Package ‘pCalibrate’

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Maintainer Manuela Ott <manuela.c.ott@gmail.com>
Description Implements transformations of p-values to the smallest possible Bayes factor within the specified class of alternative hypotheses, as described in Held & Ott (2018, <doi:10.1146/annurev-statistics-031017-100307>). Covers several common testing scenarios such as z-tests, t-tests, likelihood ratio tests and the F-test.
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Author Manuela Ott [aut, cre] (<https://orcid.org/0000-0002-8050-7279>), Leonhard Held [aut] (<https://orcid.org/0000-0002-8686-5325>)
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pCalibrate-package .................................................. 2
BF2pp .......................................................... 3
FCalibrate ....................................................... 3
formatBF .......................................................... 6
LRCalibrate .......................................................... 7
p2z ............................................................. 8
pCalibrate .......................................................... 9
tCalibrate ........................................................... 11
twoby2Calibrate ................................................... 13
z2p ............................................................. 16
zCalibrate ........................................................... 17

Index 20
Description

Implements transformations of one- and two-sided p-values to minimum Bayes factors. The minimum Bayes factor is the smallest possible Bayes factor for the point null hypothesis against the alternative within the specified class of alternatives.

The function pCalibrate() provides minimum Bayes factors for two-sided p-values which consider the p-value as the data and are directly based on the distribution of the p-value under the null hypothesis and the alternative. For one- and two-sided p-values from z-tests, zCalibrate() implements minimum Bayes factors for different classes of alternatives. The function tCalibrate() provides the same functionality for one- and two-sided p-values from t-tests. The functions FCalibrate() and LRCalibrate() transform two-sided p-values from the F-test or likelihood ratio test, respectively, to minimum Bayes factors.

Details

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Author(s)

Manuela Ott, Leonhard Held
Maintainer: Manuela Ott <manuela.c.ott@gmail.com>

References


Examples

pCalibrate(p=c(0.05, 0.01, 0.001), type="exploratory")
zCalibrate(p=c(0.05, 0.01, 0.005), type="one.sided",
          alternative="simple")
zCalibrate(p=c(0.05, 0.01, 0.005), type="two.sided")
BF2pp

Transform Bayes factors to posterior probabilities

Description
Transforms the Bayes factor for a hypothesis H_1 against a hypothesis H_2 to the posterior probability of H_1 given the prior probability of H_1 (assuming that the prior probabilities of H_1 and H_2 add up to 1).

Usage
BF2pp(BF, prior.prob)

Arguments
BF a vector of Bayes factors
prior.prob a vector of prior probabilities for H_1. Defaults to a vector with entries 0.5.

Value
A numeric vector of posterior probabilities of the hypothesis H_1

Examples
BF2pp(BF=c(2, 10, 50), prior.prob=c(0.2, 0.5, 0.9))

FCalibrate
Calibration of two-sided p-values from the F-test in the linear model

Description
Transforms two-sided p-values from the F-test of overall significance in the linear model to sample-size adjusted lower bounds on the Bayes factor for the point null hypothesis against the alternative.

Usage
FCalibrate(p, n, d, alternative="chi.squared", intercept=TRUE, transform="id")
Arguments

- **p**: a vector of two-sided p-values
- **n**: a scalar or a vector of positive integers. Specifies the sample size(s). May be a vector only if d is a scalar.
- **d**: a scalar or a vector of positive integers. Specifies the dimension(s) of the vector(s) of regression coefficients, i.e. the number(s) of explanatory variables in the linear model(s). May be a vector only if n is a scalar.
- **alternative**: either "simple" or "chi.squared". Defaults to "chi.squared". Specifies the alternative hypotheses on the non-centrality parameter of the F-distribution to consider. "simple" only considers simple point alternative hypotheses. "chi.squared" assumes a scaled chi-squared distribution.
- **intercept**: logical. If TRUE, the linear model contains an unknown intercept term, otherwise the intercept is fixed. Defaults to TRUE.
- **transform**: either "id", "log", "log2" or "log10". Defaults to "id". Specifies how to transform the lower bound on the Bayes factor. "id" corresponds to no transformation. "log" refers to the natural logarithm, "log2" to the logarithm to the base 2 and "log10" to the logarithm to the base 10.

Details

Note that under the point null hypothesis that all regression coefficients are equal to zero, the F-statistic F (which is the \((1 - p)\)-quantile of the F-distribution with \(d\) and \(n - d - 1\) degrees of freedom) has a central F-distribution with \(d\) and \(n - d - 1\) degrees of freedom if the linear model contains an unknown intercept term (otherwise F has a central F-distribution with \(d\) and \(n - d\) degrees of freedom). Under a simple point alternative, F has a non-central F-distribution with \(d\) and \(n - d - 1\) degrees of freedom.

To obtain the lower bound on the Bayes factor for alternative="simple", the likelihood under the alternative is then maximized numerically with respect to the non-centrality parameter. That calibration is described in Held & Ott (2018), Section 3.1 (in the last two paragraphs).

For alternative="chi.squared", the calibration is proposed in Held & Ott (2016), Section 3 and also described in Held & Ott (2018), Section 3.2. The corresponding minimum Bayes factor has already been derived in Johnson (2005). As described there, assigning a scaled chi-squared distribution to the non-centrality parameter of the F-distribution corresponds to assigning a (multivariate) normal prior distribution centered around the null value to the vector of regression coefficients.

Value

A matrix containing the lower bounds on the Bayes factors as entries, for all combinations of p-value and sample size n or dimension d (whichever is multidimensional). The values for the k-th sample size or dimension (k-th entry in the vector n or d) and the different p-values are given in the k-th row.

Note

Computation may fail for alternative="simple" if the p-value p is extremely small and \(\min\{n, n-d\}\) is also small. Warnings will be given in this case and the returned value is \(\text{minBF=NaN}\).
References


See Also

tCalibrate

Examples

```r
FCalibrate(p=c(0.05, 0.01, 0.005), n=20, d=2, alternative="simple")
# chi-squared alternatives
FCalibrate(p=c(0.05, 0.01, 0.005), n=20, d=2, intercept=FALSE)
FCalibrate(p=c(0.05, 0.01, 0.005), n=20, d=c(2, 5, 10))
FCalibrate(p=c(0.05, 0.01, 0.005), n=c(10, 20, 50), d=2)

# plot for chi-squared alternatives: d=2 and different sample sizes n
# note that the minimum Bayes factor decreases with decreasing sample size
p <- exp(seq(log(0.0001), log(0.3), by=0.01))
n <- c(5, 10, 20)
minBF <- FCalibrate(p, n, d=2)
# compare to the bound for large n
minTBF <- LRCalibrate(p, df=2)
par(las=1)
matplot(p, t(minBF), ylim=c(0.0003, 1), type="l",
        xlab="two-sided F-test p-value", ylab="Minimum Bayes factor",
        log="xy", lty=1, lwd=2, axes=FALSE,
        main="Local normal alternatives")
lines(p, minTBF, col="gray", lty=2, lwd=2)
axis(1, at=c(0.0001, 0.0003, 0.001, 0.003, 0.01, 0.03, 0.1, 0.3),
     as.character(c(format(c(0.0001,0.0003), nsmall=4, digits=4,
                        scientific=FALSE),
                  c(0.001, 0.003, 0.01, 0.03, 0.1, 0.3))))
my.values <- c(3000, 1000, 300, 100, 30, 10, 3, 1)
my.at <- 1/my.values
my.ylegend <- c(paste("1/", my.values[-length(my.values)], sep=""),
               "1")
axis(2, at=my.at, my.ylegend)
box()
legend("bottomright",
        legend=rev(c("n=5", "n=10", "n=20", "n large")),
        col=rev(c(1:3, "gray")), lty=rev(1, times=3), lwd=2)
```
Description

Bayes factors <1 are represented as ratios 1/x, where x is rounded to the specified number of digits. Bayes factors >=1 are rounded to the specified number of digits.

Usage

formatBF(BF, digits="default")

Arguments

- BF: a numeric vector of Bayes factors
- digits: either "default" (see Details) or a positive integer specifying the number of decimal places to round the Bayes factor (for Bayes factors >= 1) or its inverse (for Bayes factors < 1) to

Details

The default formatting, which is recommended in Held and Ott (2018), is as follows: For very small Bayes factors BF < 1/1000, "< 1/1000" is returned. Bayes factors BF with 1/1000 <= BF <= 1/10 are formatted as 1/x, where x is an integer and Bayes factors BF with 1/10 < BF < 1 as 1/x, where x is rounded to one decimal place. Accordingly, Bayes factors 1 <= BF < 10 are rounded to one decimal place, Bayes factors 10 <= BF <= 1000 are rounded to the next integer and for larger Bayes factors, "> 1000" is returned.

If digits is specified, the Bayes factor (if it is >= 1) or its inverse (if the Bayes factor is <1) is rounded to the number of decimal places specified and returned as a ratio if the Bayes factor is <1.

Value

A character vector of ratios (for inputs <1) or rounded numeric values (for inputs >=1).

References


Examples

```r
BF <- c(0.0001, 0.0049, 0.0258, 0.24, 2.798)
# use the default formatting
formatBF(BF)
# specify the number of digits
formatBF(c(0.087, 4.65), digits=1)
```
Description

Transforms two-sided p-values from likelihood ratio (deviance) tests to lower bounds on the Bayes factor for the point null hypothesis against the alternative.

Usage

LRCalibrate(p, df, alternative="gamma", transform="id")

Arguments

p  a vector of two-sided p-values
df a vector of degrees of freedom of the asymptotic chi-squared distribution(s) of likelihood ratio test statistic(s)
alternative either "simple" or "gamma". Defaults to "gamma". Specifies the alternative hypotheses on the non-centrality parameter of the chi-squared distribution to consider. "simple" only considers simple point alternative hypotheses. "gamma" assumes a specific gamma distribution.
transform either "id", "log", "log2" or "log10". Defaults to "id". Specifies how to transform the lower bound on the Bayes factor. "id" corresponds to no transformation. "log" refers to the natural logarithm, "log2" to the logarithm to the base 2 and "log10" to the logarithm to the base 10.

Details

Under the assumption that the parameter vector of interest (which has dimension df) is equal to the vector of zeros, the distribution of the deviance converges to a chi-squared distribution with df degrees of freedom. Under a simple point alternative for the parameter vector of interest and some regularity conditions, the distribution of the deviance converges to a non-central chi-squared distribution with df degrees of freedom.

For alternative = "simple", the lower bound on the Bayes factor is obtained by maximizing the (asymptotic) chi-squared distribution under the alternative with respect to the non-centrality parameter. That calibration is described in Held and Ott (2018), Section 4.2.1.

The calibration for alternative = "normal" uses the test-based Bayes factors introduced in Johnson (2008). That approach is also outlined in Held and Ott (2018), Section 4.2.2.

Using alternative = "gamma" yields a larger bound than alternative = "simple".

Typical applications of these calibrations include generalized linear models.

Value

A matrix containing the lower bounds on the Bayes factors as entries, for all combinations of p-value and degrees of freedom. The values for the k-th degrees of freedom (k-th entry in the vector df) and the different p-values are given in the k-th row.
References


Examples

```
LRCalibrate(p=c(0.05, 0.01, 0.005), df=2, alternative="simple")
# gamma alternatives
LRCalibrate(p=c(0.05, 0.01, 0.005), df=c(2, 5, 10))

# plot the minimum Bayes factor as a function of the p-value
# for different degrees of freedom df of the LR test statistic
par(mfrow=c(1,2), las=1)

p <- exp(seq(log(0.005), log(0.3), by=0.01))
df <- c(1, 5, 20)
par(las=1)
# for a simple alternative
minBF.sim <- LRCalibrate(p, df=df, alternative="simple")
matplot(p, t(minBF.sim), type="l", ylab="Minimum Bayes factor", log="xy",
       xlab="Two-sided LR-test p-value", lty=1, lwd=2, axes=FALSE,
       main="Simple alternative")
axis(1, at=c(0.01, 0.03, 0.1, 0.3), c(0.01, 0.03, 0.1, 0.3))
my.values <- c(30, 20, 10, 5, 3, 1)
my.at <- 1/my.values
my.ylegend <- c(paste("1/", my.values[-length(my.values)], sep=""), "1")
axis(2, at=my.at, my.ylegend)
box()
legend("bottomright", legend=c("df=1", "df=5", "df=20"),
       lty=1, lwd=2, , col=1:3)

# for gamma alternatives
minBF.loc <- LRCalibrate(p, df=df, alternative="gamma")
matplot(p, t(minBF.loc), type="l", ylab="Minimum Bayes factor", log="xy",
       xlab="Two-sided LR-test p-value", lty=1, lwd=2, axes=FALSE, main="Local alternatives")
axis(1, at=c(0.01, 0.03, 0.1, 0.3), c(0.01, 0.03, 0.1, 0.3))
axis(2, at=my.at, my.ylegend)
box()
legend("bottomright", legend=c("df=1", "df=5", "df=20"),
       lty=1, lwd=2, , col=1:3)
```

Transform p-values to z-values
**pCalibrate**

**Description**

Transforms the p-value(s) to the corresponding one- or two-sided z-value(s).

**Usage**

\[ p2z(p, \text{type} = \text{“two.sided”}) \]

**Arguments**

- \( p \): a vector of p-values
- \( \text{type} \): type of test. Either "two.sided" or "one.sided". Defaults to "two.sided".

**Value**

A numeric vector of z-values

**Examples**

\[ p2z(p = c(0.005, 0.01, 0.05)) \]
\[ p2z(p = c(0.005, 0.01, 0.05), \text{type} = \text{“one.sided”}) \]

---

**pCalibrate**

*Calibrations of two-sided p-values directly based on the p-value*

**Description**

Transforms a two-sided p-value to a minimum Bayes factor. That minimum Bayes factor is obtained by modelling the distributions of the p-value under the null and the alternative hypothesis, respectively.

**Usage**

\[ \text{pCalibrate}(p, \text{type} = \text{“exploratory”}, \text{transform} = \text{“id”}) \]

**Arguments**

- \( p \): a vector of two-sided p-values
- \( \text{type} \): either "exploratory" or "confirmatory". Defaults to "exploratory". Corresponds to different distributional assumptions for the p-value \( p \) under the alternative.
- \( \text{transform} \): either "id", "log", "log2" or "log10". Defaults to "id". Specifies how to transform the minimum Bayes factor(s). "id" corresponds to no transformation. "log" refers to the natural logarithm, "log2" to the logarithm to the base 2 and "log10" to the logarithm to the base 10.
Details

If `type="exploratory"` is used, the so-called "-e p log(p)" calibration (Sellke et al., 2001) is applied.

If `type="confirmatory"` is used, the so-called "-e q log(q)" calibration with \( q = 1 - p \) (Held & Ott, 2018) is applied.

`type="exploratory"` gives a larger minimum Bayes factor than `type="confirmatory"`.

Under the null hypothesis, the distribution of the p-value is assumed to be uniform. Under the alternative, the p-value is assumed to have a beta-distribution with monotonically decreasing density function under both alternatives, with different parameters however. If `type="exploratory"`, the prior sample size does not exceed 2, whereas for `type="confirmatory"`, the prior sample size is at least 2. The latter calibration may be appropriate for small sample size, but for larger sample size it is too conservative (Held & Ott, 2018).

Note that for the "-e p log(p)" calibration, alternative derivations which do not assume a beta-distribution under the alternative have also been given, see Sellke et al. (2001).

Value

A numeric vector of minimum Bayes factors for the specified p-values

Note

The argument `type` replaces the argument `alternative` in version 0.1-1 of this package.

`type="exploratory"` corresponds to `alternative="noninformative"` and `type="confirmatory"` corresponds to `alternative="informative"`.

References


Examples

```r
pCalibrate(p=c(0.05, 0.01, 0.001))
pCalibrate(p=c(0.05, 0.01, 0.001), type="confirmatory")
```

# plot the 2 calibrations as a function of the p-value
par(las=1)
p <- exp(seq(log(0.0001), log(0.3), by=0.01))
minBF1 <- pCalibrate(p=p)
minBF2 <- pCalibrate(p=p, type="confirmatory")
plot(p, minBF1, type="l", log="xy",
xlab="Two sided p-value", ylab="Minimum Bayes factor",
axes=FALSE, lwd=2, col=1)
lines(p, minBF2, col=2, lwd=2)
tCalibrate Calibration of p-values from t-tests

Description
Transforms one- and two-sided p-values from t-tests to sample-size adjusted lower bounds on the Bayes factor for the point null hypothesis against the alternative.

Usage
tCalibrate(p, n, type="two.sided", alternative="normal", transform="id")

Arguments
- **p**: a vector of p-values
- **n**: a vector of sample sizes
- **type**: either "one.sided" or "two.sided". Defaults to "two.sided". Specifies if the t-test (and the corresponding p-value) is one-sided or two-sided.
- **alternative**: either "simple" or "normal". Defaults to "normal". Specifies the alternative hypotheses for the mean to consider. See Details for more information.
- **transform**: either "id", "log", "log2" or "log10". Defaults to "id". Specifies how to transform the lower bound on the Bayes factor. "id" corresponds to no transformation. "log" refers to the natural logarithm, "log2" to the logarithm to the base 2 and "log10" to the logarithm to the base 10.

Details
For one-sided t-tests (type="one.sided"), alternative="simple" considers all simple point alternatives for the mean and alternative="normal" all shifted and possibly mirrored (if direction=less) half-normal distributions with mode at the null value.

For two-sided t-tests (type="two.sided"), alternative="simple" considers all two-point distributions on the mean which are symmetric with respect to the null value and alternative="normal" all local normal distributions centered around the null value.
Note that for `alternative="normal"`, the lower bound on the Bayes factor is the same for one-sided and two-sided p-values.

For `type="one.sided",alternative="simple"`, the calibration is available in closed form and is given in Held & Ott (2018), equation (19).

For `type="two.sided",alternative="simple"`, the calibration needs to be computed by numerical optimization and is given in Held & Ott (2018), equations (17) and (18).

For `alternative="normal"`, the corresponding lower bound on the Bayes factor has been derived in Johnson (2005) and the calibration is proposed in Held & Ott (2016), Section 3.

If `alternative="normal"`, `tCalibrate()` is a special case of `FCalibrate()`, i.e. `tCalibrate(p,n,alternative="normal")` is equivalent to `FCalibrate(p,n,d=1,alternative="chi.squared")`.

One can show that if one considers the class of all alternatives which are symmetric with respect to the null value, one obtains the same lower bound as for the subclass of all symmetric two-point distributions.

**Value**

A matrix containing the lower bounds on the Bayes factors as entries, for all combinations of p-value and sample size. The values for the k-th sample size (k-th entry in the vector `n`) and the specified p-values are given in the k-th row.

**References**


**See Also**

`FCalibrate`

**Examples**

```r
tCalibrate(p=c(0.05, 0.01, 0.005), n=10, type="one.sided", alternative="simple")
# two-sided alternatives
# for two-sided alternatives, plot the minimum Bayes factors as a function of the p-value
par(mfrow=c(1,2), pty="s", las=1)
# plot for simple alternatives
p <- exp(seq(log(0.0001), log(0.3), by=0.01))
```
n <- c(10, 20, 50)
minBF <- tCalibrate(p, n, alternative = "simple")
# compare to the bound for large n
bound1 <- zCalibrate(p, alternative="simple")
matplot(p, t(minBF), ylim=c(0.0003, 1), type="l",
      ylab="Min. Bayes factor", log="xy",
      xlab="two-sided t-test p-value", lty=1, lwd=2,
      axes=FALSE, main="Simple alternative")
lines(p, bound1, col="gray", lty=2, lwd=2)
my.at1 <- c(0.0001, 0.0003, 0.01, 0.03, 0.1, 0.3)
my.values1 <- as.character(c(format(c(0.0001,0.0003), digits=4, scientific=FALSE),
c(0.001, 0.003, 0.01, 0.03, 0.1, 0.3)))
axis(1, at=my.at1, labels=my.values1)
my.at2 <- 1/my.values2
my.ylegend2 <- c(paste("1/", my.values2[-length(my.values2)], sep=""), "1")
axis(2, at=my.at2, labels=my.ylegend2)
box()
legend("bottomright", legend=rev(c("n=10", "n=20", "n=50", "n large")),
      lty=rev(c(rep(1,3), 2)), lwd=2, col=rev(c(1:3, "gray"))

# plot for local normal alternatives
p <- exp(seq(log(0.0001), log(0.3), by=0.01))
n <- c(10, 20, 50)
minBF <- tCalibrate(p, n)
bound2 <- zCalibrate(p)
matplot(p, t(minBF), ylim=c(0.0003, 1), type="l",
      ylab="Min. Bayes factor", log="xy",
      xlab="two-sided t-test p-value", lty=1, lwd=2,
      axes=FALSE, main="Local normal alternatives")
lines(p, bound2, col="gray", lty=2, lwd=2)
axis(1, at=my.at1, labels=my.values1)
axis(2, at=my.at2, labels=my.ylegend2)
box()
legend("bottomright", legend=rev(c("n=10", "n=20", "n=50", "n large")),
      lty=rev(c(rep(1,3), 2)), lwd=2, col=rev(c(1:3, "gray"))

---

twoby2Calibrate

**Minimum Bayes factors and p-values from Fisher’s exact test for 2x2 contingency tables**

**Description**

Computes a sample-size adjusted lower bound on the Bayes factor (for the point null hypothesis against the alternative) for the given 2x2 contingency table. Also returns p-values from Fisher’s exact test (different versions in the two-sided case) and less conservative alternatives such as a mid p-value (see Details for more information).
Usage
twoby2Calibrate(x, type="two.sided", alternative="normal", direction=NULL, transform.bf="id")

Arguments

x a 2x2 contingency table in matrix form
type either "one.sided" or "two.sided". Defaults to "two.sided". Specifies if Fisher's exact test (and the corresponding p-value) is one-sided or two-sided.
alternative either "simple" or "normal". Defaults to "normal". Specifies the alternative hypotheses for the (log) odds ratio to consider for two-sided tests. Is ignored if type="one.sided" (in this case only simple alternatives are available).
direction either "greater", "less" or NULL. Defaults to NULL. Specifies the direction of the alternative for one-sided tests: "greater" corresponds to an odds ratio > 1 and "less" to an odds ratio < 1. Is ignored if type="two.sided".
transform.bf either "id", "log", "log2" or "log10". Defaults to "id". Specifies how to transform the lower bound on the Bayes factor. "id" corresponds to no transformation. "log" refers to the natural logarithm, "log2" to the logarithm to the base 2 and "log10" to the logarithm to the base 10.

Details

If type="two.sided", the point null hypothesis that the odds ratio is 1 is tested against specific two-sided alternatives: alternative="simple" considers all two-point distributions symmetric around 0 for the log odds ratio. alternative="normal" assumes a local normal prior distribution (a so-called g-prior) centered around 0 for the log odds ratio.

In the one-sided case (type="one.sided"), direction="less" tests the alternative that the odds ratio is less than 1 and considers simple point alternatives in that direction to compute the lower bound on the Bayes factor. "greater" does the same for the alternative that the odds ratio is larger than 1.

The calibration obtained with type="two.sided", alternative="normal" is based on the methodology proposed in Li & Clyde (2018) and yields an (approximate) lower bound on the Bayes factor in closed form. All the other lower bounds on the Bayes factor are computed by numerical optimization. For type="two.sided", the two calibrations are described in Ott & Held (2019).

For one-sided alternatives, the following p-value and 2 related quantities are computed:

- p.fi is the one-sided p-value from Fisher's exact test.
- p.mid is a "mid" p-value. It is obtained by subtracting half of the probability mass of the observed table from p.fi.
- p.lie is a Bayesian posterior probability. If direction="greater", it is the posterior probability that the odds ratio exceeds 1 given the observed table under the assumption of uniform priors on the success probabilities for the two groups. If direction="less", it is the posterior probability that the odds ratio does not exceed 1 given the observed table under the same priors.

For two-sided alternatives, the following 3 p-values and 2 related quantities are computed:
• p.pb is the "probability-based" p-value (the classical choice), defined as the sum of the probabilities of all tables which are at most a likely as the observed table and have the same marginals.

• p.ce is the "central" p-value, which is twice the minimum one-sided p-value (from Fisher’s exact test), bounded by 1.

• p.bl is "Blaker’s" p-value, which is the minimum one-sided p-value (from Fisher’s exact test) plus the largest tail probability from the other tail of the distribution that does not exceed that minimum.

• p.mid is a "mid" p-value. It is the mid-p modification of the central p-value, i.e. it equals twice the minimum one-sided mid p-value.

• p.lie is a two-sided version of the posterior probability for the one-sided test. Let p.lie.os be the one-sided posterior probability that the odds ratio does not exceed 1 given the observed table, as returned by the one-sided test with direction="less". Then p.lie = 2 \min\{p.lie.os, 1-p.lie.os\}.

For one-sided alternatives, the posterior probability p.lie was already studied in Liebermeister (1877) and its frequentist properties are investigated in Seneta & Phipps (2001).

For two-sided alternatives, the 3 p-values from Fisher’s exact test are defined in equations (2.24)-(2.26) in Kateri (2014) and computed using the function exact2x2() in the package exact2x2. The "mid" p-value is described in Rothman & Greenland (1998, pp. 222-223). The Bayesian significance measure p.lie is proposed in Ott & Held (2019) as a modification of the corresponding one-sided significance measure.

Value

A list of the following two elements:

- minBF the lower bound on the Bayes factor
- p.value A vector of 3 one-sided p-values/significance measures for one-sided tests, namely first the p-value p.fi from Fisher’s exact test, second the corresponding mid p-value p.mid and third the Bayesian posterior probability p.lie (see Details for more information).

A vector of 5 two-sided p-values/significance measures for two-sided tests: The first three p-values p.pb, p.ce and p.bl (see Details for the definitions) correspond to two-sided p-values from Fisher’s exact test. The 4th quantity p.mid is a mid p-value, namely the mid-p modification of the second p-value p.ce. The last element p.lie is a Bayesian significance measure (see Details for additional information).

Warning

For 2x2 tables with entries equal to 0, the minimum Bayes factor is either not defined (for alternative="normal") or the underlying numerical optimization is unstable (for alternative="simple"). A warning is displayed in such cases and minBF=NA is returned, but the different p-values/significance measures are still available.
Transform z-values to p-values

Transforms the z-value(s) to the corresponding one- or two-sided p-value(s).

Usage

```
z2p(z, type="two.sided")
```

Arguments

- `z`: a vector of z-values
- `type`: Underlying type of p-value. Either "two.sided" or "one.sided". Defaults to "two.sided".
Value
A numeric vector of p-values

Examples
z2p(z=c(1,2,5))
z2p(z=c(1,2,5), type="one.sided")

zCalibrate
Calibration of p-values from z-tests

Description
Transforms one- and two-sided p-values from z-tests to minimum Bayes factors.

Usage
zCalibrate(p=NULL, z=p2z(p), type="two.sided",
alternative="normal", transform="id")

Arguments
p a vector of p-values, default is NULL
z a vector of z-values, is calculated from p, if necessary.
type either "one.sided" or "two.sided". Defaults to "two.sided". Specifies if the z-test (and the corresponding p-value) is one-sided or two-sided.
alternative either "simple", "normal" or "local". Defaults to "normal". Specifies the alternative hypotheses for the mean to consider. See Details for more information.
transform either "id", "log", "log2" or "log10". Defaults to "id". Specifies how to transform the minimum Bayes factor(s). "id" corresponds to no transformation. "log" refers to the natural logarithm, "log2" to the logarithm to the base 2 and "log10" to the logarithm to the base 10.

Details
For one-sided z-tests (type="one.sided"), alternative="simple" considers all simple point alternatives for the mean in the specified direction, alternative="normal" all shifted and possibly mirrored (if direction=less) half-normal distributions with mode at the null value and alternative="local" all monotonic density functions with mode at the null value, which are concentrated on the parameter space of the alternative.

For two-sided z-tests (type="two.sided"), alternative="simple" considers all two-point distributions on the mean which are symmetric with respect to the null value, alternative="normal" all normal distributions centered around the null value and alternative="local" all unimodal symmetric distributions with respect the null value (i.e. these distributions are non-increasing as a function of the distance to the null value).
Note that for alternative="normal" and alternative="local", the minimum Bayes factor is the same for type="one.sided" and type="two.sided".

For type="one.sided", alternative="simple" and for alternative="normal", the calibrations have closed-form expressions and were proposed in Edwards et al. (1963).

For type="two.sided", alternative="simple" and for alternative="local", the calibrations need to be computed by numerical optimization and were derived in Berger & Sellke (1987). Most of these calibrations are also described in Held & Ott (2018).

Note that if one considers the class of all alternatives, the resulting minimum Bayes factor is the same as for type="one.sided", alternative="simple".

One can show that if one considers the class of all alternatives which are symmetric around the null value, one obtains the same minimum Bayes factor as for the subclass of all symmetric two-point distributions (Berger & Sellke, 1987).

Value

A numeric vector of minimum Bayes factors for the specified p-values

Note

For small p-values, using the corresponding z-value as an argument instead of the p-value may lead to more accurate computations.

References


See Also

tCalibrate for sample-size adjusted calibrations of p-values from t-tests

Examples

# two-sided alternatives
zCalibrate(p=c(0.05, 0.01, 0.005), alternative="simple")
zCalibrate(p=c(0.05, 0.01, 0.005))
zCalibrate(p=c(0.05, 0.01, 0.005), alternative="local")
zCalibrate(z=c(2, 3, 4), alternative="local")

# one-sided alternatives
zCalibrate(p=c(0.05, 0.01, 0.005), type="one.sided", alternative="simple")
zCalibrate(p=c(0.05, 0.01, 0.005), type="one.sided")
zCalibrate(p=c(0.05, 0.01, 0.005), type="one.sided", alternative="local")
# plot the different calibrations as a function of the p-value
par(las=1)
p <- exp(seq(log(0.0001), log(0.3), by=0.01))
minBF <- matrix(NA, ncol=4, nrow=length(p))
minBF[,1] <- zCalibrate(p)
minBF[,2] <- zCalibrate(p, type="two.sided", alternative="local")
minBF[,3] <- zCalibrate(p, type="two.sided", alternative="simple")
minBF[,4] <- zCalibrate(p, type="one.sided", alternative="simple")
matplot(p, minBF, type="l", ylab="Minimum Bayes factor", log="xy",
xlab="z-test p-value", lty=1, lwd=2, col=c(1,3,2,4), axes=FALSE)
axis(1, at=c(0.0001, 0.0003, 0.001, 0.003, 0.01, 0.03, 0.1, 0.3),
as.character(c(format(c(0.0001,0.0003), nsmall=4, digits=4, scientific=FALSE),
c(0.001, 0.003, 0.01, 0.03, 0.1, 0.3))))
my.values <- c(3000, 1000, 300, 100, 30, 10, 3, 1)
my.at <- 1/my.values
my.ylegend <- c(paste("1/", my.values[-length(my.values)], sep=""), "1")
axis(2, at=my.at, my.ylegend)
box()
legend("bottomright", lty=1, lwd=2,
  legend=c("normal", "unimodal symmetric",
    "two-sided simple", "one-sided simple"), col=c(1,3,2,4))
Index

*Topic htest
   FCcalibrate, 3
   LRCcalibrate, 7
   pcalibrate-package, 2
   tcalibrate, 11
   twoby2calibrate, 13
   zcalibrate, 17

*Topic models & regression
   FCcalibrate, 3
   LRCcalibrate, 7
   tcalibrate, 11
   twoby2calibrate, 13

*Topic package
   pcalibrate-package, 2

BF2pp, 3
exact2x2, 16

FCcalibrate, 3, 12
formatBF, 6
LRCcalibrate, 7
p2z, 8
pcalibrate, 9
pcalibrate-package, 2

tcalibrate, 5, 11, 18
twoby2calibrate, 13

z2p, 16
zcalibrate, 17