

Package: lmhelprs (via r-universe)

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Title Helper Functions for Linear Model Analysis

Version 0.4.5

Description A collection of helper functions for multiple regression models fitted by `lm()`. Most of them are simple functions for simple tasks which can be done with coding, but may not be easy for occasional users of R. Most of the tasks addressed are those sometimes needed when using the 'manymome' package (Cheung and Cheung, 2023, <[doi:10.3758/s13428-023-02224-z](https://doi.org/10.3758/s13428-023-02224-z)>) and 'stdmod' package (Cheung, Cheung, Lau, Hui, and Vong, 2022, <[doi:10.1037/hea0001188](https://doi.org/10.1037/hea0001188)>). However, they can also be used in other scenarios.

URL <https://sfcheung.github.io/lmhelprs/>

BugReports <https://github.com/sfcheung/lmhelprs/issues>

License GPL (>= 3)

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| | |
|------------|---------------------------------|
| data_test1 | <i>Sample Data: For Testing</i> |
|------------|---------------------------------|

Description

A eight-variable dataset with 100 cases.

Usage

```
data_test1
```

Format

A data frame with 100 rows and 8 variables:

x1 Predictor. Numeric.

x2 Predictor. Numeric.

x3 Predictor. Numeric.

x4 Predictor. Numeric.

x5 Predictor. Numeric.

y Outcome. Numeric.

cat1 Predictor. String. Values: "Alpha", "Beta", "Gamma"

cat2 Predictor. String. Values: "North", "South", "East", "West"

Examples

```
data(data_test1)
lm(y ~ x1 + cat2 + cat1 + cat2:cat1, data_test1)
```

`hierarchical`*Check Models Hierarchy*

Description

Check a list of 'lm' objects to see whether they are be ordered in a way for doing hierarchical regression analysis.

Usage

```
hierarchical(...)
```

Arguments

... The outputs of `lm()`, that is, one or more `lm`-class objects. The outputs of other model fitting functions may also be used, but should be used with cautions. Please refer to the "How it works" section in "Details."

Details

Two models can be compared by hierarchical regression analysis if one model can be formed by adding one or more terms to the other model.

This function checks whether a list of `lm` outputs can be ordered from the simplest model to the most complex model, with a more complex model formed by adding one or more terms to a simpler model.

How it works:

It extracts the terms in each model by `stats::terms()` and then extracts the labels of the terms by `labels()`. The labels are then used to determine the hierarchical order.

Therefore, in principle, this function can be used for the outputs of other model fitting functions as long as their outputs support the `stats::terms()` and the labels can be used to determine hierarchical order of two models.

Value

If the models can be ordered in a hierarchical way, the output is a list of the original `lm` outputs, sorted from the model with the smallest number of terms to the model with the largest number of terms. If the models cannot be ordered this way, `NA` is returned.

Author(s)

Shu Fai Cheung <https://orcid.org/0000-0002-9871-9448>

See Also

[stats::lm\(\)](#)

Examples

```

dat <- data_test1
lm1 <- lm(y ~ x1 + x2, dat)
lm2 <- lm(y ~ x1 + x2 + x3 + x4, dat)
lm3 <- lm(y ~ x1 + cat1 + cat2 + x2 + x3 + x4, dat)
lm4 <- lm(y ~ x1 + x2*x3 + x4, dat)

# The order of entry does not matter
hierarchical(lm1, lm4, lm2)

# The following three models yield NA
hierarchical(lm3, lm4, lm2)

```

hierarchical_lm *Hierarchical Regression Analysis*

Description

Do hierarchical regression analysis on two or more models fitted by 'lm()'.

Usage

```
hierarchical_lm(...)
```

Arguments

... The outputs of `lm()`, that is, one or more `lm`-class objects. The outputs of other model fitting functions may also be used, but should be used with cautions. Please refer to the "How it works" section in "Details." It also supports the output of `many_lm()`, and can mix the outputs of `many_lm()` with those of `lm()`.

Details

It conducted hierarchical regression analysis on two or more models fitted by `stats::lm()`. The models must be able to be ordered from the simplest to the most complex, with each more complex model formed by adding one or more terms to the simpler model.

ANOVA will be conducted to compare each model with the next more complex model in the order, with R-squared change computed.

Value

If the models can be ordered in a hierarchical way, the output is an ANOVA table with the R-squared estimate of each model, and the R-squared change of each model compared to the simpler model preceding this model in the order. The class of the output is `hierarchical_lm`, with a print method. If the models cannot be ordered this way, NA is returned.

How it works:

It call `hierarchical()` firsts to order the outputs for `stats::lm()`, If they can be ordered in a hierarchical way, they will be passed to `stats::anova()`. R-squared and R-squared change will be computed if they are available in the `summary()` method applied to each model.

Therefore, in principle, this function can also be used for the outputs of other model fitting functions if their outputs have `stats::anova()` and `summary()` methods.

Check Datasets Used:

The comparison is meaningful only if all models are fitted to the same datasets. There is not way to guarantee this is the case, given only the output of `lm()`. However, there are necessary conditions to claim that the same datasets are used: the number of cases are the same, the means, variances, and covariances of numerical variables, and the frequency distributions of variables common to two models are identical. If at least one of these conditions is not met, then two models must have been fitted to two different datasets.

The function will check these conditions and raise an error if any of these necessary conditions are not met.

Author(s)

Shu Fai Cheung <https://orcid.org/0000-0002-9871-9448>

See Also

`stats::lm()`, `hierarchical()`

Examples

```
dat <- data_test1
lm1 <- lm(y ~ x1 + x2, dat)
lm2 <- lm(y ~ x1 + x2 + x3 + x4, dat)
lm3 <- lm(y ~ x1 + cat1 + cat2 + x2 + x3 + x4, dat)
lm4 <- lm(y ~ x1 + x2*x3 + x4, dat)

hierarchical_lm(lm1, lm3, lm2)
hierarchical_lm(lm1, lm2, lm4)
# The following models will yield an error message:
tryCatch(hierarchical_lm(lm1, lm3, lm2, lm4), error = function(e) e)
```

lm_list_to_partable *Convert a 'lm_list' Object To a Parameter Table*

Description

Convert the output of many_lm() to a lavann-style parameter table.

Usage

```
lm_list_to_partable(
  object,
  keep_intercepts = FALSE,
  vcov_args = list(),
  pvalue_fun = NULL,
  rsquare = FALSE,
  ci = FALSE,
  ci_fun = stats::confint,
  ci_args = list(level = 0.95)
)
```

Arguments

| | |
|-----------------|--|
| object | The output of <code>many_lm()</code> or <code>manymome::lm2list()</code> . |
| keep_intercepts | Logical. If TRUE, the intercepts of the regression models and the means of the "pure" predictors (variables not being the outcome variables of any of the regression models) are kept in the parameter table. If FALSE, the default, all intercepts and means will be removed. |
| vcov_args | A named list of arguments to be passed to <code>stats::vcov()</code> when computing the standard errors of the regression coefficients. Default is <code>list()</code> , an empty list. |
| pvalue_fun | The function to be used to compute the p -values of regression coefficients. Ignored for now. Included for adding this feature in the future. |
| rsquare | Logical. Whether R-squares will be included in the output, with <code>r2</code> as the operator in the column op. Default is FALSE. Not included by default because <code>semPlot::semPaths()</code> will draw the R-squares over the residual variances. |
| ci | Logical. If TRUE, confidence intervals will be added, computed by <code>stats::confint()</code> . |
| ci_fun | The function to be used to form the confidence intervals for regression coefficients. Default is <code>stats::confint</code> |
| ci_args | A named list of arguments to be passed to <code>ci_fun</code> . Default is <code>list(level = .95)</code> , requesting 95% confidence intervals. |

Details

This function convert a a list of `lm` objects, such as the output of `many_lm()` or `manymome::lm2list()`, to a table of parameter estimates similar to the output of `lavaan::parameterTable`.

The output is designed to be used by `semPlot::semPaths()` and so contains only information necessary for the plot.

The output of `stats::lm()` is already supported by `semPlot::semPaths()`, and it can also combine a list of regression models into on single plot. However, it will convert interaction terms to knots. Moreover, if two interaction terms in two different models share the a variable, it will be incorrectly combined to become a single knot (Version 1.1.6). Therefore, this function was developed to let users to draw the model as if it were a path model in structural equation modeling.

Value

A data frame object with columns such as lhs, op, rhs, and est, major columns of the output of `lavaan::parameterTable()` necessary for plotting the model using `semPlot::semPaths()`.

Author(s)

Shu Fai Cheung <https://orcid.org/0000-0002-9871-9448>

See Also

`many_lm()` and `manymome::lm2list()`.

Examples

```
data(data_test1)
mod <- "x3 ~ x2*x1
       x4 ~ x3
       x5 ~ x4 + x3"
out <- many_lm(mod, data_test1)
out_ptable <- lm_list_to_partable(out)
out_ptable

m <- matrix(c("x1", "x2", "x2:x1", NA, "x3", NA, "x4", NA, NA, NA, "x5", NA),
            nrow = 3, ncol = 4)
m

# The output can be used by semPlot::semPaths()

if (requireNamespace("semPlot", quietly = TRUE)) {
  library(semPlot)
  p <- semPaths(out_ptable,
               what = "paths",
               whatLabels = "est",
               nCharNodes = 0,
               style = "ram",
               layout = m,
               exoCov = FALSE,
               DoNotPlot = TRUE)

  plot(p)

  # If it is desired to use knots to
  # denote interaction terms, then,
  # the output of many_lm() can be used
  # directly.

  m2 <- matrix(c("x1", NA, "x2", NA, "x3", NA, "x4", NA, NA, NA, "x5", NA),
              nrow = 3, ncol = 4)
  p2 <- semPaths(out,
               what = "paths",
               whatLabels = "est",
               nCharNodes = 0,
               style = "ram",
```

```

        layout = m2,
        exoCov = FALSE,
        intercepts = FALSE,
        DoNotPlot = TRUE)
plot(p2)

# This illustrates the problem with using
# the list of lm-outputs directly when
# a variable is involved in the interaction terms
# of two or more models.

m3 <- matrix(c("x2",  NA, "x1",  NA, "x3",
              NA,  NA,  NA,  NA,  NA,
              NA, "x4",  NA, "x5",  NA),
            nrow = 5, ncol = 3)
mod3 <- "x4 ~ x2*x1
        x5 ~ x3*x1"
out3 <- many_lm(mod3, data_test1)
p3 <- semPaths(out3,
              what = "paths",
              whatLabels = "est",
              nCharNodes = 0,
              style = "ram",
              layout = m3,
              exoCov = FALSE,
              intercepts = FALSE,
              DoNotPlot = TRUE)

plot(p3)

}

```

many_lm

Fit Linear Models Defined By Model Syntax

Description

Fit a list of linear models defined by model syntax.

Usage

```
many_lm(models, data, na_omit_all = TRUE, ...)
```

Arguments

| | |
|--------|---|
| models | Character. Model syntax. See Details. |
| data | The data frame. Must be supplied if na_omit_all is TRUE. If na_omit_all is FALSE, it can be omitted (though not suggested). |

| | |
|-------------|--|
| na_omit_all | How missing data is handled across models. If TRUE, the default, then only cases with no missing data on all variables used at least one of the models will be retained (i.e., listwise deletion). If FALSE, then missing data will be handled in each model separately by <code>lm()</code> . |
| ... | Additional arguments. To be passed to <code>lm()</code> . |

Details

This function extracts linear model formulas from a model syntax (a character vector), fits each of them by `lm()`, and stores the results in a list.

Lines with the first non-whitespace character `"#"` are treated as comments and ignored.

Each line must be a valid formula for `lm()`.

Listwise deletion:

If `na_omit_all` is TRUE, the default, then cases with missing data on at least one of the variables used in the model will be removed. Each call to `lm()` will have `subset` set to an integer vector of cases *not* removed (i.e., cases retained)

Handling the subset argument:

If `subset` is used when calling this function, it will also be used to select cases.

Note that the `subset` argument in the call in each model will be replaced by a numeric vector of cases retained, determined by both missing data and the original value of the `subset`.

Value

A list of the output of `lm()`. The class is `lm_list_lmhelpers`.

Author(s)

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See Also

[stats::lm\(\)](#)

Examples

```
data(data_test1)
mod <- "x3 ~ x2 + x1
      x4 ~ x3
      x5 ~ x4*x1"
out <- many_lm(mod, data_test1)
summary(out)
```

print.hierarchical_lm *Print a hierarchical_lm Class Object*

Description

Print the content of a 'hierarchical_lm'-class object.

Usage

```
## S3 method for class 'hierarchical_lm'
print(
  x,
  digits = 4,
  signif.stars = getOption("show.signif.stars"),
  eps.Pvalue = 0.001,
  ...
)
```

Arguments

| | |
|--------------|--|
| x | A hierarchical_lm-class object, usually the output of hierarchical_lm(). |
| digits | The minimum number of significant digits to be used for most numbers. To be used by the print method of anova-class objects. |
| signif.stars | Logical. To be used by the print method of anova-class objects. |
| eps.Pvalue | To be passed to format.pval(). It controls how small p -values are displayed. Default is .001. That is, p -values less than .001 will be displayed as <.001. |
| ... | Optional arguments. To be passed to the print method of anova-class objects. |

Details

The printout is very similar to that of the print method of an anova object. It simply overrides the default values for some arguments, notably esp.Pvalue to prevent small p -values to be presented in scientific notation.

Value

x is returned invisibly. Called for its side effect.

Author(s)

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See Also

[hierarchical_lm\(\)](#)

Examples

```
dat <- data_test1
lm1 <- lm(y ~ x1 + x2, dat)
lm2 <- lm(y ~ x1 + x2 + x3 + x4, dat)
lm3 <- lm(y ~ x1 + cat1 + cat2 + x2 + x3 + x4, dat)
lm4 <- lm(y ~ x1 + x2*x3 + x4, dat)

hierarchical_lm(lm1, lm3, lm2)
hierarchical_lm(lm1, lm2, lm4)
```

```
print.lm_list_lmhelpers
```

Print an lm_list_lmhelpers-Class Object

Description

Print the content of the output of [many_lm\(\)](#).

Usage

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

Arguments

| | |
|-----|---|
| x | The output of many_lm() . |
| ... | Other arguments. Not used. |

Details

Adapted from the package `manymome` such that `many_lm()` can be used with `manymome`.

Value

x is returned invisibly. Called for its side effect.

Examples

```
data(data_test1)
mod <- "x3 ~ x2 + x1
      x4 ~ x3
      x5 ~ x4*x1"
out <- many_lm(mod, data_test1)
out
```

```
summary.lm_list_lmhelps
```

Summary of an lm_list_lmhelps-Class Object

Description

The summary of content of the output of `many_lm()`.

Usage

```
## S3 method for class 'lm_list_lmhelps'
summary(object, ...)
```

```
## S3 method for class 'summary_lm_list_lmhelps'
print(x, digits = 3, ...)
```

Arguments

| | |
|---------------------|---|
| <code>object</code> | The output of <code>many_lm()</code> . |
| <code>...</code> | Other arguments. Not used. |
| <code>x</code> | An object of class <code>summary_lm_list_lmhelps</code> . |
| <code>digits</code> | The number of significant digits in printing numerical results. |

Value

`summary.lm_list_lmhelps()` returns a `summary_lm_list_lmhelps`-class object, which is a list of the `summary()` outputs of the `lm()` outputs stored.

`print.summary_lm_list_lmhelps()` returns `x` invisibly. Called for its side effect.

Adapted from the package `manymome` such that `many_lm()` can be used without `manymome`.

Functions

- `print(summary_lm_list_lmhelps)`: Print method for output of summary for `lm_list_lmhelps`.

Examples

```
data(data_test1)
mod <- "x3 ~ x2 + x1
       x4 ~ x3
       x5 ~ x4*x1"
out <- many_lm(mod, data_test1)
summary(out)
```

`test_highest`*Test the Highest Order Term by ANOVA*

Description

Identify the highest order terms in a model fitted by `'lm()'`, and compare this model to a model with this term removed using ANOVA.

Usage

```
test_highest(lm_out)
```

```
highest_order(lm_out)
```

Arguments

`lm_out` The output of `stats::lm()`.

Details

The function `test_highest()` first check if a model fitted by `stats::lm()` has a unique highest order term (e.g., the term `x1:x2`, in the model `y ~ x1 + x2 + x1:x2`). If yes, it will fit a model with this term removed, and then call `hierarchical_lm()` to compare the original model with this reduced model.

If the model does not have a unique highest order term, an error will be raised.

Value

A `hierarchical_lm`-class object, which is the output of `hierarchical_lm()`. Two models are compared, the original model and the model with the unique highest order term removed.

Functions

- `test_highest()`: Test the highest order term.
- `highest_order()`: Find the highest order term.

Limitation

It relies on terms created by `stats::lm()` to determine the order of each term. If a higher order term is created manually (e.g., `I(x1 * x2)`), then it cannot know that this term is a second order term.

Author(s)

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See Also[hierarchical_lm\(\)](#)**Examples**

```
dat <- data_test1

lm1 <- lm(y ~ x1 + x2 + cat1*x3, dat)
lm2 <- lm(y ~ x1 + x2*x3 + x4, dat)

test_highest(lm1)
test_highest(lm2)

highest_order(lm1)
highest_order(lm2)

# The followings will yield an error

lm3 <- lm(y ~ x1 + x2 + x3, dat)
summary(lm3)
tryCatch(test_highest(lm3), error = function(e) e)
tryCatch(highest_order(lm3), error = function(e) e)

lm4 <- lm(y ~ x1 + x2*x3 + x4*x5, dat)
summary(lm4)
tryCatch(test_highest(lm4), error = function(e) e)
tryCatch(highest_order(lm4), error = function(e) e)
```

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