

# Package ‘causaloptim’

July 22, 2025

**Encoding** UTF-8

**Type** Package

**Title** An Interface to Specify Causal Graphs and Compute Bounds on Causal Effects

**Version** 1.0.0

**Date** 2024-10-16

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**Description** When causal quantities are not identifiable from the observed data, it still may be possible to bound these quantities using the observed data. We outline a class of problems for which the derivation of tight bounds is always a linear programming problem and can therefore, at least theoretically, be solved using a symbolic linear optimizer. We extend and generalize the approach of Balke and Pearl (1994) <doi:10.1016/B978-1-55860-332-5.50011-0> and we provide a user friendly graphical interface for setting up such problems via directed acyclic graphs (DAG), which only allow for problems within this class to be depicted. The user can then define linear constraints to further refine their assumptions to meet their specific problem, and then specify a causal query using a text interface. The program converts this user defined DAG, query, and constraints, and returns tight bounds. The bounds can be converted to R functions to evaluate them for specific datasets, and to latex code for publication. The methods and proofs of tightness and validity of the bounds are described in a paper by Sachs, Jonzon, Gabriel, and Sjölander (2022) <doi:10.1080/10618600.2022.2071905>.

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**Imports** shiny, rcd

**Depends** R (>= 3.5.0), igraph

**RoxygenNote** 7.3.2

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

**VignetteBuilder** knitr

**URL** <https://sachsmc.github.io/causaloptim/>

**BugReports** <https://github.com/sachsmc/causaloptim/issues/>

**Config/testthat/edition** 3

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2024-10-17 09:00:02 UTC

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|                     |                                                                                   |
|---------------------|-----------------------------------------------------------------------------------|
| causaloctim-package | <i>An Interface to Specify Causal Graphs and Compute Bounds on Causal Effects</i> |
|---------------------|-----------------------------------------------------------------------------------|

---

**Description**

Specify causal graphs using a visual interactive interface and then analyze them and compute symbolic bounds for the causal effects in terms of the observable parameters.

**Details**

Run the shiny app by `results <- specify_graph()`. See detailed instructions in the vignette `browseVignettes("causaloctim")`.

**Author(s)**

Michael C Sachs, Arvid Sjölander, Gustav Jonzon, Alexander Balke, Colorado Reed, and Erin Gabriel Maintainer: Michael C Sachs <sachsmc at gmail.com>

**References**

Sachs, M. C., Jonzon, G., Sjölander, A., & Gabriel, E. E. (2023). A general method for deriving tight symbolic bounds on causal effects. *Journal of Computational and Graphical Statistics*, 32(2), 567-576. <https://www.tandfonline.com/doi/full/10.1080/10618600.2022.2071905>.

**See Also**

`browseVignettes('causaloctim')` [specify\\_graph](#)

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|                            |                                                                                   |
|----------------------------|-----------------------------------------------------------------------------------|
| <code>analyze_graph</code> | <i>Analyze the causal graph and effect to determine constraints and objective</i> |
|----------------------------|-----------------------------------------------------------------------------------|

---

**Description**

The graph must contain certain edge and vertex attributes which are documented in the Details below. The shiny app run by [specify\\_graph](#) will return a graph in this format.

**Usage**

```
analyze_graph(graph, constraints, effectt)
```

## Arguments

|             |                                                                                                                         |
|-------------|-------------------------------------------------------------------------------------------------------------------------|
| graph       | An <a href="#">igraph-package</a> object that represents a directed acyclic graph with certain attributes. See Details. |
| constraints | A vector of character strings that represent the constraints on counterfactual quantities                               |
| effecttt    | A character string that represents the causal effect of interest                                                        |

## Details

The graph object must contain the following named vertex attributes:

**name** The name of each vertex must be a valid R object name starting with a letter and no special characters. Good candidate names are for example, Z1, Z2, W2, X3, etc.

**leftside** An indicator of whether the vertex is on the left side of the graph, 1 if yes, 0 if no.

**latent** An indicator of whether the variable is latent (unobserved). There should always be a variable U1 on the left side that is latent and a parent of all variables on the left side, and another latent variable Ur on the right side that is a parent of all variables on the right side.

**nvals** The number of possible values that the variable can take on, the default and minimum is 2 for 2 categories (0,1). In general, a variable with nvals of K can take on values 0, 1, ..., (K-1).

In addition, there must be the following edge attributes:

**rlconnect** An indicator of whether the edge goes from the right side to the left side. Should be 0 for all edges.

**edge.monotone** An indicator of whether the effect of the edge is monotone, meaning that if  $V1 \rightarrow V2$  and the edge is monotone, then  $a > b$  implies  $V2(V1 = a) \geq V2(V1 = b)$ . Only available for binary variables (nvals = 2).

The effecttt parameter describes your causal effect of interest. The effecttt parameter must be of the form

$p\{V11(X=a)=a; V12(X=a)=b; \dots\} \text{ op1 } p\{V21(X=b)=a; V22(X=c)=b; \dots\} \text{ op2 } \dots$

where  $V_{ij}$  are names of variables in the graph,  $a, b$  are numeric values from  $0:(nvals - 1)$ , and  $op$  are either - or +. You can specify a single probability statement (i.e., no operator). Note that the probability statements begin with little  $p$ , and use curly braces, and items inside the probability statements are separated by ;. The variables may be potential outcomes which are denoted by parentheses. Variables may also be nested inside potential outcomes. Pure observations such as  $p\{Y = 1\}$  are not allowed if the left side contains any variables. There are 2 important rules to follow: 1) Only variables on the right side can be in the probability events, and if the left side is not empty: 2) none of the variables in the left side that are intervened upon can have any children in the left side, and all paths from the left to the right must be blocked by the intervention set. Here the intervention set is anything that is inside the smooth brackets (i.e., variable set to values).

All of the following are valid effect statements:

$p\{Y(X = 1) = 1\} - p\{Y(X = 0) = 1\}$

$p\{X(Z = 1) = 1; X(Z = 0) = 0\}$

$p\{Y(M(X = 0), X = 1) = 1\} - p\{Y(M(X = 0), X = 0) = 1\}$

The constraints are specified in terms of potential outcomes to constrain by writing the potential outcomes, values of their parents, and operators that determine the constraint (equalities or inequalities). For example,  $X(Z = 1) \geq X(Z = 0)$

## Value

An object of class "linearcausalproblem", which is a list with the following components. This list can be passed to `optimize_effect_2` which interfaces with the symbolic optimization program. Print and plot methods are also available.

**variables** Character vector of variable names of potential outcomes, these start with 'q' to match Balke's notation

**parameters** Character vector of parameter names of observed probabilities, these start with 'p' to match Balke's notation

**constraints** Character vector of parsed constraints

**objective** Character string defining the objective to be optimized in terms of the variables

**p.vals** Matrix of all possible values of the observed data vector, corresponding to the list of parameters.

**q.vals** Matrix of all possible values of the response function form of the potential outcomes, corresponding to the list of variables.

**parsed.query** A nested list containing information on the parsed causal query.

**objective.nonreduced** The objective in terms of the original variables, before algebraic variable reduction. The nonreduced variables can be obtained by concatenating the columns of q.vals.

**response.functions** List of response functions.

**graph** The graph as passed to the function.

**R** A matrix with coefficients relating the p.vals to the q.vals  $p = R * q$

**c0** A vector of coefficients relating the q.vals to the objective function  $\theta = c0 * q$

**iqR** A matrix with coefficients to represent the inequality constraints

## Examples

```
### confounded exposure and outcome
b <- initialize_graph(igraph::graph_from_literal(X -> Y, Ur -> X, Ur -> Y))
analyze_graph(b, constraints = NULL, effectt = "p{Y(X = 1) = 1} - p{Y(X = 0) = 1}")
```

---

btm\_var

Recursive function to get the last name in a list

---

## Description

Recursive function to get the last name in a list

## Usage

```
btm_var(x, name = NULL)
```

**Arguments**

|      |                                     |
|------|-------------------------------------|
| x    | a list                              |
| name | name of the top element of the list |

**Value**

The name of the deepest nested list element

**Examples**

```
btm_var(list(X = list(Y = list(K = 1))))
```

---

|                    |                                           |
|--------------------|-------------------------------------------|
| causalproblemcheck | <i>Check conditions on causal problem</i> |
|--------------------|-------------------------------------------|

---

**Description**

Check that a given causal problem (a causal DAG together with a causal query) satisfies conditions that guarantee that the optimization problem is linear.

**Usage**

```
causalproblemcheck(digraph, query)
```

**Arguments**

|         |                                                                                                                                                                                                                    |
|---------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| digraph | An igraph object representing a digraph.<br>Expected vertex attributes: leftside, latent and nvals.<br>Optional vertex attributes: exposure and outcome.<br>Expected edge attributes: rlconnect and edge.monotone. |
| query   | A string representing a causal query / effect.                                                                                                                                                                     |

**Value**

TRUE if conditions are met; FALSE otherwise.

**Examples**

```
b <- graph_from_literal(X ~ +Y, Ur ~ +X, Ur ~ +Y)
V(b)$leftside <- c(0, 0, 0)
V(b)$latent <- c(0, 0, 1)
V(b)$nvals <- c(2, 2, 2)
V(b)$exposure <- c(1, 0, 0)
V(b)$outcome <- c(0, 1, 0)
E(b)$rlconnect <- c(0, 0, 0)
E(b)$edge.monotone <- c(0, 0, 0)
```

```
effectt <- "p{Y(X=1)=1}-p{Y(X=0)=1}"
causalproblemcheck(digraph = b, query = effectt)
```

---

check\_constraints\_violated

*Check whether any of the observable constraints implied by the causal model are violated for a given distribution of observables*

---

## Description

Check whether any of the observable constraints implied by the causal model are violated for a given distribution of observables

## Usage

```
check_constraints_violated(obj, probs, tol = 1e-12)
```

## Arguments

|       |                                                                                        |
|-------|----------------------------------------------------------------------------------------|
| obj   | An object of class "causalmodel"                                                       |
| probs | A named vector of observable probabilities, in the same order as obj\$data\$parameters |
| tol   | Tolerance for checking (in)equalities                                                  |

## Value

Either TRUE (violated) or FALSE (not violated) with messages indicating what constraints are violated if any.

## Examples

```
graph <- initialize_graph(graph_from_literal(Z --> X, X --> Y, Ur --> X, Ur --> Y))

iv_model <- create_causalmodel(graph, prob.form = list(out = c("X", "Y"), cond = "Z"))
check_constraints_violated(iv_model, probs = sample_distribution(iv_model))
```

---

check\_linear\_objective

*Check linearity of objective function implied by a causal model and effect*

---

## Description

Check linearity of objective function implied by a causal model and effect

## Usage

```
check_linear_objective(causal_model, effectt)
```

## Arguments

**causal\_model**     An object of class "causalmodel" as produce by [create\\_causalmodel](#)

**effectt**            A character string that represents the causal effect of interest

## Details

The effectt parameter describes your causal effect of interest. The effectt parameter must be of the form

$$p\{V_{11}(X=a)=a; V_{12}(X=a)=b; \dots\} \text{ op1 } p\{V_{21}(X=b)=a; V_{22}(X=c)=b; \dots\} \text{ op2 } \dots$$

where  $V_{ij}$  are names of variables in the graph,  $a, b$  are numeric values from  $0:(nvals - 1)$ , and  $op$  are either  $-$  or  $+$ . You can specify a single probability statement (i.e., no operator). Note that the probability statements begin with little  $p$ , and use curly braces, and items inside the probability statements are separated by  $;$ . The variables may be potential outcomes which are denoted by parentheses. Variables may also be nested inside potential outcomes.

All of the following are valid effect statements:

$$p\{Y(X = 1) = 1\} - p\{Y(X = 0) = 1\}$$

$$p\{X(Z = 1) = 1; X(Z = 0) = 0\}$$

$$p\{Y(M(X = 0), X = 1) = 1\} - p\{Y(M(X = 0), X = 0) = 1\}$$

The effect must be fully specified, that is, all parents of a variable that is intervened upon need to be specified. The function cannot infer missing values or marginalize over some parents but not others.

## Value

A logical value that is TRUE if the objective function is linear

**Examples**

```
## regular IV case

ivgraph <- initialize_graph(graph_from_literal(Z -> X, X -> Y, Ur -> X, Ur -> Y))
prob.form <- list(out = c("Y", "X"), cond = "Z")

iv_model <- create_causalmodel(graph = ivgraph,
                              prob.form = prob.form)
check_linear_objective(iv_model, effectt = "p{Y(X = 1) = 1}")

#' ## contaminated IV case

civgraph <- initialize_graph(graph_from_literal(Z -> X, X -> Y, Z-> Y, Ur -> X, Ur -> Y))

cont_iv <- create_causalmodel(graph = civgraph, prob.form = prob.form)

check_linear_objective(cont_iv, effectt = "p{Y(X = 1) = 1}")
```

---

|               |                                        |
|---------------|----------------------------------------|
| check_parents | <i>Check for paths from from to to</i> |
|---------------|----------------------------------------|

---

**Description**

Check for paths from from to to

**Usage**

```
check_parents(parent_lookup, from, to, prev = NULL)
```

**Arguments**

|               |                                         |
|---------------|-----------------------------------------|
| parent_lookup | A list of vectors                       |
| from          | character                               |
| to            | character                               |
| prev          | Should always be null when first called |

**Value**

A list of paths or null if no path is found

**Examples**

```
parent_lookup <- list(M = "Am", Y = c("M", "Ay"), A = NULL, Am = "A", Ay = "A")
check_parents(parent_lookup, "A", "Y")
```

---

|                  |                          |
|------------------|--------------------------|
| constraintscheck | <i>Check constraints</i> |
|------------------|--------------------------|

---

### Description

Check that a user-provided constraint is parsable, has valid variables and relations.

### Usage

```
constraintscheck(constrainttext, graphres)
```

### Arguments

`constrainttext` A string representing a constraint.  
`graphres` An igraph object representing a DAG.

### Value

TRUE if all check pass; else FALSE.

### Examples

```
graphres <- graph_from_literal(Z -+ X, X -+ Y, U1 -+ Z, Ur -+ X, Ur -+ Y)
V(graphres)$leftside <- c(1, 0, 0, 1, 0)
V(graphres)$latent <- c(0, 0, 0, 1, 1)
V(graphres)$nvals <- c(3, 2, 2, 2, 2)
V(graphres)$exposure <- c(0, 1, 0, 0, 0)
V(graphres)$outcome <- c(0, 0, 1, 0, 0)
E(graphres)$rlconnect <- c(0, 0, 0, 0, 0)
E(graphres)$edge.monotone <- c(0, 0, 0, 0, 0)
constrainttext <- "X(Z = 1) >= X(Z = 0)"
constraintscheck(constrainttext = constrainttext, graphres = graphres) # TRUE
```

---

|                    |                                                                                     |
|--------------------|-------------------------------------------------------------------------------------|
| create_causalmodel | <i>Create a structural causal model from a graph or a set of response functions</i> |
|--------------------|-------------------------------------------------------------------------------------|

---

### Description

Given either a graph or a set of response functions (i.e., either graph or respvars may be provided), and a specification of what conditional probabilities are observed, produce a causal model.

**Usage**

```
create_causalmodel(
  graph = NULL,
  respvars = NULL,
  prob.form,
  p.vals,
  constraints = NULL,
  right.vars = NULL
)
```

**Arguments**

|             |                                                                                                                                                                                                        |
|-------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| graph       | A graph with special edge and vertex attributes, as produced by <a href="#">initialize_graph</a>                                                                                                       |
| respvars    | List of response functions as produced by <a href="#">create_response_function</a>                                                                                                                     |
| prob.form   | A list with two named elements "out", "cond" where each element is a character vector of variable names that appear in p.vals                                                                          |
| p.vals      | Data frame defining which probabilities are observable. The variable names of p.vals must all appear in prob.form. If missing, will assume that all combinations of the variables values are observed. |
| constraints | A vector of character strings that represent the constraints on counterfactual quantities                                                                                                              |
| right.vars  | A vector of character strings indicating which variables are on the right side of the graph. Only required when graph is NULL. See examples.                                                           |

**Details**

It is assumed that probabilities of the form  $p(\text{out} \mid \text{cond})$  are observed, for each combination of values in p.vals. cond may be NULL in which case nothing is conditioned on.

The constraints are specified in terms of potential outcomes to constrain by writing the potential outcomes, values of their parents, and operators that determine the constraint (equalities or inequalities). For example,  $X(Z = 1) \geq X(Z = 0)$

**Value**

An object of class "causalmodel"

**Examples**

```
## regular IV case

graph <- initialize_graph(graph_from_literal(Z -> X, X -> Y, Ur -> X, Ur -> Y))

iv_model <- create_causalmodel(graph, prob.form = list(out = c("X", "Y"), cond = "Z"))
# with monotonicity
iv_model_mono <- create_causalmodel(graph, prob.form = list(out = c("X", "Y"), cond = "Z"),
  constraints = list("X(Z = 1) >= X(Z = 0)"))

#showing the use of right.vars
```

```

b <- initialize_graph(graph_from_literal(U1 -> X -> Y -> Y2, Ur -> Y, Ur -> Y2))
V(b)$latent <- c(1, 0, 1, 0, 1)
respvars <- create_response_function(b)
create_causalmodel(graph = b, constraints = "Y2(Y = 1) >= Y2(Y = 0)",
  p.vals = expand.grid(X = 0:1, Y2 = 0:1),
  prob.form = list(out = "Y2", cond = "X"))
## need to specify right.vars because it cannot be inferred from the response functions alone
create_causalmodel(graph = NULL, respvars = respvars,
  constraints = "Y2(Y = 1) >= Y2(Y = 0)",
  p.vals = expand.grid(X = 0:1, Y2 = 0:1),
  prob.form = list(out = "Y2", cond = "X"),
  right.vars = c("Y", "Y2"))

```

---

create\_effect\_vector    *Translate target effect to vector of response variables*

---

## Description

Translate target effect to vector of response variables

## Usage

```
create_effect_vector(causal_model, effect)
```

## Arguments

**causal\_model**    An object of class "causalmodel" as produced by [create\\_causalmodel](#)

**effect**    Effect list, as returned by [parse\\_effect](#)

## Value

A list with the target effect in terms of qs

## Examples

```

graph <- initialize_graph(graph_from_literal(Z -> X, X -> Y, U1 -> Z, Ur -> X, Ur -> Y))
constraints <- "X(Z = 1) >= X(Z = 0)"
effectt = "p{Y(X = 1) = 1} - p{Y(X = 0) = 1}"
p.vals <- expand.grid(Z = 0:1, X = 0:1, Y = 0:1)
prob.form <- list(out = c("X", "Y"), cond = "Z")
effect <- parse_effect(effectt)
ivmod <- create_causalmodel(graph, respvars = NULL, p.vals = p.vals, prob.form = prob.form,
  constraints = constraints)
var.eff <- create_effect_vector(ivmod, effect)

```

---

create\_linearcausalproblem

*Create linear causal problem from causal model and effect*


---

## Description

A more flexible alternative to [analyze\\_graph](#) that takes as inputs the causal model and effect.

## Usage

```
create_linearcausalproblem(causal_model, effectt)
```

## Arguments

|              |                                                                                   |
|--------------|-----------------------------------------------------------------------------------|
| causal_model | An object of class "causalmodel" as produce by <a href="#">create_causalmodel</a> |
| effectt      | A character string that represents the causal effect of interest                  |

## Details

The effectt parameter describes your causal effect of interest. The effectt parameter must be of the form

$$p\{V_{11}(X=a)=a; V_{12}(X=a)=b; \dots\} \text{ op1 } p\{V_{21}(X=b)=a; V_{22}(X=c)=b; \dots\} \text{ op2 } \dots$$

where  $V_{ij}$  are names of variables in the graph,  $a, b$  are numeric values from  $0:(nvals - 1)$ , and  $op$  are either  $-$  or  $+$ . You can specify a single probability statement (i.e., no operator). Note that the probability statements begin with little  $p$ , and use curly braces, and items inside the probability statements are separated by  $;$ . The variables may be potential outcomes which are denoted by parentheses. Variables may also be nested inside potential outcomes. Pure observations such as  $p\{Y = 1\}$  are not allowed if the left side contains any variables. There are 2 important rules to follow: 1) Only variables on the right side can be in the probability events, and if the left side is not empty: 2) none of the variables in the left side that are intervened upon can have any children in the left side, and all paths from the left to the right must be blocked by the intervention set. Here the intervention set is anything that is inside the smooth brackets (i.e., variable set to values).

All of the following are valid effect statements:

$$p\{Y(X = 1) = 1\} - p\{Y(X = 0) = 1\}$$

$$p\{X(Z = 1) = 1; X(Z = 0) = 0\}$$

$$p\{Y(M(X = 0), X = 1) = 1\} - p\{Y(M(X = 0), X = 0) = 1\}$$

## Value

A an object of class "linearcausalproblem", which is a list with the following components. This list can be passed to [optimize\\_effect\\_2](#) which interfaces with the symbolic optimization program. Print and plot methods are also available.

**variables** Character vector of variable names of potential outcomes, these start with 'q' to match Balke's notation

- parameters** Character vector of parameter names of observed probabilities, these start with 'p' to match Balke's notation
- constraints** Character vector of parsed constraints
- objective** Character string defining the objective to be optimized in terms of the variables
- p.vals** Matrix of all possible values of the observed data vector, corresponding to the list of parameters.
- q.vals** Matrix of all possible values of the response function form of the potential outcomes, corresponding to the list of variables.
- parsed.query** A nested list containing information on the parsed causal query.
- objective.nonreduced** The objective in terms of the original variables, before algebraic variable reduction. The nonreduced variables can be obtained by concatenating the columns of q.vals.
- response.functions** List of response functions.
- graph** The graph as passed to the function.
- R** A matrix with coefficients relating the p.vals to the q.vals  $p = R * q$
- c0** A vector of coefficients relating the q.vals to the objective function  $\theta = c0 * q$
- iqR** A matrix with coefficients to represent the inequality constraints

## Examples

```
### confounded exposure and outcome
b <- initialize_graph(igraph::graph_from_literal(X -> Y, Ur -> X, Ur -> Y))
confmod <- create_causalmodel(graph = b, prob.form = list(out = c("X", "Y"), cond = NULL))
create_linearcausalproblem(confmod, effectt = "p{Y(X = 1) = 1}")
```

---

|                 |                                                                    |
|-----------------|--------------------------------------------------------------------|
| create_q_matrix | <i>Translate response functions into matrix of counterfactuals</i> |
|-----------------|--------------------------------------------------------------------|

---

## Description

Translate response functions into matrix of counterfactuals

## Usage

```
create_q_matrix(respvars, right.vars, cond.vars, constraints)
```

## Arguments

- |             |                                                                             |
|-------------|-----------------------------------------------------------------------------|
| respvars    | A list of functions as returned by <a href="#">create_response_function</a> |
| right.vars  | Vertices of graph on the right side                                         |
| cond.vars   | Vertices of graph on the left side                                          |
| constraints | A vector of character strings that represent the constraints                |

**Value**

A list of 3 data frames of counterfactuals and their associated labels

**Examples**

```
graphres <- initialize_graph(graph_from_literal(Z -> X, X -> Y, U1 -> Z, Ur -> X, Ur -> Y))
constraints <- "X(Z = 1) >= X(Z = 0)"
cond.vars <- V(graphres)[V(graphres)$leftside == 1 & names(V(graphres)) != "U1"]
right.vars <- V(graphres)[V(graphres)$leftside == 0 & names(V(graphres)) != "Ur"]
respvars <- create_response_function(graphres)
create_q_matrix(respvars, right.vars, cond.vars, constraints)
```

---

create\_response\_function

*Translate regular DAG to response functions*

---

**Description**

Translate regular DAG to response functions

**Usage**

```
create_response_function(graph)
```

**Arguments**

|       |                                                                                                                                                                                                                                                                                 |
|-------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| graph | An <a href="#">aaa-igraph-package</a> object that represents a directed acyclic graph that contains certain edge attributes. The shiny app returns a graph in this format and <a href="#">initialize_graph</a> will add them to a regular igraph object with sensible defaults. |
|-------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|

**Value**

A list of functions representing the response functions

**Examples**

```
### confounded exposure and outcome
b <- initialize_graph(igraph::graph_from_literal(X -> Y, Ur -> X, Ur -> Y))
create_response_function(b)
```

---

|                |                                         |
|----------------|-----------------------------------------|
| find_all_paths | <i>Find all paths in a causal model</i> |
|----------------|-----------------------------------------|

---

**Description**

Given a set of response functions, find all directed paths from from to to

**Usage**

```
find_all_paths(respvars, from, to)
```

**Arguments**

|          |                                                                                    |
|----------|------------------------------------------------------------------------------------|
| respvars | A set of response functions as created by <a href="#">create_response_function</a> |
| from     | A character string indicating the start of the path                                |
| to       | A character string indicating the end of the path                                  |

**Value**

A list with all the paths or a list with NULL if there are none

**Examples**

```
b <- initialize_graph(igraph::graph_from_literal(X -> Z, Z -> Y, X -> Y, Ur -> Z, Ur -> Y))
medmod <- create_response_function(b)
find_all_paths(medmod, "X", "Y")
igraph::all_simple_paths(b, "X", "Y", mode = "out")
```

---

|                    |                                                |
|--------------------|------------------------------------------------|
| get_default_effect | <i>Define default effect for a given graph</i> |
|--------------------|------------------------------------------------|

---

**Description**

Define default effect for a given graph

**Usage**

```
get_default_effect(graphres)
```

**Arguments**

|          |                                                                          |
|----------|--------------------------------------------------------------------------|
| graphres | The graph object, should have vertex attributes "outcome" and "exposure" |
|----------|--------------------------------------------------------------------------|

**Value**

A string that can be passed to [parse\\_effect](#)

**Examples**

```

graphres <- graph_from_literal(Z --> X, X --> Y, U1 --> Z, Ur --> X, Ur --> Y)
V(graphres)$leftside <- c(1, 0, 0, 1, 0)
V(graphres)$latent <- c(0, 0, 0, 1, 1)
V(graphres)$nvals <- c(3, 2, 2, 2, 2)
V(graphres)$exposure <- c(0, 1, 0, 0, 0)
V(graphres)$outcome <- c(0, 0, 1, 0, 0)
E(graphres)$rlconnect <- c(0, 0, 0, 0, 0)
E(graphres)$edge.monotone <- c(0, 0, 0, 0, 0)
get_default_effect(graphres = graphres) == "p{Y(X = 1)=1} - p{Y(X = 0)=1}" # TRUE

```

---

|               |                                    |
|---------------|------------------------------------|
| graphrescheck | <i>Check conditions on digraph</i> |
|---------------|------------------------------------|

---

**Description**

Check that a given digraph satisfies the conditions of 'no left to right edges', 'no cycles', 'valid number of categories' and 'valid variable names'. Optionally returns the digraph if all checks are passed.

**Usage**

```
graphrescheck(graphres, ret = FALSE)
```

**Arguments**

|          |                                                                                                  |
|----------|--------------------------------------------------------------------------------------------------|
| graphres | An igraph object representing a digraph.                                                         |
| ret      | A logical value. Default is FALSE. Set to TRUE to also return graphres if all checks are passed. |

**Value**

If ret=FALSE (default): TRUE if all checks pass; else FALSE. If ret=TRUE: graphres if all checks pass; else FALSE.

**Examples**

```

graphres <- graph_from_literal(X --> Y, X --> M, M --> Y, U1 --> X, Ur --> M, Ur --> Y)
V(graphres)$leftside <- c(1, 0, 0, 1, 0)
V(graphres)$latent <- c(0, 0, 0, 1, 1)
V(graphres)$nvals <- c(2, 2, 2, 2, 2)
V(graphres)$exposure <- c(0, 0, 0, 0, 0)
V(graphres)$outcome <- c(0, 0, 0, 0, 0)
E(graphres)$rlconnect <- c(0, 0, 0, 0, 0)
E(graphres)$edge.monotone <- c(0, 0, 0, 0, 0)
graphrescheck(graphres = graphres) # TRUE

```

---

|                  |                                                             |
|------------------|-------------------------------------------------------------|
| initialize_graph | <i>Initialize an igraph object for use with causaloptim</i> |
|------------------|-------------------------------------------------------------|

---

**Description**

Checks for required attributes and adds defaults if missing

**Usage**

```
initialize_graph(graph)
```

**Arguments**

|       |                           |
|-------|---------------------------|
| graph | An object of class igraph |
|-------|---------------------------|

**Value**

An igraph with the vertex attributes leftside, latent, and nvals, and edge attributes rlconnect and edge.monotone

**Examples**

```
b <- igraph::graph_from_literal(X -+ Y)
b2 <- initialize_graph(b)
V(b2)$nvals
```

---

|                  |                                            |
|------------------|--------------------------------------------|
| interpret_bounds | <i>Convert bounds string to a function</i> |
|------------------|--------------------------------------------|

---

**Description**

Convert bounds string to a function

**Usage**

```
interpret_bounds(bounds, parameters)
```

**Arguments**

|            |                                                                                    |
|------------|------------------------------------------------------------------------------------|
| bounds     | The bounds element as returned by <a href="#">optimize_effect</a>                  |
| parameters | Character vector defining parameters, as returned by <a href="#">analyze_graph</a> |

**Value**

A function that takes arguments for the parameters, i.e., the observed probabilities and returns a vector of length 2: the lower bound and the upper bound.

## Examples

```
b <- graph_from_literal(X -+ Y, Ur -+ X, Ur -+ Y)
V(b)$leftside <- c(0,0,0)
V(b)$latent <- c(0,0,1)
V(b)$nvals <- c(2,2,2)
E(b)$rconnect <- E(b)$edge.monotone <- c(0, 0, 0)
obj <- analyze_graph(b, constraints = NULL, effectt = "p{Y(X = 1) = 1} - p{Y(X = 0) = 1}")
bounds <- optimize_effect_2(obj)
bounds_func <- interpret_bounds(bounds$bounds, obj$parameters)
bounds_func(.1, .1, .4, .3)
# vectorized
do.call(bounds_func, lapply(1:4, function(i) runif(5)))
```

---

latex\_bounds

*Latex bounds equations*

---

## Description

Latex bounds equations

## Usage

```
latex_bounds(bounds, parameters, prob.sym = "P", brackets = c("(", ")"))
```

## Arguments

|            |                                                                                                                    |
|------------|--------------------------------------------------------------------------------------------------------------------|
| bounds     | Vector of bounds as returned by <a href="#">optimize_effect_2</a>                                                  |
| parameters | The parameters object as returned by <a href="#">analyze_graph</a>                                                 |
| prob.sym   | Symbol to use for probability statements in latex, usually "P" or "pr"                                             |
| brackets   | Length 2 vector with opening and closing bracket, usually <code>c("(", ")")</code> , or <code>c("\{", "\}")</code> |

## Value

A character string with latex code for the bounds

## Examples

```
b <- graph_from_literal(X -+ Y, Ur -+ X, Ur -+ Y)
V(b)$leftside <- c(0,0,0)
V(b)$latent <- c(0,0,1)
V(b)$nvals <- c(2,2,2)
E(b)$rconnect <- E(b)$edge.monotone <- c(0, 0, 0)
obj <- analyze_graph(b, constraints = NULL, effectt = "p{Y(X = 1) = 1} - p{Y(X = 0) = 1}")
bounds <- optimize_effect_2(obj)
latex_bounds(bounds$bounds, obj$parameters)
latex_bounds(bounds$bounds, obj$parameters, "Pr")
```

---

list\_to\_path

Recursive function to translate an effect list to a path sequence

---

### Description

Recursive function to translate an effect list to a path sequence

### Usage

```
list_to_path(x, name = NULL)
```

### Arguments

x                      A list of vars as returned by [parse\\_effect](#)  
name                    The name of the outcome variable

### Value

a list of characters describing the path sequence

### Examples

```
nofill <- "p{Y(X = 1, M1 = 1, M2(X = 1, M1 = 1)) = 1}"
eff2 <- parse_effect(nofill)$vars[[1]][[1]]
list_to_path(eff2, "Y")
```

---

optimize\_effect\_2

Run the optimizer to obtain symbolic bounds

---

### Description

Given an object with the linear programming problem set up, compute the bounds using rcdd. Bounds are returned as text but can be converted to R functions using [interpret\\_bounds](#), or latex code using [latex\\_bounds](#).

### Usage

```
optimize_effect_2(obj)
```

### Arguments

obj                    Object as returned by [analyze\\_graph](#) or [create\\_linearcausalproblem](#)

**Value**

An object of class "balkebound" that is a list that contains the bounds and logs as character strings, and a function to compute the bounds

**Examples**

```
b <- initialize_graph(graph_from_literal(X -+ Y, Ur -+ X, Ur -+ Y))
obj <- analyze_graph(b, constraints = NULL, effectt = "p{Y(X = 1) = 1} - p{Y(X = 0) = 1}")
optimize_effect_2(obj)
```

---

|            |                                                     |
|------------|-----------------------------------------------------|
| opt_effect | <i>Compute a bound on the average causal effect</i> |
|------------|-----------------------------------------------------|

---

**Description**

This helper function does the heavy lifting for [optimize\\_effect\\_2](#). For a given casual query, it computes either a lower or an upper bound on the corresponding causal effect.

**Usage**

```
opt_effect(opt, obj)
```

**Arguments**

|     |                                                                                                                  |
|-----|------------------------------------------------------------------------------------------------------------------|
| opt | A string. Either "min" or "max" for a lower or an upper bound, respectively.                                     |
| obj | An object as returned by the function <a href="#">analyze_graph</a> . Contains the casual query to be estimated. |

**Value**

An object of class optbound; a list with the following named components:

- `expr` is the *main* output; an expression of the bound as a print-friendly string,
- `type` is either "lower" or "upper" according to the type of the bound,
- `dual_vertices` is a numeric matrix whose rows are the vertices of the convex polytope of the dual LP,
- `dual_vrep` is a V-representation of the dual convex polytope, including some extra data.

---

|                   |                                                  |
|-------------------|--------------------------------------------------|
| parse_constraints | <i>Parse text that defines a the constraints</i> |
|-------------------|--------------------------------------------------|

---

**Description**

Parse text that defines a the constraints

**Usage**

```
parse_constraints(constraints, obsnames)
```

**Arguments**

|             |                                                        |
|-------------|--------------------------------------------------------|
| constraints | A list of character strings                            |
| obsnames    | Vector of names of the observed variables in the graph |

**Value**

A data frame with columns indicating the variables being constrained, what the values of their parents are for the constraints, and the operator defining the constraint (equality or inequalities).

**Examples**

```
constrainttext <- "X(Z = 1) >= X(Z = 0)"
obsnames <- c("Z", "X", "Y")
parse_constraints(constraints = constrainttext, obsnames = obsnames)
```

---

|              |                                                |
|--------------|------------------------------------------------|
| parse_effect | <i>Parse text that defines a causal effect</i> |
|--------------|------------------------------------------------|

---

**Description**

Parse text that defines a causal effect

**Usage**

```
parse_effect(text)
```

**Arguments**

|      |                  |
|------|------------------|
| text | Character string |
|------|------------------|

**Value**

A nested list that contains the following components:

**vars** For each element of the causal query, this indicates potential outcomes as names of the list elements, the variables that they depend on, and the values that any variables are being fixed to.

**oper** The vector of operators (addition or subtraction) that combine the terms of the causal query.

**values** The values that the potential outcomes are set to in the query.

**pcheck** List of logicals for each element of the query that are TRUE if the element is a potential outcome and FALSE if it is an observational quantity.

**Examples**

```
effectt <- "p{Y(X = 1) = 1} - p{Y(X = 0) = 1}"
parse_effect(text = effectt)
```

---

```
plot.linearcausalproblem
```

*Plot the graph from the causal problem with a legend describing attributes*

---

**Description**

Plot the graph from the causal problem with a legend describing attributes

**Usage**

```
## S3 method for class 'linearcausalproblem'
plot(x, ...)
```

**Arguments**

|     |                                       |
|-----|---------------------------------------|
| x   | object of class "linearcausalproblem" |
| ... | Not used                              |

**Value**

Nothing

**See Also**

[plot\\_graphres](#) which plots the graph only

**Examples**

```

b <- graph_from_literal(X --> Y, Ur --> X, Ur --> Y)
V(b)$leftside <- c(0,0,0)
V(b)$latent <- c(0,0,1)
V(b)$nvals <- c(2,2,2)
V(b)$exposure <- c(1,0,0)
V(b)$outcome <- c(0,1,0)
E(b)$rlconnect <- c(0,0,0)
E(b)$edge.monotone <- c(0,0,0)
q <- "p{Y(X=1)=1}-p{Y(X=0)=1}"
obj <- analyze_graph(graph = b, constraints = NULL, effectt <- q)
plot(obj)

```

---

|               |                                       |
|---------------|---------------------------------------|
| plot_graphres | <i>Plot the analyzed graph object</i> |
|---------------|---------------------------------------|

---

**Description**

Special plotting method for igraphs of this type

**Usage**

```
plot_graphres(graphres)
```

**Arguments**

graphres            an igraph object

**Value**

None

**See Also**

[plot.linearcausalproblem](#) which plots a graph with attributes

**Examples**

```

b <- graph_from_literal(X --> Y, Ur --> X, Ur --> Y)
V(b)$leftside <- c(0,0,0)
V(b)$latent <- c(0,0,1)
V(b)$nvals <- c(2,2,2)
V(b)$exposure <- c(1,0,0)
V(b)$outcome <- c(0,1,0)
E(b)$rlconnect <- c(0,0,0)
E(b)$edge.monotone <- c(0,0,0)
plot(b)

```

---

```
print.causalmodel
```

*Print relevant information about the causal model*

---

**Description**

Print relevant information about the causal model

**Usage**

```
## S3 method for class 'causalmodel'
print(x, omit_cf_constraints = FALSE, omit_obs_constraints = FALSE, ...)
```

**Arguments**

```
x                object of class "causalmodel"
omit_cf_constraints Do not print the counterfactual constraints
omit_obs_constraints Do not print the observable constraints
...              Not used
```

**Value**

x, invisibly

---

```
print.linearcausalproblem
```

*Print the causal problem*

---

**Description**

Print the causal problem

**Usage**

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

**Arguments**

```
x                object of class "linearcausaloptim"
...              Not used
```

**Value**

x, invisibly

---

|            |                                  |
|------------|----------------------------------|
| querycheck | <i>Check conditions on query</i> |
|------------|----------------------------------|

---

### Description

Given an admissible causal DAG, check that given a causal query satisfies conditions that guarantee the corresponding causal problem to be a linear program. Throws error messages detailing any conditions violated.

### Usage

```
querycheck(effecttext, graphres)
```

### Arguments

|            |                                          |
|------------|------------------------------------------|
| effecttext | A string representing a causal query.    |
| graphres   | An igraph object representing a digraph. |

### Value

TRUE if effecttext is parsable, contains only variables in  $V(\text{graphres})$  and satisfies conditions for linearity; else FALSE.

### Examples

```
graphres <- graph_from_literal(X -> Y, X -> M, M -> Y, U1 -> X, Ur -> M, Ur -> Y)
V(graphres)$leftside <- c(1, 0, 0, 1, 0)
V(graphres)$latent <- c(0, 0, 0, 1, 1)
V(graphres)$nvals <- c(2, 2, 2, 2, 2)
V(graphres)$exposure <- c(0, 0, 0, 0, 0)
V(graphres)$outcome <- c(0, 0, 0, 0, 0)
E(graphres)$rlconnect <- c(0, 0, 0, 0, 0, 0)
E(graphres)$edge.monotone <- c(0, 0, 0, 0, 0, 0)
effecttext <- "p{Y(M(X = 0), X = 1) = 1} - p{Y(M(X = 0), X = 0) = 1}"
querycheck(effecttext = effecttext, graphres = graphres) # TRUE
```

---

|            |                                             |
|------------|---------------------------------------------|
| rdirichlet | <i>Sample from a Dirichlet distribution</i> |
|------------|---------------------------------------------|

---

### Description

Generate a random vector from the k-dimensional symmetric Dirichlet distribution with concentration parameter alpha

### Usage

```
rdirichlet(k, alpha = 1)
```

**Arguments**

|       |                          |
|-------|--------------------------|
| k     | Length of the vector     |
| alpha | Concentration parameters |

**Value**

a numeric vector

**Examples**

```
qvals <- rdirichlet(16, 1)
sum(qvals)
```

---

|                     |                                                                                        |
|---------------------|----------------------------------------------------------------------------------------|
| sample_distribution | <i>Sample a distribution of observable probabilities that satisfy the causal model</i> |
|---------------------|----------------------------------------------------------------------------------------|

---

**Description**

Sample a distribution of observable probabilities that satisfy the causal model

**Usage**

```
sample_distribution(  
  obj,  
  simplex_sampler = function(k) {  
    rdirichlet(k, alpha = 1)  
  }  
)
```

**Arguments**

|                 |                                                                                                                                                                                                                      |
|-----------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| obj             | An object of class "causalmodel"                                                                                                                                                                                     |
| simplex_sampler | A function to generate a random sample from the simplex in k dimensions, where k is the number of variables (q parameters, obj\$data\$variables). By default this is uniform (symmetric dirichlet with parameter 1). |

**Value**

A vector of observable probabilities that satisfy the causal model

**Examples**

```
graph <- initialize_graph(graph_from_literal(Z -> X, X -> Y, Ur -> X, Ur -> Y))
prob.form <- list(out = c("X", "Y"), cond = "Z")

iv_model <- create_causalmodel(graph, prob.form = prob.form)
sample_distribution(iv_model)
```

---

|                 |                        |
|-----------------|------------------------|
| simulate_bounds | <i>Simulate bounds</i> |
|-----------------|------------------------|

---

**Description**

Run a simple simulation based on the bounds. For each simulation, sample the set of counterfactual probabilities from a uniform distribution, translate into a multinomial distribution, and then compute the objective and the bounds in terms of the observable variables.

**Usage**

```
simulate_bounds(obj, bounds, nsim = 1000)
```

**Arguments**

|        |                                                         |
|--------|---------------------------------------------------------|
| obj    | Object as returned by <a href="#">analyze_graph</a>     |
| bounds | Object as returned by <a href="#">optimize_effect_2</a> |
| nsim   | Number of simulation replicates                         |

**Value**

A data frame with columns: objective, bound.lower, bound.upper

**Examples**

```
b <- initialize_graph(graph_from_literal(X -> Y, Ur -> X, Ur -> Y))
obj <- analyze_graph(b, constraints = NULL, effectt = "p{Y(X = 1) = 1} - p{Y(X = 0) = 1}")
bounds <- optimize_effect_2(obj)
simulate_bounds(obj, bounds, nsim = 5)
```

specify\_graph

*Shiny interface to specify network structure and compute bounds***Description**

This launches the Shiny interface in the system's default web browser. The results of the computation will be displayed in the browser, but they can also be returned to the R session by assigning the result of the function call to an object. See below for information on what is returned.

**Usage**

```
specify_graph()
```

**Value**

If the button "Exit and return graph object" is clicked, then only the graph is returned as an [aaa-igraph-package](#) object.

If the bounds are computed and the button "Exit and return objects to R" is clicked, then a list is returned with the following elements:

**graphres** The graph as drawn and interpreted, an [aaa-igraph-package](#) object.

**obj** The objective and all necessary supporting information. This object is documented in [analyze\\_graph](#). This can be passed directly to [optimize\\_effect\\_2](#).

**bounds.obs** Object of class 'balkebound' as returned by [optimize\\_effect\\_2](#).

**constraints** Character vector of the specified constraints. NULL if no constraints.

**effect** Text describing the causal effect of interest.

**boundsFunction** Function that takes parameters (observed probabilities) as arguments, and returns a vector of length 2 for the lower and upper bounds.

update\_effect

*Update the effect in a linearcausalproblem object***Description**

If you want to use the same graph and response function, but change the effect of interest, this can save some computation time.

**Usage**

```
update_effect(obj, effectt)
```

**Arguments**

**obj** An object as returned by [analyze\\_graph](#)

**effectt** A character string that represents the causal effect of interest

**Value**

A object of class `linearcausalproblem`, see [analyze\\_graph](#) for details

**Examples**

```
b <- igraph::graph_from_literal(X -> Y, X -> M, M -> Y, U1 -> X, Ur -> Y, Ur -> M)
V(b)$leftside <- c(1, 0, 0, 1, 0)
V(b)$latent <- c(0, 0, 0, 1, 1)
V(b)$nvals <- c(2, 2, 2, 2, 2)
E(b)$rlconnect <- c(0, 0, 0, 0, 0, 0)
E(b)$edge.monotone <- c(0, 0, 0, 0, 0, 0)
CDE0_query <- "p{Y(M = 0, X = 1) = 1} - p{Y(M = 0, X = 0) = 1}"
CDE0_obj <- analyze_graph(b, constraints = NULL, effectt = CDE0_query)
CDE0_bounds <- optimize_effect_2(CDE0_obj)
CDE0_boundsfunction <- interpret_bounds(bounds = CDE0_bounds$bounds,
parameters = CDE0_obj$parameters)
CDE1_query <- "p{Y(M = 1, X = 1) = 1} - p{Y(M = 1, X = 0) = 1}"
CDE1_obj <- update_effect(CDE0_obj, effectt = CDE1_query)
CDE1_bounds <- optimize_effect_2(CDE1_obj)
CDE1_boundsfunction <- interpret_bounds(bounds = CDE1_bounds$bounds,
parameters = CDE1_obj$parameters)
```

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