Package: caugi (via r-universe)

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Title Causal Graph Interface

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Description Create, query, and modify causal graphs. 'caugi' (Causal Graph Interface) is a causality-first, high performance graph package that provides a simple interface to build, structure, and examine causal relationships.

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Language en-US

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`add-caugi_plot-caugi_plot`

Compose Plots Horizontally

Description

Arrange two plots side-by-side with configurable spacing. The `+` and `|` operators are equivalent and can be used interchangeably. Compositions can be nested to create complex multi-plot layouts.

Usage

```
## S3 method for class 'caugi_plot'
e1 + e2

## S3 method for class 'caugi_plot'
e1 | e2
```

Arguments

`e1`	A `caugi_plot` object (left plot)
`e2`	A `caugi_plot` object (right plot)

Details

The spacing between plots is controlled by the global option `caugi_options()$plot$spacing`, which defaults to `grid::unit(1, "lines")`. Compositions can be nested arbitrarily:

- `p1 + p2` - two plots side-by-side
- `(p1 + p2) + p3` - three plots in a row
- `(p1 + p2) / p3` - two plots on top, one below

Value

A `caugi_plot` object containing the composed layout

See Also

`caugi_options()` for configuring spacing and default styles

Other plotting: `caugi_layout()`, `caugi_layout_bipartite()`, `caugi_layout_circle()`, `caugi_layout_fruchterman_`
`caugi_layout_kamada_kawai()`, `caugi_layout_sugiyama()`, `caugi_layout_tiered()`, `caugi_plot()`,
`divide-caugi_plot-caugi_plot`, `plot.caugi()`

Examples

```
cg1 <- caugi(A %-->% B, B %-->% C)
cg2 <- caugi(X %-->% Y, Y %-->% Z)

p1 <- plot(cg1, main = "Graph 1")
p2 <- plot(cg2, main = "Graph 2")

# Horizontal composition
p1 + p2
p1 | p2 # equivalent

# Adjust spacing
caugi_options(plot = list(spacing = grid::unit(2, "lines")))
p1 + p2
```

`adjustment_set` *Compute an adjustment set*

Description

Computes an adjustment set for `X -> Y` in a DAG.

Usage

```
adjustment_set(
  cg,
  X = NULL,
  Y = NULL,
  X_index = NULL,
  Y_index = NULL,
  type = c("optimal", "parents", "backdoor")
)
```

Arguments

cg	A caugi object.
X, Y	Node names.
X_index, Y_index	Optional numeric 1-based indices.
type	One of "parents", "backdoor", "optimal". The optimal option computes the O-set.

Details

Types supported:

- "parents": $\bigcup \mathrm{Pa}(X)$ minus $X \cup Y$
- "backdoor": an inclusion-minimal valid backdoor adjustment set, found in linear time as a minimal d-separator of X and Y in the proper backdoor graph (van der Zander, Liśkiewicz & Textor, 2019). Unlike "parents" (which always conditions on every parent of X), this drops nodes that are not needed to block a backdoor path. Note that minimal is not the same as statistically optimal; use "optimal" for the efficient O-set.
- "optimal": O-set (only for single x and single y)

Value

A character vector of node names representing the adjustment set.

See Also

Other adjustment: all_adjustment_sets_admg(), all_backdoor_sets(), d_separated(), is_valid_adjustment_admg
is_valid_backdoor(), minimal_separator()

Examples

```
cg <- caugi(
  C %-->% X,
  X %-->% F,
  X %-->% D,
  A %-->% X,
  A %-->% K,
  K %-->% Y,
```

```
  D %-->% Y,
  D %-->% G,
  Y %-->% H,
  class = "DAG"
)

adjustment_set(cg, "X", "Y", type = "parents") # C, A
adjustment_set(cg, "X", "Y", type = "backdoor") # A
adjustment_set(cg, "X", "Y", type = "optimal") # K
```

`aid` *Adjustment Identification Distance*

Description

Compute the Adjustment Identification Distance (AID) between two graphs. AID counts how often the adjustment-identification strategy applied to `guess` yields a causal inference that is incorrect relative to `truth`. Implemented in caugi's Rust backend following Henckel, Würtzen & Weichwald (2024), doi:10.48550/arXiv.2402.08616.

Usage

```
aid(truth, guess, type = c("oset", "ancestor", "parent"), normalized = TRUE)
```

Arguments

`truth`	A `caugi` object of class `"DAG"` or `"CPDAG"`.
`guess`	A `caugi` object of class `"DAG"` or `"CPDAG"`.
`type`	A character string specifying the type of AID to compute. Options are `"oset"` (default), `"ancestor"`, and `"parent"`.
`normalized`	Logical; if `TRUE`, returns the normalized AID. If `FALSE`, returns the count.

Value

A numeric representing the AID between the two graphs, if `normalized = TRUE`, or an integer count if `normalized = FALSE`.

See Also

Other metrics: `hd()`, `shd()`

Examples

```
set.seed(1)
truth <- generate_graph(n = 100, m = 200, class = "DAG")
guess <- generate_graph(n = 100, m = 200, class = "DAG")
aid(truth, guess) # 0.0187
```

`all_adjustment_sets_admg` *Get all valid adjustment sets in an ADMG*

Description

Enumerates all valid adjustment sets for estimating the causal effect of `X` on `Y` in an ADMG, up to a specified maximum size.

Usage

```
all_adjustment_sets_admg(
  cg,
  X = NULL,
  Y = NULL,
  X_index = NULL,
  Y_index = NULL,
  minimal = TRUE,
  max_size = 3L
)
```

Arguments

`cg`	A `caugi` object of class ADMG.
`X`, `Y`	Node names (can be vectors for multiple treatments/outcomes).
`X_index`, `Y_index`	Optional 1-based indices.
`minimal`	Logical; if `TRUE` (default), only minimal sets are returned.
`max_size`	Integer; maximum size of sets to consider (default 3).

Value

A list of character vectors, each a valid adjustment set (possibly empty list if none exist).

See Also

Other adjustment: `adjustment_set()`, `all_backdoor_sets()`, `d_separated()`, `is_valid_adjustment_admg()`, `is_valid_backdoor()`, `minimal_separator()`

Examples

```
cg <- caugi(
  L %-->% X,
  X %-->% Y,
  L %-->% Y,
  M %-->% Y,
  class = "ADMG"
```

```
)

all_adjustment_sets_admg(cg, X = "X", Y = "Y", minimal = TRUE)
# Returns {L} as minimal adjustment set
```

`all_backdoor_sets` *Get all backdoor sets up to a certain size.*

Description

This function returns the backdoor sets up to size `max_size`, which per default is set to 10.

Usage

```
all_backdoor_sets(
  cg,
  X = NULL,
  Y = NULL,
  X_index = NULL,
  Y_index = NULL,
  minimal = TRUE,
  max_size = 3L
)
```

Arguments

`cg`	A `caugi`.
`X`, `Y`	Single node name.
`X_index`, `Y_index`	Optional 1-based indices (exclusive with name args).
`minimal`	Logical; if `TRUE` (default), only minimal sets are returned.
`max_size`	Integer; maximum size of sets to consider (default 3).

Value

A list of character vectors, each an adjustment set (possibly empty).

See Also

Other adjustment: `adjustment_set()`, `all_adjustment_sets_admg()`, `d_separated()`, `is_valid_adjustment_admg()`, `is_valid_backdoor()`, `minimal_separator()`

Examples

```
cg <- caugi(
  C %-->% X,
  X %-->% F,
  X %-->% D,
  A %-->% X,
  A %-->% K,
  K %-->% Y,
  D %-->% Y,
  D %-->% G,
  Y %-->% H,
  class = "DAG"
)

all_backdoor_sets(cg, X = "X", Y = "Y", max_size = 3L, minimal = FALSE)
#> [[1]]
#> [1] "A"
#>
#> [[2]]
#> [1] "K"
#>
#> [[3]]
#> [1] "C" "A"
#>
#> [[4]]
#> [1] "C" "K"
#>
#> [[5]]
#> [1] "A" "K"
#>
#> [[6]]
#> [1] "C" "A" "K"

all_backdoor_sets(cg, X = "X", Y = "Y", max_size = 3L, minimal = TRUE)
#> [[1]]
#> [1] "A"
#>
#> [[2]]
#> [1] "K"
```

`ancestors` *Get ancestors of nodes in a* `caugi`

Description

Get ancestors of nodes in a `caugi`

Usage

```
ancestors(
  cg,
  nodes = NULL,
  index = NULL,
  open = caugi_options("use_open_graph_definition")
)
```

Arguments

cg	A caugi object.
nodes	A character vector of node names.
index	A vector of node indexes.
open	Boolean. Determines how the graph is interpreted when retrieving ancestors. Default is taken from caugi_options("use_open_graph_definition"), which by default is TRUE.

Value

Either a character vector of node names (if a single node is requested) or a list of character vectors (if multiple nodes are requested).

See Also

Other queries: anteriors(), children(), components(), descendants(), districts(), edge_types(), edges(), exogenous(), is_acyclic(), is_admg(), is_ag(), is_caugi(), is_cpdag(), is_dag(), is_empty_caugi(), is_mag(), is_mpdag(), is_pdag(), is_simple(), is_ug(), m_separated(), markov_blanket(), neighbors(), nodes(), parents(), posteriors(), same_nodes(), spouses(), subgraph(), topological_sort()

Examples

```
cg <- caugi(
  A %-->% B,
  B %-->% C,
  class = "DAG"
)
ancestors(cg, "A") # NULL
ancestors(cg, "A", open = FALSE) # A
ancestors(cg, index = 2) # "A"
ancestors(cg, "B") # "A"
ancestors(cg, c("B", "C"))
#> $B
#> [1] "A"
#>
#> $C
#> [1] "A" "B"
```

`anteriors` *Get anteriors of nodes in a* `caugi`

Description

Get the anterior set of nodes in a graph. The anterior set (Richardson and Spirtes, 2002) includes all nodes reachable by following paths where every edge is either undirected or directed toward the target node.

For DAGs, the anterior set equals the ancestor set (since there are no undirected edges). For PDAGs, it includes both ancestors and nodes reachable via undirected edges.

Usage

```
anteriors(
  cg,
  nodes = NULL,
  index = NULL,
  open = caugi_options("use_open_graph_definition")
)
```

Arguments

`cg`	A `caugi` object of class DAG or PDAG.
`nodes`	A character vector of node names.
`index`	A vector of node indexes.
`open`	Boolean. Determines how the graph is interpreted when retrieving anteriors. Default is taken from `caugi_options("use_open_graph_definition")`, which by default is TRUE.

Value

Either a character vector of node names (if a single node is requested) or a list of character vectors (if multiple nodes are requested).

References

Richardson, T. and Spirtes, P. (2002). Ancestral graph Markov models. *The Annals of Statistics*, 30(4):962-1030.

See Also

Other queries: `ancestors()`, `children()`, `components()`, `descendants()`, `districts()`, `edge_types()`, `edges()`, `exogenous()`, `is_acyclic()`, `is_admg()`, `is_ag()`, `is_caugi()`, `is_cpdag()`, `is_dag()`, `is_empty_caugi()`, `is_mag()`, `is_mpdag()`, `is_pdag()`, `is_simple()`, `is_ug()`, `m_separated()`, `markov_blanket()`, `neighbors()`, `nodes()`, `parents()`, `posteriors()`, `same_nodes()`, `spouses()`, `subgraph()`, `topological_sort()`

Examples

```
# PDAG example with directed and undirected edges
cg <- caugi(
  A %-->% B %---% C,
  B %-->% D,
  class = "PDAG"
)
anteriors(cg, "A") # NULL (no anteriors)
anteriors(cg, "A", open = FALSE) # A
anteriors(cg, "C") # A, B
anteriors(cg, "D") # A, B, C

# For DAGs, anteriors equals ancestors
cg_dag <- caugi(
  A %-->% B %-->% C,
  class = "DAG"
)
anteriors(cg_dag, "C") # A, B
```

---

as_adjacency *Convert a caugi to an adjacency matrix*

Description

Does not take other edge types than the one found in a PDAG.

Usage

```
as_adjacency(x)
```

Arguments

x	A caugi object.

Value

An integer 0/1 adjacency matrix with row/col names.

See Also

Other conversions: as_bnlearn(), as_caugi(), as_dagitty(), as_igraph()

Examples

```
cg <- caugi(
  A %-->% B,
  class = "DAG"
)
adj <- as_adjacency(cg)
```

`as_bnlearn` *Convert a caugi to a bnlearn network*

Description

Convert a caugi to a bnlearn network

Usage

```
as_bnlearn(x)
```

Arguments

`x`	A `caugi` object.

Value

A `bnlearn` DAG.

See Also

Other conversions: `as_adjacency()`, `as_caugi()`, `as_dagitty()`, `as_igraph()`

Examples

```
cg <- caugi(
  A %-->% B,
  class = "DAG"
)
g_bn <- as_bnlearn(cg)
```

as_caugi *Convert to a* caugi

Description

Convert an object to a caugi. The object can be a graphNEL, matrix, tidygraph, daggity, bn, or igraph.

Usage

```
as_caugi(
  x,
 class = c("DAG", "UG", "PDAG", "MPDAG", "CPDAG", "ADMG", "AG", "PAG", "UNKNOWN"),
  simple = TRUE,
  collapse = FALSE,
  collapse_to = "---",
  ...
)
```

Arguments

x	An object to convert to a caugi.
class	Character; one of "DAG", "UG", "PDAG", "MPDAG", "CPDAG", "ADMG", "AG", or "UNKNOWN". "PAG" is only supported for integer coded matrices.
simple	logical. If TRUE (default) the graph will be simple (no multiple edges or self-loops).
collapse	logical. If TRUE collapse mutual directed edges to undirected edges. Default is FALSE.
collapse_to	Character string to use as the edge glyph when collapsing. Should be a registered symmetrical edge glyph. Default is "---".
...	Additional arguments passed to specific methods.

Details

For matrices, as_caugi assumes that the rows are the from nodes and the columns are the to nodes. Thus, for a graph, G: A –> B, we would have that G["A", "B"] == 1 and G["B", "A"] == 0. For PAGs, the integer codes are as follows (as used in pcalg):

- 0: no edge
- 1: circle (e.g., A o-o B or A --o B)
- 2: arrowhead (e.g., A --> B or A o-> B)
- 3: tail (e.g., A --o B or A --- B)

Value

A caugi object.

See Also

Other conversions: as_adjacency(), as_bnlearn(), as_dagitty(), as_igraph()

Examples

```
# igraph
ig <- igraph::graph_from_literal(A - +B, B - +C)
cg_ig <- as_caugi(ig, class = "DAG")

# graphNEL
gn <- graph::graphNEL(nodes = c("A", "B", "C"), edgemode = "directed")
gn <- graph::addEdge("A", "B", gn)
gn <- graph::addEdge("B", "C", gn)
cg_gn <- as_caugi(gn, class = "DAG")

# adjacency matrix
m <- matrix(0L, 3, 3, dimnames = list(LETTERS[1:3], LETTERS[1:3]))
m["A", "B"] <- 1L
m["B", "C"] <- 1L
cg_adj <- as_caugi(m, class = "DAG")

# bnlearn
bn <- bnlearn::model2network("[A][B|A][C|B]")
cg_bn <- as_caugi(bn, class = "DAG")

# dagitty
dg <- dagitty::dagitty("dag {
 A -> B
 B -> C
 }")
cg_dg <- as_caugi(dg, class = "DAG")

cg <- caugi(A %-->% B %-->% C, class = "DAG")

# check that all nodes are equal in all graph objects
for (cg_converted in list(cg_ig, cg_gn, cg_adj, cg_bn, cg_dg)) {
  stopifnot(identical(nodes(cg), nodes(cg_converted)))
  stopifnot(identical(edges(cg), edges(cg_converted)))
}

# collapse mutual edges
ig2 <- igraph::graph_from_literal(A - +B, B - +A, C - +D)
cg2 <- as_caugi(ig2, class = "PDAG", collapse = TRUE, collapse_to = "---")

# coded integer matrix for PAGs (pcalg style)
nm <- c("A", "B", "C", "D")
M <- matrix(0L, 4, 4, dimnames = list(nm, nm))

# A --> B
M["A", "B"] <- 2L # mark at B end
M["B", "A"] <- 3L # mark at A end
```

```
# A --- C
M["A", "C"] <- 3L
M["C", "A"] <- 3L

# B o-> C
M["B", "C"] <- 2L
M["C", "B"] <- 1L

# C o-o D
M["C", "D"] <- 1L
M["D", "C"] <- 1L

cg <- as_caugi(M, class = "PAG")
```

`as_dagitty` *Convert a caugi to a dagitty graph*

Description

Convert a caugi to a dagitty graph

Usage

```
as_dagitty(x)
```

Arguments

`x`	A `caugi` object.

Value

A `dagitty` object.

See Also

Other conversions: `as_adjacency()`, `as_bnlearn()`, `as_caugi()`, `as_igraph()`

Examples

```
cg <- caugi(
  A %-->% B,
  class = "DAG"
)
g_dg <- as_dagitty(cg)
```

as_igraph *Convert a caugi to an igraph object*

Description

Convert a caugi to an igraph object

Usage

```
as_igraph(x, ...)
```

Arguments

x	A caugi object.
...	Additional arguments passed to igraph::graph_from_data_frame().

Value

An igraph object representing the same graph structure.

See Also

Other conversions: as_adjacency(), as_bnlearn(), as_caugi(), as_dagitty()

Examples

```
cg <- caugi(
  A %-->% B,
  class = "DAG"
)
ig <- as_igraph(cg)
```

build *Build the* caugi *graph*

Description

Forces lazy compilation of the caugi graph without running a specific query. Useful to pre-initialize the graph.

Usage

```
build(cg)
```

Arguments

cg	A caugi object.

Value

The input caugi object (invisibly), with its graph built.

See Also

Other verbs: caugi_verbs

Examples

```
cg <- caugi(A %-->% B, class = "DAG")
build(cg) # initialize graph without querying
```

---

caugi *Create a* caugi *from edge expressions.*

Description

Create a caugi from a series of edge expressions using infix operators. Nodes can be specified as symbols, strings, or numbers.

The following edge operators are supported by default:

- %-->% for directed edges (A –> B)
- %---% for undirected edges (A — B)
- %<->% for bidirected edges (A <-> B)
- %o->% for partially directed edges (A o-> B)
- %--o% for partially undirected edges (A –o B)
- %o-o% for partial edges (A o-o B)

You can register additional edge types using register_caugi_edge().

Usage

```
caugi(
  ...,
  from = NULL,
  edge = NULL,
  to = NULL,
  nodes = NULL,
  edges_df = NULL,
  simple = TRUE,
  build = NULL,
 class = c("AUTO", "DAG", "UG", "PDAG", "MPDAG", "CPDAG", "ADMG", "AG", "UNKNOWN"),
```

```
  state = NULL,
  .session = NULL
)
```

Arguments

`...`	Edge expressions using the supported infix operators, or nodes given by symbols or strings. Multiple edges can be combined using `+`: `A --> B + C`, indicating an edge from `A` to both `B` and `C`. Nodes can also be grouped using `c(...)` or parentheses.
`from`	Character vector of source node names. Optional; mutually exclusive with `....`
`edge`	Character vector of edge types. Optional; mutually exclusive with `....`
`to`	Character vector of target node names. Optional; mutually exclusive with `....`
`nodes`	Character vector of node names to declare as isolated nodes. An optional, but recommended, option is to provide all node names in the graph, including those that appear in edges. If `nodes` is provided, the order of nodes in the graph will follow the order in `nodes`.
`edges_df`	Optional data.frame or data.table with columns `from`, `edge`, and `to` to specify edges. Mutually exclusive with `...` and `from`, `edge`, `to`. Can be used to create graphs using `edges(cg)` from another `caugi` object, `cg`.
`simple`	Logical; if `TRUE` (default), the graph is a simple graph, and the function will throw an error if the input contains parallel edges or self-loops.
`build`	DEPRECATED. The graph is always built lazily, so this argument is ignored. Can use `build()` to force lazy compilation if desired.
`class`	Character; one of `"AUTO"`, `"DAG"`, `"UG"`, `"PDAG"`, `"MPDAG"`, `"CPDAG"`, `"ADMG"`, `"AG"`, or `"UNKNOWN"`. `"AUTO"` will automatically pick the appropriate class based on the first match in the order of `"DAG"`, `"UG"`, `"MPDAG"`, `"PDAG"`, `"ADMG"`, and `"AG"`. It will default to `"UNKNOWN"` if no match is found.
`state`	DEPRECATED. Replaced by `.session`.
`.session`	For internal use. Build a graph by supplying a pre-constructed session pointer from Rust.

Value

A `caugi` S7 object containing the nodes, edges, and a pointer to the underlying Rust graph structure.

Examples

```
# create a simple DAG (using NSE)
cg <- caugi(
  A %-->% B + C,
  B %-->% D,
  class = "DAG"
)

# create a PDAG with undirected edges (using NSE)
cg2 <- caugi(
```

```
  A %-->% B + C,
  B %---% D,
  E, # no neighbors for this node
  class = "PDAG"
)

# create a DAG (using SE)
cg3 <- caugi(
  from = c("A", "A", "B"),
  edge = c("-->", "-->", "-->"),
  to = c("B", "C", "D"),
  nodes = c("A", "B", "C", "D", "E"),
  class = "DAG"
)

# create a non-simple graph
cg4 <- caugi(
  A %-->% B,
  B %-->% A,
  class = "UNKNOWN",
  simple = FALSE
)

cg4@simple # FALSE
cg4@graph_class # "UNKNOWN"
```

`caugi_default_options` *Default options for caugi*

Description

Returns the default options for the caugi package. Useful for resetting options to their original state.

Usage

```
caugi_default_options()
```

Value

A list of default options for caugi.

See Also

`caugi_options()` for setting and getting options

Examples

```
# Get defaults
caugi_default_options()

# Reset to defaults
caugi_options(caugi_default_options())
```

`caugi_deserialize` *Deserialize caugi Graph from JSON String*

Description

Converts a JSON string in the native caugi format back to a caugi graph. This is a lower-level function; consider using `read_caugi()` for reading from files.

Usage

```
caugi_deserialize(json, lazy)
```

Arguments

`json`	Character string containing the JSON representation.
`lazy`	DEPRECATED, no longer necessary. The graph is always built lazily, so this argument is ignored.

Value

A `caugi` object.

See Also

Other export: `caugi_dot()`, `caugi_export()`, `caugi_graphml()`, `caugi_mermaid()`, `caugi_serialize()`, `export-classes`, `format-caugi`, `format-dot`, `format-graphml`, `format-mermaid`, `knit_print.caugi_export()`, `read_caugi()`, `read_graphml()`, `to_dot()`, `to_graphml()`, `to_mermaid()`, `write_caugi()`, `write_dot()`, `write_graphml()`, `write_mermaid()`

Examples

```
cg <- caugi(A %-->% B, class = "DAG")
json <- caugi_serialize(cg)
cg2 <- caugi_deserialize(json)
```

caugi_dot *S7 Class for DOT Export*

Description

An S7 object that wraps a DOT format string for displaying caugi graphs. When printed interactively, displays the DOT string cleanly.

Usage

```
caugi_dot(content)
```

Arguments

content	A character string containing the DOT format graph.

Value

A caugi_dot S7 object wrapping the DOT string.

See Also

Other export: caugi_deserialize(), caugi_export(), caugi_graphml(), caugi_mermaid(), caugi_serialize(), export-classes, format-caugi, format-dot, format-graphml, format-mermaid, knit_print.caugi_export(), read_caugi(), read_graphml(), to_dot(), to_graphml(), to_mermaid(), write_caugi(), write_dot(), write_graphml(), write_mermaid()

caugi_export *S7 Base Class for Caugi Exports*

Description

A base class for all caugi export formats. Provides common structure and behavior for different export formats (DOT, GraphML, etc.).

Usage

```
caugi_export(content = character(0), format = character(0))
```

Arguments

content	A character string containing the exported graph.
format	A character string indicating the export format.

Value

A caugi_export S7 object with content and format properties.

See Also

Other export: caugi_deserialize(), caugi_dot(), caugi_graphml(), caugi_mermaid(), caugi_serialize(), export-classes, format-caugi, format-dot, format-graphml, format-mermaid, knit_print.caugi_export(), read_caugi(), read_graphml(), to_dot(), to_graphml(), to_mermaid(), write_caugi(), write_dot(), write_graphml(), write_mermaid()

---

caugi_graphml *S7 Class for GraphML Export*

Description

An S7 object that wraps a GraphML format string for caugi graphs.

Usage

```
caugi_graphml(content)
```

Arguments

content	A character string containing the GraphML format graph.

Value

A caugi_graphml S7 object wrapping the GraphML string.

See Also

Other export: caugi_deserialize(), caugi_dot(), caugi_export(), caugi_mermaid(), caugi_serialize(), export-classes, format-caugi, format-dot, format-graphml, format-mermaid, knit_print.caugi_export(), read_caugi(), read_graphml(), to_dot(), to_graphml(), to_mermaid(), write_caugi(), write_dot(), write_graphml(), write_mermaid()

---

caugi_layout *Compute Graph Layout*

Description

Computes node coordinates for graph visualization using specified layout algorithm. If the graph has not been built yet, it will be built automatically before computing the layout.

Usage

```
caugi_layout(
  x,
 method = c("auto", "sugiyama", "fruchterman-reingold", "kamada-kawai", "bipartite",
    "tiered", "circle"),
  packing_ratio = 1.618034,
  ...
)
```

Arguments

x	A caugi object. Must contain only directed edges for Sugiyama layout.
method	Character string specifying the layout method. Options: • "auto": Automatically choose the best layout (default). Selection order: 1. If tiers is provided, uses "tiered" 2. If partition is provided, uses "bipartite" 3. If graph has only directed edges, uses "sugiyama" 4. Otherwise, uses "fruchterman-reingold" • "sugiyama": Hierarchical layout for DAGs (requires only directed edges) • "fruchterman-reingold": Fast spring-electrical layout (works with all edge types) • "kamada-kawai": High-quality stress minimization (works with all edge types) • "bipartite": Bipartite layout (requires partition parameter) • "tiered": Multi-tier layout (requires tiers parameter) • "circle": Place nodes evenly along a circle
packing_ratio	Aspect ratio for packing disconnected components (width/height). Default is the golden ratio (1.618) which works well with widescreen displays. Use 1.0 for square grid, 2.0 for wider layouts, 0.5 for taller layouts, Inf for single row, or 0.0 for single column.
...	Additional arguments passed to the specific layout function. For bipartite layouts, use partition (logical vector) and orientation ("columns" or "rows"). For tiered layouts, use tiers (list, named vector, or data.frame) and orientation ("rows" or "columns").

Value

A data.frame with columns name, x, and y containing node names and their coordinates.

Layout Algorithms

Sugiyama (Hierarchical Layout)

Optimized for directed acyclic graphs (DAGs). Places nodes in layers to emphasize hierarchical structure and causal flow from top to bottom. Edges are routed to minimize crossings. Best for visualizing clear cause-effect relationships. Only works with directed edges.

Fruchterman-Reingold (Spring-Electrical)

Fast force-directed layout using a spring-electrical model. Treats edges as springs and nodes as electrically charged particles. Produces organic, symmetric layouts with uniform edge lengths. Good for general-purpose visualization and works with all edge types. Results are deterministic.

Kamada-Kawai (Stress Minimization)

High-quality force-directed layout that minimizes "stress" by making Euclidean distances proportional to graph-theoretic distances. Better preserves the global structure and path lengths compared to Fruchterman-Reingold. Ideal for publication-quality visualizations where accurate distance representation matters. Works with all edge types and produces deterministic results.

Circle

Places nodes evenly along the perimeter of a circle. The first node is at the top and subsequent nodes proceed counter-clockwise. Useful for small graphs, cycle visualization, and as a deterministic fallback. Works with all edge types and ignores edge structure.

Source

Fruchterman, T. M. J., & Reingold, E. M. (1991). Graph drawing by force-directed placement. Software: Practice and Experience, 21(11), 1129-1164. doi:10.1002/spe.4380211102

Kamada, T., & Kawai, S. (1989). An algorithm for drawing general undirected graphs. Information Processing Letters, 31(1), 7-15. doi:10.1016/00200190(89)901026

Sugiyama, K., Tagawa, S., & Toda, M. (1981). Methods for visual understanding of hierarchical system structures. IEEE Transactions on Systems, Man, and Cybernetics, 11(2), 109-125. doi:10.1109/TSMC.1981.4308636

See Also

Other plotting: add-caugi_plot-caugi_plot, caugi_layout_bipartite(), caugi_layout_circle(), caugi_layout_fruchterman_reingold(), caugi_layout_kamada_kawai(), caugi_layout_sugiyama(), caugi_layout_tiered(), caugi_plot(), divide-caugi_plot-caugi_plot, plot.caugi()

Examples

```
cg <- caugi(
  A %-->% B + C,
  B %-->% D,
  C %-->% D,
  class = "DAG"
)

# Default: auto-selects best layout
layout <- caugi_layout(cg)

# Auto-selects tiered when tiers provided
cg_tiered <- caugi(X1 %-->% M1, X2 %-->% M2, M1 %-->% Y, M2 %-->% Y)
tiers <- list(c("X1", "X2"), c("M1", "M2"), "Y")
layout_auto <- caugi_layout(cg_tiered, tiers = tiers) # Uses "tiered"

# Explicitly use hierarchical layout
```

```
layout_sug <- caugi_layout(cg, method = "sugiyama")

# Use force-directed for organic appearance
layout_fr <- caugi_layout(cg, method = "fruchterman-reingold")

# Use stress minimization for publication quality
layout_kk <- caugi_layout(cg, method = "kamada-kawai")

# Place nodes on a circle
layout_circle <- caugi_layout(cg, method = "circle")

# Bipartite layout with auto-detected partition
cg_bp <- caugi(A %-->% X, A %-->% Y, B %-->% X, B %-->% Y)
layout_bp_rows <- caugi_layout(
  cg_bp,
  method = "bipartite",
  orientation = "rows"
)

# Explicit partition
partition <- c(TRUE, TRUE, FALSE, FALSE)
layout_bp_cols <- caugi_layout(
  cg_bp,
  method = "bipartite",
  partition = partition,
  orientation = "columns"
)

# Tiered layout with three tiers
cg_tiered <- caugi(
  X1 %-->% M1 + M2,
  X2 %-->% M1 + M2,
  M1 %-->% Y,
  M2 %-->% Y
)
tiers <- list(c("X1", "X2"), c("M1", "M2"), "Y")
layout_tiered <- caugi_layout(
  cg_tiered,
  method = "tiered",
  tiers = tiers,
  orientation = "rows"
)
```

---

caugi_layout_bipartite

Bipartite Graph Layout

Description

Computes node coordinates for bipartite graphs, placing nodes in two parallel lines (rows or columns) based on a partition. If the graph has not been built yet, it will be built automatically before computing the layout.

Usage

```
caugi_layout_bipartite(x, partition = NULL, orientation = c("columns", "rows"))
```

Arguments

x	A caugi object.
partition	Optional logical vector indicating node partitions. Nodes with TRUE are placed in one partition and nodes with FALSE in the other. Length must equal the number of nodes. Both partitions must be non-empty. If NULL (default), attempts to detect bipartite structure automatically by assigning nodes without incoming edges to one partition and others to the second partition.
orientation	Character string specifying the layout orientation: • "columns": Two vertical columns. First partition on right (x=1), second partition on left (x=0). • "rows": Two horizontal rows. First partition on top (y=1), second partition on bottom (y=0).

Value

A data.frame with columns name, x, and y containing node names and their coordinates.

See Also

Other plotting: add-caugi_plot-caugi_plot, caugi_layout(), caugi_layout_circle(), caugi_layout_fruchterman
caugi_layout_kamada_kawai(), caugi_layout_sugiyama(), caugi_layout_tiered(), caugi_plot(),
divide-caugi_plot-caugi_plot, plot.caugi()

Examples

```
# Create a bipartite graph (causes -> effects)
cg <- caugi(A %-->% X, A %-->% Y, B %-->% X, B %-->% Y)
partition <- c(TRUE, TRUE, FALSE, FALSE) # A, B = causes, X, Y = effects

# Two horizontal rows (causes on top)
layout_rows <- caugi_layout_bipartite(cg, partition, orientation = "rows")

# Two vertical columns (causes on right)
layout_cols <- caugi_layout_bipartite(cg, partition, orientation = "columns")
```

caugi_layout_circle *Circle Layout*

Description

Computes node coordinates by placing nodes evenly along the perimeter of a circle. The first node is placed at the top of the circle, and subsequent nodes proceed counter-clockwise. Edge structure is ignored. Works with all edge types and produces deterministic results.

Usage

```
caugi_layout_circle(x, ...)
```

Arguments

x	A caugi object.
...	Ignored. For future extensibility.

Value

A data.frame with columns name, x, and y containing node names and their coordinates.

See Also

Other plotting: add-caugi_plot-caugi_plot, caugi_layout(), caugi_layout_bipartite(), caugi_layout_fruchterman_reingold(), caugi_layout_kamada_kawai(), caugi_layout_sugiyama(), caugi_layout_tiered(), caugi_plot(), divide-caugi_plot-caugi_plot, plot.caugi()

Examples

```
cg <- caugi(
  A %-->% B,
  B %-->% C,
  C %-->% D,
  D %-->% A
)
layout <- caugi_layout_circle(cg)
```

caugi_layout_fruchterman_reingold *Fruchterman-Reingold Force-Directed Layout*

Description

Computes node coordinates using the Fruchterman-Reingold force-directed layout algorithm. Fast spring-electrical model that treats edges as springs and nodes as electrically charged particles. Produces organic, symmetric layouts with uniform edge lengths. Works with all edge types and produces deterministic results.

Usage

```
caugi_layout_fruchterman_reingold(x, packing_ratio = 1.618034, ...)
```

Arguments

x	A caugi object.
packing_ratio	Aspect ratio for packing disconnected components (width/height). Default is the golden ratio (1.618) which works well with widescreen displays. Use 1.0 for square grid, 2.0 for wider layouts, 0.5 for taller layouts, Inf for single row, or 0.0 for single column.
...	Ignored. For future extensibility.

Value

A data.frame with columns name, x, and y containing node names and their coordinates.

Source

Fruchterman, T. M. J., & Reingold, E. M. (1991). Graph drawing by force-directed placement. Software: Practice and Experience, 21(11), 1129-1164. doi:10.1002/spe.4380211102

See Also

Other plotting: add-caugi_plot-caugi_plot, caugi_layout(), caugi_layout_bipartite(), caugi_layout_circle(), caugi_layout_kamada_kawai(), caugi_layout_sugiyama(), caugi_layout_tiered(), caugi_plot(), divide-caugi_plot-caugi_plot, plot.caugi()

Examples

```
cg <- caugi(
  A %-->% B,
  B %<->% C,
  C %-->% D
)
layout <- caugi_layout_fruchterman_reingold(cg)
```

caugi_layout_kamada_kawai
Kamada-Kawai Stress Minimization Layout

Description

Computes node coordinates using the Kamada-Kawai stress minimization algorithm. High-quality force-directed layout that minimizes "stress" by making Euclidean distances proportional to graph-theoretic distances. Better preserves global structure and path lengths compared to Fruchterman-Reingold. Ideal for publication-quality visualizations. Works with all edge types and produces deterministic results.

Usage

```
caugi_layout_kamada_kawai(x, packing_ratio = 1.618034, ...)
```

Arguments

`x`	A `caugi` object.
`packing_ratio`	Aspect ratio for packing disconnected components (width/height). Default is the golden ratio (1.618) which works well with widescreen displays. Use `1.0` for square grid, `2.0` for wider layouts, `0.5` for taller layouts, `Inf` for single row, or `0.0` for single column.
`...`	Ignored. For future extensibility.

Value

A `data.frame` with columns `name`, `x`, and `y` containing node names and their coordinates.

Source

Kamada, T., & Kawai, S. (1989). An algorithm for drawing general undirected graphs. Information Processing Letters, 31(1), 7-15. doi:10.1016/00200190(89)901026

See Also

Other plotting: `add-caugi_plot-caugi_plot`, `caugi_layout()`, `caugi_layout_bipartite()`, `caugi_layout_circle()`, `caugi_layout_fruchterman_reingold()`, `caugi_layout_sugiyama()`, `caugi_layout_tiered()`, `caugi_plot()`, `divide-caugi_plot-caugi_plot`, `plot.caugi()`

Examples

```
cg <- caugi(
  A %-->% B,
  B %<->% C,
  C %-->% D
)
layout <- caugi_layout_kamada_kawai(cg)
```

`caugi_layout_sugiyama` *Sugiyama Hierarchical Layout*

Description

Computes node coordinates using the Sugiyama hierarchical layout algorithm. Optimized for directed acyclic graphs (DAGs), placing nodes in layers to emphasize hierarchical structure and causal flow from top to bottom.

Usage

```
caugi_layout_sugiyama(x, packing_ratio = 1.618034, ...)
```

Arguments

`x`	A `caugi` object. Must contain only directed edges.
`packing_ratio`	Aspect ratio for packing disconnected components (width/height). Default is the golden ratio (1.618) which works well with widescreen displays. Use `1.0` for square grid, `2.0` for wider layouts, `0.5` for taller layouts, `Inf` for single row, or `0.0` for single column.
`...`	Ignored. For future extensibility.

Value

A `data.frame` with columns `name`, `x`, and `y` containing node names and their coordinates.

Source

Sugiyama, K., Tagawa, S., & Toda, M. (1981). Methods for visual understanding of hierarchical system structures. IEEE Transactions on Systems, Man, and Cybernetics, 11(2), 109-125. doi:10.1109/TSMC.1981.4308636

See Also

Other plotting: `add-caugi_plot-caugi_plot`, `caugi_layout()`, `caugi_layout_bipartite()`, `caugi_layout_circle()`, `caugi_layout_fruchterman_reingold()`, `caugi_layout_kamada_kawai()`, `caugi_layout_tiered()`, `caugi_plot()`, `divide-caugi_plot-caugi_plot`, `plot.caugi()`

Examples

```
cg <- caugi(A %-->% B + C, B %-->% D, C %-->% D, class = "DAG")
layout <- caugi_layout_sugiyama(cg)
```

caugi_layout_tiered *Tiered Graph Layout*

Description

Computes node coordinates for graphs with multiple tiers (layers), placing nodes in parallel rows or columns based on tier assignments. If the graph has not been built yet, it will be built automatically before computing the layout.

Usage

```
caugi_layout_tiered(x, tiers, orientation = c("columns", "rows"))
```

Arguments

`x`	A `caugi` object.
`tiers`	Tier assignments specifying which tier each node belongs to. Can be provided in multiple formats: • **Named list**: List where each element is a character vector of node names belonging to that tier. Element names are ignored; tier order is determined by list order (first element = tier 0, etc.). • **Named numeric vector**: Vector where names are node names and values are tier indices (starting from 0 or 1). • **Data.frame**: Must contain columns `name` (node names) and `tier` (tier indices). All nodes must be assigned to a tier, all tiers must be non-empty, and tier indices must be consecutive starting from 0 or 1.
`orientation`	Character string specifying the layout orientation: • `"columns"`: Vertical tiers. First tier at left (x=0), subsequent tiers to the right, last tier at right (x=1). • `"rows"`: Horizontal tiers. First tier at top (y=1), subsequent tiers below, last tier at bottom (y=0).

Value

A `data.frame` with columns `name`, `x`, `y`, and `tier` containing node names, their coordinates, and tier assignments (0-indexed). The returned data.frame also has an `orientation` attribute storing the orientation used. When passed to `plot()`, tier information is automatically extracted, so you don't need to specify `tiers` again.

See Also

Other plotting: `add-caugi_plot-caugi_plot`, `caugi_layout()`, `caugi_layout_bipartite()`, `caugi_layout_circle()`, `caugi_layout_fruchterman_reingold()`, `caugi_layout_kamada_kawai()`, `caugi_layout_sugiyama()`, `caugi_plot()`, `divide-caugi_plot-caugi_plot`, `plot.caugi()`

Examples

```
# Create a three-tier causal graph (exposures -> mediators -> outcome)
cg <- caugi(
  X1 %-->% M1 + M2,
  X2 %-->% M1 + M2,
  M1 %-->% Y,
  M2 %-->% Y
)

# Option 1: Named list (tier names are just labels)
tiers <- list(
  exposures = c("X1", "X2"),
  mediators = c("M1", "M2"),
  outcome = "Y"
)
layout_rows <- caugi_layout_tiered(cg, tiers, orientation = "rows")

# Option 2: Named numeric vector (0-indexed or 1-indexed both work)
tiers <- c(X1 = 1, X2 = 1, M1 = 2, M2 = 2, Y = 3)
layout_cols <- caugi_layout_tiered(cg, tiers, orientation = "columns")

# Option 3: Data.frame
tiers <- data.frame(
  name = c("X1", "X2", "M1", "M2", "Y"),
  tier = c(1, 1, 2, 2, 3)
)
layout <- caugi_layout_tiered(cg, tiers, orientation = "rows")

# The layout includes tier information, so plot() works without passing tiers
plot(cg, layout = layout)
```

---

caugi_mermaid *S7 Class for Mermaid Export*

Description

An S7 object that wraps a Mermaid format string for displaying caugi graphs. When printed interactively, displays the Mermaid string cleanly.

Usage

```
caugi_mermaid(content)
```

Arguments

content	A character string containing the Mermaid format graph.

Value

A caugi_mermaid S7 object wrapping the Mermaid string.

See Also

Other export: caugi_deserialize(), caugi_dot(), caugi_export(), caugi_graphml(), caugi_serialize(), export-classes, format-caugi, format-dot, format-graphml, format-mermaid, knit_print.caugi_export(), read_caugi(), read_graphml(), to_dot(), to_graphml(), to_mermaid(), write_caugi(), write_dot(), write_graphml(), write_mermaid()

---

caugi_options *Get or set global options for caugi*

Description

Configure global defaults for caugi, including plot composition spacing and default visual styles for nodes, edges, labels, and titles.

Usage

```
caugi_options(...)
```

Arguments

...	Named values to update options with, or unnamed option names to retrieve. Multiple unnamed arguments drill down through nested options. To query all options, call without arguments. Attempting to access a non-existent option will raise an error.

Details

The use_open_graph_definition option (TRUE/FALSE, default TRUE) controls how graph queries interpret reachability relations. When TRUE (open definition), queries such as ancestors(), descendants(), posteriors(),and anteriors() exclude the queried node itself. When FALSE (closed definition), the queried node is included in the results.

The plot options are nested under the plot key:

- spacing: A grid::unit() controlling space between composed plots (default: grid::unit(1, "lines"))
- node_style: List of default node appearance parameters:
  - fill: Fill color (default: "lightgrey")
  - padding: Padding around labels in mm (default: 2)
  - size: Size multiplier (default: 1)
- edge_style: List of default edge appearance parameters:
  - arrow_size: Arrow size in mm (default: 3)

  - `circle_size`: Radius of endpoint circles for partial edges in mm (default: `1.5`)
  - `fill`: Arrow/line color (default: `"black"`)
  - `route`: Whether edges automatically bend around non-incident nodes they would otherwise cross (default: `TRUE`)
- `label_style`: List of label text parameters (see `grid::gpar()`)
- `title_style`: List of title text parameters:
  - `col`: Text color (default: `"black"`)
  - `fontface`: Font face (default: `"bold"`)
  - `fontsize`: Font size in pts (default: `14.4`)

Options set via `caugi_options()` serve as global defaults that can be overridden by arguments to `plot.caugi()`.

Value

When setting, returns (invisibly) the previous values for the updated options. When getting (no arguments or unnamed character vector), returns the requested options.

See Also

`plot.caugi()` for per-plot style arguments, `grid::gpar()` for available graphical parameters

Examples

```
# Query all options
caugi_options()

# Use closed graph definition
caugi_options(use_open_graph_definition = FALSE)

# Query specific option
caugi_options("plot")

# Query nested option
caugi_options("plot", "tier_style")
caugi_options("plot", "node_style", "fill")

# Set plot spacing
caugi_options(plot = list(spacing = grid::unit(2, "lines")))

# Set default node style
caugi_options(plot = list(
  node_style = list(fill = "lightblue", padding = 3)
))

# Set multiple options at once
caugi_options(plot = list(
  spacing = grid::unit(1.5, "lines"),
  node_style = list(fill = "lightblue", padding = 3),
  edge_style = list(arrow_size = 4, fill = "darkgray"),
```

```
  title_style = list(col = "blue", fontsize = 16)
))

# Reset to defaults
caugi_options(caugi_default_options())
```

`caugi_plot` *S7 Class for caugi Plot*

Description

An S7 object that wraps a grid gTree for displaying caugi graphs. Similar to ggplot objects, these are created by the plot method but not drawn until explicitly printed or plotted. This allows for returning plot objects from functions and controlling when/where they are displayed.

Usage

```
caugi_plot(grob = NULL)
```

Arguments

`grob`	A grid gTree representing the graph plot.

Value

A `caugi_plot` S7 object wrapping the supplied `grob`.

See Also

Other plotting: `add-caugi_plot-caugi_plot`, `caugi_layout()`, `caugi_layout_bipartite()`, `caugi_layout_circle()`, `caugi_layout_fruchterman_reingold()`, `caugi_layout_kamada_kawai()`, `caugi_layout_sugiyama()`, `caugi_layout_tiered()`, `divide-caugi_plot-caugi_plot`, `plot.caugi()`

`caugi_serialize` *Serialize caugi Graph to JSON String*

Description

Converts a caugi graph to a JSON string in the native caugi format. This is a lower-level function; consider using `write_caugi()` for writing to files.

Usage

```
caugi_serialize(x, comment = NULL, tags = NULL)
```

Arguments

x	A caugi object or an object coercible to caugi.
comment	Optional character string with a comment about the graph.
tags	Optional character vector of tags for categorizing the graph.

Value

A character string containing the JSON representation.

See Also

Other export: caugi_deserialize(), caugi_dot(), caugi_export(), caugi_graphml(), caugi_mermaid(), export-classes, format-caugi, format-dot, format-graphml, format-mermaid, knit_print.caugi_export(), read_caugi(), read_graphml(), to_dot(), to_graphml(), to_mermaid(), write_caugi(), write_dot(), write_graphml(), write_mermaid()

Examples

```
cg <- caugi(A %-->% B, class = "DAG")
json <- caugi_serialize(cg)
cat(json)
```

---

caugi_verbs *Manipulate nodes and edges of a* caugi

Description

Add, remove, or and set nodes or edges to / from a caugi object. Edges can be specified using expressions with the infix operators. Alternatively, the edges to be added are specified using the from, edge, and to arguments.

Usage

```
add_edges(cg, ..., from = NULL, edge = NULL, to = NULL, inplace = FALSE)

remove_edges(cg, ..., from = NULL, edge = NULL, to = NULL, inplace = FALSE)

set_edges(cg, ..., from = NULL, edge = NULL, to = NULL, inplace = FALSE)

add_nodes(cg, ..., name = NULL, inplace = FALSE)

remove_nodes(cg, ..., name = NULL, inplace = FALSE)
```

Arguments

cg	A caugi object.
...	Expressions specifying edges to add using the infix operators, or nodes to add using unquoted names, vectors via c(), or + composition.
from	Character vector of source node names. Default is NULL.
edge	Character vector of edge types. Default is NULL.
to	Character vector of target node names. Default is NULL.
inplace	DEPRECATED This parameter is deprecated and will be ignored. Graphs are always modified via copy-on-write.
name	Character vector of node names. Default is NULL.

Details

Caugi graph verbs

Value

The updated caugi.

Functions

- add_edges(): Add edges.
- remove_edges(): Remove edges.
- set_edges(): Set edge type for given pair(s).
- add_nodes(): Add nodes.
- remove_nodes(): Remove nodes.

See Also

Other verbs: build()

Examples

```
# initialize empty graph and build slowly
cg <- caugi(class = "PDAG")

cg <- cg |>
  add_nodes(c("A", "B", "C", "D", "E")) |> # A, B, C, D, E
  add_edges(A %-->% B %-->% C) |> # A --> B --> C, D, E
  set_edges(B %---% C) # A --> B --- C, D, E

cg <- remove_edges(cg, B %---% C) |> # A --> B, C, D, E
  remove_nodes(c("C", "D", "E")) # A --> B

# Graphs are now built lazily when needed
parents(cg, "B") # triggers compilation
```

`children` *Get children of nodes in a* `caugi`

Description

Get children of nodes in a graph (nodes with directed edges pointing OUT from the target nodes). This is equivalent to `neighbors(cg, nodes, mode = "out")`.

Usage

```
children(cg, nodes = NULL, index = NULL)
```

Arguments

`cg`	A `caugi` object.
`nodes`	A character vector of node names.
`index`	A vector of node indexes.

Value

Either a character vector of node names (if a single node is requested) or a list of character vectors (if multiple nodes are requested).

See Also

Other queries: `ancestors()`, `anteriors()`, `components()`, `descendants()`, `districts()`, `edge_types()`, `edges()`, `exogenous()`, `is_acyclic()`, `is_admg()`, `is_ag()`, `is_caugi()`, `is_cpdag()`, `is_dag()`, `is_empty_caugi()`, `is_mag()`, `is_mpdag()`, `is_pdag()`, `is_simple()`, `is_ug()`, `m_separated()`, `markov_blanket()`, `neighbors()`, `nodes()`, `parents()`, `posteriors()`, `same_nodes()`, `spouses()`, `subgraph()`, `topological_sort()`

Examples

```
cg <- caugi(
  A %-->% B,
  B %-->% C,
  class = "DAG"
)
children(cg, "A") # "B"
children(cg, index = 2) # "C"
children(cg, "B") # "C"
children(cg, c("B", "C"))
#> $B
#> [1] "C"
#>
#> $C
#> NULL
```

components *Get connected components of a graph*

Description

Partition a graph into maximal weakly or strongly connected components. This query supports every graph class, including cyclic graphs of class "UNKNOWN".

Usage

```
components(cg, mode = c("weak", "strong"))
```

Arguments

cg	A caugi object.
mode	Character; "weak" (default) or "strong". Weak connectivity ignores edge directions and includes all edge types. Strong connectivity uses only fully directed edges: every node in a component can reach every other node by following directed edges. Undirected, bidirected, and partial edges are ignored in strong mode.

Details

Every strong component of a DAG is a singleton. Strong components describe mutual directed reachability, whereas districts() describe connectivity through bidirected edges.

Value

A list of character vectors, one per component. Nodes within each component follow the graph's node order, and components are ordered by their first node in that order. Isolated nodes form singleton components. An empty graph returns list().

See Also

Other queries: ancestors(), anteriors(), children(), descendants(), districts(), edge_types(), edges(), exogenous(), is_acyclic(), is_admg(), is_ag(), is_caugi(), is_cpdag(), is_dag(), is_empty_caugi(), is_mag(), is_mpdag(), is_pdag(), is_simple(), is_ug(), m_separated(), markov_blanket(), neighbors(), nodes(), parents(), posteriors(), same_nodes(), spouses(), subgraph(), topological_sort()

Examples

```
cg <- caugi(A %-->% B, C %-->% B, D, class = "DAG")
components(cg) # list(c("A", "B", "C"), "D")
components(cg, mode = "strong") # Four singleton components

cyclic <- caugi(
  A %-->% B, B %-->% C, C %-->% A, C %-->% D,
```

```
  class = "UNKNOWN"
)
components(cyclic, mode = "strong") # list(c("A", "B", "C"), "D")
```

`condition_marginalize` *Marginalize and/or condition on variables in an ancestral graph (AG)*

Description

Marginalize variables out of an AG, and/or condition on variables. Depending on the structure, it could produce a graph with directed, bidirected, and undirected edges.

Usage

```
condition_marginalize(cg, cond_vars = NULL, marg_vars = NULL)
```

Arguments

`cg`	A `caugi` ancestral graph of class `"AG"`.
`cond_vars`	Character vector of nodes to condition on.
`marg_vars`	Character vector of nodes to marginalize over.

Value

A `caugi` object of class `"AG"`.

References

Definition 4.2.1 in Thomas Richardson. Peter Spirtes. "Ancestral graph Markov models." Ann. Statist. 30 (4) 962 - 1030, August 2002. doi:10.1214/aos/1031689015

See Also

Other operations: `count_dags()`, `dag_from_pdag()`, `enumerate_dags()`, `exogenize()`, `latent_project()`, `meek_closure()`, `moralize()`, `mutate_caugi()`, `normalize_latent_structure()`, `skeleton()`

Examples

```
mg <- caugi(
  U %-->% X + Y,
  A %-->% X,
  B %-->% Y,
  class = "DAG"
)

condition_marginalize(mg, marg_vars = "U") # ADMG
condition_marginalize(mg, cond_vars = "U") # DAG
```

count_dags *Count DAGs in a Markov equivalence class*

Description

Returns the number of DAGs in the Markov equivalence class of a PDAG without materializing each one. Useful for sizing an enumeration before calling `enumerate_dags()`.

Usage

```
count_dags(cg)
```

Arguments

`cg`	A `caugi` object of class `"PDAG"` or `"MPDAG"`.

Value

A single numeric value, the cardinality of the MEC. Counts above `2^53` lose integer precision; in practice no realistic PDAG yields a MEC anywhere near that size.

References

Chickering, D. M. (2002). "Learning Equivalence Classes of Bayesian-Network Structures". *Journal of Machine Learning Research*, 2:445–498.

See Also

Other operations: `condition_marginalize()`, `dag_from_pdag()`, `enumerate_dags()`, `exogenize()`, `latent_project()`, `meek_closure()`, `moralize()`, `mutate_caugi()`, `normalize_latent_structure()`, `skeleton()`

Examples

```
pdag <- caugi(
  A %---% B,
  B %---% C,
  class = "PDAG"
)
count_dags(pdag) # 3
```

d_separated *Are X and Y d-separated given Z?*

Description

Checks whether every node in X is d-separated from every node in Y given Z in a DAG.

Usage

```
d_separated(
  cg,
  X = NULL,
  Y = NULL,
  Z = NULL,
  X_index = NULL,
  Y_index = NULL,
  Z_index = NULL
)
```

Arguments

cg	A caugi object.
X, Y, Z	Character vectors of node names, or NULL. Use *_index to pass 1-based indices. If Z is NULL or missing, no nodes are conditioned on.
X_index, Y_index, Z_index	Optional numeric 1-based indices (exclusive with X,Y,Z respectively).

Value

TRUE if d-separated, FALSE otherwise.

See Also

Other adjustment: adjustment_set(), all_adjustment_sets_admg(), all_backdoor_sets(), is_valid_adjustment_admg(), is_valid_backdoor(), minimal_separator()

Examples

```
cg <- caugi(
  C %-->% X,
  X %-->% F,
  X %-->% D,
  A %-->% X,
  A %-->% K,
  K %-->% Y,
  D %-->% Y,
  D %-->% G,
  Y %-->% H,
```

```
  class = "DAG"
)

d_separated(cg, "X", "Y", Z = c("A", "D")) # TRUE
d_separated(cg, "X", "Y", Z = NULL) # FALSE
```

---

dag_from_pdag *Extend a PDAG to a DAG using the Dor-Tarsi Algorithm*

Description

Given a Partially Directed Acyclic Graph (PDAG), this function attempts to extend it to a Directed Acyclic Graph (DAG) by orienting the undirected edges while preserving acyclicity and all existing directed edges. The procedure implements the Dor-Tarsi algorithm.

If the PDAG cannot be consistently extended to a DAG, the function will raise an error.

Usage

```
dag_from_pdag(cg, PDAG)
```

Arguments

cg	A caugi object of class "PDAG", "MPDAG", or "CPDAG".
PDAG	Deprecated alias for cg. Use cg instead.

Value

A caugi object of class "DAG" representing a DAG extension of the input PDAG.

References

Dor, D., & Tarsi, M. (1992). "A simple algorithm to construct a consistent extension of a partially directed acyclic graph".

See Also

Other operations: condition_marginalize(), count_dags(), enumerate_dags(), exogenize(), latent_project(), meek_closure(), moralize(), mutate_caugi(), normalize_latent_structure(), skeleton()

Examples

```
pdag <- caugi(
  A %---% B,
  B %---% C,
  class = "PDAG"
)
dag <- dag_from_pdag(pdag)
edges(dag)
```

`descendants` *Get descendants of nodes in a* `caugi`

Description

Get descendants of nodes in a `caugi`

Usage

```
descendants(
  cg,
  nodes = NULL,
  index = NULL,
  open = caugi_options("use_open_graph_definition")
)
```

Arguments

`cg`	A `caugi` object.
`nodes`	A character vector of node names.
`index`	A vector of node indexes.
`open`	Boolean. Determines how the graph is interpreted when retrieving descendants. Default is taken from `caugi_options("use_open_graph_definition")`, which by default is TRUE.

Value

Either a character vector of node names (if a single node is requested) or a list of character vectors (if multiple nodes are requested).

See Also

Other queries: `ancestors()`, `anteriors()`, `children()`, `components()`, `districts()`, `edge_types()`, `edges()`, `exogenous()`, `is_acyclic()`, `is_admg()`, `is_ag()`, `is_caugi()`, `is_cpdag()`, `is_dag()`, `is_empty_caugi()`, `is_mag()`, `is_mpdag()`, `is_pdag()`, `is_simple()`, `is_ug()`, `m_separated()`, `markov_blanket()`, `neighbors()`, `nodes()`, `parents()`, `posteriors()`, `same_nodes()`, `spouses()`, `subgraph()`, `topological_sort()`

Examples

```
cg <- caugi(
  A %-->% B,
  B %-->% C,
  class = "DAG"
)
descendants(cg, "A") # "B" "C"
descendants(cg, "A", open = FALSE) # "A" "B" "C"
descendants(cg, index = 2) # "C"
descendants(cg, "B") # "C"
descendants(cg, c("B", "C"))
#> $B
#> [1] "C"
#>
#> $C
#> NULL
```

---

districts *Get districts (c-components) of an ADMG or AG*

Description

Get districts (c-components) for all nodes, or for selected nodes in an ADMG/AG. A district is a maximal set of nodes connected via bidirected edges. If both `nodes` and `index` are `NULL`, returns all districts in the graph.

Usage

```
districts(cg, nodes = NULL, index = NULL, all = NULL)
```

Arguments

`cg`	A `caugi` object of class ADMG or AG.
`nodes`	Optional character vector of node names. If supplied, returns district(s) containing these nodes.
`index`	Optional numeric vector of 1-based node indices. If supplied, returns district(s) containing these indices.
`all`	DEPRECATED (If `TRUE`, return all districts explicitly. Cannot be combined with `nodes` or `index`.)

Value

If all districts are requested: a list of character vectors, one per district. If `nodes`/`index` are supplied: either a character vector (single target) or a named list of character vectors (multiple targets).

See Also

Other queries: ancestors(), anteriors(), children(), components(), descendants(), edge_types(), edges(), exogenous(), is_acyclic(), is_admg(), is_ag(), is_caugi(), is_cpdag(), is_dag(), is_empty_caugi(), is_mag(), is_mpdag(), is_pdag(), is_simple(), is_ug(), m_separated(), markov_blanket(), neighbors(), nodes(), parents(), posteriors(), same_nodes(), spouses(), subgraph(), topological_sort()

Examples

```
cg <- caugi(
  A %-->% B,
  A %<->% C,
  D %<->% E,
  class = "ADMG"
)
districts(cg)
# Returns list with districts: {A, C}, {B}, {D, E}
districts(cg, nodes = "A") # Returns c("A", "C")
districts(cg, index = c(1, 4))
```

---

divide-caugi_plot-caugi_plot

Compose Plots Vertically

Description

Stack two plots vertically with configurable spacing. Compositions can be nested to create complex multi-plot layouts.

Usage

```
## S3 method for class 'caugi_plot'
e1 / e2
```

Arguments

e1	A caugi_plot object (top plot)
e2	A caugi_plot object (bottom plot)

Details

The spacing between plots is controlled by the global option caugi_options()$plot$spacing, which defaults to grid::unit(1, "lines"). Compositions can be nested arbitrarily:

- p1 / p2 - two plots stacked vertically
- p1 / p2 / p3 - three plots in a column
- (p1 + p2) / p3 - two plots on top, one below

Value

A caugi_plot object containing the composed layout

See Also

caugi_options() for configuring spacing and default styles

Other plotting: add-caugi_plot-caugi_plot, caugi_layout(), caugi_layout_bipartite(), caugi_layout_circle(), caugi_layout_fruchterman_reingold(), caugi_layout_kamada_kawai(), caugi_layout_sugiyama(), caugi_layout_tiered(), caugi_plot(), plot.caugi()

Examples

```
cg1 <- caugi(A %-->% B, B %-->% C)
cg2 <- caugi(X %-->% Y, Y %-->% Z)

p1 <- plot(cg1, main = "Graph 1")
p2 <- plot(cg2, main = "Graph 2")

# Vertical composition
p1 / p2

# Mixed composition
(p1 + p2) / p1
```

---

edge_types *Get the edge types of a* caugi.

Description

Get the edge types of a caugi.

Usage

```
edge_types(cg)
```

Arguments

cg	A caugi object.

Value

A character vector of edge types.

See Also

Other queries: ancestors(), anteriors(), children(), components(), descendants(), districts(), edges(), exogenous(), is_acyclic(), is_admg(), is_ag(), is_caugi(), is_cpdag(), is_dag(), is_empty_caugi(), is_mag(), is_mpdag(), is_pdag(), is_simple(), is_ug(), m_separated(), markov_blanket(), neighbors(), nodes(), parents(), posteriors(), same_nodes(), spouses(), subgraph(), topological_sort()

Examples

```
cg <- caugi(
  A %-->% B,
  B %--o% C,
  C %<->% D,
  D %---% E,
  A %o-o% E,
  class = "UNKNOWN"
)
edge_types(cg) # returns c("-->", "o-o", "--o", "<->", "---")
```

---

edges *Get edges of a* caugi.

Description

Get edges of a caugi.

Usage

```
edges(cg, ...)

E(cg, ...)
```

Arguments

cg	A caugi object.
...	Additional arguments (currently unused).

Value

A data.table with columns from, edge, and to.

See Also

Other queries: ancestors(), anteriors(), children(), components(), descendants(), districts(), edge_types(), exogenous(), is_acyclic(), is_admg(), is_ag(), is_caugi(), is_cpdag(), is_dag(), is_empty_caugi(), is_mag(), is_mpdag(), is_pdag(), is_simple(), is_ug(), m_separated(), markov_blanket(), neighbors(), nodes(), parents(), posteriors(), same_nodes(), spouses(), subgraph(), topological_sort()

Examples

```
cg <- caugi(
  A %-->% B,
  B %-->% C,
  D,
  class = "DAG"
)
edges(cg) # returns the data.table with columns from, edge, to
```

`enumerate_dags` *Enumerate all DAGs in a Markov equivalence class*

Description

Given a PDAG, enumerate every Directed Acyclic Graph (DAG) in its Markov equivalence class – i.e. every acyclic orientation of the undirected edges that introduces no new v-structures.

Usage

```
enumerate_dags(cg)
```

Arguments

`cg`	A `caugi` object of class `"PDAG"` or `"MPDAG"`.

Details

Implements the recursive listing algorithm of Chickering (2002). The input is normalized via `meek_closure()` so any background-knowledge orientations are preserved and propagated before enumeration. The number of returned DAGs can grow super-exponentially in the size of the chain components; use `count_dags()` first to size the problem.

Value

A list of `caugi` objects of class `"DAG"`, one per DAG in the MEC.

References

Chickering, D. M. (2002). "Learning Equivalence Classes of Bayesian-Network Structures". *Journal of Machine Learning Research*, 2:445–498.

See Also

Other operations: `condition_marginalize()`, `count_dags()`, `dag_from_pdag()`, `exogenize()`, `latent_project()`, `meek_closure()`, `moralize()`, `mutate_caugi()`, `normalize_latent_structure()`, `skeleton()`

Examples

```
pdag <- caugi(
  A %---% B,
  B %---% C,
  class = "PDAG"
)
dags <- enumerate_dags(pdag)
length(dags) # 3
```

`exogenize` *Exogenize a graph*

Description

Exogenize a graph by removing all ingoing edges to the set of nodes specified (i.e., make the nodes exogenous), as well as joining the parents of the nodes specified to the children of the nodes specified.

Usage

```
exogenize(cg, nodes)
```

Arguments

`cg`	A `caugi` object of class `"DAG"`.
`nodes`	A character vector of node names to exogenize. Must be a subset of the nodes in the graph.

Value

A `caugi` object representing the exogenized graph.

See Also

Other operations: `condition_marginalize()`, `count_dags()`, `dag_from_pdag()`, `enumerate_dags()`, `latent_project()`, `meek_closure()`, `moralize()`, `mutate_caugi()`, `normalize_latent_structure()`, `skeleton()`

Examples

```
cg <- caugi(A %-->% B, class = "DAG")
exogenize(cg, nodes = "B") # A, B
```

exogenous *Get all exogenous nodes in a* caugi

Description

Get all exogenous nodes (nodes with no parents) in a caugi.

Usage

```
exogenous(cg, undirected_as_parents = FALSE)
```

Arguments

cg	A caugi object.
undirected_as_parents	Logical; if TRUE, undirected edges are treated as (possible) parents, if FALSE (default), undirected edges are ignored.

Value

Either a character vector of node names (if a single node is requested) or a list of character vectors (if multiple nodes are requested).

See Also

Other queries: ancestors(), anteriors(), children(), components(), descendants(), districts(), edge_types(), edges(), is_acyclic(), is_admg(), is_ag(), is_caugi(), is_cpdag(), is_dag(), is_empty_caugi(), is_mag(), is_mpdag(), is_pdag(), is_simple(), is_ug(), m_separated(), markov_blanket(), neighbors(), nodes(), parents(), posteriors(), same_nodes(), spouses(), subgraph(), topological_sort()

Examples

```
cg <- caugi(
  A %-->% B,
  B %-->% C,
  class = "DAG"
)
exogenous(cg) # "A"
```

export-classes *Export Format Classes*

Description

S7 classes for representing caugi graphs in various export formats. These classes provide a common interface for serializing graphs to different text formats like DOT, GraphML, JSON, etc.

Base Class

`caugi_export` is the base class for all export formats. It provides:

- `content` property: Character string containing the serialized graph
- `format` property: Character string indicating the format type
- Common methods: `print()`, `as.character()`, `knit_print()`

Subclasses

- `caugi_dot`: DOT format for Graphviz visualization
- `caugi_mermaid`: Mermaid format for web-based visualization

See Also

Other export: `caugi_deserialize()`, `caugi_dot()`, `caugi_export()`, `caugi_graphml()`, `caugi_mermaid()`, `caugi_serialize()`, `format-caugi`, `format-dot`, `format-graphml`, `format-mermaid`, `knit_print.caugi_export()`, `read_caugi()`, `read_graphml()`, `to_dot()`, `to_graphml()`, `to_mermaid()`, `write_caugi()`, `write_dot()`, `write_graphml()`, `write_mermaid()`

format-caugi *Caugi Native Format Serialization*

Description

Functions for converting caugi graphs to and from the native caugi JSON format. This format provides efficient, reproducible serialization for saving and sharing caugi graphs.

See Also

Other export: `caugi_deserialize()`, `caugi_dot()`, `caugi_export()`, `caugi_graphml()`, `caugi_mermaid()`, `caugi_serialize()`, `export-classes`, `format-dot`, `format-graphml`, `format-mermaid`, `knit_print.caugi_export()`, `read_caugi()`, `read_graphml()`, `to_dot()`, `to_graphml()`, `to_mermaid()`, `write_caugi()`, `write_dot()`, `write_graphml()`, `write_mermaid()`

format-dot *DOT Format Export and Import*

Description

Functions for converting caugi graphs to and from Graphviz DOT format. The DOT format is a plain text graph description language used by Graphviz tools for visualization.

See Also

Other export: caugi_deserialize(), caugi_dot(), caugi_export(), caugi_graphml(), caugi_mermaid(), caugi_serialize(), export-classes, format-caugi, format-graphml, format-mermaid, knit_print.caugi_export(read_caugi(), read_graphml(), to_dot(), to_graphml(), to_mermaid(), write_caugi(), write_dot(), write_graphml(), write_mermaid()

format-graphml *GraphML Format Export and Import*

Description

Functions for converting caugi graphs to and from GraphML format. GraphML is an XML-based file format for graphs supported by many graph tools and libraries.

See Also

Other export: caugi_deserialize(), caugi_dot(), caugi_export(), caugi_graphml(), caugi_mermaid(), caugi_serialize(), export-classes, format-caugi, format-dot, format-mermaid, knit_print.caugi_export(), read_caugi(), read_graphml(), to_dot(), to_graphml(), to_mermaid(), write_caugi(), write_dot(), write_graphml(), write_mermaid()

format-mermaid *Mermaid Format Export*

Description

Functions for converting caugi graphs to Mermaid flowchart format. Mermaid is a JavaScript-based diagramming tool that renders in web browsers and is natively supported by Quarto, GitHub, and many other platforms.

See Also

Other export: caugi_deserialize(), caugi_dot(), caugi_export(), caugi_graphml(), caugi_mermaid(), caugi_serialize(), export-classes, format-caugi, format-dot, format-graphml, knit_print.caugi_export(), read_caugi(), read_graphml(), to_dot(), to_graphml(), to_mermaid(), write_caugi(), write_dot(), write_graphml(), write_mermaid()

generate_graph *Generate a* caugi *using Erdős-Rényi.*

Description

Sample a random DAG or CPDAG using Erdős-Rényi for random graph generation.

Usage

```
generate_graph(n, m = NULL, p = NULL, class = c("DAG", "CPDAG"), seed = NULL)
```

Arguments

n	Integer >= 0. Number of nodes in the graph.
m	Integer in `0, n*(n-1)/2`. Number of edges in the graph. Exactly one of `m` or `p` must be supplied.
p	Numeric in `[0,1]`. Probability of edge creation. Exactly one of `m` or `p` must be supplied.
class	"DAG" or "CPDAG". When `"CPDAG"`, the result is the CPDAG (essential graph) of the sampled DAG's Markov equivalence class, returned with class `"CPDAG"`.
seed	Optional integer; random seed for reproducibility.

Value

The sampled caugi object. `class = "DAG"` returns a `"DAG"`; `class = "CPDAG"` returns a `"CPDAG"`.

See Also

Other simulation functions: `simulate_data()`

Examples

```
# generate a random DAG with 5 nodes and 4 edges
dag <- generate_graph(n = 5, m = 4, class = "DAG")

# generate a random CPDAG with 5 nodes and edge probability 0.3
cpdag <- generate_graph(n = 5, p = 0.3, class = "CPDAG")
```

hd *Hamming Distance*

Description

Compute the Hamming Distance between two graphs.

Usage

```
hd(cg1, cg2, normalized = FALSE)
```

Arguments

cg1	A caugi object.
cg2	A caugi object.
normalized	Logical; if TRUE, returns the normalized Hamming Distance.

Value

An integer representing the Hamming Distance between the two graphs, if normalized = FALSE, or a numeric between 0 and 1 if normalized = TRUE.

See Also

Other metrics: aid(), shd()

Examples

```
cg1 <- caugi(A %-->% B %-->% C, D %-->% C, class = "DAG")
cg2 <- caugi(A %-->% B %-->% C, D %---% C, class = "PDAG")
hd(cg1, cg2) # 0
```

is_acyclic *Is the* caugi *acyclic?*

Description

Checks if the given caugi graph is acyclic.

Usage

```
is_acyclic(cg, force_check = FALSE)
```

Arguments

cg	A caugi object.
force_check	Logical; if TRUE, the function will test if the graph is acyclic, if FALSE (default), it will look at the graph class and match it, if possible.

Details

Logically, it should not be possible to have a graph class of "DAG", "PDAG", "MPDAG", or "CPDAG" that has cycles, but in case the user modified the graph after creation in some unforeseen way that could have introduced cycles, this function allows to force a check of acyclicity, if needed.

Value

A logical value indicating whether the graph is acyclic.

See Also

Other queries: ancestors(), anteriors(), children(), components(), descendants(), districts(), edge_types(), edges(), exogenous(), is_admg(), is_ag(), is_caugi(), is_cpdag(), is_dag(), is_empty_caugi(), is_mag(), is_mpdag(), is_pdag(), is_simple(), is_ug(), m_separated(), markov_blanket(), neighbors(), nodes(), parents(), posteriors(), same_nodes(), spouses(), subgraph(), topological_sort()

Examples

```
cg_acyclic <- caugi(
  A %-->% B,
  B %-->% C,
  class = "DAG"
)
is_acyclic(cg_acyclic) # TRUE
cg_cyclic <- caugi(
  A %-->% B,
  B %-->% C,
  C %-->% A,
  class = "UNKNOWN"
)
is_acyclic(cg_cyclic) # FALSE
```

---

is_admg *Is the* caugi *graph an ADMG?*

Description

Checks if the given caugi graph is an Acyclic Directed Mixed Graph (ADMG).

An ADMG contains only directed (-->) and bidirected (<->) edges, and the directed part must be acyclic.

Usage

```
is_admg(cg, force_check = FALSE)
```

Arguments

cg	A caugi object.
force_check	Logical; if TRUE, the function will test if the graph is an ADMG, if FALSE (default), it will look at the graph class and match it, if possible.

Value

A logical value indicating whether the graph is an ADMG.

See Also

Other queries: ancestors(), anteriors(), children(), components(), descendants(), districts(), edge_types(), edges(), exogenous(), is_acyclic(), is_ag(), is_caugi(), is_cpdag(), is_dag(), is_empty_caugi(), is_mag(), is_mpdag(), is_pdag(), is_simple(), is_ug(), m_separated(), markov_blanket(), neighbors(), nodes(), parents(), posteriors(), same_nodes(), spouses(), subgraph(), topological_sort()

Examples

```
cg_admg <- caugi(
  A %-->% B,
  A %<->% C,
  class = "ADMG"
)
is_admg(cg_admg) # TRUE

cg_dag <- caugi(
  A %-->% B,
  class = "DAG"
)
is_admg(cg_dag) # TRUE (DAGs are valid ADMGs)
```

---

is_ag *Is the* caugi *graph an AG?*

Description

Checks if the given caugi graph is an Ancestral Graph (AG).

An AG contains directed (-->), bidirected (<->), and undirected (---) edges, and must satisfy ancestral graph constraints (no directed cycles, anterior constraint, and undirected constraint).

Usage

```
is_ag(cg, force_check = FALSE)
```

Arguments

cg	A caugi object.
force_check	Logical; if TRUE, the function will test if the graph is an AG, if FALSE (default), it will look at the graph class and match it, if possible.

Value

A logical value indicating whether the graph is an AG.

See Also

Other queries: ancestors(), anteriors(), children(), components(), descendants(), districts(), edge_types(), edges(), exogenous(), is_acyclic(), is_admg(), is_caugi(), is_cpdag(), is_dag(), is_empty_caugi(), is_mag(), is_mpdag(), is_pdag(), is_simple(), is_ug(), m_separated(), markov_blanket(), neighbors(), nodes(), parents(), posteriors(), same_nodes(), spouses(), subgraph(), topological_sort()

Examples

```
cg_ag <- caugi(
  A %-->% B,
  C %<->% D,
  E %---% F,
  class = "AG"
)
is_ag(cg_ag) # TRUE

cg_ug <- caugi(
  A %---% B,
  class = "UG"
)
is_ag(cg_ug) # TRUE (UGs are valid AGs)
```

---

is_caugi *Is it a* caugi *graph?*

Description

Checks if the given object is a caugi. Mostly used internally to validate inputs.

Usage

```
is_caugi(x, throw_error = FALSE)
```

Arguments

x	An object to check.
throw_error	Logical; if TRUE, throws an error if x is not a caugi.

Value

A logical value indicating whether the object is a caugi.

See Also

Other queries: ancestors(), anteriors(), children(), components(), descendants(), districts(), edge_types(), edges(), exogenous(), is_acyclic(), is_admg(), is_ag(), is_cpdag(), is_dag(), is_empty_caugi(), is_mag(), is_mpdag(), is_pdag(), is_simple(), is_ug(), m_separated(), markov_blanket(), neighbors(), nodes(), parents(), posteriors(), same_nodes(), spouses(), subgraph(), topological_sort()

Examples

```
cg <- caugi(
  A %-->% B,
  class = "DAG"
)

is_caugi(cg) # TRUE
```

---

is_cpdag *Is the* caugi *graph a CPDAG?*

Description

Checks if the given caugi graph is a Complete Partially Directed Acyclic Graph (CPDAG).

Usage

```
is_cpdag(cg)
```

Arguments

cg	A caugi object.

Value

A logical value indicating whether the graph is a CPDAG.

References

C. Meek (1995). Causal inference and causal explanation with background knowledge. In *Proceedings of the Eleventh Conference on Uncertainty in Artificial Intelligence (UAI-95)*, pp. 403–411. Morgan Kaufmann.

See Also

Other queries: `ancestors()`, `anteriors()`, `children()`, `components()`, `descendants()`, `districts()`, `edge_types()`, `edges()`, `exogenous()`, `is_acyclic()`, `is_admg()`, `is_ag()`, `is_caugi()`, `is_dag()`, `is_empty_caugi()`, `is_mag()`, `is_mpdag()`, `is_pdag()`, `is_simple()`, `is_ug()`, `m_separated()`, `markov_blanket()`, `neighbors()`, `nodes()`, `parents()`, `posteriors()`, `same_nodes()`, `spouses()`, `subgraph()`, `topological_sort()`

Examples

```
cg_cpdag <- caugi(
  A %---% B,
  A %-->% C,
  B %-->% C,
  class = "PDAG"
)
is_cpdag(cg_cpdag) # TRUE

cg_not_cpdag <- caugi(
  A %---% B,
  A %---% C,
  B %-->% C,
  class = "PDAG"
)
is_cpdag(cg_not_cpdag) # FALSE
```

---

is_dag *Is the* caugi *graph a DAG?*

Description

Checks if the given caugi graph is a Directed Acyclic Graph (DAG).

Usage

```
is_dag(cg, force_check = FALSE)
```

Arguments

cg	A caugi object.
force_check	Logical; if TRUE, the function will test if the graph is a DAG, if FALSE (default), it will look at the graph class and match it, if possible.

Value

A logical value indicating whether the graph is a DAG.

See Also

Other queries: ancestors(), anteriors(), children(), components(), descendants(), districts(), edge_types(), edges(), exogenous(), is_acyclic(), is_admg(), is_ag(), is_caugi(), is_cpdag(), is_empty_caugi(), is_mag(), is_mpdag(), is_pdag(), is_simple(), is_ug(), m_separated(), markov_blanket(), neighbors(), nodes(), parents(), posteriors(), same_nodes(), spouses(), subgraph(), topological_sort()

Examples

```
cg_dag_class <- caugi(
  A %-->% B,
  class = "DAG"
)
is_dag(cg_dag_class) # TRUE
cg_dag_but_pdag_class <- caugi(
  A %-->% B,
  class = "PDAG"
)
is_dag(cg_dag_but_pdag_class) # TRUE
cg_cyclic <- caugi(
  A %-->% B,
  B %-->% C,
  C %-->% A,
  class = "UNKNOWN",
  simple = FALSE
)
is_dag(cg_cyclic) # FALSE

cg_undirected <- caugi(
  A %---% B,
  class = "UNKNOWN"
)
is_dag(cg_undirected) # FALSE
```

---

is_empty_caugi *Is the* caugi *graph empty?*

Description

Checks if the given caugi graph is empty (has no nodes).

Usage

```
is_empty_caugi(cg)
```

Arguments

cg	A caugi object.

Value

A logical value indicating whether the graph is empty.

See Also

Other queries: ancestors(), anteriors(), children(), components(), descendants(), districts(), edge_types(), edges(), exogenous(), is_acyclic(), is_admg(), is_ag(), is_caugi(), is_cpdag(), is_dag(), is_mag(), is_mpdag(), is_pdag(), is_simple(), is_ug(), m_separated(), markov_blanket(), neighbors(), nodes(), parents(), posteriors(), same_nodes(), spouses(), subgraph(), topological_sort()

Examples

```
cg_empty <- caugi(class = "DAG")
is_empty_caugi(cg_empty) # TRUE
cg_non_empty <- caugi(
  A %-->% B,
  class = "DAG"
)
is_empty_caugi(cg_non_empty) # FALSE

cg_no_edges_but_has_nodes <- caugi(
  A, B,
  class = "DAG"
)
is_empty_caugi(cg_no_edges_but_has_nodes) # FALSE
```

---

is_mag *Is the* caugi *graph a MAG?*

Description

Checks if the given caugi graph is a Maximal Ancestral Graph (MAG).

A MAG is an ancestral graph where no additional edge can be added without violating the ancestral graph constraints or changing the encoded independence model.

Usage

```
is_mag(cg, force_check = FALSE)
```

Arguments

cg	A caugi object.
force_check	Logical; if TRUE, the function will test if the graph is a MAG, if FALSE (default), it will look at the graph class and match it, if possible.

Value

A logical value indicating whether the graph is a MAG.

See Also

Other queries: ancestors(), anteriors(), children(), components(), descendants(), districts(), edge_types(), edges(), exogenous(), is_acyclic(), is_admg(), is_ag(), is_caugi(), is_cpdag(), is_dag(), is_empty_caugi(), is_mpdag(), is_pdag(), is_simple(), is_ug(), m_separated(), markov_blanket(), neighbors(), nodes(), parents(), posteriors(), same_nodes(), spouses(), subgraph(), topological_sort()

Examples

```
cg_ag <- caugi(
  A %-->% B,
  B %-->% C,
  class = "AG"
)
is_mag(cg_ag) # TRUE (0 and 2 are m-separated by {B})
```

---

is_mpdag *Is the* caugi *graph an MPDAG?*

Description

Checks if the given caugi graph is a Maximally oriented Partially Directed Acyclic Graph (MPDAG), i.e. a PDAG where no additional edge orientations are implied by Meek's rules (R1–R4).

Usage

```
is_mpdag(cg)
```

Arguments

cg	A caugi object.

Details

If the graph is not PDAG-compatible, the function returns FALSE.

Value

A logical value indicating whether the graph is an MPDAG.

References

C. Meek (1995). Causal inference and causal explanation with background knowledge. In *Proceedings of the Eleventh Conference on Uncertainty in Artificial Intelligence (UAI-95)*, pp. 403–411. Morgan Kaufmann.

See Also

Other queries: `ancestors()`, `anteriors()`, `children()`, `components()`, `descendants()`, `districts()`, `edge_types()`, `edges()`, `exogenous()`, `is_acyclic()`, `is_admg()`, `is_ag()`, `is_caugi()`, `is_cpdag()`, `is_dag()`, `is_empty_caugi()`, `is_mag()`, `is_pdag()`, `is_simple()`, `is_ug()`, `m_separated()`, `markov_blanket()`, `neighbors()`, `nodes()`, `parents()`, `posteriors()`, `same_nodes()`, `spouses()`, `subgraph()`, `topological_sort()`

Examples

```
cg_not_mpdag <- caugi(
  A %---% B,
  A %-->% C,
  C %-->% B,
  class = "PDAG"
)
is_mpdag(cg_not_mpdag) # FALSE
```

---

is_pdag *Is the* caugi *graph a PDAG?*

Description

Checks if the given `caugi` graph is a Partially Directed Acyclic Graph (PDAG).

Usage

```
is_pdag(cg, force_check = FALSE)
```

Arguments

`cg`	A `caugi` object.
`force_check`	Logical; if `TRUE`, the function will test if the graph is a PDAG, if `FALSE` (default), it will look at the graph class and match it, if possible.

Value

A logical value indicating whether the graph is a PDAG.

See Also

Other queries: ancestors(), anteriors(), children(), components(), descendants(), districts(), edge_types(), edges(), exogenous(), is_acyclic(), is_admg(), is_ag(), is_caugi(), is_cpdag(), is_dag(), is_empty_caugi(), is_mag(), is_mpdag(), is_simple(), is_ug(), m_separated(), markov_blanket(), neighbors(), nodes(), parents(), posteriors(), same_nodes(), spouses(), subgraph(), topological_sort()

Examples

```
cg_dag_class <- caugi(
  A %-->% B,
  class = "DAG"
)
is_pdag(cg_dag_class) # TRUE
cg_dag_but_pdag_class <- caugi(
  A %-->% B,
  class = "PDAG"
)
is_pdag(cg_dag_but_pdag_class) # TRUE
cg_cyclic <- caugi(
  A %-->% B,
  B %-->% C,
  C %-->% A,
  D %---% A,
  class = "UNKNOWN",
  simple = FALSE
)
is_pdag(cg_cyclic) # FALSE

cg_undirected <- caugi(
  A %---% B,
  class = "UNKNOWN"
)
is_pdag(cg_undirected) # TRUE

cg_pag <- caugi(
  A %o-% B,
  class = "UNKNOWN"
)
is_pdag(cg_pag) # FALSE
```

---

is_simple *Is the* caugi *graph simple?*

Description

Checks if the given caugi graph is simple (no self-loops and no parallel edges).

Usage

```
is_simple(cg, force_check = FALSE)
```

Arguments

cg	A caugi object.
force_check	Logical; if TRUE, force a check against the compiled graph representation. If FALSE (default), return the declared simple property.

Value

A logical value indicating whether the graph is simple.

See Also

Other queries: ancestors(), anteriors(), children(), components(), descendants(), districts(), edge_types(), edges(), exogenous(), is_acyclic(), is_admg(), is_ag(), is_caugi(), is_cpdag(), is_dag(), is_empty_caugi(), is_mag(), is_mpdag(), is_pdag(), is_ug(), m_separated(), markov_blanket(), neighbors(), nodes(), parents(), posteriors(), same_nodes(), spouses(), subgraph(), topological_sort()

Examples

```
cg_simple <- caugi(
  A %-->% B,
  class = "DAG"
)
is_simple(cg_simple) # TRUE

cg_nonsimple <- caugi(
  A %-->% B,
  A %<->% B,
  class = "UNKNOWN",
  simple = FALSE
)
is_simple(cg_nonsimple) # FALSE
```

---

is_ug *Is the* caugi *graph an UG?*

Description

Checks if the given caugi graph is an undirected graph (UG).

Usage

```
is_ug(cg, force_check = FALSE)
```

Arguments

cg	A caugi object.
force_check	Logical; if TRUE, the function will test if the graph is an UG, if FALSE (default), it will look at the graph class and match it, if possible.

Value

A logical value indicating whether the graph is an UG.

See Also

Other queries: ancestors(), anteriors(), children(), components(), descendants(), districts(), edge_types(), edges(), exogenous(), is_acyclic(), is_admg(), is_ag(), is_caugi(), is_cpdag(), is_dag(), is_empty_caugi(), is_mag(), is_mpdag(), is_pdag(), is_simple(), m_separated(), markov_blanket(), neighbors(), nodes(), parents(), posteriors(), same_nodes(), spouses(), subgraph(), topological_sort()

Examples

```
cg_ug_class <- caugi(
  A %---% B,
  class = "UG"
)
is_ug(cg_ug_class) # TRUE
cg_not_ug <- caugi(
  A %-->% B,
  class = "DAG"
)
is_ug(cg_not_ug) # FALSE
```

---

is_valid_adjustment_admg

Is a set a valid adjustment set in an ADMG?

Description

Checks whether Z is a valid adjustment set for estimating the causal effect of X on Y in an ADMG using the generalized adjustment criterion.

Usage

```
is_valid_adjustment_admg(
  cg,
  X = NULL,
  Y = NULL,
  Z = NULL,
  X_index = NULL,
```

```
  Y_index = NULL,
  Z_index = NULL
)
```

Arguments

cg	A caugi object of class ADMG.
X, Y	Node names (can be vectors for multiple treatments/outcomes).
Z	Conditioning set (character vector of node names).
X_index, Y_index, Z_index	Optional 1-based indices.

Value

Logical value indicating if the adjustment set is valid.

See Also

Other adjustment: adjustment_set(), all_adjustment_sets_admg(), all_backdoor_sets(), d_separated(), is_valid_backdoor(), minimal_separator()

Examples

```
# Classic confounding
cg <- caugi(
  L %-->% X,
  X %-->% Y,
  L %-->% Y,
  class = "ADMG"
)

is_valid_adjustment_admg(cg, X = "X", Y = "Y", Z = NULL) # FALSE
is_valid_adjustment_admg(cg, X = "X", Y = "Y", Z = "L") # TRUE
```

---

is_valid_backdoor *Is a backdoor set valid?*

Description

Checks whether Z is a valid backdoor adjustment set for X --> Y.

Usage

```
is_valid_backdoor(
  cg,
  X = NULL,
  Y = NULL,
  Z = NULL,
  X_index = NULL,
  Y_index = NULL,
  Z_index = NULL
)
```

Arguments

cg	A caugi object.
X, Y	Single node names.
Z	Optional node set for conditioning
X_index, Y_index, Z_index	Optional 1-based indices.

Value

Logical value indicating if backdoor is valid or not.

See Also

Other adjustment: adjustment_set(), all_adjustment_sets_admg(), all_backdoor_sets(), d_separated(), is_valid_adjustment_admg(), minimal_separator()

Examples

```
cg <- caugi(
  C %-->% X,
  X %-->% F,
  X %-->% D,
  A %-->% X,
  A %-->% K,
  K %-->% Y,
  D %-->% Y,
  D %-->% G,
  Y %-->% H,
  class = "DAG"
)

is_valid_backdoor(cg, X = "X", Y = "Y", Z = NULL) # FALSE
is_valid_backdoor(cg, X = "X", Y = "Y", Z = "K") # TRUE
is_valid_backdoor(cg, X = "X", Y = "Y", Z = c("A", "C")) # TRUE
```

knit_print.caugi_export *Knit Print Method for caugi_export*

Description

Renders caugi export objects as code blocks in Quarto/R Markdown documents. This method is automatically invoked when an export object is the last expression in a code chunk.

Usage

```
## S3 method for class 'caugi_export'
knit_print(x, ...)
```

Arguments

x	A caugi_export object.
...	Additional arguments (currently unused).

Details

This method enables seamless rendering of caugi graphs in Quarto and R Markdown. The code block type is determined by the export format. Simply use an export function (e.g., to_dot(cg)) as the last expression in a chunk with output: asis:

```
#| output: asis
to_dot(cg)
```

Value

A knit_asis object for rendering by knitr.

See Also

Other export: caugi_deserialize(), caugi_dot(), caugi_export(), caugi_graphml(), caugi_mermaid(), caugi_serialize(), export-classes, format-caugi, format-dot, format-graphml, format-mermaid, read_caugi(), read_graphml(), to_dot(), to_graphml(), to_mermaid(), write_caugi(), write_dot(), write_graphml(), write_mermaid()

`latent_project` *Project latent variables from a DAG to an ADMG*

Description

Projects out latent (unobserved) variables from a DAG to produce an Acyclic Directed Mixed Graph (ADMG) over the observed variables.

Usage

```
latent_project(cg, latents)
```

Arguments

`cg`	A `caugi` object of class `"DAG"`.
`latents`	Character vector of latent variable names to project out.

Value

A `caugi` object of class `"ADMG"` containing only the observed variables.

See Also

Other operations: `condition_marginalize()`, `count_dags()`, `dag_from_pdag()`, `enumerate_dags()`, `exogenize()`, `meek_closure()`, `moralize()`, `mutate_caugi()`, `normalize_latent_structure()`, `skeleton()`

Examples

```
# DAG with latent confounder U
dag <- caugi(
  U %-->% X,
  U %-->% Y,
  X %-->% Y,
  class = "DAG"
)

# Project out the latent variable
admg <- latent_project(dag, latents = "U")
# Result: X -> Y, X <-> Y (children of U become bidirected-connected)
edges(admg)

# DAG with directed path through latent
dag2 <- caugi(
  X %-->% L,
  L %-->% Y,
  class = "DAG"
)
```

```
# Project out the latent variable
admg2 <- latent_project(dag2, latents = "L")
# Result: X -> Y (directed path X -> L -> Y becomes X -> Y)
edges(admg2)
```

`length.caugi` *Length of a* `caugi`

Description

Returns the number of nodes in the graph.

Usage

```
## S3 method for class 'caugi'
length(x)
```

Arguments

`x`	A `caugi` object.

Value

An integer representing the number of nodes.

See Also

Other caugi methods: `caugi-equality`, `print.caugi()`

Examples

```
cg <- caugi(
  A %-->% B,
  class = "DAG"
)
length(cg) # 2

cg2 <- caugi(
  A %-->% B + C,
  nodes = LETTERS[1:5],
  class = "DAG"
)
length(cg2) # 5
```

`m_separated` *M-separation test for AGs and ADMGs*

Description

Test whether two sets of nodes are m-separated given a conditioning set in an ancestral graph (AG) or an ADMG.

M-separation generalizes d-separation to AGs/ADMGs and applies to DAGs.

Usage

```
m_separated(
  cg,
  X = NULL,
  Y = NULL,
  Z = NULL,
  X_index = NULL,
  Y_index = NULL,
  Z_index = NULL
)
```

Arguments

`cg`	A `caugi` object of class AG, ADMG, or DAG.
`X`, `Y`, `Z`	Character vectors of node names, or `NULL`. Use `*_index` to pass 1-based indices. If `Z` is `NULL` or missing, no nodes are conditioned on.
`X_index`, `Y_index`, `Z_index`	Optional numeric 1-based indices (exclusive with `X`,`Y`,`Z` respectively).

Value

A logical value; `TRUE` if `X` and `Y` are m-separated given `Z`.

See Also

Other queries: `ancestors()`, `anteriors()`, `children()`, `components()`, `descendants()`, `districts()`, `edge_types()`, `edges()`, `exogenous()`, `is_acyclic()`, `is_admg()`, `is_ag()`, `is_caugi()`, `is_cpdag()`, `is_dag()`, `is_empty_caugi()`, `is_mag()`, `is_mpdag()`, `is_pdag()`, `is_simple()`, `is_ug()`, `markov_blanket()`, `neighbors()`, `nodes()`, `parents()`, `posteriors()`, `same_nodes()`, `spouses()`, `subgraph()`, `topological_sort()`

Examples

```
# Classic confounding example
cg <- caugi(
  L %-->% X,
  X %-->% Y,
```

```
  L %-->% Y,
  class = "ADMG"
)
m_separated(cg, X = "X", Y = "Y") # FALSE (connected via L)
m_separated(cg, X = "X", Y = "Y", Z = "L") # TRUE (L blocks the path)
```

`markov_blanket` *Get Markov blanket of nodes in a* `caugi`

Description

Get Markov blanket of nodes in a `caugi`

Usage

```
markov_blanket(cg, nodes = NULL, index = NULL)
```

Arguments

`cg`	A `caugi` object.
`nodes`	A character vector of node names.
`index`	A vector of node indexes.

Value

Either a character vector of node names (if a single node is requested) or a list of character vectors (if multiple nodes are requested).

See Also

Other queries: `ancestors()`, `anteriors()`, `children()`, `components()`, `descendants()`, `districts()`, `edge_types()`, `edges()`, `exogenous()`, `is_acyclic()`, `is_admg()`, `is_ag()`, `is_caugi()`, `is_cpdag()`, `is_dag()`, `is_empty_caugi()`, `is_mag()`, `is_mpdag()`, `is_pdag()`, `is_simple()`, `is_ug()`, `m_separated()`, `neighbors()`, `nodes()`, `parents()`, `posteriors()`, `same_nodes()`, `spouses()`, `subgraph()`, `topological_sort()`

Examples

```
cg <- caugi(
  A %-->% B,
  B %-->% C,
  class = "DAG"
)
markov_blanket(cg, "A") # "B"
markov_blanket(cg, index = 2) # "A" "C"
markov_blanket(cg, "B") # "A" "C"
markov_blanket(cg, c("B", "C"))
```

```
#> $B
#> [1] "A" "C"
#>
#> $C
#> [1] "B"
```

`meek_closure` *Apply Meek closure to a PDAG*

Description

Applies Meek's orientation rules (R1–R4) repeatedly to a PDAG until no more orientations are implied.

Usage

```
meek_closure(cg)
```

Arguments

`cg`	A `caugi` object. Must be PDAG-compatible.

Value

A `caugi` object closed under Meek's rules. Class `"MPDAG"` in general, or `"DAG"` if the closure orients every edge.

References

C. Meek (1995). Causal inference and causal explanation with background knowledge. In *Proceedings of the Eleventh Conference on Uncertainty in Artificial Intelligence (UAI-95)*, pp. 403–411. Morgan Kaufmann.

See Also

Other operations: `condition_marginalize()`, `count_dags()`, `dag_from_pdag()`, `enumerate_dags()`, `exogenize()`, `latent_project()`, `moralize()`, `mutate_caugi()`, `normalize_latent_structure()`, `skeleton()`

Examples

```
pdag <- caugi(
  A %---% B,
  A %-->% C,
  C %-->% B,
  class = "PDAG"
)
mpdag <- meek_closure(pdag)
```

```
edges(mpdag)
```

`minimal_separator` *Compute a minimal separator*

Description

Computes a minimal separator Z for sets X and Y, optionally with mandatory inclusions and restrictions on the separator. Supports DAGs (where the result is a d-separator), ADMGs, and ancestral graphs (where the result is an m-separator).

Usage

```
minimal_separator(
  cg,
  X = NULL,
  Y = NULL,
  I = character(0),
  R = NULL,
  X_index = NULL,
  Y_index = NULL,
  I_index = NULL,
  R_index = NULL
)

minimal_d_separator(
  cg,
  X = NULL,
  Y = NULL,
  I = character(0),
  R = NULL,
  X_index = NULL,
  Y_index = NULL,
  I_index = NULL,
  R_index = NULL
)
```

Arguments

`cg`	A `caugi` object (DAG, ADMG, or AG).
`X`, `Y`	Character vectors of node names. Use `*_index` to pass 1-based indices.
`I`	Nodes that must be included in the separator.
`R`	Nodes allowed in the separator. If `NULL`, uses all nodes excluding X and Y.
`X_index`, `Y_index`, `I_index`, `R_index`	Optional numeric 1-based indices (exclusive with corresponding name parameters).

Details

A separator Z for X and Y is a set of nodes such that conditioning on Z d- or m-separates X from Y in the graph. This function returns a minimal separator: no proper subset of Z (excluding I) still separates X and Y.

The algorithm runs in linear time O(n + m) and is unified across graph classes via the Bayes-ball reachability of van der Zander & Liśkiewicz (2020). For DAGs the algorithm specializes to FINDMINSEPINDAG; for ADMGs and AGs (and their subclasses CPDAG, RCG, MAG) it uses the general FINDMINSEP over mixed graphs.

Value

A character vector of node names representing the minimal separator, or `NULL` if no valid separator exists within the restriction R.

Source

van der Zander, B. & Liśkiewicz, M. (2020). Finding Minimal d-separators in Linear Time and Applications. Proceedings of The 35th Uncertainty in Artificial Intelligence Conference, in Proceedings of Machine Learning Research 115:637-647 Available from https://proceedings.mlr.press/v115/van-der-zander20a.html.

References

van der Zander, B. & Liśkiewicz, M. (2020). Finding Minimal d-separators in Linear Time and Applications. In *Proceedings of the 35th Conference on Uncertainty in Artificial Intelligence (UAI 2020)*, PMLR 115:637–647. https://proceedings.mlr.press/v115/van-der-zander20a.html.

See Also

Other adjustment: `adjustment_set()`, `all_adjustment_sets_admg()`, `all_backdoor_sets()`, `d_separated()`, `is_valid_adjustment_admg()`, `is_valid_backdoor()`

Examples

```
cg <- caugi(
  A %-->% X,
  X %-->% M,
  M %-->% Y,
  A %-->% Y,
  class = "DAG"
)

# Find any minimal separator between X and Y
minimal_separator(cg, "X", "Y")

# Force M to be in the separator
minimal_separator(cg, "X", "Y", I = "M")

# Restrict separator to only {A, M}
minimal_separator(cg, "X", "Y", R = c("A", "M"))
```

```
# Works on ADMGs (returns a minimal m-separator)
admg <- caugi(
  X %-->% Y,
  L %-->% X,
  L %-->% Y,
  class = "ADMG"
)
minimal_separator(admg, "X", "Y")
```

`moralize` *Moralize a DAG*

Description

Moralizing a DAG involves connecting all parents of each node and then converting all directed edges into undirected edges.

Usage

```
moralize(cg)
```

Arguments

`cg`	A `caugi` object (DAG).

Details

This changes the graph from a Directed Acyclic Graph (DAG) to an Undirected Graph (UG), also known as a Markov Graph.

Value

A `caugi` object representing the moralized graph (UG).

See Also

Other operations: `condition_marginalize()`, `count_dags()`, `dag_from_pdag()`, `enumerate_dags()`, `exogenize()`, `latent_project()`, `meek_closure()`, `mutate_caugi()`, `normalize_latent_structure()`, `skeleton()`

Examples

```
cg <- caugi(A %-->% C, B %-->% C, class = "DAG")
moralize(cg) # A -- B, A -- C, B -- C
```

mutate_caugi *Mutate* caugi *class*

Description

Mutate the caugi class from one graph class to another, if possible. For example, convert a DAG to a PDAG, or a fully directed caugi of class UNKNOWN to a DAG. Throws an error if not possible.

Usage

```
mutate_caugi(cg, class)
```

Arguments

cg	A caugi object.
class	A character string specifying the new class.

Details

This function returns a copy of the object, and the original remains unchanged.

Value

A caugi object of the specified class.

See Also

Other operations: condition_marginalize(), count_dags(), dag_from_pdag(), enumerate_dags(), exogenize(), latent_project(), meek_closure(), moralize(), normalize_latent_structure(), skeleton()

Examples

```
cg <- caugi(A %-->% B, class = "UNKNOWN")
cg_dag <- mutate_caugi(cg, "DAG")
```

neighbors *Get neighbors of nodes in a* caugi

Description

Get neighbors of a node in the graph, optionally filtered by edge direction or type. This function works for all graph classes including UNKNOWN.

Usage

```
neighbors(cg, nodes = NULL, index = NULL, mode = "all")

neighbours(cg, nodes = NULL, index = NULL, mode = "all")
```

Arguments

cg	A caugi object.
nodes	A character vector of node names.
index	A vector of node indexes.
mode	Character; specifies which types of neighbors to return:

"all" All neighbors (default)

"in" Parents: nodes with directed edges pointing INTO the target node (equivalent to parents())

"out" Children: nodes with directed edges pointing OUT from the target node (equivalent to children())

"undirected" Nodes connected via undirected (---) edges

"bidirected" Nodes connected via bidirected (<->) edges (equivalent to spouses() for ADMGs)

"partial" Nodes connected via partial edges (edges with circle endpoints: o-o, o->, --o)

Not all modes are valid for all graph classes:

- DAG: "in", "out", "all" only
- PDAG: "in", "out", "undirected", "all"
- UG: "undirected", "all" only
- ADMG: "in", "out", "bidirected", "all"
- UNKNOWN: all modes allowed

Value

Either a character vector of node names (if a single node is requested) or a list of character vectors (if multiple nodes are requested).

See Also

Other queries: ancestors(), anteriors(), children(), components(), descendants(), districts(), edge_types(), edges(), exogenous(), is_acyclic(), is_admg(), is_ag(), is_caugi(), is_cpdag(), is_dag(), is_empty_caugi(), is_mag(), is_mpdag(), is_pdag(), is_simple(), is_ug(), m_separated(), markov_blanket(), nodes(), parents(), posteriors(), same_nodes(), spouses(), subgraph(), topological_sort()

Examples

```
cg <- caugi(
  A %-->% B,
  B %-->% C,
  class = "DAG"
)
neighbors(cg, "A") # "B"
neighbors(cg, index = 2) # "A" "C"
neighbors(cg, "B") # "A" "C"
neighbors(cg, c("B", "C"))
#> $B
#> [1] "A" "C"
#>
#> $C
#> [1] "B"

# Using mode to filter by edge direction
neighbors(cg, "B", mode = "in") # "A" (parents)
neighbors(cg, "B", mode = "out") # "C" (children)

# Works for UNKNOWN graphs too
cg_unknown <- caugi(
  A %-->% B,
  B %---% C,
  C %o->% D,
  class = "UNKNOWN"
)
neighbors(cg_unknown, "B", mode = "in") # "A"
neighbors(cg_unknown, "B", mode = "undirected") # "C"
neighbors(cg_unknown, "C", mode = "partial") # "D"
```

---

nodes *Get nodes or edges of a* caugi

Description

Get nodes or edges of a caugi

Usage

```
nodes(cg, ...)

vertices(cg, ...)

V(cg, ...)
```

Arguments

cg	A caugi object.
...	Additional arguments (currently unused).

Value

A data.table with a name column.

See Also

Other queries: ancestors(), anteriors(), children(), components(), descendants(), districts(), edge_types(), edges(), exogenous(), is_acyclic(), is_admg(), is_ag(), is_caugi(), is_cpdag(), is_dag(), is_empty_caugi(), is_mag(), is_mpdag(), is_pdag(), is_simple(), is_ug(), m_separated(), markov_blanket(), neighbors(), parents(), posteriors(), same_nodes(), spouses(), subgraph(), topological_sort()

Examples

```
cg <- caugi(
  A %-->% B,
  B %-->% C,
  D,
  class = "DAG"
)
nodes(cg) # returns the data.table with nodes A, B, C, D
```

---

normalize_latent_structure

Normalize latent structure in a DAG

Description

Normalizes a DAG with latent variables while preserving the induced marginal model over the observed variables. This is done by:

(1) exogenizing all latent nodes (making them parentless), (2) removing exogenous latent nodes with at most one child, and (3) removing exogenous latent nodes whose child sets are strict subsets of another latent node's child set.

This corresponds to Lemmas 1–3 in Evans (2016).

Usage

```
normalize_latent_structure(cg, latents)
```

Arguments

cg	A caugi object of class "DAG".
latents	Character vector of latent node names.

Value

A caugi object of class "DAG".

References

Evans, R. J. (2016). Graphs for margins of Bayesian networks. Scandinavian Journal of Statistics, 43(3), 625–648. doi:10.1111/sjos.12194

See Also

Other operations: condition_marginalize(), count_dags(), dag_from_pdag(), enumerate_dags(), exogenize(), latent_project(), meek_closure(), moralize(), mutate_caugi(), skeleton()

Examples

```
dag <- caugi(
  A %-->% U,
  U %-->% X + Y,
  class = "DAG"
)

normalize_latent_structure(dag, latents = "U")

# More complex example with two latents and nested child sets
dag2 <- caugi(
  A %-->% U,
  U %-->% X + Y + Z,
  U2 %-->% Y + Z,
  class = "DAG"
)
normalize_latent_structure(dag2, c("U", "U2"))
```

parents *Get parents of nodes in a* caugi

Description

Get parents of nodes in a graph (nodes with directed edges pointing INTO the target node). This is equivalent to `neighbors(cg, nodes, mode = "in")`.

Note that not both nodes and index can be given.

Usage

```
parents(cg, nodes = NULL, index = NULL)
```

Arguments

cg	A caugi object.
nodes	A character vector of node names.
index	A vector of node indexes.

Value

Either a character vector of node names (if a single node is requested) or a list of character vectors (if multiple nodes are requested).

See Also

Other queries: ancestors(), anteriors(), children(), components(), descendants(), districts(), edge_types(), edges(), exogenous(), is_acyclic(), is_admg(), is_ag(), is_caugi(), is_cpdag(), is_dag(), is_empty_caugi(), is_mag(), is_mpdag(), is_pdag(), is_simple(), is_ug(), m_separated(), markov_blanket(), neighbors(), nodes(), posteriors(), same_nodes(), spouses(), subgraph(), topological_sort()

Examples

```
cg <- caugi(
  A %-->% B,
  B %-->% C,
  class = "DAG"
)
parents(cg, "A") # NULL
parents(cg, index = 2) # "A"
parents(cg, "B") # "A"
parents(cg, c("B", "C"))
#> $B
#> [1] "A"
#>
#> $C
#> [1] "B"
```

plot.caugi *Create a caugi Graph Plot Object*

Description

Creates a grid graphics object (gTree) representing a caugi graph. If the graph has not been built yet, it will be built automatically before plotting. This implementation uses idiomatic grid graphics with viewports for proper coordinate handling.

Usage

```
## S3 method for class 'caugi'
plot(x, layout = "auto", node_style = list(),
  edge_style = list(), label_style = list(), tier_style = list(),
  main = NULL, title_style = list(), asp = NA,
  outer_margin = grid::unit(2, "mm"), title_gap = grid::unit(1, "lines"), ...)
```

Arguments

x	A caugi object. Must contain only directed edges for Sugiyama layout.
layout	Specifies the graph layout method. Can be: • A character string: "auto" (default), "sugiyama", "fruchterman-reingold", "kamada-kawai", "bipartite". See caugi_layout() for details. • A layout function: e.g., caugi_layout_sugiyama, caugi_layout_bipartite, etc. The function will be called with x and any additional arguments passed via .... • A pre-computed layout data.frame with columns name, x, and y.
node_style	List of node styling parameters. Supports: • Appearance (passed to gpar()): fill, col, lwd, lty, alpha • Geometry: padding (text padding inside nodes in mm, default 2), size (node size multiplier, default 1) • Local overrides via by_node: a named list of nodes with their own style lists, e.g. by_node = list(A = list(fill = "red"), B = list(col = "blue"))
edge_style	List of edge styling parameters. Can specify global options or per-type options via directed, undirected, bidirected, partial. Supports: • Appearance (passed to gpar()): col, lwd, lty, alpha, fill. • Geometry: arrow_size (arrow length in mm, default 3), circle_size (radius of endpoint circles for partial edges in mm, default 1.5), route (logical, default TRUE; when TRUE, edges automatically bend around non-incident nodes they would otherwise pass through) • Local overrides via by_edge: a named list with: – Node-wide styles: applied to all edges touching a node, e.g. A = list(col = "red", lwd = 2)

- Specific edges: nested named lists for particular edges, e.g. `A = list(B = list(col = "blue", lwd = 4))`

Multiple levels can be combined: **Style precedence** (highest to lowest): specific edge settings > node-wide settings > edge type settings > global settings.

`label_style` List of label styling parameters. Supports:

- Appearance (passed to `gpar()`): `col`, `fontsize`, `fontface`, `fontfamily`, `cex`

`tier_style` List of tier box styling parameters. Tier boxes are shown when `boxes = TRUE` is set within this list. Supports:

- Appearance (passed to `gpar()`): `fill`, `col` (border color), `lwd`, `lty`, `alpha`
- Geometry: `padding` (padding around tier nodes as proportion of plot range, default 0.05)
- Labels: `labels` (logical or character vector). If `TRUE`, uses tier names from `tiers` argument. If a character vector, uses custom labels (one per tier). If `FALSE` or `NULL` (default), no labels are shown.
- Label styling: `label_style` (list with `col`, `fontsize`, `fontface`, etc.)
- Values can be scalars (applied to all tiers) or vectors (auto-expanded to each tier in order)
- Local overrides via `by_tier`: a named list (using tier names from `tiers` argument) or indexed list for per-tier customization, e.g. `by_tier = list(exposures = list(fill = "lightblue"), outcome = list(fill = "yellow"))` or `by_tier = list("1" = list(fill = "lightblue"))`

`main` Optional character string for plot title. If `NULL` (default), no title is displayed.

`title_style` List of title styling parameters. Supports:

- Appearance (passed to `gpar()`): `col`, `fontsize`, `fontface`, `fontfamily`, `cex`

`asp` Numeric value for the y/x aspect ratio. If `NA` or `NULL` (default), the aspect ratio is automatically determined to fill the available space. Use `asp = 1` to ensure that one unit on the x-axis equals one unit on the y-axis, which respects the layout coordinates. Values other than 1 will stretch the plot accordingly (e.g., `asp = 2` makes the y-axis twice as tall as the x-axis for the same data range).

`outer_margin` Grid unit specifying outer margin around the plot. Default is `grid::unit(2, "mm")`.

`title_gap` Grid unit specifying gap between title and graph. Default is `grid::unit(1, "lines")`.

`...` Additional arguments passed to `caugi_layout()`. For bipartite layouts, include `partition` (logical vector) and `orientation` (`"rows"` or `"columns"`).

Value

A `caugi_plot` object that wraps a `gTree` for grid graphics display. The plot is automatically drawn when printed or explicitly plotted.

See Also

Other plotting: add-caugi_plot-caugi_plot, caugi_layout(), caugi_layout_bipartite(), caugi_layout_circle(), caugi_layout_fruchterman_reingold(), caugi_layout_kamada_kawai(), caugi_layout_sugiyama(), caugi_layout_tiered(), caugi_plot(), divide-caugi_plot-caugi_plot

Examples

```
cg <- caugi(
  A %-->% B + C,
  B %-->% D,
  C %-->% D,
  class = "DAG"
)

plot(cg)

# Use a specific layout method (as string)
plot(cg, layout = "kamada-kawai")

# Use a layout function
plot(cg, layout = caugi_layout_sugiyama)

# Pre-compute layout and use it
coords <- caugi_layout_fruchterman_reingold(cg)
plot(cg, layout = coords)

# Bipartite layout with a function
cg_bp <- caugi(A %-->% X, B %-->% X, C %-->% Y)
partition <- c(TRUE, TRUE, TRUE, FALSE, FALSE)
plot(cg_bp, layout = caugi_layout_bipartite, partition = partition)

# Customize nodes
plot(cg, node_style = list(fill = "lightgreen", padding = 0.8))

# Customize edges by type
plot(
  cg,
  edge_style = list(
    directed = list(col = "blue", arrow_size = 4),
    undirected = list(col = "red")
  )
)

# Add a title
plot(cg, main = "Causal Graph")

# Customize title
plot(
  cg,
  main = "My Graph",
  title_style = list(fontsize = 18, col = "blue", fontface = "italic")
)
```

```
# Respect aspect ratio (1:1)
plot(cg, asp = 1)
```

`posteriors` *Get posteriors of nodes in a* `caugi`

Description

Get the posterior set of nodes in a graph. The posterior set (dual of the anterior set from Richardson and Spirtes, 2002) includes all nodes reachable by following paths where every edge is either undirected or directed away from the source node.

For DAGs, the posterior set equals the descendant set (since there are no undirected edges). For PDAGs, it includes both descendants and nodes reachable via undirected edges.

Usage

```
posteriors(
  cg,
  nodes = NULL,
  index = NULL,
  open = caugi_options("use_open_graph_definition")
)
```

Arguments

`cg`	A `caugi` object of class DAG, PDAG, or AG.
`nodes`	A character vector of node names.
`index`	A vector of node indexes.
`open`	Boolean. Determines how the graph is interpreted when retrieving posteriors. Default is taken from `caugi_options("use_open_graph_definition")`, which by default is TRUE.

Value

Either a character vector of node names (if a single node is requested) or a list of character vectors (if multiple nodes are requested).

See Also

Other queries: `ancestors()`, `anteriors()`, `children()`, `components()`, `descendants()`, `districts()`, `edge_types()`, `edges()`, `exogenous()`, `is_acyclic()`, `is_admg()`, `is_ag()`, `is_caugi()`, `is_cpdag()`, `is_dag()`, `is_empty_caugi()`, `is_mag()`, `is_mpdag()`, `is_pdag()`, `is_simple()`, `is_ug()`, `m_separated()`, `markov_blanket()`, `neighbors()`, `nodes()`, `parents()`, `same_nodes()`, `spouses()`, `subgraph()`, `topological_sort()`

Examples

```
# PDAG example with directed and undirected edges
cg <- caugi(
  A %-->% B %---% C,
  B %-->% D,
  class = "PDAG"
)

posteriors(cg, "A") # B, C, D
posteriors(cg, "A", open = FALSE) # A, B, C, D
posteriors(cg, "B") # C, D
posteriors(cg, "D") # NULL (no posteriors)

# For DAGs, posteriors equals descendants
cg_dag <- caugi(
  A %-->% B %-->% C,
  class = "DAG"
)
posteriors(cg_dag, "A") # B, C
```

---

print.caugi *Print a* caugi

Description

Print a caugi

Usage

```
## S3 method for class 'caugi'
print(x, max_nodes = getOption("caugi.max_nodes"),
  max_edges = getOption("caugi.max_edges"), ...)
```

Arguments

x	A caugi object.
max_nodes	Optional numeric; maximum number of node names to consider. If NULL, the method automatically prints as many as fit on one console line (plus a separate truncation line if needed).
max_edges	Optional numeric; maximum number of edges to consider. If NULL, the method automatically prints as many edges as fit on two console lines (plus a separate truncation line if needed).
...	Not used.

Value

The input caugi object, invisibly.

See Also

Other caugi methods: caugi-equality, length.caugi()

Examples

```
cg <- caugi(A %-->% B, class = "DAG")
print(cg)
```

---

read_caugi *Read caugi Graph from File*

Description

Reads a caugi graph from a file in the native caugi JSON format.

Usage

```
read_caugi(path, lazy)
```

Arguments

path	Character string specifying the file path.
lazy	DEPRECATED, no longer necessary. The graph is always built lazily, so this argument is ignored.

Details

The function validates the file format and version, ensuring compatibility with the current version of the caugi package.

Value

A caugi object.

See Also

Other export: caugi_deserialize(), caugi_dot(), caugi_export(), caugi_graphml(), caugi_mermaid(), caugi_serialize(), export-classes, format-caugi, format-dot, format-graphml, format-mermaid, knit_print.caugi_export(), read_graphml(), to_dot(), to_graphml(), to_mermaid(), write_caugi(), write_dot(), write_graphml(), write_mermaid()

Examples

```
cg <- caugi(
  A %-->% B + C,
  class = "DAG"
)

# Write and read
tmp <- tempfile(fileext = ".caugi.json")
write_caugi(cg, tmp)
cg2 <- read_caugi(tmp)

# Clean up
unlink(tmp)
```

---

read_graphml *Read GraphML File to caugi Graph*

Description

Imports a GraphML file as a caugi graph. Supports GraphML files exported from caugi with full edge type information.

Usage

```
read_graphml(path, class = NULL)
```

Arguments

path	File path to the GraphML file.
class	Graph class to assign. If NULL (default), attempts to read from the GraphML metadata. If not present, defaults to "UNKNOWN".

Details

This function provides basic GraphML import support. It reads:

- Nodes and their IDs
- Edges with source and target
- Edge types (if present in edge_type attribute)
- Graph class (if present in graph data)

For GraphML files not created by caugi, edge types default to "–>" for directed graphs and "—" for undirected graphs.

Value

A caugi object.

See Also

Other export: caugi_deserialize(), caugi_dot(), caugi_export(), caugi_graphml(), caugi_mermaid(), caugi_serialize(), export-classes, format-caugi, format-dot, format-graphml, format-mermaid, knit_print.caugi_export(), read_caugi(), to_dot(), to_graphml(), to_mermaid(), write_caugi(), write_dot(), write_graphml(), write_mermaid()

Examples

```
# Create and export a graph
cg <- caugi(
  A %-->% B,
  B %-->% C,
  class = "DAG"
)

tmp <- tempfile(fileext = ".graphml")
write_graphml(cg, tmp)

# Read it back
cg2 <- read_graphml(tmp)

# Clean up
unlink(tmp)
```

---

register_caugi_edge *Register a new edge type in the global registry.*

Description

Register a new edge type in the global registry.

Usage

```
register_caugi_edge(glyph, tail_mark, head_mark, class, symmetric = FALSE)
```

Arguments

glyph	A string representing the edge glyph (e.g., "-->", "<->").
tail_mark	One of "arrow", "tail", "circle", "other".
head_mark	One of "arrow", "tail", "circle", "other".
class	One of "directed","undirected","bidirected","partial".
symmetric	Logical.

Value

TRUE, invisibly.

See Also

Other registry: registry

Examples

```
# first, for reproducability, we reset the registry to default
reset_caugi_registry()

# create a new registry
reg <- caugi_registry()

# register an edge
register_caugi_edge(
  glyph = "<--",
  tail_mark = "arrow",
  head_mark = "tail",
  class = "directed",
  symmetric = FALSE
)

# now, this edge is available for caugi graphs:
cg <- caugi(A %-->% B, B %<--% C, class = "DAG")

# reset the registry to default
reset_caugi_registry()
```

---

registry caugi *edge registry*

Description

The caugi edge registry stores information about the different edge types that can be used in caugi graphs. It maps edge glyphs (e.g., "-->", "<->", "o->", etc.) to their specifications, including tail and head marks, class, and symmetry. The registry allows for dynamic registration of new edge types, enabling users to extend the set of supported edges in caugi. It is implemented as a singleton, ensuring that there is a single global instance of the registry throughout the R session.

Usage

```
caugi_registry()

list_caugi_edges()

reset_caugi_registry()

seal_caugi_registry()
```

Details

The intended use of the caugi registry is mostly for advanced users and developers. The registry enables users who need to define their own custom edge types in caugi directly. . It currently mostly supports the *representation* of new edges, but for users that might want to represent reverse edges, this preserves correctness of reason over these edges.

Value

An edge_registry external pointer.

A data.table with columns glyph, tail, head, class, and symmetric, where each row corresponds to a registered edge type.

Functions

- caugi_registry(): Access the global edge registry, creating it if needed.
- list_caugi_edges(): List all registered edge types in the global registry.
- reset_caugi_registry(): Reset the global edge registry to its default state.
- seal_caugi_registry(): Seal the global edge registry to prevent further modifications.

See Also

Other registry: register_caugi_edge()

Examples

```
# first, for reproducability, we reset the registry to default
reset_caugi_registry()

# create a new registry
reg <- caugi_registry()

# list registered edges
list_caugi_edges()

# register an edge
register_caugi_edge(
  glyph = "<--",
  tail_mark = "arrow",
  head_mark = "tail",
  class = "directed",
  symmetric = FALSE
)

# now, this edge is available for caugi graphs:
list_caugi_edges()
cg <- caugi(A %-->% B, B %<--% C, class = "DAG")

# reset the registry to default
reset_caugi_registry()
```

`same_nodes` *Same nodes?*

Description

Check if two `caugi` objects have the same nodes.

Usage

```
same_nodes(cg1, cg2, throw_error = FALSE)
```

Arguments

`cg1`	A `caugi` object.
`cg2`	A `caugi` object.
`throw_error`	Logical; if `TRUE`, throws an error if the graphs do not have the same nodes.

Value

A logical indicating if the two graphs have the same nodes.

See Also

Other queries: `ancestors()`, `anteriors()`, `children()`, `components()`, `descendants()`, `districts()`, `edge_types()`, `edges()`, `exogenous()`, `is_acyclic()`, `is_admg()`, `is_ag()`, `is_caugi()`, `is_cpdag()`, `is_dag()`, `is_empty_caugi()`, `is_mag()`, `is_mpdag()`, `is_pdag()`, `is_simple()`, `is_ug()`, `m_separated()`, `markov_blanket()`, `neighbors()`, `nodes()`, `parents()`, `posteriors()`, `spouses()`, `subgraph()`, `topological_sort()`

Examples

```
cg1 <- caugi(
  A %-->% B,
  class = "DAG"
)
cg2 <- caugi(
  A %-->% B + C,
  class = "DAG"
)
same_nodes(cg1, cg2) # FALSE
```

shd *Structural Hamming Distance*

Description

Compute the Structural Hamming Distance (SHD) between two graphs.

Usage

```
shd(cg1, cg2, normalized = FALSE)
```

Arguments

cg1	A caugi object.
cg2	A caugi object.
normalized	Logical; if TRUE, returns the normalized SHD.

Value

An integer representing the Hamming Distance between the two graphs, if normalized = FALSE, or a numeric between 0 and 1 if normalized = TRUE.

See Also

Other metrics: aid(), hd()

Examples

```
cg1 <- caugi(A %-->% B %-->% C, D %-->% C, class = "DAG")
cg2 <- caugi(A %-->% B %-->% C, D %---% C, class = "PDAG")
shd(cg1, cg2) # 1
```

simulate_data *Simulate data from a* caugi *DAG.*

Description

Simulate data from a caugi object of class DAG using a linear structural equation model (SEM). As standard, the data is simulated from a DAG, where each node is generated as a linear combination of its parents plus Gaussian noise, following the topological order of the graph. Nodes without custom equations are simulated using auto-generated linear Gaussian relationships.

Usage

```
simulate_data(
  cg,
  n,
  ...,
  standardize = TRUE,
  coef_range = c(0.1, 0.9),
  error_sd = 1,
  seed = NULL
)
```

Arguments

cg	A caugi object of class DAG.
n	Integer; number of observations to simulate.
...	Named expressions for custom structural equations. Names must match node names in the graph. Expressions can reference parent node names and the variable n (sample size). Nodes without custom equations use auto-generated linear Gaussian relationships.
standardize	Logical; if TRUE, standardize all variables to have mean 0 and standard deviation 1. Default is TRUE.
coef_range	Numeric vector of length 2; range for random edge coefficients that will be sampled uniformly. Default is c(0.1, 0.9).
error_sd	Numeric; standard deviation for error terms in auto-generated equations. Default is 1.
seed	Optional integer; random seed for reproducibility.

Value

A data.frame with n rows and one column per node, ordered according to the node order in the graph.

See Also

Other simulation functions: generate_graph()

Examples

```
cg <- caugi(A %-->% B, B %-->% C, A %-->% C, class = "DAG")

# Fully automatic simulation
df <- simulate_data(cg, n = 100)

# With standardization
df <- simulate_data(cg, n = 100, standardize = TRUE)

# Custom equations for some nodes
df <- simulate_data(cg, n = 100,
```

```
  A = rnorm(n, mean = 10, sd = 2),
  B = 0.5 * A + rnorm(n, sd = 0.5)
)

# Reproducible simulation
df <- simulate_data(cg, n = 100, seed = 42)
```

`skeleton` *Get the skeleton of a graph*

Description

The skeleton of a graph is obtained by replacing all directed edges with undirected edges.

Usage

```
skeleton(cg)
```

Arguments

`cg`	A `caugi` object. Either a DAG or PDAG.

Details

This changes the graph from any class to an Undirected Graph (UG), also known as a Markov Graph.

Value

A `caugi` object representing the skeleton of the graph (UG).

See Also

Other operations: `condition_marginalize()`, `count_dags()`, `dag_from_pdag()`, `enumerate_dags()`, `exogenize()`, `latent_project()`, `meek_closure()`, `moralize()`, `mutate_caugi()`, `normalize_latent_structure()`

Examples

```
cg <- caugi(A %-->% B, class = "DAG")
skeleton(cg) # A --- B
```

spouses *Get spouses (bidirected neighbors) of nodes in an ADMG*

Description

Get nodes connected via bidirected edges in an ADMG.

Usage

```
spouses(cg, nodes = NULL, index = NULL)
```

Arguments

cg	A caugi object of class ADMG.
nodes	A character vector of node names.
index	A vector of node indexes.

Value

Either a character vector of node names (if a single node is requested) or a list of character vectors (if multiple nodes are requested).

See Also

Other queries: ancestors(), anteriors(), children(), components(), descendants(), districts(), edge_types(), edges(), exogenous(), is_acyclic(), is_admg(), is_ag(), is_caugi(), is_cpdag(), is_dag(), is_empty_caugi(), is_mag(), is_mpdag(), is_pdag(), is_simple(), is_ug(), m_separated(), markov_blanket(), neighbors(), nodes(), parents(), posteriors(), same_nodes(), subgraph(), topological_sort()

Examples

```
cg <- caugi(
  A %-->% B,
  A %<->% C,
  B %<->% C,
  class = "ADMG"
)
spouses(cg, "A") # "C"
spouses(cg, "C") # c("A", "B")
```

subgraph *Get the induced subgraph*

Description

Get the induced subgraph

Usage

```
subgraph(cg, nodes = NULL, index = NULL)
```

Arguments

cg	A caugi object.
nodes	A character vector of node names.
index	A vector of node indexes.

Value

A new caugi that is a subgraph of the selected nodes.

See Also

Other queries: ancestors(), anteriors(), children(), components(), descendants(), districts(), edge_types(), edges(), exogenous(), is_acyclic(), is_admg(), is_ag(), is_caugi(), is_cpdag(), is_dag(), is_empty_caugi(), is_mag(), is_mpdag(), is_pdag(), is_simple(), is_ug(), m_separated(), markov_blanket(), neighbors(), nodes(), parents(), posteriors(), same_nodes(), spouses(), topological_sort()

Examples

```
cg <- caugi(
  A %-->% B,
  B %-->% C,
  class = "DAG"
)
sub_cg <- subgraph(cg, c("B", "C"))
cg2 <- caugi(B %-->% C, class = "DAG")
all(nodes(sub_cg) == nodes(cg2)) # TRUE
all(edges(sub_cg) == edges(cg2)) # TRUE
```

to_dot *Export caugi Graph to DOT Format*

Description

Converts a caugi graph to the Graphviz DOT format as a string. The DOT format can be used with Graphviz tools for visualization and analysis.

Usage

```
to_dot(x, graph_attrs = list(), node_attrs = list(), edge_attrs = list())
```

Arguments

x	A caugi object.
graph_attrs	Named list of graph attributes (e.g., list(rankdir = "LR")).
node_attrs	Named list of default node attributes.
edge_attrs	Named list of default edge attributes.

Details

The function handles different edge types:

- Directed edges (-->) use -> in DOT
- Undirected edges (---) use -- in DOT (or -> with dir=none in digraphs)
- Bidirected edges (<->) use -> with [dir=both] attribute
- Partial edges (o->) use -> with [dir=both, arrowtail=odot] attribute
- Partial edges (--o) use -> with [arrowhead=odot] attribute
- Partial edges (o-o) use -> with [dir=both, arrowtail=odot, arrowhead=odot] attribute

Value

A caugi_dot object containing the DOT representation.

See Also

Other export: caugi_deserialize(), caugi_dot(), caugi_export(), caugi_graphml(), caugi_mermaid(), caugi_serialize(), export-classes, format-caugi, format-dot, format-graphml, format-mermaid, knit_print.caugi_export(), read_caugi(), read_graphml(), to_graphml(), to_mermaid(), write_caugi(), write_dot(), write_graphml(), write_mermaid()

Examples

```
cg <- caugi(
  A %-->% B + C,
  B %-->% D,
  C %-->% D,
  class = "DAG"
)

# Get DOT string
dot <- to_dot(cg)
dot@content

# With custom attributes
dot <- to_dot(
  cg,
  graph_attrs = list(rankdir = "LR"),
  node_attrs = list(shape = "box")
)
```

---

to_graphml *Export caugi Graph to GraphML Format*

Description

Converts a caugi graph to the GraphML XML format as a string. GraphML is widely supported by graph analysis tools and libraries.

Usage

```
to_graphml(x)
```

Arguments

x	A caugi object.

Details

The GraphML export includes:

- Node IDs and labels
- Edge types stored as a custom edge_type attribute
- Graph class stored as a graph-level attribute

Edge types are encoded using the caugi DSL operators (e.g., "–>", "<->"). This allows for perfect round-trip conversion back to caugi.

Value

A caugi_graphml object containing the GraphML representation.

See Also

Other export: caugi_deserialize(), caugi_dot(), caugi_export(), caugi_graphml(), caugi_mermaid(), caugi_serialize(), export-classes, format-caugi, format-dot, format-graphml, format-mermaid, knit_print.caugi_export(), read_caugi(), read_graphml(), to_dot(), to_mermaid(), write_caugi(), write_dot(), write_graphml(), write_mermaid()

Examples

```
cg <- caugi(
  A %-->% B + C,
  B %-->% D,
  C %-->% D,
  class = "DAG"
)

# Get GraphML string
graphml <- to_graphml(cg)
cat(graphml@content)

# Write to file
## Not run:
write_graphml(cg, "graph.graphml")

## End(Not run)
```

---

to_mermaid *Export caugi Graph to Mermaid Format*

Description

Converts a caugi graph to the Mermaid flowchart format as a string. Mermaid diagrams can be rendered in Quarto, R Markdown, GitHub, and many other platforms.

Usage

```
to_mermaid(x, direction = "TD")
```

Arguments

x	A caugi object.
direction	Graph direction: "TB" (top-bottom), "TD" (top-down), "BT" (bottom-top), "LR" (left-right), or "RL" (right-left). Default is "TD".

Details

The function handles different edge types:

- Directed edges (`-->`) use `-->` in Mermaid
- Undirected edges (`---`) use `---` in Mermaid
- Bidirected edges (`<->`) use `<-->` in Mermaid
- Partial edges (`o->`) use `o-->` in Mermaid (circle tail)
- Partial edges (`--o`) use `--o` in Mermaid (circle head)
- Partial edges (`o-o`) use `o--o` in Mermaid (circle both ends)

Node names are automatically escaped if they contain special characters.

Value

A `caugi_mermaid` object containing the Mermaid representation.

See Also

Other export: `caugi_deserialize()`, `caugi_dot()`, `caugi_export()`, `caugi_graphml()`, `caugi_mermaid()`, `caugi_serialize()`, `export-classes`, `format-caugi`, `format-dot`, `format-graphml`, `format-mermaid`, `knit_print.caugi_export()`, `read_caugi()`, `read_graphml()`, `to_dot()`, `to_graphml()`, `write_caugi()`, `write_dot()`, `write_graphml()`, `write_mermaid()`

Examples

```
cg <- caugi(
  A %-->% B + C,
  B %-->% D,
  C %-->% D,
  class = "DAG"
)

# Get Mermaid string
mmd <- to_mermaid(cg)
mmd@content

# With custom direction
mmd <- to_mermaid(cg, direction = "LR")
```

---

topological_sort *Get a topological ordering of a DAG*

Description

Returns a topological ordering of the nodes in a DAG. For every directed edge u -> v in the graph, u will appear before v in the returned ordering.

Usage

```
topological_sort(cg)
```

Arguments

cg	A caugi object of class DAG.

Value

A character vector of node names in topological order.

See Also

Other queries: ancestors(), anteriors(), children(), components(), descendants(), districts(), edge_types(), edges(), exogenous(), is_acyclic(), is_admg(), is_ag(), is_caugi(), is_cpdag(), is_dag(), is_empty_caugi(), is_mag(), is_mpdag(), is_pdag(), is_simple(), is_ug(), m_separated(), markov_blanket(), neighbors(), nodes(), parents(), posteriors(), same_nodes(), spouses(), subgraph()

Examples

```
# Simple DAG: A -> B -> C
cg <- caugi(
  A %-->% B,
  B %-->% C,
  class = "DAG"
)
topological_sort(cg) # Returns c("A", "B", "C") or equivalent valid ordering

# DAG with multiple valid orderings
cg2 <- caugi(
  A %-->% C,
  B %-->% C,
  class = "DAG"
)
# Could return c("A", "B", "C") or c("B", "A", "C")
topological_sort(cg2)
```

---

write_caugi *Write caugi Graph to File*

Description

Writes a caugi graph to a file in the native caugi JSON format. This format is designed for reproducibility, caching, and sharing caugi graphs across R sessions.

Usage

```
write_caugi(x, path, comment = NULL, tags = NULL)
```

Arguments

x	A caugi object or an object coercible to caugi.
path	Character string specifying the file path.
comment	Optional character string with a comment about the graph.
tags	Optional character vector of tags for categorizing the graph.

Details

The caugi format is a versioned JSON schema that captures:

- Graph structure (nodes and edges with their types)
- Graph class (DAG, PDAG, ADMG, UG, etc.)
- Optional metadata (comments and tags)

Edge types are encoded using their DSL operators (e.g., "-->", "<->", "--").

For a complete guide to the format, see `vignette("serialization", package = "caugi")`. The formal JSON Schema is available at: https://caugi.org/schemas/caugi-v1.schema.json

Value

Invisibly returns the input x.

See Also

Other export: caugi_deserialize(), caugi_dot(), caugi_export(), caugi_graphml(), caugi_mermaid(), caugi_serialize(), export-classes, format-caugi, format-dot, format-graphml, format-mermaid, knit_print.caugi_export(), read_caugi(), read_graphml(), to_dot(), to_graphml(), to_mermaid(), write_dot(), write_graphml(), write_mermaid()

Examples

```
cg <- caugi(
  A %-->% B + C,
  B %-->% D,
  C %-->% D,
  class = "DAG"
)

# Write to file
tmp <- tempfile(fileext = ".caugi.json")
write_caugi(cg, tmp, comment = "Example DAG")

# Read back
cg2 <- read_caugi(tmp)
identical(edges(cg), edges(cg2))
```

```
# Clean up
unlink(tmp)
```

`write_dot` *Write caugi Graph to DOT File*

Description

Writes a caugi graph to a file in Graphviz DOT format.

Usage

```
write_dot(x, file, ...)
```

Arguments

`x`	A `caugi` object.
`file`	Path to output file.
`...`	Additional arguments passed to `to_dot()`, such as `graph_attrs`, `node_attrs`, and `edge_attrs`.

Value

Invisibly returns the path to the file.

See Also

Other export: `caugi_deserialize()`, `caugi_dot()`, `caugi_export()`, `caugi_graphml()`, `caugi_mermaid()`, `caugi_serialize()`, `export-classes`, `format-caugi`, `format-dot`, `format-graphml`, `format-mermaid`, `knit_print.caugi_export()`, `read_caugi()`, `read_graphml()`, `to_dot()`, `to_graphml()`, `to_mermaid()`, `write_caugi()`, `write_graphml()`, `write_mermaid()`

Examples

```
cg <- caugi(
  A %-->% B + C,
  B %-->% D,
  C %-->% D,
  class = "DAG"
)

## Not run:
# Write to file
write_dot(cg, "graph.dot")

# With custom attributes
```

```
write_dot(
  cg,
  "graph.dot",
  graph_attrs = list(rankdir = "LR")
)

## End(Not run)
```

`write_graphml` *Write caugi Graph to GraphML File*

Description

Exports a caugi graph to a GraphML file.

Usage

```
write_graphml(x, path)
```

Arguments

`x`	A `caugi` object.
`path`	File path for the output GraphML file.

Value

Invisibly returns `NULL`. Called for side effects.

See Also

Other export: `caugi_deserialize()`, `caugi_dot()`, `caugi_export()`, `caugi_graphml()`, `caugi_mermaid()`, `caugi_serialize()`, `export-classes`, `format-caugi`, `format-dot`, `format-graphml`, `format-mermaid`, `knit_print.caugi_export()`, `read_caugi()`, `read_graphml()`, `to_dot()`, `to_graphml()`, `to_mermaid()`, `write_caugi()`, `write_dot()`, `write_mermaid()`

Examples

```
cg <- caugi(A %-->% B + C, class = "DAG")

tmp <- tempfile(fileext = ".graphml")
write_graphml(cg, tmp)

# Read it back
cg2 <- read_graphml(tmp)

# Clean up
unlink(tmp)
```

write_mermaid *Write caugi Graph to Mermaid File*

Description

Writes a caugi graph to a file in Mermaid format.

Usage

```
write_mermaid(x, file, ...)
```

Arguments

x	A caugi object.
file	Path to output file.
...	Additional arguments passed to to_mermaid(), such as direction.

Value

Invisibly returns the path to the file.

See Also

Other export: caugi_deserialize(), caugi_dot(), caugi_export(), caugi_graphml(), caugi_mermaid(), caugi_serialize(), export-classes, format-caugi, format-dot, format-graphml, format-mermaid, knit_print.caugi_export(), read_caugi(), read_graphml(), to_dot(), to_graphml(), to_mermaid(), write_caugi(), write_dot(), write_graphml()

Examples

```
cg <- caugi(
  A %-->% B + C,
  B %-->% D,
  C %-->% D,
  class = "DAG"
)

## Not run:
# Write to file
write_mermaid(cg, "graph.mmd")

# With custom direction
write_mermaid(cg, "graph.mmd", direction = "LR")

## End(Not run)
```

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