Package ‘perturb’
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Title Tools for evaluating collinearity
Version 2.05
Author John Hendrickx
Description ```perturb``` evaluates collinearity by adding random noise to
selected variables. ```colldiag``` calculates condition numbers and
variance decomposition proportions to test for collinearity and
uncover its sources.
Maintainer John Hendrickx <John_Hendrickx@yahoo.com>
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R topics documented:

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```
colldiag Condition indexes and variance decomposition proportions
```

Description

Calculates condition indexes and variance decomposition proportions in order to test for collinearity
among the independent variables of a regression model and identifies the sources of collinearity if
present
Usage

colldiag(mod, scale = TRUE, center = FALSE, add.intercept = TRUE)

## S3 method for class 'colldiag'
print(x, dec.places = 3, fuzz = NULL, fuzzchar = ".", ...)

Arguments

mod
A model object or data-frame

scale
If FALSE, the data are left unscaled. Default is TRUE

center
If TRUE, data are centered. Default is FALSE

add.intercept
if TRUE, an intercept is added. Default is TRUE

x
A colldiag object

dec.places
number of decimal places to use when printing

fuzz
variance decomposition proportions less than fuzz are printed as fuzzchar

fuzzchar
character for small variance decomposition proportion values

... arguments to be passed on to or from other methods

Details

Colldiag is an implementation of the regression collinearity diagnostic procedures found in Belsley, Kuh, and Welsch (1980). These procedures examine the “conditioning” of the matrix of independent variables.

Colldiag computes the condition indexes of the matrix. If the largest condition index (the condition number) is large (Belsley et al suggest 30 or higher), then there may be collinearity problems. All large condition indexes may be worth investigating.

Colldiag also provides further information that may help to identify the source of these problems, the variance decomposition proportions associated with each condition index. If a large condition index is associated with two or more variables with large variance decomposition proportions, these variables may be causing collinearity problems. Belsley et al suggest that a large proportion is 50 percent or more.

Value

A colldiag object

condindx A vector of condition indexes

pi A matrix of variance decomposition proportions

print.colldiag prints the condition indexes as the first column of a table with the variance decomposition proportions beside them. print.colldiag has a fuzz option to suppress printing of small numbers. If fuzz is used, small values are replaced by a period ".". Fuzzchar can be used to specify an alternative character.
Note

Colldiag is based on the Stata program coldiag by Joseph Harkness <joe.harkness@jhu.edu>, Johns Hopkins University.

Author(s)

John Hendrickx <John_Hendrickx@yahoo.com>

References


See Also

lm, scale, svd, [car]vif, [rms]vif, perturb

Examples

# The Consumption Function (pp. 149-154)
data(consumption)

ct1 <- with(consumption, c(NA, cons[-length(cons)]))

# compare (5.3)
m1 <- lm(cons ~ ct1+dpi+rate+d_dpi, data = consumption)
anova(m1)
summary(m1)

# compare exhibit 5.11
with(consumption, cor(cbind(ct1, dpi, rate, d_dpi), use="complete.obs"))

# compare exhibit 5.12
cd<-colldiag(m1)
cd
print(cd,fuzz=.3)

## Not run:
# Example of reading UCLA data files from
# http://www.ats.ucla.edu/stat/r/dae/rreg.htm
library(foreign)
elemapi <- read.dta("http://www.ats.ucla.edu/stat/data/elemapi2.dta")
attach(elemapi)

# Example of SAS collinearity diagnostics from
# http://www.ats.ucla.edu/stat/sas/webbooks/reg/chapter2/sasreg2.htm
# 2.4 Tests for Collinearity
m2 <- lm(api00 ~ acs_k3+avg_ed+grad_sch+col_grad+some_col)
summary(m2)
The Consumption Function

Description

Example from pp 149-154 of Belsley (1991), Conditioning Diagnostics

Usage

data(consumption)

Format

A data frame with 28 observations on the following 5 variables.

- **year**: 1947 to 1974
- **cons**: total consumption, 1958 dollars
- **rate**: the interest rate (Moody’s Aaa)
- **dpi**: disposable income, 1958 dollars
- **d_dpi**: annual change in disposable income

Source

pp 149-154 of Belsley (1991), Conditioning Diagnostics

References


Examples

data(consumption)
**perturb**

**Perturbation analysis to evaluate collinearity**

**Description**

Adds random noise to selected variables to evaluate collinearity. Also suitable for other models than linear regression and for categorical independent variables.

**Usage**

```r
perturb(mod, pvars = NULL, prange = NULL, ptrans = NULL, pfac = NULL, uniform = FALSE, niter = 100)
```

```r
## S3 method for class 'perturb'
summary(object, dec.places=3, full=FALSE,...)
```

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

**Arguments**

- `mod` A model object, not necessarily type `lm`
- `pvars` Contains an array of variables to be perturbed. Random values are added to the variable, after which the model is re-estimated.
- `prange` Contains an array of values determining the magnitude of perturbations. There should be as many `prange` values as `pvars` variables.
- `ptrans` Contains an array of transformations to be applied. Each element should contain valid R syntax in quotes for deriving one of the `pvars` as a function of other variables.
- `pfac` Contains a list of categorical variables to be perturbed and parameters controlling the reclassification process. The first component must be a factor name. The name for the first component is ignored. Other list components should correspond with options for `reclassify`. The usage of these parameters is discussed more fully below under the heading "Categorical variables".
- `uniform` If `uniform=TRUE`, random values from a uniform distribution \( \text{unif}(-x/2, x/2) \) are added to the perturb variables, where \( x \) is the `prange` value corresponding with each `pvars` variable. The default is to add values from a normal distribution \( N(0,x) \).
- `niter` Indicates the number of times to re-estimate the model. Default is 100.
- `object` a `perturb` object to be summarized
- `x` a `summary.perturb` object to be printed
- `dec.places` number of decimal places to use when printing
- `full` if `TRUE`, some extra information is printed
- `...` arguments to be passed on to or from other methods. Print options for class `matrix` may be used, e.g. `print.gap`
Details

Perturb is a tool for assessing the impact of small random changes (perturbations) to variables on parameter estimates. It is an alternative for collinearity diagnostics such as vif in the car package, vif in the rms package or colldiag in this package. Perturb is particularly useful for evaluating collinearity if interactions are present or nonlinear transformations of variables, e.g. a squared term. Perturb can show how the perturbations affect the estimates of a variable and terms derived from it whereas other collinearity diagnostics simply treat interactions and transformations as regular independent variables. Perturb is not limited to linear regression but can be used for all regression-like models. Perturb can also deal with categorical variables by randomly misclassifying them to assess the impact on parameter estimates.

Perturb works by adding a small random “perturbation” value to selected independent variables, then re-estimating the model. This process is repeated niter times, after which a summary of the means, standard deviation, minimum and maximum of the parameter estimates is displayed. If collinearity is a serious problem in the data, then the estimates will be unstable and vary strongly.

Perturb can be used with categorical variables. Categorical variables are reclassified according to a table of reclassification probabilities. Random numbers determine to which category each case is reclassified at each iteration. The reclassification probabilities are specified to make reclassification to the same category highly likely. For ordered variables, short distance reclassification can be made more likely than long distance. See the section on “Categorical variables” and reclassify for further details.

Value

An object of class “perturb”. The main result is contained in coef.table, which contains the parameter estimates for each iteration of the perturbation analysis. summary prints the mean, standard deviation, minimum and maximum of the parameter estimates over the iterations. If the option full is specified, reclassify prints additional information on how the reclassification probabilities were derived. Summary also prints information on the transformed model formula.

coeff.table Estimated coefficients for each iteration of the perturbation analysis
formula The model formula used
pvars The continuous variables perturbed in the analysis
prange Magnitude of the perturbations
ptrans2 The transformations using the temporary variables of the perturbation analysis
reclassify.tables objects produced by reclassify for each factor in the perturbation analysis
formula2 The model formula using temporary variables
distribution “normal” or “uniform”, the distribution from which to draw random numbers

Categorical variables

In a perturbation analysis, categorical variables are reclassified with a high probability of remaining in the same category. This could be accomplished in several ways. reclassify lets you specify the target percentage reclassification, then adjusts the reclassification frequencies so that the expected frequencies of the reclassified variable are the same as those of the original. In addition, reclassify
perturb

imposes a meaningful pattern of association between the original and the reclassified variable. See reclassify for details.

Categorical variables are specified in perturb as a list in the pfac option. The first (unnamed) component is the factor to be reclassified. The names of following components should be valid reclassify options follows by appropriate values. For example, to reclassify the factor “type” with a 95% probability of reclassify to the same category, use:

```r
p2<-perturb(m2,pvars=c("income","education"),prange=c(1,1),
          pfac=list("type",pcnt=95))
```

This command will iteratively re-estimate model m2 100 times (default). Random values from a normal distribution with a standard deviation of 1 will be added to the variables income and education. 

reclassify creates a table of initial reclassification probabilities for type with a 95% probability of reclassification to the same category. This initial table is adjusted and the final reclassification probabilities printed in the output are subsequently used to reclassify type at each iteration.

Use a list of lists to specify a model with more than one reclassification factor, for example:

```r
pfac=list(list("fegp6",pcnt=95),list("eyrc",pcnt=m1),list("expc",pcnt=m2))
q<-perturb(r1, pfac=pfac)
```

Note

Perturb can be used with estimation procedures other than `lm`. On the other hand, collinearity is a result of extreme (multiple) correlation among independent variables. Another option is `vif` in the `rms` package or `colldiag`, which use only the independent variables of a regression model. This will usually be a faster solution since maximum likelihood procedures require iterative estimation for each iteration of the perturbation analysis. It is possible though that certain procedures are more sensitive to collinearity than `lm`, in which case perturb could be a better solution.

Author(s)

John Hendrickx <John_Hendrickx@yahoo.com>

References


See Also

reclassify, colldiag, [car]vif, [rms]vif
Examples

```r
library(car)
data(Duncan)
attach(Duncan)
m1<-lm(prestige~income+education)
summary(m1)
anova(m1)
vif(m1)
p1<-perturb(m1,pvars=c("income","education"),prange=c(1,1))
summary(p1)
m2<-lm(prestige~income+education+type)
summary(m2)
anova(m2)
vif(m2)
p2<-perturb(m2,pvars=c("income","education"),prange=c(1,1),pfac=list("type",pcnt=95))
summary(p2)

## Not run:
r1<-lm(ses~fegp6+educyr+eyr+exp2)
summary(r1)
q<-perturb(r1,c("eyr","exp"),c(2.5,2.5),ptrans="exp2<-exp^2")
summary(q)

fegp6<-as.factor(fegp6)

# eyr and exp also as factors
eyr<-cut(eyr,c(min(eyr),40,50,60,70,80,max(eyr)),include.lowest=T,right=F)
table(eyr)
exp<-cut(exp,c(0,10,20,max(exp)),include.lowest=T,right=F)
table(exp)

# rough initial reclassification probabilities,
# program will ensure they sum to 100 row-wise
m1<-matrix(0,nlevels(eyr),nlevels(eyr))
m1[row(m1)]==col(m1)]<-80
m1[abs(row(m1)-col(m1))==1]<-8
m1[abs(row(m1)-col(m1))==2]<-2
m1

m2<-matrix(0,nlevels(exp),nlevels(exp))
m2[row(m2)]==col(m2)]<-80
m2[abs(row(m2)-col(m2))==1]<-10
m2[abs(row(m2)-col(m2))==2]<-2
m2

r2<-lm(ses~fegp6+eyr+exp)
summary(r2)
pfac=list(list("fegp6",pcnt=95),list("eyr",pcnt=m1),list("exp",pcnt=m2))
q2<-perturb(r2,pfac=pfac,niter=1)
summary(q2)

## End(Not run)
```
Description

reclassify is called by perturb to calculate reclassification probabilities for categorical variables. Use separately to experiment with reclassification probabilities.

Usage

reclassify(varname, pcnt = NULL, adjust = TRUE, bestmod = TRUE, min.val = .1, diag = NULL, unif = NULL, dist = NULL, assoc = NULL)

## S3 method for class 'reclassify'
print(x, dec.places = 3, full = FALSE, ...)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>varname</td>
<td>a factor to be reclassified</td>
</tr>
<tr>
<td>pcnt</td>
<td>initial reclassification percentages</td>
</tr>
<tr>
<td>adjust</td>
<td>makes the expected frequency distribution of the reclassified variable equal to that of the original</td>
</tr>
<tr>
<td>bestmod</td>
<td>imposes an appropriate pattern of association between the original and the reclassified variable</td>
</tr>
<tr>
<td>min.val</td>
<td>value to add to empty cells of the initial expected table when estimating the best model</td>
</tr>
<tr>
<td>diag</td>
<td>The odds of same versus different category reclassification</td>
</tr>
<tr>
<td>unif</td>
<td>Controls short distance versus long distance reclassification for ordered variables</td>
</tr>
<tr>
<td>dist</td>
<td>alternative parameter for short versus long distance reclassification</td>
</tr>
<tr>
<td>assoc</td>
<td>a matrix defining a loglinear pattern of association</td>
</tr>
<tr>
<td>x</td>
<td>a reclassify object to be printed</td>
</tr>
<tr>
<td>dec.places</td>
<td>number of decimal places to use when printing</td>
</tr>
<tr>
<td>full</td>
<td>if TRUE, some extra information is printed</td>
</tr>
<tr>
<td>...</td>
<td>arguments to be passed on to or from other methods. Print options for class matrix may be used, e.g. print.gap</td>
</tr>
</tbody>
</table>

Details

reclassify creates a table of reclassification probabilities for varname. By default, the reclassification probabilities are defined so that the expected frequency distribution of the reclassified variable is identical to that of the original. In addition, a meaningful pattern of association is imposed
between the original and the reclassified variable. reclassify is called by perturb to calculate reclassification probabilities for categorical variables. reclassify can be used separately to find a suitable reclassification probabilities.

Reclassify has several options but the most relevant will generally be the pcnt option. The argument for pcnt can be

- a scalar
- a vector of length \( n \)
- a vector of length \( n^2 \), where \( n \) is the number of categories of the variable to be reclassified.

If the argument for pcnt is a scalar, its value is taken to be the percentage of cases to be reclassified to the same category, which is the same for all categories. A table of initial reclassification probabilities for the original by the reclassified variable is created with this value divided by 100 on the diagonal and equal values on off-diagonal cells.

If the argument for pcnt is a vector of length \( n \), its values indicate the percentage to be reclassified to the same category for each category separately. These values divided by 100 form the diagonal of the table of initial reclassification probabilities. Off-diagonal cells have the same values for rows so that the row sum is equal to 1.

If the argument for pcnt is a vector of length \( n^2 \), its values form the table of initial reclassification probabilities. prop.table is used to ensure that these values sum to 1 over the columns. Specifying a complete table of initial reclassification probabilities will be primarily useful when an ordered variable is being reclassified.

Reclassify prints an initial table of reclassification probabilities based on the pcnt option. This table is not used directly though but adjusted to make the expected frequencies of the reclassified variable identical to those of the original. In addition, a meaningful pattern of association is imposed between the original and the reclassified variable. Details are given in the section “Adjusting the reclassification probabilities”.

Knowledgeable users can specify a suitable pattern of association directly, bypassing the pcnt option. Details are given in the section “Specifying a pattern of association directly”.

Value

An object of class reclassify. By default, print.reclassify prints the variable name and the reclass.prob. If the full option is used with print.reclassify, additional information such as the initial reclassification probabilities, initial expected table, best model, are printed as well.

```r
variable  The variable specified
reclass.prob Row-wise proportions of fitted.table
cum.reclass.prob Cumulative row-wise proportions
exptab$init.pcnt initial reclassification probabilities (option pcnt)
exptab$init.tbl initial expected frequencies (option pcnt)
bestmod The best model found for the table of initial expected frequencies (option pcnt)
assoc The log pattern of association specified using pcnt and bestmod=FALSE
```
The coefficients of a fitted loglinear model

The adjusted table of expected frequencies

Adjusting the reclassification probabilities

A problem with the initial reclassification probabilities created using pcnt is that the expected frequencies of the reclassified variable will not be the same as those of the original. Smaller categories will become larger in the expected frequencies, larger categories will become smaller. This can be seen in the column marginal of the initial table of expected frequencies in the reclassify output. This could have a strong impact on the standard errors of reclassified variables, particularly as categories differ strongly in size.

To avoid this, the initial expected table is adjusted so that the column margin is the same as the row margin, i.e. the expected frequencies of the reclassified variable are the same as those of the original. Use adjust=FALSE to skip this step. In that case the initial reclassification probabilities are also the final reclassification probabilities.

A second objection to the initial reclassification probabilities is that the pattern of association between the original and the reclassified variable is arbitrary. The association between some combinations of categories is higher than for others. Reclassify therefore derives an appropriate pattern of association for the initial expected table of the original by reclassified variable. This pattern of association is used when “adjusting” the marginals to make the frequency distribution of the reclassified variable identical to that of the original. Use the option bestmod=FALSE to skip this step.

The patterns of association used by reclassify are drawn from loglinear models for square tables, also known as “mobility models” (Goodman 1984, Hout 1983). Many texts on loglinear modelling contain a brief discussion of such models as well. For unordered variables, a “quasi-independent” pattern of association would be appropriate. Under quasi-independent association, the row variable is independent of the column variable if the diagonal cells are ignored.

If the argument for pcnt was a scalar, reclassify fits a “quasi-independent (constrained)” model. This model has a single parameter diag which indicates the log-odds of same versus different reclassification. This log-odds is the same for all categories. If the argument was of vector of length n, then a regular quasi-independence model is fitted with parameters diag1 to diagn. These parameters indicate the log-odds of same versus different category reclassification, which is different for each category. For both models, the reclassified category is independent of the original category if the diagonal cells are ignored.

If the argument for pcnt was a vector of length n^2, reclassify fits two models, a “quasi-distance model” and a “quasi-uniform association” model, and selects the one with the best fit to the initial expected table. Both have the diag parameter of the “quasi-independence (constrained)” model. An additional parameter is added to make short distance reclassification more likely than long distance reclassification. The quasi-uniform model is stricter: it makes reclassification less likely proportionately to the squared difference between the two categories. The distance model makes reclassification less likely proportionately to the absolute difference between the two categories.

In some cases, the initial expected table based on the pcnt option contains empty cells. To avoid problems when estimating the best model for this table, a value of .1 is added to these cells. Use the min.val option to specify a different value.
Specifying a pattern of association directly

If the pcnt option is used, reclassify automatically determines a suitable pattern of association between the original and the reclassified variable. Knowledgeable users can also specify a pattern of association directly. The final reclassification probabilities will then be based on these values. Built-in options for specifying the loglinear parameters of selected mobility models are:

- **diag** quasi-independence constrained (same versus different category reclassification)
- **unif** uniform association (long versus short distance reclassification for ordered categories)
- **dist** linear distance model (allows more long distance reclassification than uniform association)

The assoc option can be used to specify an association pattern of one’s own choice. The elements of assoc should refer to matrices with an appropriate loglinear pattern of association. Such matrices can be created in many ways. An efficient method is:

```r
wrk<-diag(table(factor))
myassoc<-abs(row(wrk)-col(wrk))*-log(5)
```

This creates a square diagonal matrix called wrk with the same number of rows and columns as the levels of factor. row(wrk) and col(wrk) can now be used to define a loglinear pattern of association, in this case a distance model with parameter 5. reclassify checks the length of the matrix equals \( n^2 \), where \( n \) is the number of categories of varname and ensures that the pattern of association is symmetric.

Imposing a pattern of association

A table with given margins and a given pattern of association can be created by

- estimating a loglinear model of independence for a table with the desired margins
- while specifying the log pattern of association as an offset variable (cf. Kaufman & Schervish (1986), Hendrickx (2004)).

The body of the table is unimportant as long as it has the appropriate margins. The predicted values of the model form a table with the desired properties.

The expected table of the original by the reclassified variable is adjusted by creating a table with the frequency distribution of the original variable on the diagonal cells. This table then has the same marginals for the row and column variables. The pattern of association is determined by the reclassify options. If pcnt is used and bestmod=TRUE then the predicted values of the best model are used as the offset variable. If bestmod=FALSE, the log values of the initial expected table are made symmetric and used as the offset variable. If a loglinear model was specified directly, a variable is created in the manner of the assoc example.

A small modification in procedure is that reclassify uses a model of equal main effects rather than independence. Since the pattern of association is always symmetric, the created table will then also be exactly symmetric with the frequency distribution of the original variable as row and column marginal.

Author(s)

John Hendrickx <John_Hendrickx@yahoo.com>
reclassify

References


See Also

perturb, colldiag, [car]vif, [rms]vif

Examples

```r
library(car)
data(Duncan)
attach(Duncan)

reclassify(type,pcnt=95)
```
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