Package ‘dagitty’
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Description A port of the web-based software 'DAGitty', available at
<http://dagitty.net>, for analyzing structural causal models
(also known as directed acyclic graphs or DAGs).
This package computes covariate adjustment sets for estimating causal
effects, enumerates instrumental variables, derives testable
implications (d-separation and vanishing tetrads), generates equivalent
models, and includes a simple facility for data simulation.

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**adjustmentSets**

Covariate Adjustment Sets

**Description**

Enumerates sets of covariates that (asymptotically) allow unbiased estimation of causal effects from observational data, assuming that the input causal graph is correct.

**Usage**

```r
adjustmentSets(
  x,
  exposure = NULL,
  outcome = NULL,
  type = c("minimal", "canonical", "all"),
  effect = c("total", "direct"),
  max.results = Inf
)
```

**Arguments**

- **x**: the input graph, a DAG, MAG, PDAG, or PAG.
- **exposure**: name(s) of the exposure variable(s). If not given (default), then the exposure variables are supposed to be defined in the graph itself.
- **outcome**: name(s) of the outcome variable(s), also taken from the graph if not given.
- **type**: which type of adjustment set(s) to compute. If type="minimal", then only minimal sufficient adjustment sets are returned (default). For type="all", all valid adjustment sets are returned. For type="canonical", a single adjustment set is returned that consists of all (possible) ancestors of exposures and outcomes, minus (possible) descendants of nodes on proper causal paths. This canonical adjustment set is always valid if any valid set exists at all.
- **effect**: which effect is to be identified. If effect="total", then the total effect is to be identified, and the adjustment criterion by Perkovic et al (2015; see also van der Zander et al., 2014), an extension of Pearl’s back-door criterion, is used. Otherwise, if effect="direct", then the average direct effect is to be identified, and Pearl’s single-door criterion is used (Pearl, 2009). In a structural equation model (Gaussian graphical model), direct effects are simply the path coefficients.
- **max.results**: integer. The listing of adjustment set is stopped once this many results have been found. Use Inf to generate them all. This only applies when type="minimal".

**Details**

If the input graph is a MAG or PAG, then it must not contain any undirected edges (=hidden selection variables).
References


Examples

```r
# The M-bias graph showing that adjustment for
# pre-treatment covariates is not always valid
f <- dagitty("dag\{ x \rightarrow y ; x \leftrightarrow m \leftrightarrow y \}\")
adjustmetsets( f, "x", "y" ) # empty set

# Generate data where true effect (=path coefficient) is .5
set.seed( 123 ); d <- simulateSEM( f, .5, .5 )
confint( lm( y ~ x, d ) )["x",] # includes .5
confint( lm( y ~ x + m, d ) )["x",] # does not include .5

# Adjustment sets can also sometimes be computed for graphs in which not all
# edge directions are known
f <- dagitty("pdag \{ x[e] y[o] a \rightarrow \{ i z b \}; \{ a z i \} \rightarrow x \rightarrow y \rightarrow \{ z b \}\}")
adjustmetsets( f )
```

ancestorGraph

**Ancestor Graph**

**Description**

Creates the induced subgraph containing only the vertices in `v`, their ancestors, and the edges between them. All other vertices and edges are discarded.

**Usage**

```r
ancestorGraph(x, v = NULL)
```

**Arguments**

- `x`: the input graph, a DAG, MAG, or PDAG.
- `v`: variable names.

**Details**

If the input graph is a MAG or PDAG, then all *possible* ancestors will be returned (see Examples).
Ancestral Relations

Examples

```r
g <- dagitty("dag{ z <- x -> y }")
ancestorGraph( g, "z" )

ans <- dagitty("pdag{ z -- x -> y }")
ancestorGraph( g, "y" ) # includes z
```

Description

Retrieve the names of all variables in a given graph that are in the specified ancestral relationship to the input variable \( v \).

Usage

- `descendants(x, v)` retrieves variables that are reachable from \( v \) via a directed path.
- `ancestors(x, v)` retrieves variables from which \( v \) is reachable via a directed path.
- `children(x, v)` finds all variables \( w \) connected to \( v \) by an edge \( v \rightarrow w \).
- `parents(x, v)` finds all variables \( w \) connected to \( v \) by an edge \( w \rightarrow v \).
- `markovBlanket(x, v)` returns \( x \)'s parents, its children, and all other parents of its children. The Markov blanket always renders \( x \) independent of all other nodes in the graph.

Arguments

- \( x \) the input graph, of any type.
- \( v \) name(s) of variable(s).
By convention, $\text{descendants}(x,v)$ and $\text{ancestors}(x,v)$ include $v$ but $\text{children}(x,v)$ and $\text{parents}(x,v)$ do not.

**Examples**

```r
g <- dagitty("graph{ a <-> x <-> b ; c -- x <- d }")
descendants(g,"x")
parents(g,"x")
spouses(g,"x")
```

---

**as.dagitty**

*Convert to DAGitty object*

---

**Description**

Converts its argument to a DAGitty object, if possible.

**Usage**

```r
as.dagitty(x, ...)
```

**Arguments**

- `x` an object.
- `...` further arguments passed on to methods.

---

**backDoorGraph**

*Back-Door Graph*

---

**Description**

Removes every first edge on a proper causal path from $x$. If $x$ is a MAG or PAG, then only “visible” directed edges are removed (Zhang, 2008).

**Usage**

```r
backDoorGraph(x)
```

**Arguments**

- `x` the input graph, a DAG, MAG, PDAG, or PAG.

**References**

canonicalize

Examples

```r
# Create a DAG
g <- dagitty("dag { x <-> m <-> y <- x }")
backDoorGraph(g) # x->y edge is removed

# Create a MAG
g <- dagitty("mag { x <-> m <-> y <- x }")
backDoorGraph(g) # x->y edge is not removed

# Create a MAG with additional edges
f <- dagitty("mag { x <-> m <-> y <- x <- i }")
backDoorGraph(g) # x->y edge is removed
```

canonicalize

**canonicalize**

*Canonicalize an Ancestral Graph*

**Description**

Takes an input ancestral graph (a graph with directed, bidirected and undirected edges) and converts it to a DAG by replacing every bidirected edge `x <-> y` with a substructure `x <- L -> y`, where `L` is a latent variable, and every undirected edge `x - y` with a substructure `x -> S < y`, where `S` is a selection variable. This function does not check whether the input is actually an ancestral graph.

**Usage**

```r
canonicalize(x)
```

**Arguments**

- `x` the input graph, a DAG or MAG.

**Value**

A list containing the following components:

- `g` The resulting graph.
- `L` Names of newly inserted latent variables.
- `S` Names of newly inserted selection variables.

**Examples**

```r
canonicalize("mag(x <-> y -- z)") # introduces two new variables
```
### completeDAG

**Generate Complete DAG**

**Description**
Generates a complete DAG on the given variable names. The order in which the variables are given corresponds to the topological ordering of the DAG. Returns a named list.

**Usage**

```r
completeDAG(x)
```

**Arguments**

- `x` variable names. Can also be a positive integer, in which case the variables will be called `x1,...,xN`.

### coordinates

**Plot Coordinates of Variables in Graph**

**Description**

The DAGitty syntax allows specification of plot coordinates for each variable in a graph. This function extracts these plot coordinates from the graph description in a dagitty object. Note that the coordinate system is undefined, typically one needs to compute the bounding box before plotting the graph.

**Usage**

```r
coordinates(x)
```

```r
coordinates(x) <- value
```

**Arguments**

- `x` the input graph, of any type.
- `value` a list with components `x` and `y`, giving relative coordinates for each variable. This format is suitable for `xy.coords`.

**See Also**

Function `graphLayout` for automatically generating layout coordinates, and function `plot.dagitty` for plotting graphs.
Examples

```r
## Plot localization of each node in the Shrier example
plot( coordinates( getExample("Shrier") ) )

## Define a graph and set coordinates afterwards
x <- dagitty('dag(
  G <-> H <-> I <-> G
  D <-> B -> C -> I <-> F <-> B <-> A
  H <-> E <-> C -> G <-> D
)
coordinates( x ) <-
  list( x=c(A=1, B=2, D=3, C=3, F=3, E=4, G=5, H=5, I=5),
       y=c(A=0, B=0, D=1, C=0, F=-1, E=0, G=1, H=0, I=-1) )
plot( x )
```

**dagitty**  
*Parse DAGitty Graph*

**Description**

Constructs a dagitty graph object from a textual description.

**Usage**

```r
dagitty(x, layout = FALSE)
```

**Arguments**

- `x` character, string describing a graphical model in dagitty syntax.
- `layout` logical, whether to automatically generate layout coordinates for each variable (see `graphLayout`)

**Details**

The textual syntax for DAGitty graph is based on the dot language of the graphviz software ([https://graphviz.gitlab.io/_pages/doc/info/lang.html](https://graphviz.gitlab.io/_pages/doc/info/lang.html)). This is a fairly intuitive syntax – use the examples below and in the other functions to get you started. An important difference to graphviz is that the DAGitty language supports several types of graphs, which have different semantics. However, many users will mainly focus on DAGs.

A DAGitty graph description has the following form:

```
[graph type] '{' [statements] '}'
```

where `[graph type]` is one of `dag`, 'mag', 'pdag', or 'pag' and `[statements]` is a list of variables statements and edge statements, which may (optionally) be separated by semicolons. Whitespace, including newlines, has no semantic role.

Variable statements look like
For example, the statement
\[ x \text{[exposure, pos="1,0"]} \]
declares a variable with ID x that is an exposure variable and has a layout position of 1,0.

The edge statement
\[ x \rightarrow y \]
declares a directed edge from variable x to variable y. Explicit variable statements are not required for the variables involved in edge statements, unless attributes such as position or exposure/outcome status need to be set.

DAGs (directed acyclic graphs) can contain the following edges: ->, <->. Bidirected edges in DAGs are simply shorthands for substructures <-U ->, where U is an unobserved variable.

MAGs (maximal ancestral graphs) can contain the following edges: ->, <->, --. The bidirected and directed edges of MAGs can represent latent confounders, and the undirected edges represent latent selection variables. For details, see Richardson and Spirtes (2002).

PDAGs (partially directed acyclic graphs) can contain the following edges: ->, <->, --. The bidirected edges mean the same thing as in DAGs. The undirected edges represent edges whose direction is not known. Thus, PDAGs are used to represent equivalence classes of DAGs (see also the function `equivalenceClass`).

PAGs (partial ancestral graphs) are to MAGs what PDAGs are to DAGs: they represent equivalence classes of MAGs. MAGs can contain the following edges: @-@, ->, @->, --, @-- (the @ symbols are written as circle marks in most of the literature). For details on PAGs, see Zhang et al (2008). For now, only a few DAGitty functions support PAGs (for instance, `adjustmentSets`).

The DAGitty parser does not perform semantic validation. That is, it will not check whether a DAG is actually acyclic, or whether all chain components in a PAG are actually chordal. This is not done because it can be computationally rather expensive.

References


B. van der Zander and M. Liskiewicz (2016), Separators and Adjustment Sets in Markov Equivalent DAGs. In *Proceedings of the Thirtieth AAAI Conference on Artificial Intelligence (AAAI’16)*, Phoenix, Arizona, USA.

Examples

```
# Specify a simple DAG containing one path
g <- dagitty("dag{
  a -> b ;
  b -> c ;
  d -> c
}")
```

# Newlines and semicolons are optional
d-connected

d-Separation

Description

A set $Z$ d-separates a path $p$ if (1) $Z$ contains a non-collider on $p$, e.g. $x\rightarrow m \rightarrow y$ with $Z = \{m\}$; or (2) some collider on $p$ is not on $Z$, e.g. $x \rightarrow m \leftarrow y$ with $Z = \phi$. 

```r
g <- dagitty("dag(
  a -> b -> c ; c -> d
)")
# Paths can be specified in one go; the semicolon below is # optional

g <- dagitty("dag("
  a -> b ; b -> c ; c -> d
")")
# Edges can be written in reverse notation


g <- dagitty("dag(
  a -> b -> c <- d
)")
# Spaces are optional as well


g <- dagitty("dag(a->b->c<d)")
# Variable attributes can be set in square brackets
# Example: DAG with one exposure, one outcome, and one unobserved variable

g <- dagitty("dag(
  x -> y ; x <- z -> y
  x [exposure]
  y [outcome]
  z [unobserved]
)")
# The same graph as above

g <- dagitty("dag(x[e]y[o]z[u]x<-z->y<-x)")
# A two-factor latent variable model

g <- dagitty("dag (X <=> Y
  X -> a X -> b X -> c X -> d
  Y -> a Y -> b Y -> c Y -> d
)")
# Curly braces can be used to "group" variables and
# specify edges to whole groups of variables
# The same two-factor model

g <- dagitty("dag( {X<->Y} -> {a b c d} )")
# A MAG

g <- dagitty("mag(a -- x -> y <-> z )")
# A PDAG

g <- dagitty("pdag( x -- y -- z )")
# A PAG

g <- dagitty("pag( x @-@ y @-@ z )")
```
Usage

dconnected(x, X, Y = list(), Z = list())
dseparated(x, X, Y = list(), Z = list())

Arguments

x the input graph, a DAG, PDAG, or MAG.
X vector of variable names.
Y vector of variable names.
Z vector of variable names.

dseparated(x, X, Y, Z) checks if all paths between X and Y are d-separated by Z.
dconnected(x, X, Y, Z) checks if at least one path between X and Y is not d-separated by Z.

Details

The functions also work for mixed graphs with directed, undirected, and bidirected edges. The definition of a collider in such graphs is: a node where two arrowheads collide, e.g. x<->m<y but not x->m->y.

Examples

dconnected( "dag(x->m->y)", "x", "y", c() ) # TRUE
dconnected( "dag(x->m->y)", "x", "y", c("m") ) # FALSE
dseparated( "dag(x->m->y)", "x", "y", c() ) # FALSE
dseparated( "dag(x->m->y)", "x", "y", c("m") ) # TRUE

downloadGraph

Download Graph from dagitty.net

Description

Downloads a graph that has been built and stored online using the dagitty.net GUI. Users who store graphs online will receive a unique URL for their graph, which can be fed into this function to continue working with the graph in R.

Usage

downloadGraph(x = "dagitty.net/mz-Tuw9")

Arguments

x dagitty model URL.
**edges**

*Graph Edges*

**Description**

Extracts edge information from the input graph.

**Usage**

```r
edges(x)
```

**Arguments**

- `x` the input graph, of any type.

**Value**

A data frame with the following variables:

- `v` name of the start node.
- `w` name of the end node. For symmetric edges (bidirected and undirected), the order of start and end node is arbitrary.
- `e` type of edge. Can be one of `"->"`, `"<->"` and `"--"`.
- `x` X coordinate for a control point. If this is not NA, then the edge is drawn as an `xspline` through the start point, this control point, and the end point. This is especially important for cases where there is more than one edge between two variables (for instance, both a directed and a bidirected edge).
- `y` Y coordinate for a control point.

**Examples**

```r
## Which kinds of edges are used in the Shrier example?
levels( edges( getExample("Shrier") )$e )
```

---

**EquivalentModels**

*Generating Equivalent Models*

**Description**

equivalenceClass(x) generates a complete partially directed acyclic graph (CPDAG) from an input DAG x. The CPDAG represents all graphs that are Markov equivalent to x: undirected edges in the CPDAG can be oriented either way, as long as this does not create a cycle or a new v-structure (a sugraph a -> m <- b, where a and b are not adjacent).
exogenousVariables

Usage

equivalenceClass(x)

equivalentDAGs(x, n = 100)

Arguments

x the input graph, a DAG.
n maximal number of returned graphs.

Details

equivalentDAGs(x, n) enumerates at most n DAGs that are Markov equivalent to x.

Examples

# How many equivalent DAGs are there for the sports DAG example?
g <- getExample("Shrier")
length(equivalentDAGs(g))
# Plot all equivalent DAGs
par( mfrow=c(2,3) )
lapply(equivalentDAGs(g), plot )
# How many edges can be reversed without changing the equivalence class?
sum(edges(equivalenceClass(g))$e == "--")

exogenousVariables Retrieve Exogenous Variables

Description

Returns the names of all variables that have no directed arrow pointing to them. Note that this does not preclude variables connected to bidirected arrows.

Usage

exogenousVariables(x)

Arguments

x the input graph, of any type.
getExample

Get Bundled Examples

Description

Provides access to the built-in examples of the dagitty website.

Usage

getExample(x)

Arguments

x name of the example, or part thereof. Supported values are:

- "M-bias" the M-bias graph.
- "confounding" an extended confounding triangle.
- "mediator" a small model with a mediator.
- "paths" a graph with many variables but few paths
- "Sebastiani" a small part of a genetics study (Sebastiani et al., 2005)
- "Polzer" DAG from a dentistry study (Polzer et al., 2012)
- "Schipf" DAG from a study on diabetes (Schipf et al., 2010)
- "Shrier" DAG from a classic sports medicine example (Shrier & Platt, 2008)
- "Thoemmes" DAG with unobserved variables (communicated by Felix Thoemmes, 2013).
- "Kampen" DAG from a psychiatry study (van Kampen, 2014)

References

Sabine Schipf, Robin Haring, Nele Friedrich, Matthias Nauck, Katharina Lau, Dietrich Alte, Andreas Stang, Henry Voelzke, and Henri Wallaschowski (2011), Low total testosterone is associated with increased risk of incident type 2 diabetes mellitus in men: Results from the study of health in pomerania (SHIP). The Aging Male 14(3):168–75.


Ian Shrier and Robert W. Platt (2008), Reducing bias through directed acyclic graphs. BMC Medical Research Methodology, 8(70).


graphLayout

Generate Graph Layout

Description

This function generates plot coordinates for each variable in a graph that does not have them already. To this end, the well-known “Spring” layout algorithm is used. Note that this is a stochastic algorithm, so the generated layout will be different every time (which also means that you can try several times until you find a decent layout).

Usage

graphLayout(x, method = "spring")

Arguments

x the input graph, of any type.
method the layout method; currently, only "spring" is supported.

Value

the same graph as x but with layout coordinates added.

Examples

```r
# Generate a layout for the M-bias graph and plot it
plot( graphLayout( dagitty( "dag ( X <- U1 -> M <- U2 -> Y ) " ) ) )
# Plot larger graph and abbreviate its variable names.
plot( getExample("Shrier"), abbreviate.names=TRUE )
```
graphType

Get Graph Type

Description

Get Graph Type

Usage

graphType(x)

Arguments

x  the input graph.

Examples

graphType("mag(x<->y)") == "mag"

impliedConditionalIndependencies

List Implied Conditional Independencies

Description

Generates a list of conditional independence statements that must hold in every probability distribution compatible with the given model.

Usage

impliedConditionalIndependencies(x, type = "missing.edge", max.results = Inf)

Arguments

x  the input graph, a DAG, MAG, or PDAG.

type  can be one of "missing.edge", "basis.set", or "all.pairs". With the first, one or more minimal testable implication (with the smallest possible conditioning set) is returned per missing edge of the graph. With "basis.set", one testable implication is returned per vertex of the graph that has non-descendants other than its parents. Basis sets can be smaller, but they involve higher-dimensional independencies, whereas missing edge sets involve only independencies between two variables at a time. With "all.pairs", the function will return a list of all implied conditional independencies between two variables at a time. Beware, because this can be a very long list and it may not be feasible to compute this except for small graphs.

max.results  integer. The listing of conditional independencies is stopped once this many results have been found. Use Inf to generate them all. This applies only when type="missing.edge" or type="all".
Examples

g <- dagitty( "dag( x -> m -> y )" )
impliedConditionalIndependencies( g ) # one
latents( g ) <- c("m")
impliedConditionalIndependencies( g ) # none

impliedCovarianceMatrix

Implied Covariance Matrix of a Gaussian Graphical Model

Description

Implied Covariance Matrix of a Gaussian Graphical Model

Usage

impliedCovarianceMatrix(
  x, 
  b.default = NULL, 
  b.lower = -0.6, 
  b.upper = 0.6, 
  eps = 1, 
  standardized = TRUE 
)

Arguments

x the input graph, a DAG (which may contain bidirected edges).

b.default default path coefficient applied to arrows for which no coefficient is defined in the model syntax.

b.lower lower bound for random path coefficients, applied if b.default=NULL.

b.upper upper bound for path coefficients.

eps residual variance (only meaningful if standardized=FALSE).

standardized logical. If true, a standardized population covariance matrix is generated (all variables have variance 1).
instrumentalVariables  Find Instrumental Variables

Description

Generates a list of instrumental variables that can be used to infer the total effect of an exposure on an outcome in the presence of latent confounding, under linearity assumptions.

Usage

instrumentalVariables(x, exposure = NULL, outcome = NULL)

Arguments

x the input graph, a DAG.

exposure name of the exposure variable. If not given (default), then the exposure variable is supposed to be defined in the graph itself. Only a single exposure variable and a single outcome variable supported.

outcome name of the outcome variable, also taken from the graph if not given. Only a single outcome variable is supported.

References


Examples

# The classic IV model
instrumentalVariables( "dag( i->x->y; x<->y )", "x", "y" )

# A conditional instrumental variable
instrumentalVariables( "dag( i->x->y; x<->y ; y<-z->i )", "x", "y" )

is.dagitty  Test for Graph Class

Description

A function to check whether an object has class dagitty.

Usage

is.dagitty(x)

Arguments

x object to be tested.
isAcyclic  
Test for Cycles

Description

Returns TRUE if the given graph does not contain a directed cycle.

Usage

isAcyclic(x)

Arguments

x  
the input graph, of any graph type.

Details

This function will only consider simple directed edges in the given graph.

Examples

```r
  g1 <- dagitty("dag(X -> Y -> Z)")
  stopifnot( isTRUE(isAcyclic( g1 )) )
  g2 <- dagitty("dag(X -> Y -> Z -> X)")
  stopifnot( isTRUE(!isAcyclic( g2 )) )
  g3 <- dagitty("mag[X -- Y -- Z -- X]")
  stopifnot( isTRUE(isAcyclic( g3 )) )
```

isAdjustmentSet  
Adjustment Criterion

Description

Test whether a set fulfills the adjustment criterion, that means, it removes all confounding bias when estimating a *total* effect. This is an # Back-door criterion (Shpitser et al, 2010; van der Zander et al, 2014; Perkovic et al, 2015) which is complete in the sense that either a set fulfills this criterion, or it does not remove all confounding bias.

Usage

```r
  isAdjustmentSet(x, Z, exposure = NULL, outcome = NULL)
```
Arguments

- **x**: the input graph, a DAG, MAG, PDAG, or PAG.
- **Z**: vector of variable names.
- **exposure**: name(s) of the exposure variable(s). If not given (default), then the exposure variables are supposed to be defined in the graph itself.
- **outcome**: name(s) of the outcome variable(s), also taken from the graph if not given.

Details

If the input graph is a MAG or PAG, then it must not contain any undirected edges (=hidden selection variables).

References


---

**isCollider**

*Test for Colliders*

Description

Returns TRUE if three given variables form a collider in a given graph.

Usage

```r
isCollider(x, u, v, w)
```

Arguments

- **x**: the input graph, a DAG.
- **u**: the first endpoint of the putative collider
- **v**: the midpoint of the putative collider
- **w**: the second endpoint of the putative collider

Examples

```r
g1 <- dagitty("dag(X -> Y -> Z)")
stopifnot( isTRUE(!isCollider( g1, "X", "Y", "Z" )) )
g2 <- dagitty("dag(X -> Y <-> Z )")
stopifnot( isTRUE(isCollider( g2, "X", "Y", "Z" )) )
```
lavaanToGraph  
*Convert Lavaan Model to DAGitty Graph*

**Description**

The lavaan package is a popular package for structural equation modeling. To provide interoperability with lavaan, this function converts models specified in lavaan syntax to dagitty graphs.

**Usage**

```r
lavaanToGraph(x, digits = 3, ...)
```

**Arguments**

- `x`  
  data frame, lavaan parameter table such as returned by `lavaanify`. Can also be a lavaan object or a lavaan model string.

- `digits`  
  number of significant digits to use when representing path coefficients, if any

- `...`  
  Not used.

**Examples**

```r
if( require(lavaan) ){  
  mdl <- lavaanify("  
X ~ C1 + C3  
M ~ X + C3  
Y ~ X + M + C3 + C5  
C1 ~ C2  
C3 ~ C2 + C4  
C5 ~ C4  
C1 ~~ C2 \n C1 ~~ C3 \n C1 ~~ C4 \n C1 ~~ C5  
C2 ~~ C3 \n C2 ~~ C4 \n C2 ~~ C5  
C3 ~~ C4 \n C3 ~~ C5",fixed.x=FALSE)  
  plot( lavaanToGraph( mdl ) )
}
```

---

**localTests**  
*Test Graph against Data*

**Description**

Derives testable implications from the given graphical model and tests them against the given dataset.
Usage

localTests(
  x = NULL,
  data = NULL,
  type = c("cis", "cis.loess", "cis.chisq", "tetrads", "tetrads.within",
            "tetrads.between", "tetrads.epistemic"),
  tests = NULL,
  sample.cov = NULL,
  sample.nobs = NULL,
  conf.level = 0.95,
  R = NULL,
  max.conditioning.variables = NULL,
  tol = NULL,
  loess.pars = NULL
)

ciTest(X, Y, Z = NULL, data, ...)

Arguments

x
  the input graph, a DAG, MAG, or PDAG. Either an input graph or an explicit list of tests needs to be specified.

data
  matrix or data frame containing the data.

type
  character indicating which kind of local test to perform. Supported values are "cis" (linear conditional independence), "cis.loess" (conditional independence using loess regression), "cis.chisq" (for categorical data, based on the chi-square test), "tetrads" and "tetrads.type", where "type" is one of the items of the tetrad typology, e.g. "tetrads.within" (see vanishingTetrads). Tetrads testing is only implemented for DAGs.

tests
  list of the precise tests to perform. If not given, the list of tests is automatically derived from the input graph. Can be used to restrict testing to only a certain subset of tests (for instance, to test only those conditional independencies for which the conditioning set is of a reasonably low dimension, such as shown in the example).

sample.cov
  the sample covariance matrix; ignored if data is supplied. Either data or sample.cov and sample.nobs must be supplied.

sample.nobs
  number of observations; ignored if data is supplied.

conf.level
  determines the size of confidence intervals for test statistics.

R
  how many bootstrap replicates for estimating confidence intervals. If NULL, then confidence intervals are based on normal approximation. For tetrads, the normal approximation is only valid in large samples even if the data are normally distributed.

max.conditioning.variables
  for conditional independence testing, this parameter can be used to perform only those tests where the number of conditioning variables does not exceed the given value. High-dimensional conditional independence tests can be very unreliable.
tol bound value for tolerated deviation from local test value. By default, we perform a two-sided test of the hypothesis theta=0. If this parameter is given, the test changes to abs(theta)=tol versus abs(theta)>tol.

loess.pars list of parameter to be passed on to loess (for type="cis.loess"), for example the smoothing range.

ciTest(X,Y,Z,data) is a convenience function to test a single conditional independence independently of a DAG.

X vector of variable names.

Y vector of variable names.

Z vector of variable names.

... parameters passed on from ciTest to localTests

Details

Tetrad implications can only be derived if a Gaussian model (i.e., a linear structural equation model) is postulated. Conditional independence implications (CI) do not require this assumption. However, both Tetrad and CI implications are tested parametrically: for Tetrads, Wishart's confidence interval formula is used, whereas for CIs, a Z test of zero conditional covariance (if the covariance matrix is given) or a test of residual independence after linear regression (if the raw data is given) is performed. Both tetrad and CI tests also support bootstrapping instead of estimating parametric confidence intervals.

Examples

# Simulate full mediation model with measurement error of M1
set.seed(123)
d <- simulateSEM("dag(X->{U1 M2}->Y U1->M1}",.6,.6)

# Postulate and test full mediation model without measurement error
r <- localTests("dag( X -> {M1 M2} -> Y )", d, "cis")
plotLocalTestResults( r )

# Simulate data from example SEM
g <- getExample("Polzer")
d <- simulateSEM(g,.1,.1)

# Compute independencies with at most 3 conditioning variables
r <- localTests( g, d, "cis.loess", R=100, loess.pars=list(span=0.6),
max.conditioning.variables=3 )
plotLocalTestResults( r )

# Test independencies for categorical data using chi-square test
d <- simulateLogistic("dag(X->{U1 M2}->Y U1->M1}",2)
localTests( "dag(X->{M1 M2}->Y)", d, type="cis.chisq" )
measurementPart

Extract Measurement Part from Structural Equation Model

Description

Removes all edges between latent variables, then removes any latent variables without adjacent edges, then returns the graph.

Usage

measurementPart(x)

Arguments

x the input graph, a DAG.

Details

Assumes that x is a graph where there are edges between the latent variables, between the observed variables, and from latent to observed variables, but no edge between a latent L and an observed X may have an arrowhead at L.

moralize

Moral Graph

Description

Graph obtained from x by (1) “marrying” (inserting an undirected edge between) all nodes that have common children, and then replacing all edges by undirected edges. If x contains bidirected edges, then all sets of nodes connected by a path containing only bidirected edges are treated like a single node (see Examples).

Usage

moralize(x)

Arguments

x the input graph, a DAG, MAG, or PDAG.

Examples

# returns a complete graph
moralize("dag( x->m<y )")
# also returns a complete graph
moralize("dag( x -> m1 <-> m2 <-> m3 <-> m4 <-> y )")
names.dagitty  

Names of Variables in Graph

Description

Extracts the variable names from an input graph. Useful for iterating over all variables.

Usage

```r
## S3 method for class 'dagitty'
names(x)
```

Arguments

- `x`: the input graph, of any type.

Examples

```r
## A "DAG" with Romanian and Swedish variable names. These can be
## input using quotes to overcome the limitations on unquoted identifiers.
g <- dagitty("digraph {
  "coração" [pos="0.297,0.502"]
  "hjärta" [pos="0.482,0.387"]
  "coração" -> "hjärta"
}
")
names(g)
```

orientPDAG  

Orient Edges in PDAG.

Description

Orients as many edges as possible in a partially directed acyclic graph (PDAG) by converting induced subgraphs $X \rightarrow Y \rightarrow Z$ to $X \rightarrow Y \rightarrow Z$.

Usage

```r
orientPDAG(x)
```

Arguments

- `x`: the input graph, a PDAG.

Examples

```r
orientPDAG( "pdag { x -> y -- z }" )
```
**paths**

*Show Paths*

---

### Description

Returns a list with two components: `path` gives the actual paths, and `open` shows whether each path is open (d-connected) or closed (d-separated).

### Usage

```r
paths(
  x, 
  from = exposures(x),
  to = outcomes(x),
  Z = list(),
  limit = 100,
  directed = FALSE
)
```

### Arguments

- **x**: the input graph, a DAG, PDAG, or MAG.
- **from**: name(s) of first variable(s).
- **to**: name(s) of last variable(s).
- **Z**: names of variables to condition on for determining open paths.
- **limit**: maximum amount of paths to show. In general, the number of paths grows exponentially with the number of variables in the graph, such that path inspection is not useful except for the most simple models.
- **directed**: logical; should only directed (i.e., causal) paths be shown?

### Examples

```r
sum( paths(backDoorGraph(getExample("Shrier")))$open ) # Any open Back-Door paths?
```

---

**plot.dagitty**

*Plot Graph*

---

### Description

A simple plot method to quickly visualize a graph. This is intended mainly for simple visualization purposes and not as a full-fledged graph drawing function.
## S3 method for class 'dagitty'
plot(
    x, 
    abbreviate.names = FALSE, 
    show.coefficients = FALSE, 
    adjust.coefficients = NA, 
    ...
)

### Arguments

- **x**
  - the input graph, a DAG, MAG, or PDAG.
- **abbreviate.names**
  - logical. Whether to abbreviate variable names.
- **show.coefficients**
  - logical. Whether to plot coefficients defined in the graph syntax on the edges.
- **adjust.coefficients**
  - numerical. Adjustment for coefficient labels; the distance between the edge labels and the midpoint of the edge can be controlled using this parameter. Can also be a vector of 2 numbers for separate horizontal and vertical adjustment. NA means no adjustment (default).
- **...**
  - not used.

---

### plotLocalTestResults

Plot Results of Local Tests

### Description

Generates a summary plot of the results of local tests (see `localTests`). For each test, a test statistic and the confidence interval are shown.

### Usage

```r
plotLocalTestResults(
    x, 
    xlab = "test statistic (95% CI)", 
    xlim = range(x[, c(ncol(x) - 1, ncol(x))]), 
    sort.by.statistic = TRUE, 
    n = Inf, 
    axis.pars = list(las = 1), 
    auto.margin = TRUE, 
    ...
)
```
randomDAG

Generate DAG at Random

Description

Generates a random DAG with N variables called x1,...,xN. For each pair of variables xi,xj with i<j, an edge i->j will be present with probability p.

Usage

randomDAG(N, p)

Arguments

N desired number of variables.

p connectivity parameter, a number between 0 and 1.

Examples

d <- simulateSEM("dag(X->{U1 M2}->Y U1->M1}",.6,.6)
par(mar=c(2,8,1,1)) # so we can see the test names
plotLocalTestResults(localTests("dag( X -> {M1 M2} -> Y }", d, "cis" ))

Arguments

x data frame; results of the local tests as returned by localTests.
xlab X axis label.
xlim numerical vector with 2 elements; range of X axis.
sort.by.statistic logical. Sort the rows of x by the absolute value of the test statistic before plotting.
n plot only the n tests for which the absolute value of the test statistics diverges most from 0.
axis.pars arguments to be passed on to axis when generating the Y axis for the plot.
auto.margin logical. Computes the left margin to fit the Y axis labels.
... further arguments to be passed on to plot.
**simulateLogistic**  
*Simulate Binary Data from DAG Structure*

**Description**

Interprets input DAG as a structural description of a logistic model in which each variable is binary and its log-odds ratio is a linear combination of its parent values.

**Usage**

```r
simulateLogistic(
  x,
  b.default = NULL,
  b.lower = -0.6,
  b.upper = 0.6,
  eps = 0,
  N = 500,
  verbose = FALSE
)
```

**Arguments**

- `x`: the input graph, a DAG (which may contain bidirected edges).
- `b.default`: default path coefficient applied to arrows for which no coefficient is defined in the model syntax.
- `b.lower`: lower bound for random path coefficients, applied if `b.default=NULL`.
- `b.upper`: upper bound for path coefficients.
- `eps`: base log-odds ratio.
- `N`: number of samples to generate.
- `verbose`: logical. If true, prints the order in which the data are generated (which should be a topological order).

**simulateSEM**  
*Simulate Data from Structural Equation Model*

**Description**

Interprets the input graph as a structural equation model, generates random path coefficients, and simulates data from the model. This is a very bare-bones function and probably not very useful except for quick validation purposes (e.g. checking that an implied vanishing tetrad truly vanishes in simulated data). For more elaborate simulation studies, please use the lavaan package or similar facilities in other packages.
simulateSEM

Usage

simulateSEM(
  x,
  b.default = NULL,
  b.lower = -0.6,
  b.upper = 0.6,
  eps = 1,
  N = 500,
  standardized = TRUE,
  empirical = FALSE,
  verbose = FALSE
)

Arguments

x the input graph, a DAG (which may contain bidirected edges).

b.default default path coefficient applied to arrows for which no coefficient is defined in
  the model syntax.

b.lower lower bound for random path coefficients, applied if b.default=NULL.

b.upper upper bound for path coefficients.

eps residual variance (only meaningful if standardized=FALSE).

N number of samples to generate.

standardized logical. If true, a standardized population covariance matrix is generated (all
  variables have variance 1).

empirical logical. If true, the empirical covariance matrix will be equal to the population
  covariance matrix.

verbose logical. If true, prints the generated population covariance matrix.

Details

Data are generated in the following manner. Each directed arrow is assigned a path coefficient that
  can be given using the attribute "beta" in the model syntax (see the examples). All coefficients not
  set in this manner are set to the b.default argument, or if that is not given, are chosen uniformly at
  random from the interval given by b.lower and b.upper (inclusive; set both parameters to the same
  value for constant path coefficients). Each bidirected arrow a <-> b is replaced by a substructure a
  <- L -> b, where L is an exogenous latent variable. Path coefficients on such substructures are set
to sqrt(x), where x is again chosen at random from the given interval; if x is negative, one path
  coefficient is set to -sqrt(x) and the other to sqrt(x). All residual variances are set to eps.

If standardized=TRUE, all path coefficients are interpreted as standardized coefficients. But not all
  standardized coefficients are compatible with all graph structures. For instance, the graph structure
  z <- x -> y -> z is incompatible with standardized coefficients of 0.9, since this would imply that
  the variance of z must be larger than 1. For large graphs with many parallel paths, it can be very
difficult to find coefficients that work.

Value

Returns a data frame containing N values for each variable in x.
Examples

```r
## Simulate data with pre-defined path coefficients of -.6
g <- dagitty('dag(z -> x [beta=-.6] x <- y [beta=-.6] )')
x <- simulateSEM( g )
cov(x)
```

---

**structuralPart**  
*Extract Structural Part from Structural Equation Model*

**Description**

Removes all observed variables from the input graph.

**Usage**

```r
structuralPart(x)
```

**Arguments**

`x`  
the input graph, a DAG.

**Details**

Assumes that `x` is a graph where there are edges between the latent variables, between the observed variables, and from latent to observed variables, but no edge between a latent `L` and an observed `X` may have an arrowhead at `L`.

---

**toMAG**  
*Convert DAG to MAG.*

**Description**

Given a DAG, possibly with latent variables, construct a MAG that represents its marginal independence model.

**Usage**

```r
toMAG(x)
```

**Arguments**

`x`  
the input graph, a DAG
Examples

toMAG("dag { ParentalSmoking->Smoking (Profession [latent] ) -> {Income->Smoking) Genotype -> {Smoking->LungCancer} })")

---

topologicalOrdering Get Topological Ordering of DAG

Description

Computes a topological ordering of the nodes, i.e., a number for each node such that every node’s number is smaller than the one of all its descendants. Bidirected edges (<->) are ignored.

Usage

topologicalOrdering(x)

Arguments

x the input graph, a DAG

---

vanishingTetrads List Implied Vanishing Tetrads

Description

Interpret the given graph as a structural equation model and list all the vanishing tetrads that it implies.

Usage

vanishingTetrads(x, type = NA)

Arguments

x the input graph, a DAG.

type restrict output to one level of Kenny’s tetrad typology. Possible values are "within" (homogeneity within constructs; all four variables have the same parents), "between" (homogeneity between constructs; two pairs of variables each sharing one parent) and "epistemic" (consistency of epistemic correlations; three variables have the same parent). By default, all tetrads are listed.

Value

a data frame with four columns, where each row of the form i,j,k,l means that the tetrad Cov(i,j)Cov(k,l) - Cov(i,k)Cov(j,l) vanishes (is equal to 0) according to the model.
VariableStatus

References

Examples
# Specify two-factor model with 4 indicators each
g <- dagitty("dag{{x1 x2 x3 x4} <- x <-> y -> {y1 y2 y3 y4}}")
latents(g) <- c("x","y")

# Check how many tetrads are implied
nrow(vanishingTetrads(g))
# Check how these distribute across the typology
nrow(vanishingTetrads(g,"within"))
nrow(vanishingTetrads(g,"between"))
nrow(vanishingTetrads(g,"epistemic"))

<table>
<thead>
<tr>
<th>VariableStatus</th>
<th>Variable Statuses</th>
</tr>
</thead>
</table>

Description
Get or set variables with a given status in a graph. Variables in dagitty graphs can have one of several statuses. Variables with status exposure and outcome are important when determining causal effects via the functions adjustmentSets and instrumentalVariables. Variables with status latent are assumed to be unobserved variables or latent constructs, which is respected when deriving testable implications of a graph via the functions impliedConditionalIndependencies or vanishingTetrads.

Usage
exposures(x)
exposures(x) <- value
outcomes(x)
outcomes(x) <- value
latents(x)
latents(x) <- value
adjustedNodes(x)
adjustedNodes(x) <- value
setVariableStatus(x, status, value)
VariableStatus

Arguments
- x: the input graph, of any type.
- value: character vector; names of variables to receive the given status.
- status: character, one of "exposure", "outcome" or "latent".

Details
setVariableStatus first removes the given status from all variables in the graph that had it, and then sets it on the given variables. For instance, if status="exposure" and value="X" are given, then X will be the only exposure in the resulting graph.

Examples
```r
g <- dagitty("dag{ x<->m<->y<->x }") # m-bias graph
exposures(g) <- "x"
outcomes(g) <- "y"
adjustmentSets(g)
```
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