

Package ‘MTest’

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Type Package

Title A Procedure for Multicollinearity Testing using Bootstrap

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Description

Functions for detecting multicollinearity. This test gives statistical support to two of the most famous methods for detecting multicollinearity in applied work: Klein’s rule and Variance Inflation Factor (VIF). See the URL for the papers associated with this package, as for instance, Morales-Oñate and Morales-Oñate (2015) <[doi:10.33333/rp.vol51n2.05](https://doi.org/10.33333/rp.vol51n2.05)>.

Depends R (>= 4.1.0)

License GPL (>= 3)

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Repository CRAN

URL <https://github.com/vmoprojs/MTest>

BugReports <https://github.com/vmoprojs/MTest/issues>

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MTest

*Bootstrap-based test for multicollinearity (Klein and VIF)***Description**

MTest implements a nonparametric (pairs) bootstrap to assess multicollinearity by providing achieved significance levels (ASL) for two widely used diagnostics: Klein's rule and the Variance Inflation Factor (VIF). It returns bootstrap distributions of the global R^2 and the auxiliary R_j^2 (from regressions of each predictor on the remaining predictors), along with p-values for both rules.

Usage

```
MTest(object, nboot = 100, nsam = NULL, trace = FALSE, seed = NULL,
      valor_vif = 0.9)
```

Arguments

| | |
|-----------|---|
| object | A fitted model, typically of class "lm". The function uses its <code>model.frame</code> and <code>model.matrix</code> as the fixed design for resampling. |
| nboot | Integer. Number of bootstrap iterations (rows resampled with replacement). |
| nsam | Integer. Bootstrap sample size per iteration. Defaults to the original number of rows. |
| trace | Logical. If TRUE, shows a progress bar. |
| seed | Integer. Optional RNG seed for reproducibility. |
| valor_vif | Numeric in $[0, 1)$. Threshold applied to R_j^2 for the VIF rule: the ASL is $P(R_j^2 > c)$, where $c = \text{valor_vif}$. Since $\text{VIF}_j = 1/(1 - R_j^2)$, $\text{valor_vif} = 0.9$ corresponds roughly to $\text{VIF} \geq 10$. |

Details

Model. Consider the linear regression model

$$Y_i = \beta_0 + \beta_1 X_{1i} + \cdots + \beta_p X_{pi} + u_i, \quad i = 1, \dots, n,$$

and the *auxiliary* regressions obtained by regressing each predictor X_j on the remaining predictors X_{-j} . Let R_g^2 be the global coefficient of determination and R_j^2 the coefficient of determination of the j -th auxiliary regression.

Diagnostics and achieved significance levels (ASL).

- *Klein's rule*: flag multicollinearity if $R_j^2 > R_g^2$. We estimate the ASL as $P(R_g^2 < R_j^2)$ using the bootstrap distribution.
- *VIF rule*: flag multicollinearity if VIF exceeds a threshold. Since $\text{VIF}_j = 1/(1 - R_j^2)$, this is equivalent to testing R_j^2 against valor_vif . We estimate $P(R_j^2 > \text{valor_vif})$.

Bootstrap scheme. The function resamples rows of the model frame (pairs bootstrap) and, for each bootstrap sample, computes R_g^2 and R_j^2 (hence VIF) using the same expanded design matrix as the original fit. This makes the procedure robust to transformed terms on either side of the formula (e.g., $\log(y)$, $I(X^2)$, interactions, factors, `poly()`, etc.).

Value

An object of class MTest, which is a list containing:

| | |
|------------|---|
| pval_vif | Named numeric vector of ASL for the VIF rule, $P(R_j^2 > \text{valor_vif})$. |
| pval_klein | Named numeric vector of ASL for Klein's rule, $P(R_g^2 < R_j^2)$. |
| Bvals | Numeric matrix of size nboot x (p+1) with columns "global" for R_g^2 and one column per predictor for R_j^2 . |
| VIFvals | Numeric matrix nboot x p with VIF values per predictor (one column per design column). |
| vif.tot | Observed VIF per predictor from the original design. |
| R.tot | Named numeric vector with observed R_g^2 and all R_j^2 . |
| nsam | Bootstrap sample size actually used. |
| nboot | Number of bootstrap iterations actually performed. |

Interpretation

- Larger pval_klein[j] indicates stronger evidence that predictor j violates Klein's rule (R_j^2 often exceeds R_g^2).
- Larger pval_vif[j] indicates that R_j^2 frequently exceeds valor_vif (equivalently, VIF exceeds the implied threshold).

Notes

For factor predictors, the underlying design includes multiple columns; VIFvals and VIF-related summaries are returned *per design column*. In singular bootstrap samples some statistics may be NA.

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References

Morales-Oñate, V., and Morales-Oñate, B. (2023). *MTest: a Bootstrap Test for Multicollinearity*. Revista Politécnica, 51(2), 53–62. doi:10.33333/rp.vol51n2.05

See Also

[vif](#) for classical VIF computation.

Examples

```
## Minimal example (small nboot for speed)
set.seed(1)
data(simDataMTest, package = "MTest")
m1 <- stats::lm(y ~ ., data = simDataMTest)

boot.sol <- MTest(m1, nboot = 50, trace = FALSE, seed = 123, valor_vif = 0.90)

boot.sol$pval_vif
boot.sol$pval_klein
head(boot.sol$Bvals)
print(boot.sol)
```

pairwiseKStest

Pairwise Kolmogorov–Smirnov tests for matrix columns

Description

Computes pairwise Kolmogorov–Smirnov (KS) tests between all columns of a numeric matrix or data frame, returning the matrix of p-values. Typical inputs include the Bvals matrix from MTest. For one-sided alternatives ("greater" or "less"), the p-value matrix is directional: rows correspond to x and columns to y.

Usage

```
pairwiseKStest(X,
               alternative = c("greater", "less", "two.sided"),
               use = c("asis", "pairwise.complete.obs"),
               exact = NULL)
```

Arguments

| | |
|-------------|---|
| X | Numeric matrix or data frame. Columns are compared pairwise by KS tests. A common use is Bvals from MTest. If you want to compare only predictors, pass Bvals[, -1] to exclude the "global" column. |
| alternative | Character string: "greater", "less", or "two.sided". See ks.test for the meaning of these options. |
| use | Character string: "asis" (default; no NA filtering, replicates the original behavior), or "pairwise.complete.obs" (remove NAs pairwise for each test). |
| exact | Logical or NULL. Forwarded to ks.test . Leave as NULL to use the default decision of ks.test (as in the original function). |

Details

The function performs a KS test for each ordered pair of columns (i , j) using `ks.test(X[, i], X[, j], alternative = alternative, exact = exact)`. For one-sided alternatives, the result is not symmetric, since rows play the role of x and columns the role of y .

The returned Suggestion follows the same rule as the original function: for `alternative = "greater"`, it sorts the row sums of the p-value matrix (descending); for `"less"`, it sorts the column sums; for `"two.sided"`, no suggestion is returned.

Value

A list of class `pairwiseKStest` with components:

| | |
|--------------------------|--|
| <code>KSpwMatrix</code> | Numeric matrix of p-values. Rows are x , columns are y . |
| <code>alternative</code> | Character string describing the alternative hypothesis used. |
| <code>Suggestion</code> | For <code>"greater"</code> : row sums of <code>KSpwMatrix</code> (sorted decreasing). For <code>"less"</code> : column sums (sorted decreasing). For <code>"two.sided"</code> : a message indicating no suggestions. |

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References

Morales-Oñate, V., and Morales-Oñate, B. (2023). *MTest: a Bootstrap Test for Multicollinearity*. *Revista Politécnica*, 51(2), 53–62. doi:10.33333/rp.vol51n2.05

See Also

[ks.test](#), [MTest](#)

Examples

```
## Typical workflow with MTest:
## (use small nboot for speed in examples)
set.seed(1)
data(simDataMTest, package = "MTest")
m1 <- stats::lm(y ~ ., data = simDataMTest)
boot.sol <- MTest(m1, nboot = 30, trace = FALSE, seed = 123)

## Compare only predictors (exclude "global"):
ks_res_greater <- pairwiseKStest(boot.sol$Bvals[, -1],
                                alternative = "greater",
                                use = "asis",      # same behavior as the original
                                exact = NULL)     # let ks.test decide

ks_res_greater$KSpwMatrix
```

```

ks_res_greater$Suggestion

## Two-sided (no suggestion by design):
ks_res_twosided <- pairwiseKStest(boot.sol$Bvals[, -1],
                                 alternative = "two.sided")
ks_res_twosided$KSpwMatrix

```

plot.MTest

Plot density or empirical cumulative distribution from MTest

Description

Plot density or empirical cumulative distribution from Bvals in [MTest](#) output.

Usage

```

## S3 method for class 'MTest'
plot(x, type=1, plotly = FALSE, ...)

```

Arguments

| | |
|--------|---|
| x | an object of the class "MTest" |
| type | Numeric; 1 if density, 2 if ecdf plot is returned |
| plotly | Logical; if FALSE, a ggplotly plot is returned |
| ... | other arguments to be passed to the function ggplot |

Details

This function plots density or empirical cumulative distribution function from MTest bootstrap replications.

Value

Produces a plot. No values are returned.

See Also

[MTest](#) for procedure and examples.

`simDataMTest`*Simulated data for MTest*

Description

This data set helps testing functions in MTest package, the generating process is documented in the reference.

Usage`simDataMTest`**Format**

A dataframe containing 10000 observations and four columns.

References

Morales-Oñate, V., and Morales-Oñate, B. (2023). *MTest: a Bootstrap Test for Multicollinearity*. *Revista Politécnica*, 51(2), 53–62. doi:[10.33333/rp.vol51n2.05](https://doi.org/10.33333/rp.vol51n2.05)

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