

Package: SimiCviz (via r-universe)

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Type Package

Title Visualization Tools for Gene Regulatory Network Analysis

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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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.compute_cell_auc *Compute AUC for a single cell*

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

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

Value

named vector of AUC scores (one per TF)

.ensure_genes_x_cells_format
Validate expression matrix is in genes x cells format

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

expr_mat expression matrix
 cell_labels data.frame with cell identifiers in 'cell' column

Value

expression matrix (genes x cells) with validated dimensions

auc_list_to_df	<i>Collect per-label AUC matrices using cell labels</i>
----------------	---

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)
```

AUCProcessor

*Initialize AUCProcessor***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

weights	list with weight matrices per label (if simic input) or data.frame with columns: tf, target, weight, label, tf (if data.frame input). adj_p_val (optional, for p-value filtering 'qc_type' = "p_value").
expression	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.
cell_labels	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")

ValueA [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", "example1_expression.pickle"),
                                   package = "SimiCviz")
cell_labels_path <- system.file("extdata",
                                file.path("inputFiles", "treatment_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 *AUCProcessor class*

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)
```

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 *Calculate ECDF AUC*

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("Pms1", "Ets1"))
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.

get_auc *Extract activity scores from an object*

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"))
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 0.5157082 0.5900224 0.5445804
# Cell2 0.5139540 0.5453391 0.5365168

```

```
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	<i>Extract stacked TF-target weight matrix across labels</i>
----------------	--

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

<code>x</code>	A <code>SimiCvizExperiment</code> object.
<code>tf_name</code>	Character; name of the transcription factor.
<code>labels</code>	Integer vector of labels to include (default: all).
<code>r2_threshold</code>	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("Tet2"),
                          labels = c(1, 2),
                          r2_threshold = 0.7)

print(network)
```

is.SimiCvizExperiment	<i>Check if object is a SimiCvizExperiment</i>
-----------------------	--

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 *Load cell-to-label mapping*

Description

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

Usage

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

Arguments

x One of:

- character (length 1)** Path to a CSV / TSV file. If the file has columns named cell and label they are used directly. Otherwise the first column is treated as cell and the second as label. 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 cell_1, cell_2,
- named vector** Names are used as cell IDs and values as labels.
- data.frame** Must contain columns cell and label, or exactly two columns (first = cell, second = label).

... Additional arguments passed to file readers when x 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", "treatment_annotation.csv"),
                                package = "SimiCviz")
cell_labels <- load_cell_labels(cell_labels_path, header = TRUE, sep = ",")
head(cell_labels)
#   cell category label
# 1 05_87_62__s5 control    0
# 2 02_84_27__s3 control    0
# 3 02_95_13__s5 control    0
# 4 06_61_12__s1 control    0
# 5 03_14_11__s5 control    0
# 6 05_46_81__s4 control    0
```

load_collected_auc *Load a collected AUC CSV into a data.frame*

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

`file` Path to a CSV file with cells in rows and TFs in columns.
`...` 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/example1_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", "example1_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", "treatment_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 × TF, all labels merged) load_collected_auc
2. Per-label pickle → collect → save CSV read_auc_pickle → auc_list_to_df → .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   = "example1",  
#   lambda1    = "0.01",  
#   lambda2    = "0.001")
```

plot_auc_cumulative *Plot AUC cumulative (ECDF) curves by label*

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

x	A SimiCvizExperiment object.
tf_names	Optional TF identifiers to plot. Defaults to all available.
labels	Optional labels to include.
alpha	Line transparency for ECDF curves.
rug	Logical; draw rug marks at the x-axis.
grid	Integer vector c(nrow, ncol) for page layout.
percentile	Percentile used in ECDF summary metrics.
include_table	Logical; add ECDF metrics table below each panel.
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 list of grobs/plots.

Examples

```
simic <- readRDS(system.file("extdata", "simic_full.rds", package = "SimiCviz"))
plot_auc_cumulative(
  simic,
  tf_names = c("Pms1", "Ets1"),
  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 c(nrow, ncol) for page layout. Use NULL for a single auto-sized page.
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 list of ggplot objects.

Examples

```
simic <- readRDS(system.file("extdata", "simic_full.rds", package = "SimiCviz"))
plot_auc_distributions(
  simic,
  tf_names = c("Pms1", "Ets1"),
  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, <code>calculate_dissimilarity</code> is called internally.
cmap	Colour palette specification. Can be: <ul style="list-style-type: none"> • 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 <code>calculate_dissimilarity</code> .

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`.

plot_target_weights *Plot weight barplots for target genes*

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

<code>x</code>	<code>SimiCvizExperiment</code>
<code>target_names</code>	character vector of targets to plot (default: all)
<code>labels</code>	integer or character vector of labels (default: all)
<code>grid</code>	integer vector <code>c(nrow, ncol)</code> per page (default <code>c(4, 1)</code>). Set <code>NULL</code> for a single page.
<code>top_n</code>	Optional integer. Currently accepted for API compatibility; ignored in target mode.
<code>save</code>	logical; save to PDF (default <code>FALSE</code>)
<code>filename</code>	PDF filename (default <code>"target_weights.pdf"</code>)
<code>out_dir</code>	output directory (default <code>getwd()</code>)
<code>width, height</code>	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("Slit2", "Kif20b"),
                    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

x	A SimiCvizExperiment object.
tf_name	Character; name of the transcription factor to plot.
labels	Integer or character vector of labels to include (default: all).
top_n	Integer; number of top target genes to display, ranked by maximum absolute weight across labels (default: 10).
r2_threshold	Numeric or NULL. Targets with adjusted R^2 below this value receive NA and are rendered as grey tiles. Passed to .get_tf_network().

cmap	Colour palette specification, identical to <code>plot_dissimilarity_heatmap</code> . 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> .
show_values	Logical; annotate each cell with its weight or " $< R^2$ threshold" text (default TRUE).
save	Logical; save the plot to a PDF file (default TRUE).
filename	Custom filename (default: auto-generated from <code>tf_name</code>).
out_dir	Output directory for the PDF (default: working directory).
width, height	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, "Pms1")

# Custom palette and top targets
plot_tf_network_heatmap(simic, "Ets1", top_n = 15,
                        cmap = c("white", "red", "darkred"),
                        r2_threshold = 0.7)

# Only specific labels, no saving
plot_tf_network_heatmap(simic, "Gli3", labels = c(0, 3),
                        show_values = FALSE)
```

plot_tf_weights

Plot weight barplots for transcription factors

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

<code>x</code>	<code>SimiCvizExperiment</code>
<code>tf_names</code>	character vector of TFs to plot (default: all)
<code>labels</code>	integer or character vector of labels (default: all)
<code>top_n</code>	integer; show only the top N targets by mean absolute weight (default 50). Applied after <code>allowed_targets</code> filtering.
<code>allowed_targets</code>	character vector or NULL; restrict targets to this pre-filtered set before applying <code>top_n</code> . Useful for passing targets that pass an external significance filter.
<code>grid</code>	integer vector <code>c(nrow, ncol)</code> per page (default <code>c(4, 1)</code>). Set NULL for a single page.
<code>save</code>	logical; save to PDF (default FALSE)
<code>filename</code>	PDF filename (default "TF_weights.pdf")
<code>out_dir</code>	output directory (default <code>getwd()</code>)
<code>width, height</code>	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("Pms1", "Tet2"),
  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 <code>utils::read.csv()</code> .

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).

read_pickle	<i>Read pickle files</i>
-------------	--------------------------

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/example1_simic_weights.pickle"),  
                             package = "SimiCviz")  
simic_weights <- read_pickle(weights_file)
```

read_weights_csv	<i>Read Long-style TF-target weights from CSV (compatibility)</i>
------------------	---

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 Pms1 Brinp3 0.0000000  0
# 2 Prrx2 Brinp3 1.5622762  0
# 3 Ets1 Brinp3 0.0000000  0
# 4 Tet2 Brinp3 0.8540945  0
# 5 Crebrf Brinp3 0.0000000  0
# 6 Gli3 Brinp3 0.0000000  0
```

read_weights_pickle *Read SimiCPipeline output weights (pickle file)*

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/example1_simic_weights.pickle"),
                             package = "SimiCviz")
simic_weights <- read_weights_pickle(weights_file)
```

setCellLabels *Set or update cell-to-label mapping*

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 *Set or update label names and colors*

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"))
```

SimiCvizExperiment *Construct a SimiCvizExperiment object*

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> data.frame. A plain data.frame 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 data.frame 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)
```

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