

Package: AncReg (via r-universe)

May 13, 2026

Title Ancestor Regression

Version 1.0.1

Description Causal discovery in linear structural equation models (Schultheiss, and Bühlmann (2023) <[doi:10.1093/biomet/asad008](https://doi.org/10.1093/biomet/asad008)>) and vector autoregressive models (Schultheiss, Ulmer, and Bühlmann (2025) <[doi:10.1515/jci-2024-0011](https://doi.org/10.1515/jci-2024-0011)>) with explicit error control for false discovery, at least asymptotically.

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Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

Imports tsutils, Rdpack, methods

Suggests pcalg, MASS, igraph, testthat (>= 3.0.0)

Config/testthat/edition 3

RdMacros Rdpack

URL <http://www.markus-ulmer.ch/AncReg/>

Config/pak/sysreqs cmake texlive libssl-dev

Repository <https://markusul.r-universe.dev>

Date/Publication 2025-07-11 13:50:08 UTC

RemoteUrl <https://github.com/markusul/ancreg>

RemoteRef HEAD

RemoteSha 7ba35e10c46bfa1070231e112ce7619efd1a8ede

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AncReg *Ancestor Regression*

Description

This function performs ancestor regression for linear structural equation models (Schultheiss et al. 2025) and vector autoregressive models (Schultheiss and Bühlmann 2023) with explicit error control for false discovery, at least asymptotically.

Usage

```
AncReg(x, degree = 0, targets = colnames(x), f = function(x) x^3)
```

Arguments

| | |
|---------|--|
| x | A named numeric matrix containing the observational data. |
| degree | An integer specifying the order of the SVAR process to be considered. Default is 0 for no time series. |
| targets | A character vector specifying the variables whose ancestors should be estimated. Default is all variables. |
| f | A function specifying the non-linearity used in the ancestor regression. Default is a cubic function. |

Value

An object of class "AncReg" containing:

| | |
|-------|--------------------------------------|
| z.val | A numeric matrix of test statistics. |
| p.val | A numeric matrix of p-values. |

References

Schultheiss C, Bühlmann P (2023). "Ancestor regression in linear structural equation models." *Biometrika*, **110**(4), 1117-1124. ISSN 1464-3510. doi:10.1093/biomet/asad008. <https://academic.oup.com/biomet/article-pdf/110/4/1117/53472115/asad008.pdf>.

Schultheiss C, Ulmer M, Bühlmann P (2025). "Ancestor regression in structural vector autoregressive models." doi:10.1515/jci20240011.

See Also

[summary.AncReg](#), [instant_graph](#), [summary_graph](#), [instant_p.val](#), [summary_p.val](#)

Examples

```
##### simulated example for linear structural equation models

# random DAGs for simulation
set.seed(1234)

p <- 5 #number of nodes
DAG <- pcalg::randomDAG(p, prob = 0.5)

B <- matrix(0, p, p) # represent DAG as matrix
for (i in 2:p){
  for(j in 1:(i-1)){
    # store edge weights
    B[i,j] <- max(0, DAG@edgeData@data[[paste(j,"|",i, sep="")]]$weight)
  }
}
colnames(B) <- rownames(B) <- LETTERS[1:p]

# solution in terms of noise
Bprime <- MASS::ginv(diag(p) - B)

n <- 5000
N <- matrix(rexp(n * p), ncol = p)
X <- t(Bprime %*% t(N))
colnames(X) <- LETTERS[1:p]

# fit ancestor regression
fit <- AncReg(X)
# collect ancestral p-values and graph
res <- summary(fit)
res

#compare true and estimated ancestral graph
trueGraph <- igraph::graph_from_adjacency_matrix(recAncestor(B != 0))
ancGraph <- igraph::graph_from_adjacency_matrix(res$graph)

oldpar <- par(mfrow = c(1, 2))
plot(trueGraph, main = 'true ancestral graph', vertex.size = 30)
plot(ancGraph, main = 'Ancestor Regression', vertex.size = 30)

##### SVAR-example with geysers timeseries
geyser <- MASS::geyser
# shift waiting such that it is waiting after eruption
geyser2 <- data.frame(waiting = geyser$waiting[-1], duration = geyser$duration[-nrow(geyser)])

# fit ancestor regression with 6 lags considered
fit2 <- AncReg(as.matrix(geyser2), degree = 6)
res2 <- summary(fit2)
res2

# visualize instantaneous ancestry
instGraph <- igraph::graph_from_adjacency_matrix(res2$inst.graph)
```

```

plot(instGraph, edge.label = round(diag(res2$inst.p.val[1:2, 2:1]), 2),
     main = 'instantaneous effects', vertex.size = 90)

# visualize summary of lagged ancestry
sumGraph <- igraph::graph_from_adjacency_matrix(res2$sum.graph)
plot(sumGraph, edge.label = round(diag(res2$sum.p.val[1:2, 2:1]), 2),
     main = 'summary graph', vertex.size = 90)
par(oldpar)

```

instant_graph

Instantaneous graph

Description

Construct instantaneous graph from p-values and significance level. Recursively constructs all ancestral connections by adding ancestors of ancestors.

Usage

```
instant_graph(lin.anc, alpha = 0.05, verbose = FALSE, corr = TRUE)
```

Arguments

| | |
|---------|--|
| lin.anc | output from AncReg() |
| alpha | significance level |
| verbose | should information be printed? |
| corr | should multiplicity correction be applied? |

Value

A list containing:

| | |
|----------|--|
| rec.ancs | A boolean matrix indicating whether one variable affects another instantaneously |
| alpha | The significance level to avoid cycles |

See Also

[AncReg](#), [instant_p.val](#)

Examples

```

# random DAGS for simulation
set.seed(1234)

p <- 5 #number of nodes
DAG <- pcalg::randomDAG(p, prob = 0.5)

B <- matrix(0, p, p) # represent DAG as matrix

```

```
for (i in 2:p){
  for(j in 1:(i-1)){
    # store edge weights
    B[i,j] <- max(0, DAG@edgeData@data[[paste(j,"|",i, sep="")]]$weight)
  }
}
colnames(B) <- rownames(B) <- LETTERS[1:p]

# solution in terms of noise
Bprime <- MASS::ginv(diag(p) - B)

n <- 500
N <- matrix(rexp(n * p), ncol = p)
X <- t(Bprime %*% t(N))
colnames(X) <- LETTERS[1:p]

# fit ancestor regression
fit <- AncReg(X)

# generate instantaneous graph
instant_graph(fit, alpha = 0.01, verbose = TRUE)
```

instant_p.val

P-values for instantaneous graph

Description

Collect p-values for instantaneous graph.

Usage

```
instant_p.val(lin.anc)
```

Arguments

lin.anc output from AncReg()

Value

A numeric matrix of p-values for the instantaneous graph

See Also

[AncReg](#)

Examples

```

# random DAGS for simulation
set.seed(1234)

p <- 5 #number of nodes
DAG <- pcalg::randomDAG(p, prob = 0.5)

B <- matrix(0, p, p) # represent DAG as matrix
for (i in 2:p){
  for(j in 1:(i-1)){
    # store edge weights
    B[i,j] <- max(0, DAG@edgeData@data[[paste(j,"|",i, sep=")"]])$weight)
  }
}
colnames(B) <- rownames(B) <- LETTERS[1:p]

# solution in terms of noise
Bprime <- MASS::ginv(diag(p) - B)

n <- 500
N <- matrix(rexp(n * p), ncol = p)
X <- t(Bprime %*% t(N))
colnames(X) <- LETTERS[1:p]

# fit ancestor regression
fit <- AncReg(X)

# collect instantaneous p-values
instant_p.val(fit)

```

recAncestor

Recursive Ancestor Detection

Description

This function recursively detects all ancestors of a given set of variables in a matrix. Adds ancestors of ancestors to the output matrix.

Usage

```
recAncestor(pmat)
```

Arguments

`pmat` A boolean matrix indicating whether a connection was detected.

Value

A boolean matrix indicating whether a connection was detected or constructed.

See Also[AncReg](#), [summary_graph](#)**Examples**

```
# random DAGS for simulation
set.seed(1234)

p <- 5 #number of nodes
DAG <- pcalg::randomDAG(p, prob = 0.5)

B <- matrix(0, p, p) # represent DAG as matrix
for (i in 2:p){
  for(j in 1:(i-1)){
    # store edge weights
    B[i,j] <- max(0, DAG@edgeData@data[[paste(j,"|",i, sep=")"]])$weight)
  }
}
colnames(B) <- rownames(B) <- LETTERS[1:p]

# edge effects to adjacency matrix
B <- B != 0

# transform adjacency matrix to ancestral matrix
recAncestor(B)
```

summary.AncReg

*Summary of AncReg***Description**

Summarize the results of AncReg. For models with degree = 0 only the instantaneous graph is returned and for models with degree > 0 the summary graph is returned as well.

Usage

```
## S3 method for class 'AncReg'
summary(object, alpha = 0.05, verbose = FALSE, corr = TRUE, ...)
```

Arguments

| | |
|---------|---|
| object | output from AncReg() |
| alpha | significance level for determin whether a connection is significant |
| verbose | should information be printed? |
| corr | should multiplicity correction be applied? |
| ... | Further arguments passed to or from other methods. |

Value

A list containing: If degree = 0:

p.val A numeric matrix of p-values for the instantaneous graph
 graph A boolean matrix indicating whether one variable affects another instantaneously
 alpha The significance level to avoid cycles

If degree > 0:

inst.p.val A numeric matrix of p-values for the instantaneous graph
 inst.graph A boolean matrix indicating whether one variable affects another instantaneously
 inst.alpha The significance level to avoid cycles
 sum.p.val A numeric matrix of p-values for the summary graph
 sum.graph A boolean matrix indicating whether one variable affects another

See Also

[AncReg](#), [instant_graph](#), [summary_graph](#), [instant_p.val](#), [summary_p.val](#)

Examples

```
# random DAGS for simulation
set.seed(1234)

p <- 5 #number of nodes
DAG <- pcalg::randomDAG(p, prob = 0.5)

B <- matrix(0, p, p) # represent DAG as matrix
for (i in 2:p){
  for(j in 1:(i-1)){
    # store edge weights
    B[i,j] <- max(0, DAG@edgeData@data[[paste(j,"|",i, sep="")]]$weight)
  }
}
colnames(B) <- rownames(B) <- LETTERS[1:p]

# solution in terms of noise
Bprime <- MASS::ginv(diag(p) - B)

n <- 500
N <- matrix(rexp(n * p), ncol = p)
X <- t(Bprime %*% t(N))
colnames(X) <- LETTERS[1:p]

# fit ancestor regression
fit <- AncReg(X)
# collect ancestral p-values and graph
res <- summary(fit, alpha = 1)
res
```

| | |
|---------------|----------------------|
| summary_graph | <i>Summary graph</i> |
|---------------|----------------------|

Description

Construct summary graph from p-values and significance level. Recursively constructs all ancestral connections by adding ancestors of ancestors.

Usage

```
summary_graph(lin.anc, alpha = 0.05, corr = TRUE)
```

Arguments

| | |
|---------|--|
| lin.anc | output from AncReg() |
| alpha | significance level |
| corr | should multiplicity correction be applied? |

Value

A boolean matrix indicating whether one variable affects another

See Also

[AncReg](#), [summary_p.val](#)

Examples

```
# random DAGS for simulation
set.seed(1234)

p <- 5 #number of nodes
DAG <- pcalg::randomDAG(p, prob = 0.5)

B <- matrix(0, p, p) # represent DAG as matrix
for (i in 2:p){
  for(j in 1:(i-1)){
    # store edge weights
    B[i,j] <- max(0, DAG@edgeData@data[[paste(j,"|",i, sep=")"]])$weight)
  }
}
colnames(B) <- rownames(B) <- LETTERS[1:p]

# solution in terms of noise
Bprime <- MASS::ginv(diag(p) - B)

n <- 500
N <- matrix(rexp(n * p), ncol = p)
X <- t(Bprime %*% t(N))
```

```

colnames(X) <- LETTERS[1:p]

# fit ancestor regression
fit <- AncReg(X)

# generate summary graph
summary_graph(fit, alpha = 0.1)

```

summary_p.val

P-values for summary graph

Description

Collect p-values for summary graph.

Usage

```
summary_p.val(lin.anc)
```

Arguments

lin.anc output from AncReg()

Value

A numeric matrix of p-values for the summary graph

See Also

[AncReg](#)

Examples

```

# random DAGS for simulation
set.seed(1234)

p <- 5 #number of nodes
DAG <- pcalg::randomDAG(p, prob = 0.5)

B <- matrix(0, p, p) # represent DAG as matrix
for (i in 2:p){
  for(j in 1:(i-1)){
    # store edge weights
    B[i,j] <- max(0, DAG@edgeData@data[[paste(j,"|",i, sep="")]]$weight)
  }
}
colnames(B) <- rownames(B) <- LETTERS[1:p]

# solution in terms of noise
Bprime <- MASS::ginv(diag(p) - B)

```

```
n <- 500
N <- matrix(rexp(n * p), ncol = p)
X <- t(Bprime %% t(N))
colnames(X) <- LETTERS[1:p]

# fit ancestor regression
fit <- AncReg(X)

# collect summary p-values
summary_p.val(fit)
```

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