

# Package ‘caugi’

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**Title** Causal Graph Interface

**Version** 0.3.1

**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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**URL** <https://frederikfabriciusbjerre.github.io/caugi/>

**BugReports** <https://github.com/frederikfabriciusbjerre/caugi/issues>

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## Contents

adjustment_set . . . . .	3
aid . . . . .	4
all_backdoor_sets . . . . .	5
ancestors . . . . .	6
as_adjacency . . . . .	7
as_bnlearn . . . . .	8
as_caugi . . . . .	9
as_dagitty . . . . .	11
as_igraph . . . . .	12
build . . . . .	12
caugi . . . . .	13
caugi_verbs . . . . .	15
children . . . . .	17
descendants . . . . .	18
d_separated . . . . .	19
edges . . . . .	20
edge_types . . . . .	21
exogenous . . . . .	22
generate_graph . . . . .	23
hd . . . . .	23
is_acyclic . . . . .	24
is_caugi . . . . .	25
is_cpdag . . . . .	26
is_dag . . . . .	27
is_empty_caugi . . . . .	28
is_pdag . . . . .	29
is_ug . . . . .	30
is_valid_backdoor . . . . .	31
length . . . . .	32
markov_blanket . . . . .	33
moralize . . . . .	34
mutate_caugi . . . . .	34
neighbors . . . . .	35
nodes . . . . .	36
parents . . . . .	37
print . . . . .	38
register_caugi_edge . . . . .	39
registry . . . . .	40
same_nodes . . . . .	41
shd . . . . .	42
skeleton . . . . .	43
subgraph . . . . .	43

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adjustment_set	<i>Compute an adjustment set</i>
----------------	----------------------------------

---

## Description

Computes an adjustment set for  $X \rightarrow Y$  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":  $\bigcup \text{Pa}(X)$  minus  $X \cup Y$
- "backdoor": Pearl backdoor formula
- "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\\_backdoor\\_sets\(\)](#), [d\\_separated\(\)](#), [is\\_valid\\_backdoor\(\)](#)

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

aid

*Adjustment Identification Distance*

## Description

Compute the Adjustment Identification Distance (AID) between two graphs using the `gadjid` Rust package.

## Usage

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

## Arguments

truth	A <code>caugi</code> object.
guess	A <code>caugi</code> object.
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_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

<code>cg</code>	A <code>caugi</code> .
<code>X, Y</code>	Single node name.
<code>X_index, Y_index</code>	Optional 1-based indices (exclusive with name args).
<code>minimal</code>	Logical; if <code>TRUE</code> (default), only minimal sets are returned.
<code>max_size</code>	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\(\)](#), [d\\_separated\(\)](#), [is\\_valid\\_backdoor\(\)](#)

## 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)
```

**Arguments**

cg	A caugi object.
nodes	A vector of node names, a vector of unquoted node names, or an expression combining these with + and c().
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: [children\(\)](#), [descendants\(\)](#), [edge\\_types\(\)](#), [edges\(\)](#), [exogenous\(\)](#), [is\\_acyclic\(\)](#), [is\\_caugi\(\)](#), [is\\_cpdag\(\)](#), [is\\_dag\(\)](#), [is\\_empty\\_caugi\(\)](#), [is\\_pdag\(\)](#), [is\\_ug\(\)](#), [markov\\_blanket\(\)](#), [neighbors\(\)](#), [nodes\(\)](#), [parents\(\)](#), [same\\_nodes\(\)](#), [subgraph\(\)](#)

**Examples**

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

---

<code>as_caugi</code>	<i>Convert to a caugi</i>
-----------------------	---------------------------

---

## 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", "PDAG", "PAG", "UNKNOWN"),
  simple = TRUE,
  build = TRUE,
  collapse = FALSE,
  collapse_to = "---",
  ...
)
```

## Arguments

<code>x</code>	An object to convert to a caugi.
<code>class</code>	"DAG", "PDAG", "PAG", or "UNKNOWN". "PAG" is only supported for integer coded matrices.
<code>simple</code>	logical. If TRUE (default) the graph will be simple (no multiple edges or self-loops).
<code>build</code>	logical. If TRUE (default) build the graph now, otherwise build lazily on first query or when using <code>build()</code> .
<code>collapse</code>	logical. If TRUE collapse mutual directed edges to undirected edges. Default is FALSE.
<code>collapse_to</code>	Character string to use as the edge glyph when collapsing. Should be a registered symmetrical edge glyph. Default is "---".
<code>...</code>	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,  $G: A \rightarrow B$ , 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.,  $A \circ-o B$  or  $A \circ-- B$ )
- 2: arrowhead (e.g.,  $A \dashrightarrow B$  or  $A \circ-> B$ )
- 3: tail (e.g.,  $A \circ-- B$  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 <code>igraph::graph_from_data_frame()</code> .

**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 graph now***Description**

If a caugi has been modified (nodes or edges added or removed), it is marked as *not built*, i.e `cg@built = FALSE`. This function builds the graph using the Rust backend and updates the internal pointer to the graph. If the graph is already built, it is returned.

**Usage**

```
build(CG, ...)
```

**Arguments**

cg	A caugi object.
...	Not used.

**Value**

The built caugi object.

**See Also**

Other verbs: [caugi\\_verbs](#)

**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

# verbs do not build the Rust backend
cg@built # FALSE
build(cg)
cg@built # TRUE
```

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 = TRUE,
  class = c("UNKNOWN", "DAG", "PDAG", "UG"),
  state = 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	Logical; if TRUE (default), the graph will be built using the Rust backend. If FALSE, the graph will not be built, and the Rust backend cannot be used. The graph will build, when queries are made to the graph or if calling <a href="#">build()</a> . <b>Note:</b> Even if build = TRUE, if no edges or nodes are provided, the graph will not be built and the pointer will be NULL.
class	Character; one of "UNKNOWN", "DAG", "PDAG", or "UG".
state	For internal use. Build a graph by supplying a pre-constructed state environment.

## 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@built # TRUE
cg4@graph_class # "UNKNOWN"

# create graph, but don't built Rust object yet, which is needed for queries
cg5 <- caugi(
  A %-->% B + C,
  B %-->% D,
  class = "DAG",
  build = FALSE
)

cg@built # FALSE

```

## 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	Logical, whether to modify the graph inplace or not. If FALSE (default), a copy of the caugi is made and modified.
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

# verbs do not build the Rust backend
cg@built # FALSE
build(cg)
cg@built # TRUE
```

---

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

---

**Description**

Get children of nodes in a caugi

**Usage**

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

**Arguments**

cg	A caugi object.
nodes	A vector of node names, a vector of unquoted node names, or an expression combining these with + and c().
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\(\)](#), [descendants\(\)](#), [edge\\_types\(\)](#), [edges\(\)](#), [exogenous\(\)](#), [is\\_acyclic\(\)](#), [is\\_caugi\(\)](#), [is\\_cpdag\(\)](#), [is\\_dag\(\)](#), [is\\_empty\\_caugi\(\)](#), [is\\_pdag\(\)](#), [is\\_ug\(\)](#), [markov\\_blanket\(\)](#), [neighbors\(\)](#), [nodes\(\)](#), [parents\(\)](#), [same\\_nodes\(\)](#), [subgraph\(\)](#)

**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
```

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

Get descendants of nodes in a caugi

**Usage**

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

**Arguments**

<code>cg</code>	A caugi object.
<code>nodes</code>	A vector of node names, a vector of unquoted node names, or an expression combining these with + and <code>c()</code> .
<code>index</code>	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\(\)](#), [children\(\)](#), [edge\\_types\(\)](#), [edges\(\)](#), [exogenous\(\)](#), [is\\_acyclic\(\)](#), [is\\_caugi\(\)](#), [is\\_cpdag\(\)](#), [is\\_dag\(\)](#), [is\\_empty\\_caugi\(\)](#), [is\\_pdag\(\)](#), [is\\_ug\(\)](#), [markov\\_blanket\(\)](#), [neighbors\(\)](#), [nodes\(\)](#), [parents\(\)](#), [same\\_nodes\(\)](#), [subgraph\(\)](#)

**Examples**

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

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	Node selectors: character vector of names, unquoted expression (supports + and c()), 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\\_backdoor\\_sets\(\)](#), [is\\_valid\\_backdoor\(\)](#)

### 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
```

edges

*Get edges of a caugi.*

### Description

Get edges of a caugi.

### Usage

edges(cg)

E(cg)

### Arguments

cg                   A caugi object.

### Value

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

**See Also**

Other queries: [ancestors\(\)](#), [children\(\)](#), [descendants\(\)](#), [edge\\_types\(\)](#), [exogenous\(\)](#), [is\\_acyclic\(\)](#), [is\\_caugi\(\)](#), [is\\_cpdag\(\)](#), [is\\_dag\(\)](#), [is\\_empty\\_caugi\(\)](#), [is\\_pdag\(\)](#), [is\\_ug\(\)](#), [markov\\_blanket\(\)](#), [neighbors\(\)](#), [nodes\(\)](#), [parents\(\)](#), [same\\_nodes\(\)](#), [subgraph\(\)](#)

**Examples**

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

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\(\)](#), [children\(\)](#), [descendants\(\)](#), [edges\(\)](#), [exogenous\(\)](#), [is\\_acyclic\(\)](#), [is\\_caugi\(\)](#), [is\\_cpdag\(\)](#), [is\\_dag\(\)](#), [is\\_empty\\_caugi\(\)](#), [is\\_pdag\(\)](#), [is\\_ug\(\)](#), [markov\\_blanket\(\)](#), [neighbors\(\)](#), [nodes\(\)](#), [parents\(\)](#), [same\\_nodes\(\)](#), [subgraph\(\)](#)

**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", "<->", "---")

```

**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

<code>cg</code>	A caugi object.
<code>undirected_as_parents</code>	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\(\)](#), [children\(\)](#), [descendants\(\)](#), [edge\\_types\(\)](#), [edges\(\)](#), [is\\_acyclic\(\)](#), [is\\_caugi\(\)](#), [is\\_cpdag\(\)](#), [is\\_dag\(\)](#), [is\\_empty\\_caugi\(\)](#), [is\\_pdag\(\)](#), [is\\_ug\(\)](#), [markov\\_blanket\(\)](#), [neighbors\(\)](#), [nodes\(\)](#), [parents\(\)](#), [same\\_nodes\(\)](#), [subgraph\(\)](#)

## Examples

```

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

```

---

generate_graph	<i>Generate a caugi using Erdős-Rényi.</i>
----------------	--

---

**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"))
```

**Arguments**

n	Integer $\geq 0$ . 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".

**Value**

The sampled caugi object.

**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	<i>Hamming Distance</i>
----	-------------------------

---

**Description**

Compute the Hamming Distance between two graphs.

**Usage**

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

**Arguments**

<code>cg1</code>	A caugi object.
<code>cg2</code>	A caugi object.
<code>normalized</code>	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
```

<code>is_acyclic</code>	<i>Is the caugi acyclic?</i>
-------------------------	------------------------------

**Description**

Checks if the given caugi graph is acyclic.

**Usage**

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

**Arguments**

<code>cg</code>	A caugi object.
<code>force_check</code>	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" or "PDAG" 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\(\)](#), [children\(\)](#), [descendants\(\)](#), [edge\\_types\(\)](#), [edges\(\)](#), [exogenous\(\)](#), [is\\_caugi\(\)](#), [is\\_cpdag\(\)](#), [is\\_dag\(\)](#), [is\\_empty\\_caugi\(\)](#), [is\\_pdag\(\)](#), [is\\_ug\(\)](#), [markov\\_blanket\(\)](#), [neighbors\(\)](#), [nodes\(\)](#), [parents\(\)](#), [same\\_nodes\(\)](#), [subgraph\(\)](#)

**Examples**

```
cgACYCLIC <- caugi(
  A %-->% B,
  B %-->% C,
  class = "DAG"
)
isACYCLIC(cgACYCLIC) # TRUE
cgCYCLIC <- caugi(
  A %-->% B,
  B %-->% C,
  C %-->% A,
  class = "UNKNOWN"
)
isACYCLIC(cgCYCLIC) # FALSE
```

**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\(\)](#), [children\(\)](#), [descendants\(\)](#), [edge\\_types\(\)](#), [edges\(\)](#), [exogenous\(\)](#), [is\\_caugi\(\)](#), [is\\_cpdag\(\)](#), [is\\_dag\(\)](#), [is\\_empty\\_caugi\(\)](#), [is\\_pdag\(\)](#), [is\\_ug\(\)](#), [markov\\_blanket\(\)](#), [neighbors\(\)](#), [nodes\(\)](#), [parents\(\)](#), [same\\_nodes\(\)](#), [subgraph\(\)](#)

### 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.

### See Also

Other queries: [ancestors\(\)](#), [children\(\)](#), [descendants\(\)](#), [edge\\_types\(\)](#), [edges\(\)](#), [exogenous\(\)](#), [is\\_acyclic\(\)](#), [is\\_caugi\(\)](#), [is\\_dag\(\)](#), [is\\_empty\\_caugi\(\)](#), [is\\_pdag\(\)](#), [is\\_ug\(\)](#), [markov\\_blanket\(\)](#), [neighbors\(\)](#), [nodes\(\)](#), [parents\(\)](#), [same\\_nodes\(\)](#), [subgraph\(\)](#)

### 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\(\)](#), [children\(\)](#), [descendants\(\)](#), [edge\\_types\(\)](#), [edges\(\)](#), [exogenous\(\)](#), [is\\_acyclic\(\)](#), [is\\_caugi\(\)](#), [is\\_cpdag\(\)](#), [is\\_empty\\_caugi\(\)](#), [is\\_pdag\(\)](#), [is\\_ug\(\)](#), [markov\\_blanket\(\)](#), [neighbors\(\)](#), [nodes\(\)](#), [parents\(\)](#), [same\\_nodes\(\)](#), [subgraph\(\)](#)

**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\(\)](#), [children\(\)](#), [descendants\(\)](#), [edge\\_types\(\)](#), [edges\(\)](#), [exogenous\(\)](#), [is\\_acyclic\(\)](#), [is\\_caugi\(\)](#), [is\\_cpdag\(\)](#), [is\\_dag\(\)](#), [is\\_pdag\(\)](#), [is\\_ug\(\)](#), [markov\\_blanket\(\)](#), [neighbors\(\)](#), [nodes\(\)](#), [parents\(\)](#), [same\\_nodes\(\)](#), [subgraph\(\)](#)

## 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

```

<code>is_pdag</code>	<i>Is the caugi graph a PDAG?</i>
----------------------	-----------------------------------

## 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\(\)](#), [children\(\)](#), [descendants\(\)](#), [edge\\_types\(\)](#), [edges\(\)](#), [exogenous\(\)](#), [is\\_acyclic\(\)](#), [is\\_caugi\(\)](#), [is\\_cpdag\(\)](#), [is\\_dag\(\)](#), [is\\_empty\\_caugi\(\)](#), [is\\_ug\(\)](#), [markov\\_blanket\(\)](#), [neighbors\(\)](#), [nodes\(\)](#), [parents\(\)](#), [same\\_nodes\(\)](#), [subgraph\(\)](#)

## 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\_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**

<code>cg</code>	A caugi object.
<code>force_check</code>	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\(\)](#), [children\(\)](#), [descendants\(\)](#), [edge\\_types\(\)](#), [edges\(\)](#), [exogenous\(\)](#), [is\\_acyclic\(\)](#), [is\\_caugi\(\)](#), [is\\_cpdag\(\)](#), [is\\_dag\(\)](#), [is\\_empty\\_caugi\(\)](#), [is\\_pdag\(\)](#), [markov\\_blanket\(\)](#), [neighbors\(\)](#), [nodes\(\)](#), [parents\(\)](#), [same\\_nodes\(\)](#), [subgraph\(\)](#)

**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_backdoor`     *Is a backdoor set valid?*

## Description

Checks whether Z is a valid backdoor adjustment set for X  $\dashrightarrow$  Y.

## Usage

```

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

```

## Arguments

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

## Value

Logical value indicating if backdoor is valid or not.

## See Also

Other adjustment: [adjustment\\_set\(\)](#), [all\\_backdoor\\_sets\(\)](#), [d\\_separated\(\)](#)

## 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

```

length

*Length of a caugi***Description**

Returns the number of nodes in the graph.

**Arguments**

x	A caugi object.
---	-----------------

**Value**

An integer representing the number of nodes.

**See Also**

Other caugi methods: [print\(\)](#)

**Examples**

```

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

cg2 <- caugi(
  A %-->% B + C,
  nodes = LETTERS[1:5],
  class = "DAG"
)
length(CG2) # 5

```

---

markov_blanket	<i>Get Markov blanket of nodes in a caugi</i>
----------------	---

---

## Description

Get Markov blanket of nodes in a caugi

## Usage

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

## Arguments

cg	A caugi object.
nodes	A vector of node names, a vector of unquoted node names, or an expression combining these with + and c().
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\(\)](#), [children\(\)](#), [descendants\(\)](#), [edge\\_types\(\)](#), [edges\(\)](#), [exogenous\(\)](#), [isACYCLIC\(\)](#), [is\\_caugi\(\)](#), [is\\_cpdag\(\)](#), [is\\_dag\(\)](#), [is\\_empty\\_caugi\(\)](#), [is\\_pdag\(\)](#), [is\\_ug\(\)](#), [neighbors\(\)](#), [nodes\(\)](#), [parents\(\)](#), [same\\_nodes\(\)](#), [subgraph\(\)](#)

## 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"
```

**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: [mutate\\_caugi\(\)](#), [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: [moralize\(\)](#), [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 nodes in a caugi

**Usage**

```
neighbors(cg, nodes = NULL, index = NULL)
neighbours(cg, nodes = NULL, index = NULL)
```

**Arguments**

- |       |   |
|-------|---|
| cg    | A caugi object.   |
| nodes | A vector of node names, a vector of unquoted node names, or an expression combining these with + and c(). |
| 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\(\)](#), [children\(\)](#), [descendants\(\)](#), [edge\\_types\(\)](#), [edges\(\)](#), [exogenous\(\)](#), [is\\_acyclic\(\)](#), [is\\_caugi\(\)](#), [is\\_cpdag\(\)](#), [is\\_dag\(\)](#), [is\\_empty\\_caugi\(\)](#), [is\\_pdag\(\)](#), [is\\_ug\(\)](#), [markov\\_blanket\(\)](#), [nodes\(\)](#), [parents\(\)](#), [same\\_nodes\(\)](#), [subgraph\(\)](#)

**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"
```

**nodes***Get nodes or edges of a caugi***Description**

Get nodes or edges of a caugi

**Usage**

```
nodes(cg)
```

```
vertices(cg)
```

```
V(cg)
```

**Arguments**

<code>cg</code>	A caugi object.
-----------------	-----------------

**Value**

A `data.table` with a `name` column.

**See Also**

Other queries: [ancestors\(\)](#), [children\(\)](#), [descendants\(\)](#), [edge\\_types\(\)](#), [edges\(\)](#), [exogenous\(\)](#), [is\\_acyclic\(\)](#), [is\\_caugi\(\)](#), [is\\_cpdag\(\)](#), [is\\_dag\(\)](#), [is\\_empty\\_caugi\(\)](#), [is\\_pdag\(\)](#), [is\\_ug\(\)](#), [markov\\_blanket\(\)](#), [neighbors\(\)](#), [parents\(\)](#), [same\\_nodes\(\)](#), [subgraph\(\)](#)

**Examples**

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

---

**parents***Get parents of nodes in a caugi*

---

**Description**

Get parents of node in a graph. Note that not both nodes and index can be given.

**Usage**

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

**Arguments**

- |                    |   |
|--------------------|---|
| <code>cg</code>    | A caugi object.   |
| <code>nodes</code> | A vector of node names, a vector of unquoted node names, or an expression combining these with + and c(). |
| <code>index</code> | 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\(\)](#), [children\(\)](#), [descendants\(\)](#), [edge\\_types\(\)](#), [edges\(\)](#), [exogenous\(\)](#), [is\\_acyclic\(\)](#), [is\\_caugi\(\)](#), [is\\_cpdag\(\)](#), [is\\_dag\(\)](#), [is\\_empty\\_caugi\(\)](#), [is\\_pdag\(\)](#), [is\\_ug\(\)](#), [markov\\_blanket\(\)](#), [neighbors\(\)](#), [nodes\(\)](#), [same\\_nodes\(\)](#), [subgraph\(\)](#)

## 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"
```

**print**

*Print a caugi*

## Description

Print a caugi

## Arguments

<code>x</code>	A caugi object.
<code>max_nodes</code>	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).
<code>max_edges</code>	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).
<code>...</code>	Not used.

## Value

The input caugi object, invisibly.

## See Also

Other caugi methods: [length\(\)](#)

## Examples

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

---

```
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()
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.

## Functions

- `caugi_registry()`: Access the global edge registry, creating it if needed.
- `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()

# 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()
```

---

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\(\)](#), [children\(\)](#), [descendants\(\)](#), [edge\\_types\(\)](#), [edges\(\)](#), [exogenous\(\)](#), [is\\_acyclic\(\)](#), [is\\_caugi\(\)](#), [is\\_cpdag\(\)](#), [is\\_dag\(\)](#), [is\\_empty\\_caugi\(\)](#), [is\\_pdag\(\)](#), [is\\_ug\(\)](#), [markov\\_blanket\(\)](#), [neighbors\(\)](#), [nodes\(\)](#), [parents\(\)](#), [subgraph\(\)](#)

## 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
```

---

**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: [moralize\(\)](#), [mutate\\_caugi\(\)](#)

**Examples**

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

---

**subgraph***Get the induced subgraph*

---

**Description**

Get the induced subgraph

**Usage**

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

**Arguments**

<code>cg</code>	A <code>caugi</code> object.
<code>nodes</code>	A vector of node names, a vector of unquoted node names, or an expression combining these with <code>+</code> and <code>c()</code> .
<code>index</code>	A vector of node indexes.

**Value**

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

**See Also**

Other queries: `ancestors()`, `children()`, `descendants()`, `edge_types()`, `edges()`, `exogenous()`, `is_acyclic()`, `is_caugi()`, `is_cpdag()`, `is_dag()`, `is_empty_caugi()`, `is_pdag()`, `is_ug()`, `markov_blanket()`, `neighbors()`, `nodes()`, `parents()`, `same_nodes()`

**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
```

# Index

- \* **adjustment**
  - adjustment\_set, 3
  - all\_backdoor\_sets, 5
  - d\_separated, 19
  - is\_valid\_backdoor, 31
- \* **caugi methods**
  - length, 32
  - print, 38
- \* **caugi**
  - caugi, 13
- \* **conversions**
  - as\_adjacency, 7
  - as\_bnlearn, 8
  - as\_caugi, 9
  - as\_dagitty, 11
  - as\_igraph, 12
- \* **methods**
  - length, 32
  - print, 38
- \* **metrics**
  - aid, 4
  - hd, 23
  - shd, 42
- \* **operations**
  - moralize, 34
  - mutate\_caugi, 34
  - skeleton, 43
- \* **queries**
  - ancestors, 6
  - children, 17
  - descendants, 18
  - edge\_types, 21
  - edges, 20
  - exogenous, 22
  - isACYCLIC, 24
  - is\_caugi, 25
  - is\_CPDAG, 26
  - is\_dag, 27
  - is\_EMPTY\_caugi, 28
- is\_pdag, 29
- is\_ug, 30
- markov\_blanket, 33
- neighbors, 35
- nodes, 36
- parents, 37
- same\_nodes, 41
- subgraph, 43
- \* **registry**
  - register\_caugi\_edge, 39
  - registry, 40
- \* **simulation functions**
  - generate\_graph, 23
- \* **simulation**
  - generate\_graph, 23
- \* **verbs**
  - build, 12
  - caugi\_verbs, 15
- add\_edges (caugi\_verbs), 15
- add\_nodes (caugi\_verbs), 15
- adjustment\_set, 3, 5, 20, 31
- aid, 4, 24, 42
- all\_backdoor\_sets, 3, 5, 20, 31
- ancestors, 6, 18, 19, 21, 22, 25–30, 33, 36, 37, 41, 44
- as\_adjacency, 7, 8, 10–12
- as\_bnlearn, 8, 8, 10–12
- as\_caugi, 8, 9, 11, 12
- as\_dagitty, 8, 10, 11, 12
- as\_igraph, 8, 10, 11, 12
- build, 12, 17
- build(), 9, 14
- caugi, 13
- caugi\_registry (registry), 40
- caugi\_verbs, 13, 15
- children, 7, 17, 19, 21, 22, 25–30, 33, 36, 37, 41, 44

**d\_separated**, 3, 5, 19, 31  
**descendants**, 7, 18, 18, 21, 22, 25–30, 33, 36, 37, 41, 44  
  
**E** (edges), 20  
**edge\_types**, 7, 18, 19, 21, 21, 22, 25–30, 33, 36, 37, 41, 44  
**edges**, 7, 18, 19, 20, 21, 22, 25–30, 33, 36, 37, 41, 44  
**exogenous**, 7, 18, 19, 21, 22, 25–30, 33, 36, 37, 41, 44  
  
**generate\_graph**, 23  
  
**hd**, 4, 23, 42  
  
**is\_acyclic**, 7, 18, 19, 21, 22, 24, 25–30, 33, 36, 37, 41, 44  
**is\_caugi**, 7, 18, 19, 21, 22, 25, 25, 26–30, 33, 36, 37, 41, 44  
**is\_cpdag**, 7, 18, 19, 21, 22, 25, 26, 27–30, 33, 36, 37, 41, 44  
**is\_dag**, 7, 18, 19, 21, 22, 25, 26, 27, 28–30, 33, 36, 37, 41, 44  
**is\_empty\_caugi**, 7, 18, 19, 21, 22, 25–27, 28, 29, 30, 33, 36, 37, 41, 44  
**is\_pdag**, 7, 18, 19, 21, 22, 25–28, 29, 30, 33, 36, 37, 41, 44  
**is\_ug**, 7, 18, 19, 21, 22, 25–29, 30, 33, 36, 37, 41, 44  
**is\_valid\_backdoor**, 3, 5, 20, 31  
  
**length**, 32, 38  
  
**markov\_blanket**, 7, 18, 19, 21, 22, 25–30, 33, 36, 37, 41, 44  
**moralize**, 34, 35, 43  
**mutate\_caugi**, 34, 34, 43  
  
**neighbors**, 7, 18, 19, 21, 22, 25–30, 33, 35, 37, 41, 44  
**neighbours** (**neighbors**), 35  
**nodes**, 7, 18, 19, 21, 22, 25–30, 33, 36, 36, 37, 41, 44  
  
**parents**, 7, 18, 19, 21, 22, 25–30, 33, 36, 37, 37, 41, 44  
**print**, 32, 38  
  
**register\_caugi\_edge**, 39, 40  
  
**register\_caugi\_edge()**, 13  
**registry**, 39, 40  
**remove\_edges** (**caugi\_verbs**), 15  
**remove\_nodes** (**caugi\_verbs**), 15  
**reset\_caugi\_registry** (**registry**), 40  
  
**same\_nodes**, 7, 18, 19, 21, 22, 25–30, 33, 36, 37, 41, 44  
**seal\_caugi\_registry** (**registry**), 40  
**set\_edges** (**caugi\_verbs**), 15  
**shd**, 4, 24, 42  
**skeleton**, 34, 35, 43  
**subgraph**, 7, 18, 19, 21, 22, 25–30, 33, 36, 37, 41, 43  
  
**V** (**nodes**), 36  
**vertices** (**nodes**), 36