

Package ‘pCalibrate’

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Type Package

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Depends epitools, exact2x2, MCMCpack

Description Implements transformations of P-values to the smallest possible Bayes factor within the specified class of alternative hypotheses, as described in Held & Ott (2017, On p-values and Bayes factors, Annual Review of Statistics and Its Application, 5, to appear). Covers several common testing scenarios such as z-tests, t-tests, likelihood ratio tests and the F-test of overall significance in the linear model.

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pCalibrate-package *Bayesian Calibrations of P-Values*

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 transformations (called calibrations in the sequel) 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 calibrations 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()` calibrate two-sided P-values from the F-test of overall significance in the linear model or likelihood ratio tests, respectively.

Details

Package: pCalibrate
Type: Package
Title: Bayesian Calibrations of P-Values
Version: 0.1-1
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Author: Manuela Ott [aut, cre], Leonhard Held [aut]
Maintainer: Manuela Ott <manuela.ott@uzh.ch>
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Author(s)

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References

Held, L. and Ott, M. (2017). On p-values and Bayes factors. To appear in *Annual Review of Statistics and Its Application*, Volume 5.

Examples

```
pCalibrate(p=c(0.05, 0.01, 0.001), alternative="noninformative")
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", alternative="normal")
tCalibrate(p=c(0.05, 0.01, 0.005), n=c(10, 20, 50), type="two.sided", alternative="normal")
FCalibrate(p=c(0.05, 0.01, 0.005), n=20, d=c(2, 5, 10), alternative="chi.squared")
LRCalibrate(p=c(0.05, 0.01, 0.005), df=2, alternative="simple")
```

`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=0.5)
```

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 minimum Bayes factors.

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. 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 non-central 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 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

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 minimum 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 (2017), 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 (2017), 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 minimum 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 `minBF=NaN`.

References

- Held, L. and Ott, M. (2016). How the maximal evidence of P-values against point null hypotheses depends on sample size. *American Statistician*, **70**, 335–341
- Held, L. and Ott, M. (2017). On p-values and Bayes factors. To appear in *Annual Review of Statistics and Its Application*, Volume 5.
- Johnson, V. E. (2005). Bayes factors based on test statistics. *Journal of the Royal Statistical Society, Series B*, **67**, 689–701.

See Also

[tCalibrate](#)

Examples

```
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 minimum Bayes factor for large n
minTBF <- LRCalibrate(p, df=2)
par(las=1)
matplot(p, t(minBF), ylim=c(0.0003, 1), type="l", ylab="Minimum Bayes factor", log="xy",
        xlab="two-sided F-test P-value", lty=1, lwd=2, axes=FALSE,
        main="Local normal alternatives, d=2")
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=c(2, rep(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 (2017), is as follows : For very small Bayes factors $BF < 1/1000$, " $< 1/1000$ " is returned. Bayes factors BF with $1/1000 \leq BF \leq 1/10$ 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 $1 \leq BF < 10$ are rounded to one decimal place, Bayes factors $10 \leq BF \leq 1000$ 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

Held, L. and Ott, M. (2017). On p-values and Bayes factors. To appear in *Annual Review of Statistics and Its Application, Volume 5*.

Examples

```
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)
```

LRCalibrate	<i>Calibration of two-sided P-values obtained from the likelihood ratio test statistic</i>
-------------	--

Description

Transforms two-sided P-values from likelihood ratio (deviance) tests to minimum Bayes factors.

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 non-central 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 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

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 minimum Bayes factor is obtained by maximizing the density function of the (asymptotic) non-central chi-squared distribution under the alternative with respect to the non-centrality parameter. That calibration is described in Held and Ott (2017), 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 (2017), Section 4.2.2.

Using `alternative = "gamma"` yields a larger minimum Bayes factor than `alternative = "simple"`. Typical applications of these calibrations include generalized linear models.

Value

A matrix containing the minimum 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

Held, L. and Ott, M. (2017). On p-values and Bayes factors. To appear in *Annual Review of Statistics and Its Application, Volume 5*.

Johnson, V. E. (2008). Properties of Bayes factors based on test statistics. *Scandinavian Journal of Statistics*, **35**, 354–368.

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)
```


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

```
pCalibrate(p, alternative="noninformative", transform="id")
```

Arguments

p	a vector of two-sided P-values
alternative	either "noninformative" or "informative". Defaults to "noninformative". Corresponds to different distributional assumptions for the P-value p under the alternative.
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 `alternative="noninformative"` is used, the so-called " $-e p \log(p)$ " calibration (Sellke et al., 2001) is applied.

If `alternative="informative"` is used, the the so-called " $-e q \log(q)$ " calibration with $q=1-p$ (Held & Ott, 2017) is applied.

`alternative="noninformative"` gives a larger minimum Bayes factor than `alternative="informative"`.

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 `alternative="noninformative"`, the prior sample size does not exceed 2, whereas for `alternative="informative"`, 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, 2017).

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

References

- Held, L. and Ott, M. (2017). On p-values and Bayes factors. To appear in *Annual Review of Statistics and Its Application*, Volume 5.
- Sellke, T., Bayarri, M. J. and Berger, J. O. (2001). Calibration of p values for testing precise null hypotheses. *The American Statistician*, **55**, 62–71.

Vovk, V. G. (1993). A logic of probability, with application to the foundations of statistics (with discussion and a reply by the author). *Journal of the Royal Statistical Society, Series B*, **55**, 317–351.

Examples

```
pCalibrate(p=c(0.05, 0.01, 0.001))
pCalibrate(p=c(0.05, 0.01, 0.001), alternative="informative")

# 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, alternative="informative")
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)
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("- e p log(p)", "- e q log(q)"),
      , col=c(1,2))
```

tCalibrate

Calibration of P-values from t-tests

Description

Transforms one- and two-sided P-values from t-tests to sample-size adjusted minimum Bayes factors.

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 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 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 minimum 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 (2017), equation (19).

For type="two.sided", alternative="simple", the calibration needs to be computed by numerical optimization and is given in Held & Ott (2017), equations (17) and (18).

For alternative="normal", the corresponding minimum 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="normal").

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 minimum Bayes factor as for the subclass of all symmetric two-point distributions.

Value

A matrix containing the minimum 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

- Held, L. and Ott, M. (2017). On p-values and Bayes factors. To appear in *Annual Review of Statistics and Its Application*, Volume 5.
- Held, L. and Ott, M. (2016). How the maximal evidence of P-values against point null hypotheses depends on sample size. *The American Statistician*, **70**, 335–341.
- Johnson, V. E. (2005). Bayes factors based on test statistics. *Journal of the Royal Statistical Society, Series B*, **67**, 689–701.

See Also

[FCalibrate](#)

Examples

```

tCalibrate(p=c(0.05, 0.01, 0.005), n=10, type="one.sided", alternative="simple")
# two-sided alternatives
tCalibrate(p=c(0.05, 0.01, 0.005), n=20, alternative="simple")
tCalibrate(p=c(0.05, 0.01, 0.005), n=c(10, 20, 50))

# 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 minimum Bayes factor 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",
        xlabel="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, 0.001, 0.003, 0.01, 0.03, 0.1, 0.3)
my.values1 <- 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)))
axis(1, at=my.at1, labels=my.values1)
my.values2 <- c(3000, 1000, 300, 100, 30, 10, 3, 1)
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",
        xlabel="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, 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 minimum Bayes factor 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 minimum 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 minimum 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 (2016) and yields an (approximate) minimum Bayes factor in closed form. All the other minimum Bayes factors are computed by numerical optimization. For type="two.sided", the two calibrations are described in Ott & Held (2017).

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 as 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 `exact2x2()`-function in the `exact2x2`-package. The "mid" P-value is described in Rothman & Greenland (1998, pp. 222-223) and computed using the `tab2by2.test()`-function in the package `epi.tools`. The Bayesian significance measure `p.lie` is proposed in Ott & Held (2017) as a modification of the corresponding one-sided significance measure.

Value

A list of the following two elements:

<code>minBF</code>	the minimum Bayes factor
<code>p.value</code>	A vector of 3 one-sided P-values/significance measures for one-sided tests, namely first the P-value <code>p.fi</code> from Fisher's exact test, second the corresponding mid P-value <code>p.mid</code> and third the Bayesian posterior probability <code>p.lie</code> (see Details for more information). A vector of 5 two-sided P-values/significance measures for two-sided tests: The first three P-values <code>p.pb</code> , <code>p.ce</code> and <code>p.bl</code> (see Details for the definitions) correspond to two-sided P-values from Fisher's exact test. The 4th quantity <code>p.mid</code> is a mid P-value, namely the mid-p modification of the second P-value <code>p.ce</code> . The last element <code>p.lie</code> 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.

References

- Li, Y. and Clyde, M. A. (2016). Mixtures of g-priors in generalized linear models. Technical report, Clemson/Duke University. <https://arxiv.org/abs/1503.06913v2>
- Liebermeister, C. (1877). Ueber Wahrscheinlichkeitsrechnung in Anwendung auf therapeutische Statistik. Sammlung klinischer Vortraege. *Innere Medizin*, **110**(31–64), 935–962.
- Kateri, M. (2014). Contingency Table Analysis - Methods and Implementation using R. Statistics for Industry and Technology. Birkhaeuser.
- Ott, M. and Held, L. (2017). Bayesian calibration of P-values from Fisher's exact test. Technical report, University of Zurich.
- Rothman, K. J. and Greenland, S. (1998). Modern Epidemiology. 2nd ed. Lippincott-Raven.
- Seneta, E. and Phipps, M. C. (2001). On the comparison of two observed frequencies. *Biometrical Journal*, **43**(1), 23–43.

See Also

For computation of P-values: [exact2x2](#) in package `exact2x2` and [tab2by2.test](#) in package `epi-tools`.

Examples

```
tab <- matrix(c(1,15,5,10), nrow=2, byrow=TRUE)
minBF.plus <- twoby2Calibrate(x=tab, type="one.sided", direction="greater")$minBF
minBF.minus <- twoby2Calibrate(x=tab, type="one.sided", direction="less")$minBF
minBF.sim <- twoby2Calibrate(x=tab, type="two.sided", alternative="simple")$minBF
minBF.nor <- twoby2Calibrate(x=tab)$minBF
p.plus <- twoby2Calibrate(x=tab, type="one.sided", direction="greater")$p.value
p.minus <- twoby2Calibrate(x=tab, type="one.sided", direction="less")$p.value
pvals.twosid <- twoby2Calibrate(x=tab)$p.value
```

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, type="two.sided", alternative="normal", transform="id")
```

Arguments

p	a vector of P-values
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 (2017).

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

References

- Berger, J. O. and Sellke, T. (1987). Testing a point null hypothesis: The irreconcilability of P values and evidence (with discussion). *Journal of the American Statistical Association*, **82**, 112–139.
- Edwards, W., Lindman, H. and Savage, L. J. (1963). Bayesian statistical inference for psychological research. *Psychological Review*, **70**, 193–242.

Held, L. and Ott, M. (2017). On p-values and Bayes factors. To appear in *Annual Review of Statistics and Its Application, Volume 5*.

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")
# 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))
```

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