Package ‘detectnorm’

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Type Package

Title Detect Nonnormality in Meta-Analysis without Raw Data

Version 1.0.0

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Description Non-normality could greatly distort the meta-analytic results, according to the simulation in Sun and Cheung (2020) <doi:10.3758/s13428-019-01334-x>. This package aims to detect non-normality for two independent groups with only limited descriptive statistics, including mean, standard deviation, minimum, and maximum.

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URL https://github.com/irissun/detectnorm

BugReports https://github.com/irissun/detectnorm/issues

Encoding UTF-8

LazyData true

Depends R (>= 2.10)

Imports nleqslv, ggplot2, truncnorm, Rdpack, psych

Suggests knitr, metafor (>= 3.4-0), rmarkdown, testthat (>= 3.0.0)

RdMacros Rdpack

RoxygenNote 7.2.0

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Example meta-analysis: Extremely Non-normal Data

Description
This dataset is generated by nonnormal data with function rnonnorm. It contains the descriptive data in individual studies in the meta-analysis.

Usage
beta_mdat

Format
A data.frame with 40 studies:

- **study** No of studies
- **n1** sample size of group 1 with equal sample size for the two studies. Generated with uniform distribution.
- **m1** mean of group 1. Population mean is equal to 1. The data of group 1 is generated with skewness = 4 and kurtosis = 2.
- **sd1** standard deviation of group 1. Population sd of group 1 is equal to 1.
- **lo1** minimum of the generated sample for group 1.
- **hi1** maximum of the generated sample for group 1.
- **n2** sample size of study 2; n1 = n2 for each study
- **m2** mean of group 2. Population mean is equal to 1.5. The data of group 2 is generated with skewness = -4 and kurtosis = 2.
- **sd2** standard deviation of group 2. Population sd of group 2 is equal to 1.
- **lo2** minimum of the generated sample for group 2.
- **hi2** maximum of the generated sample for group 2.
- **skew1** sample skewness for group 1.
- **skew2** sample skewness for group 2.
desbeta

Calculate skewness and kurtosis based on Beta distribution in one group

Description

This function can be used to calculate the skewness and kurtosis based on the Beta distribution. Also, this function estimate the shape parameters alpha and beta.

Usage

```
desbeta(
  vmean,  # sample mean of the truncated data
  vsd,  # sample standard deviation of the truncated data
  lo,  # minimum possible value
  hi,  # maximum possible value
  method = "MM",  # when method = 'MM', the method used is the method of moments, when method = "ML", the method used to estimate the distribution is maximum likelihood
  rawdata = NULL,  # when raw data is available, we could still use it to check it figuratively, if the data was closed to the normal distribution, or truncated normal distribution.
  showFigure = FALSE,  # when showFigure = TRUE, it will display the plots with theoretical normal curve and the truncated normal curve.
  ...  # other arguments
)
```

Arguments

- **vmean**: sample mean of the truncated data
- **vsd**: sample standard deviation of the truncated data
- **lo**: minimum possible value
- **hi**: maximum possible value
- **method**: when method = 'MM', the method used is the method of moments, when method = "ML", the method used to estimate the distribution is maximum likelihood
- **rawdata**: when raw data is available, we could still use it to check it figuratively, if the data was closed to the normal distribution, or truncated normal distribution.
- **showFigure**: when showFigure = TRUE, it will display the plots with theoretical normal curve and the truncated normal curve.
- **...**: other arguments

Value

If ‘showFigure = TRUE’, the output will be a list with two objects: one is the data frame of shape parameters (alpha and beta), mean and standard deviation of standard beta distribution (mean and sd), and skewness and kurtosis; the other is the theoretical figures of beta and normal distributions. If ‘showFigure = FALSE’, the output will be only the data frame.
References


See Also
destrunc

Examples

data('beta_mdat')
desbeta(vmean=beta_mdat$m2[6], vsd=beta_mdat$sd2[6],
hi = beta_mdat$hi2[6], lo = beta_mdat$lo2[6], showFigure = TRUE)

destrunc Calculate skewness and kurtosis based on truncated normal distribution in one group

Description

This function can be used to calculate the skewness and kurtosis based on the truncated normal distribution. Also, it can be used to estimate the mean and variance of the parent distribution (the distribution before truncated).

Usage

destrunc(
  vmean,
  vsd,
  lo,
  hi,
  rawdata = NULL,
  showFigure = FALSE,
  xstart,
  btol,
  ftol,
  ...
)
**Arguments**

- **vmean**: sample mean of the truncated data
- **vsd**: sample standard deviation of the truncated data
- **lo**: minimum possible value
- **hi**: maximum possible value
- **rawdata**: when raw data is available, we could still use it to check it figuratively, if the data was closed to the normal distribution, or truncated normal distribution.
- **showFigure**: when `showFigure = TRUE`, it will display the plots with theoretical normal curve and the truncated normal curve.
- **xstart**: see the package `nleqslv`
- **btol**: see the package `nleqslv`
- **ftol**: see the package `nleqslv`
- **...**: other arguments

**Value**

If `showFigure = TRUE`; the output will be a list with two objects: one is the data frame of parent mean and standard deviation (pmean and psd), mean and standard deviation of truncated normal distribution (mean and sd), and skewness and kurtosis; the other is the theoretical figures of beta and normal distributions. If `showFigure = FALSE`; the output will be only the data frame.

**References**


**See Also**

- `desbeta`

**Examples**

```r
data("trun_mdat")
destrunc(vmean=trun_mdat$m2[6], vsd=trun_mdat$sd2[6],
hi = 4, lo = 0, showfigure = TRUE)
#example2
destrunc(vmean=trun_mdat$m1[17], vsd=trun_mdat$sd1[17],
hi = 4, lo = 0, showfigure = TRUE)
```
detectnorm

*Calculate skewness and kurtosis based on Beta or truncated normal distribution in a meta-analysis for SMD (Two independent groups)*

**Description**

This function can be used to calculate the skewness and kurtosis based on the Beta distribution with the dataset used to conduct meta-analysis.

**Usage**

```r
detectnorm(
    m1i,  # vector to the means of first group
    sd1i, # vector to specify the standard deviation of first group
    n1i,  # vector to specify the sample size of first group
    lo1i, # vector to specify the possible minimum of the first group
    hi1i, # vector to specify the possible maximum of the first group
    m2i,  # vector to the means of second group
    sd2i, # vector to specify the standard deviation of second group
    n2i,  # vector to specify the sample size of second group
    lo2i, # vector to specify the possible minimum of the second group
    hi2i, # vector to specify the possible maximum of the second group
    data, # the optional original data frame containing the data for the function
    showFigure = FALSE, # when showFigure = TRUE, it will display all the plots (within the result as a list, result$fig) with theoretical normal curve and the truncated normal curve.
    distri = "beta", #
    ...)
```

**Arguments**

- **m1i**: vector to the means of first group
- **sd1i**: vector to specify the standard deviation of first group
- **n1i**: vector to specify the sample size of first group
- **lo1i**: vector to specify the possible minimum of the first group
- **hi1i**: vector to specify the possible maximum of the first group
- **m2i**: vector to the means of second group
- **sd2i**: vector to specify the standard deviation of second group
- **n2i**: vector to specify the sample size of second group
- **lo2i**: vector to specify the possible minimum of the second group
- **hi2i**: vector to specify the possible maximum of the second group
- **data**: the optional original data frame containing the data for the function
- **showFigure**: when showFigure = TRUE, it will display all the plots (within the result as a list, result$fig) with theoretical normal curve and the truncated normal curve.
detectnorm

```
distri
```

Beta distribution is used when using `distri = "beta"`; Truncated normal distribution is used when using `distri = "truncnorm"`.

... other arguments

**Value**

The output of the data frame adding some columns of the possible skewness and kurtosis for each groups.

**References**


**Examples**

```{r}
#truncated normal data
data("trun_mdat")
ex <- detectnorm(m1i = m1,sd1i = sd1,n1i = n1,
hi1i = 4,lo1i = 0,m2i = m2,sd2i = sd2,n2i = n2,
hi2i = 4,lo2i=0,distri = "truncnorm", data = trun_mdat)
head(ex)

#extremely non-normal data
data("beta_mdat")
ex2 <- detectnorm(m1i = m1,sd1i = sd1,n1i = n1,
hi1i = h11,lo1i = l1,m2i = m2,sd2i = sd2,n2i = n2,
hi2i = hi2,lo2i=lo2,distri = "beta", data = beta_mdat)
head(ex2)
mean(ex2$skew1)#sample skewness calculated from the sample
mean(ex2$g1_skewness) #estimated using beta
```
Non-normal Distribution

Description

Generating non-normal data with specified skewness and kurtosis using Fleishman’s Method.

Usage

rnonnorm(n, mean = 0, sd = 1, skew = 0, kurt = 0)

Arguments

- **n** number of observations
- **mean** mean
- **sd** standard deviation
- **skew** skewness
- **kurt** kurtosis

Details

This function can be used to generate non-normal data with specified skewness and kurtosis using Fleishman’s Power Method.

Value

A list of two objects: non-normal data is 'dat'; and the other is the Fleishman Coefficients used to generate the distributions.

References


Examples

```r
set.seed(341031)
exdat <- rnonnorm(n = 100, mean = 1, sd = 2, skew = 3, kurt = 2)$dat
hist(exdat)
```
trun_mdat

Example meta-analysis: Truncated Normal Data

Description
This dataset is generated by truncated normal data with function `rtruncnorm` with the scale of 0-4.

Usage
trun_mdat

Format
A data frame with 40 studies:

- **study**  No of studies
- **n1** sample size of group 1 with equal sample size for the two studies. Generated with uniform distribution.
- **m1** mean of group 1. Population mean is equal to 1. The data of group 1 is generated with the scale 0-4.
- **sd1** standard deviation of group 1. Population sd of group 1 is equal to 1.
- **lo1** minimum of the generated sample for group 1.
- **hi1** maximum of the generated sample for group 1.
- **n2** sample size of study 2; n1 = n2 for each study
- **m2** mean of group 2. Population mean is equal to 1.5. The data of group 2 is generated with the scale 0-4.
- **sd2** standard deviation of group 2. Population sd of group 2 is equal to 1.
- **lo2** minimum of the generated sample for group 2.
- **hi2** maximum of the generated sample for group 2.
- **skew1** sample skewness for group 1.
- **skew2** sampble skewness for group 2.
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