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Description Statistical tolerance limits provide the limits between which we can expect to find a specified proportion of a sampled population with a given level of confidence. This package provides functions for estimating tolerance limits (intervals) for various univariate distributions (binomial, Cauchy, discrete Pareto, exponential, two-parameter exponential, extreme value, hypergeometric, Laplace, logistic, negative binomial, negative hypergeometric, normal, Pareto, Poisson-Lindley, Poisson, uniform, and Zipf-Mandelbrot), Bayesian normal tolerance limits, multivariate normal tolerance regions, nonparametric tolerance intervals, tolerance bands for regression settings (linear regression, nonlinear regression, nonparametric regression, and multivariate regression), and analysis of variance tolerance intervals. Visualizations are also available for most of these settings.
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R topics documented:

tolerance-package ...................................................... 3
acc.samp ................................................................. 4
anovatol.int ............................................................ 5
bayesnormtol.int ........................................................ 7
bintol.int ................................................................. 9
bonftol.int ............................................................... 12
cautol.int ............................................................... 13
2

R topics documented:

diffnormtol.int .......................................................... 14
DiffProp ................................................................. 16
DiscretePareto .......................................................... 18
distfree.est .............................................................. 19
dpareto.ll ................................................................. 20
dparetotol.int ........................................................... 21
exp2tol.int .............................................................. 23
exptol.int .............................................................. 25
exttol.int .............................................................. 26
F1 ................................................................. 28
fidbintol.int ........................................................... 29
fidnegbintol.int ........................................................ 31
fidpoistol.int .......................................................... 33
gamtol.int ............................................................ 35
hypertol.int ............................................................ 37
K.factor ................................................................. 38
K.factor.sim ............................................................ 40
K.table ................................................................. 42
laptol.int .............................................................. 44
logistol.int ............................................................ 45
mvregtol.region ......................................................... 47
mvtol.region ........................................................... 48
negbintol.int ........................................................... 50
NegHypergeometric ....................................................... 52
neghypertol.int ........................................................ 54
nlregtol.int ............................................................ 55
norm.OC ................................................................. 57
norm.ss ................................................................. 59
normtol.int ............................................................ 61
np.order ............................................................... 63
npbetol.int ............................................................ 64
npmvtol.region ......................................................... 65
npregtol.int ........................................................... 67
nptol.int .............................................................. 69
paretotol.int .......................................................... 71
plottol ................................................................. 73
poislind.ll .............................................................. 75
poislindtol.int ........................................................ 76
PoissonLindley .......................................................... 77
poistol.int ............................................................ 78
regtol.int ............................................................. 81
simnormtol.int ........................................................ 82
TwoParExponential ...................................................... 84
umatol.int ............................................................. 85
uniftol.int ............................................................ 87
ZipfMandelbrot .......................................................... 88
zipftol.int ............................................................ 90
zm.ll ................................................................. 93
Description

Statistical tolerance limits provide the limits between which we can expect to find a specified proportion of a sampled population with a given level of confidence. This package provides functions for estimating tolerance limits (intervals) for various univariate distributions (binomial, Cauchy, discrete Pareto, exponential, two-parameter exponential, extreme value, hypergeometric, Laplace, logistic, negative binomial, negative hypergeometric, normal, Pareto, Poisson-Lindley, Poisson, uniform, and Zipf-Mandelbrot), Bayesian normal tolerance limits, multivariate normal tolerance regions, nonparametric tolerance intervals, tolerance bands for regression settings (linear regression, nonlinear regression, nonparametric regression, and multivariate regression), and analysis of variance tolerance intervals. Visualizations are also available for most of these settings.

Details

Package: tolerance
Type: Package
Version: 2.0.0
Date: 2020-02-04
Imports: MASS, rgl, stats4
License: GPL (>= 2)

Author(s)

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References


See Also

`confint`

---

**acc.samp**

*Acceptance Sampling*

**Description**

Provides an upper bound on the number of acceptable rejects or nonconformities in a process. This is similar to a 1-sided upper tolerance bound for a hypergeometric random variable.

**Usage**

```r
acc.samp(n, N, alpha = 0.05, P = 0.99, AQL = 0.01, RQL = 0.02)
```

**Arguments**

- `n`: The sample size to be drawn from the inventory.
- `N`: The total inventory (or lot) size.
- `alpha`: $1 - \alpha$ is the confidence level for bounding the probability of accepting the inventory.
- `P`: The proportion of accountable items.
- `AQL`: The acceptable quality level, which is the largest proportion of defects in a process considered acceptable. Note that $0 < AQL < 1$.
- `RQL`: The rejectable quality level, which is the largest proportion of defects in an independent lot that one is willing to tolerate. Note that $AQL < RQL < 1$.

**Value**

`acc.samp` returns a matrix with the following quantities:

- `acceptance.limit`: The number of items in the sample which may be unaccountable, yet still be able to attain the desired confidence level $1 - \alpha$.
- `lot.size`: The total inventory (or lot) size $N$.
- `confidence`: The confidence level $1 - \alpha$.
- `P`: The proportion of accountable items specified by the user.
- `AQL`: The acceptable quality level as specified by the user. If the sampling were to be repeated numerous times as a process, then this quantity specifies the proportion of missing items considered acceptable from the process as a whole. Conditioning on the calculated value for `acceptance.limit`, the `AQL` is used to estimate the producer’s risk (see `prod.risk` below).
The rejectable quality level as specified by the user. This is the proportion of individual items in a sample one is willing to tolerate missing. Conditioning on the calculated value for acceptance.limit, the RQL is used to estimate the consumer’s risk (see cons.risk below).

The sample size drawn as specified by n.

The producer’s risk at the specified AQL. This is the probability of rejecting an audit of a good inventory (also called the Type I error). A good inventory can be rejected if an unfortunate random sample is selected (e.g., most of the missing items happened to be selected for the audit). 1 - prod.risk gives the confidence level of this sampling plan for the specified AQL and RQL. If it is lower than the confidence level desired (e.g., because the AQL is too high), then a warning message will be displayed.

The consumer’s risk at the specified RQL. This is the probability of accepting an audit of a bad inventory (also called the Type II error). A bad inventory can be accepted if a fortunate random sample is selected (e.g., most of the missing items happened to not be selected for the audit).


See Also

Hypergeometric

Examples

## A 90%/90% acceptance sampling plan for a sample of 450
## drawn from a lot size of 960.

acc samp(n = 450, N = 960, alpha = 0.10, P = 0.90, AQL = 0.07,
RQL = 0.10)

Tolerance intervals for each factor level in a balanced (or nearly-balanced) ANOVA.

Usage

anovatol.int(lm.out, data, alpha = 0.05, P = 0.99, side = 1,
method = c("HE", "HE2", "WBE", "ELL", "KM",
"EXACT", "OCT"), m = 50)
Arguments

lm.out  An object of class `lm` (i.e., the results from the linear model fitting routine such that the `anova` function can act upon).

data  A data frame consisting of the data fitted in `lm.out`. Note that `data` must have one column for each main effect (i.e., factor) that is analyzed in `lm.out` and that these columns must be of class `factor`.

alpha  The level chosen such that 1-`alpha` is the confidence level.

P  The proportion of the population to be covered by this tolerance interval.

side  Whether a 1-sided or 2-sided tolerance interval is required (determined by `side = 1` or `side = 2`, respectively).

method  The method for calculating the k-factors. The k-factor for the 1-sided tolerance intervals is performed exactly and thus is the same for the chosen method. "HE" is the Howe method and is often viewed as being extremely accurate, even for small sample sizes. "HE2" is a second method due to Howe, which performs similarly to the Weissberg-Beatty method, but is computationally simpler. "WBE" is the Weissberg-Beatty method (also called the Wald-Wolfowitz method), which performs similarly to the first Howe method for larger sample sizes. "ELL" is the Ellison correction to the Weissberg-Beatty method when \( f \) is appreciably larger than \( n^2 \). A warning message is displayed if \( f \) is not larger than \( n^2 \). "KM" is the Krishnamoorthy-Mathew approximation to the exact solution, which works well for larger sample sizes. "EXACT" computes the k-factor exactly by finding the integral solution to the problem via the `integrate` function. Note the computation time of this method is largely determined by \( m \). "OCT" is the Owen approach to compute the k-factor when controlling the tails so that there is not more than \((1-P)/2\) of the data in each tail of the distribution.

m  The maximum number of subintervals to be used in the `integrate` function. This is necessary only for `method = "EXACT"` and `method = "OCT"`. The larger the number, the more accurate the solution. Too low of a value can result in an error. A large value can also cause the function to be slow for `method = "EXACT"`.

Value

`anovatol.int` returns a list where each element is a data frame corresponding to each main effect (i.e., factor) tested in the ANOVA and the rows of each data frame are the levels of that factor. The columns of each data frame report the following:

mean  The mean for that factor level.

n  The effective sample size for that factor level.

k  The k-factor for constructing the respective factor level’s tolerance interval.

1-sided.lower  The 1-sided lower tolerance bound. This is given only if `side = 1`.

1-sided.upper  The 1-sided upper tolerance bound. This is given only if `side = 1`.

2-sided.lower  The 2-sided lower tolerance bound. This is given only if `side = 2`.

2-sided.upper  The 2-sided upper tolerance bound. This is given only if `side = 2`. 
References


See Also

*K.factor, normtol.int, lm, anova*

Examples

```r
## 90%/95% 2-sided tolerance intervals for a 2-way ANOVA
## using the "warpbreaks" data.

attach(warpbreaks)

lm.out <- lm(breaks ~ wool + tension)
out <- anovatol.int(lm.out, data = warpbreaks, alpha = 0.10,
                  P = 0.95, side = 2, method = "HE")
out
plottol(out, x = warpbreaks)
```

---

Bayesian Normal Tolerance Intervals

Description

Provides 1-sided or 2-sided Bayesian tolerance intervals under the conjugate prior for data distributed according to a normal distribution.

Usage

```r
bayesnormtol.int(x = NULL, norm.stats = list(x.bar = NA,
    s = NA, n = NA), alpha = 0.05, P = 0.99,
    side = 1, method = c("HE", "HE2", "WBE",
    "ELL", "KM", "EXACT", "OCT"), m = 50,
    hyper.par = list(mu.0 = NULL,
    sig2.0 = NULL, m.0 = NULL, n.0 = NULL))
```

Arguments

- **x**: A vector of data which is distributed according to a normal distribution.
- **norm.stats**: An optional list of statistics that can be provided in-lieu of the full dataset. If provided, the user must specify all three components: the sample mean (x.bar), the sample standard deviation (s), and the sample size (n).
alpha: The level chosen such that 1 - alpha is the confidence level.

P: The proportion of the population to be covered by this tolerance interval.

side: Whether a 1-sided or 2-sided tolerance interval is required (determined by side = 1 or side = 2, respectively).

method: The method for calculating the k-factors. The k-factor for the 1-sided tolerance intervals is performed exactly and thus is the same for the chosen method. "HE" is the Howe method and is often viewed as being extremely accurate, even for small sample sizes. "HE2" is a second method due to Howe, which performs similarly to the Weissberg-Beatty method, but is computationally simpler. "WBE" is the Weissberg-Beatty method (also called the Wald-Wolfowitz method), which performs similarly to the first Howe method for larger sample sizes. "ELL" is the Ellison correction to the Weissberg-Beatty method when f is appreciably larger than n^2. A warning message is displayed if f is not larger than n^2. "KM" is the Krishnamoorthy-Mathew approximation to the exact solution, which works well for larger sample sizes. "EXACT" computes the k-factor exactly by finding the integral solution to the problem via the integrate function. Note the computation time of this method is largely determined by m. "OCT" is the Owen approach to compute the k-factor when controlling the tails so that there is not more than (1-P)/2 of the data in each tail of the distribution.

m: The maximum number of subintervals to be used in the integrate function. This is necessary only for method = "EXACT" and method = "OCT". The larger the number, the more accurate the solution. Too low of a value can result in an error. A large value can also cause the function to be slow for method = "EXACT".

hyper.par: A list consisting of the hyperparameters for the conjugate prior: the hyperparameters for the mean (mu.0 and n.0) and the hyperparameters for the variance (sig2.0 and m.0).

Details

Note that if one considers the non-informative prior distribution, then the Bayesian tolerance intervals are the same as the classical solution, which can be obtained by using normtol.int.

Value

bayesnormtol.int returns a data frame with items:

alpha: The specified significance level.

P: The proportion of the population covered by this tolerance interval.

x.bar: The sample mean.

1-sided.lower: The 1-sided lower Bayesian tolerance bound. This is given only if side = 1.

1-sided.upper: The 1-sided upper Bayesian tolerance bound. This is given only if side = 1.

2-sided.lower: The 2-sided lower Bayesian tolerance bound. This is given only if side = 2.

2-sided.upper: The 2-sided upper Bayesian tolerance bound. This is given only if side = 2.
References


See Also

Normal, normtol.int, K.factor

Examples

```r
## 95%/85% 1-sided Bayesian normal tolerance limits for
## a sample of size 100.

set.seed(100)
x <- rnorm(100)
out <- bayesnormtol.int(x = x, alpha = 0.05, P = 0.85,
side = 1, method = "EXACT",
hyper.par = list(mu.0 = 0,
sig2.0 = 1, n.0 = 10, m.0 = 10))

out

plottol(out, x, plot.type = "both", side = "upper",
x.lab = "Normal Data")
```

--

**bintol.int**  
*Binomial Tolerance Intervals*

Description

Provides 1-sided or 2-sided tolerance intervals for binomial random variables. From a statistical quality control perspective, these limits use the proportion of defective (or acceptable) items in a sample to bound the number of defective (or acceptable) items in future productions of a specified quantity.

Usage

```r
bintol.int(x, n, m = NULL, alpha = 0.05, P = 0.99, side = 1,
method = c("LS", "WS", "AC", "JF", "CP", "AS",
"LO", "PR", "PO", "CL", "CC", "CWS"),
a1 = 0.5, a2 = 0.5)
```
Arguments

- **x**: The number of defective (or acceptable) units in the sample. Can be a vector of length \( n \), in which case the sum of \( x \) is used.
- **n**: The size of the random sample of units selected for inspection.
- **m**: The quantity produced in future groups. If \( m = \text{NULL} \), then the tolerance limits will be constructed assuming \( n \) for this quantity.
- **alpha**: The level chosen such that \( 1 - \alpha \) is the confidence level.
- **P**: The proportion of the defective (or acceptable) units in future samples of size \( m \) to be covered by this tolerance interval.
- **side**: Whether a 1-sided or 2-sided tolerance interval is required (determined by \( \text{side} = 1 \) or \( \text{side} = 2 \), respectively).
- **method**: The method for calculating the lower and upper confidence bounds, which are used in the calculation of the tolerance bounds. The default method is "LS", which is the large-sample method. "WS" is Wilson’s method, which is just the score confidence interval. "AC" gives the Agresti-Coull method, which is also appropriate when the sample size is large. "JE" is Jeffreys' method, which is a Bayesian approach to the estimation. "CP" is the Clopper-Pearson (exact) method, which is based on beta percentiles and provides a more conservative interval. "AS" is the arcsine method, which is appropriate when the sample proportion is not too close to 0 or 1. "LO" is the logit method, which also is appropriate when the sample proportion is not too close to 0 or 1, but yields a more conservative interval. "PR" uses a probit transformation and is accurate for large sample sizes. "PO" is based on a Poisson parameterization, but it tends to be more erratic compared to the other methods. "CL" is the complementary log transformation and also tends to perform well for large sample sizes. "CC" gives a continuity-corrected version of the large-sample method. "CWS" gives a continuity-corrected version of Wilson’s method. More information on these methods can be found in the "References".
- **a1**: This specifies the first shape hyperparameter when using Jeffreys’ method.
- **a2**: This specifies the second shape hyperparameter when using Jeffreys’ method.

Value

*bintol.int* returns a data frame with items:

- **alpha**: The specified significance level.
- **P**: The proportion of defective (or acceptable) units in future samples of size \( m \).
- **p.hat**: The proportion of defective (or acceptable) units in the sample, calculated by \( x/n \).
- **1-sided.lower**: The 1-sided lower tolerance bound. This is given only if \( \text{side} = 1 \).
- **1-sided.upper**: The 1-sided upper tolerance bound. This is given only if \( \text{side} = 1 \).
- **2-sided.lower**: The 2-sided lower tolerance bound. This is given only if \( \text{side} = 2 \).
- **2-sided.upper**: The 2-sided upper tolerance bound. This is given only if \( \text{side} = 2 \).
References


See Also

*Binomial, umatol.int*

Examples

```r
## 85%/90% 2-sided binomial tolerance intervals for a future
## lot of 2500 when a sample of 230 were drawn from a lot of
## 1000. All methods but Jeffreys' method are compared
## below.

bintol.int(x = 230, n = 1000, m = 2500, alpha = 0.15, P = 0.90,
    side = 2, method = "LS")
bintol.int(x = 230, n = 1000, m = 2500, alpha = 0.15, P = 0.90,
    side = 2, method = "WS")
bintol.int(x = 230, n = 1000, m = 2500, alpha = 0.15, P = 0.90,
    side = 2, method = "AC")
bintol.int(x = 230, n = 1000, m = 2500, alpha = 0.15, P = 0.90,
    side = 2, method = "CP")
bintol.int(x = 230, n = 1000, m = 2500, alpha = 0.15, P = 0.90,
    side = 2, method = "AS")
bintol.int(x = 230, n = 1000, m = 2500, alpha = 0.15, P = 0.90,
    side = 2, method = "LO")
bintol.int(x = 230, n = 1000, m = 2500, alpha = 0.15, P = 0.90,
    side = 2, method = "PR")
bintol.int(x = 230, n = 1000, m = 2500, alpha = 0.15, P = 0.90,
    side = 2, method = "PO")
bintol.int(x = 230, n = 1000, m = 2500, alpha = 0.15, P = 0.90,
    side = 2, method = "CL")
bintol.int(x = 230, n = 1000, m = 2500, alpha = 0.15, P = 0.90,
    side = 2, method = "CC")
bintol.int(x = 230, n = 1000, m = 2500, alpha = 0.15, P = 0.90,
    side = 2, method = "CWS")

## Using Jeffreys' method to construct the 85%/90% 1-sided
## binomial tolerance limits. The first calculation assumes
## a prior on the proportion of defects which places greater
## density on values near 0. The second calculation assumes
## a prior on the proportion of defects which places greater
## density on values near 1.

bintol.int(x = 230, n = 1000, m = 2500, alpha = 0.15, P = 0.90,
    method = "J")
```
bonftol.int

Approximate 2-Sided Tolerance Intervals that Control the Tails Using Bonferroni’s Inequality

Description

This function allows the user to control what proportion of the population is to be in the tails of the given distribution for a 2-sided tolerance interval. The result is a conservative approximation based on Bonferroni’s inequality.

Usage

bonftol.int(fn, P1 = 0.005, P2 = 0.005, alpha = 0.05, ...)

Arguments

fn
The function name for the 2-sided tolerance interval to be calculated.

P1
The proportion of the population not covered in the lower tail of the distribution.

P2
The proportion of the population not covered in the upper tail of the distribution.

alpha
The level chosen such that 1 - alpha is the confidence level.

... Additional arguments passed to fn, including the data. All arguments that would be specified in fn must also be specified here.

Value

The results for the 2-sided tolerance interval procedure are reported. See the corresponding help file for fn about specific output. Note that the (minimum) proportion of the population to be covered by this interval is 1 - (P1 + P2).

Note

This function can be used with any 2-sided tolerance interval function, including the regression tolerance interval functions.

References


Examples

```r
# 95%/97% tolerance interval for normally distributed
# data controlling 1% of the data is in the lower tail
# and 2% of the data in the upper tail.

set.seed(100)
x <- rnorm(100, 0, 0.2)
bonfintol.int(normtol.int, x = x, P1 = 0.01, P2 = 0.02,
alpha = 0.05, method = "HE")
```

cautol.int

### Cauchy Tolerance Intervals

**Description**

Provides 1-sided or 2-sided tolerance intervals for Cauchy distributed data.

**Usage**

```r
cautol.int(x, alpha = 0.05, P = 0.99, side = 1)
```

**Arguments**

- `x` A vector of data which is Cauchy distributed.
- `alpha` The level chosen such that 1-\(\alpha\) is the confidence level.
- `P` The proportion of the population to be covered by this tolerance interval.
- `side` Whether a 1-sided or 2-sided tolerance interval is required (determined by `side = 1` or `side = 2`, respectively).

**Value**

cautol.int returns a data.frame with items:

- `alpha` The specified significance level.
- `P` The proportion of the population covered by this tolerance interval.
- `1-sided.lower` The 1-sided lower tolerance bound. This is given only if `side = 1`.
- `1-sided.upper` The 1-sided upper tolerance bound. This is given only if `side = 1`.
- `2-sided.lower` The 2-sided lower tolerance bound. This is given only if `side = 2`.
- `2-sided.upper` The 2-sided upper tolerance bound. This is given only if `side = 2`.

**References**

diffnormtol.int

1-Sided Tolerance Limits for the Distribution of the Difference Between Two Independent Normal Random Variables

Description

Provides 1-sided tolerance limits for the difference between two independent normal random variables. If the ratio of the variances is known, then an exact calculation is performed. Otherwise, approximation methods are implemented.

Usage

diffnormtol.int(x1, x2, var.ratio = NULL, alpha = 0.05, P = 0.99, method = c("HALL", "GK", "RG"))

Arguments

x1
A vector of sample data which is distributed according to a normal distribution (sample 1).

x2
Another vector of sample data which is distributed according to a normal distribution (sample 2). It can be of a different sample size than the sample specified by x1.

var.ratio
A specified, known value of the variance ratio (i.e., the ratio of the variance for population 1 to the variance of population 2). If NULL, then the variance ratio is estimated according to one of the three methods specified in the method argument.

alpha
The level chosen such that 1-alpha is the confidence level.

P
The proportion of the population to be covered by the tolerance limits.
The method for estimating the variance ratio. This only needs to be specified in the case when `var.ratio` is not `NULL`. "HALL" is Hall's method, which takes a bias-corrected version of the ratio between the sample variance for sample 1 to the sample variance for sample 2. "GK" is the Guo-Krishnamoorthy method, which first calculates a bias-corrected version of the ratio between the sample variance for sample 2 to the sample variance for sample 1. The resulting limit is then compared to the limit from Hall's method and the most conservative limit is chosen. "RG" is the Reiser-Guttman method, which is a biased version of the variance ratio that is calculated by taking the sample variance for sample 1 to the sample variance for sample 2. Typically, Hall's method or the Guo-Krishnamoorthy method are preferred to the Reiser-Guttman method.

Details

Satterthwaite's approximation for the degrees of freedom is used when the variance ratio is unknown.

Value
diffnormtol.int returns a data frame with items:

- `alpha`: The specified significance level.
- `p`: The proportion of the population covered by this tolerance interval.
- `diff.bar`: The difference between the sample means.
- `1-sided.lower`: The 1-sided lower tolerance bound.
- `1-sided.upper`: The 1-sided upper tolerance bound.

Note

Unlike other tolerance interval functions, the output from diffnormtol.int cannot be passed to plottol.

References


See Also

`Normal`, `K.factor.normtol.int`
Examples

```r
## 90%/99% tolerance limits for the difference between two
## simulated normal data sets. This data is taken from
## Krishnamoorthy and Mathew (2009). Note that there is a
## calculational error in their example, which yields different
## results with the output below.

x1 <- c(10.166, 5.889, 8.258, 7.303, 8.757)
x2 <- c(-0.204, 2.578, 1.182, 1.892, 0.786, -0.517, 1.156,
       0.980, 0.323, 0.437, 0.397, 0.050, 0.812, 0.720)
diffnormtol.int(x1, x2, alpha = 0.10, P = 0.99, method = "HALL")
diffnormtol.int(x1, x2, alpha = 0.10, P = 0.99, method = "GK")
diffnormtol.int(x1, x2, alpha = 0.10, P = 0.99, method = "RG")
diffnormtol.int(x1, x2, var.ratio = 3.8, alpha = 0.10, P = 0.99)
```

### Description

Density (mass), distribution function, quantile function, and random generation for the difference between two proportions. This is determined by taking the difference between two independent beta distributions.

### Usage

```r
ddiffprop(x, k1, k2, n1, n2, a1 = 0.5, a2 = 0.5, log = FALSE, ...)
pdiffprop(q, k1, k2, n1, n2, a1 = 0.5, a2 = 0.5, lower.tail = TRUE, log.p = FALSE, ...)
qdiffprop(p, k1, k2, n1, n2, a1 = 0.5, a2 = 0.5, lower.tail = TRUE, log.p = FALSE, ...)
rdiffprop(n, k1, k2, n1, n2, a1 = 0.5, a2 = 0.5)
```

### Arguments

- `x, q`: Vector of quantiles.
- `p`: Vector of probabilities.
- `n`: The number of observations. If `length>1`, then the length is taken to be the number required.
- `k1, k2`: The number of successes drawn from groups 1 and 2, respectively.
- `n1, n2`: The sample sizes for groups 1 and 2, respectively.
The shift parameters for the beta distributions. For the fiducial approach, we know that the lower and upper limits are set at $a_1 = a_2 = 0$ and $a_1 = a_2 = 1$, respectively, for the true $p_1$ and $p_2$. While computations can be performed on real values outside the unit interval, a warning message will be returned if such values are specified. For practical purposes, the default value of 0.5 should be used for each parameter.

`log, log.p` Logical vectors. If `TRUE`, then the probabilities are given as $\log(p)$.

`lower.tail` Logical vector. If `TRUE`, then probabilities are $P[X \leq x]$, else $P[X > x]$.

... Additional arguments passed to the Appell $F_1$ function.

### Details

The difference between two proportions distribution has a fairly complicated functional form. Please see the article by Chen and Luo (2011), who corrected a typo in the article by Nadarajah and Kotz (2007), for the functional form of this distribution.

### Value

`ddiffprop` gives the density (mass), `pdiffprop` gives the distribution function, `qdiffprop` gives the quantile function, and `rdiffprop` generates random deviates.

### References


### See Also

`runif` and `.Random.seed` about random number generation.

### Examples

```r
## Randomly generated data from the difference between
## two proportions distribution.

set.seed(100)
x <- rdiffprop(n = 100, k1 = 2, k2 = 10, n1 = 17, n2 = 13)
hist(x, main = "Randomly Generated Data", prob = TRUE)
x.1 <- sort(x)
y <- ddiffprop(x = x.1, k1 = 2, k2 = 10, n1 = 17, n2 = 13)
lines(x.1, y, col = 2, lwd = 2)
plot(x.1, pdiffprop(q = x.1, k1 = 2, k2 = 10, n1 = 17,
          n2 = 13), type = "l", xlab = "x",
     ylab = "Cumulative Probabilities")
qdiffprop(p = 0.20, k1 = 2, k2 = 10, n1 = 17, n2 = 13,
```
```r
lower.tail = FALSE
qdiffprop(p = 0.80, k1 = 2, k2 = 10, n1 = 17, n2 = 13)
```

---

### Discrete Pareto Distribution

**Description**

Density (mass), distribution function, quantile function, and random generation for the discrete Pareto distribution.

**Usage**

```r
ddpareto(x, theta, log = FALSE)
pdpareto(q, theta, lower.tail = TRUE, log.p = FALSE)
qdpareto(p, theta, lower.tail = TRUE, log.p = FALSE)
rdpareto(n, theta)
```

**Arguments**

- **x, q** Vector of quantiles.
- **p** Vector of probabilities.
- **n** The number of observations. If `length>1`, then the length is taken to be the number required.
- **theta** The shape parameter, which must be greater than 0 and less than 1.
- **log, log.p** Logical vectors. If `TRUE`, then the probabilities are given as `log(p)`.
- **lower.tail** Logical vector. If `TRUE`, then probabilities are \( P[X \leq x] \), else \( P[X > x] \).

**Details**

The discrete Pareto distribution has mass

\[
p(x) = \theta^{\log(1+x)} - \theta^{\log(2+x)},
\]

where \( x = 0, 1, \ldots \) and \( 0 < \theta < 1 \) is the shape parameter.

**Value**

ddpareto gives the density (mass), pdpareto gives the distribution function, qdpareto gives the quantile function, and rdpareto generates random deviates for the specified distribution.

**References**


distfree.est

See Also
runif and .Random.seed about random number generation.

Examples

```
## Randomly generated data from the discrete Pareto
## distribution.
set.seed(100)
x <- rdpareto(n = 150, theta = 0.2)
hist(x, main = "Randomly Generated Data", prob = TRUE)
x.1 <- sort(x)
y <- ddpareto(x = x.1, theta = 0.2)
lines(x.1, y, col = 2, lwd = 2)
plot(x.1, pdpareto(q = x.1, theta = 0.2), type = "l",
xlab = "x", ylab = "Cumulative Probabilities")
qdpareto(p = 0.80, theta = 0.2, lower.tail = FALSE)
qdpareto(p = 0.95, theta = 0.2)
```

---

distfree.est

Estimating Various Quantities for Distribution-Free Tolerance Intervals

Description

When providing two of the three quantities \( n \), \( \alpha \), and \( P \), this function solves for the third quantity in the context of distribution-free tolerance intervals.

Usage

```
distfree.est(n = NULL, alpha = NULL, P = NULL, side = 1)
```

Arguments

- **n**
  The necessary sample size to cover a proportion \( P \) of the population with confidence \( 1 - \alpha \). Can be a vector.

- **alpha**
  1 minus the confidence level attained when it is desired to cover a proportion \( P \) of the population and a sample size \( n \) is provided. Can be a vector.

- **P**
  The proportion of the population to be covered with confidence \( 1 - \alpha \) when a sample size \( n \) is provided. Can be a vector.

- **side**
  Whether a 1-sided or 2-sided tolerance interval is assumed (determined by side = 1 or side = 2, respectively).
Value

When providing two of the three quantities n, alpha, and P, distfree.est returns the third quantity. If more than one value of a certain quantity is specified, then a table will be returned.

References


See Also

nptol.int

Examples

```r
## Solving for 1 minus the confidence level.
distfree.est(n = 59, P = 0.95, side = 1)

## Solving for the sample size.
distfree.est(alpha = 0.05, P = 0.95, side = 1)

## Solving for the proportion of the population to cover.
distfree.est(n = 59, alpha = 0.05, side = 1)

## Solving for sample sizes for many tolerance specifications.
distfree.est(alpha = seq(0.01, 0.05, 0.01),
              P = seq(0.80, 0.99, 0.01), side = 2)
```

dpareto.ll

Maximum Likelihood Estimation for the Discrete Pareto Distribution

Description

Performs maximum likelihood estimation for the parameter of the discrete Pareto distribution.

Usage

dpareto.ll(x, theta = NULL, ...)

Arguments

- **x**: A vector of raw data which is distributed according to a Poisson-Lindley distribution.
- **theta**: Optional starting value for the parameter. If `NULL`, then the method of moments estimator is used.
- ...: Additional arguments passed to the `mle` function.

Details

The discrete Pareto distribution is a discretized of the continuous Type II Pareto distribution (also called the Lomax distribution).

Value

See the help file for `mle` to see how the output is structured.

References


See Also

`mle`, `DiscretePareto`

Examples

```r
## Maximum likelihood estimation for randomly generated data
## from the discrete Pareto distribution.

set.seed(100)

dp.data <- rdpareto(n = 500, theta = 0.2)
out.dp <- dpareto.ll(dp.data)
stats4::coef(out.dp)
stats4::vcov(out.dp)
```

Description

Provides 1-sided or 2-sided tolerance intervals for data distributed according to the discrete Pareto distribution.
Usage
dparetotol.int(x, m = NULL, alpha = 0.05, P = 0.99, side = 1, ...)

Arguments
x A vector of raw data which is distributed according to a discrete Pareto distribution.
m The number of observations in a future sample for which the tolerance limits will be calculated. By default, \( m = \text{NULL} \) and, thus, \( m \) will be set equal to the original sample size.
alpha The level chosen such that \( 1 - \alpha \) is the confidence level.
P The proportion of the population to be covered by this tolerance interval.
side Whether a 1-sided or 2-sided tolerance interval is required (determined by \( \text{side} = 1 \) or \( \text{side} = 2 \), respectively).
... Additional arguments passed to the dpareto.ll function, which is used for maximum likelihood estimation.

Details
The discrete Pareto is a discretized of the continuous Type II Pareto distribution (also called the Lomax distribution). Discrete Pareto distributions are heavily right-skewed distributions and potentially good models for discrete lifetime data and extremes in count data. For most practical applications, one will typically be interested in 1-sided upper bounds.

Value
dparetotol.int returns a data frame with the following items:
alpha The specified significance level.
P The proportion of the population covered by this tolerance interval.
theta MLE for the shape parameter \( \theta \).
1-sided.lower The 1-sided lower tolerance bound. This is given only if \( \text{side} = 1 \).
1-sided.upper The 1-sided upper tolerance bound. This is given only if \( \text{side} = 1 \).
2-sided.lower The 2-sided lower tolerance bound. This is given only if \( \text{side} = 2 \).
2-sided.upper The 2-sided upper tolerance bound. This is given only if \( \text{side} = 2 \).

References

See Also
DiscretePareto, dpareto.ll
Examples

```r
# 95%/95% 1-sided tolerance intervals for data assuming
# the discrete Pareto distribution.
set.seed(100)
x <- rdpareto(n = 500, theta = 0.5)
out <- dparetotol.int(x, alpha = 0.05, P = 0.95, side = 1)
out
```

## Description

Provides 1-sided or 2-sided tolerance intervals for data distributed according to a 2-parameter exponential distribution. Data with Type II censoring is permitted.

## Usage

```r
exp2tol.int(x, alpha = 0.05, P = 0.99, side = 1,
method = c("GPU", "DUN", "KM"), type.2 = FALSE)
```

## Arguments

- `x`: A vector of data which is distributed according to the 2-parameter exponential distribution.
- `alpha`: The level chosen such that \(1 - \alpha\) is the confidence level.
- `P`: The proportion of the population to be covered by this tolerance interval.
- `side`: Whether a 1-sided or 2-sided tolerance interval is required (determined by `side` = 1 or `side` = 2, respectively).
- `method`: The method for how the upper tolerance bound is approximated. "GPU" is the Guenther-Patil-Upppuluri method. "DUN" is the Dunsmore method, which has been empirically shown to be an improvement for samples greater than or equal to 8. "KM" is the Krishnamoorthy-Mathew method, which is typically more liberal than the other methods. More information on these methods can be found in the "References", which also highlight general sample size conditions as to when these different methods should be used.
- `type.2`: Select `TRUE` if Type II censoring is present (i.e., the data set is censored at the maximum value present). The default is `FALSE`.
Value

exp2tol.int returns a data frame with items:

<table>
<thead>
<tr>
<th>Item</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>alpha</td>
<td>The specified significance level.</td>
</tr>
<tr>
<td>( p )</td>
<td>The proportion of the population covered by this tolerance interval.</td>
</tr>
<tr>
<td>1-sided.lower</td>
<td>The 1-sided lower tolerance bound. This is given only if ( \text{side} = 1 ).</td>
</tr>
<tr>
<td>1-sided.upper</td>
<td>The 1-sided upper tolerance bound. This is given only if ( \text{side} = 1 ).</td>
</tr>
<tr>
<td>2-sided.lower</td>
<td>The 2-sided lower tolerance bound. This is given only if ( \text{side} = 2 ).</td>
</tr>
<tr>
<td>2-sided.upper</td>
<td>The 2-sided upper tolerance bound. This is given only if ( \text{side} = 2 ).</td>
</tr>
</tbody>
</table>

References


See Also

TwoParExponential

Examples

```r
## 95%/90% 1-sided 2-parameter exponential tolerance intervals
## for a sample of size 50.

set.seed(100)
x <- r2exp(50, 6, shift = 55)
out <- exp2tol.int(x = x, alpha = 0.05, P = 0.90, side = 1,
                   method = "DUN", type.2 = FALSE)
out
plottol(out, x, plot.type = "both", side = "upper",
ex.lab = "2-Parameter Exponential Data")```
Description

Provides 1-sided or 2-sided tolerance intervals for data distributed according to an exponential distribution. Data with Type II censoring is permitted.

Usage

```r
exptol.int(x, alpha = 0.05, P = 0.99, side = 1, type.2 = FALSE)
```

Arguments

- **x**: A vector of data which is distributed according to an exponential distribution.
- **alpha**: The level chosen such that 1-alpha is the confidence level.
- **P**: The proportion of the population to be covered by this tolerance interval.
- **side**: Whether a 1-sided or 2-sided tolerance interval is required (determined by `side = 1` or `side = 2`, respectively).
- **type.2**: Select `TRUE` if Type II censoring is present (i.e., the data set is censored at the maximum value present). The default is `FALSE`.

Value

`exptol.int` returns a data frame with items:

- **alpha**: The specified significance level.
- **P**: The proportion of the population covered by this tolerance interval.
- **lambda.hat**: The mean of the data (i.e., 1/rate).
- **1-sided.lower**: The 1-sided lower tolerance bound. This is given only if `side = 1`.
- **1-sided.upper**: The 1-sided upper tolerance bound. This is given only if `side = 1`.
- **2-sided.lower**: The 2-sided lower tolerance bound. This is given only if `side = 2`.
- **2-sided.upper**: The 2-sided upper tolerance bound. This is given only if `side = 2`.

References


See Also

`Exponential`
Examples

## 95%/99% 1-sided exponential tolerance intervals for a
## sample of size 50.

set.seed(100)
x <- rexp(100, 0.004)
out <- exptol.int(x = x, alpha = 0.05, P = 0.99, side = 1,
    type.2 = FALSE)
out

plottol(out, x, plot.type = "both", side = "lower",
x.lab = "Exponential Data")

---

exttol.int

Weibull (or Extreme-Value) Tolerance Intervals

Description

Provides 1-sided or 2-sided tolerance intervals for data distributed according to either a Weibull distribution or extreme-value (also called Gumbel) distributions.

Usage

```r
exttol.int(x, alpha = 0.05, P = 0.99, side = 1,
    dist = c("Weibull", "Gumbel"), ext = c("min", "max"),
    NR.delta = 1e-8)
```

Arguments

- **x**: A vector of data which is distributed according to either a Weibull distribution or an extreme-value distribution.
- **alpha**: The level chosen such that 1 - alpha is the confidence level.
- **P**: The proportion of the population to be covered by this tolerance interval.
- **side**: Whether a 1-sided or 2-sided tolerance interval is required (determined by `side = 1` or `side = 2`, respectively).
- **dist**: Select either `dist = "Weibull"` or `dist = "Gumbel"` if the data is distributed according to the Weibull or extreme-value distribution, respectively.
- **ext**: If `dist = "Gumbel"`, then select which extreme is to be modeled for the Gumbel distribution. The Gumbel distribution for the minimum (i.e., `ext = "min"`) corresponds to a left-skewed distribution and the Gumbel distribution for the maximum (i.e., `ext = "max"`) corresponds to a right-skewed distribution.
- **NR.delta**: The stopping criterion used for the Newton-Raphson algorithm when finding the maximum likelihood estimates of the Weibull or extreme-value distribution.
Details

Recall that the relationship between the Weibull distribution and the extreme-value distribution for the minimum is that if the random variable $X$ is distributed according to a Weibull distribution, then the random variable $Y = \ln(X)$ is distributed according to an extreme-value distribution for the minimum.

If `dist = "Weibull"`, then the natural logarithm of the data are taken so that a Newton-Raphson algorithm can be employed to find the MLEs of the extreme-value distribution for the minimum and then the data and MLEs are transformed back appropriately. No transformation is performed if `dist = "Gumbel"`. The Newton-Raphson algorithm is initialized by the method of moments estimators for the parameters.

Value

`exttol.int` returns a data frame with items:

- **alpha**: The specified significance level.
- **P**: The proportion of the population covered by this tolerance interval.
- **shape.1**: MLE for the shape parameter if `dist = "Weibull"` or for the location parameter if `dist = "Gumbel"`
- **shape.2**: MLE for the scale parameter if `dist = "Weibull"` or `dist = "Gumbel"`
- **1-sided.lower**: The 1-sided lower tolerance bound. This is given only if `side = 1`.
- **1-sided.upper**: The 1-sided upper tolerance bound. This is given only if `side = 1`.
- **2-sided.lower**: The 2-sided lower tolerance bound. This is given only if `side = 2`.
- **2-sided.upper**: The 2-sided upper tolerance bound. This is given only if `side = 2`.

References


See Also

`Weibull`

Examples

```r
## 85%/90% 1-sided Weibull tolerance intervals for a sample
## of size 150.
set.seed(100)
x <- rweibull(150, 3, 75)
out <- exttol.int(x = x, alpha = 0.15, P = 0.90, side = 1,
                 dist = "Weibull")
out
```
F1

Appell's F1 Hypergeometric Function

Description

The Appell function of the first kind, which is a two variable extension of the hypergeometric distribution.

Usage

F1(a, b, b.prime, c, x, y, ...)

Arguments

a, b, b.prime, c
  Appropriate parameters for this function.

x, y
  The inputted values to evaluate this function such that each is less than 1 in absolute value.

...
  Additional arguments passed to the integrate function.

Value

F1 returns the simple integral result for the Appell function of the first kind with the arguments specified above.

Note

This function is solved by using a simple integral representation for real numbers. While all four of the Appell functions can be extended to the complex plane, this is not an option for this code.

References


See Also

DiffProp, integrate

Examples

## Sample calculation.

F1(a = 3, b = 4, b.prime = 5, c = 13, x = 0.2, y = 0.4)
**Fiducial-Based Tolerance Intervals for the Function of Two Binomial Proportions**

**Description**

Provides 1-sided or 2-sided tolerance intervals for the function of two binomial proportions using fiducial quantities.

**Usage**

```r
fidbintol.int(x1, x2, n1, n2, m1 = NULL, m2 = NULL, FUN,
               alpha = 0.05, P = 0.99, side = 1, K = 1000,
               B = 1000)
```

**Arguments**

- `x1`: A value of observed "successes" from group 1.
- `x2`: A value of observed "successes" from group 2.
- `n1`: The total number of trials for group 1.
- `n2`: The total number of trials for group 2.
- `m1`: The total number of future trials for group 1. If `NULL`, then it is set to `n1`.
- `m2`: The total number of future trials for group 2. If `NULL`, then it is set to `n2`.
- `FUN`: Any reasonable (and meaningful) function taking exactly two arguments that we are interested in constructing a tolerance interval on.
- `alpha`: The level chosen such that 1-alpha is the confidence level.
- `P`: The proportion of the population to be covered by this tolerance interval.
- `side`: Whether a 1-sided or 2-sided tolerance interval is required (determined by `side = 1` or `side = 2`, respectively).
- `K`: The number of fiducial quantities to be generated. The number of iterations should be at least as large as the default value of 1000. See Details for the definition of the fiducial quantity for a binomial proportion.
- `B`: The number of iterations used for the Monte Carlo algorithm which determines the tolerance limits. The number of iterations should be at least as large as the default value of 1000.

**Details**

If \( X \) is observed from a \( \text{Bin}(n, p) \) distribution, then the fiducial quantity for \( p \) is \( \text{Beta}(X + 0.5, n - X + 0.5) \).
Value

`fidbintol.int` returns a list with two items. The first item (`tol.limits`) is a data frame with the following items:

- **alpha**: The specified significance level.
- **P**: The proportion of the population covered by this tolerance interval.
- **fn.est**: A point estimate of the functional form of interest using the maximum likelihood estimates calculated with the inputted values of `x1`, `x2`, `n1`, and `n2`.
- **1-sided.lower**: The 1-sided lower tolerance bound. This is given only if `side = 1`.
- **1-sided.upper**: The 1-sided upper tolerance bound. This is given only if `side = 1`.
- **2-sided.lower**: The 2-sided lower tolerance bound. This is given only if `side = 2`.
- **2-sided.upper**: The 2-sided upper tolerance bound. This is given only if `side = 2`.

The second item (`fn`) simply returns the functional form specified by `FUN`.

References

Clopper, C. J. and Pearson, E. S. (1934), The Use of Confidence or Fiducial Limits Illustrated in the Case of the Binomial, *Biometrika*, 26, 404–413.


See Also

`fidnegbintol.int`, `fidpoistol.int`

Examples

```r
## 95%/99% 1-sided and 2-sided tolerance intervals for
## the difference between binomial proportions.

c <- 100

p1 <- 0.2
p2 <- 0.4
n1 <- n2 <- 200
x1 <- rbinom(1, n1, p1)
x2 <- rbinom(1, n2, p2)
fun.ti <- function(x, y) x - y

fidbintol.int(x1, x2, n1, n2, m1 = 500, m2 = 500, FUN = fun.ti,
              alpha = 0.05, P = 0.99, side = 1)

fidbintol.int(x1, x2, n1, n2, m1 = 500, m2 = 500, FUN = fun.ti,
              alpha = 0.05, P = 0.99, side = 2)
```
Fiducial-Based Tolerance Intervals for the Function of Two Negative Binomial Proportions

Description

Provides 1-sided or 2-sided tolerance intervals for the function of two negative binomial proportions using fiducial quantities.

Usage

`fidnegbintol.int(x1, x2, n1, n2, m1 = NULL, m2 = NULL, FUN, alpha = 0.05, P = 0.99, side = 1, K = 1000, B = 1000)`

Arguments

- `x1`: A value of observed "failures" from group 1.
- `x2`: A value of observed "failures" from group 2.
- `n1`: The target number of successes for group 1.
- `n2`: The target number of successes for group 2.
- `m1`: The total number of future trials for group 1. If `NULL`, then it is set to `n1`.
- `m2`: The total number of future trials for group 2. If `NULL`, then it is set to `n2`.
- `FUN`: Any reasonable (and meaningful) function taking exactly two arguments that we are interested in constructing a tolerance interval on.
- `alpha`: The level chosen such that 1-alpha is the confidence level.
- `P`: The proportion of the population to be covered by this tolerance interval.
- `side`: Whether a 1-sided or 2-sided tolerance interval is required (determined by `side = 1` or `side = 2`, respectively).
- `K`: The number of fiducial quantities to be generated. The number of iterations should be at least as large as the default value of 1000. See Details for the definition of the fiducial quantity for a negative binomial proportion.
- `B`: The number of iterations used for the Monte Carlo algorithm which determines the tolerance limits. The number of iterations should be at least as large as the default value of 1000.

Details

If `X` is observed from a `NegBin(n, p)` distribution, then the fiducial quantity for `p` is `Beta(n, X + 0.5)`. 
Value

`fidnegbintol.int` returns a list with two items. The first item (`tol.limits`) is a data frame with the following items:

- **alpha**: The specified significance level.
- **P**: The proportion of the population covered by this tolerance interval.
- **fn.est**: A point estimate of the functional form of interest using the maximum likelihood estimates calculated with the inputted values of `x1`, `x2`, `n1`, and `n2`.
- **1-sided.lower**: The 1-sided lower tolerance bound. This is given only if `side = 1`.
- **1-sided.upper**: The 1-sided upper tolerance bound. This is given only if `side = 1`.
- **2-sided.lower**: The 2-sided lower tolerance bound. This is given only if `side = 2`.
- **2-sided.upper**: The 2-sided upper tolerance bound. This is given only if `side = 2`.

The second item (`fn`) simply returns the functional form specified by `FUN`.

References


Clopper, C. J. and Pearson, E. S. (1934), The Use of Confidence or Fiducial Limits Illustrated in the Case of the Binomial, *Biometrika*, 26, 404–413.


See Also

`fidbintol.int`, `fidpoistol.int`

Examples

```r
## 95%/99% 1-sided and 2-sided tolerance intervals for
## the ratio of odds ratios for negative binomial proportions.

set.seed(100)

p1 <- 0.6
p2 <- 0.2
n1 <- n2 <- 50
x1 <- rnbinom(1, n1, p1)
x2 <- rnbinom(1, n2, p2)
fun.ti <- function(x, y) x * (1 - y) / (y * (1 - x))

fidnegbintol.int(x1, x2, n1, n2, m1 = 50, m2 = 50, FUN = fun.ti,
alpha = 0.05, P = 0.99, side = 1)
 fidnegbintol.int(x1, x2, n1, n2, m1 = 50, m2 = 50, FUN = fun.ti,
```
Description

Provides 1-sided or 2-sided tolerance intervals for the function of two Poisson rates using fiducial quantities.

Usage

fidpoistol.int(x1, x2, n1, n2, m1 = NULL, m2 = NULL, FUN,
   alpha = 0.05, P = 0.99, side = 1, K = 1000,
   B = 1000)

Arguments

x1 A value of observed counts from group 1.
x2 A value of observed counts from group 2.
n1 The length of time that x1 was recorded over.
n2 The length of time that x2 was recorded over.
m1 The total number of future trials for group 1. If NULL, then it is set to n1.
m2 The total number of future trials for group 2. If NULL, then it is set to n2.
FUN Any reasonable (and meaningful) function taking exactly two arguments that we are interested in constructing a tolerance interval on.
alpha The level chosen such that 1-alpha is the confidence level.
P The proportion of the population to be covered by this tolerance interval.
side Whether a 1-sided or 2-sided tolerance interval is required (determined by side = 1 or side = 2, respectively).
K The number of fiducial quantities to be generated. The number of iterations should be at least as large as the default value of 1000. See Details for the definition of the fiducial quantity for a Poisson rate.
B The number of iterations used for the Monte Carlo algorithm which determines the tolerance limits. The number of iterations should be at least as large as the default value of 1000.

Details

If X is observed from a Pois(n * λ) distribution, then the fiducial quantity for λ is \( \chi^2_{2x+1}/(2*n) \).
Value

fidpoistol.int returns a list with two items. The first item (tol.limits) is a data frame with the following items:

- **alpha**: The specified significance level.
- **P**: The proportion of the population covered by this tolerance interval.
- **fn.est**: A point estimate of the functional form of interest using the maximum likelihood estimates calculated with the inputted values of \( x_1, x_2, n_1, \) and \( n_2 \).
- **1-sided.lower**: The 1-sided lower tolerance bound. This is given only if \( \text{side} = 1 \).
- **1-sided.upper**: The 1-sided upper tolerance bound. This is given only if \( \text{side} = 1 \).
- **2-sided.lower**: The 2-sided lower tolerance bound. This is given only if \( \text{side} = 2 \).
- **2-sided.upper**: The 2-sided upper tolerance bound. This is given only if \( \text{side} = 2 \).

The second item (fn) simply returns the functional form specified by FUN.

References


See Also

 fidbintol.int, fidnegbintol.int

Examples

```r
## 95%/99% 1-sided and 2-sided tolerance intervals for
## the ratio of two Poisson rates.

set.seed(100)

lambda1 <- 10
lambda2 <- 2
n1 <- 3000
n2 <- 3250
x1 <- rpois(1, n1 * lambda1)
x2 <- rpois(1, n2 * lambda2)
fun.ti <- function(x, y) x / y

fidpoistol.int(x1, x2, n1, n2, m1 = 2000, m2 = 2500,
               FUN = fun.ti, alpha = 0.05, P = 0.99, side = 1)
 fidpoistol.int(x1, x2, n1, n2, m1 = 2000, m2 = 2500,
               FUN = fun.ti, alpha = 0.05, P = 0.99, side = 2)
```
Description

Provides 1-sided or 2-sided tolerance intervals for data distributed according to either a gamma distribution or log-gamma distribution.

Usage

```r
gamtol.int(x, alpha = 0.05, P = 0.99, side = 1,
method = c("HE", "HE2", "WBE", "ELL", "KM", "EXACT",
"OCT"), m = 50, log.gamma = FALSE)
```

Arguments

- `x`: A vector of data which is distributed according to either a gamma distribution or a log-gamma distribution.
- `alpha`: The level chosen such that 1-alpha is the confidence level.
- `P`: The proportion of the population to be covered by this tolerance interval.
- `side`: Whether a 1-sided or 2-sided tolerance interval is required (determined by `side = 1` or `side = 2`, respectively).
- `method`: The method for calculating the k-factors. The k-factor for the 1-sided tolerance intervals is performed exactly and thus is the same for the chosen method. "HE" is the Howe method and is often viewed as being extremely accurate, even for small sample sizes. "HE2" is a second method due to Howe, which performs similarly to the Weissberg-Beatty method, but is computationally simpler. "WBE" is the Weissberg-Beatty method (also called the Wald-Wolfowitz method), which performs similarly to the first Howe method for larger sample sizes. "ELL" is the Ellison correction to the Weissberg-Beatty method when f is appreciably larger than n^2. A warning message is displayed if f is not larger than n^2. "KM" is the Krishnamoorthy-Mathew approximation to the exact solution, which works well for larger sample sizes. "EXACT" computes the k-factor exactly by finding the integral solution to the problem via the `integrate` function. Note the computation time of this method is largely determined by `m`. "OCT" is the Owen approach to compute the k-factor when controlling the tails so that there is not more than (1-P)/2 of the data in each tail of the distribution.
- `m`: The maximum number of subintervals to be used in the `integrate` function. This is necessary only for `method = "EXACT"` and `method = "OCT"`. The larger the number, the more accurate the solution. Too low of a value can result in an error. A large value can also cause the function to be slow for `method = "EXACT"`.
- `log.gamma`: If TRUE, then the data is considered to be from a log-gamma distribution, in which case the output gives tolerance intervals for the log-gamma distribution. The default is FALSE.
Details

Recall that if the random variable $X$ is distributed according to a log-gamma distribution, then the random variable $Y = \ln(X)$ is distributed according to a gamma distribution.

Value

`gamtol.int` returns a data frame with items:

- `alpha` The specified significance level.
- `P` The proportion of the population covered by this tolerance interval.
- `1-sided.lower` The 1-sided lower tolerance bound. This is given only if `side = 1`.
- `1-sided.upper` The 1-sided upper tolerance bound. This is given only if `side = 1`.
- `2-sided.lower` The 2-sided lower tolerance bound. This is given only if `side = 2`.
- `2-sided.upper` The 2-sided upper tolerance bound. This is given only if `side = 2`.

References


See Also

`GammaDist`, `K.factor`

Examples

```r
## 99%/99% 1-sided gamma tolerance intervals for a sample
## of size 50.
set.seed(100)
x <- rgamma(50, 0.30, scale = 2)
out <- gamtol.int(x = x, alpha = 0.01, P = 0.99, side = 1,
                 method = "HE")
out
plottol(out, x, plot.type = "both", side = "upper",
x.lab = "Gamma Data")
```
hypertol.int

Hypergeometric Tolerance Intervals

Description

Provides 1-sided or 2-sided tolerance intervals for hypergeometric random variables. From a sampling without replacement perspective, these limits use the proportion of units from group A (e.g., "black balls" in an urn) in a sample to bound the number of potential units drawn from group A in a future sample taken from the universe.

Usage

```r
hypertol.int(x, n, N, m = NULL, alpha = 0.05, P = 0.99, side = 1, method = c("EX", "LS", "CC"))
```

Arguments

- `x`: The number of units from group A in the sample. Can be a vector, in which case the sum of `x` is used.
- `n`: The size of the random sample of units selected.
- `N`: The population size.
- `m`: The quantity of units to be sampled from the universe for a future study. If `m = NULL`, then the tolerance limits will be constructed assuming `n` for this quantity.
- `alpha`: The level chosen such that 1 - `alpha` is the confidence level.
- `P`: The proportion of units from group A in future samples of size `m` to be covered by this tolerance interval.
- `side`: Whether a 1-sided or 2-sided tolerance interval is required (determined by `side = 1` or `side = 2`, respectively).
- `method`: The method for calculating the lower and upper confidence bounds, which are used in the calculation of the tolerance bounds. The default method is "EX", which is an exact-based method. "LS" is the large-sample method. "CC" gives a continuity-corrected version of the large-sample method.

Value

`hypertol.int` returns a data frame with items:

- `alpha`: The specified significance level.
- `P`: The proportion of units from group A in future samples of size `m`.
- `rate`: The sampling rate determined by `n/N`.
- `p.hat`: The proportion of units in the sample from group A, calculated by `x/n`.
- `1-sided.lower`: The 1-sided lower tolerance bound. This is given only if `side = 1`.
- `1-sided.upper`: The 1-sided upper tolerance bound. This is given only if `side = 1`.
- `2-sided.lower`: The 2-sided lower tolerance bound. This is given only if `side = 2`.
- `2-sided.upper`: The 2-sided upper tolerance bound. This is given only if `side = 2`.
Note

As this methodology is built using large-sample theory, if the sampling rate is less than 0.05, then a warning is generated stating that the results are not reliable. Also, compare the functionality of this procedure with the `acc.samp` procedure, which is to determine a minimal acceptance limit for a particular sampling plan.

References


See Also

`acc.samp`, `Hypergeometric`

Examples

```r
## 90%/95% 1-sided and 2-sided hypergeometric tolerance
## intervals for a future sample of 30 when the universe
## is of size 100.

hypertol.int(x = 15, n = 50, N = 100, m = 30, alpha = 0.10, P = 0.95, side = 1, method = "LS")
hypertol.int(x = 15, n = 50, N = 100, m = 30, alpha = 0.10, P = 0.95, side = 1, method = "CC")
hypertol.int(x = 15, n = 50, N = 100, m = 30, alpha = 0.10, P = 0.95, side = 2, method = "LS")
hypertol.int(x = 15, n = 50, N = 100, m = 30, alpha = 0.10, P = 0.95, side = 2, method = "CC")
```

K.factor

Estimating K-factors for Tolerance Intervals Based on Normality

Description

Estimates k-factors for tolerance intervals based on normality.

Usage

```r
K.factor(n, f = NULL, alpha = 0.05, P = 0.99, side = 1,
method = c("HE", "HE2", "WBE", "ELL", "KM", "EXACT",
"OCT"), m = 50)
```
K.factor

Arguments

n
The (effective) sample size.

f
The number of degrees of freedom associated with calculating the estimate of the population standard deviation. If NULL, then f is taken to be n-1.

alpha
The level chosen such that 1-alpha is the confidence level.

P
The proportion of the population to be covered by the tolerance interval.

side
Whether a 1-sided or 2-sided tolerance interval is required (determined by side = 1 or side = 2, respectively).

method
The method for calculating the k-factors. The k-factor for the 1-sided tolerance intervals is performed exactly and thus is the same for the chosen method. "HE" is the Howe method and is often viewed as being extremely accurate, even for small sample sizes. "HE2" is a second method due to Howe, which performs similarly to the Weissberg-Beatty method, but is computationally simpler. "WBE" is the Weissberg-Beatty method (also called the Wald-Wolfowitz method), which performs similarly to the first Howe method for larger sample sizes. "ELL" is the Ellison correction to the Weissberg-Beatty method when f is appreciably larger than n^2. A warning message is displayed if f is not larger than n^2. "KM" is the Krishnamoorthy-Mathew approximation to the exact solution, which works well for larger sample sizes. "EXACT" computes the k-factor exactly by finding the integral solution to the problem via the integrate function. Note the computation time of this method is largely determined by m. "OCT" is the Owen approach to compute the k-factor when controlling the tails so that there is not more than (1-P)/2 of the data in each tail of the distribution.

m
The maximum number of subintervals to be used in the integrate function. This is necessary only for method = "EXACT" and method = "OCT". The larger the number, the more accurate the solution. Too low of a value can result in an error. A large value can also cause the function to be slow for method = "EXACT".

Value

K.factor returns the k-factor for tolerance intervals based on normality with the arguments specified above.

Note

For larger sample sizes, there may be some accuracy issues with the 1-sided calculation since it depends on the noncentral t-distribution. The code is primarily intended to be used for moderate values of the noncentrality parameter. It will not be highly accurate, especially in the tails, for large values. See TDist for further details.

References


See Also

`integrate`, `K.table`, `normtol.int`, `TDist`

Examples

```r
## Showing the effect of the Howe, Weissberg-Beatty, 
## and exact estimation methods as the sample size increases.

K.factor(10, P = 0.95, side = 2, method = "HE")
K.factor(10, P = 0.95, side = 2, method = "WBE")
K.factor(10, P = 0.95, side = 2, method = "EXACT", m = 50)

K.factor(100, P = 0.95, side = 2, method = "HE")
K.factor(100, P = 0.95, side = 2, method = "WBE")
K.factor(100, P = 0.95, side = 2, method = "EXACT", m = 50)
```

---

**K.factor.sim**

*Estimating K-factors for Simultaneous Tolerance Intervals Based on Normality*

**Description**

Estimates k-factors for simultaneous tolerance intervals based on normality.

**Usage**

```r
K.factor.sim(n, l = NULL, alpha = 0.05, P = 0.99, side = 1,
             method = c("EXACT", "BONF"), m = 50)
```
Arguments

- **n**: If method = "EXACT", this is the sample size of each of the l groups. If method = "BONF", then n can be a vector of different sample sizes for the l groups.

- **l**: The number of normal populations for which the k-factors will be constructed simultaneously. If NULL, then it is taken to be the length of n.

- **alpha**: The level chosen such that 1-alpha is the confidence level.

- **P**: The proportion of the population to be covered by the tolerance interval.

- **side**: Whether a k-factor for a 1-sided or 2-sided tolerance interval is required (determined by side = 1 or side = 2, respectively).

- **method**: The method for calculating the k-factors. "EXACT" is an exact method that can be used when all l groups have the same sample size. "BONF" is an approximate method using the Bonferroni inequality, which can be used when the l groups have different sample sizes.

- **m**: The maximum number of subintervals to be used in the integrate function. This is necessary only for method = "EXACT". The larger the number, the more accurate the solution. Too low of a value can result in an error. A large value can also cause the function to be slow for method = "EXACT".

Value

K.factor returns the k-factor for simultaneous tolerance intervals based on normality with the arguments specified above.

Note

For larger combinations of n and l when side = 2 and method = "EXACT", the calculation can be slow. For larger sample sizes when side = "BONF", there may be some accuracy issues with the 1-sided calculation since it depends on the noncentral t-distribution. The code is primarily intended to be used for moderate values of the noncentrality parameter. It will not be highly accurate, especially in the tails, for large values. See TDist for further details.

Thanks to Andrew Landgraf for providing the basic code for the method = "EXACT" procedure.

References


See Also

integrate, K.factor
Examples

```r
## Reproducing part of Table B5 from Krishnamoorthy and Mathew (2009).

n_sizes <- c(2:20, seq(30, 100, 10))
l_sizes <- 2:10
KM_table <- sapply(1:length(l_sizes), function(i)
  sapply(1:length(n_sizes), function(j)
    round(K.factor.sim(n = n_sizes[j], l = l_sizes[i], side=1, alpha = 0.1,
    P = 0.9),3)))
dimnames(KM_table) <- list(n = n_sizes, l = l_sizes)
KM_table
```

K.table

### Tables of K-factors for Tolerance Intervals Based on Normality

#### Description
Tabulated summary of k-factors for tolerance intervals based on normality. The user can specify multiple values for each of the three inputs.

#### Usage

```r
K.table(n, alpha, P, side = 1, f = NULL, method = c("HE", "HE2", "WBE", "ELL", "KM", "EXACT", "OCT"), m = 50,
by.arg = c("n", "alpha", "P"))
```

#### Arguments

- **n**  
  A vector of (effective) sample sizes.

- **alpha**  
  The level chosen such that 1-\alpha is the confidence level. Can be a vector.

- **P**  
  The proportion of the population to be covered by this tolerance interval. Can be a vector.

- **side**  
  Whether a 1-sided or 2-sided tolerance interval is required (determined by side = 1 or side = 2, respectively).

- **f**  
  The number of degrees of freedom associated with calculating the estimate of the population standard deviation. If NULL, then f is taken to be n-1. Only a single value can be specified for f.

- **method**  
  The method for calculating the k-factors. The k-factor for the 1-sided tolerance intervals is performed exactly and thus is the same for the chosen method. "HE" is the Howe method and is often viewed as being extremely accurate, even for small sample sizes. "HE2" is a second method due to Howe, which performs similarly to the Weissberg-Beatty method, but is computationally simpler. "WBE" is the Weissbeig-Beatty method (also called the Wald-Wolfowitz
method), which performs similarly to the first Howe method for larger sample sizes. "ELL" is the Ellison correction to the Weissberg-Beatty method when \( f \) is appreciably larger than \( n^2 \). A warning message is displayed if \( f \) is not larger than \( n^2 \). "KM" is the Krishnamoorthy-Mathew approximation to the exact solution, which works well for larger sample sizes. "EXACT" computes the k-factor exactly by finding the integral solution to the problem via the integrate function. Note the computation time of this method is largely determined by \( m \). "OCT" is the Owen approach to compute the k-factor when controlling the tails so that there is not more than \((1-P)/2 \) of the data in each tail of the distribution.

\( m \) The maximum number of subintervals to be used in the integrate function. This is necessary only for \( \text{method} = "EXACT" \) and \( \text{method} = "OCT" \). The larger the number, the more accurate the solution. Too low of a value can result in an error. A large value can also cause the function to be slow for \( \text{method} = "EXACT" \).

\( \text{by.arg} \) How you would like the output organized. If \( \text{by.arg} = "n" \), then the output provides a list of matrices sorted by the values specified in \( n \). The matrices have rows corresponding to the values specified by \( 1-\alpha \) and columns corresponding to the values specified by \( P \). If \( \text{by.arg} = "\alpha" \), then the output provides a list of matrices sorted by the values specified in \( 1-\alpha \). The matrices have rows corresponding to the values specified by \( n \) and columns corresponding to the values specified by \( P \). If \( \text{by.arg} = "P" \), then the output provides a list of matrices sorted by the values specified in \( P \). The matrices have rows corresponding to the values specified by \( 1-\alpha \) and columns corresponding to the values specified by \( n \).

Details

The method used for estimating the k-factors is that due to Howe as it is generally viewed as more accurate than the Weissberg-Beatty method.

Value

\( K.\text{table} \) returns a list with a structure determined by the argument \( \text{by.arg} \) described above.

References


See Also

\( K.\text{factor} \)

Examples

```r
## Tables generated for each value of the sample size.
```
K.table(n = seq(50, 100, 10), alpha = c(0.01, 0.05, 0.10),
   P = c(0.90, 0.95, 0.99), by.arg = "n")

## Tables generated for each value of the confidence level.

K.table(n = seq(50, 100, 10), alpha = c(0.01, 0.05, 0.10),
   P = c(0.90, 0.95, 0.99), by.arg = "alpha")

## Tables generated for each value of the coverage proportion.

K.table(n = seq(50, 100, 10), alpha = c(0.01, 0.05, 0.10),
   P = c(0.90, 0.95, 0.99), by.arg = "P")

---

**laptol.int**

*Laplace Tolerance Intervals*

**Description**

Provides 1-sided or 2-sided tolerance intervals for data distributed according to a Laplace distribution.

**Usage**

laptol.int(x, alpha = 0.05, P = 0.99, side = 1)

**Arguments**

- **x** A vector of data which is distributed according to a Laplace distribution.
- **alpha** The level chosen such that 1-alpha is the confidence level.
- **P** The proportion of the population to be covered by this tolerance interval.
- **side** Whether a 1-sided or 2-sided tolerance interval is required (determined by side = 1 or side = 2, respectively).

**Value**

laptol.int returns a data frame with items:

- **alpha** The specified significance level.
- **P** The proportion of the population covered by this tolerance interval.
- **1-sided.lower** The 1-sided lower tolerance bound. This is given only if side = 1.
- **1-sided.upper** The 1-sided upper tolerance bound. This is given only if side = 1.
- **2-sided.lower** The 2-sided lower tolerance bound. This is given only if side = 2.
- **2-sided.upper** The 2-sided upper tolerance bound. This is given only if side = 2.
logistol.int

References


Examples

```r
## First generate data from a Laplace distribution with location
## parameter 70 and scale parameter 3.
set.seed(100)
tmp <- runif(40)
x <- rep(70, 40) - sign(tmp - 0.5)*rep(3, 40)*
    log(2*ifelse(tmp < 0.5, tmp, 1-tmp))

## 95%/90% 1-sided Laplace tolerance intervals for the sample
## of size 40 generated above.
out <- laptol.int(x = x, alpha = 0.05, P = 0.90, side = 1)
out
plottol(out, x, plot.type = "hist", side = "two",
    x.lab = "Laplace Data")
```

logistol.int

**Logistic (or Log-Logistic) Tolerance Intervals**

**Description**

Provides 1-sided or 2-sided tolerance intervals for data distributed according to a logistic or log-logistic distribution.

**Usage**

```r
logistol.int(x, alpha = 0.05, P = 0.99, log.log = FALSE, side = 1)
```

**Arguments**

- `x`: A vector of data which is distributed according to a logistic or log-logistic distribution.
- `alpha`: The level chosen such that 1-alpha is the confidence level.
- `P`: The proportion of the population to be covered by this tolerance interval.
- `log.log`: If TRUE, then the data is considered to be from a log-logistic distribution, in which case the output gives tolerance intervals for the log-logistic distribution. The default is FALSE.
- `side`: Whether a 1-sided or 2-sided tolerance interval is required (determined by side = 1 or side = 2, respectively).
Details

Recall that if the random variable $X$ is distributed according to a log-logistic distribution, then the random variable $Y = \ln(X)$ is distributed according to a logistic distribution.

Value

`logistol.int` returns a data frame with items:

- `alpha`: The specified significance level.
- `P`: The proportion of the population covered by this tolerance interval.
- `1-sided.lower`: The 1-sided lower tolerance bound. This is given only if `side = 1`.
- `1-sided.upper`: The 1-sided upper tolerance bound. This is given only if `side = 1`.
- `2-sided.lower`: The 2-sided lower tolerance bound. This is given only if `side = 2`.
- `2-sided.upper`: The 2-sided upper tolerance bound. This is given only if `side = 2`.

References


See Also

`Logistic`

Examples

```r
## 90%/95% 1-sided logistic tolerance intervals for a sample
## of size 20.

set.seed(100)
x <- rlogis(20, 5, 1)
out <- logistol.int(x = x, alpha = 0.10, P = 0.95,
                   log.log = FALSE, side = 1)
out

plottol(out, x, plot.type = "control", side = "two",
x.lab = "Logistic Data")
```
mvregtol.region  

Multivariate (Multiple) Linear Regression Tolerance Regions

Description

Determines the appropriate tolerance factor for computing multivariate (multiple) linear regression tolerance regions based on Monte Carlo simulation.

Usage

mvregtol.region(mvreg, new.x = NULL, alpha = 0.05, P = 0.99, 
               B = 1000)

Arguments

- **mvreg**: A multivariate (multiple) linear regression fit, having class `mlm`.
- **new.x**: An optional data frame of new values for which to approximate k-factors. This must be a data frame with named columns that match those in the data frame used for the `mvreg` fitted object.
- **alpha**: The level chosen such that $1 - \alpha$ is the confidence level.
- **P**: The proportion of the population to be covered by this tolerance region.
- **B**: The number of iterations used for the Monte Carlo algorithm which determines the tolerance factor. The number of iterations should be at least as large as the default value of 1000.

Details

A basic sketch of how the algorithm works is as follows:

1. Generate independent chi-square random variables and Wishart random matrices.
2. Compute the eigenvalues of the randomly generated Wishart matrices.
3. Iterate the above steps to generate a set of $B$ sample values such that the $100(1-\alpha)$-th percentile is an approximate tolerance factor.

Value

`mvregtol.region` returns a matrix where the first column is the k-factor, the next q columns are the estimated responses from the least squares fit, and the final m columns are the predictor values. The first n rows of the matrix pertain to the raw data as specified by y and x. If values for `new.x` are specified, then there is one additional row appended to this output for each row in the matrix `new.x`.

Note

As of tolerance version 2.0.0, the arguments to this function have changed. This function no longer depends on inputted y and x matrices or an `int` argument. Instead, the function requires `mvreg`, which is of class "mlm", and provides all of the necessary components for the way the output is formatted. Also, `new.x` must now be a data frame with columns matching those from the data frame used in the `mvreg` fitted object.
References


Examples

```r
## 95%/95% multivariate regression tolerance factors using
grain <- c(40, 17, 9, 15, 6, 12, 5, 9)
straw <- c(53, 19, 10, 29, 13, 27, 19, 30)
fert <- c(24, 11, 5, 12, 7, 14, 11, 18)
DF <- data.frame(grain, straw, fert)
new.x <- data.frame(fert = c(10, 15, 20))
mvreg <- lm(cbind(grain, straw) ~ fert + I(fert^2), data = DF)
set.seed(100)
out <- mvregtol.region(mvreg, new.x = new.x, alpha = 0.05,
P = 0.95, B = 5000)
out
```

mvtol.region

Multivariate Normal Tolerance Regions

Description

Determines the appropriate tolerance factor for computing multivariate normal tolerance regions based on Monte Carlo methods or other approximations.

Usage

```r
mvtol.region(x, alpha = 0.05, P = 0.99, B = 1000, M = 1000,
method = c("KM", "AM", "GM", "HM", "MHM", "V11",
"HM.V11", "MC"))
```

Arguments

- **x**: An n x p matrix of data assumed to be drawn from a p-dimensional multivariate normal distribution. n pertains to the sample size.
- **alpha**: The level chosen such that 1 - alpha is the confidence level. A vector of alpha values may be specified.
- **P**: The proportion of the population to be covered by this tolerance region. A vector of P values may be specified.
The number of iterations used for the Monte Carlo algorithms (i.e., when `method` = "KM" or "MC"), which determines the tolerance factor. The number of iterations should be at least as large as the default value of 1000.

The number of iterations used for the inner loop of the Monte Carlo algorithm specified through `method = "MC"`. The number of iterations should be at least as large as the default value of 1000. Note that this is not required for `method = "KM"` since that algorithm handles the eigenvalues differently in the estimation of the tolerance factor.

The method for estimating the tolerance factors. "KM" is the Krishnamoorthy-Mondal method, which is the method implemented in previous versions of the tolerance package. It is one of the more accurate methods available. "AM" is an approximation method based on the arithmetic mean. "GM" is an approximation method based on the geometric mean. "HM" is an approximation method based on the harmonic mean. "HM.M" is a modified approach based on the harmonic mean. "V11" is a method that utilizes a certain partitioning of a Wishart random matrix for deriving an approximate tolerance factor. "HM.V11" is a hybrid method of the "HM" and "V11" methods. "MC" is a simple Monte Carlo approach to estimating the tolerance factor, which is computationally expensive as the values of B and M increase.

All of the methods are outlined in the references that we provided. In practice, we recommend using the Krishnamoorthy-Mondal approach. A basic sketch of how the Krishnamoorthy-Mondal algorithm works is as follows:

1. Generate independent chi-square random variables and Wishart random matrices.
2. Compute the eigenvalues of the randomly generated Wishart matrices.
3. Iterate the above steps to generate a set of B sample values such that the 100(1-alpha)-th percentile is an approximate tolerance factor.

mvto1.region returns a matrix where the rows pertain to each confidence level 1-alpha specified and the columns pertain to each proportion level P specified.

References


Examples

```R
## 90%/90% bivariate normal tolerance region.
set.seed(100)
```
negbintol.int

Description

Provides 1-sided or 2-sided tolerance intervals for negative binomial random variables. From a statistical quality control perspective, these limits use the number of failures that occur to reach \( n \) successes to bound the number of failures for a specified amount of future successes (\( m \)).

Usage

```r
negbintol.int(x, n, m = NULL, alpha = 0.05, P = 0.99, 
side = 1, method = c("LS", "WU", "CB", 
"CS", "SC", "LR", "SP", "CC"))
```

Arguments

- **x**
  - The total number of failures that occur from a sample of size \( n \). Can be a vector of length \( n \), in which case the sum of \( x \) is computed.

- **n**
  - The target number of successes (sometimes called size) for each trial.

- **m**
  - The target number of successes in a future lot for which the tolerance limits will be calculated. If \( m = NULL \), then the tolerance limits will be constructed assuming \( n \) for the target number of future successes.

- **alpha**
  - The level chosen such that 1-\( \alpha \) is the confidence level.
The proportion of the defective (or acceptable) units in future samples of size \( m \) to be covered by this tolerance interval.

Whether a 1-sided or 2-sided tolerance interval is required (determined by \( \text{side} = 1 \) or \( \text{side} = 2 \), respectively).

The method for calculating the lower and upper confidence bounds, which are used in the calculation of the tolerance bounds. The default method is "LS", which is the large-sample method based on the MLE. "WU" is a Wald-type interval based on the UMVUE of the negative binomial proportion. "CB" is the Casella-Berger exact method. "CS" is a method based on chi-square percentiles. "SC" is the score method. "LR" is a likelihood ratio-based method. "SP" is a method using a saddlepoint approximation for the confidence intervals. "CC" gives a continuity-corrected version of the large-sample method and is appropriate when \( n \) is large. More information on these methods can be found in the "References".

This function takes the approach for Poisson and binomial random variables developed in Hahn and Chandra (1981) and applies it to the negative binomial case.

negbintol.int returns a data frame with items:

- \( \alpha \) The specified significance level.
- \( P \) The proportion of defective (or acceptable) units in future samples of size \( m \).
- \( \hat{p} \) The probability of success in each trial, calculated by \( n/(n+x) \).
- 1-sided.lower The 1-sided lower tolerance bound. This is given only if \( \text{side} = 1 \).
- 1-sided.upper The 1-sided upper tolerance bound. This is given only if \( \text{side} = 1 \).
- 2-sided.lower The 2-sided lower tolerance bound. This is given only if \( \text{side} = 2 \).
- 2-sided.upper The 2-sided upper tolerance bound. This is given only if \( \text{side} = 2 \).

Recall that the geometric distribution is the negative binomial distribution where the size is 1. Therefore, the case when \( n = m = 1 \) will provide tolerance limits for a geometric distribution.

See Also

NegBinomial, umatol.int

Examples

```r
## Comparison of 95%/99% 1-sided tolerance limits with
## 50 failures before 10 successes are reached.

negbintol.int(x = 50, n = 10, side = 1, method = "LS")
negbintol.int(x = 50, n = 10, side = 1, method = "WU")
negbintol.int(x = 50, n = 10, side = 1, method = "CB")
negbintol.int(x = 50, n = 10, side = 1, method = "CS")
negbintol.int(x = 50, n = 10, side = 1, method = "SC")
negbintol.int(x = 50, n = 10, side = 1, method = "LR")
negbintol.int(x = 50, n = 10, side = 1, method = "SP")
negbintol.int(x = 50, n = 10, side = 1, method = "CC")

## 95%/99% 1-sided tolerance limits and 2-sided tolerance
## interval for the same setting above, but when we are
## interested in a future experiment that requires 20 successes
## be reached for each trial.

negbintol.int(x = 50, n = 10, m = 20, side = 1)
negbintol.int(x = 50, n = 10, m = 20, side = 2)
```

NegHypergeometric

The Negative Hypergeometric Distribution

Description

Density, distribution function, quantile function, and random generation for the negative hypergeometric distribution.

Usage

```r
dnhyper(x, m, n, k, log = FALSE)
pnhyper(q, m, n, k, lower.tail = TRUE, log.p = FALSE)
qnhyper(p, m, n, k, lower.tail = TRUE, log.p = FALSE)
rnhyper(nn, m, n, k)
```

Arguments

- `x, q` Vector of quantiles representing the number of trials until `k` successes have occurred (e.g., until `k` white balls have been drawn from an urn without replacement).
- `m` The number of successes in the population (e.g., the number of white balls in the urn).
The population size (e.g., the total number of balls in the urn).

The number of successes (e.g., white balls) to achieve with the sample.

Vector of probabilities, which must be between 0 and 1.

The number of observations. If length>1, then the length is taken to be the number required.

Logical vectors. If TRUE, then probabilities are given as log(p).

Logical vector. If TRUE, then probabilities are $P[X \leq x]$, else $P[X > x]$.

A negative hypergeometric distribution (sometimes called the inverse hypergeometric distribution) models the total number of trials until $k$ successes occur. Compare this to the negative binomial distribution, which models the number of failures that occur until a specified number of successes has been reached. The negative hypergeometric distribution has density

$$
p(x) = \frac{(x-1)^{k-1}}{m-k \choose x-m} \frac{n-x}{n-m}
$$

for $x = k, k+1, \ldots, n - m + k$.

Value

dnhyper gives the density, pnhyper gives the distribution function, qnhyper gives the quantile function, and rnhyper generates random deviates.

Invalid arguments will return value NaN, with a warning.

References


See Also

runif and .Random.seed about random number generation.

Examples

```r
## Randomly generated data from the negative hypergeometric distribution.

set.seed(100)
x <- rnhyper(nn = 1000, m = 15, n = 40, k = 10)
hist(x, main = "Randomly Generated Data", prob = TRUE)
x.1 = sort(x)
y <- dnhyper(x = x.1, m = 15, n = 40, k = 10)
lines(x.1, y, col = 2, lwd = 2)
plot(x.1, pnhyper(q = x.1, m = 15, n = 40, k = 10),
     type = "l", xlab = "x", ylab = "Cumulative Probabilities")
```
neghypertol.int

Description

Provides 1-sided or 2-sided tolerance intervals for negative hypergeometric random variables. When sampling without replacement, these limits are on the total number of expected draws in a future sample in order to achieve a certain number from group A (e.g., "black balls" in an urn).

Usage

neghypertol.int(x, n, N, m = NULL, alpha = 0.05, P = 0.99, side = 1, method = c("EX", "LS", "CC"))

Arguments

- **x**: The number of units drawn in order to achieve \( n \) successes. Can be a vector, in which case the sum of \( x \) is used.
- **n**: The target number of successes in the sample drawn (e.g., the number of "black balls" you are to draw in the sample).
- **N**: The population size (e.g., the total number of balls in the urn).
- **m**: The target number of successes to be sampled from the universe for a future study. If \( m = \) NULL, then the tolerance limits will be constructed assuming \( n \) for this quantity.
- **alpha**: The level chosen such that \( 1 - \alpha \) is the confidence level.
- **P**: The proportion of units from group A in future samples of size \( m \) to be covered by this tolerance interval.
- **side**: Whether a 1-sided or 2-sided tolerance interval is required (determined by \( \text{side} = 1 \) or \( \text{side} = 2 \), respectively).
- **method**: The method for calculating the lower and upper confidence bounds, which are used in the calculation of the tolerance bounds. The default method is "EX", which is an exact-based method. "LS" is the large-sample method. "CC" gives a continuity-corrected version of the large-sample method.

Value

neghypertol.int returns a data frame with items:

- **alpha**: The specified significance level.
- **P**: The proportion of units from group A in future samples of size \( m \).
- **rate**: The sampling rate determined by \( x/N \).
p.hat The proportion of units in the sample from group A, calculated by \( n/x \).

1-sided.lower The 1-sided lower tolerance bound. This is given only if \( side = 1 \).

1-sided.upper The 1-sided upper tolerance bound. This is given only if \( side = 1 \).

2-sided.lower The 2-sided lower tolerance bound. This is given only if \( side = 2 \).

2-sided.upper The 2-sided upper tolerance bound. This is given only if \( side = 2 \).

Note

As this methodology is built using large-sample theory, if the sampling rate is less than 0.05, then a warning is generated stating that the results are not reliable.

References


See Also

`acc.samp`, `NegHypergeometric`

Examples

```r
## 90%/95% 2-sided negative hypergeometric tolerance
## intervals for a future number of 20 successes when
## the universe is of size 100. The estimates are
## based on having drawn 50 in another sample to achieve
## 20 successes.

neghypertol.int(50, 20, 100, m = 20, alpha = 0.05,
               P = 0.95, side = 2, method = "LS")
```

nlregtol.int

**Nonlinear Regression Tolerance Bounds**

**Description**

Provides 1-sided or 2-sided nonlinear regression tolerance bounds.

**Usage**

```
nlregtol.int(formula, xy.data = data.frame(), x.new = NULL,
             side = 1, alpha = 0.05, P = 0.99, maxiter = 50,
             ...)
```
Arguments

- **formula**: A nonlinear model formula including variables and parameters.
- **xy.data**: A data frame in which to evaluate the formulas in `formula`. The first column of `xy.data` must be the response variable.
- **x.new**: Any new levels of the predictor(s) for which to report the tolerance bounds. The number of columns must be 1 less than the number of columns for `xy.data`.
- **side**: Whether a 1-sided or 2-sided tolerance bound is required (determined by `side = 1` or `side = 2`, respectively).
- **alpha**: The level chosen such that `1-alpha` is the confidence level.
- **P**: The proportion of the population to be covered by the tolerance bound(s).
- **maxiter**: A positive integer specifying the maximum number of iterations that the nonlinear least squares routine (`nls`) should run.
- **...**: Optional arguments passed to `nls` when estimating the nonlinear regression equation.

Details

It is highly recommended that the user specify starting values for the `nls` routine.

Value

`nlregtol.int` returns a data frame with items:

- **alpha**: The specified significance level.
- **P**: The proportion of the population covered by the tolerance bound(s).
- **y.hat**: The predicted value of the response for the fitted nonlinear regression model.
- **y**: The value of the response given in the first column of `xy.data`. This data frame is sorted by this value.
- **1-sided.lower**: The 1-sided lower tolerance bound. This is given only if `side = 1`.
- **1-sided.upper**: The 1-sided upper tolerance bound. This is given only if `side = 1`.
- **2-sided.lower**: The 2-sided lower tolerance bound. This is given only if `side = 2`.
- **2-sided.upper**: The 2-sided upper tolerance bound. This is given only if `side = 2`.

References


See Also

- `nls`
Examples

```r
## 95%/95% 2-sided nonlinear regression tolerance bounds
## for a sample of size 50.

set.seed(100)
x <- runif(50, 5, 45)
f1 <- function(x, b1, b2) b1 + (0.49 - b1)*exp(-b2*(x - 8)) +
    rnorm(50, sd = 0.01)
y <- f1(x, 0.39, 0.11)
formula <- as.formula(y ~ b1 + (0.49 - b1)*exp(-b2*(x - 8)))
out <- nlregtol.int(formula = formula,
    xy.data = data.frame(cbind(y, x)),
    x.new=cbind(c(10, 20)), side = 2,
    alpha = 0.05, P = 0.95)
out
plottol(out, x = x, y = y, side = "two", x.lab = "X",
y.lab = "Y")
```

### norm.OC

**Operating Characteristic (OC) Curves for K-Factors for Tolerance Intervals Based on Normality**

**Description**

Provides OC-type curves to illustrate how values of the k-factors for normal tolerance intervals, confidence levels, and content levels change as a function of the sample size.

**Usage**

```r
norm.OC(k = NULL, alpha = NULL, P = NULL, n, side = 1,
    method = c("HE", "HE2", "WBE", "ELL", "KM", "EXACT",
    "OCT"), m = 50)
```

**Arguments**

- **k**
  
  If wanting OC curves where the confidence level or content level is on the y-axis, then a single positive value of k must be specified. This would be the target k-factor for the desired tolerance interval. If k = NULL, then OC curves will be constructed where the k-factor value is found for given levels of alpha, P, and n.

- **alpha**
  
  The set of levels chosen such that 1-alpha are confidence levels. If wanting OC curves where the content level is being calculated, then each curve will correspond to a level in the set of alpha. If a set of P values is specified, then OC curves will be constructed where the k-factor is found and each curve will correspond to each combination of alpha and P. If alpha = NULL, then OC curves will be constructed to find the confidence level for given levels of k, P, and n.
The set of content levels to be considered. If wanting OC curves where the confidence level is being calculated, then each curve will correspond to a level in the set of \( P \). If a set of \( \alpha \) values is specified, then OC curves will be constructed where the k-factor is found and each curve will correspond to each combination of \( \alpha \) and \( P \). If \( P = \) NULL, then OC curves will be constructed to find the content level for given levels of \( k \), \( \alpha \), and \( n \).

A sequence of sample sizes to consider. This must be a vector of at least length 2 since all OC curves are constructed as functions of \( n \).

Whether a 1-sided or 2-sided tolerance interval is required (determined by \( \text{side} = 1 \) or \( \text{side} = 2 \), respectively).

The method for calculating the k-factors. The k-factor for the 1-sided tolerance intervals is performed exactly and thus is the same for the chosen method. "HE" is the Howe method and is often viewed as being extremely accurate, even for small sample sizes. "HE2" is a second method due to Howe, which performs similarly to the Weissberg-Beatty method, but is computationally simpler. "WBE" is the Weissberg-Beatty method (also called the Wald-Wolfowitz method), which performs similarly to the first Howe method for larger sample sizes. "ELL" is the Ellison correction to the Weissberg-Beatty method when \( f \) is appreciably larger than \( n^2 \). A warning message is displayed if \( f \) is not larger than \( n^2 \). "KM" is the Krishnamoorthy-Mathew approximation to the exact solution, which works well for larger sample sizes. "EXACT" computes the k-factor exactly by finding the integral solution to the problem via the integrate function. Note the computation time of this method is largely determined by \( m \). "OCT" is the Owen approach to compute the k-factor when controlling the tails so that there is not more than \((1-P)/2\) of the data in each tail of the distribution.

The maximum number of subintervals to be used in the integrate function, which is used for the underlying exact method for calculating the normal tolerance intervals.

Value

\( \text{norm.OC} \) returns a figure with the OC curves constructed using the specifications in the arguments.

References


See Also

\texttt{K.factor}, \texttt{normtol.int}

Examples

```r
## The three types of OC-curves that can be constructed
## with the \texttt{norm.OC} function.

norm.OC(k = 4, alpha = NULL, P = c(0.90, 0.95, 0.99),
```
norm.ss

\[
n = 10:20, \text{ side } = 1
\]

\[
norm.OC(k = 4, \alpha = c(0.01, 0.05, 0.10), P = \text{NULL},
n = 10:20, \text{ side } = 1)
\]

\[
norm.OC(k = \text{NULL}, P = c(0.90, 0.95, 0.99),
\alpha = c(0.01, 0.05, 0.10), n = 10:20, \text{ side } = 1)
\]

---

**Sample Size Determination for Normal Tolerance Intervals**

**Description**

Provides minimum sample sizes for a future sample size when constructing normal tolerance intervals. Various strategies are available for determining the sample size, including strategies that incorporate known specification limits.

**Usage**

\[
norm.ss(x = \text{NULL}, \alpha = 0.05, P = 0.99, \delta = \text{NULL},
P.prime = \text{NULL}, \text{ side } = 1, m = 50, \text{ spec } = c(\text{NA, NA}),
\text{ hyper.par } = \text{list}(\mu.0 = \text{NULL}, \sigma^2.0 = \text{NULL},
m.0 = \text{NULL}, n.0 = \text{NULL}), \text{ method } = c(\text{"DIR", "FW", "YGZO"}))
\]

**Arguments**

- **x**
  A vector of current data that is distributed according to a normal distribution. This is only required for method = "YGZO".

- **alpha**
  The level chosen such that 1-alpha is the confidence level.

- **P**
  The proportion of the population to be covered by this tolerance interval.

- **delta**
  The precision measure for the future tolerance interval as specified under the Faulkenberry-Weeks method.

- **P.prime**
  The proportion of the population (greater than P) such that the tolerance interval of interest will only exceed P.prime by the probability given by delta.

- **side**
  Whether a 1-sided or 2-sided tolerance interval is required (determined by side = 1 or side = 2, respectively).

- **m**
  The maximum number of subintervals to be used in the integrate function, which is used for the underlying exact method for calculating the normal tolerance intervals.

- **spec**
  A vector of length 2 given known specification limits. These are required when method = "DIR" or method = "YGZO". By default, the values are NA. The two elements of the vector are for the lower and upper specification limits, respectively. If side = 1, then only one of the specification limits must be specified. If side = 2, then both specification limits must be specified.
Necessary parameter values for the different methods. If method = "DIR" or method = "YGZO", then mu.0 and sig2.0 must be specified, which correspond to the assumed population mean and variance of the underlying normal distribution, which further pertains to the historical data for method = "YGZO". If method = "YGZO" and the sample size is to be determined using Bayesian normal tolerance intervals, then this is a required list consisting of the hyperparameters for the conjugate prior – the hyperparameters for the mean (mu.0 and n.0) and the hyperparameters for the variance (sig2.0 and m.0).

The method for performing the sample size determination. "DIR" is the direct method (intended as a simple calculation for planning purposes) where the mean and standard deviation are taken as truth and the sample size is determined with respect to the given specification limits. "FW" is for the traditional Faulkenberry-Weeks approach for sample size determination. "YGZO" is for the Young-Gordon-Zhu-Olin approach, which incorporates historical data and specification limits for determining the value of delta and/or P.prime in the Faulkenberry-Weeks approach. Note that for "YGZO", at least one of delta and P.prime must be NULL.

Value

norm.ss returns a data frame with items:

- alpha: The specified significance level.
- P: The proportion of the population covered by this tolerance interval.
- delta: The user-specified or calculated precision measure. Not returned if method = "DIR".
- P.prime: The user-specified or calculated closeness measure. Not returned if method = "DIR".
- n: The minimum sample size determined using the conditions specified for this function.

References


See Also

bayesnormtol.int, Normal, normtol.int

Examples

```r
## Sample size determination for 95%/95% 2-sided normal
## tolerance intervals using the direct method.
```
set.seed(100)
norm.ss(alpha = 0.05, P = 0.95, side = 2, spec = c(-3, 3),
method = "DIR", hyper.par = list(mu.0 = 0,
sig2.0 = 1))

---

**normtol.int**

*Normal (or Log-Normal) Tolerance Intervals*

**Description**

Provides 1-sided or 2-sided tolerance intervals for data distributed according to either a normal distribution or log-normal distribution.

**Usage**

```r
normtol.int(x, alpha = 0.05, P = 0.99, side = 1,
method = c("HE", "HE2", "WBE", "ELL", "KM",
"EXACT", "OCT"), m = 50, log.norm = FALSE)
```

**Arguments**

- **x**: A vector of data which is distributed according to either a normal distribution or a log-normal distribution.
- **alpha**: The level chosen such that 1-alpha is the confidence level.
- **P**: The proportion of the population to be covered by this tolerance interval.
- **side**: Whether a 1-sided or 2-sided tolerance interval is required (determined by `side = 1` or `side = 2`, respectively).
- **method**: The method for calculating the k-factors. The k-factor for the 1-sided tolerance intervals is performed exactly and thus is the same for the chosen method. "HE" is the Howe method and is often viewed as being extremely accurate, even for small sample sizes. "HE2" is a second method due to Howe, which performs similarly to the Weissberg-Beatty method, but is computationally simpler. "WBE" is the Weissberg-Beatty method (also called the Wald-Wolfowitz method), which performs similarly to the first Howe method for larger sample sizes. "ELL" is the Ellison correction to the Weissberg-Beatty method when f is appreciably larger than n^2. A warning message is displayed if f is not larger than n^2. "KM" is the Krishnamoorthy-Mathew approximation to the exact solution, which works well for larger sample sizes. "EXACT" computes the k-factor exactly by finding the integral solution to the problem via the `integrate` function. Note the computation time of this method is largely determined by m. "OCT" is the Owen approach to compute the k-factor when controlling the tails so that there is not more than (1-P)/2 of the data in each tail of the distribution.
The maximum number of subintervals to be used in the integrate function. This is necessary only for method = "EXACT" and method = "OCT". The larger the number, the more accurate the solution. Too low of a value can result in an error. A large value can also cause the function to be slow for method = "EXACT".

If TRUE, then the data is considered to be from a log-normal distribution, in which case the output gives tolerance intervals for the log-normal distribution. The default is FALSE.

Recall that if the random variable $X$ is distributed according to a log-normal distribution, then the random variable $Y = \ln(X)$ is distributed according to a normal distribution.

normtol.int returns a data frame with items:

- `alpha` The specified significance level.
- `P` The proportion of the population covered by this tolerance interval.
- `x.bar` The sample mean.
- `1-sided.lower` The 1-sided lower tolerance bound. This is given only if side = 1.
- `1-sided.upper` The 1-sided upper tolerance bound. This is given only if side = 1.
- `2-sided.lower` The 2-sided lower tolerance bound. This is given only if side = 2.
- `2-sided.upper` The 2-sided upper tolerance bound. This is given only if side = 2.

References


See Also

`Normal`, `K.factor`

Examples

```r
## 95%/95% 2-sided normal tolerance intervals for a sample
## of size 100.
set.seed(100)
x <- rnorm(100, 0, 0.2)
out <- normtol.int(x = x, alpha = 0.05, P = 0.95, side = 2,
```
np.order

```r
method = "HE", log.norm = FALSE)

out

plottol(out, x, plot.type = "both", side = "two",
x.lab = "Normal Data")
```

Sample Size Determination for Tolerance Limits Based on Order Statistics

Description

For given values of \( m, \alpha \), and \( P \), this function solves the necessary sample size such that the \( r \)-th (or \((n-s+1)\)-th) order statistic is the \([100(1-\alpha)\%, 100(P)\%]\) lower (or upper) tolerance limit (see the Details section below for further explanation). This function can also report all combinations of order statistics for 2-sided intervals.

Usage

```r
np.order(m, alpha = 0.05, P = 0.99, indices = FALSE)
```

Arguments

- **m**: See the Details section below for how \( m \) is defined.
- **alpha**: 1 minus the confidence level attained when it is desired to cover a proportion \( P \) of the population with the order statistics.
- **P**: The proportion of the population to be covered with confidence \( 1-\alpha \) with the order statistics.
- **indices**: An optional argument to report all combinations of order statistics indices for the upper and lower limits of the 2-sided intervals. Note that this can only be calculated when \( m>1 \).

Details

For the 1-sided tolerance limits, \( m=s+r \) such that the probability is at least \( 1-\alpha \) that at least the proportion \( P \) of the population is below the \((n-s+1)\)-th order statistic for the upper limit or above the \( r \)-th order statistic for the lower limit. This means for the 1-sided upper limit that \( r=1 \), while for the 1-sided lower limit it means that \( s=1 \). For the 2-sided tolerance intervals, \( m=s+r \) such that the probability is at least \( 1-\alpha \) that at least the proportion \( P \) of the population is between the \( r \)-th and \((n-s+1)\)-th order statistics. Thus, all combinations of \( r>0 \) and \( s>0 \) such that \( m=s+r \) are considered.

Value

If \( indices = FALSE \), then a single number is returned for the necessary sample size such that the \( r \)-th (or \((n-s+1)\)-th) order statistic is the \([100(1-\alpha)\%, 100(P)\%]\) lower (or upper) tolerance limit. If \( indices = TRUE \), then a list is returned with a single number for the necessary sample size and a matrix with 2 columns where each row gives the pairs of indices for the order statistics for all permissible \([100(1-\alpha)\%, 100(P)\%]\) 2-sided tolerance intervals.
References


See Also

nptol.int

Examples

```r
## Only requesting the sample size.
np.order(m = 5, alpha = 0.05, P = 0.95)

## Requesting the order statistics indices as well.
np.order(m = 5, alpha = 0.05, P = 0.95, indices = TRUE)
```

---

**npbetol.int**

*Nonparametric Beta-Expectation Tolerance Intervals*

Description

Provides 1-sided or 2-sided nonparametric (i.e., distribution-free) beta-expectation tolerance intervals for any continuous data set. These are equivalent to nonparametric prediction intervals based on order statistics.

Usage

```r
npbetol.int(x, Beta = 0.95, side = 1, upper = NULL, lower = NULL)
```

Arguments

- **x**: A vector of data which no distributional assumptions are made. The data is only assumed to come from a continuous distribution.
- **Beta**: The confidence level.
- **side**: Whether a 1-sided or 2-sided tolerance interval is required (determined by `side` = 1 or `side` = 2, respectively).
- **upper**: The upper bound of the data. When `NULL`, then the maximum of `x` is used.
- **lower**: The lower bound of the data. When `NULL`, then the minimum of `x` is used.
Value

`nptol.int` returns a data frame with items:

- **Beta**
  - The specified confidence level.
- **1-sided.lower**
  - The 1-sided lower tolerance bound. This is given only if `side = 1`.
- **1-sided.upper**
  - The 1-sided upper tolerance bound. This is given only if `side = 1`.
- **2-sided.lower**
  - The 2-sided lower tolerance bound. This is given only if `side = 2`.
- **2-sided.upper**
  - The 2-sided upper tolerance bound. This is given only if `side = 2`.

References


See Also

distfree.est, npregtol.int, nptol.int

Examples

```r
## Nonparametric 90%-expectation tolerance intervals
## for a sample of size 100.
set.seed(100)
x <- rexp(100, 5)
out <- npbetol.int(x = x, Beta = 0.90, side = 2,
                   upper = NULL, lower = NULL)
out
```

npmvtol.region

**Nonparametric Multivariate Hyperrectangular Tolerance Regions**

Description

Provides depth-based multivariate central or semi-space nonparametric tolerance regions. These can be calculated for any continuous multivariate data set. Either (P, 1-alpha) tolerance regions or beta-expectation tolerance regions can be specified.

Usage

```r
npmvtol.region(x, alpha = NULL, P = NULL, Beta = NULL, depth.fn,
                 adjust = c("no", "floor", "ceiling"),
                 type = c("central", "semi-space"),
                 semi.order = list(lower = NULL, center = NULL, upper = NULL),
                 L = -Inf, U = Inf, ...)
```
Arguments

x  An n x p matrix of data assumed to be drawn from a p-dimensional multivariate distribution. n pertains to the sample size.

alpha The level chosen such that 1 - alpha is the confidence level. Note that if a (P, 1-alpha) tolerance region is required, then both alpha and P must be specified, but Beta must be set to NULL.

P  The proportion of the population to be covered by this tolerance interval. Note that if a (P, 1-alpha) tolerance region is required, then both alpha and P must be specified, but Beta must be set to NULL.

Beta The confidence level for a beta-expectation tolerance region. Note that if a beta-expectation tolerance region is required, then Beta must be specified, but both alpha and P must be set to NULL.

depth.fn The data depth function used to perform the ordering of the multivariate data. Thus function must be coded in such a way that the first argument is multivariate data for which to calculate the depth values and the second argument is the original multivariate sample, x. For the purpose of this tolerance region calculation, these two arguments should both be the original multivariate sample.

adjust Whether an adjustment should be made during an intermediate calculation for determining the number of points that need to be included in the multivariate region. If adjust = "no", the default, then no adjustment is made during the intermediate calculation. If adjust = "floor", then the intermediate calculation is rounded down to the next nearest integer. If adjust = "ceiling", then the intermediate calculation is rounded up to the next nearest integer.

type The type of multivariate hyperrectangular region to calculate. If type = "central", then two-sided intervals are reported for each dimension of the data x. If type = "semispace", then a combination of one-sided intervals and two-sided intervals are reported for the dimensions of x. Which interval is calculated for each dimension in this latter setting is dictated by the semi.order argument.

semi.order If type = "semispace", then this argument must be specified. This argument is a list of length 3, such that each element gives the indices of the dimensions of x for which the type of interval should be calculated. Indices specified for the element of lower will return one-sided lower limits for those dimensions, indices specified for the element of center will return two-sided intervals for those dimensions, and indices specified for the element of upper will return one-sided upper limits for those dimensions.

L  If type = "semispace", these are the lower limits for any dimensions for which one requests one-sided lower limits.

U  If type = "semispace", these are the upper limits for any dimensions for which one requests one-sided lower limits.

... Additional arguments passed to the depth.fn function.

Value

npmvtol.region returns a p x 2 matrix where the columns give the lower and upper limits, respectively, of the multivariate hyperrectangular tolerance region.
References


See Also

distfree.est, mvtol.region, npregtol.int

Examples

## 90%/95% semi-space tolerance region for a sample
## of size 20 generated from a multivariate normal
## distribution. The mdepth function below is not
## a true depth function, but used only for
## illustrative purposes.

mdepth <- function(pts, x){
    mahalanobis(pts, center = rep(0, 3),
               cov = diag(1, 3))
}

set.seed(100)
x <- cbind(rnorm(100), rnorm(100), rnorm(100))
out <- npmvtol.region(x = x, alpha = 0.10, P = 0.95, depth.fn = mdepth,
                      type = "semispace", semi.order = list(lower = 2,
                      center = 3, upper = 1))
out

npregtol.int

Nonparametric Regression Tolerance Bounds

Description

Provides 1-sided or 2-sided nonparametric regression tolerance bounds.

Usage

npregtol.int(x, y, y.hat, side = 1, alpha = 0.05, P = 0.99,
            method = c("WILKS", "WALD", "HM"), upper = NULL,
            lower = NULL)

Arguments

x A vector of values for the predictor variable. Currently, this function is only capable of handling a single predictor.

y A vector of values for the response variable.

y.hat A vector of fitted values extracted from a nonparametric smoothing routine.
Whether a 1-sided or 2-sided tolerance bound is required (determined by side = 1 or side = 2, respectively).

alpha  The level chosen such that 1-\alpha is the confidence level.

P  The proportion of the population to be covered by the tolerance bound(s).

method  The method for determining which indices of the ordered residuals will be used for the tolerance bounds. "WILKS", "WALD", and "HM" are each described in nptol.int. However, since only one tolerance bound can actually be reported for this procedure, only the first tolerance bound will be returned. Note that this is not an issue when method = "WILKS" is used as it only produces one set of tolerance bounds.

upper  The upper bound of the data. When NULL, then the maximum of x is used.

lower  The lower bound of the data. When NULL, then the minimum of x is used.

Value

nptol.int returns a data frame with items:

alpha  The specified significance level.

P  The proportion of the population covered by the tolerance bound(s).

x  The values of the predictor variable.

y  The values of the response variable.

y.hat  The predicted value of the response for the fitted nonparametric smoothing routine.

1-sided.lower  The 1-sided lower tolerance bound. This is given only if side = 1.

1-sided.upper  The 1-sided upper tolerance bound. This is given only if side = 1.

2-sided.lower  The 2-sided lower tolerance bound. This is given only if side = 2.

2-sided.upper  The 2-sided upper tolerance bound. This is given only if side = 2.

References


See Also

loess, nptol.int, spline

Examples

```r
## 95%/95% 2-sided nonparametric regression tolerance bounds
## for a sample of size 50.
set.seed(100)
x <- runif(50, 5, 45)
f1 <- function(x, b1, b2) b1 + (0.49 - b1)*exp(-b2*(x - 8)) +
```
rnorm(50, sd = 0.01)
y <- f1(x, 0.39, 0.11)
y.hat <- loess(y~x)$fit
out <- npregtol.int(x = x, y = y, y.hat = y.hat, side = 2,
                   alpha = 0.05, P = 0.95, method = "WILKS")
out

plottol(out, x = x, y = y, y.hat = y.hat, side = "two",
        x.lab = "X", y.lab = "Y")

### nptol.int

**Nonparametric Tolerance Intervals**

**Description**

Provides 1-sided or 2-sided nonparametric (i.e., distribution-free) tolerance intervals for any continuous data set.

**Usage**

```r
nptol.int(x, alpha = 0.05, P = 0.99, side = 1,
          method = c("WILKS", "WALD", "HM", "YM"),
          upper = NULL, lower = NULL)
```

**Arguments**

- **x**
  A vector of data which no distributional assumptions are made. The data is only assumed to come from a continuous distribution.

- **alpha**
  The level chosen such that 1-alpha is the confidence level.

- **P**
  The proportion of the population to be covered by this tolerance interval.

- **side**
  Whether a 1-sided or 2-sided tolerance interval is required (determined by side = 1 or side = 2, respectively).

- **method**
  The method for determining which indices of the ordered observations will be used for the tolerance intervals. "WILKS" is the Wilks method, which produces tolerance bounds symmetric about the observed center of the data by using the beta distribution. "WALD" is the Wald method, which produces (possibly) multiple tolerance bounds for side = 2 (each having at least the specified confidence level), but is the same as method = "WILKS" for side = 1. "HM" is the Hahn-Meeker method, which is based on the binomial distribution, but the upper and lower bounds may exceed the minimum and maximum of the sample data. For side = 2, this method will yield two intervals if an odd number of observations are to be trimmed from each side. "YM" is the Young-Mathew method for performing interpolation or extrapolation based on the order statistics. See below for more information on this method.

- **upper**
  The upper bound of the data. When NULL, then the maximum of x is used. If method = "YM" and extrapolation is performed, then upper will be greater than the maximum.
lower

The lower bound of the data. When NULL, then the minimum of x is used. If method = "YM" and extrapolation is performed, then lower will be less than the minimum.

Details

For the Young-Mathew method, interpolation or extrapolation is performed. When side = 1, two intervals are given: one based on linear interpolation/extrapolation of order statistics (OS-Based) and one based on fractional order statistics (FOS-Based). When side = 2, only an interval based on linear interpolation/extrapolation of order statistics is given.

Value

nptol.int returns a data frame with items:

- **alpha**
  - The specified significance level.
- **P**
  - The proportion of the population covered by this tolerance interval.
- **1-sided.lower**
  - The 1-sided lower tolerance bound. This is given only if side = 1.
- **1-sided.upper**
  - The 1-sided upper tolerance bound. This is given only if side = 1.
- **2-sided.lower**
  - The 2-sided lower tolerance bound. This is given only if side = 2.
- **2-sided.upper**
  - The 2-sided upper tolerance bound. This is given only if side = 2.

References


See Also

distfree.est, npregtol.int

Examples

```r
## 90%/95% 2-sided nonparametric tolerance intervals for a
## sample of size 20.

set.seed(100)
x <- rlogis(20, 5, 1)
out <- nptol.int(x = x, alpha = 0.10, P = 0.95, side = 1,
                method = "WILKS", upper = NULL, lower = NULL)
```
Description

Provides 1-sided or 2-sided tolerance intervals for data distributed according to either a Pareto distribution or a power distribution (i.e., the inverse Pareto distribution).

Usage

```r
paretotol.int(x, alpha = 0.05, P = 0.99, side = 1,
             method = c("GPU", "DUN"), power.dist = FALSE)
```

Arguments

- `x`: A vector of data which is distributed according to either a Pareto distribution or a power distribution.
- `alpha`: The level chosen such that `1-alpha` is the confidence level.
- `P`: The proportion of the population to be covered by this tolerance interval.
- `side`: Whether a 1-sided or 2-sided tolerance interval is required (determined by `side = 1` or `side = 2`, respectively).
- `method`: The method for how the upper tolerance bound is approximated when transforming to utilize the relationship with the 2-parameter exponential distribution. "GPU" is the Guenther-Patil-Upppuluri method. "DUN" is the Dunsmore method, which was empirically shown to be an improvement for samples greater than or equal to 8. More information on these methods can be found in the "References".
- `power.dist`: If `TRUE`, then the data is considered to be from a power distribution, in which case the output gives tolerance intervals for the power distribution. The default is `FALSE`.

Details

Recall that if the random variable $X$ is distributed according to a Pareto distribution, then the random variable $Y = \ln(X)$ is distributed according to a 2-parameter exponential distribution. Moreover, if the random variable $W$ is distributed according to a power distribution, then the random variable $X = 1/W$ is distributed according to a Pareto distribution, which in turn means that the random variable $Y = \ln(1/W)$ is distributed according to a 2-parameter exponential distribution.
Value

paretotol.int returns a data frame with items:

- **alpha**: The specified significance level.
- **P**: The proportion of the population covered by this tolerance interval.
- **1-sided.lower**: The 1-sided lower tolerance bound. This is given only if `side = 1`.
- **1-sided.upper**: The 1-sided upper tolerance bound. This is given only if `side = 1`.
- **2-sided.lower**: The 2-sided lower tolerance bound. This is given only if `side = 2`.
- **2-sided.upper**: The 2-sided upper tolerance bound. This is given only if `side = 2`.

References


See Also

`TwoParExponential`, `exp2tol.int`

Examples

```r
## 95%/99% 2-sided Pareto tolerance intervals
## for a sample of size 500.
set.seed(100)
x <- exp(r2exp(500, rate = 0.15, shift = 2))
out <- paretotol.int(x = x, alpha = 0.05, P = 0.99, side = 2,
                     method = "DUN", power.dist = FALSE)
out
plottol(out, x, plot.type = "both", side = "two",
x.lab = "Pareto Data")
```
Description

Provides control charts and/or histograms for tolerance bounds on continuous data as well as tolerance ellipses for data distributed according to bivariate and trivariate normal distributions. Scatterplots with regression tolerance bounds and interval plots for ANOVA tolerance intervals may also be produced.

Usage

```r
plottol(tol.out, x, y = NULL, y.hat = NULL,
side = c("two", "upper", "lower"),
plot.type = c("control", "hist", "both"),
x.lab = NULL, y.lab = NULL, z.lab = NULL, ...)
```

Arguments

- `tol.out` Output from any continuous (including ANOVA) tolerance interval procedure or from a regression tolerance bound procedure.
- `x` Either data from a continuous distribution or the predictors for a regression model. If this is a design matrix for a linear regression model, then it must be in matrix form AND include a column of 1's if there is to be an intercept. Note that multiple predictors are only allowed if considering polynomial regression. If the output for `tol.out` concerns ANOVA tolerance intervals, then `x` must be a data frame.
- `y` The response vector for a regression setting. Leave as `NULL` if not doing regression tolerance bounds.
- `y.hat` The fitted values from a nonparametric smoothing routine if plotting nonparametric regression tolerance bounds. Otherwise, leave as `NULL`.
- `side` `side = "two"` produces plots for either the two-sided tolerance intervals or both one-sided tolerance intervals. This will be determined by the output in `tol.out`. `side = "upper"` produces plots showing the upper tolerance bounds. `side = "lower"` produces plots showing the lower tolerance bounds.
- `plot.type` `plot.type = "control"` produces a control chart of the data along with the tolerance bounds specified by `side`. `plot.type = "hist"` produces a histogram of the data along with the tolerance bounds specified by `side`. `plot.type = "both"` produces both the control chart and histogram. This argument is ignored when plotting regression data.
- `x.lab` Specify the label for the x-axis.
- `y.lab` Specify the label for the y-axis.
- `z.lab` Specify the label for the z-axis.
- `...` Additional arguments passed to the plotting function used for the control charts or regression scatterplots.
Value

`plottol` can return a control chart, histogram, or both for continuous data along with the calculated tolerance intervals. For regression data, `plottol` returns a scatterplot along with the regression tolerance bounds. For ANOVA output, `plottol` returns an interval plot for each factor.

References


Examples

```r
## 90%/90% 1-sided Weibull tolerance intervals for a sample
## of size 150.

set.seed(100)
x <- rweibull(150, 3, 75)
out <- exttol.int(x = x, alpha = 0.15, P = 0.90,
dist = "Weibull")
out
plottol(out, x, plot.type = "both", side = "lower",
x.lab = "Weibull Data")

## 90%/90% trivariate normal tolerance region.

set.seed(100)
x1 <- rnorm(100, 0, 0.2)
x2 <- rnorm(100, 0, 0.5)
x3 <- rnorm(100, 5, 1)
x <- cbind(x1, x2, x3)
mvtol.region(x = x, alpha = c(0.10, 0.05, 0.01),
P = c(0.90, 0.95, 0.99), B = 1000)
out2 <- mvtol.region(x = x, alpha = 0.10, P = 0.90, B = 1000)
plottol(out2, x)

## 95%/95% 2-sided linear regression tolerance bounds
## for a sample of size 100.

set.seed(100)
x <- runif(100, 0, 10)
y <- 20 + 5*x + rnorm(100, 0, 3)
out3 <- regtol.int(reg = lm(y ~ x), new.x = data.frame(x = c(3, 6, 9)),
side = 2, alpha = 0.05, P = 0.95)
plottol(out3, x = cbind(1, x), y = y, side = "two", x.lab = "X",
y.lab = "Y")
```
poislind.ll

Maximum Likelihood Estimation for the Discrete Poisson-Lindley Distribution

Description

Performs maximum likelihood estimation for the parameter of the Poisson-Lindley distribution.

Usage

poislind.ll(x, theta = NULL, ...)

Arguments

x A vector of raw data which is distributed according to a Poisson-Lindley distribution.
theta Optional starting value for the parameter. If NULL, then the method of moments estimator is used.
... Additional arguments passed to the mle function.

Details

The discrete Poisson-Lindley distribution is a compound distribution that, potentially, provides a better fit for count data relative to the traditional Poisson and negative binomial distributions.

Value

See the help file for mle to see how the output is structured.

References


See Also

mle, PoissonLindley

Examples

## Maximum likelihood estimation for randomly generated data
## from the Poisson-Lindley distribution.

set.seed(100)

pl.data <- rpoislind(n = 500, theta = 0.5)
out.pl <- poislind.ll(pl.data)
poislindtol.int

Poisson-Lindley Tolerance Intervals

Description

Provides 1-sided or 2-sided tolerance intervals for data distributed according to the Poisson-Lindley distribution.

Usage

poislindtol.int(x, m = NULL, alpha = 0.05, P = 0.99, side = 1, ...)

Arguments

x
A vector of raw data which is distributed according to a Poisson-Lindley distribution.

m
The number of observations in a future sample for which the tolerance limits will be calculated. By default, m = NULL and, thus, m will be set equal to the original sample size.

alpha
The level chosen such that 1-alpha is the confidence level.

P
The proportion of the population to be covered by this tolerance interval.

side
Whether a 1-sided or 2-sided tolerance interval is required (determined by side = 1 or side = 2, respectively).

... Additional arguments passed to the poislind.ll function, which is used for maximum likelihood estimation.

Details

The discrete Poisson-Lindley distribution is a compound distribution that, potentially, provides a better fit for count data relative to the traditional Poisson and negative binomial distributions. Poisson-Lindley distributions are heavily right-skewed distributions. For most practical applications, one will typically be interested in 1-sided upper bounds.

Value

poislindtol.int returns a data frame with the following items:

alpha
The specified significance level.

P
The proportion of the population covered by this tolerance interval.

theta
MLE for the shape parameter theta.

1-sided.lower
The 1-sided lower tolerance bound. This is given only if side = 1.

1-sided.upper
The 1-sided upper tolerance bound. This is given only if side = 1.

2-sided.lower
The 2-sided lower tolerance bound. This is given only if side = 2.

2-sided.upper
The 2-sided upper tolerance bound. This is given only if side = 2.
References


See Also

PoissonLindley, poislind.ll

Examples

```r
## 90%/90% 1-sided tolerance intervals for data assuming
## the Poisson-Lindley distribution.

x <- c(rep(0, 447), rep(1, 132), rep(2, 42), rep(3, 21),
      rep(4, 3), rep(5, 2))
out <- poislindtol.int(x, alpha = 0.10, P = 0.90, side = 1)
out
```

---

**PoissonLindley**  
*Discrete Poisson-Lindley Distribution*

Description

Density (mass), distribution function, quantile function, and random generation for the Poisson-Lindley distribution.

Usage

```r
dpoislind(x, theta, log = FALSE)
ppoislind(q, theta, lower.tail = TRUE, log.p = FALSE)
qpoislind(p, theta, lower.tail = TRUE, log.p = FALSE)
rpoislind(n, theta)
```

Arguments

- `x, q`  
  Vector of quantiles.
- `p`  
  Vector of probabilities.
- `n`  
  The number of observations. If `length>1`, then the length is taken to be the number required.
- `theta`  
  The shape parameter, which must be greater than 0.
- `log, log.p`  
  Logical vectors. If TRUE, then the probabilities are given as \(\log(p)\).
- `lower.tail`  
  Logical vector. If TRUE, then probabilities are \(P[X \leq x]\), else \(P[X > x]\).
Details

The Poisson-Lindley distribution has mass

\[ p(x) = \frac{\theta^2(x + \theta + 2)}{(\theta + 1)x + 3}, \]

where \( x = 0, 1, \ldots \) and \( \theta > 0 \) is the shape parameter.

Value

dpoislind gives the density (mass), ppoislind gives the distribution function, qpoislind gives the quantile function, and rpoislind generates random deviates for the specified distribution.

References


See Also

runif and .Random.seed about random number generation.

Examples

```r
## Randomly generated data from the Poisson-Lindley
## distribution.

set.seed(100)
x <- rpoislind(n = 150, theta = 0.5)
hist(x, main = "Randomly Generated Data", prob = TRUE)
x.1 <- sort(x)
y <- dpoislind(x = x.1, theta = 0.5)
lines(x.1, y, col = 2, lwd = 2)
plot(x.1, ppoislind(q = x.1, theta = 0.5), type = "l",
xlab = "x", ylab = "Cumulative Probabilities")
qpoislind(p = 0.20, theta = 0.5, lower.tail = FALSE)
qpoislind(p = 0.80, theta = 0.5)
```

---

**poistol.int**

Poisson Tolerance Intervals

Description

Provides 1-sided or 2-sided tolerance intervals for Poisson random variables. From a statistical quality control perspective, these limits bound the number of occurrences (which follow a Poisson distribution) in a specified future time period.
Usage

poistol.int(x, n, m = NULL, alpha = 0.05, P = 0.99, side = 1, method = c("TAB", "LS", "SC", "CC", "VS", "RVS", "FT", "CSC"))

Arguments

x The number of occurrences of the event in time period n. Can be a vector of length n, in which case the sum of x is used.
n The time period of the original measurements.
m The specified future length of time. If m = NULL, then the tolerance limits will be constructed assuming n for the future length of time.
alpha The level chosen such that 1-alpha is the confidence level.
P The proportion of occurrences in future time lengths of size m to be covered by this tolerance interval.
side Whether a 1-sided or 2-sided tolerance interval is required (determined by side = 1 or side = 2, respectively).
method The method for calculating the lower and upper confidence bounds, which are used in the calculation of the tolerance bounds. The default method is "TAB", which is the tabular method and is usually preferred for a smaller number of occurrences. "LS" gives the large-sample (Wald) method, which is usually preferred when the number of occurrences is x > 20. "SC" gives the score method, which again is usually used when the number of occurrences is relatively large. "CC" gives a continuity-corrected version of the large-sample method. "VS" gives a variance-stabilized version of the large-sample method. "RVS" is a recentered version of the variance-stabilization method. "FT" is the Freeman-Tukey method. "CSC" is the continuity-corrected version of the score method. More information on these methods can be found in the "References".

Value

poistol.int returns a data frame with items:

alpha The specified significance level.
P The proportion of occurrences in future time periods of length m.
\( \lambda \text{hat} \) The mean occurrence rate per unit time, calculated by \( x/n \).
1-sided.lower The 1-sided lower tolerance bound. This is given only if side = 1.
1-sided.upper The 1-sided upper tolerance bound. This is given only if side = 1.
2-sided.lower The 2-sided lower tolerance bound. This is given only if side = 2.
2-sided.upper The 2-sided upper tolerance bound. This is given only if side = 2.
References


See Also

Poisson, umatol.int

Examples

```r
## 95%/90% 1-sided Poisson tolerance limits for future occurrences in a period of length 3. All seven methods are presented for comparison.
poistol.int(x = 45, n = 9, m = 3, alpha = 0.05, P = 0.90, side = 1, method = "TAB")
poistol.int(x = 45, n = 9, m = 3, alpha = 0.05, P = 0.90, side = 1, method = "LS")
poistol.int(x = 45, n = 9, m = 3, alpha = 0.05, P = 0.90, side = 1, method = "SC")
poistol.int(x = 45, n = 9, m = 3, alpha = 0.05, P = 0.90, side = 1, method = "CC")
poistol.int(x = 45, n = 9, m = 3, alpha = 0.05, P = 0.90, side = 1, method = "VS")
poistol.int(x = 45, n = 9, m = 3, alpha = 0.05, P = 0.90, side = 1, method = "RVS")
poistol.int(x = 45, n = 9, m = 3, alpha = 0.05, P = 0.90, side = 1, method = "FT")
poistol.int(x = 45, n = 9, m = 3, alpha = 0.05, P = 0.90, side = 1, method = "CSC")

## 95%/90% 2-sided Poisson tolerance intervals for future occurrences in a period of length 15. All seven methods are presented for comparison.
poistol.int(x = 45, n = 9, m = 15, alpha = 0.05, P = 0.90, side = 2, method = "TAB")
poistol.int(x = 45, n = 9, m = 15, alpha = 0.05, P = 0.90, side = 2, method = "LS")
poistol.int(x = 45, n = 9, m = 15, alpha = 0.05, P = 0.90, side = 2, method = "SC")
poistol.int(x = 45, n = 9, m = 15, alpha = 0.05, P = 0.90, side = 2, method = "CC")
poistol.int(x = 45, n = 9, m = 15, alpha = 0.05, P = 0.90, side = 2, method = "VS")
poistol.int(x = 45, n = 9, m = 15, alpha = 0.05, P = 0.90, side = 2, method = "RVS")
poistol.int(x = 45, n = 9, m = 15, alpha = 0.05, P = 0.90, side = 2, method = "FT")
```
(Multiple) Linear Regression Tolerance Bounds

Description

Provides 1-sided or 2-sided (multiple) linear regression tolerance bounds. It is also possible to fit a regression through the origin model.

Usage

regtol.int(reg, new.x = NULL, side = 1, alpha = 0.05, P = 0.99)

Arguments

reg An object of class lm (i.e., the results from a linear regression routine).
new.x An optional data frame in which to look for variables with which to predict. If omitted, the fitted values are used.
side Whether a 1-sided or 2-sided tolerance bound is required (determined by side = 1 or side = 2, respectively).
alpha The level chosen such that 1-alpha is the confidence level.
P The proportion of the population to be covered by the tolerance bound(s).

Value

regtol.int returns a data frame with items:

alpha The specified significance level.
P The proportion of the population covered by the tolerance bound(s).
y The value of the response given on the left-hand side of the model in reg.
y.hat The predicted value of the response for the fitted linear regression model. This data frame is sorted by this value.
1-sided.lower The 1-sided lower tolerance bound. This is given only if side = 1.
1-sided.upper The 1-sided upper tolerance bound. This is given only if side = 1.
2-sided.lower The 2-sided lower tolerance bound. This is given only if side = 2.
2-sided.upper The 2-sided upper tolerance bound. This is given only if side = 2.
References


See Also

lm

Examples

```r
## 95%/95% 2-sided linear regression tolerance bounds
## for a sample of size 100.

set.seed(100)
x <- runif(100, 0, 10)
y <- 20 + 5*x + rnorm(100, 0, 3)
out <- regtol.int(reg = lm(y ~ x), new.x = data.frame(x = c(3, 6, 9)),
                 side = 2, alpha = 0.05, P = 0.95)
out
plottol(out, x = cbind(1, x), y = y, side = "two", x.lab = "X",
        y.lab = "Y")
```

---

**simnormtol.int**  
*Simultaneous Normal (or Log-Normal) Tolerance Intervals*

**Description**

Provides simultaneous 1-sided or 2-sided tolerance intervals for data distributed according to either a normal distribution or log-normal distribution.

**Usage**

```r
simnormtol.int(x, alpha = 0.05, P = 0.99, side = 1,
                method = c("EXACT", "BONF"), m = 50, log.norm = FALSE)
```

**Arguments**

- `x`  
  Either a matrix or list of vectors of the data. If a matrix, then the columns are the samples from the different normal (or log-normal) populations. If `method = "EXACT"`, then `x` must be a matrix.

- `alpha`  
  The level chosen such that `1-\alpha` is the confidence level.

- `P`  
  The proportion of the population to be covered by this tolerance interval.
Whether simultaneous 1-sided or 2-sided tolerance intervals are required (determined by `side = 1` or `side = 2`, respectively).

The method for calculating the k-factors. "EXACT" is an exact method that can be used when all 1 groups have the same sample size. "BONF" is an approximate method using the Bonferroni inequality, which can be used when the 1 groups have different sample sizes.

The maximum number of subintervals to be used in the integrate function. This is necessary only for `method = "EXACT"`. The larger the number, the more accurate the solution. Too low of a value can result in an error. A large value can also cause the function to be slow for `method = "EXACT"`.

If TRUE, then the data is considered to be from a log-normal distribution, in which case the output gives tolerance intervals for the log-normal distribution. The default is FALSE.

Recall that if the random variable \( X \) is distributed according to a log-normal distribution, then the random variable \( Y = \ln(X) \) is distributed according to a normal distribution.

`normtol.int` returns a data frame with items:

- `alpha`: The specified significance level.
- `P`: The proportion of the population covered by this tolerance interval.
- `x.bar`: The sample means.
- `1-sided.lower`: The simultaneous 1-sided lower tolerance bounds. This is given only if `side = 1`.
- `1-sided.upper`: The simultaneous 1-sided upper tolerance bounds. This is given only if `side = 1`.
- `2-sided.lower`: The simultaneous 2-sided lower tolerance bounds. This is given only if `side = 2`.
- `2-sided.upper`: The simultaneous 2-sided upper tolerance bounds. This is given only if `side = 2`.

The code for this functions is built upon code provided by Andrew Landgraf.


See Also

Normal, K.factor.sim

Examples

## 95%/95% simultaneous 2-sided normal tolerance
## intervals for three samples of unequal size.

set.seed(100)
x <- list(rnorm(20), rnorm(10, 1), rnorm(12, 1, 2))
out <- simnormtol.int(x = x, alpha = 0.05, P = 0.95,
                      side = 2, method = "BONF")
out

TwoParExponential

The 2-Parameter Exponential Distribution

Description

Density, distribution function, quantile function, and random generation for the 2-parameter exponential distribution with rate equal to rate and shift equal to shift.

Usage

d2exp(x, rate = 1, shift = 0, log = FALSE)
p2exp(q, rate = 1, shift = 0, lower.tail = TRUE, log.p = FALSE)
q2exp(p, rate = 1, shift = 0, lower.tail = TRUE, log.p = FALSE)
r2exp(n, rate = 1, shift = 0)

Arguments

x, q  Vector of quantiles.
p      Vector of probabilities.
n  The number of observations. If length > 1, then the length is taken to be the number required.
rate  Vector of rates.
shift Vector of shifts.
log, log.p  Logical vectors. If TRUE, then probabilities are given as log(p).
lower.tail Logical vector. If TRUE, then probabilities are \( P[X \leq x] \), else \( P[X > x] \).
Details
If rate or shift are not specified, then they assume the default values of 1 and 0, respectively.
The 2-parameter exponential distribution has density
\[
    f(x) = \frac{1}{\beta} e^{(x-\mu)/\beta}
\]
where \(x \geq \mu\), \(\mu\) is the shift parameter, and \(\beta > 0\) is the scale parameter.

Value
d2exp gives the density, p2exp gives the distribution function, q2exp gives the quantile function,
and r2exp generates random deviates.

See Also
runif and .Random.seed about random number generation.

Examples
```r
## Randomly generated data from the 2-parameter exponential
distribution.
set.seed(100)
x <- r2exp(n = 500, rate = 3, shift = -10)
hist(x, main = "Randomly Generated Data", prob = TRUE)
x.1 = sort(x)
y <- d2exp(x = x.1, rate = 3, shift = -10)
lines(x.1, y, col = 2, lwd = 2)
plot(x.1, p2exp(q = x.1, rate = 3, shift = -10), type = "l",
    xlab = "x", ylab = "Cumulative Probabilities")
q2exp(p = 0.20, rate = 3, shift = -10, lower.tail = FALSE)
q2exp(p = 0.80, rate = 3, shift = -10)
```

umatol.int

**Uniformly Most Accurate Upper Tolerance Limits for Certain Discrete Distributions**

Description
Provides uniformly most accurate upper tolerance limits for the binomial, negative binomial, and
Poisson distributions.

Usage
```r
umatol.int(x, n = NULL, dist = c("Bin", "NegBin", "Pois"), N,
    alpha = 0.05, P = 0.99)
```
Arguments

- **x**: A vector of data which is distributed according to one of the binomial, negative binomial, or Poisson distributions. If the length of `x` is 1, then it is assumed that this number is the sum of iid values from the assumed distribution.
- **n**: The sample size of the data. If null, then `n` is calculated as the length of `x`.
- **dist**: The distribution for the data given by `x`. The options are "Bin" for the binomial distribution, "NegBin" for the negative binomial distribution, and "Pois" for the Poisson distribution.
- **N**: Must be specified for the binomial and negative binomial distributions. If `dist` = "Bin", then `N` is the number of Bernoulli trials and must be a positive integer. If `dist` = "NegBin", then `N` is the total number of successful trials (or dispersion parameter) and must be strictly positive.
- **alpha**: The level chosen such that 1-alpha is the confidence level.
- **P**: The proportion of the population to be covered by this tolerance interval.

Value

`umatol.int` returns a data frame with items:

- **alpha**: The specified significance level.
- **P**: The proportion of the population covered by this tolerance interval.
- **p.hat**: The maximum likelihood estimate for the probability of success in each trial; reported if `dist` = "Bin".
- **nu.hat**: The maximum likelihood estimate for the probability of success in each trial; reported if `dist` = "NegBin".
- **lambda.hat**: The maximum likelihood estimate for the rate of success; reported if `dist` = "Pois".
- **1-sided.upper**: The 1-sided upper tolerance limit.

References


See Also

`Binomial, NegBinomial, Poisson`

Examples

```r
## Examples from Zacks (1970).
umatol.int(25, n = 4, dist = "Bin", N = 10, alpha = 0.10, P = 0.95)
umatol.int(13, n = 10, dist = "NegBin", N = 2, alpha = 0.10, P = 0.95)
umatol.int(37, n = 10, dist = "Pois", alpha = 0.10, P = 0.95)
```
Description

Provides 1-sided or 2-sided tolerance intervals for data distributed according to a uniform distribution.

Usage

uniftol.int(x, alpha = 0.05, P = 0.99, upper = NULL, lower = NULL, side = 1)

Arguments

- **x**: A vector of data which is distributed according to a uniform distribution.
- **alpha**: The level chosen such that 1-\(\alpha\) is the confidence level.
- **P**: The proportion of the population to be covered by this tolerance interval.
- **upper**: The upper bound of the data. When `NULL`, then the maximum of `x` is used.
- **lower**: The lower bound of the data. When `NULL`, then the minimum of `x` is used.
- **side**: Whether a 1-sided or 2-sided tolerance interval is required (determined by `side = 1` or `side = 2`, respectively).

Value

`uniftol.int` returns a data frame with items:

- **alpha**: The specified significance level.
- **P**: The proportion of the population covered by this tolerance interval.
- **1-sided.lower**: The 1-sided lower tolerance bound. This is given only if `side = 1`.
- **1-sided.upper**: The 1-sided upper tolerance bound. This is given only if `side = 1`.
- **2-sided.lower**: The 2-sided lower tolerance bound. This is given only if `side = 2`.
- **2-sided.upper**: The 2-sided upper tolerance bound. This is given only if `side = 2`.

References

Examples

```r
## 90%/90% 1-sided uniform tolerance intervals for a sample
## of size 50 with a known lower bound of 0.
set.seed(100)
x <- runif(50, 0, 50)
out <- uniftol.int(x = x, alpha = 0.10, P = 0.90, lower = 0,
                  side = 1)
out
plottol(out, x, plot.type = "hist", side = "two",
xlab = "Uniform Data")
```

### ZipfMandelbrot

#### Zipf-Mandelbrot Distributions

**Description**

Density (mass), distribution function, quantile function, and random generation for the Zipf, Zipf-Mandelbrot, and zeta distributions.

**Usage**

```r
dzipfman(x, s, b = NULL, N = NULL, log = FALSE)
pzipfman(q, s, b = NULL, N = NULL, lower.tail = TRUE,
         log.p = FALSE)
qzipfman(p, s, b = NULL, N = NULL, lower.tail = TRUE,
         log.p = FALSE)
rzipfman(n, s, b = NULL, N = NULL)
```

**Arguments**

- `x, q` Vector of quantiles.
- `p` Vector of probabilities.
- `n` The number of observations. If `length(n) > 1`, then the length is taken to be the number required.
- `s, b` The shape parameters, both of which must be greater than 0. `b` must be specified for Zipf-Mandelbrot distributions.
- `N` The number of categories, which must be integer-valued for Zipf and Zipf-Mandelbrot distributions. For a zeta distribution, `N = Inf` must be used.
- `log, log.p` Logical vectors. If `TRUE`, then the probabilities are given as `log(p)`.
- `lower.tail` Logical vector. If `TRUE`, then probabilities are `P[X \leq x]`, else `P[X > x]`.

**Arguments**

- `x, q` Vector of quantiles.
- `p` Vector of probabilities.
- `n` The number of observations. If `length(n) > 1`, then the length is taken to be the number required.
- `s, b` The shape parameters, both of which must be greater than 0. `b` must be specified for Zipf-Mandelbrot distributions.
- `N` The number of categories, which must be integer-valued for Zipf and Zipf-Mandelbrot distributions. For a zeta distribution, `N = Inf` must be used.
- `log, log.p` Logical vectors. If `TRUE`, then the probabilities are given as `log(p)`.
- `lower.tail` Logical vector. If `TRUE`, then probabilities are `P[X \leq x]`, else `P[X > x]`.  

Details

The Zipf-Mandelbrot distribution has mass

\[ p(x) = \frac{(x + b)^{-s}}{\sum_{i=1}^{N}(i + b)^{-s}}, \]

where \( x = 1, \ldots, N \), \( s, b > 0 \) are shape parameters, and \( N \) is the number of distinct categories. The Zipf distribution is just a special case of the Zipf-Mandelbrot distribution where the second shape parameter \( b = 0 \). The zeta distribution has mass

\[ p(x) = \frac{x^{-s}}{\zeta(s)}, \]

where \( x = 1, 2, \ldots, s > 1 \) is the shape parameter, and \( \zeta() \) is the Riemann zeta function given by:

\[ \zeta(t) = \sum_{i=1}^{\infty} \frac{1}{i^t} < \infty. \]

Note that the zeta distribution is just a special case of the Zipf distribution where \( s > 1 \) and \( N \) goes to infinity.

Value

dzipfman gives the density (mass), pzipfman gives the distribution function, qzipfman gives the quantile function, and rzipfman generates random deviates for the specified distribution.

Note

These functions may be updated in a future version of the package so as to allow greater flexibility with the inputs.

References


See Also

runif and .Random.seed about random number generation.
Examples

## Randomly generated data from the Zipf distribution.

```r
set.seed(100)
x <- rzipfman(n = 150, s = 2, N = 100)
hist(x, main = "Randomly Generated Data", prob = TRUE)

x.1 <- sort(x)
y <- dzipfman(x = x.1, s = 2, N = 100)
lines(x.1, y, col = 2, lwd = 2)

plot(x.1, pzipfman(q = x.1, s = 2, N = 100), type = "l",
     xlab = "x", ylab = "Cumulative Probabilities")
qzipfman(p = 0.20, s = 2, N = 100)
qzipfman(p = 0.80, s = 2, N = 100)

## Randomly generated data from the Zipf-Mandelbrot distribution.

set.seed(100)
x <- rzipfman(n = 150, s = 2, b = 3, N = 100)
hist(x, main = "Randomly Generated Data", prob = TRUE)

x.1 <- sort(x)
y <- dzipfman(x = x.1, s = 2, b = 3, N = 100)
lines(x.1, y, col = 2, lwd = 2)

plot(x.1, pzipfman(q = x.1, s = 2, b = 3, N = 100), type = "l",
     xlab = "x", ylab = "Cumulative Probabilities")
qzipfman(p = 0.20, s = 2, b = 3, N = 100)
qzipfman(p = 0.80, s = 2, b = 3, N = 100)

## Randomly generated data from the zeta distribution.

set.seed(100)
x <- rzipfman(n = 100, s = 1.3, N = Inf)
hist(x, main = "Randomly Generated Data", prob = TRUE)

x.1 <- sort(x)
y <- dzipfman(x = x.1, s = 1.3, N = Inf)
lines(x.1, y, col = 2, lwd = 2)

plot(x.1, pzipfman(q = x.1, s = 1.3, N = Inf), type = "l",
     xlab = "x", ylab = "Cumulative Probabilities")
qzipfman(p = 0.20, s = 1.3, N = Inf)
qzipfman(p = 0.80, s = 1.3, N = Inf)
```

(zipftol.int) Zipf-Mandelbrot Tolerance Intervals
Description

Provides 1-sided or 2-sided tolerance intervals for data distributed according to Zipf, Zipf-Mandelbrot, and zeta distributions.

Usage

```r
zipftol.int(x, m = NULL, N = NULL, alpha = 0.05, P = 0.99,
          side = 1, s = 1, b = 1, dist = c("Zipf",
          "Zipf-Man", "Zeta"), ties = FALSE, ...)
```

Arguments

- `x`: A vector of raw data or a table of counts which is distributed according to a Zipf, Zipf-Mandelbrot, or zeta distribution. Do not supply a vector of counts!
- `m`: The number of observations in a future sample for which the tolerance limits will be calculated. By default, `m = NULL` and, thus, `m` will be set equal to the original sample size.
- `N`: The number of categories when `dist = "Zipf"` or `dist = "Zipf-Man"`. This is not used when `dist = "Zeta"`. If `N = NULL`, then N is estimated based on the number of categories observed in the data.
- `alpha`: The level chosen such that 1-alpha is the confidence level.
- `P`: The proportion of the population to be covered by this tolerance interval.
- `side`: Whether a 1-sided or 2-sided tolerance interval is required (determined by `side = 1` or `side = 2`, respectively).
- `s`: The initial value to estimate the shape parameter in the `zm.ll` function.
- `b`: The initial value to estimate the second shape parameter in the `zm.ll` function when `dist = "Zipf-Man"`.
- `dist`: Options are `dist = "Zipf"`, `dist = "Zipf-Man"`, or `dist = "Zeta"` if the data is distributed according to the Zipf, Zipf-Mandelbrot, or zeta distribution, respectively.
- `ties`: How to handle if there are other categories with the same frequency as the category at the estimated tolerance limit. The default is `FALSE`, which does no correction. If `TRUE`, then the highest ranked (i.e., lowest number) of the tied categories is selected for the lower limit and the lowest ranked (i.e., highest number) of the tied categories is selected for the upper limit.
- `...`: Additional arguments passed to the `zm.ll` function, which is used for maximum likelihood estimation.

Details

Zipf-Mandelbrot models are commonly used to model phenomena where the frequencies of categorical data are approximately inversely proportional to its rank in the frequency table. Zipf-Mandelbrot distributions are heavily right-skewed distributions with a (relatively) large mass placed on the first category. For most practical applications, one will typically be interested in 1-sided upper bounds.
zipftol.int returns a data frame with the following items:

- **alpha**: The specified significance level.
- **P**: The proportion of the population covered by this tolerance interval.
- **s.hat**: MLE for the shape parameter \( s \).
- **b.hat**: MLE for the shape parameter \( b \) when \( \text{dist} = \text{"Zipf-Man"} \).
- **1-sided.lower**: The 1-sided lower tolerance bound. This is given only if \( \text{side} = 1 \).
- **1-sided.upper**: The 1-sided upper tolerance bound. This is given only if \( \text{side} = 1 \).
- **2-sided.lower**: The 2-sided lower tolerance bound. This is given only if \( \text{side} = 2 \).
- **2-sided.upper**: The 2-sided upper tolerance bound. This is given only if \( \text{side} = 2 \).

**Note**

This function may be updated in a future version of the package so as to allow greater flexibility with the inputs.

**References**


**See Also**

`ZipfMandelbrot`, `zm.ll`

**Examples**

```r
## 95%/99% 1-sided tolerance intervals for the Zipf, Zipf-Mandelbrot, and zeta distributions.

set.seed(100)

s <- 2
b <- 5
N <- 50

zipf.data <- rzipfman(n = 150, s = s, N = N)
zipfman.data <- rzipfman(n = 150, s = s, b = b, N = N)
zeta.data <- rzipfman(n = 150, s = s, N = Inf)

out.zipf <- zipftol.int(zipf.data, dist = "Zipf")
```
out.zipfman <- zipftol.int(zipfman.data, dist = "Zipf-Man")
out.zeta <- zipftol.int(zeta.data, N = Inf, dist = "Zeta")

zm.ll

Maximum Likelihood Estimation for Zipf-Mandelbrot Models

Description

Performs maximum likelihood estimation for the parameters of the Zipf, Zipf-Mandelbrot, and zeta distributions.

Usage

zm.ll(x, N = NULL, s = 1, b = 1, dist = c("Zipf", "Zipf-Man", "Zeta"), ...)  

Arguments

x A vector of raw data or a table of counts which is distributed according to a Zipf, Zipf-Mandelbrot, or zeta distribution. Do not supply a vector of counts!
N The number of categories when dist = "Zipf" or dist = "Zipf-Man". This is not used when dist = "Zeta". If N = NULL, then N is estimated based on the number of categories observed in the data.
s The initial value to estimate the shape parameter, which is set to 1 by default. If a poor initial value is specified, then a WARNING message is returned.
b The initial value to estimate the second shape parameter when dist = "Zipf-Man", which is set to 1 by default. If a poor initial value is specified, then a WARNING message is returned.
dist Options are dist = "Zipf", dist = "Zipf-Man", or dist = "Zeta" if the data is distributed according to the Zipf, Zipf-Mandelbrot, or zeta distribution, respectively.
... Additional arguments passed to the mle function.

Details

Zipf-Mandelbrot models are commonly used to model phenomena where the frequencies of categorical data are approximately inversely proportional to its rank in the frequency table.

Value

See the help file for mle to see how the output is structured.
Note

This function may be updated in a future version of the package so as to allow greater flexibility with the inputs.

References


See Also

mle, ZipfMandelbrot

Examples

## Maximum likelihood estimation for randomly generated data
## from the Zipf, Zipf-Mandelbrot, and zeta distributions.

```r
set.seed(100)

s <- 2
b <- 5
N <- 50

zipf.data <- rzipfman(n = 500, s = s, N = N)
out.zipf <- zm.ll(zipf.data, N = N, dist = "Zipf")
stats4::coef(out.zipf)
stats4::vcov(out.zipf)

zipfman.data <- rzipfman(n = 500, s = s, b = b, N = N)
out.zipfman <- zm.ll(zipfman.data, N = N, dist = "Zipf-Man")
stats4::coef(out.zipfman)
diag(stats4::vcov(out.zipfman))

zeta.data <- rzipfman(n = 200, s = s, N = Inf)
out.zeta <- zm.ll(zeta.data, N = Inf, dist = "Zeta")
stats4::coef(out.zeta)
stats4::vcov(out.zeta)
```
Index

+Topic file
  acc.samp, 4
  anovatol.int, 5
  bayesnormtol.int, 7
  bintol.int, 9
  bonftol.int, 12
  cautol.int, 13
  diffnormtol.int, 14
  DiffProp, 16
  DiscretePareto, 18
  distfree.est, 19
  dpareto.ll, 20
  dparetotol.int, 21
  exp2tol.int, 23
  exptol.int, 25
  exttol.int, 26
  F1, 28
  fidbintol.int, 29
  fidnegbintol.int, 31
  fidpoistol.int, 33
  gamtol.int, 35
  hypertol.int, 37
  K.factor, 38
  K.factor.sim, 40
  K.table, 42
  laptol.int, 44
  logistol.int, 45
  mvregtol.region, 47
  mvtol.region, 48
  negbintol.int, 50
  NegHypergeometric, 52
  neghypertol.int, 54
  nlregtol.int, 55
  norm.OC, 57
  norm.ss, 59
  normtol.int, 61
  np.order, 63
  npbetol.int, 64
  npmvvtol.region, 65
  npregtol.int, 67
  nptol.int, 69
  paretotol.int, 71
  plottol, 73
  poisind.11, 75
  poisindtol.int, 76
  PoissonLindley, 77
  poistol.int, 78
  regtol.int, 81
  simnormtol.int, 82
  TwoParExponential, 84
  umatol.int, 85
  unifitol.int, 87
  ZipfMandelbrot, 88
  ziptol.int, 90
  zm.11, 93
  .Random.seed, 17, 19, 53, 78, 85, 89

  acc.samp, 4, 38, 55
  anova, 7
  anovatol.int, 5
  bayesnormtol.int, 7, 60
  Binomial, 11, 86
  bintol.int, 9
  bonftol.int, 12
  Cauchy, 14
  cautol.int, 13
  confint, 4
  d2exp(TwoParExponential), 84
diffprop(DiffProp), 16
ddpareto(DiscretePareto), 18
diffnormtol.int, 14
  DiffProp, 16, 28
  DiscretePareto, 18, 21, 22
distfree.est, 19, 65, 67, 70
  dhyp (NegHypergeometric), 52
dpareto.11, 20, 22
INDEX

dparetotol.int, 21

dpoislind (PoissonLindley), 77
dzipfman (ZipfMandelbrot), 88

exp2tol.int, 23, 72
Exponential, 25
exptol.int, 25
exttol.int, 26

F1, 28
fidbintol.int, 29, 32, 34
fidnegbintol.int, 30, 31, 34
fidpoistol.int, 30, 32, 33

GammaDist, 36
gamtol.int, 35

Hypergeometric, 5, 38
hypertol.int, 37

integrate, 28, 40, 41
K.factor, 7, 9, 15, 36, 38, 41, 43, 58, 62
K.factor.sim, 40, 84
K.table, 40, 42

laptotol.int, 44
lm, 7, 82
loess, 68
Logistic, 46
logistol.int, 45

mle, 21, 75, 94
mvregtol.region, 47
mvtdtol.region, 48, 67

NegBinomial, 52, 86
negbintol.int, 50
NegHypergeometric, 52, 55
neghypertol.int, 54
nlregtol.int, 55
nls, 56
norm.OC, 57
norm.ss, 59
Normal, 9, 15, 60, 62, 84
normtol.int, 7–9, 15, 40, 58, 60, 61
np.order, 63
npbetol.int, 64
npmvtol.region, 65
npregtol.int, 65, 67, 67, 70

nptol.int, 20, 64, 65, 68, 69

p2exp (TwoParExponential), 84
paretotol.int, 71
pdfprop (DiffProp), 16
pdpareto (DiscretePareto), 18
plottol, 73
pnhyper (NegHypergeometric), 52
poislind.11, 75, 77
poislindtol.int, 76
Poisson, 80, 86
PoissonLindley, 75, 77, 77
poistol.int, 78
ppoislind (PoissonLindley), 77
pzipfman (ZipfMandelbrot), 88

q2exp (TwoParExponential), 84
qdiffprop (DiffProp), 16
qdppareto (DiscretePareto), 18
qnhyper (NegHypergeometric), 52
qpoislind (PoissonLindley), 77
qzipfman (ZipfMandelbrot), 88

r2exp (TwoParExponential), 84
rdiffprop (DiffProp), 16
rdpareto (DiscretePareto), 18
regtol.int, 81
rnhyper (NegHypergeometric), 52
rpoislind (PoissonLindley), 77
rzipfman (ZipfMandelbrot), 88

simnormtol.int, 82
spline, 68

TDist, 39–41
tolerance (tolerance-package), 3
tolerance-package, 3
TwoParExponential, 24, 72, 84

umatol.int, 11, 52, 80, 85
uniftol.int, 87

Weibull, 27

ZipfMandelbrot, 88, 92, 94
zipftol.int, 90
zm.11, 92, 93