

Package ‘piecewiseSEM’

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Type Package

Title Piecewise Structural Equation Modeling

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Description Implements piecewise structural equation modeling from a single list of structural equations, with new methods for non-linear, latent, and composite variables, standardized coefficients, query-based prediction and indirect effects. See <<http://jslefcche.github.io/piecewiseSEM/>> for more.

Depends R (>= 3.5.0)

URL <https://github.com/jslefcche/>

BugReports <https://github.com/jslefcche/piecewiseSEM/issues>

Imports car, lme4, MASS, nlme, methods, pbkrtest

License GPL-3

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piecewiseSEM-package *Piecewise Structural Equation Modeling*

Description

Fitting and evaluation of piecewise structural equation models, complete with goodness-of-fit tests, estimates of (standardized) path coefficients, and evaluation of individual model fits (e.g., through R-squared values). Compared with traditional variance-covariance based SEM, piecewise SEM allows for fitting of models to different distributions through GLM and/or hierarchical/nested random structures through (G)LMER. Supported model classes include: `lm`, `glm`, `gls`, `pgls`, `sarlm`, `lme`, `glmmPQL`, `lmerMod`, `m`

Details

Package: piecewiseSEM
 Type: Package
 Version: 2.0.2
 Date: 2018-07-24
 Depends: R (>= 3.5.0), nlme, pbkrtest
 Suggests: MASS, lme4
 License: MIT

The primary functions in the package are `psem` which unites structural equations in a single model. `summary.psem` can be used on an object of class `psem` to provide various summary statistics for evaluation and interpretation.

Author(s)

Jon Lefcheck <jslefc@bigelow.org>

References

- Shiple, Bill. "A new inferential test for path models based on directed acyclic graphs." *Structural Equation Modeling* 7.2 (2000): 206-218.
- Shiple, Bill. *Cause and correlation in biology: a user's guide to path analysis, structural equations and causal inference*. Cambridge University Press, 2002.
- Shiple, Bill. "Confirmatory path analysis in a generalized multilevel context." *Ecology* 90.2 (2009): 363-368.
- Shiple, Bill. "The AIC model selection method applied to path analytic models compared using a d-separation test." *Ecology* 94.3 (2013): 560-564.
- Grace, J.B., Johnson, D.A., Lefcheck, J.S., and Byrnes, J.E. "Standardized Coefficients in Regression and Structural Models with Binary Outcomes." *Ecosphere* 9(6): e02283.
- Nakagawa, Shinichi, Paul CD Johnson, and Holger Schielzeth. "The coefficient of determination R² and intra-class correlation coefficient from generalized linear mixed-effects models revisited and expanded." *Journal of the Royal Society Interface* 14.134 (2017): 20170213.

AIC.psem

Generalized function for SEM AIC(c) score

Description

Generalized function for SEM AIC(c) score

Usage

```
## S3 method for class 'psem'
AIC(object, ..., aicc = FALSE)
```

Arguments

object	a psem object
...	additional arguments to AIC
aicc	whether correction for small sample size should be applied. Default is FALSE

as.psem	<i>Convert list to psem object</i>
---------	------------------------------------

Description

Convert list to psem object

Usage

```
as.psem(object, Class = "psem")
```

Arguments

object	any R object
Class	the name of the class to which object should be coerced

basisSet	<i>Derivation of the basis set</i>
----------	------------------------------------

Description

Acquires the set of independence claims—or the 'basis set'—for use in evaluating the goodness-of-fit for piecewise structural equation models.

Usage

```
basisSet(modelList, direction = NULL)
```

Arguments

modelList	A list of structural equations.
direction	a vector of claims defining the specific directionality of any independence claim(s)

Details

This function returns a list of independence claims. Each claim is a vector of the predictor of interest, followed by the response, and, if present, any conditioning variables.

Relationships among exogenous variables are omitted from the basis set because the directionality is unclear—e.g., does temperature cause latitude or does latitude cause temperature?—and the assumptions of the variables are not specified in the list of structural equations, so evaluating the relationship becomes challenging without further input from the user. This creates a circular scenario whereby the user specifies relationships among exogenous variables, raising the issue of whether they should be included as directed paths if they can be assigned directional relationships.

Paths can be omitted from the basis set by specifying them as correlated errors using `%~~%` or by assigning a directionality using the argument `direction`, e.g. `direction = c("X <- Y")`. This can be done if post hoc examination of the d-sep tests reveals nonsensical independence claims (e.g., arthropod abundance predicting photosynthetically-active radiation) that the user may wish to exclude from evaluation.

Value

A list of independence claims.

Author(s)

Jon Lefcheck <jlefcheck@bigelow.org>

References

Shipley, Bill. "A new inferential test for path models based on directed acyclic graphs." *Structural Equation Modeling* 7.2 (2000): 206-218.

See Also

[dSep](#)

BIC.psem

Generalized function for SEM BIC score

Description

Generalized function for SEM BIC score

Usage

```
## S3 method for class 'psem'
BIC(object, ...)
```

Arguments

<code>object</code>	a psem object
<code>...</code>	additional arguments to BIC

cerror	<i>Correlated errors</i>
--------	--------------------------

Description

Calculates partial correlations and partial significance tests.

Usage

```
cerror(formula., modellist, data = NULL)
```

Arguments

formula.	A formula specifying the two correlated variables using %~~%.
modellist	A list of structural equations.
data	A data.frame containing the data used in the list of equations.

Details

If the variables are exogenous, then the correlated error is the raw bivariate correlation.

If the variables are endogenous, then the correlated error is the partial correlation, accounting for the influence of any predictors.

The significance of the correlated error is conducted using `cor.test` if the variables are exogenous. Otherwise, a t-statistic is constructed and compared to a t-distribution with $N - k - 2$ degrees of freedom (where N is the total number of replicates, and k is the total number of variables informing the relationship) to derive a P-value.

Value

Returns a data.frame containing the (partial) correlation and associated significance test.

Author(s)

Jon Lefcheck <jlefccheck@bigelow.org>

See Also

[%~%tilde%tilde%](#)

Examples

```
# Generate example data
dat <- data.frame(x1 = runif(50),
  x2 = runif(50), y1 = runif(50),
  y2 = runif(50))

# Create list of structural equations
```

```

sem <- psem(
  lm(y1 ~ x1 + x2, dat),
  lm(y2 ~ y1 + x1, dat)
)

# Look at correlated error between x1 and x2
# (exogenous)
cerror(x1 %~~% x2, sem, dat)

# Same as cor.test
with(dat, cor.test(x1, x2))

# Look at correlated error between x1 and y1
# (endogenous)
cerror(y1 %~~% x1, sem, dat)

# Not the same as cor.test
# (accounts for influence of x1 and x2 on y1)
with(dat, cor.test(y1, x1))

# Specify in psem
sem <- update(sem, x1 %~~% y1)

coefs(sem)

```

coefs

Extract path coefficients

Description

Extracts (standardized) path coefficients from a psem object.

Usage

```
coefs(modellist, standardize = "scale", standardize.type = "latent.linear",
intercepts = FALSE)
```

Arguments

modellist	A list of structural equations.
standardize	The type of standardization: none, scale, range. Default is scale.
standardize.type	The type of standardized for non-Gaussian responses: latent.linear, Menard.OE. Default is latent.linear.
intercepts	Whether intercepts should be included in the coefficients table. Default is FALSE.

Details

P-values for models constructed using `lme4` are obtained using the Kenward-Roger approximation of the denominator degrees of freedom as implemented in the `pbkrtest` package.

Different forms of standardization can be implemented using the `standardize` argument:

- `none` No standardized coefficients are reported.
- `scale` Raw coefficients are scaled by the ratio of the standard deviation of `x` divided by the standard deviation of `y`. See below for cases pertaining to GLM.
- `range` Raw coefficients are scaled by a pre-selected range of `x` divided by a preselected range of `y`. The default argument is `range` which takes the two extremes of the data, otherwise the user must supply a named `list` where the names are the variables to be standardized, and each entry contains a vector of length 2 to the ranges to be used in standardization.

For binary response models (i.e., binomial responses), standardized coefficients are obtained in one of two ways:

- `latent.linear` Referred to in Grace et al. (in review) as the standard form of the latent-theoretic (LT) approach. In this method, there is assumed to be a continuous latent propensity, y^* , that underlies the observed binary responses. The standard deviation of y^* is computed as the square-root of the variance of the predictions (on the linear or 'link' scale) plus the distribution-specific assumed variance (for logit links: $\pi^2/3$, for probit links: 1).
- `Menard.OE` Referred to in Grace et al. (in review) as the standard form of the observed-empirical (OE) approach. In this method, error variance is based on the differences between predicted scores and the observed binary data. The standard deviation used for standardization is computed as the square-root of the variance of the predictions (on the linear scale) plus the correlation between the observed and predicted (on the original or 'response' scale) values of `y`.

Value

Returns a `data.frame` of coefficients, their standard errors, degrees of freedom, and significance tests.

Author(s)

Jon Lefcheck <jlefccheck@bigelow.org>, Jim Grace

References

Grace, J.B., Johnson, D.A., Lefcheck, J.S., and Byrnes, J.E. "Standardized Coefficients in Regression and Structural Models with Binary Outcomes." *Ecosphere* 9(6): e02283.

See Also

[KRmodcomp](#)

Dag	<i>Generate adjacency matrix from list of structural equations</i>
-----	--

Description

Generate adjacency matrix from list of structural equations

Usage

```
Dag(formulaList)
```

Arguments

formulaList a list of formulae corresponding to structural equations

dSep	<i>Tests of directed separation</i>
------	-------------------------------------

Description

Evaluation of conditional independence claims to be used in determining the goodness-of-fit for piecewise structural equation models.

Usage

```
dSep(modellist, direction = NULL, conserve = FALSE, conditioning = FALSE,
      .progressBar = TRUE)
```

Arguments

modellist	A list of structural equations created using psem.
direction	A vector of claims defining the specific directionality of independence claims; for use in special cases (see Details).
conserve	Whether the most conservative P-value should be returned; for use in special cases (see Details). Default is FALSE.
conditioning	Whether the conditioning variables should be shown in the summary table. Default is FALSE.
.progressBar	An optional progress bar. Default is TRUE.

Details

In cases involving non-normally distributed responses in the independence claims that are modeled using generalized linear models, the significance of the independence claim is not reversible (e.g., the P-value of $Y \sim X$ is not the same as $X \sim Y$). This is due to the transformation of the response via the link function. In extreme cases, this can bias the goodness-of-fit tests. `summary.psem` will issue a warning when this case is present and provide guidance for solutions.

One solution is to specify the directionality of the relationship using the `direction` argument, e.g. `direction = c("X <- Y")`. Another is to run both tests ($Y \sim X$, $X \sim Y$) and return the most conservative (i.e., lowest) P-value, which can be toggled using the `conserve = TRUE` argument.

Value

Returns a `data.frame` of independence claims and their significance values.

Author(s)

Jon Lefcheck <jlefcheck@bigelow.org>

References

Shipley, Bill. "A new inferential test for path models based on directed acyclic graphs." *Structural Equation Modeling* 7.2 (2000): 206-218.

See Also

[basisSet](#)

evaluateClasses	<i>Evaluate model classes and stop if unsupported model class</i>
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Description

Evaluate model classes and stop if unsupported model class

Usage

```
evaluateClasses(modellist)
```

Arguments

`modellist` a list of structural equations or a model object

 fisherC

Summarize tests of directed separation using Fisher's C statistic

Description

Summarize tests of directed separation using Fisher's C statistic

Usage

```
fisherC(dTable, add.claims = NULL, direction = NULL, conserve = FALSE,
        conditional = FALSE, .progressBar = FALSE)
```

Arguments

dTable	a data.frame containing tests of directed separation from dSep
add.claims	an optional vector of additional independence claims (i.e., P-values) to be added to the basis set
direction	a vector of claims defining the specific directionality of any independence claim(s)
conserve	whether the most conservative P-value should be returned. Default is FALSE
conditional	whether the conditioning variables should be shown in the table. Default is FALSE
.progressBar	an optional progress bar. Default is FALSE

Value

a vector corresponding to the C statistic, d.f., and P-value

 infCrit

Information criterion values for SEM

Description

Information criterion values for SEM

Usage

```
infCrit(modelList, Cstat, add.claims = NULL, direction = NULL,
        conserve = FALSE, conditional = FALSE, .progressBar = FALSE)
```

Arguments

<code>modellist</code>	a list of structural equations
<code>Cstat</code>	Fisher's C statistic obtained from <code>fisherC</code>
<code>add.claims</code>	an optional vector of additional independence claims (P-values) to be added to the basis set
<code>direction</code>	a vector of claims defining the specific directionality of any independence claim(s)
<code>conserve</code>	whether the most conservative P-value should be returned (See Details) Default is FALSE
<code>conditional</code>	whether the conditioning variables should be shown in the table. Default is FALSE
<code>.progressBar</code>	an optional progress bar. Default is FALSE

Value

a vector of AIC, AICc, BIC, d.f., and sample size

<code>keeley</code>	<i>Data set from Keeley et al.</i>
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Description

Data set from Keeley et al.

Usage

`keeley`

Format

A data.frame with 90 observations of 8 variables.

distance Distance to coast
elev Elevation from sea level
abiotic Abiotic favorability
age Age of stand before fire
hetero Plot heterogeneity
firesev Severity of fire
cover Cover of plants
rich Plant species richness

partial.resid	<i>partial.resid</i>
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Description

Obtains partial residuals

Usage

```
partial.resid(...)
```

Arguments

... any input

Value

a warning

partialResid	<i>Computing partial effects</i>
--------------	----------------------------------

Description

Extracts partial residuals from a model or psem object for a given x and y.

Usage

```
partialResid(formula., modellist, data = NULL)
```

Arguments

formula.	A formula where the lhs is the response and the rhs is the predictor whose partial effect is desired.
modellist	A list of structural equations.
data	A data.frame used to fit the equations.

Details

This function computes the partial residuals of $y \sim x + Z$ in a two-step procedure to remove the variation explained by Z: (1) remove x from the equation and model $y \sim Z$, and (2) replace y with x and model $x \sim Z$.

Value

Returns a data.frame of residuals of $y \sim Z$ called yresids, of $x \sim Z$ called xresids.

Author(s)

Jon Lefcheck <jlefcheck@bigelow.org>

See Also

[cerror](#)

Examples

```
# Generate data
dat <- data.frame(y = rnorm(100), x1 = rnorm(100), x2 = rnorm(100))

# Build model
model <- lm(y ~ x1 + x2, dat)

# Compute partial residuals of y ~ x1
yresid <- resid(lm(y ~ x2, dat))

xresid <- resid(lm(x1 ~ x2, dat))

plot(yresid, xresid)

# Use partialResid
presid <- partialResid(y ~ x1, model)

plot(presid) # identical plot!
```

print.psem

Print psem

Description

Print psem

Usage

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

Arguments

x an object of class psem
... further arguments passed to or from other methods

```
print.summary.psem
```

Print summary

Description

Print summary

Usage

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

Arguments

`x` an object of class `summary.psem`
`...` further arguments passed to or from other methods

```
psem
```

Fitting piecewise structural equation models

Description

`psem` is used to unite a list of structural equations into a single structural equation model.

Usage

```
psem(...)
```

Arguments

`...` A list of structural equations

Details

`psem` takes a list of structural equations, which can be model objects of classes: `lm`, `glm`, `gls`, `pgls`, `sarlm`, `lme`, `glmmPQ`

It also takes objects of class `formula`, `formula.error`, corresponding to additional variables to be included in the tests of directed separation ($X \sim 1$) or correlated errors ($X1 \sim\sim X2$).

The function optionally accepts data objects of classes: `matrix`, `data.frame`, `SpatialPointsDataFrame`, `comparative.d` or these are derived internally from the structural equations.

Value

Returns an object of class `psem`

Author(s)

Jon Lefcheck <jlecheck@bigelow.org>

See Also

[summary.psem, %\textasciitilde\textasciitilde%](#)

residuals.psem	<i>Residual values from fit models</i>
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Description

Residual values from fit models

Usage

```
## S3 method for class 'psem'
residuals(object, ...)
```

Arguments

object	a psem object
...	additional arguments to residuals

Value

a data.frame of residuals for endogenous variables as columns

rsquared	<i>R-squared for linear regression</i>
----------	--

Description

Returns (pseudo)-R² values for all linear, generalized linear, and generalized linear mixed effects models.

Usage

```
rsquared(modelList, method = NULL)
```

Arguments

modelList	a regression, or a list of structural equations.
method	The method used to compute the R ² value (See Details)

Details

For mixed models, marginal R2 considers only the variance by the fixed effects, and the conditional R2 by both the fixed and random effects.

For GLMs (`glm`), supported methods include:

- `mcfadden` 1 - ratio of likelihoods of full vs. null models
- `coxsne11` McFadden's R2 but raised to 2/N. Upper limit is < 1
- `nagelkerke` Adjusts Cox-Snell R2 so that upper limit = 1. The DEFAULT method

For GLMERs fit to Poisson, Gamma, and negative binomial distributions (`glmer`, `glmmPQL`, `glmer.nb`), supported methods include

- `delta` Approximates the observation variance based on second-order Taylor series expansion. Can be used with many families and link functions
- `lognormal` Observation variance is the variance of the log-normal distribution
- `trigamma` Provides most accurate estimate of the observation variance but is limited to only the log link. The DEFAULT method

For GLMERs fit to the binomial distribution (`glmer`, `glmmPQL`), supported methods include:

- `theoretical` Assumes observation variance is $\pi^2/3$
- `delta` Approximates the observation variance as above. The DEFAULT method

Value

Returns a `data.frame` with the response, its family and link, the method used to estimate R2, and the R2 value itself. Mixed models also return marginal and conditional R2 values.

Author(s)

Jon Lefcheck <jlefcheck@bigelow.org>

References

Nakagawa, Sinichi, Johnson, Paul C.D., and Holger Schielzeth. "The coefficient of determination R2 and intra-class correlation coefficient from generalized linear mixed-effects models revisited and expanded." *bioRxiv* 095851 (2017).

Examples

```
## Not run:
# Create data
dat <- data.frame(
  ynorm = rnorm(100),
  ypois = rpois(100, 100),
  x1 = rnorm(100),
  random = letters[1:5]
)
```

```

# Get R2 for linear model
rsquared(lm(ynorm ~ x1, dat))

# Get R2 for generalized linear model
rsquared(glm(y pois ~ x1, "poisson", dat))

rsquared(glm(y pois ~ x1, "poisson", dat), method = "mcfadden") # McFadden R2

# Get R2 for generalized least-squares model
rsquared(gls(ynorm ~ x1, dat))

# Get R2 for linear mixed effects model (nlme)
rsquared(nlme::lme(ynorm ~ x1, random = ~ 1 | random, dat))

# Get R2 for linear mixed effects model (lme4)
rsquared(lme4::lmer(ynorm ~ x1 + (1 | random), dat))

# Get R2 for generalized linear mixed effects model (lme4)
rsquared(lme4::glmer(y pois ~ x1 + (1 | random), family = poisson, dat))

rsquared(lme4::glmer(y pois ~ x1 + (1 | random), family = poisson, dat), method = "delta")

# Get R2 for generalized linear mixed effects model (glmmPQL)
rsquared(MASS::glmmPQL(y pois ~ x1, random = ~ 1 | random, family = poisson, dat))

## End(Not run)

```

sem.aic

sem.aic

Description

AIC for piecewiseSEM (old)

Usage

```

sem.aic(modellist, data, corr.errors = NULL, add.vars = NULL,
        grouping.vars = NULL, grouping.fun = mean, adjust.p = FALSE,
        basis.set = NULL, pvalues.df = NULL, model.control = NULL,
        .progressBar = TRUE)

```

Arguments

modellist	a list of regressions representing the structural equation model
data	a data.frame used to construct the structured equations
corr.errors	a vector of variables with correlated errors (separated by "~")
add.vars	a vector of additional variables whose independence claims should be evaluated, but which do not appear in the model list

grouping.vars	an optional variable that represents the levels of data aggregation for a multi-level dataset
grouping.fun	a function defining how variables are aggregated in grouping.vars. Default is mean
adjust.p	whether p-values degrees of freedom should be adjusted. Default is FALSE
basis.set	provide an optional basis set
pvalues.df	an optional data.frame corresponding to p-values for independence claims
model.control	a list of model control arguments to be passed to d-sep models
.progressBar	enable optional text progress bar. Default is TRUE

Details

This function calculates AIC and AICc (corrected for small sample sizes) values for a piecewise structural equation model (SEM).

For linear mixed effects models, p-values can be adjusted to accommodate the full model degrees of freedom using the argument `p.adjust = TRUE`. For more information, see Shipley 2013.

Value

Returns a data.frame where the first entry is the AIC score, and the second is the AICc score, and the third is the likelihood degrees of freedom (K)

sem.basis.set	<i>sem.basis.set</i>
---------------	----------------------

Description

Derive independence claims for SEM (old)

Usage

```
sem.basis.set(modelList, corr.errors = NULL, add.vars = NULL)
```

Arguments

modelList	a list of regressions representing the structural equation model
corr.errors	a vector of variables with correlated errors (separated by "~")
add.vars	a vector of additional variables whose independence claims should be

Details

Variables with correlated errors have no direct relationship but rather are hypothesized to be driven by the same underlying factor. This covariance should be reflected as correlated errors (double-headed arrow). Correlated errors are specified using the same syntax as the lavaan package: `var1 ~~ var2`. Variables with correlated errors are ignored in the basis set under the assumption that their correlations will be quantified later using the function `sem.coefs`. The argument `add.vars` requires a vector of character strings corresponding to column names in the dataset used to construct the models in `modelList`. This is useful if comparing nested SEMs where one wishes to account for additional variables whose independence claims should be evaluated, but which do not have any hypothesized paths in the current SEM. The default assumes there is no additional independence claims that do not appear in the model list.

Value

Returns a list of independence claims. Each entry in the list is a vector where the first entry is the predictor whose independence from the response is being evaluated, the second is the response, and remaining entries represent the variables on which the independence claim are conditional

<code>sem.coefs</code>	<i>sem.coefs</i>
------------------------	------------------

Description

Standardized coefficients for linear models (old)

Usage

```
sem.coefs(modelList, data = NULL, standardize = "none",
  corr.errors = NULL, intercept = FALSE)
```

Arguments

<code>modelList</code>	a list of regressions representing the structural equation model
<code>data</code>	a data.frame used to construct the structured equations
<code>standardize</code>	whether coefficients should be scaled by their standard deviations ("scale") or by their ranges ("range")
<code>corr.errors</code>	a vector of variables with correlated errors (separated by "~")
<code>intercept</code>	whether intercepts should also be returned. Default is FALSE

 sem.fisher.c

sem.fisher.c

Description

Fisher's C test for SEM (old)

Usage

```
sem.fisher.c(modellist, data, corr.errors = NULL, add.vars = NULL,
  grouping.vars = NULL, grouping.fun = mean, adjust.p = FALSE,
  basis.set = NULL, pvalues.df = NULL, model.control = NULL,
  .progressBar = TRUE)
```

Arguments

modellist	a list of regressions representing the structural equation model
data	a data.frame used to construct the structured equations
corr.errors	a vector of variables with correlated errors (separated by "~")
add.vars	a vector of additional variables whose independence claims should be evaluated, but which do not appear in the model list
grouping.vars	an optional variable that represents the levels of data aggregation for a multi-level dataset
grouping.fun	a function defining how variables are aggregated in grouping.vars. Default is mean
adjust.p	whether p-values degrees of freedom should be adjusted. Default is FALSE
basis.set	provide an optional basis set
pvalues.df	an optional data.frame corresponding to p-values for independence claims
model.control	a list of model control arguments to be passed to d-sep models
.progressBar	enable optional text progress bar. Default is TRUE

sem.fit

sem.fit

Description

Goodness-of-fit tests for piecewise SEM (old)

Usage

```
sem.fit(modellist, data, conditional = FALSE, corr.errors = NULL,
  add.vars = NULL, grouping.vars = NULL, grouping.fun = mean,
  adjust.p = FALSE, basis.set = NULL, pvalues.df = NULL,
  model.control = NULL, .progressBar = TRUE)
```

Arguments

modellist	a list of regressions representing the structural equation model
data	a data.frame used to construct the structured equations
conditional	whether the full set of conditioning variables should be returned. Default is FALSE
corr.errors	a vector of variables with correlated errors (separated by "~")
add.vars	a vector of additional variables whose independence claims should be evaluated, but which do not appear in the model list
grouping.vars	an optional variable that represents the levels of data aggregation for a multi-level dataset
grouping.fun	a function defining how variables are aggregated in grouping.vars. Default is mean
adjust.p	whether p-values degrees of freedom should be adjusted. Default is FALSE
basis.set	provide an optional basis set
pvalues.df	an optional data.frame corresponding to p-values for independence claims
model.control	a list of model control arguments to be passed to d-sep models
.progressBar	enable optional text progress bar. Default is TRUE

Details

Tests independence claims and calculates Fisher's C statistic and associated p-value, and AIC and AICc, for a piecewise structural equation model (SEM).

Value

a list corresponding to: the tests of directed separation, the Fisher's C statistic, and the AIC of the model

sem.missing.paths	<i>sem.missing.paths</i>
-------------------	--------------------------

Description

Tests of directed separation (old)

Usage

```
sem.missing.paths(modellist, data, conditional = FALSE, corr.errors = NULL,
  add.vars = NULL, grouping.vars = NULL, grouping.fun = mean,
  adjust.p = FALSE, basis.set = NULL, model.control = NULL,
  .progressBar = TRUE)
```

Arguments

modellist	a list of regressions representing the structural equation model
data	a data.frame used to construct the structured equations
conditional	whether the full set of conditioning variables should be returned. Default is FALSE
corr.errors	a vector of variables with correlated errors (separated by "~~")
add.vars	a vector of additional variables whose independence claims should be evaluated, but which do not appear in the model list
grouping.vars	an optional variable that represents the levels of data aggregation for a multi-level dataset
grouping.fun	a function defining how variables are aggregated in grouping.vars. Default is mean
adjust.p	whether p-values degrees of freedom should be adjusted. Default is FALSE
basis.set	provide an optional basis set
model.control	a list of model control arguments to be passed to d-sep models
.progressBar	enable optional text progress bar. Default is TRUE

 sem.model.fits

sem.model.fits

Description

Goodness-of-fit statistics for linear models (old)

Usage

```
sem.model.fits(...)
```

Arguments

... a linear model or list of models

shipley

Data set from Shipley (2009)

Description

Data set from Shipley (2009)

Usage

shipley

Format

A data.frame with 1900 observations of 9 variables.

site Site of observation

tree Tree of observation

lat Latitude

year Year of observation

Date Julian date of first bud burst

DD Cumulative degree days until first bud burst

Growth Increase in stem diameter

Survival Plant species richness

Live Alive (1) or dead (0)

summary.psem

Summarizing piecewise structural equation models

Description

Returns information necessary to interpret piecewise structural equation models, including tests of directed separation, path coefficients, information criterion values, and R-squared values of individual models.

Usage

```
## S3 method for class 'psem'
summary(object, ..., direction = NULL, conserve = FALSE,
  conditional = FALSE, add.claims = NULL, standardize = "scale",
  standardize.type = "latent.linear", intercepts = FALSE,
  .progressBar = TRUE)
```

Arguments

<code>object</code>	a list of structural equations
<code>...</code>	additional arguments to <code>summary</code>
<code>direction</code>	a vector of claims defining the specific directionality of any independence claim(s)
<code>conserve</code>	whether the most conservative P-value should be returned (See Details) Default is FALSE
<code>conditional</code>	whether all conditioning variables should be shown in the table Default is FALSE
<code>add.claims</code>	an optional vector of additional independence claims (P-values) to be added to the basis set
<code>standardize</code>	whether standardized path coefficients should be reported Default is "scale"
<code>standardize.type</code>	the type of standardized for non-Gaussian responses: <code>latent.linear</code> (default), <code>standard.OE</code>
<code>intercepts</code>	whether intercepts should be included in the coefficient table Default is FALSE
<code>.progressBar</code>	an optional progress bar. Default is TRUE

Details

The forthcoming argument `groups` splits the analysis based on an optional grouping factor, conducts separate d-sep tests, and reports goodness-of-fit and path coefficients for each submodel. The procedure is approximately similar to a multigroup analysis in traditional variance-covariance SEM. Coming in version 2.1.

In cases involving non-normally distributed responses in the independence claims that are modeled using generalized linear models, the significance of the independence claim is not reversible (e.g., the P-value of $Y \sim X$ is not the same as $X \sim Y$). This is due to the transformation of the response via the link function. In extreme cases, this can bias the goodness-of-fit tests. `summary.psem` will issue a warning when this case is present and provide guidance for solutions. One solution is to specify the directionality of the relationship using the `direction` argument, e.g. `direction = c("X <- Y")`. Another is to run both tests ($Y \sim X$, $X \sim Y$) and return the most conservative (i.e., lowest) P-value, which can be toggled using the `conserve = TRUE` argument.

In some cases, additional claims that were excluded from the basis set can be added back in using the argument `add.claims`. These could be, for instance, independence claims among exogenous variables. See Details in [basisSet](#).

Standardized path coefficients are scaled by standard deviations.

Value

The function `summary.psem` returns a list of summary statistics:

<code>dTable</code>	A summary table of the tests of directed separation, from dSep .
<code>CStat</code>	Fisher's C statistic, degrees of freedom, and significance value based on a Chi-square test.
<code>IC</code>	Information criterion (Akaike, Bayesian, corrected Akaike) as well as degrees of freedom and sample size.
<code>coefficients</code>	A summary table of the path coefficients, from <code>link{coefs}</code> .
<code>R2</code>	(Pseudo)-R2 values, from rsquared .

Author(s)

Jon Lefcheck <jlefcheck@bigelow.org>

References

Shipley, Bill. "A new inferential test for path models based on directed acyclic graphs." *Structural Equation Modeling* 7.2 (2000): 206-218.

Shipley, Bill. *Cause and correlation in biology: a user's guide to path analysis, structural equations and causal inference*. Cambridge University Press, 2002.

Shipley, Bill. "Confirmatory path analysis in a generalized multilevel context." *Ecology* 90.2 (2009): 363-368.

Shipley, Bill. "The AIC model selection method applied to path analytic models compared using a d-separation test." *Ecology* 94.3 (2013): 560-564.

See Also

The model fitting function [psem](#).

update.psem

Update psem model object with additional values.

Description

Update psem model object with additional values.

Usage

```
## S3 method for class 'psem'  
update(object, ...)
```

Arguments

object	a psem object to update
...	additional arguments to update

%textasciitilde%
Correlated error operator

Description

Specifies correlated errors among predictors

Usage

e1

Details

For use in `psem` to identify correlated sets of variables.

Author(s)

Jon Lefcheck <jlefcheck@bigelow.org>

See Also

[cerror](#)

Examples

```
# Generate example data
dat <- data.frame(x1 = runif(50),
  x2 = runif(50), y1 = runif(50),
  y2 = runif(50))

# Create list of structural equations
sem <- psem(
  lm(y1 ~ x1 + x2, dat),
  lm(y2 ~ y1 + x1, dat)
)

# Look at correlated error between x1 and x2
# (exogenous)
cerror(x1 %~~% x2, sem, dat)

# Same as cor.test
with(dat, cor.test(x1, x2))

# Look at correlated error between x1 and y1
# (endogenous)
cerror(y1 %~~% x1, sem, dat)
```

```
# Not the same as cor.test
# (accounts for influence of x1 and x2 on y1)
with(dat, cor.test(y1, x1))

# Specify in psem
sem <- update(sem, x1 %~~% y1)

coefs(sem)
```

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