Package ‘influence.SEM’

April 14, 2018

Type Package
Title Case Influence in Structural Equation Models
Version 2.2
Date 2018-04-14
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Depends lavaan
Suggests tcltk
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Description A set of tools for evaluating several measures of case influence for structural equation models.
License GPL (>= 2)
NeedsCompilation no
Repository CRAN
Date/Publication 2018-04-14 10:06:26 UTC

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**bollen.loglik**

*Log-Likelihood of a sem model (Internal function)*

---

**Description**

Internal function, called by `likedist`.

**Usage**

```r
bollen.loglik(N, S, Sigma)
```

**Arguments**

- `N`: Sample size.
- `S`: Observed covariance matrix.
- `Sigma`: Model fitted covariance matrix, \( \Sigma(\theta) \).

**Details**

The log-likelihood is computed by the function `bollen.loglik` using the formula 4B2 described by Bollen (1989, pag. 135).

**Value**

Returns the Log-likelihood.

**Author(s)**

Massimiliano Pastore, Gianmarco Altoe’

**References**


**See Also**

`likedist`

**Examples**

```r
data("PIDI")
model <- "
  F1 =~ y1+y2+y3+y4
"
fit0 <- sem(model, data=PIDI)
N <- fit0@data@nobs[[1]]
S <- fit0@SampleStats@cov[[1]]
Sigma <- fitted(fit0)$cov
bollen.loglik(N,S,Sigma)
```
Deltachi

Chi-square difference.

Description
Quantifies case influence on overall model fit by change in the test statistic

\[ \Delta \chi^2_i = \chi^2 - \chi^2_{(i)} \]

where \( \chi^2 \) and \( \chi^2_{(i)} \) are the test statistics obtained from original and deleted \( i \) samples.

Usage
Deltachi(model, data, \ldots, scaled = FALSE)

Arguments
- **model**: A description of the user-specified model using the lavaan model syntax. See lavaan for more information.
- **data**: A data frame containing the observed variables used in the model. If any variables are declared as ordered factors, this function will treat them as ordinal variables.
- \ldots: Additional parameters for sem function.
- **scaled**: Logical, if TRUE the function uses the scaled \( \chi^2 \) (Rosseel, 2013).

Value
Returns a vector of \( \Delta \chi^2_i \).

Note
If for observation \( i \) model does not converge or yields a solution with negative estimated variances, the associated value of \( \Delta \chi^2_i \) is set to NA.

This function is a particular case of fitinfluence, see example below.

Author(s)
Massimiliano Pastore

References
explore.influence

Examples

```r
## not run: this example take several minutes
data("PDII")
model <- 
  F1 <- y1+y2+y3+y4

# fit0 <- sem(model, data=PDII)
# Dchi <- deltachi(model, data=PDII)
# plot(Dchi,pch=19,xlab="observations",ylab="Delta chisquare")

## not run: this example take several minutes
## an example in which the deletion of a case yelds a solution
## with negative estimated variances
model <- 
  F1 <- x1+x2+x3
  F2 <- y1+y2+y3+y4
  F3 <- y5+y6+y7+y8

# fit0 <- sem(model, data=PDII)
# Dchi <- deltachi(model, data=PDII)
# plot(Dchi,pch=19,xlab="observations",ylab="Delta chisquare",main="Deltachi function")

## the case that produces negative estimated variances
# sem(model, data=PDII[-which(is.na(Dchi)),])

## same results
# Dchi <- fitinfluence("chisq", model, data=PDII)$Dind$chisq
# plot(Dchi,pch=19,xlab="observations",ylab="Delta chisquare",main="fitinfluence function")
```

explore.influence  

Explores case influence.

Description

It explores case influence. Cases with extreme values of the considered measure of influence are reported. Extreme values are determined using the boxplot criterion (Tukey, 1977) or user-defined cut-offs. Cases for which deletion leads to a model that does not converge or yields a solution with negative estimated variances are also reported. In addition, explore.influence provides a graphical representation of case influence.

Usage

explore.influence(x, cut offs = 'default',
                  plot = 'TRUE', cook = 'FALSE', ...)
Arguments

- **x**: A vector containing the influence of each case as returned by `Deltachi`, `fitinfluence`, `genCookDist`, `Likedist` or `parinfluence` functions.
- **cut-offs**: A vector of two numeric elements containing the lower and the upper cut-offs to be considered. If default, the cut-offs are calculated according to the boxplot criterion for outliers (see also, `cook`).
- **plot**: If TRUE (the default) a graphical representation of case influence is given.
- **cook**: If TRUE, x is interpreted as a vector containing Cook’s distances, and so the lower cut-off is forced to be greater or equal to zero.
- ... Additional parameters for `plot` function.

Value

A list with the following components:

- **n**: number of cases.
- **cook**: logical, indicating if x is treated as a vector of Cook’s distances.
- **cut.low**: the lower cut-off.
- **cut.upp**: the upper cut-off.
- **not.allowed**: a vector containing cases with negative variance or not converging models.
- **less.cut.low**: a vector containing cases with influence value less than the lower cut-off.
- **greater.cut.low**: a vector containing cases with influence value greater than the upper cut-off.

Author(s)

Gianmarco Altoe'

References


Examples

data("PDII")
model <- "
F1 = - y1+y2+y3+y4
"
fit0 <- sem(model, data=PDII, std.lv=TRUE)
## not run
# gCD <- genCookDist(model, data=PDII, std.lv=TRUE)
# explore.influence(gCD, cook=TRUE)

##
## not run: this example take several minutes
model <- "
F1 = - x1+x2+x3"
fitinfluence

Case influence on model fit.

Description

This function evaluates the case’s effect on a user-defined fit index.

Usage

fitinfluence(index, model, data, ...)

Arguments

- **index**: A model fit index.
- **model**: A description of the user-specified model using the lavaan model syntax. See lavaan for more information.
- **data**: A data frame containing the observed variables used in the model. If any variables are declared as ordered factors, this function will treat them as ordinal variables.
- **...**: Additional parameters for sem function.

Details

For each case evaluate the influence on one or more fit indices: the difference between the chosen fit index calculated for the SEM target model $M$ and the same index computed for the SEM model $M_{(i)}$ excluding case $i$.

Value

Returns a list:

- **dind**: a data.frame of case influence.
- **oind**: observed fit indices.

Note

If for observation $i$ model does not converge or yields a solution with negative estimated variances, the associated value of influence is set to NA.
Author(s)

Massimiliano Pastore

References


Examples

```r
## not run: this example take several minutes
data("PDII")
model <- "
  F1 <- y1+y2+y3+y4
"

# fit0 <- sem(model, data=PDII)
# FI <- fitinfluence("cfi",model,data=PDII)
# plot(FI$ind,pch=19)

## not run: this example take several minutes
## an example in which the deletion of a case yelds a solution
## with negative estimated variances
model <- "
  F1 <- x1+x2+x3
  F2 <- y1+y2+y3+y4
  F3 <- y5+y6+y7+y8
"

# fit0 <- sem(model, data=PDII)
# FI <- fitinfluence(c("tli","rmsea"),model,PDII)
# explore.influence(FI$ind$tli)
# explore.influence(FI$ind$rmsea)
```

description

Case influence on a vector of parameters may be quantified by generalized Cook’s Distance (\(gCD\); Cook 1977, 1986):

\[
gCD_i = (\hat{\theta} - \hat{\theta}_{(i)})' \hat{\Sigma} (\hat{\theta}_{(i)})^{-1} (\hat{\theta} - \hat{\theta}_{(i)})
\]

where \(\hat{\theta}\) and \(\hat{\theta}_{(i)}\) are \(l \times 1\) vectors of parameter estimates obtained from the original and delete \(i\) samples, and \(\hat{\Sigma} (\hat{\theta}_{(i)})\) is the estimated asymptotic covariance matrix of the parameter estimates obtained from reduced sample.
Usage

genCookDist(model, data, ...)

Arguments

model  A description of the user-specified model using the lavaan model syntax. See lavaan for more information.
data  A data frame containing the observed variables used in the model. If any variables are declared as ordered factors, this function will treat them as ordinal variables.
...  Additional parameters for sem function.

Value

Returns a vector of $gCD_i$.

Note

If for observation $i$ model does not converge or yields a solution with negative estimated variances, the associated value of $gCD_i$ is set to \texttt{NA}.

Author(s)

Massimiliano Pastore

References


Examples

```r
## not run: this example take several minutes
data("PDII")
model <- "
  F1 =~ y1+y2+y3+y4
"
# fit0 <- sem(model, data=PDII)
# gCD <- genCookDist(model, data=PDII)
# plot(gCD,pch=19,xlab="observations",ylab="Cook distance")

## not run: this example take several minutes
## an example in which the deletion of a case produces solution
## with negative estimated variances
model <- "
  F1 =~ y1+y2+y3+y4
  y1 ~ y1
" `}
```
A general model-based measure of case influence on model fit is likelihood distance (Cook, 1977, 1986; Cook & Weisberg, 1982) defined as

\[ LD_i = 2[L(\hat{\theta}) - L(\hat{\theta}_{(i)})] \]

where \( \hat{\theta} \) and \( \hat{\theta}_{(i)} \) are the \( k \times 1 \) vectors of estimated model parameters on the original and deleted \( i \) samples, respectively, where \( i = 1, \ldots, N \). The subscript \( (i) \) indicates that the estimate was computed on the sample excluding case \( i \). \( L(\hat{\theta}) \) and \( L(\hat{\theta}_{(i)}) \) are the log-likelihoods based on the original and the deleted \( i \) samples, respectively.

**Usage**

```
likedist(model, data, ...)  
```

**Arguments**

- `model`: A description of the user-specified model using the lavaan model syntax. See `lavaan` for more information.
- `data`: A data frame containing the observed variables used in the model. If any variables are declared as ordered factors, this function will treat them as ordinal variables.
- `...`: Additional parameters for `sem` function.

**Details**

The log-likelihoods \( L(\hat{\theta}) \) and \( L(\hat{\theta}_{(i)}) \) are computed by the function `bollen.loglik` using the formula 4B2 described by Bollen (1989, pag. 135).

The likelihood distance gives the amount by which the log-likelihood of the full data changes if one were to evaluate it at the reduced-data estimates. The important point is that \( L(\hat{\theta}_{(i)}) \) is not the log-likelihood obtained by fitting the model to the reduced data set. It is obtained by evaluating the likelihood function based on the full data set (containing all \( n \) observations) at the reduced-data estimates (Schabenberger, 2005).
Value

Returns a vector of \( LD_i \).

Note

If for observation \( i \) model does not converge or yields a solution with negative estimated variances, the associated value of \( LD_i \) is set to \( \text{NA} \).

Author(s)

Massimiliano Pastore, Gianmarco Altoe’

References


See Also

*bollen.loglik*

Examples

```r
# not run: this example take several minutes
data("PDII")
model <- "
  F1 <- y1+y2+y3+y4
  "
# fit0 <- sem(model, data=PDII)
# LD <- Likedist(model, data=PDII)
# plot(LD,pch=19,xlab="observations",ylab="Likelihood distances")

# not run: this example take several minutes
# an example in which the deletion of a case yields a solution
# with negative estimated variances
model <- "
  F1 <- x1+x2+x3
  F2 <- y1+y2+y3+y4
  F3 <- y5+y6+y7+y8
  "
```
parinfluence (Case influence on model parameters)

Description

Computes direction of change in parameter estimates with

$$\Delta \hat{\theta}_{ji} = \frac{\hat{\theta}_j - \hat{\theta}_{j(i)}}{\sqrt{\text{VAR}(\hat{\theta}_{j(i)})}}$$

where $\hat{\theta}_j$ and $\hat{\theta}_{j(i)}$ are the parameter estimates obtained from original and deleted $i$ samples.

Usage

parinfluence(parm, model, data, cook = FALSE, ...)

Arguments

- **parm**: Single parameter or vector of parameters.
- **model**: A description of the user-specified model using the lavaan model syntax. See lavaan for more information.
- **data**: A data frame containing the observed variables used in the model. If any variables are declared as ordered factors, this function will treat them as ordinal variables.
- **cook**: Logical, if TRUE returns generalized Cook’s Distance computed as $[\Delta \hat{\theta}_{ji}]^2$.
- **...**: Additional parameters for sem function.

Value

Returns a list:

- **gCD**: Generalized Cook’s Distance, if cook=TRUE.
- **dparm**: Direction of change in parameter estimates.

Note

If for observation $i$ model does not converge or yields a solution with negative estimated variances or NA parameter values, the associated values of $\Delta \hat{\theta}_{ji}$ are set to NA.

Author(s)

Massimiliano Pastore
References


Examples

```r
## not run: this example take several minutes
data("PDII")
model <- "
  F1 =~ y1+y2+y3+y4
"
# fit0 <- sem(model, data=PDII)
# PAR <- c("F1=-y2","F1=-y3","F1=-y4")
# LY <- parinfluence(PAR,model,PDII)
# str(LY)
# explore.influence(LY$Dparm[,1])

## not run: this example take several minutes
## an example in which the deletion of a case yields a solution
## with negative estimated variances
model <- "
  F1 =~ x1+x2+x3
  F2 =~ y1+y2+y3+y4
  F3 =~ y5+y6+y7+y8
"
# fit0 <- sem(model, data=PDII)
# PAR <- c("F2=-y2","F2=-y3","F2=-y4")
# LY <- parinfluence(PAR,model,PDII)

## not run: this example take several minutes
## dealing with ordinal data
data(Q)
model <- "
  F1 =~ it1+it2+it3+it4+it5+it6+it7+it8+it9+it10
"
# fit0 <- sem(model, data=Q, ordered=colnames(Q))
# LY <- parinfluence("F1=-it4",model,Q,ordered=colnames(Q))
# explore.influence(LY$Dparm[,1])
```

Description

Simulated data set from covariance matrix reported in Bollen (1989).
Usage
data(PDII)

Format
This data frame contains 75 obs. of 11 variables:
- x1: num, gross national product per capita.
- x2: num, consumption per capita.
- x3: num, percentage of the labor force in industrial occupations.
- y7: num, fairness of elections in 1965.
- y8: num, elective nature and effectiveness of the legislative body in 1965.

References

Examples
data(PDII)

---

Q Simulated data set.

Description
Simulated data set.

Usage
data(Q)

Format
This data frame contains 919 obs. of 10 ordinal discrete variables.

Examples
data(Q)
sem.fitres

Fitted values and residuals

Description

It calculates the expected values and the residuals of a sem model.

Usage

sem.fitres(object)
obs.fitres(object)
lat.fitres(object)

Arguments

object       An object of class lavaan.

Details

The main function, sem.fitres(), calls one of the other two routines depending on the type of the model. If model does not contain latent variables, sem.fitres() calls the function obs.fitres(), otherwise calls the function lat.fitres().

The functions obs.fitres() and lat.fitres() are internal functions, do not use it directly.

Value

Returns a data frame containing:

The observed model variables.
The expected values on dependent variables (indicated with hat.)
The residuals on dependent variables (indicated with e.)

Note

In order to compute more interpretable fitted values and residuals, model is forced to have meanstructure = TRUE and std.lv = TRUE.

Author(s)

Massimiliano Pastore
Examples

data("PDII")
model <- "
  F1 <- y1+y2+y3+y4
"

fit0 <- sem(model, data=PDII)
out <- sem.fitres(fit0)
head(out)

par(mfrow=c(2,2))
plot(e.y1-hat.y1, data=out)
plot(e.y2-hat.y2, data=out)
plot(e.y3-hat.y3, data=out)
plot(e.y4-hat.y4, data=out)

qqnorm(out$e.y1); qline(out$e.y1)
qqnorm(out$e.y2); qline(out$e.y2)
qqnorm(out$e.y3); qline(out$e.y3)
qqnorm(out$e.y4); qline(out$e.y4)
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