Package 'ess'

January 10, 2026

Title Efficient Stepwise Selection in Decomposable Models

Version 1.1.2.1

Description An implementation of the ESS algorithm following Amol Deshpande, Minos Garofalakis, Michael I Jordan (2013) <doi:10.48550/arXiv.1301.2267>. The ESS algorithm is used for model selection in decomposable graphical models.

URL https://github.com/mlindsk/ess

Depends R (>= 3.5.0)

License GPL-3

Encoding UTF-8

LazyData true

Imports Rcpp, igraph

LinkingTo Rcpp

RoxygenNote 7.1.1

Suggests tinytest

BugReports https://github.com/mlindsk/ess/issues

NeedsCompilation yes

Author Mads Lindskou [aut, cre]

Maintainer Mads Lindskou <mads@math.aau.dk>

Repository CRAN

Date/Publication 2026-01-10 16:08:14 UTC

Contents

`ess-package` *ess: Eficient Stepwise Selection in Decomposable Models*

Description

The class of graphical models is a family of probability distributions for which conditional dependencies can be read off from a graph. If the graph is decomposable, the maximum likelihood estimates of the parameters in the model can be shown to be on exact form. This is what enables ESS to be fast and efficient for model selection in decomposable graphical models.

Author(s)

Maintainer: Mads Lindskou <mads@math.aau.dk>

See Also

Useful links:

- https://github.com/mlindsk/ess
- Report bugs at https://github.com/mlindsk/ess/issues

adj_lst *Adjacency List*

Description

Extracts the adjacency list of a gengraph

Usage

```
adj_lst(x)

## S3 method for class 'gengraph'
adj_lst(x)
```

Arguments

x	gengraph

Value

An adjacency list

adj_mat *Adjacency Matrix*

Description

Extracts the adjacency matrix of a gengraph object

Usage

```
adj_mat(x)

## S3 method for class 'gengraph'
adj_mat(x)
```

Arguments

x	gengraph object

Value

An adjacency matrix

as_adj_lst *Converts an adjacency matrix to an adjacency list*

Description

Converts an adjacency matrix to an adjacency list

Usage

```
as_adj_lst(A)
```

Arguments

A	Adjacency matrix

as_adj_mat *Converts an adjacency list to an adjacency matrix*

Description

Converts an adjacency list to an adjacency matrix

Usage

```
as_adj_mat(adj)
```

Arguments

adj	Adjacency list

Value

An adjacency matrix

Examples

```
adj <- list(a = c("b", "d"), b = c("a", "c", "d"), c = c("b", "d"), d = c("a", "c", "b"))
as_adj_mat(adj)
```

as_igraph *Gengraph as igraph*

Description

Convert a gengraph object to an igraph object

Usage

```
as_igraph(x)

## S3 method for class 'gengraph'
as_igraph(x)
```

Arguments

x	gengraph object

Value

An igraph object

components *Finds the components of a graph*

Description

Finds the components of a graph

Usage

```
components(adj)
```

Arguments

adj	Adjacency list or gengraph object

Value

A list where the elements are the components of the graph

derma *Dermatology Database*

Description

This data set contains 358 observations (we have removed 8 with missing values). It contains 12 clinical attributes and 21 histopathological attributes. The age attribute has been discretized. The class variable "ES" has six levels; each describing a skin disease.

Usage

```
derma
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 358 rows and 35 columns.

References

Dermatology Data Set

dfs *Depth First Search*

Description

Finds the elements in the component of `root`

Usage

```
dfs(adj, root)
```

Arguments

`adj`	A named adjacency list of a decomposable grah
`root`	The node from which the component should be found

Value

All nodes connected to `root`

Examples

```
x <- list(a = c("b", "d"), b = c("a", "d"), c = c("b", "a"),
          d = c("e", "f"), e = c("d", "f"), f = c("d", "e"))
dfs(x, "a")
```

`dgm_sim_from_graph` *Simulate observations from a decomposable graphical model*

Description

Simulate observations from a decomposable graphical model

Usage

```
dgm_sim_from_graph(g, lvls, nsim = 1000, cell_rate = 0.5)
```

Arguments

`g`	An adjacency list
`lvls`	Named list with levels of the discrete variables
`nsim`	Number of simulations
`cell_rate`	Control discrete cell probabilities

Value

This function returns a matrix of dimension where each row correspond to a simulated observation from a DGM represented by g.

Examples

```
g = list(
  A = c("B", "X", "Y"),
  B = c("A", "Y"),
  X = c("A", "Y"),
  Y = c("A", "X", "B")
)

lvls <- list(
  A = c("0", "1"),
  B = c("0", "1"),
  X = c("a", "b", "c"),
  Y = c("0", "1", "2")
)

dgm_sim_from_graph(g, lvls, nsim = 10)
#'
```

entropy *Joint Entropy*

Description

Calculates the joint entropy over discrete variables in `df`

Usage

```
entropy(df, thres = 5, npc = new.env())
```

Arguments

`df`	data.frame
`thres`	A threshold mechanism for choosing between two different ways of calculating the entropy. Can Speed up the procedure with the "correct" value.
`npc`	An environment. If supplied, the number of positive cells in the underlying pmf will be stored in the environment with the name `value`

Value

A number representing the entropy of the variables in `df`.

Examples

```
entropy(derma[1:100, 1:3])
```

fit_components *Fit a decomposable graphical model on each component*

Description

Structure learning in decomposable graphical models on several components

Usage

```
fit_components(
  df,
  comp,
  type = "fwd",
  q = 0.5,
  trace = FALSE,
  thres = 5,
  wrap = TRUE
)
```

Arguments

df	Character data.frame
comp	A list with character vectors. Each element in the list is a component in the graph (using expert knowledge)
type	Character ("fwd", "bwd", "tree" or "tfwd")
q	Penalty term in the stopping criterion where 0 = AIC and 1 = BIC. Anything in between is referred to as qic
trace	Logical indicating whether or not to trace the procedure
thres	A threshold mechanism for choosing between two different ways of calculating the entropy.
wrap	logical specifying if the result of a run with type = "tree" should be converted to a "fwd" object

Value

An adjacency list object

See Also

fit_graph, adj_lst.gengraph, adj_mat.gengraph, walk.fwd, walk.bwd, gengraph

---

fit_graph *Fit a decomposable graphical model*

Description

A generic method for structure learning in decomposable graphical models

Usage

```
fit_graph(
  df,
  type = "fwd",
  q = 0.5,
  trace = FALSE,
  sparse_qic = FALSE,
  thres = 5,
  wrap = TRUE
)
```

Arguments

df	Character data.frame
type	Character ("fwd", "bwd", "tree" or "tfwd")
q	Penalty term in the stopping criterion where 0 = AIC and 1 = BIC. Anything in between is referred to as qic
trace	Logical indicating whether or not to trace the procedure
sparse_qic	Logical. If nrow(df) is small, the tables tends to be sparse. In these cases the usual penalty term of AIC and BIC is often too restrictive. If sparse_qic is TRUE this penality is computed according to a sparse criteria. The criteria resembles the usual penalty as nrow(df) grows.
thres	A threshold mechanism for choosing between two different ways of calculating the entropy.
wrap	logical specifying if the result of a run with type = "tree" should be converted to a "fwd" object

Details

The types are

- "fwd": forward selection
- "bwd": backward selection
- "tree": Chow-Liu tree (first order interactions only)
- "tfwd": A combination of "tree" and "fwd". This can speed up runtime considerably in high dimensions.

Using adj_lst on an object returned by fit_graph gives the adjacency list corresponding to the graph. Similarly one can use adj_mat to obtain an adjacency matrix. Applying the rip function on an adjacency list returns the cliques and separators of the graph.

Value

A gengraph object representing a decomposable graph.

References

https://arxiv.org/abs/1301.2267, doi:10.1109/ictai.2004.100

See Also

adj_lst, adj_mat, as_igraph, gengraph

Examples

```
g <- fit_graph(derma)
print(g)
plot(g)

# Adjacency matrix and adjacency list
adjm <- adj_mat(g)
adjl <- adj_lst(g)
```

---

gengraph *A generic and extendable structure for decomposable graphical models*

Description

A generic structure for decomposable graphical models

Usage

```
gengraph(df, type = "fwd", q = 0.5, sparse_qic = TRUE)
```

Arguments

df	Character data.frame
type	Character ("fwd", "bwd", "tree" or "tfwd")
q	Penalty term in the stopping criterion where 0 = AIC and 1 = BIC. Anything in between is referred to as qic
sparse_qic	Logical. If nrow(df) is small, the tables tends to be sparse. In these cases the usual penalty term of AIC and BIC is often too restrictive. If sparse_qic is TRUE this penality is computed according to a sparse criteria. The criteria resembles the usual penalty as nrow(df) grows.

Value

A gengraph object with child class type used for model selection.

See Also

adj_lst.gengraph, adj_mat.gengraph, fit_graph, walk.fwd, walk.bwd

Examples

```
gengraph(derma, type = "fwd")
gengraph(derma, type = "bwd")
```

is_decomposable *A test for decomposability in undirected graphs*

Description

This function returns TRUE if the graph is decomposable and FALSE otherwise

Usage

```
is_decomposable(adj)
```

Arguments

adj	Adjacency list of an undirected graph

Value

Logial describing whether or not adj is decomposable

Examples

```
# 4-cycle:
adj <- list(a = c("b", "d"), b = c("a", "c"), c = c("b", "d"), d = c("a", "c"))
is_decomposable(adj) # FALSE
# Two triangles:
adj2 <- list(a = c("b", "d"), b = c("a", "c", "d"), c = c("b", "d"), d = c("a", "c", "b"))
is_decomposable(adj2) # TRUE
```

make_complete_graph *Make a complete graph*

Description

A helper function to make an adjacency list corresponding to a complete graph

Usage

```
make_complete_graph(nodes)
```

Arguments

nodes	A character vector containing the nodes to be used in the graph

Value

An adjacency list of a complete graph

Examples

```
d  <- derma[, 5:8]
cg <- make_complete_graph(colnames(d))
```

---

make_null_graph *Make a null graph*

Description

A helper function to make an adjacency list corresponding to a null graph (no edges)

Usage

```
make_null_graph(nodes)
```

Arguments

nodes	A character vector containing the nodes to be used in the graph

Value

An adjacency list the null graph with no edges

Examples

```
d  <- derma[, 5:8]
ng <- make_null_graph(colnames(d))
```

---

mcs *Maximum Cardinality Search*

Description

Maximum Cardinality Search

Usage

```
mcs(adj, check = TRUE)
```

Arguments

adj	A named adjacency list of a decomposable graph
check	Boolean: check if adj is decomposable

Details

If adj is not the adjacency list of a decomposable graph an error is raised

Value

A list with a perfect numbering of the nodes and a perfect sequence of sets

Examples

```
x <- list(a = c("b", "d"), b = c("a", "c", "d"), c = c("b", "d"), d = c("a", "c", "b"))
mcs(x)
```

`plot.gengraph` *Plot*

Description

A wrapper around igraphs plot method for gengraph objects

Usage

```
## S3 method for class 'gengraph'
plot(x, vc = NULL, ...)
```

Arguments

x	A gengraph object
vc	Named character vector; the names are the vertices and the elements are the colors of the nodes
...	Extra arguments. See the igraph package

Value

No return value, called for side effects

Examples

```
d <- derma[, 10:25]
g <- fit_graph(d)
vs <- colnames(d)
vcol <- structure(vector("character", length(vs)), names = vs)
vcol[1:4]  <- "lightsteelblue2"
vcol[5:7]  <- "orange"
vcol[8:16] <- "pink"
plot(g, vcol)
```

print.gengraph *Print*

Description

A print method for gengraph objects

Usage

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

Arguments

x	A gengraph object
...	Not used (for S3 compatability)

print.tree *Print*

Description

A print method for tree objects

Usage

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

Arguments

x	A tree object
...	Not used (for S3 compatability)

rip *Runnining Intersection Property*

Description

Given a decomposable graph, this functions finds a perfect numbering on the vertices using maximum cardinality search, and hereafter returns a list with two elements: "C" - A RIP-ordering of the cliques and "S" - A RIP ordering of the separators.

Usage

```
rip(adj, check = TRUE)
```

Arguments

adj	A named adjacency list of a decomposable graph
check	Boolean: check if adj is decomposable

Value

A list with cliques and separators of adj

See Also

mcs, is_decomposable

Examples

```
x <- list(a = c("b", "d"), b = c("a", "c", "d"), c = c("b", "d"), d = c("a", "c", "b"))
y <- rip(x)
# Cliques:
y$C
# Separators:
y$S
```

subgraph *Subgraph*

Description

Construct a subgraph with a given set of nodes removed

Usage

```
subgraph(x, g)
```

Arguments

x	Character vector of nodes
g	Adjacency list (named) or a adjacency matrix with dimnames given as the nodes

Value

An adjacency list or adjacency matrix.

Examples

```
adj <- list(a = c("b", "d"), b = c("a", "c", "d"), c = c("b", "d"), d = c("a", "c", "b"))
d <- data.frame(a = "", b = "", c ="", d = "") # Toy data so we can plot the graph
subgraph(c("c", "b"), adj)
subgraph(c("b", "d"), as_adj_mat(adj))
```

---

walk *Stepwise model selection*

Description

Stepwise model selection in decomposable graphical models

Usage

```
walk(x, df, q, thres)
```

Arguments

x	fwd or bwd objects
df	data.frame
q	Penalty term in the stopping criterion (0 = AIC and 1 = BIC)
thres	A threshold mechanism for choosing between two different ways of calculating the entropy. Can Speed up the procedure with the "correct" value.

Details

A fwd (or bwd) object can be created using the gengraph constructor with type = "fwd".

Value

A fwd or bwd object with one additional edge than the input object.

See Also

fit_graph, walk.fwd, gengraph

Examples

```
d <- derma[, 10:25]

g <- gengraph(d, type = "fwd")
s <- walk(g, d)
print(s)
plot(s)
adj_lst(s)
adj_mat(s)
```

`walk.bwd` *Stepwise backward selection*

Description

Stepwise backward selection in decomposable graphical models

Usage

```
## S3 method for class 'bwd'
walk(x, df, q = 0.5, thres = 5)
```

Arguments

`x`	gengraph
`df`	data.frame
`q`	Penalty term in the stopping criterion (`0` = AIC and `1` = BIC)
`thres`	A threshold mechanism for choosing between two different ways of calculating the entropy. Can Speed up the procedure with the "correct" value.

Details

A `bwd` object can be created using the `gengraph` constructor with `type = "bwd"`

Value

A `bwd` object; a subclass of `gengraph`) used for backward selection.

See Also

`fit_graph`, `walk.fwd`, `gengraph`

Examples

```
d <- derma[, 10:25]

g <- gengraph(d, type = "bwd")
s <- walk(g, d)
print(s)
plot(s)
adj_lst(s)
adj_mat(s)
```

`walk.fwd` *Stepwise efficient forward selection in decomposable graphical models*

Description

Stepwise efficient forward selection in decomposable graphical models

Usage

```
## S3 method for class 'fwd'
walk(x, df, q = 0.5, thres = 5)
```

Arguments

`x`	A `fwd` object
`df`	data.frame
`q`	Penalty term in the stopping criterion (`0` = AIC and `1` = BIC)
`thres`	A threshold mechanism for choosing between two different ways of calculating the entropy. Can Speed up the procedure with the "correct" value.

Details

A `fwd` object can be created using the `gengraph` constructor with `type = "fwd"`

Value

A `fwd` object; a subclass of `gengraph`) used for forward selection.

References

https://arxiv.org/abs/1301.2267, doi:10.1109/ictai.2004.100

See Also

`fit_graph`, `walk.bwd`, `gengraph`

Examples

```
d <- derma[, 10:25]

g <- gengraph(d, type = "fwd")
s <- walk(g, d)
print(s)
plot(s)
adj_lst(s)
adj_mat(s)
```

Index