

Package ‘SimiCviz’

September 10, 2026

Type Package

Title Visualization Tools for Gene Regulatory Network Analysis

Version 0.99.2

Description Visualization and export utilities for SimiC and SimiCPipeline outputs.
The package focuses on importing SimiC-style results (e.g., weights, AUC metrics) from pickle/CSV files, processing and generating publication-ready plots (networks, heatmaps, distributions) and tables saved into a reproducible, ordered directory hierarchy.

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Encoding UTF-8

LazyData false

SystemRequirements Python (>= 3.8)

Depends R (>= 4.6)

Imports methods, stats, BiocParallel, viridisLite, utils, Matrix,
graphics, SummarizedExperiment, colorspace, gridExtra, ggplot2,
dplyr, tibble, tidyr, reshape2, scales, reticulate (>= 1.45.0)

Suggests knitr, rmarkdown, BiocStyle, testthat (>= 3.0.0)

VignetteBuilder knitr

URL <https://github.com/ML4BM-Lab/SimiCviz>

BugReports <https://github.com/ML4BM-Lab/SimiCviz/issues>

biocViews Software, Visualization, GeneRegulation, NetworkInference,
Network, SingleCell

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

git_url <https://git.bioconductor.org/packages/SimiCviz>

git_branch devel

git_last_commit ba290d2

git_last_commit_date 2026-07-04

Repository Bioconductor 3.24

Date/Publication 2026-09-09

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Contents

.compute_cell_auc	3
.ensure_genes_x_cells_format	3
.make_weight_barplot	4
.plot_weights_paginated	4
.subset_auc_for_label	5
.weights_to_long	6
AUCProcessor	6
AUCProcessor-class	7
auc_list_to_df	8
calculate_activity_scores	9
calculate_dissimilarity	10
calculate_ecdf_auc	11
compute_auc	12
compute_auc,AUCProcessor-method	13
export_SimiCviz_csv	13
get_auc	14
get_auc,AUCProcessor-method	15
get_tf_network	15
is.SimiCvizExperiment	16
load_cell_labels	17
load_collected_auc	18
load_expression_matrix	18
load_from_csv	19
load_SimiCPipeline	20
plot_auc_cumulative	21
plot_auc_distributions	22
plot_auc_heatmap	23
plot_auc_summary_statistics	24
plot_dissimilarity_heatmap	25
plot_r2_distribution	26
plot_target_weights	27
plot_tf_network_heatmap	28
plot_tf_weights	30
read_auc_csv	31
read_auc_pickle	31
read_pickle	32
read_weights_csv	32
read_weights_pickle	33
setCellLabels	34
setLabelNames	34
SimiCviz	35
SimiCvizExperiment	36
SimiCvizExperiment-class	37

<code>.compute_cell_auc</code>	<i>Compute AUC for a single cell</i>
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Description

Compute AUC for a single cell

Usage

```
.compute_cell_auc(  
  expr_row,  
  weight_df,  
  target_norm,  
  sort_by,  
  select_top_k = NULL,  
  percent_of_target = 1  
)
```

Arguments

<code>expr_row</code>	expression values for target genes (vector)
<code>weight_df</code>	weight data.frame subset for this cell's label (columns: tf, target, weight)
<code>target_norm</code>	precomputed Euclidean norm of target expression (vector)
<code>sort_by</code>	sorting criterion ("expression" or "weight")
<code>select_top_k</code>	keep only top K targets per TF (NULL = all)
<code>percent_of_target</code>	percentage of targets to use (0-1)

Value

named vector of AUC scores (one per TF)

<code>.ensure_genes_x_cells_format</code>	<i>Validate expression matrix is in genes x cells format</i>
---	--

Description

Strictly enforces that expression matrix is in genes x cells format with column names matching cell identifiers in `cell_labels`.

Usage

```
.ensure_genes_x_cells_format(expr_mat, cell_labels)
```

Arguments

<code>expr_mat</code>	expression matrix
<code>cell_labels</code>	data.frame with cell identifiers in 'cell' column

Value

expression matrix (genes x cells) with validated dimensions

`.make_weight_barplot` *Render a single weight barplot on a ggplot*

Description

Render a single weight barplot on a ggplot

Usage

```
.make_weight_barplot(
  df,
  gene_name,
  gene_type,
  col_map,
  top_n = NULL,
  allowed_genes = NULL
)
```

Arguments

<code>df</code>	long-format data.frame (already subsetting) with columns: <code>gene</code> , <code>weight</code> , <code>label_name</code>
<code>gene_name</code>	character
<code>gene_type</code>	character; "tf" or "target"
<code>col_map</code>	named character vector of colours (keyed by <code>label_name</code>)
<code>top_n</code>	integer or NULL; keep only top N partners by mean abs weight
<code>allowed_genes</code>	character vector or NULL; restrict partner genes to this set

Value

ggplot object

`.plot_weights_paginated`
Shared paginated weight barplot engine

Description

Shared paginated weight barplot engine

Usage

```
.plot_weights_paginated(
  x,
  gene_names = NULL,
  gene_type = c("tf", "target"),
  labels = NULL,
  top_n = NULL,
  allowed_targets = NULL,
  grid = c(4L, 1L),
  save = FALSE,
  filename = NULL,
  out_dir = getwd(),
  width = 16,
  height = NULL
)
```

Arguments

<code>x</code>	SimiCvizExperiment
<code>gene_names</code>	character vector or NULL (all genes of that type)
<code>gene_type</code>	"tf" or "target"
<code>labels</code>	integer vector of labels (default: all)
<code>top_n</code>	integer or NULL; max partners shown per gene (TF mode only)
<code>allowed_targets</code>	character vector or NULL; restrict targets to this set (TF mode only; use to pass pre-filtered target lists)
<code>grid</code>	integer vector c(nrow, ncol) per page; NULL = single page
<code>save</code>	logical
<code>filename</code>	PDF filename
<code>out_dir</code>	output directory
<code>width, height</code>	page dimensions in inches

Value

Invisibly, list of page grobs.

`.subset_auc_for_label` *Subset collected AUC for a specific label*

Description

Subset collected AUC for a specific label

Usage

```
.subset_auc_for_label(x, label)
```

<code>.weights_to_long</code>	<i>Convert weight list to long-format data frame</i>
-------------------------------	--

Description

Convert weight list to long-format data frame

Usage

```
.weights_to_long(x)
```

Arguments

<code>x</code>	<code>SimiCvizExperiment</code>
----------------	---------------------------------

Value

data.frame with columns: tf, target, weight, label, label_name

<code>AUCProcessor</code>	<i>Initialize AUCProcessor</i>
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Description

Initialize AUCProcessor

Usage

```
AUCProcessor(
  weights,
  expression,
  cell_labels,
  qc_type = NULL,
  qc_threshold = 0.7,
  adj_r2_list = NULL,
  n_cores = 1,
  backend = "sequential"
)
```

Arguments

<code>weights</code>	list with weight matrices per label (if simic input) or data.frame with columns: tf, target, weight, label, tf (if data.frame input). <code>adj_p_val</code> (optional, for p-value filtering <code>'qc_type' = "p_value"</code>).
<code>expression</code>	expression matrix (cells x cells) or path to file. IMPORTANT: Expression must be in genes x cells format (genes as rows, cells as columns), matching Seurat/SingleCellExperiment conventions.
<code>cell_labels</code>	data.frame with cell-to-label mapping

qc_type	character type of quality metric. Values: "adj_r2" or other column name (pvalue, adj_p_val, etc.) provided in weights in data.frame format. If "adj_r2", targets with R2 below threshold are filtered out. If other (i.e. "p_value"), targets with qc_metric above threshold are filtered out.
qc_threshold	threshold for filtering targets based on qc_metric (default: 0.7 for R2).
adj_r2_list	(optional) A list of R2 values per label per Only used if weights are provided in list format qc_type is "adj_r2".
n_cores	number of cores for parallelization (default: 1)
backend	parallelization backend ("sequential", "multicore", "multisession")

Value

A [AUCProcessor](#) object with initialized slots.

Examples

```
weight_path <- system.file("extdata", "example_weights.csv",
                           package = "SimiCviz")
weights_df <- read_weights_csv(weight_path)
expression_mat_path <- system.file("extdata",
                                   file.path("inputFiles", "example_expression.pickle"),
                                   package = "SimiCviz")
cell_labels_path <- system.file("extdata",
                                file.path("inputFiles", "disease_stage_annotation.csv"),
                                package = "SimiCviz")
cell_labels <- load_cell_labels(cell_labels_path, header = TRUE, sep = ",")

AS_processor <- AUCProcessor(weights = weights_df,
                             expression = expression_mat_path,
                             cell_labels = cell_labels,
                             qc_type = "adj_p_val",
                             qc_threshold = 0.05, # Filter targets above
                             n_cores = 2,
                             backend = "multisession")
```

AUCProcessor-class	<i>AUCProcessor class</i>
--------------------	---------------------------

Description

Efficient calculator for TF activity scores (AUC) based on GRN weights and cell-specific expression.

Usage

```
## S4 method for signature 'AUCProcessor'
show(object)
```

Arguments

object A [AUCProcessor](#) object.

Value

An object of class AUCProcessor with slots for weights, expression, and computed AUC scores.

Slots

weights list with weight matrices per label (TFs x targets)
 expression data.frame or matrix (genes x cells)
 cell_labels data.frame with columns 'cell' and 'label'
 target_ids character vector of target gene IDs
 tf_ids character vector of TF gene IDs
 auc_results matrix to store computed activity scores (cells x TFs)
 parallel_params list with parallelization settings

Examples

```
# Initialize an AUCProcessor object
weights_list <- list("0" = as.data.frame(matrix(rnorm(90), nrow = 3,
                                                dimnames = list(paste0("TF", 1:3),
                                                                paste0("Gene", 1:30)))),
                    "1" = as.data.frame(matrix(rnorm(90), nrow = 3,
                                                dimnames = list(paste0("TF", 1:3),
                                                                paste0("Gene", 1:30)))))
cell_labels <- data.frame(cell= c("Cell1", "Cell2"), label = c("0", "1"))
expr <- matrix(rnorm(60), nrow=2, byrow = FALSE,
              dimnames = list(c("Cell1", "Cell2"),paste0("Gene", 1:30)))

processor <- AUCProcessor(weights = weights_list,
                          expression = expr,
                          cell_labels = cell_labels)
```

auc_list_to_df

Collect per-label AUC matrices using cell labels

Description

Given a list of AUC matrices (one per label) and a cell-labels data.frame, subsets each matrix to include only the cells belonging to that label and collects them into a single data.frame. This is a helper function to transform raw per-label AUC outputs into the "collected" format used by SimiCvizExperiment@auc.

Usage

```
auc_list_to_df(auc_list, cell_labels_df)
```

Arguments

auc_list Named list of AUC matrices (cells × TFs). Names should correspond to label identifiers (e.g. "0", "1").

cell_labels_df A data.frame with columns cell and label, as returned by [load_cell_labels](#).

Value

A data.frame with cells in rows and TFs in columns, containing the activity scores for the specific labels.

Examples

```
# Example usage with per-label AUC matrices
auc_list <- list("0" = matrix(rnorm(100), nrow = 10,
                             dimnames = list(paste0("cell_", 1:10),
                                             paste0("TF", 1:10))),
               "1" = matrix(rnorm(100), nrow = 10,
                             dimnames = list(paste0("cell_", 1:10),
                                             paste0("TF", 1:10))))
cell_labels_df <- data.frame(cell = paste0("cell_", 1:10),
                             label = c(rep(0, 5), rep(1, 5)))
collected_auc <- auc_list_to_df(auc_list, cell_labels_df)
```

calculate_activity_scores

Calculate activity scores from SimiCvizExperiment weights

Description

Efficiently computes TF activity scores for all cells using label-specific GRNs. Avoids redundant computation by calculating only for each cell's corresponding label.

Usage

```
calculate_activity_scores(
  simic,
  expression = NULL,
  adj_r2_threshold = NULL,
  sort_by = "expression",
  select_top_k = NULL,
  percent_of_target = 1,
  n_cores = 1,
  backend = "sequential",
  verbose = TRUE
)
```

Arguments

simic	SimiCvizExperiment object with weights and expression data
expression	expression matrix (cells x genes). If NULL, uses data from metadata or file path if available.
adj_r2_threshold	minimum adjusted R2 for target filtering (default: 0.7)
sort_by	sorting criterion ("expression", "weight", or "adj_r2")
select_top_k	keep only top K targets per TF (NULL = all)

percent_of_target	percentage of targets to use (0-1)
n_cores	number of cores for parallelization (1 = sequential)
backend	parallelization backend ("sequential", "multicore", "multisession")
verbose	print progress messages

Value

SimiCvizExperiment with computed AUC scores added to @auc slot

Examples

```
# Generate minimal example data
weights_list <- list("0" = as.data.frame(matrix(rnorm(90), nrow = 3,
                                                dimnames = list(paste0("TF", 1:3),
                                                                paste0("Gene", 1:30)))),
                    "1" = as.data.frame(matrix(rnorm(90), nrow = 3,
                                                dimnames = list(paste0("TF", 1:3),
                                                                paste0("Gene", 1:30))))))
cell_labels <- data.frame(cell= c("Cell1", "Cell2"), label = c("0", "1"))
simic <- SimiCvizExperiment(weights = weights_list, cell_labels = cell_labels)
expr <- matrix(rnorm(60), nrow=2, byrow = FALSE,
              dimnames = list(c("Cell1", "Cell2"),paste0("Gene", 1:30)))
simic <- calculate_activity_scores(simic,
                                expression = expr,
                                sort_by = "expression",
                                n_cores = 2,
                                backend ="multicore")
```

calculate_dissimilarity

Calculate dissimilarity scores across phenotype labels

Description

Compares per-cell TF activity-score distributions between phenotype labels using a histogram-based MinMax divergence.

Usage

```
calculate_dissimilarity(
  x,
  labels = NULL,
  cell_groups = NULL,
  n_breaks = 100L,
  verbose = TRUE
)
```

Arguments

x	A SimiCvizExperiment object.
labels	Integer vector of label keys or character vector of label display names to compare (default: all labels). Mixing types is allowed.
cell_groups	Optional named list mapping group names to character vectors of cell identifiers.
n_breaks	Number of histogram bins (default 100).
verbose	Logical; print progress messages (default TRUE).

Value

A data.frame with TFs as rows, sorted by score (descending).

Examples

```
simic <- readRDS(system.file("extdata", "simic_full.rds",
                             package = "SimiCviz"))
dis_score <- calculate_dissimilarity(simic)
```

calculate_ecdf_auc	<i>Calculate ECDF AUC</i>
--------------------	---------------------------

Description

Calculates the area under the empirical cumulative distribution function.

Usage

```
calculate_ecdf_auc(
  x,
  tf_names = NULL,
  labels = NULL,
  integration_range = c(0, 1),
  percentile = 0.5
)
```

Arguments

x	A SimiCvizExperiment object.
tf_names	Optional TF identifiers to evaluate. Defaults to all TFs in collected AUC data.
labels	Optional labels to evaluate. Accepts label ids or label names.
integration_range	Numeric vector of length 2 defining lower and upper bounds for integration.
percentile	Percentile used to compute the auxiliary AUC50/x_at_p50 metrics.

Value

A data.frame with one row per TF and per-label ECDF-derived metrics.

Examples

```
simic <- readRDS(system.file("extdata", "simic_full.rds", package = "SimiCviz"))
ecdf_metrics <- calculate_ecdf_auc(simic, tf_names = c("MEF2D", "SATB1"))
head(ecdf_metrics)
```

compute_auc

Compute activity scores for an object

Description

S4 generic for computing TF activity scores (AUC-like metrics).

Usage

```
compute_auc(object, ...)
```

Arguments

object An object that implements a compute_auc method.

... Additional method-specific arguments.

Value

Object with computed activity scores.

Examples

```
weights_list <- list("0" = as.data.frame(matrix(rnorm(90), nrow = 3,
  dimnames = list(paste0("TF", 1:3),
    paste0("Gene", 1:30)))),
  "1" = as.data.frame(matrix(rnorm(90), nrow = 3,
  dimnames = list(paste0("TF", 1:3),
    paste0("Gene", 1:30))))))
cell_labels <- data.frame(cell= c("Cell1", "Cell2"), label = c("0", "1"))
expr <- matrix(rnorm(60), nrow=2, byrow = FALSE,
  dimnames = list(c("Cell1", "Cell2"),paste0("Gene", 1:30)))

processor <- AUCProcessor(weights = weights_list,
  expression = expr,
  cell_labels = cell_labels)
processor <- compute_auc(processor, sort_by = "expression")
```

compute_auc, AUCProcessor-method

Compute activity scores for all cells

Description

Efficiently calculates TF activity scores for each cell using its corresponding label-specific GRN. Uses BiocParallel for parallelization.

Usage

```
## S4 method for signature 'AUCProcessor'
compute_auc(
  object,
  sort_by = "expression",
  select_top_k = NULL,
  percent_of_target = 1,
  verbose = TRUE
)
```

Arguments

object	A AUCProcessor object.
sort_by	sorting criterion ("expression" or "weight")
select_top_k	keep only top K targets per TF (NULL = use all)
percent_of_target	percentage of targets to use (0-1)
verbose	print progress messages

Value

A [AUCProcessor](#) object with computed scores in the auc_results slot.

export_SimiCviz_csv *Export SimiCvizExperiment tables to CSV*

Description

Exports weights and AUC tables into an organized directory structure:

data/weights weights tables

data/auc AUC tables (collected cells × TF format)

Usage

```
export_SimiCviz_csv(x, out_dir, prefix = "SimiCviz", overwrite = FALSE)
```

Arguments

x [SimiCvizExperiment](#) object.
out_dir root output directory.
prefix filename prefix (default: "SimiCviz").
overwrite logical; overwrite existing files.

Value

Invisibly, a list of file paths.

Examples

```
simic <- readRDS(system.file("extdata", "simic_full.rds",
                             package = "SimiCviz"))
export_SimiCviz_csv(simic, out_dir = tempdir(), prefix = "simic_export")
```

get_auc	<i>Extract activity scores from an object</i>
---------	---

Description

S4 generic for retrieving computed TF activity scores.

Usage

```
get_auc(object, ...)
```

Arguments

object An object that implements a get_auc method.
... Additional method-specific arguments.

Value

Extracted activity scores.

Examples

```
#' # Generate minimal example data
weights_list <- list("0" = as.data.frame(matrix(rnorm(90), nrow = 3,
                                                dimnames = list(paste0("TF", 1:3),
                                                                paste0("Gene", 1:30)))),
                    "1" = as.data.frame(matrix(rnorm(90), nrow = 3,
                                                dimnames = list(paste0("TF", 1:3),
                                                                paste0("Gene", 1:30))))))
cell_labels <- data.frame(cell= c("Cell1", "Cell2"), label = c("0", "1"))
set.seed(123)
expr <- matrix(rnorm(60), nrow=2, byrow = FALSE,
              dimnames = list(c("Cell1", "Cell2"), paste0("Gene", 1:30)))

processor <- AUCProcessor(weights = weights_list,
                        expression = expr,
```

```

                                cell_labels = cell_labels)
processor <- compute_auc(processor, sort_by = "expression")
auc_scores <- get_auc(processor)
head(auc_scores)
#           TF1           TF2           TF3
# Cell1 0.5308869 0.5307807 0.5618426
# Cell2 0.5752393 0.5399460 0.5304443

```

get_auc,AUCProcessor-method

Get computed activity scores

Description

Get computed activity scores

Usage

```

## S4 method for signature 'AUCProcessor'
get_auc(object, format = "wide")

```

Arguments

object	A AUCProcessor object.
format	Output format: "wide" for cells x TF table, or "long" for long format with columns cell, tf, score, and label.

Value

A data.frame with activity scores in the requested format.

get_tf_network

Extract stacked TF-target weight matrix across labels

Description

For a given TF, extracts the regulatory weight for every target gene in each label. Targets whose adjusted R^2 falls below `r2_threshold` in a given label receive NA (analogous to Python's `get_TF_network(..., stacked=TRUE)`).

Usage

```
get_tf_network(x, tf_name, labels = NULL, r2_threshold = NULL)
```

Arguments

x	A <code>SimiCvizExperiment</code> object.
tf_name	Character; name of the transcription factor.
labels	Integer vector of labels to include (default: all).
r2_threshold	Numeric or NULL. If non-NULL, weights for targets with adjusted R^2 below this value are set to NA.

Value

A data.frame with target genes as rows and one column per label (named by label_names).

Examples

```
# Example usage
simic <- readRDS(system.file("extdata", "simic_full.rds",
                             package = "SimiCviz"))
network <- get_tf_network(simic, c("MEF2D"),
                          labels = c(0, 1),
                          r2_threshold = 0.7)

print(network)
```

is.SimiCvizExperiment *Check if object is a SimiCvizExperiment*

Description

Tests whether an object is of class SimiCvizExperiment.

Usage

```
is.SimiCvizExperiment(x)
```

Arguments

x An object to test.

Value

Logical, TRUE if x is a SimiCvizExperiment.

Examples

```
weights_list <- list("0" = as.data.frame(matrix(rnorm(90), nrow = 3,
                                                dimnames = list(paste0("TF", 1:3),
                                                                paste0("Gene", 1:30)))),
                    "1" = as.data.frame(matrix(rnorm(90), nrow = 3),
                                                dimnames = list(paste0("TF", 1:3),
                                                                paste0("Gene", 1:30))))

simic <- SimiCvizExperiment(weights = weights_list)
is.SimiCvizExperiment(simic) # should return TRUE
```

load_cell_labels	<i>Load cell-to-label mapping</i>
------------------	-----------------------------------

Description

Reads or constructs a two-column `data.frame` (`cell`, `label`) from various input formats.

Usage

```
load_cell_labels(x, ...)
```

Arguments

<code>x</code>	One of: character (length 1) Path to a CSV / TSV file. If the file has columns named <code>cell</code> and <code>label</code> they are used directly. Otherwise the first column is treated as <code>cell</code> and the second as <code>label</code> . A single-column file (or headerless file with one field) is treated as a label-only vector — see next bullet. character / integer / numeric vector A vector of labels, one per cell, in the same order as rows of the AUC matrix. Cell IDs are generated as <code>cell_1</code> , <code>cell_2</code> , named vector Names are used as cell IDs and values as labels. data.frame Must contain columns <code>cell</code> and <code>label</code> , or exactly two columns (first = <code>cell</code> , second = <code>label</code>).
<code>...</code>	Additional arguments passed to file readers when <code>x</code> is a path.

Value

A `data.frame` with columns `cell` (`character`) and `label` (`integer`), sorted by `cell`.

Examples

```
cell_labels_path <- system.file("extdata",
                                file.path("inputFiles", "disease_stage_annotation.csv"),
                                package = "SimiCviz")
cell_labels <- load_cell_labels(cell_labels_path, header = TRUE, sep = ",")
head(cell_labels)
#           cell category label
# 1 AGGGTGATCTGAGGGA-1-NBM-10.138P      NBM      0
# 2 CCTAGCTTCTCCAACC-1-NBM-1.138P      NBM      0
# 3 ATTACTCTCGTGGTCG-1-NBM-10.138P      NBM      0
# 4 TAAGAGAAGCCGCCTA-1-NBM-8.138P      NBM      0
# 5 GATCGATTGAGAGGTG-1-NBM-8.138P      NBM      0
# 6 ACATCAGGTCGCGGTT-1-NBM-10.138P      NBM      0
```

load_collected_auc	<i>Load a collected AUC CSV into a data.frame</i>
--------------------	---

Description

Reads a cells $\times$ TF CSV file (as written by internal function `.save_collected_auc` or `SimiCPipeline`). This is the canonical import for any GRN method that produces per-cell TF activity scores.

Usage

```
load_collected_auc(file, ...)
```

Arguments

<code>file</code>	Path to a CSV file with cells in rows and TFs in columns.
<code>...</code>	Additional arguments passed to read.csv .

Value

A data.frame with cell IDs as row names.

Examples

```
auc_file <- system.file("extdata",
  file.path("outputSimic/example_simic_auc_collected.csv"),
  package = "SimiCviz")
auc_df <- load_collected_auc(auc_file)
```

load_expression_matrix

Load expression matrix from various sources /file formats Allowed formats:

- *CSV file*
 - *h5ad file*
 - *rds file (Seurat or SingleCellExperiment object)*
 - *matrix or data.frame in R*
-

Description

Load expression matrix from various sources /file formats Allowed formats:

- CSV file
- h5ad file
- rds file (Seurat or SingleCellExperiment object)
- matrix or data.frame in R

Usage

```
load_expression_matrix(expression)
```

Arguments

expression file path, matrix, or data.frame

Value

expression matrix

Examples

```
expression_mat_path <- system.file("extdata",
                                   file.path("inputFiles", "example_expression.pickle"),
                                   package = "SimiCviz")
expression_mat <- load_expression_matrix(expression_mat_path)
```

load_from_csv

*Create a SimiCvizExperiment from CSV files***Description**

Create a SimiCvizExperiment from CSV files

Usage

```
load_from_csv(
  weights_file,
  auc_file = NULL,
  cell_labels_file = NULL,
  meta = list()
)
```

Arguments

weights_file CSV with weights (long format: tf, target, weight, and optionally label).
 auc_file optional CSV with AUC metrics (collected cells × TF format).
 cell_labels_file optional CSV with cell labels (required columns: cell, label).
 meta optional named list with metadata.

Value

[SimiCvizExperiment](#) object.

Examples

```
# Example usage with CSV files
weight_path <- system.file("extdata", "example_weights.csv",
                           package = "SimiCviz")
auc_path <- system.file("extdata", "example_auc.csv",
                        package = "SimiCviz")
cell_labels_path <- system.file("extdata",
                                file.path("inputFiles", "disease_stage_annotation.csv"),
                                package = "SimiCviz")
simic <- load_from_csv(weights_file = weight_path,
                      auc_file = auc_path,
                      cell_labels_file = cell_labels_path,
                      meta = list(run_name = "example_run"))
is.SimiCvizExperiment(simic) # TRUE
```

load_SimiCPipeline	Create a SimiCvizExperiment from SimiCPipeline output path
--------------------	--

Description

Loads weights and AUC data following this priority chain for AUC:

1. Collected CSV (cells $\times$ TF, all labels merged) load_collected_auc
2. Per-label pickle $\rightarrow$ collect $\rightarrow$ save CSV read_auc_pickle $\rightarrow$ auc_list_to_df $\rightarrow$.save_collected_auc (internal)

Usage

```
load_SimiCPipeline(
  project_dir,
  run_name = NULL,
  lambda1 = NULL,
  lambda2 = NULL,
  meta = list()
)
```

Arguments

project_dir	root directory of a SimiCPipeline project.
run_name	name of the run experiment.
lambda1	L1 regularization parameter.
lambda2	L2 regularization parameter.
meta	optional named list with metadata.

Details

The canonical AUC format stored in `SimiCvizExperiment@auc` is always a single data.frame with cells in rows and TFs in columns (the "collected" format), compatible with any GRN method producing per-cell TF activity scores.

Value

`SimiCvizExperiment` object.

Examples

```
# simic_full <- load_SimiCPipeline(
#   project_dir = "path/to/simic_run",
#   run_name    = "example",
#   lambda1     = "0.01",
#   lambda2     = "0.001")
```

plot_auc_cumulative	<i>Plot AUC cumulative (ECDF) curves by label</i>
---------------------	---

Description

Plot AUC cumulative (ECDF) curves by label

Usage

```
plot_auc_cumulative(
  x,
  tf_names = NULL,
  labels = NULL,
  alpha = 0.8,
  rug = FALSE,
  grid = c(4L, 2L),
  percentile = 0.5,
  include_table = TRUE,
  save = FALSE,
  filename = NULL,
  out_dir = getwd(),
  width = 14,
  height = NULL
)
```

Arguments

<code>x</code>	A <code>SimiCvizExperiment</code> object.
<code>tf_names</code>	Optional TF identifiers to plot. Defaults to all available.
<code>labels</code>	Optional labels to include.
<code>alpha</code>	Line transparency for ECDF curves.
<code>rug</code>	Logical; draw rug marks at the x-axis.
<code>grid</code>	Integer vector <code>c(nrow, ncol)</code> for page layout.
<code>percentile</code>	Percentile used in ECDF summary metrics.
<code>include_table</code>	Logical; add ECDF metrics table below each panel.
<code>save</code>	Logical; save to PDF.
<code>filename</code>	Output filename when <code>save = TRUE</code> .
<code>out_dir</code>	Output directory when <code>save = TRUE</code> .
<code>width, height</code>	Output page dimensions.

Value

Invisibly, a list of grobs/plots.

Examples

```
simic <- readRDS(system.file("extdata", "simic_full.rds", package = "SimiCviz"))
plot_auc_cumulative(
  simic,
  tf_names = c("MEF2D", "SATB1"),
  rug = TRUE,
  grid = c(1L, 2L)
)
```

plot_auc_distributions

Plot AUC density distributions by label

Description

Plot AUC density distributions by label

Usage

```
plot_auc_distributions(
  x,
  tf_names = NULL,
  labels = NULL,
  fill = TRUE,
  alpha = 0.5,
  bw_adjust = 1,
  rug = FALSE,
  grid = c(4L, 2L),
  save = FALSE,
  filename = NULL,
  out_dir = getwd(),
  width = 14,
  height = NULL
)
```

Arguments

x	A SimiCvizExperiment object.
tf_names	Optional TF identifiers to plot. Defaults to all available.
labels	Optional labels to include.
fill	Logical; if TRUE, draw filled densities.
alpha	Density transparency.
bw_adjust	Bandwidth adjustment passed to density estimation.
rug	Logical; draw rug marks.

grid	Integer vector <code>c(nrow, ncol)</code> for page layout. Use <code>NULL</code> for a single auto-sized page.
save	Logical; save to PDF.
filename	Output filename when <code>save = TRUE</code> .
out_dir	Output directory when <code>save = TRUE</code> .
width, height	Output page dimensions.

Value

Invisibly, a list of ggplot objects.

Examples

```
simic <- readRDS(system.file("extdata", "simic_full.rds", package = "SimiCviz"))
plot_auc_distributions(
  simic,
  tf_names = c("MEF2D", "SATB1"),
  fill      = TRUE,
  alpha     = 0.6,
  bw_adjust = 1/8,
  rug       = TRUE,
  grid      = c(1L, 2L)
)
```

plot_auc_heatmap	<i>Plot mean AUC heatmap by TF and label</i>
------------------	--

Description

Plot mean AUC heatmap by TF and label

Usage

```
plot_auc_heatmap(
  x,
  tf_names = NULL,
  labels = NULL,
  top_n = NULL,
  cmap = "cividis",
  save = FALSE,
  filename = NULL,
  out_dir = getwd(),
  width = 10,
  height = NULL
)
```

Arguments

x	A SimiCvizExperiment object.
tf_names	Optional TF identifiers to plot. Defaults to all available.
labels	Optional labels to include.
top_n	Optional number of TFs to keep by dynamic range.
cmap	Colour map specification passed to internal palette helpers.
save	Logical; save to PDF.
filename	Output filename when save = TRUE.
out_dir	Output directory when save = TRUE.
width, height	Output page dimensions.

Value

Invisibly, the ggplot object.

Examples

```
simic <- readRDS(system.file("extdata", "simic_full.rds", package = "SimiCviz"))
plot_auc_heatmap(simic, top_n = 5)
```

```
plot_auc_summary_statistics
```

Plot AUC summary statistics

Description

Plot AUC summary statistics

Usage

```
plot_auc_summary_statistics(
  x,
  labels = NULL,
  high_threshold = 0.5,
  save = FALSE,
  filename = NULL,
  out_dir = getwd(),
  width = 14,
  height = 10
)
```

Arguments

x	A SimiCvizExperiment object.
labels	Optional labels to include.
high_threshold	Threshold used to count highly active TFs.
save	Logical; save to PDF.
filename	Output filename when save = TRUE.
out_dir	Output directory when save = TRUE.
width, height	Output page dimensions.

Value

Invisibly, a named list of plot objects.

Examples

```
simic <- readRDS(system.file("extdata", "simic_full.rds", package = "SimiCviz"))
plot_auc_summary_statistics(simic)
```

```
plot_dissimilarity_heatmap
      Plot dissimilarity heatmap
```

Description

Displays a heatmap of TF regulatory dissimilarity scores, optionally broken down by cell group. Uses **ggplot2** tile geometry.

Usage

```
plot_dissimilarity_heatmap(
  x,
  top_n = NULL,
  sort_by = NULL,
  dissim_df = NULL,
  cmap = NULL,
  show_values = TRUE,
  save = FALSE,
  out_dir = getwd(),
  filename = NULL,
  width = NULL,
  height = NULL,
  ...
)
```

Arguments

x	A SimiCvizExperiment object.
top_n	Integer; number of top TFs to display (default: all).
sort_by	Column name to sort TFs by. Default: "MinMax_score" (no groups) or "mean_score" (groups).
dissim_df	Optional pre-computed dissimilarity data.frame. If NULL, calculate_dissimilarity is called internally.
cmap	Colour palette specification. Can be: • A viridis palette name: "viridis", "magma", "plasma", "inferno", or "cividis" (requires viridisLite). • A single colour string (gradient from white to that colour). • A character vector of 2+ colours for a custom gradient. • NULL (default): built-in viridis-like gradient.
show_values	Logical; annotate cells with numeric values (default TRUE).

save	Logical; save the plot to a PDF file (default TRUE).
out_dir	Output directory for the PDF (default: working directory).
filename	Custom filename (default: auto-generated).
width, height	PDF dimensions in inches.
...	Additional arguments passed to calculate_dissimilarity.

Value

Invisibly, a list with plot (the ggplot object) and data (the dissimilarity data.frame).

Examples

```
simic <- readRDS(system.file("extdata", "simic_full.rds",
                             package = "SimiCviz"))
plot_dissimilarity_heatmap(simic, top_n = 20)
plot_dissimilarity_heatmap(simic, top_n = 5, cmap = "magma")
plot_dissimilarity_heatmap(simic, cmap = c("white", "red", "darkred"),
                           show_values = FALSE)
```

plot_r2_distribution *Plot adjusted R² distributions*

Description

Plots histograms of adjusted R² values per label, similar to the Python SimiCVisualization\$plot_r2_distribution.

Usage

```
plot_r2_distribution(
  adjusted_r_squared,
  x = NULL,
  labels = NULL,
  threshold = 0.7,
  grid = NULL,
  save = FALSE,
  filename = NULL,
  out_dir = getwd(),
  width = 10,
  height = NULL
)
```

Arguments

adjusted_r_squared

A **named list** of numeric vectors, one per label. Names must be label identifiers (e.g. "0", "1", ...). This metric is specific to SimiC's regression step; other methods may not produce it, so it is kept as an explicit input rather than extracted from the experiment object.

x	Optional SimiCvizExperiment object used solely to resolve display names and colors for labels. If NULL, default "Label i" naming and a built-in palette are used.
labels	Optional vector of labels to plot (subset of names(adjusted_r_squared)). Defaults to all.
threshold	Numeric R^2 threshold line and summary-statistic cutoff (default 0.7).
grid	Optional numeric vector of length 2: c(nrow, ncol). If NULL, one label per row is used.
save	logical; save to PDF (default FALSE).
filename	PDF filename (default "R2_distributions.pdf").
out_dir	output directory (default getwd()).
width, height	page dimensions in inches (defaults 10 x 5*nrow).

Value

Called for side effects (plots). Returns invisible(NULL).

Examples

```
simic <- readRDS(system.file("extdata", "simic_full.rds",
                             package = "SimiCviz"))
plot_r2_distribution(simic@meta$adjusted_r_squared, simic,
                    grid = c(2, 2))
plot_r2_distribution(simic@meta$adjusted_r_squared, simic,
                    threshold = 0.9, labels = c(0, 1))
```

plot_target_weights	<i>Plot weight barplots for target genes</i>
---------------------	--

Description

For each target gene, shows a grouped bar chart of incoming regulatory weights from all TFs, coloured by phenotype label. Mirrors SimiCVisualization.plot_target_weights from the Python package.

Usage

```
plot_target_weights(
  x,
  target_names = NULL,
  labels = NULL,
  grid = c(4L, 1L),
  top_n = NULL,
  save = FALSE,
  filename = NULL,
  out_dir = getwd(),
  width = 12,
  height = NULL
)
```

Arguments

x	SimiCvizExperiment
target_names	character vector of targets to plot (default: all)
labels	integer or character vector of labels (default: all)
grid	integer vector c(nrow, ncol) per page (default c(4, 1)). Set NULL for a single page.
top_n	Optional integer. Currently accepted for API compatibility; ignored in target mode.
save	logical; save to PDF (default FALSE)
filename	PDF filename (default "target_weights.pdf")
out_dir	output directory (default getwd())
width, height	page dimensions in inches

Value

Invisibly, a list of page grobs.

Examples

```
simic <- readRDS(system.file("extdata", "simic_full.rds",
                             package = "SimiCviz"))
plot_target_weights(simic,
                    target_names = c("CD79A", "IGHM"),
                    labels = c(0, 1), grid = c(2, 1))
```

plot_tf_network_heatmap

Plot heatmap of a TF regulatory network across phenotypes

Description

Displays a heatmap showing the regulatory weights of a single transcription factor across its top target genes, with one column per phenotype label. Targets that fail the adjusted- R^2 filter are shown as grey cells labelled " $< R^2$ threshold", mirroring the Python SimiCVisualization.plot_tf_network_heatmap() method.

Usage

```
plot_tf_network_heatmap(
  x,
  tf_name,
  labels = NULL,
  top_n = 10L,
  r2_threshold = NULL,
  cmap = c("blue", "white", "red"),
  show_values = TRUE,
  save = FALSE,
  filename = NULL,
  out_dir = getwd(),
```

```

    width = NULL,
    height = NULL
  )

```

Arguments

<code>x</code>	A SimiCvizExperiment object.
<code>tf_name</code>	Character; name of the transcription factor to plot.
<code>labels</code>	Integer or character vector of labels to include (default: all).
<code>top_n</code>	Integer; number of top target genes to display, ranked by maximum absolute weight across labels (default: 10).
<code>r2_threshold</code>	Numeric or NULL. Targets with adjusted R^2 below this value receive NA and are rendered as grey tiles. Passed to <code>.get_tf_network()</code> .
<code>cmap</code>	Colour palette specification, identical to plot_dissimilarity_heatmap . Recommended diverging palettes such as "RdBu_r" (red-white-blue, reversed) or a two-colour vector like <code>c("blue", "white", "red")</code> . Default: <code>c("blue", "white", "red")</code> .
<code>show_values</code>	Logical; annotate each cell with its weight or "< R^2 threshold" text (default TRUE).
<code>save</code>	Logical; save the plot to a PDF file (default TRUE).
<code>filename</code>	Custom filename (default: auto-generated from <code>tf_name</code>).
<code>out_dir</code>	Output directory for the PDF (default: working directory).
<code>width, height</code>	PDF dimensions in inches (auto-calculated if NULL).

Value

Invisibly, a list with components:

plot The ggplot object.

data The (filtered) data.frame of weights used for the plot.

Examples

```

simic <- readRDS(system.file("extdata", "simic_full.rds",
                             package = "SimiCviz"))
plot_tf_network_heatmap(simic, "SATB1")

# Custom palette and top targets
plot_tf_network_heatmap(simic, "E2F4", top_n = 15,
                        cmap = c("white", "red", "darkred"),
                        r2_threshold = 0.7)

# Only specific labels, no saving
plot_tf_network_heatmap(simic, "MEF2D", labels = c(0, 2),
                        show_values = FALSE)

```

plot_tf_weights	<i>Plot weight barplots for transcription factors</i>
-----------------	---

Description

For each TF, shows a grouped bar chart of regulatory weights across all target genes, coloured by phenotype label. Mirrors SimiCVisualization.plot_tf_weights from the Python package.

Usage

```
plot_tf_weights(
  x,
  tf_names = NULL,
  labels = NULL,
  top_n = 50L,
  allowed_targets = NULL,
  grid = c(4L, 1L),
  save = FALSE,
  filename = NULL,
  out_dir = getwd(),
  width = 16,
  height = NULL
)
```

Arguments

x	SimiCvizExperiment
tf_names	character vector of TFs to plot (default: all)
labels	integer or character vector of labels (default: all)
top_n	integer; show only the top N targets by mean absolute weight (default 50). Applied after allowed_targets filtering.
allowed_targets	character vector or NULL; restrict targets to this pre-filtered set before applying top_n. Useful for passing targets that pass an external significance filter.
grid	integer vector c(nrow, ncol) per page (default c(4, 1)). Set NULL for a single page.
save	logical; save to PDF (default FALSE)
filename	PDF filename (default "TF_weights.pdf")
out_dir	output directory (default getwd())
width, height	page dimensions in inches

Value

Invisibly, a list of page grobs.

Examples

```
simic <- readRDS(system.file("extdata", "simic_full.rds",
                             package = "SimiCviz"))
plot_tf_weights(simic, tf_names = c("MEF2D", "SATB1"),
                 top_n = 20, grid = c(2, 1))
```

read_auc_csv	<i>Read SimiC-style AUC results from CSV (compatibility)</i>
--------------	--

Description

Read SimiC-style AUC results from CSV (compatibility)

Usage

```
read_auc_csv(file, ...)
```

Arguments

file	path to a CSV file containing AUC metrics. Expected columns include at least cell, tf, and score.
...	additional arguments passed to utils::read.csv() .

Value

data.frame with AUC metrics.

Examples

```
auc_path <- system.file("extdata", "example_auc.csv",
                        package = "SimiCviz")
auc_df <- read_auc_csv(auc_path)
```

read_auc_pickle	<i>Read SimiCPipeline output AUC matrices (pickle file)</i>
-----------------	---

Description

Returns a list of matrices (one per label), each with cells in rows and TFs in columns.

Usage

```
read_auc_pickle(file)
```

Arguments

file	path to a pickle file containing per-label AUC matrices.
------	--

Value

A named list of data.frames / matrices (one per label).

Examples

```
# This file does not exist in the package due to size constraints, but if you have a SimiCPipeline output, you can

# auc_file <- system.file("extdata",paste0("outputSimic/example_simic_wAUC.pickle"))
# auc_list <- read_auc_pickle(auc_file)
```

read_pickle*Read pickle files*

Description

Read pickle files

Usage

```
read_pickle(file)
```

Arguments

file path to the pickle file

Value

object containing the contents of the pickle file

Examples

```
weights_file <- system.file("extdata",
                             file.path("outputSimic/example_simic_weights.pickle"),
                             package = "SimiCviz")
simic_weights <- read_pickle(weights_file)
```

read_weights_csv*Read Long-style TF-target weights from CSV (compatibility)*

Description

Read Long-style TF-target weights from CSV (compatibility)

Usage

```
read_weights_csv(file, ...)
```

Arguments

file path to a CSV file containing TF-target weights. Expected minimal columns: tf, target, weight. Additional columns such as label, etc. are preserved.

... additional arguments passed to [utils::read.csv\(\)](#).

Value

data.frame with weights.

Examples

```
weight_path <- system.file("extdata", "example_weights.csv",
                           package = "SimiCviz")
weights_df <- read_weights_csv(weight_path)
head(weights_df)
#      tf target    weight label
# 1 MEF2D  RPLP1 -0.7501612      0
# 2  E2F4  RPLP1  0.0000000      0
# 3 SATB1  RPLP1  0.0000000      0
# 4  IRF1  RPLP1 -0.8536968      0
# 5  ATF6  RPLP1 -2.6133661      0
# 6   JUN  RPLP1  0.0000000      0
```

read_weights_pickle	<i>Read SimiCPipeline output weights (pickle file)</i>
---------------------	--

Description

Read SimiCPipeline output weights (pickle file)

Usage

```
read_weights_pickle(file)
```

Arguments

file path to the pickle file containing SimiC weights.

Value

A list of length n_labels (phenotypes) with GRN weight matrices (TFs x targets).

Examples

```
weights_file <- system.file("extdata",
                           file.path("outputSimic/example_simic_weights.pickle"),
                           package = "SimiCviz")
simic_weights <- read_weights_pickle(weights_file)
```

setCellLabels	<i>Set or update cell-to-label mapping</i>
---------------	--

Description

Set or update cell-to-label mapping

Usage

```
setCellLabels(x, cell_labels)
```

Arguments

x SimiCvizExperiment.
cell_labels Any format accepted by [load_cell_labels](#).

Value

Modified SimiCvizExperiment object.

Examples

```
wt <- data.frame(tf      = c("TF1", "TF2"),
                 target = c("Gene1", "Gene2"),
                 weight = c(0.5, 0.8),
                 label  = c(0, 1)
                )
simic <- SimiCvizExperiment(weights = wt)

cell_labels <- data.frame(cell = c("Cell1", "Cell2"),
                         label = c(0, 1))
simic <- setCellLabels(simic, cell_labels)
```

setLabelNames	<i>Set or update label names and colors</i>
---------------	---

Description

Validates that the provided vectors match the number of labels in `cell_labels` (preferred) or `weights`.

Usage

```
setLabelNames(x, label_names, colors = NULL)
```

Arguments

x SimiCvizExperiment.
label_names named character vector mapping labels to display names.
colors optional named character vector mapping labels to colors.

Value

Modified SimiCvizExperiment object.

Examples

```
wt <- data.frame(tf      = c("TF1", "TF2"),
                 target = c("Gene1", "Gene2"),
                 weight  = c(0.5, 0.8),
                 label   = c(0, 1)
                )
cell_labels <- data.frame(cell = c("Cell1", "Cell2"),
                          label = c(0, 1)
                         )
simic <- SimiCvizExperiment(weights = wt, cell_labels = cell_labels)
simic <- setLabelNames(simic,
                       label_names = c("control", "treated"),
                       colors = c("#e0e0e0", "#a8c8ff"))
```

SimiCviz

SimiCviz: Visualization and Activity Score analysis of Gene Regulatory Networks

Description

SimiCviz provides utilities to:

- Read SimiC or SimiCPipeline output tables from CSV and pickle files.
- Organize weights, AUCs, and metadata into a coherent object.
- Visualize regulatory networks and performance metrics.
- Compute and visualize regulatory dissimilarity across phenotypes (see [calculate_dissimilarity](#) and [plot_dissimilarity_heatmap](#)).
- Export plots (PDF) and processed data tables (CSV) into a reproducible directory hierarchy.

Details

The package is designed to be lightweight and focused on visualization, leaving modeling and inference to SimiCPipeline itself.

Author(s)

Maintainer: Irene Marín-Goñi <imarin.4@alumni.unav.es> ([ORCID](#))

See Also

Useful links:

- <https://github.com/ML4BM-Lab/SimiCviz>
- Report bugs at <https://github.com/ML4BM-Lab/SimiCviz/issues>

SimiCvizExperiment	<i>Construct a SimiCvizExperiment object</i>
--------------------	--

Description

Construct a SimiCvizExperiment object

Usage

```
SimiCvizExperiment(
  weights = NULL,
  auc = NULL,
  cell_labels = NULL,
  label_names = NULL,
  colors = NULL,
  meta = list()
)
```

Arguments

weights	list with weight matrices and adjusted R ² .
auc	optional list containing AUC data. The preferred format is <code>list(collected = df)</code> where <code>df</code> is a <code>cells × TF</code> <code>data.frame</code> . A plain <code>data.frame</code> is automatically wrapped into this structure. This canonical format is compatible with any GRN method that produces per-cell TF activity scores.
cell_labels	optional <code>data.frame</code> or vector with cell-to-label mapping. If a plain vector is provided (no cell ids), it must be in the same row order as the AUC matrix.
label_names	optional named character vector mapping labels to display names. Length must match the number of unique labels in <code>cell_labels</code> (if provided) or <code>weights</code> .
colors	optional named character vector mapping labels to colors. Same length requirement as <code>label_names</code> .
meta	optional list of additional metadata.

Value

An object of class "SimiCvizExperiment".

Examples

```
# Create a minimal SimiCvizExperiment with weights
weights_list <- list("0" = as.data.frame(matrix(rnorm(90), nrow = 3,
  dimnames = list(paste0("TF", 1:3),
    paste0("Gene", 1:30)))),
  "1" = as.data.frame(matrix(rnorm(90), nrow = 3),
    dimnames = list(paste0("TF", 1:3),
      paste0("Gene", 1:30))))
simic <- SimiCvizExperiment(weights = weights_list)
```

SimiCvizExperiment-class

SimiCvizExperiment class

Description

Lightweight S4 container for SimiC visualization data.

Usage

```
## S4 method for signature 'SimiCvizExperiment'
show(object)
```

Arguments

object A [SimiCvizExperiment](#) object.

Value

An object of class `SimiCvizExperiment` with initialized slots.

Slots

`weights` list with weight matrices and adjusted R^2 per label.

`auc` list containing the collected AUC data. The canonical element is `$collected`: a `data.frame` with cells in rows, TFs in columns, and an optional label column. This format is shared across all GRN methods that produce per-cell TF activity scores.

`cell_labels` `data.frame` with columns `cell` (character) and `label` (integer). Provides the mapping between cell identifiers and phenotype labels. Required for label-specific AUC visualizations.

`tf_ids` character vector of TF identifiers.

`target_ids` character vector of target gene identifiers.

`label_names` named character vector mapping integer labels to display names.

`colors` named character vector mapping integer labels to colors.

`meta` list with arbitrary metadata.

Examples

```
# Create a SimiCvizExperiment from weights and AUC data
weights_list <- list("0" = as.data.frame(matrix(rnorm(90), nrow = 3,
                                                dimnames = list(paste0("TF", 1:3),
                                                                paste0("Gene", 1:30)))),
                    "1" = as.data.frame(matrix(rnorm(90), nrow = 3,
                                                dimnames = list(paste0("TF", 1:3),
                                                                paste0("Gene", 1:30))))))
cell_labels <- data.frame(cell= c("Cell1", "Cell2"), label = c("0", "1"))
simic <- SimiCvizExperiment(weights = weights_list, cell_labels = cell_labels)
```

Index

* internal

- .make_weight_barplot, [4](#)
 - .plot_weights_paginated, [4](#)
 - .subset_auc_for_label, [5](#)
 - .weights_to_long, [6](#)
- SimiCviz, [35](#)
- .compute_cell_auc, [3](#)
- .ensure_genes_x_cells_format, [3](#)
- .make_weight_barplot, [4](#)
- .plot_weights_paginated, [4](#)
- .subset_auc_for_label, [5](#)
- .weights_to_long, [6](#)
- auc_list_to_df, [8](#)
- AUCProcessor, [6](#), [7](#), [13](#), [15](#)
- AUCProcessor-class, [7](#)
- calculate_activity_scores, [9](#)
- calculate_dissimilarity, [10](#), [25](#), [35](#)
- calculate_ecdf_auc, [11](#)
- compute_auc, [12](#)
- compute_auc, AUCProcessor-method, [13](#)
- export_SimiCviz_csv, [13](#)
- get_auc, [14](#)
- get_auc, AUCProcessor-method, [15](#)
- get_tf_network, [15](#)
- is.SimiCvizExperiment, [16](#)
- load_cell_labels, [8](#), [17](#), [34](#)
- load_collected_auc, [18](#)
- load_expression_matrix, [18](#)
- load_from_csv, [19](#)
- load_SimiCPipeline, [20](#)
- plot_auc_cumulative, [21](#)
- plot_auc_distributions, [22](#)
- plot_auc_heatmap, [23](#)
- plot_auc_summary_statistics, [24](#)
- plot_dissimilarity_heatmap, [25](#), [29](#), [35](#)
- plot_r2_distribution, [26](#)
- plot_target_weights, [27](#)
- plot_tf_network_heatmap, [28](#)

- plot_tf_weights, [30](#)
- read.csv, [18](#)
- read_auc_csv, [31](#)
- read_auc_pickle, [31](#)
- read_pickle, [32](#)
- read_weights_csv, [32](#)
- read_weights_pickle, [33](#)
- setCellLabels, [34](#)
- setLabelNames, [34](#)
- show, AUCProcessor-method
(AUCProcessor-class), [7](#)
- show, SimiCvizExperiment-method
(SimiCvizExperiment-class), [37](#)
- SimiCviz, [35](#)
- SimiCviz-package (SimiCviz), [35](#)
- SimiCvizExperiment, [14](#), [19](#), [21](#), [36](#), [37](#)
- SimiCvizExperiment-class, [37](#)
- utils::read.csv(), [31](#), [32](#)