Package ‘Transform’

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Title Statistical Transformations

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Suggests MASS

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Description Performs various statistical transformations; Box-Cox and Log (Box and Cox, 1964) <doi:10.1111/j.2517-6161.1964.tb00553.x>, Glog (Durbin et al., 2002) <doi:10.1093/bioinformatics/18.suppl_1.S105>, Neglog (Whittaker et al., 2005) <doi:10.1111/j.1467-9876.2005.00520.x>, Reciprocal (Tukey, 1957), Log Shift (Feng et al., 2016) <doi:10.1002/sta4.104>, Bickel-Docksum (Bickel and Doksum, 1981) <doi:10.1080/01621459.1981.10477649>, Yeo-Johnson (Yeo and Johnson, 2000) <doi:10.1093/biomet/87.4.954>, Square Root (Medina et al., 2019), Manly (Manly, 1976) <doi:10.2307/2988129>, Modulus (John and Draper, 1980) <doi:10.2307/2986305>, Dual (Yang, 2006) <doi:10.1016/j.econlet.2006.01.011>, Gpower (Ko
mansky et al., 2013) <doi:10.1515/sagmb-2012-0030>. It also performs graphical approaches, assesses the success of the transformation via tests and plots.

License GPL (>= 2)

NeedsCompilation no

Repository CRAN

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Contents

`bcTransform` *Box-Cox Transformation for Normality*

Description

`bcTransform` performs Box-Cox transformation for normality of a variable and provides graphical analysis.

Usage

```
bcTransform(data, lambda = seq(-3,3,0.01), lambda2 = NULL, plot = TRUE,
  alpha = 0.05, verbose = TRUE)
```

Arguments

`data`	a numeric vector of data values.
`lambda`	a vector which includes the sequence of candidate lambda values. Default is set to (-3,3) with increment 0.01.
`lambda2`	a numeric for an additional shifting parameter. Default is set to lambda2 = NULL.
`plot`	a logical to plot histogram with its density line and qqplot of raw and transformed data. Defaults plot = TRUE.
`alpha`	the level of significance to check the normality after transformation. Default is set to alpha = 0.05.
`verbose`	a logical for printing output to R console.

Details

Denote y the variable at the original scale and y' the transformed variable. The Box-Cox power transformation is defined by:

$$y' = \begin{cases} \frac{y^\lambda - 1}{\lambda} \text{ , if } \lambda \neq 0 \\ log(y) \text{ , if } \lambda = 0 \end{cases}$$

If the data include any non- positive observations, a shifting parameter λ_2 can be included in the transformation given by:

$$y' = \begin{cases} \frac{(y+\lambda_2)^\lambda - 1}{\lambda}, \text{ if } \lambda \neq 0 \\ log(y+\lambda_2), \text{ if } \lambda = 0 \end{cases}$$

Value

A list with class "bc" containing the following elements:

`method`	method to estimate Box-Cox transformation parameter
`lambda.hat`	estimate of Box-Cox Power transformation parameter
`lambda2`	additional shifting parameter
`statistic`	Shapiro-Wilk test statistic for transformed data
`p.value`	Shapiro-Wilk test p.value for transformed data
`alpha`	level of significance to assess normality
`tf.data`	transformed data set
`var.name`	variable name

Author(s)

Muge Coskun Yildirim, Osman Dag

References

Asar, O., Ilk, O., Dag, O. (2017). Estimating Box-Cox Power Transformation Parameter via Goodness of Fit Tests. *Communications in Statistics - Simulation and Computation*, **46:1**, 91–105.

Box, G.E., Cox, D.R. (1964). An Analysis of Transformations. *Journal of the Royal Statistical Society: Series B (Methodological)*, **26:2**, 211–43.

Examples

```
library(Transform)
out <- bcTransform(MASS::Cushings$Tetrahydrocortisone)
out$lambda.hat # the estimate of Box-Cox parameter based on Shapiro-Wilk test statistic
out$p.value # p.value of Shapiro-Wilk test for transformed data
out$tf.data # transformed data set
```

`bdTransform` *Bickel-Docksum Transformation for Normality*

Description

`bdTransform` performs Bickel-Docksum transformation for normality of a variable and provides graphical analysis.

Usage

```
bdTransform(data, lambda = seq(0.01,6,0.01), plot = TRUE, alpha = 0.05,
  verbose = TRUE)
```

Arguments

`data`	a numeric vector of data values.
`lambda`	a vector which includes the sequence of candidate lambda values. Default is set to (0.01,6) with increment 0.01.
`plot`	a logical to plot histogram with its density line and qqplot of raw and transformed data. Defaults plot = TRUE.
`alpha`	the level of significance to check the normality after transformation. Default is set to alpha = 0.05.
`verbose`	a logical for printing output to R console.

Details

Denote y the variable at the original scale and y' the transformed variable. The Bickel-Docksum power transformation is defined by:

$$y' = \frac{|y|^{\lambda} Sign(y) - 1}{\lambda} \text{, if } \lambda > 0$$

Value

A list with class "bd" containing the following elements:

`method`	method to estimate Bickel-Docksum transformation parameter
`lambda.hat`	estimate of Bickel-Docksum transformation parameter
`statistic`	Shapiro-Wilk test statistic for transformed data
`p.value`	Shapiro-Wilk test p.value for transformed data
`alpha`	level of significance to assess normality
`tf.data`	transformed data set
`var.name`	variable name

Author(s)

Muge Coskun Yildirim, Osman Dag

References

Asar, O., Ilk, O., Dag, O. (2017). Estimating Box-Cox Power Transformation Parameter via Goodness of Fit Tests. *Communications in Statistics - Simulation and Computation*, **46:1**, 91–105.

Bickel, P.J., Doksum, K.A. (1981). An Analysis of Transformations Revisited. *Journal of the American Statistical Association*, **76:374**, 296–311.

Examples

```
library(Transform)
out <- bdTransform(MASS::Cushings$Tetrahydrocortisone)
out$lambda.hat # the estimate of Bickel-Docksum parameter based on Shapiro-Wilk test statistic
out$p.value # p.value of Shapiro-Wilk test for transformed data
out$tf.data # transformed data set
```

`dlTransform` *Dual Transformation for Normality*

Description

`dlTransform` performs Dual transformation for normality of a variable and provides graphical analysis.

Usage

```
dlTransform(data, lambda = seq(0,6,0.01), plot = TRUE, alpha = 0.05,
  verbose = TRUE)
```

Arguments

`data`	a numeric vector of data values.
`lambda`	a vector which includes the sequence of candidate lambda values. Default is set to (0,6) with increment 0.01.
`plot`	a logical to plot histogram with its density line and qqplot of raw and transformed data. Defaults plot = TRUE.
`alpha`	the level of significance to check the normality after transformation. Default is set to alpha = 0.05.
`verbose`	a logical for printing output to R console.

Details

Denote y the variable at the original scale and y' the transformed variable. The Dual power transformation is defined by:

$$y' = \begin{cases} \frac{y^{\lambda} - y^{-\lambda}}{2\lambda} \text{ , if } \lambda > 0 \\ \log(y) \text{ , if } \lambda = 0 \end{cases}$$

Value

A list with class "dl" containing the following elements:

`method`	method to estimate Dual transformation parameter
`lambda.hat`	estimate of Dual transformation parameter
`statistic`	Shapiro-Wilk test statistic for transformed data
`p.value`	Shapiro-Wilk test p.value for transformed data
`alpha`	level of significance to assess normality
`tf.data`	transformed data set
`var.name`	variable name

Author(s)

Muge Coskun Yildirim, Osman Dag

References

Asar, O., Ilk, O., Dag, O. (2017). Estimating Box-Cox Power Transformation Parameter via Goodness of Fit Tests. *Communications in Statistics - Simulation and Computation*, **46:1**, 91–105.

Yang, Z. (2006). A Modified Family of Power Transformations. *Economics Letters*. **92:1**, 14–9.

Examples

```
library(Transform)
out <- dlTransform(MASS::Cushings$Tetrahydrocortisone)
out$lambda.hat # the estimate of Dual parameter based on Shapiro-Wilk test statistic
out$p.value # p.value of Shapiro-Wilk test for transformed data
out$tf.data # transformed data set
```

`glTransform` *Glog Transformation for Normality*

Description

`glTransform` performs Glog transformation for normality of a variable and provides graphical analysis.

Usage

```
glTransform(data, plot = TRUE, alpha = 0.05, verbose = TRUE)
```

Arguments

`data`	a numeric vector of data values.
`plot`	a logical to plot histogram with its density line and qqplot of raw and transformed data. Defaults plot = TRUE.
`alpha`	the level of significance to check the normality after transformation. Default is set to alpha = 0.05.
`verbose`	a logical for printing output to R console.

Details

Denote y the variable at the original scale and y' the transformed variable. The Glog power transformation is defined by:

$$y' = \log(y + \sqrt{y^2 + 1})$$

Value

A list with class "gl" containing the following elements:

`method`	method name
`statistic`	Shapiro-Wilk test statistic for transformed data
`p.value`	Shapiro-Wilk test p.value for transformed data
`alpha`	level of significance to assess normality
`tf.data`	transformed data set
`var.name`	variable name

Author(s)

Muge Coskun Yildirim, Osman Dag

References

Asar, O., Ilk, O., Dag, O. (2017). Estimating Box-Cox Power Transformation Parameter via Goodness of Fit Tests. *Communications in Statistics - Simulation and Computation*, **46:1**, 91–105.

Durbin, B.P., Hardin, J.S., Hawkins, D.M., Rocke, D.M. (2002). A Variance-Stabilizing Transformation for Gene-expression Microarray Data. *Bioinformatics*, **18(suppl_1)**, 105–110.

Examples

```
library(Transform)
out <- glTransform(MASS::Cushings$Tetrahydrocortisone)
out$p.value # p.value of Shapiro-Wilk test for transformed data
out$tf.data # transformed data set
```

`gpTransform` *Gpower Transformation for Normality*

Description

`gpTransform` performs Gpower transformation for normality of a variable and provides graphical analysis.

Usage

```
gpTransform(data, lambda = seq(-3,3,0.01), plot = TRUE, alpha = 0.05,
  verbose = TRUE)
```

Arguments

`data`	a numeric vector of data values.
`lambda`	a vector which includes the sequence of candidate lambda values. Default is set to (-3,3) with increment 0.01.
`plot`	a logical to plot histogram with its density line and qqplot of raw and transformed data. Defaults plot = TRUE.
`alpha`	the level of significance to check the normality after transformation. Default is set to alpha = 0.05.
`verbose`	a logical for printing output to R console.

Details

Denote y the variable at the original scale and y' the transformed variable. The Gpower power transformation is defined by:

$$y' = \begin{cases} \frac{(y+\sqrt{y^2+1})^\lambda - 1}{\lambda}\text{ , if } \lambda \neq 0 \\ \log(y+\sqrt{y^2+1})\text{ , if } \lambda = 0 \end{cases}$$

Value

A list with class "gp" containing the following elements:

`method`	method to estimate Gpower transformation parameter
`lambda.hat`	estimate of Gpower transformation parameter
`statistic`	Shapiro-Wilk test statistic for transformed data
`p.value`	Shapiro-Wilk test p.value for transformed data
`alpha`	level of significance to assess normality
`tf.data`	transformed data set
`var.name`	variable name

Author(s)

Muge Coskun Yildirim, Osman Dag

References

Asar, O., Ilk, O., Dag, O. (2017). Estimating Box-Cox Power Transformation Parameter via Goodness of Fit Tests. *Communications in Statistics - Simulation and Computation*, **46:1**, 91–105.

Kelmansky, D.M., Martinez, E.J., Leiva, V. (2013). A New Variance Stabilizing Transformation for Gene Expression Data Analysis. *Statistical Applications in Genetics and Molecular Biology*, **12:6**, 653–66.

Examples

```
library(Transform)
out <- gpTransform(MASS::Cushings$Tetrahydrocortisone)
out$lambda.hat # the estimate of Gpower parameter based on Shapiro-Wilk test statistic
out$p.value # p.value of Shapiro-Wilk test for transformed data
out$tf.data # transformed data set
```

`lgTransform` *Log Transformation for Normality*

Description

`lgTransform` performs Log transformation for normality of a variable and provides graphical analysis.

Usage

```
lgTransform(data, lambda2 = NULL, plot = TRUE, alpha = 0.05, verbose = TRUE)
```

Arguments

`data`	a numeric vector of data values.
`lambda2`	a numeric for an additional shifting parameter. Default is set to lambda2 = NULL.
`plot`	a logical to plot histogram with its density line and qqplot of raw and transformed data. Defaults plot = TRUE.
`alpha`	the level of significance to check the normality after transformation. Default is set to alpha = 0.05.
`verbose`	a logical for printing output to R console.

Details

Denote y the variable at the original scale and y' the transformed variable. The Log power transformation is defined by:

$$y' = \log(y)$$

If the data include any nonpositive observations, a shifting parameter λ_2 can be included in the transformation given by:

$$y' = \log(y + \lambda_2)$$

Value

A list with class "lg" containing the following elements:

`method`	method name
`lambda2`	additional shifting parameter
`statistic`	Shapiro-Wilk test statistic for transformed data
`p.value`	Shapiro-Wilk test p.value for transformed data
`alpha`	level of significance to assess normality
`tf.data`	transformed data set
`var.name`	variable name

Author(s)

Muge Coskun Yildirim, Osman Dag

References

Asar, O., Ilk, O., Dag, O. (2017). Estimating Box-Cox Power Transformation Parameter via Goodness of Fit Tests. *Communications in Statistics - Simulation and Computation*, **46:1**, 91–105.

Box, G.E., Cox, D.R. (1964). An Analysis of Transformations. *Journal of the Royal Statistical Society: Series B (Methodological)*, **26:2**, 211–43.

Examples

```
library(Transform)
out <- lgTransform(MASS::Cushings$Tetrahydrocortisone)
out$p.value # p.value of Shapiro-Wilk test for transformed data
out$tf.data # transformed data set
```

`lsTransform` *Log-shift Transformation for Normality*

Description

`lsTransform` performs Log-shift transformation for normality of a variable and provides graphical analysis.

Usage

```
lsTransform(data, lambda = seq(-3,3,0.01), plot = TRUE, alpha = 0.05,
  verbose = TRUE)
```

Arguments

`data`	a numeric vector of data values.
`lambda`	a vector which includes the sequence of candidate lambda values. Default is set to (-3,3) with increment 0.01.
`plot`	a logical to plot histogram with its density line and qqplot of raw and transformed data. Defaults plot = TRUE.
`alpha`	the level of significance to check the normality after transformation. Default is set to alpha = 0.05.
`verbose`	a logical for printing output to R console.

Details

Denote y the variable at the original scale and y' the transformed variable. The Log-shift power transformation is defined by:

$$y' = \log(y + \lambda)$$

Value

A list with class "ls" containing the following elements:

`method`	method to estimate Log-shift transformation parameter
`lambda.hat`	estimate of Log-shift transformation parameter
`statistic`	Shapiro-Wilk test statistic for transformed data

`p.value`	Shapiro-Wilk test p.value for transformed data
`alpha`	level of significance to assess normality
`tf.data`	transformed data set
`var.name`	variable name

Author(s)

Muge Coskun Yildirim, Osman Dag

References

Asar, O., Ilk, O., Dag, O. (2017). Estimating Box-Cox Power Transformation Parameter via Goodness of Fit Tests. *Communications in Statistics - Simulation and Computation*, **46:1**, 91–105.

Feng, Q., Hannig, J., Marron, J. (2015). A Note on Automatic Data Transformation. *Stat*, **5:1**, 82–7.

Examples

```
library(Transform)
out <- lsTransform(MASS::Cushings$Tetrahydrocortisone)
out$lambda.hat # the estimate of Log-shift parameter based on Shapiro-Wilk test statistic
out$p.value # p.value of Shapiro-Wilk test for transformed data
out$tf.data # transformed data set
```

`mdTransform` *Modulus Transformation for Normality*

Description

`mdTransform` performs Modulus transformation for normality of a variable and provides graphical analysis.

Usage

```
mdTransform(data, lambda = seq(-3,3,0.01), plot = TRUE, alpha = 0.05,
  verbose = TRUE)
```

Arguments

`data`	a numeric vector of data values.
`lambda`	a vector which includes the sequence of candidate lambda values. Default is set to (-3,3) with increment 0.01.
`plot`	a logical to plot histogram with its density line and qqplot of raw and transformed data. Defaults plot = TRUE.
`alpha`	the level of significance to check the normality after transformation. Default is set to alpha = 0.05.
`verbose`	a logical for printing output to R console.

Details

Denote y the variable at the original scale and y' the transformed variable. The Modulus power transformation is defined by:

$$y' = \begin{cases} Sign(y)\frac{(|y|+1)^{\lambda}-1}{\lambda} \text{ , if } \lambda \neq 0 \\ Sign(y)\log\left(|y|+1\right) \text{ , if } \lambda = 0 \end{cases}$$

Value

A list with class "md" containing the following elements:

`method`	method to estimate Modulus transformation parameter
`lambda.hat`	estimate of Modulus transformation parameter
`statistic`	Shapiro-Wilk test statistic for transformed data
`p.value`	Shapiro-Wilk test p.value for transformed data
`alpha`	level of significance to assess normality
`tf.data`	transformed data set
`var.name`	variable name

Author(s)

Muge Coskun Yildirim, Osman Dag

References

Asar, O., Ilk, O., Dag, O. (2017). Estimating Box-Cox Power Transformation Parameter via Goodness of Fit Tests. *Communications in Statistics - Simulation and Computation*, **46:1**, 91–105.

John, J., Draper, N.R. (1980). An Alternative Family of Transformations. *Journal of the Royal Statistical Society Series C: Applied Statistics*, **29:2**, 190–7.

Examples

```
library(Transform)
out <- mdTransform(MASS::Cushings$Tetrahydrocortisone)
out$lambda.hat # the estimate of Modulus parameter based on Shapiro-Wilk test statistic
out$p.value # p.value of Shapiro-Wilk test for transformed data
out$tf.data # transformed data set
```

`mnTransform` *Manly Transformation for Normality*

Description

`mnTransform` performs Manly transformation for normality of a variable and provides graphical analysis.

Usage

```
mnTransform(data, lambda = seq(-3,3,0.01), plot = TRUE, alpha = 0.05,
  verbose = TRUE)
```

Arguments

`data`	a numeric vector of data values.
`lambda`	a vector which includes the sequence of candidate lambda values. Default is set to (-3,3) with increment 0.01.
`plot`	a logical to plot histogram with its density line and qqplot of raw and transformed data. Defaults plot = TRUE.
`alpha`	the level of significance to check the normality after transformation. Default is set to alpha = 0.05.
`verbose`	a logical for printing output to R console.

Details

Denote y the variable at the original scale and y' the transformed variable. The Manly power transformation is defined by:

$$y' = \begin{cases} \frac{e^{\lambda y}-1}{\lambda} \text{ , if } \lambda \neq 0 \\ y \text{ , if } \lambda = 0 \end{cases}$$

Value

A list with class "mn" containing the following elements:

`method`	method to estimate Manly transformation parameter
`lambda.hat`	estimate of Manly transformation parameter
`statistic`	Shapiro-Wilk test statistic for transformed data
`p.value`	Shapiro-Wilk test p.value for transformed data
`alpha`	level of significance to assess normality
`tf.data`	transformed data set
`var.name`	variable name

Author(s)

Muge Coskun Yildirim, Osman Dag

References

Asar, O., Ilk, O., Dag, O. (2017). Estimating Box-Cox Power Transformation Parameter via Goodness of Fit Tests. *Communications in Statistics - Simulation and Computation*, **46:1**, 91–105.

Manly, B.F. (1976). Exponential Data Transformations. *Journal of the Royal Statistical Society: Series D (The Statistician)*, **25:1**, 37–42.

Examples

```
library(Transform)
out <- mnTransform(MASS::Cushings$Tetrahydrocortisone)
out$lambda.hat # the estimate of Manly parameter based on Shapiro-Wilk test statistic
out$p.value # p.value of Shapiro-Wilk test for transformed data
out$tf.data # transformed data set
```

`nlTransform` *Neglog Transformation for Normality*

Description

`nlTransform` performs Neglog transformation for normality of a variable and provides graphical analysis.

Usage

```
nlTransform(data, plot = TRUE, alpha = 0.05, verbose = TRUE)
```

Arguments

`data`	a numeric vector of data values.
`plot`	a logical to plot histogram with its density line and qqplot of raw and transformed data. Defaults plot = TRUE.
`alpha`	the level of significance to check the normality after transformation. Default is set to alpha = 0.05.
`verbose`	a logical for printing output to R console.

Details

Denote y the variable at the original scale and y' the transformed variable. The Neglog power transformation is defined by:

$$y' = Sign(y)\log(|y| + 1)$$

Value

A list with class "nl" containing the following elements:

`method`	method name
`statistic`	Shapiro-Wilk test statistic for transformed data
`p.value`	Shapiro-Wilk test p.value for transformed data
`alpha`	level of significance to assess normality
`tf.data`	transformed data set
`var.name`	variable name

Author(s)

Muge Coskun Yildirim, Osman Dag

References

Asar, O., Ilk, O., Dag, O. (2017). Estimating Box-Cox Power Transformation Parameter via Goodness of Fit Tests. *Communications in Statistics - Simulation and Computation*, **46:1**, 91–105.

Whittaker, J., Whitehead, C., Somers, M. (2005). The Neglog Transformation and Quantile Regression for the Analysis of a Large Credit Scoring Database. *Journal of the Royal Statistical Society: Series C (Applied Statistics)*, **54:5**, 863–78.

Examples

```
library(Transform)
out <- nlTransform(MASS::Cushings$Tetrahydrocortisone)
out$p.value # p.value of Shapiro-Wilk test for transformed data
out$tf.data # transformed data set
```

`rpTransform` *Reciprocal Transformation for Normality*

Description

`rpTransform` performs Reciprocal transformation for normality of a variable and provides graphical analysis.

Usage

```
rpTransform(data, plot = TRUE, alpha = 0.05, verbose = TRUE)
```

Arguments

`data`	a numeric vector of data values.
`plot`	a logical to plot histogram with its density line and qqplot of raw and transformed data. Defaults plot = TRUE.
`alpha`	the level of significance to check the normality after transformation. Default is set to alpha = 0.05.
`verbose`	a logical for printing output to R console.

Details

Denote y the variable at the original scale and y' the transformed variable. The Dual power transformation is defined by:

$$y' = \frac{1}{y}$$

Value

A list with class "rp" containing the following elements:

`method`	method name
`statistic`	Shapiro-Wilk test statistic for transformed data
`p.value`	Shapiro-Wilk test p.value for transformed data
`alpha`	level of significance to assess normality
`tf.data`	transformed data set
`var.name`	variable name

Author(s)

Muge Coskun Yildirim, Osman Dag

References

Asar, O., Ilk, O., Dag, O. (2017). Estimating Box-Cox Power Transformation Parameter via Goodness of Fit Tests. *Communications in Statistics - Simulation and Computation*, **46:1**, 91–105.

Tukey, J.W. (1957). On the Comparative Anatomy of Transformations. *The Annals of Mathematical Statistics*, 602–32.

Examples

```
library(Transform)
out <- rpTransform(MASS::Cushings$Tetrahydrocortisone)
out$p.value # p.value of Shapiro-Wilk test for transformed data
out$tf.data # transformed data set
```

`selectTransform` *Data-Driven Selection of the Optimal Transformation Method*

Description

`selectTransform` performs an automated evaluation to identify the optimal transformation method for a dataset.

Usage

```
selectTransform(data, alpha = 0.05, na.rm = TRUE, verbose = TRUE)
```

Arguments

`data`	a numeric vector to be transformed.
`alpha`	the level of significance used to assess normality based on the Shapiro-Wilk test. Default is set to `alpha = 0.05`.
`na.rm`	a logical value indicating whether missing values should be removed before the computation proceeds.
`verbose`	a logical value indicating whether the output should be printed to the R console.

Details

The function applies several transformation methods to the data and evaluates the normality of the transformed data using the Shapiro-Wilk test.

For each transformation method, the function reports the estimated transformation parameter, when applicable, the Shapiro-Wilk test statistic, and the corresponding p-value. The transformation method yielding the maximum Shapiro-Wilk test statistic is recommended as the optimal transformation method.

The transformation methods evaluated by the function include Box-Cox, Manly, Modulus, Bickel-Doksum, Yeo-Johnson, Dual, Gpower, Log-shift, Square-root shift, Log, Reciprocal, Glog, and Neglog transformations. For transformation methods without a transformation parameter, the lambda value is reported as `NA`.

Value

A data frame presenting the name of the transformation method, the corresponding transformation function call, the estimated transformation parameter, the Shapiro-Wilk test statistic, the corresponding p-value of the Shapiro-Wilk normality test.

Author(s)

Muge Coskun Yildirim and Osman Dag

Examples

```
library(Transform)
selectTransform(MASS::Cushings$Tetrahydrocortisone)
```

`ssTransform` *Square Root Transformation for Normality*

Description

`ssTransform` performs Square Root transformation for normality of a variable and provides graphical analysis.

Usage

```
ssTransform(data, lambda = seq(-3,3,0.01), plot = TRUE, alpha = 0.05,
  verbose = TRUE)
```

Arguments

`data`	a numeric vector of data values.
`lambda`	a vector which includes the sequence of candidate lambda values. Default is set to (-3,3) with increment 0.01.
`plot`	a logical to plot histogram with its density line and qqplot of raw and transformed data. Defaults plot = TRUE.
`alpha`	the level of significance to check the normality after transformation. Default is set to alpha = 0.05.
`verbose`	a logical for printing output to R console.

Details

Denote y the variable at the original scale and y' the transformed variable. The Square Root power transformation is defined by:

$$y' = \sqrt{y + \lambda}$$

Value

A list with class "ss" containing the following elements:

`method`	method to estimate Square Root transformation parameter
`lambda.hat`	estimate of Square Root transformation parameter
`statistic`	Shapiro-Wilk test statistic for transformed data
`p.value`	Shapiro-Wilk test p.value for transformed data

`alpha`	level of significance to assess normality
`tf.data`	transformed data set
`var.name`	variable name

Author(s)

Muge Coskun Yildirim, Osman Dag

References

Asar, O., Ilk, O., Dag, O. (2017). Estimating Box-Cox Power Transformation Parameter via Goodness of Fit Tests. *Communications in Statistics - Simulation and Computation*, **46:1**, 91–105.

Medina, L., Castro, P., Kreutzmann, A. (2018). Rojas-Perilla N. trafo: Estimation, Comparison and Selection of Transformations. *R package version*. **1.0.1**.

Examples

```
library(Transform)
out <- ssTransform(MASS::Cushings$Tetrahydrocortisone)
out$lambda.hat # the estimate of Square Root parameter based on Shapiro-Wilk test statistic
out$p.value # p.value of Shapiro-Wilk test for transformed data
out$tf.data # transformed data set
```

`Transform` *Statistical Transformations for Normality*

Description

`Transform` performs transformations for normality of a variable and provides graphical analysis.

Usage

```
Transform(data, method = "dl", lambda = seq(0,6,0.01), lambda2 = NULL, plot = TRUE,
  alpha = 0.05, verbose = TRUE)
```

Arguments

`data`	a numeric vector of data values.
`method`	a character string. Different transformation methods can be used for the estimation of the optimal transformation parameter: Box-Cox ("bc"), Log-shift ("ls"), Bickel-Doksum ("bd"), Yeo-Johnson ("yj"), Square Root ("ss"), Manly ("mn"), Modulus ("md"), Dual ("dl"), Gpower ("gp"), Log ("lg"), Glog ("gl"), Neglog ("nl"), Reciprocal ("rp"). Default is set to method = "dl".

`lambda`	a vector which includes the sequence of candidate lambda values. Please see the corresponding method to learn the lambda range. Default is set to (0,6) with increment 0.01.
`lambda2`	a numeric for an additional shifting parameter. Please see the corresponding method to learn the lambda2. Default is set to lambda2 = NULL.
`plot`	a logical to plot histogram with its density line and qqplot of raw and transformed data. Defaults plot = TRUE.
`alpha`	the level of significance to check the normality after transformation. Default is set to alpha = 0.05.
`verbose`	a logical for printing output to R console.

Value

See the corresponding transformation method.

Author(s)

Muge Coskun Yildirim, Osman Dag

Examples

```
library(Transform)
out <- Transform(MASS::Cushings$Tetrahydrocortisone, method = "bc")
out$lambda.hat # the estimate of Box-Cox parameter based on Shapiro-Wilk test statistic
out$p.value # p.value of Shapiro-Wilk test for transformed data
out$tf.data # transformed data set
```

`yjTransform` *Yeo- Johnson Transformation for Normality*

Description

`yjTransform` performs Yeo- Johnson transformation for normality of a variable and provides graphical analysis.

Usage

```
yjTransform(data, lambda = seq(-3,3,0.01), plot = TRUE, alpha = 0.05,
  verbose = TRUE)
```

Arguments

`data`	a numeric vector of data values.
`lambda`	a vector which includes the sequence of candidate lambda values. Default is set to (-3,3) with increment 0.01.
`plot`	a logical to plot histogram with its density line and qqplot of raw and transformed data. Defaults plot = TRUE.
`alpha`	the level of significance to check the normality after transformation. Default is set to alpha = 0.05.
`verbose`	a logical for printing output to R console.

Details

Denote y the variable at the original scale and y' the transformed variable. The Yeo-Johnson power transformation is defined by:

$$y' = \begin{cases} \frac{(y+1)^\lambda - 1}{\lambda} \text{ , if } \lambda \neq 0, y \geq 0 \\ \log(y+1) \text{ , if } \lambda = 0, y \geq 0 \\ \frac{(1-y)^{2-\lambda} - 1}{\lambda - 2} \text{ , if } \lambda \neq 2, y < 0 \\ -\log(1-y) \text{ , if } \lambda = 2, y < 0 \end{cases}$$

Value

A list with class "yj" containing the following elements:

`method`	method to estimate Yeo-Johnson transformation parameter
`lambda.hat`	estimate of Yeo-Johnson transformation parameter
`statistic`	Shapiro-Wilk test statistic for transformed data
`p.value`	Shapiro-Wilk test p.value for transformed data
`alpha`	level of significance to assess normality
`tf.data`	transformed data set
`var.name`	variable name

Author(s)

Muge Coskun Yildirim, Osman Dag

References

Asar, O., Ilk, O., Dag, O. (2017). Estimating Box-Cox Power Transformation Parameter via Goodness of Fit Tests. *Communications in Statistics - Simulation and Computation*, **46:1**, 91–105.

Yeo, I.K., Johnson, R.A. (2000). A New Family of Power Transformations to Improve Normality or Symmetry. *Biometrika*, **87:4**, 954–9.

Examples

```
library(Transform)
out <- yjTransform(MASS::Cushings$Tetrahydrocortisone)
out$lambda.hat # the estimate of Yeo- Johnson parameter based on Shapiro-Wilk test statistic
out$p.value # p.value of Shapiro-Wilk test for transformed data
out$tf.data # transformed data set
```

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