Package ‘piecewiseSEM’

Type Package

Title Piecewise Structural Equation Modeling

Version 2.1.0

Date 2019-12-05

Maintainer Jon Lefcheck <lefcheckj@si.edu>

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://jslefche.github.io/piecewiseSEM/> for more.

Depends R (>= 3.5.0)

URL https://github.com/jslefche/

BugReports https://github.com/jslefche/piecewiseSEM/issues

Imports car, DiagrammeR, emmeans, igraph, lme4, MASS, methods, nlme

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 7.0.2

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

Author Jon Lefcheck [aut, cre], Jarrett Byrnes [aut], James Grace [aut]

Repository CRAN

Date/Publication 2019-12-05 16:50:02 UTC
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, merMod.
piecewiseSEM-package

Details
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 <lefcheckj@si.edu>

**References**


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**AIC.psem**

*Generalized function for SEM AIC(c) score*

**Description**

Generalized function for SEM AIC(c) score

**Usage**

```r
## 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

Description

Compute analysis of variance table for one or more structural equation models.

Usage

## S3 method for class 'psem'
anova(object, ..., digits = 3, anovafun = "Anova")

Arguments

object a psem object
... additional objects of the same type
digits number of digits to round results. Default is 3
anovafun The function used for ANOVA. Defaults to Anova

Details

Additional models will be tested against the first model using a Chi-squared difference test.

Value

an F, LRT, or other table for a single model, or a list of comparisons between multiple models

Author(s)

Jon Lefcheck <lefcheckj@si.edu>, Jarrett Byrnes <jarrett.byrnes@umb.edu>

See Also

Anova
Examples

```r
data(keeley)

mod1 <- psem(
  lm(rich ~ cover, data = keeley),
  lm(cover ~ firesev, data = keeley),
  lm(firesev ~ age, data = keeley),
  data = keeley
)

# get type II Anova
anova(mod1)

# conduct LRT
mod2 <- psem(
  lm(rich ~ cover, data = keeley),
  lm(cover ~ firesev, data = keeley),
  age ~ 1,
  data = keeley
)

anova(mod1, mod2)
```

---

**as.psem**  
*Convert list to psem object*

**Description**

Convert list to psem object

**Usage**

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

**Arguments**

- **object**: any R object
- **Class**: the name of the class to which object should be coerced
**basisSet**

*Derivation of the basis set*

**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**

```r
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 <lefcheckj@si.edu>

**References**

See Also

dSep

---

**BIC.psem**  
*Generalized function for SEM BIC score*

---

**Description**

Generalized function for SEM BIC score

**Usage**

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

**Arguments**

- `object`  
a psem object
- `...`  
additional arguments to BIC

---

**cbind_fill**  
*Bind data.frames of differing dimensions*

---

**Description**

From: https://stackoverflow.com/a/31678079

**Usage**

```r
cbind_fill(...)```

**Arguments**

- `...`  
data.frames to be bound, separated by commas
- @keywords internal
**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 <lefcheckj@si.edu>

**See Also**

%~~%

**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

coops(
  modelList,
  standardize = "scale",
  standardize.type = "latent.linear",
  test.statistic = "F",
  test.type = "II",
  intercepts = FALSE
)

Arguments

  modelList       A list of structural equations, or a model.
  standardize     The type of standardization: none, scale, range. Default is scale.
coefs

standardize.type
The type of standardized for non-Gaussian responses: latent.linear, Menard.OE. Default is latent.linear.

test.statistic
the type of test statistic generated by Anova

test.type
the type of test for significance of categorical variables from Anova. Default is type "II".

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 Anova function.

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 must 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.

For categorical predictors: significance is determined using ANOVA (or analysis of deviance). Because n-1 coefficients are reported for n levels, the output instead reports model-estimated means in the Estimate column. This is done so all n paths in the corresponding path diagram have assignable values.

The means are generated using function emmeans in the emmeans package. Pairwise contrasts are further conducted among all levels using the default correction for multiple testing. The results of those comparisons are given in the significance codes (e.g., "a", "b", "ab") as reported in the emmeans::cld function.
Value

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

Author(s)

Jon Lefcheck <lefcheckj@si.edu>, Jim Grace

References


See Also

Anova, emmeans, CLD

Examples

```r
mod <- psem(
  lm(rich ~ cover, data = keeley),
  lm(cover ~ firesev, data = keeley),
  lm(firesev ~ age, data = keeley),
  data = keeley
)

coefs(mod)
```

---

dSep Test of directed separation

Description

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

Usage

```r
dSep(
  modellist,
  basis.set = NULL,
  direction = NULL,
  conserve = FALSE,
  conditioning = FALSE,
  .progressBar = TRUE
)
```
Arguments

- **modelList**: A list of structural equations created using `psem`.
- **basis.set**: An optional list of independence claims.
- **direction**: A vector of claims defining the specific directionality of independence claims; for use in special cases (see Details). Default is FALSE.
- **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 ~ X is not the same as X ~ 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 ~ X, X ~ 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 <lefcheckj@si.edu>, Jarrett Byrnes

References


See Also

- `basisSet`
evaluateClasses  
Evaluate model classes and stop if unsupported model class

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,
basis.set = 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
basis.set An optional list of independence claims.
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
getDAG

Value

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

dag

Generate adjacency matrix from list of structural equations

Description

Generate adjacency matrix from list of structural equations

Usage

getDAG(modelList)

Arguments

modelList A list of structural equations

infCrit

Information criterion values for SEM

Description

Information criterion values for SEM

Usage

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

- `modelList` a list of structural equations
- `Cstat` Fisher's C statistic obtained from `fisherC`
- `add.claims` an optional vector of additional independence claims (P-values) to be added to the basis set
- `basis.set` An optional list of independence claims.
- `direction` a vector of claims defining the specific directionality of any independence claim(s)
- `conserve` whether the most conservative P-value should be returned (See Details) 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 of AIC, AICc, BIC, d.f., and sample size

---

keeley

*Data set from Grace & Keeley (2006)*

Description

Data set from Grace & Keeley (2006)

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
Data set from Grace & Jutila (1999)

Description
Data set from Grace & Jutila (1999)

Usage
meadows

Format
A data.frame with 354 observations of 4 variables.

- **grazed** Whether meadows were exposed to grazing: 0 = no, 1 = yes
- **mass** Plant biomass in g m\(^{-2}\)
- **elev** Elevation of the plot above mean sea level
- **rich** Plant species richness per m\(^2\)

Multigroup Analysis for Piecewise SEM

Description
Multigroup Analysis for Piecewise SEM

Usage

```r
multigroup(
  modelList,
  group,
  standardize = "scale",  # The type of standardization: none, scale, range. Default is scale.
  standardize.type = "latent.linear",  # The type of standardized for non-Gaussian responses: latent.linear, Menard.OE. Default is latent.linear.
  test.type = "III"  # what kind of ANOVA should be reported. Default is type III
)
```

Arguments

- **modelList** a list of structural equations
- **group** the name of the grouping variable in quotes
- **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.
- **test.type** what kind of ANOVA should be reported. Default is type III
Partial Residuals

Author(s)

Jon Lefcheck <lefcheckj@si.edu>

Examples

data(meadows)

jutila <- psem(
lm(rich ~ elev + mass, data = meadows),
lm(mass ~ elev, data = meadows)
)

jutila.multigroup <- multigroup(jutila, group = "grazed")

jutila.multigroup

partialResid

Computing Partial Effects

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 <lefcheckj@si.edu>
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!

plot.psem

Description

plot.psem uses [DiagrammeR] to generate path diagrams of 'piecewiseSEM' fits within R.

Usage

## S3 method for class 'psem'
plot(
x, 
return = FALSE,
node_attrs = data.frame(shape = "rectangle", color = "black", fillcolor = "white"),
edge_attrs = data.frame(style = "solid", color = "black"),
ns_dashed = T,
alpha = 0.05,
show = "std",
digits = 3,
add_edge_label_spaces = TRUE,
...
**Arguments**

- **x**  
  a `psem()` object

- **return**  
  whether to return the output from `DiagrammeR::create_graph()` for modification and later plotting

- **node_attrs**  
  List of node attributes to override defaults of rectangular nodes with black outline and white fill. See [here](http://visualizers.co/diagrammer/articles/node-edge-data-frames.html) and [here](http://visualizers.co/diagrammer/articles/graphviz-mermaid.html) for a more complete rundown of options.

- **edge_attrs**  
  List of edge attributes to override defaults of solid black arrows. See [here](http://visualizers.co/diagrammer/articles/node-edge-data-frames.html) and [here](http://visualizers.co/diagrammer/articles/graphviz-mermaid.html) for a more complete rundown of options.

- **ns_dashed**  
  If TRUE, paths that are not different from 0 will be dashed rather than solid, unless the whole is overridden in `edge_attrs`

- **alpha**  
  The alpha level for assessing whether a path is different from 0

- **show**  
  What types of path coefficients are shown? Default "std" is standardized coefficients. For unstandardized, use "unstd".

- **digits**  
  How many significant digits should be shown?

- **add_edge_label_spaces**  
  Should spaces by added on either side of edge labels? Default is 'TRUE' as otherwise paths too often overlap edges.

- **...**  
  Other arguments to `DiagrammeR::render_graph()`

**Value**

Returns an object of class `DiagrammeR::dgr_graph`

**Author(s)**

Jarrett Byrnes <jarrett.byynes@umb.edu>

**Examples**

```r
data(keeley)
mod <- psem(
  lm(rich ~ cover, data=keeley),
  lm(cover ~ firesev, data=keeley),
  lm(firesev ~ age, data=keeley),
  data = keeley
)
plot(mod)

### More customized plot
plot(mod, node_attrs = list(
  shape = "rectangle", color = "black",
```
print.anova.psem

fillna = "orange", x = 3, y=1:4))

print.anova.psem  Print anova

Description
Print anova

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

Arguments
x  an object of class anova.psem
...

print.basisSet  Print basis set

Description
Print basis set

Usage
## S3 method for class 'basisSet'
print(x, ...)

Arguments
x  a basis set
...

... further arguments passed to or from other methods
print.multigroup.psem  Print multigroup

Description
Print multigroup

Usage

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

Arguments

x                  an object to print
...

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**

```r
## 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**

```r
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, pgl,sarlm, lme, glmmPQL, lmerMod, glmerMod`

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

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

**Value**

Returns an object of class `psem`
residuals.psem

Residual values from fit models

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

**rsquared**

*R-squared for linear regression*

**Description**

Returns (pseudo)-$R^2$ values for all linear, generalized linear, and generalized linear mixed effects models.

**Usage**

```r
r_squared(modelList, method = NULL)
```

**Arguments**

- `modelList`: a regression, or a list of structural equations.
- `method`: The method used to compute the R2 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
- `coxsnell`: 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 <lefcheckj@si.edu>

References


Examples

```r
## 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(ypois ~ x1, "poisson", dat))
rsquared(glm(ypois ~ 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)
rquared(nlme::lme(ynorm ~ x1, random = ~ 1 | random, dat))

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

# Get R2 for generalized linear mixed effects model (lme4)
rquared(lme4::glmer(ypois ~ x1 + (1 | random), family = poisson, dat))
rsquared(lme4::glmer(ypois ~ x1 + (1 | random), family = poisson, dat), method = "delta")

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

## End(Not run)
```
Description

Data set from Shipley (2006)

Usage

shipley

Format

A data.frame with 1900 observations of 9 variables.

- **site**: Site of observation
- **tree**: Individual 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**: Proportional survival
- **Live**: Alive (1) or dead (0)

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

```r
## S3 method for class 'psem'
summary(
  object,
  ..., 
  basis.set = NULL, 
  direction = NULL, 
  conserve = FALSE,
)```
conditioning = FALSE,
add.claims = NULL,
standardize = "scale",
standardize.type = "latent.linear",
test.statistic = "F",
test.type = "II",
intercepts = FALSE,
.progressBar = TRUE
)

Arguments

object a list of structural equations
...
additional arguments to summary
basis.set an optional 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 (See Details) Default is FALSE
conditioning whether all conditioning variables should be shown in the table Default is FALSE
add.claims an optional vector of additional independence claims (P-values) to be added to the basis set
standardize whether standardized path coefficients should be reported Default is "scale"
standardize.type the type of standardized for non-Gaussian responses: latent.linear (default), Mendard.OE
test.statistic the type of test statistic generated by Anova
test.type the type of test ("II" or "III") for significance of categorical variables (from car::Anova)
intercepts whether intercepts should be included in the coefficient table Default is FALSE
.progressBar 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 ~ X is not the same as X ~ 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 ~ X, X ~ 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:

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

**Author(s)**

Jon Lefcheck <lefcheckj@si.edu>

**References**


**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**

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

object a psem object
...
additional arguments to update

Description

Specifies correlated errors among predictors

Usage

e1 %~~% e2

Arguments

e1 one variable to be correlated
e2 the other variable to be correlated

Details

For use in psem to identify correlated sets of variables.

Author(s)

Jon Lefcheck <lefcheckj@si.edu>

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 correlatde 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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