNIVAL to find a subset of the prior knowledge network based on optimization that (1) includes the most measured and input nodes and (2) which is in agreement with the data. Use [preprocess\\_COSMOS\\_metabolism\\_to\\_signaling](#) to prepare the the inputs, measurements and the prior knowledge network.

**Usage**

```
run_COSMOS_metabolism_to_signaling(
  data,
  CARNIVAL_options = default_CARNIVAL_options("lpSolve")
)
```

**Arguments**

`data` [cosmos\\_data](#) object. Use the [preprocess\\_COSMOS\\_metabolism\\_to\\_signaling](#) function to create an instance.

`CARNIVAL_options` List that controls the options of CARNIVAL. See details in [default\\_CARNIVAL\\_options](#).

**Value**

List with the following elements:

`weightedSIF` The averaged networks found by optimization in a format of a Simple Interaction network, i.e. each row codes an edge

`N_networks` Number of solutions found by the optimization

`nodesAttributes` Estimated node properties

`individual_networks` List of optimal networks found

`individual_networks_node_attributes` Node activity in each network

**See Also**

[preprocess\\_COSMOS\\_metabolism\\_to\\_signaling](#), [runCARNIVAL](#), [cosmos\\_data](#)

**Examples**

```
data(toy_network)
data(toy_signaling_input)
data(toy_metabolic_input)
data(toy_RNA)
test_back <- preprocess_COSMOS_metabolism_to_signaling(meta_network = toy_network,
  signaling_data = toy_signaling_input,
  metabolic_data = toy_metabolic_input,
  diff_expression_data = toy_RNA,
  maximum_network_depth = 15,
  remove_unexpressed_nodes = TRUE,
  CARNIVAL_options = default_CARNIVAL_options("lpSolve"))

test_result_back <- run_COSMOS_metabolism_to_signaling(data = test_back,
  CARNIVAL_options = default_CARNIVAL_options("lpSolve"))
```

---

```
run_COSMOS_signaling_to_metabolism  
  run COSMOS signaling to metabolism
```

---

## Description

Runs COSMOS from signaling to metabolism. This function uses CARNIVAL to find a subset of the prior knowledge network based on optimisation that (1) includes the most measured and input nodes and (2) which is in agreement with the data. Use [preprocess\\_COSMOS\\_signaling\\_to\\_metabolism](#) to prepare inputs, measurements and prior knowledge network.

## Usage

```
run_COSMOS_signaling_to_metabolism(  
  data,  
  CARNIVAL_options = default_CARNIVAL_options("lpSolve")  
)
```

## Arguments

**data** [cosmos\\_data](#) object. Use the [preprocess\\_COSMOS\\_signaling\\_to\\_metabolism](#) function to create an instance.

**CARNIVAL\_options** List that controls the options of CARNIVAL. See details in [default\\_CARNIVAL\\_options](#).

## Value

List with the following elements:

**weightedSIF** The averaged networks found by optimization in a format of a Simple Interaction network, i.e. each row codes an edge

**N\_networks** Number of solutions found by the optimization

**nodesAttributes** Estimated node properties

**individual\_networks** List of optimal networks found

**individual\_networks\_node\_attributes** Node activity in each network

## See Also

[preprocess\\_COSMOS\\_metabolism\\_to\\_signaling](#), [runCARNIVAL](#), [cosmos\\_data](#)

## Examples

```
data(toy_network)  
data(toy_signaling_input)  
data(toy_metabolic_input)  
data(toy_RNA)  
test_for <- preprocess_COSMOS_signaling_to_metabolism(meta_network = toy_network,
```

```
signaling_data = toy_signaling_input,  
metabolic_data = toy_metabolic_input,  
diff_expression_data = toy_RNA,  
maximum_network_depth = 15,  
remove_unexpressed_nodes = TRUE,  
CARNIVAL_options = default_CARNIVAL_options("lpSolve"))  
  
test_result_for <- run_COSMOS_signaling_to_metabolism(data = test_for,  
CARNIVAL_options = default_CARNIVAL_options("lpSolve"))
```

---

toy\_metabolic\_input    *Toy Metabolic Input Data*

---

### Description

This metabolic data are a subset from the metabolic measurements of the 786-O cell line from the NCI60 dataset.

### Usage

```
data(toy_metabolic_input)
```

### Format

An object of class “numeric” containing the t-values of 2 metabolites, which are named with metabolite HMDB Ids matching the toy network.

### Source

Subset of: [https://github.com/saezlab/COSMOS\\_MSB/blob/main/data/metab\\_input\\_COSMOS.csv](https://github.com/saezlab/COSMOS_MSB/blob/main/data/metab_input_COSMOS.csv)

### References

Dugourd, A., Kuppe, C. and Sciacovelli, M. et. al. (2021) *Molecular Systems Biology*. **17**, e9730.

### Examples

```
data(toy_metabolic_input)
```



---

toy_network	<i>Toy Input Network</i>
-------------	--------------------------

---

### Description

This signaling network is the reduced COSMOS network solution obtained in the cosmos test on 786-O NCI60 data. Here, this network solution is reused as an exemplary input prior knowledge network (PKN).

### Usage

```
data(toy_network)
```

### Format

An object of class “data.frame” with 19 rows (interactions) and three variables:

source Source node, either metabolite or protein

interaction Type of interaction, 1 = Activation, -1 = Inhibition

target Target node, either metabolite or protein A detailed description of the identifier formatting can be found under [https://metapkn.omnipathdb.org/00\\_\\_README.txt](https://metapkn.omnipathdb.org/00__README.txt).

### Source

The network data are available on github: [https://github.com/saezlab/COSMOS\\_MSB/tree/main/results/COSMOS\\_result/COSMOS\\_res\\_session.RData](https://github.com/saezlab/COSMOS_MSB/tree/main/results/COSMOS_result/COSMOS_res_session.RData). The toy\_network is the combined network of the COSMOS network solutions CARNIVAL\_Result2 and CARNIVAL\_Result\_rerun subsequently reduced to 19 exemplary nodes.

### References

Dugourd, A., Kuppe, C. and Sciacovelli, M. et. al. (2021) *Molecular Systems Biology*. **17**, e9730.

### Examples

```
data(toy_network)
```

---

toy_RNA	<i>Toy Input Transcription Data Set</i>
---------	---

---

**Description**

This exemplary transcription data are the specific deregulated gene expression of the 786-O cell line from the NCI60 dataset.

**Usage**

```
data(toy_RNA)
```

**Format**

An object of class “numeric” containing the t-values of 9300 genes, which are named with gene symbols matching the toy network.

**Source**

[https://github.com/saezlab/COSMOS\\_MSB/blob/main/data/RNA\\_ttop\\_tumorvshealthy.csv](https://github.com/saezlab/COSMOS_MSB/blob/main/data/RNA_ttop_tumorvshealthy.csv)

**References**

Dugourd, A., Kuppe, C. and Sciacovelli, M. et. al. (2021) *Molecular Systems Biology*. **17**, e9730.

**Examples**

```
data(toy_RNA)
```

---

toy_signaling_input	<i>Toy Signaling Input</i>
---------------------	----------------------------

---

**Description**

This signaling data are a subset of the footprint-based signaling activity estimates of transcription factors of the 786-O cell line from the NCI60 dataset.

**Usage**

```
data(toy_signaling_input)
```

**Format**

An object of class “data.frame” containing the normalised enrichment scores (NES) of 2 signaling proteins, which are named with their respective gene Entrez ID matching the toy network.

**Source**

Subset of: [https://github.com/saezlab/COSMOS\\_MSB/blob/main/data/signaling\\_input\\_COSMOS.csv](https://github.com/saezlab/COSMOS_MSB/blob/main/data/signaling_input_COSMOS.csv)

**References**

Dugourd, A., Kuppe, C. and Sciacovelli, M. et. al. (2021) *Molecular Systems Biology*. **17**, e9730.

**Examples**

```
data(toy_signaling_input)
```

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