Package 'IMaGES'

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Title Independent Multiple-Sample Greedy Equivalence Search
Implementation

Description Functions for the implementation of Independent Multiple-sample
Greedy Equivalence Search (IMaGES), a causal inference algorithm for creating
aggregate graphs and structural equation modeling data for one or more
datasets. This package is useful for time series data with specific regions of
interest. This implementation is inspired by the paper ``Six problems
for causal inference from fMRI'' by Ramsey, Hanson, Hanson, Halchenko, Poldrack,
and Glymour (2010) <DOI:10.1016/j.neuroimage.2009.08.065>. The IMaGES algo-
rithm uses a modified BIC score to compute goodness
of fit of edge additions, subtractions, and turns across all datasets and
returns a representative graph, along with structural equation modeling data for
the global graph and individual datasets, means, and standard errors. Functions
for plotting the resulting graph(s) are provided. This package is built upon the
'pcalg' package.

Maintainer Noah Frazier-Logue <n.frazier.logue@nyu.edu>

Author Noah Frazier-Logue [aut, cre],
Stephen Jose Hanson [aut],
Markus Kalisch [ctb],
Alain Hauser [ctb],
Martin Maechler [ctb],
Diego Colombo [ctb],
Doris Entner [ctb],
Patrik Hoyer [ctb],
Antti Hyttinen [ctb],
Jonas Peters [ctb],
Nicoletta Andri [ctb],
Emilija Perkovic [ctb],
Preetam Nandy [ctb],
Philipp Ruetimann [ctb],
Daniel Stekhoven [ctb],
Manuel Schuerch [ctb]

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R **topics documented:**

IMaGES	*Estimate the DAG and Markov equivalence class of multiple datasets using the IMaGES algorithm*

Description

Estimate the DAG using the IMaGES algorithm of Ramsey, Hanson, Hanson, Halchenko, Poldrack, Glymour (2010). Adapted from 'GES' as implemented in the 'pcalg' package.

Usage

```
IMaGES(matrices, penalty=3, num.markovs=5,
       use.verbose=FALSE)
```

Arguments

`matrices`	A list of (at least one) matrix object(s) to run in the algorithm
`penalty`	Node labels; by default, they are determined from the scoring object.
`num.markovs`	Number of graphs to store in the Markov equivalence class.
`use.verbose`	boolean value indicating whether or not the run will output things such as step direction, current IMScore, step number, and whether or not early stopping is kicking in.

Details

IMaGES (Independent Multi-sample Greedy Equivalence Search) is a score-based algorithm that greedily maximizes a score function similar to the one used in the pcalg implementation of GES. It modifies the scoring by creating a global score across all datasets and uses this score to determine which step from the individual datasets best represents all of the datasets. It accomplishes this by using forward, backward, and turning steps as described below:

Forward phase In the forward phase, IMaGES moves through the space of essential graphs in steps that correspond to the addition of a single edge in the space of DAGs; the phase is aborted as soon as the score cannot be augmented any more.

Backward phase In the backward phase, the algorithm performs moves that correspond to the removal of a single edge in the space of DAGs until the score cannot be augmented any more.

Turning phase In the turning phase, the algorithm performs moves that correspond to the reversal of a single arrow in the space of DAGs until the score cannot be augmented any more.

During each step, the IMaGES algorithm simulates the addition, deletion, or turning of an edge for each individual dataset. The step that most augments the score (each edge is assigned a SEM BIC score) for the individual dataset is selected, and the global step across all datasets is selected by finding the most commonly recommended step. The algorithm then executes that step and updated the IMScore accordingly. This repeats for (number of nodes)**2 or until the algorithm detects that no steps augment the score for five consecutive iterations (also known as 'early stopping').

These operations are carried out and result in a global representative graph and a Markov Equivalence Class.

Value

IMaGES returns a list with the following components:

`results`	A named list containing:
	`global` a named list containing `.graph`, the global graphNEL object, and `.params`, the Structural Equation Modeling data for the global graph
	`.single.graphs` a list containing named lists of the same structure as above that corresponds to each individual dataset passsed into IMaGES
	`.markovs` a list containing named lists of the same structure as above that corresponds to each Markov Equivalence Class (the size of which is specified by the user)
	`.means` a list containing the mean values for the SEM data for each edge in the graph

.std.errs a list containing the standard errors for the SEM data for each edge
            in the graph

.graphs   A list containing the individual graph information, including raw graph data,
                 score information, and intermediary variables

Author(s)

Noah Frazier-Logue (`<n.frazier.logue@nyu.edu>`)

Stephen Jose Hanson (`<jose@rubic.rutgers.edu>`)

References

J.D. Ramsey, S.J. Hanson, et al. (2010) Six problems for causal inference from fMRI. *NeuroImage* **49**, 1545-1558.

D.M. Chickering (2002). Optimal structure identification with greedy search. *Journal of Machine Learning Research* **3**, 507–554

A. Hauser and P. Bühlmann (2012). Characterization and greedy learning of interventional Markov equivalence classes of directed acyclic graphs. *Journal of Machine Learning Research* **13**, 2409–2464.

P. Nandy, A. Hauser and M. Maathuis (2015). Understanding consistency in hybrid causal structure learning. *arXiv preprint* 1507.02608

P. Spirtes, C.N. Glymour, and R. Scheines (2000). *Causation, Prediction, and Search*, MIT Press, Cambridge (MA).

See Also

plotIMGraph, plotAll, plotMarkovs

Examples

```
library(graph)
## Load predefined data
data(IMData)
data(IMTrue)

#run IMaGES
im.fits <- IMaGES(matrices=IMData, penalty=3, num.markovs=5)

#plot global graph and all individual graphs with own SEM data
plotAll(im.fits)

#plot true individual graphs as a comparison
for (i in 1:length(IMTrue)) {
  plot(IMTrue[[1]])
}

#plot graph with SEM data from first dataset
plotIMGraph(im.fits$.single.graph[[1]])
```

```
#plot MEC
plotMarkovs(im.fits)

#print mean SEM values for each edge
print(im.fits$.means)

#print standard errors for each edge
print(im.fits$.std.errs)
```

IMData *IMaGES Test Data*

Description

Test data to be used with IMaGES. Included is a list called `IMData`, a list containing three data files that can be passed into IMaGES.

Usage

```
data(IMData)
```

Format

Objects of class `"list"`.

Examples

```
data(IMData)

result <- IMaGES(matrices=IMData)

plotAll(result)
```

IMTrue *IMaGES Test Data*

Description

Test data to be used with IMaGES. Included is a list called `IMTrue`, a list containing the original graph structures for each dataset in `IMTrue`.

Usage

```
data(IMData)
```

Format

Objects of class "list".

Examples

```
data(IMData)
data(IMTrue)

result <- IMaGES(matrices=IMData)

plotAll(result)

par(mfrow=c(1,length(IMTrue)))

for (i in 1:length(IMTrue)) {
  graph::plot(IMTrue[[i]])
}
```

---

plotAll   *plotAll*

Description

This function takes the object returned by an IMaGES run and plots the global structure with its SEM (structural equation modeling) data, as well as the SEM data for each dataset imposed on the global structure. The function determines the dimensions that most closely represent a square and plots the graphs in that fashion.

Usage

```
plotAll(im.fits)
```

Arguments

im.fits   Object returned by IMaGES run

Value

plot   Prints plot to the screen

Author(s)

Noah Frazier-Logue (<n.frazier.logue@nyu.edu>)

Stephen Jose Hanson (<jose@rubic.rutgers.edu>)

References

J.D. Ramsey, S.J. Hanson, et al. (2010) Six problems for causal inference from fMRI. *NeuroImage* **49**, 1545-1558.

See Also

[plotIMGraph](#), [plotMarkovs](#), [IMaGES](#)

Examples

```
## Load predefined data
data(IMData)

#run IMaGES
im.fits <- IMaGES(matrices=IMData, penalty=3, num.markovs=5)

#plot global graph and all individual graphs with own SEM data
plotAll(im.fits)
```

---

plotIMGraph   *plotIMGraph*

Description

This function takes a graph object returned from IMaGES (takes the form of a named list containing .graph and .params) and plots it. Using plotAll or plotMarkovs is recommended unless you only want to see one specific graph.

Usage

```
plotIMGraph(graph.object, title="Global")
```

Arguments

graph.object   Graph object returned as part of IMaGES run

title   Title of resulting plot of IMGraph

Value

plot   Prints plot to the screen

Author(s)

Noah Frazier-Logue (<n.frazier.logue@nyu.edu>)

Stephen Jose Hanson (<jose@rubic.rutgers.edu>)

References

J.D. Ramsey, S.J. Hanson, et al. (2010) Six problems for causal inference from fMRI. *NeuroImage* **49**, 1545-1558.

See Also

[plotMarkovs](#), [plotAll](#), [IMaGES](#)

Examples

```
## Load predefined data
data(IMData)

#run IMaGES
im.fits <- IMaGES(matrices=IMData, penalty=3, num.markovs=5)

#plot individual graph
plotIMGraph(im.fits$.single.graph[[1]], title="Global")
```

---

plotMarkovs	*plotMarkovs*

Description

This function takes the object returned by an IMaGES run and plots the global structure with its SEM (structural equation modeling) data, as well as the SEM data for each Markov Equivalence Class (MEC) and their respective structures. The function determines the dimensions that most closely represent a square and plots the graphs in that fashion.

Usage

```
## Load predefined data
data(IMData)

plotMarkovs(im.fits)
```

Arguments

im.fits   Object returned by IMaGES run

Value

plot   Prints plot to the screen

Author(s)

Noah Frazier-Logue (<n.frazier.logue@nyu.edu>)

Stephen Jose Hanson (<jose@rubic.rutgers.edu>)

References

J.D. Ramsey, S.J. Hanson, et al. (2010) Six problems for causal inference from fMRI. *NeuroImage* **49**, 1545-1558.

See Also

plotIMGraph, plotAll, IMaGES

Examples

```
## Load predefined data
data(IMData)

#run IMaGES
im.fits <- IMaGES(matrices=IMData, penalty=3, num.markovs=5)

#plot global graph and all individual graphs with own SEM data
plotMarkovs(im.fits)
```

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