Package: evidence (via r-universe)

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Title Analysis of Scientific Evidence Using Bayesian and Likelihood Methods

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BugReports https://github.com/rvhulst/evidence/

Depends rstan, rstanarm, loo, lattice, stats, utils, graphics, grDevices

Imports LearnBayes, LaplacesDemon,

ByteCompile TRUE

Description Bayesian (and some likelihoodist) functions as alternatives to hypothesis-testing functions in R base using a user interface patterned after those of R's hypothesis testing functions. See McElreath (2016, ISBN: 978-1-4822-5344-3), Gelman and Hill (2007, ISBN: 0-521-68689-X) (new edition in preparation) and Albert (2009, ISBN: 978-0-387-71384-7) for good introductions to Bayesian analysis and Pawitan (2002, ISBN: 0-19-850765-8) for the Likelihood approach. The functions in the package also make extensive use of graphical displays for data exploration and model comparison.

License GPL (>= 2)

NeedsCompilation no

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Contents

evidence-package   *evidence: Functions and Data for Bayesian and Likelihood Analysis*

Description

The functions in this package include Bayesian and likelihood alternatives to the standard statistical hypothesis tests that form part of base R. Their aim is to provide a wider perspective on how statistical evidence can be analyzed than the usual hypothesis-testing one. In view of the increasing importance in science of Bayesian and likelihood inference a wider exposure to these alternatives has become overdue.

This package makes Bayesian and likelihood analyses of simple statistical problems as convenient as traditional frequentist ones are in R. In addition, it makes effective use of R's excellent plotting capabilities, and facilitates exploratory data analysis and an interactive approach to modeling. Both data exploration and model exploration are crucial in data analysis, and these are facilitated by an interactive and graphics-centered approach.

Details

Package:	evidence
Type:	Package
Version:	0.8.10
Date:	2018-04-15
License:	GPL

Author(s)

Robert van Hulst

Maintainer: <rvhulst.ubishops.ca>

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

AOV1 *Made-up data for a balanced one-way anova.*

Description

Made-up data with easy numbers for practicing one-way anova by hand to understand how an anova works.

Usage

```
data(AOV1)
```

Format

A data frame with 15 observations on the following 2 variables.

y response

i predictor, a factor with 3 levels

Details

Note that the design is balanced.

Source

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

Examples

```
data(AOV1)
summary(aov(y ~ i, data=AOV1))
```

AOV2 *Made-up data for an unbalanced one-way anova.*

Description

Made-up data with easy numbers for practicing one-way anova by hand to understand how an anova works.

Usage

```
data(AOV2)
```

Format

A data frame with 22 observations on the following 2 variables:

y response

i predictor: a factor with 4 levels

Details

Note that the design is unbalanced.

Source

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

Examples

```
data(AOV2, package)
summary(aov(y ~ i, data=AOV2))
```

Aspirin   *A contingency table for heart attacks and aspirin use.*

Description

The Physicians health study data cross-classified according to Infarct (heart attack or not) and Group (Placebo or Aspirin).

Usage

```
data(Aspirin)
```

Format

A 2 by 2 matrix of counts with row names:

Infarct:Yes and Infarct:No,

and column names:

Group:placebo and Group:aspirin.

Source

Steering Committee of the Physicians' Health Study Research Group. 1989. Final report of the aspirin component of the ongoing Physicians' Health Study. N Engl J Med, 321:129–135.

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

B1Nmean   *Bayesian analysis of one sample from a Normal distribution with imprecise priors.*

Description

This function performs a standard Bayesian analysis of a single sample of a population presumably following a Normal distribution. Imprecise priors for the mean and the standard deviation are used.

Usage

```
B1Nmean(x, plotit = TRUE, hists = FALSE, pdf = FALSE)
```

Arguments

x	a vector of sample values
plotit	should the function produce plots? Defaults to TRUE.
hists	should histograms of the posterior distribution for the data with twenty posterior predictive histograms also be plotted? Defaults to FALSE.
pdf	should the histograms be saved as a pdf-file? Defaults to FALSE.

Value

none produced: text and graphical output are produced

Author(s)

Robert van Hulst

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

See Also

B1Nsir

Examples

```
## Not run:
data(Fat)
B1Nmean(Fat$Height)

## End(Not run)
```

B1Nsir   *Bayesian analysis of a Normal sample using a SIR prior.*

Description

This function performs a standard Bayesian analysis of a single sample of a population assumed to follow a Normal distribution. A Standard Improper Reference prior is assumed.

Usage

```
B1Nsir(x, r = 10000, alpha = 0.05)
```

Arguments

x	a vector of sample values
r	the number of samples to be taken from the posterior distribution (defaults to 10000)
alpha	1 - level of credibility, so that for alpha = 0.05 (the default) credible intervals will have 95% credibility

Value

none returned; the function produces a plot of the posterior distribution and prints some statistics.

Author(s)

Robert van Hulst

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

See Also

[B1Nmean](#)

Examples

```
data(darwin)
B1Nsir(darwin$difference)
```

B1prop   *Bayesian analysis of the binomial parameter for one sample.*

Description

This function computes the posterior distribution of the binomial probability π when given the number of "successes" and the sample size, as well as one of a choice of priors. A plot of the posterior distribution is produced with the 95% credible interval of π.

Usage

```
B1prop(s, n, p = 0.5, alpha = 0.05, prior = c("uniform", "near_0.5",
  "not_near_0.5", "near_0", "near_1", "custom"), params = NULL)
```

Arguments

s	the number of sampling units with the feature
n	the number of sampling units examined
p	an optional hypothesized probability
alpha	1 - alpha is the desired level of credibility of a credible interval
prior	one of: "uniform", "near_0.5", "not_near_0.5", "near_0", "near_1", "custom", which are all beta distributions with appropriate parameter values. Note that if prior="custom" the following argument has to be supplied:
params	a vector with the a and b parameters of the custom beta prior

Value

the posterior probability

Author(s)

Robert van Hulst

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

See Also

B2props

prop.test

Examples

```
B1prop(13, 100, .1, prior="near_0")
```

B1propSim   *simulates Bayesian updating of the binomial parameter π.*

Description

Provides a simple demonstration of how the posterior distribution improves as increasing amounts of data become available. A Binomial variable with a known parametric probability is sampled, and as increasing numbers of samples become available the posterior distribution is re-evaluated and plotted.

Usage

```
B1propSim(p, N = 100, prior = c("uniform", "near_0.5",
  "not_near_0.5", "near_0", "near_1"))
```

Arguments

p   the "real" binomial probability; if a number samller than 0 or one lager than 1
             isentered the function will choose an arbitrary probability

N   the number of observations to accumulate

prior   one of: "uniform", "near_0.5", "not_near_0.5", "near_0", or "near_1".

Value

none returned; the function is run for the plot it produces.

Author(s)

Robert van Hulst

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

Examples

```
B1propSim(p = 0.44, prior = "near_0.5")
```

| B2Nsir | *Bayesian analysis of the means of two Normal samples using SIR priors.* |

Description

Produces exploratory plots (boxplots and, if the sample sizes are equal), a quantile-quantile plot of the two samples. Also produces Bayesian posterior densities of the two sample means and of the difference between the means. The priors used are standard improper reference priors.

Usage

```
B2Nsir(formula, data, var.equal = TRUE, alpha = 0.05, plotit = TRUE, r = 10000)
```

Arguments

formula	the standard formula interface: response ~ factor
data	a data.frame containing the response and the two-level factor
var.equal	if TRUE the group variances are assumed to be equal, if FALSE two separate group variances are estimated
alpha	1 - level of credibility, so that for alpha = 0.05 (the default) credible intervals will have 95% credibility
plotit	should plots be produced?
r	the number of samples from the posterior distribution; can usually be left at its default value of 10000

Details

Note that in the first plot the second sub-plot is NOT a normality plot but a quantile-quantile plot that compares the observations in the two groups.

Value

none returned; the function produces several plots and prints some statistics.

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

See Also

[BnNsir](#)
[t.test](#)

Examples

```
data(bodytemp)
B2Nsir(temperature ~ gender, bodytemp)
```

B2props   *Bayesian analysis of the binomial parameters for two samples.*

Description

This function computes the posterior distributions of the binomial parameters $\pi[1]$ and $\pi[2]$ when given the numbers of "successes" and the sample sizes for the two samples. It uses uniform priors. A plot of the posterior distributions of the two π's is produced, and a plot of the posterior distribution of $\pi[1] - \pi[2]$ with its 95% credible interval.

Usage

```
B2props(s, n, alpha = 0.05)
```

Arguments

s	a vector containing the 2 numbers of sampling units with the feature ("success")
n	a vector containing the 2 numbers of sampling units examined
alpha	1 - level of credibility, so that for alpha = 0.05 (the default) credible intervals will have 95% credibility

Value

None, the inferred difference between the probabilities and its 95% credible interval is calculated and several plots are produced

Author(s)

Robert van Hulst

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

See Also

B1prop

prop.test

Examples

```
B2props(c(13, 22), c(78, 92))
```

Bft2x2   *Bayesian analysis of a 2 x 2 contingency table.*

Description

A 2 x 2 contingency table (in matrix form) is analyzed in a Bayesian way using uniform priors. The posterior probabilities of each of the the two outcomes given the other factor levels are calculated. See MacKay(2003, p. 460).

Usage

```
Bft2x2(X, div = 100, plotit = TRUE)
```

Arguments

X	a contingency table in the form of a 2 x 2 matrix with row and column names
div	optional: the number of divisions for the row and column variables for use in calculations (can be left at 100)
plotit	should plots be produced? (defaults to TRUE)

Details

Note that the rows of the 2 x 2 matrix are assumed to represent the "outcomes" and the columns the "treatments"—where these expressions are applicable. Note also that to obtain properly labeled plots the matrix has to be supplied with dimnames.

Value

the matrix of `div` x `div` posterior probabilities that was plotted

Author(s)

Robert van Hulst

References

MacKay, D.J.C. 2003. Information Theory, Inference, and Learning Algorithms. Cambridge University Press, Cambridge.

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

See Also

fisher.test

Examples

```
data(Glasses)
Bft2x2(Glasses)
```

BiasVarTO	*a simple example of the bias–variance trade-off.*

Description

A total of eight models are fitted to a data set consisting of seven predictors. The response is the exact fit with a variable amount of zero-mean noise added. This is repeated a certain number of times (by default, 100 times). Plots of Bias^2 and variance vs. the number of parameters are produced.

Usage

```
BiasVarTO(times = 100)
```

Arguments

times   the number of repeats to average bias and variance over (default 100)

Value

none produced, the function produces two plots

Author(s)

Robert van Hulst

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

---

binPriorsPlot	*function to plot diverse Beta distributions for use as Binomial priors*

Description

This function just plots some Beta distributions with commonly used parameters

Usage

```
binPriorsPlot()
```

Value

none produced, the function just produces one (compound) plot

Author(s)

Robert van Hulst

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

Examples

```
binPriorsPlot()
```

BirdsCS	*Simulated clutch size data for birds with different nesting locations.*

Description

These made-up data do respect the average clutch sizes (number of eggs laid in a single brood) and incubation periods that were observed in different European bird species with four different types of nests, as reported in Case(2000).

Usage

```
data(BirdsCS)
```

Format

A data frame with 40 observations on the following 3 variables:

Nest kind of nest, a factor with levels `hole`, `roofed`, `niche`, and `open`

Inc.Per average duration of the incubation period (days)

ClutchSize the typical number of eggs in a nest

Source

Case, T.J. An Illustrated Guide to Theoretical Ecology. Oxford University Press, New York.

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

Examples

```
data(BirdsCS)
library(graphics)
coplot(ClutchSize ~ Inc.Per | Nest, BirdsCS, panel=panel.smooth)
```

BnNsir	*Bayesian analysis of n >= 2 Normal means with standard improper reference priors.*

Description

Several exploratory plots are produced, after which this function calculates and plots the posterior densities of the treatment means and their differences. Pooled or separate variances can be specified. Note that this function uses Standard Improper Reference (SIR) priors.

Usage

```
BnNsir(formula, data, var.equal = TRUE, alpha = 0.05, plotit = TRUE,
 r = 10000)
```

Arguments

formula	the usual formula interface: response ~ factor
data	a data.frame containing the response and the factor variables
var.equal	should a pooled variance be used? Specify var.equal = FALSE if you want separate variances to be fitted
alpha	1 - level of credibility, so that for alpha = 0.05 (the default) credible intervals will have 95% credibility
plotit	are plots desired?
r	the number of samples of the posterior that should be taken

Value

none returned: the function is used for the plots and the printed information it produces

Author(s)

Robert van Hulst

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

See Also

[B2Nsir](#)

Examples

```
data(PlantGrowth)
BnNsir(weight ~ group, PlantGrowth)
```

---

bodytemp   *Data on body temperature, heart rate, and gender of 130 human subjects.*

Description

These data were collected by Mackowiak, Wasserman, and Levine(1992), and have been used, among others, by Ntzoufras(2009).

Usage

```
data(bodytemp)
```

Format

A data frame with 130 observations on the following 3 variables:

temperature body temperature in degrees Fahrenheit

gender a factor with levels 'female' and 'male'

heart.rate heart rate in beats per minute

Source

Mackowiak, P.A., Wasserman, S.S., and Levine, M.M.(1992) A critical appraisal of 98.6 degrees F, the upper limit of the normal body temperature, and other legacies of Carl Reinhold August Wunderlich. JASA 268, 1578–1580.

Ntzoufras, I.(2009) Bayesian Modeling Using Winbugs. Wiley, Hoboken, N.J.

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

Examples

```
data(bodytemp)
B2Nsir(temperature ~ gender, bodytemp)
```

Bregbf   *Bayesian regression model comparison with Bayes factors.*

Description

This function compares different linear models on the basis of their Bayes factors and by graphically comparing posterior model probabilities.

Usage

```
Bregbf(form.list, data, l=length(form.list))
```

Arguments

form.list	a list of linear models, each expressed by a model formula, that should be compared; the models must all be applicable to the same data frame and use the same response variable
data	a data frame to be analyzed
l	the number of models to be compared; defaults to all models in the form.list

Details

Note that a list containing several appropriate models for the data frame should be prepared beforehand. See the example for how to do this.

Value

A list with model parameter probabilities is silently returned.

Author(s)

Robert van Hulst

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

Examples

```
## Not run:
data(PlantGrowth)
frmlst <- list(
model0 = formula(weight ~ 1),
model1 = formula(weight ~ group) )
Bregbf(form.list=frmlst, data=PlantGrowth)
data(fev)
frmlst.fev <- list(
formula(FEV ~ Age),
formula(FEV ~ Smoke),
formula(FEV ~ Age + Smoke),
formula(FEV ~ Age * Smoke)
)
Bregbf(frmlst.fev, fev)

## End(Not run)
```

Bt.test | *Bayesian t-test using reference priors.*

Description

The Bayesian "t-test" developed by Bernardo and Perez (2007) that calculates the Bayes-factor against the null hypothesis of no difference.

Usage

```
Bt.test(formula, data, plotit = TRUE)
```

Arguments

formula   the usual formula interface: response ~ factor

data   a data.frame with the response values and the factor values for all samples; the factor can only have two factor levels

plotit   is plotted output required?

Value

none supplied: the function is used for the plotted and printed output it produces

Author(s)

Robert van Hulst

References

J. Bernardo and S. Perez. Comparing normal means: New methods for an old problem. Bayesian Analysis, 2:45–58, 2007.

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

See Also

[B2Nsir](#)

[t.test](#)

Examples

```
data(bodytemp)
Bt.test(temperature ~ gender, bodytemp)

Bt.test(heart.rate ~ gender, bodytemp)
```

budworm	*Mortality data of moth larvae due to increasing doses of insecticide.*

Description

Batches of twenty larvae were exposed to increasing doses of insecticide, and the number of survivors and their sexes were noted. These data were reported by Collett(1991) and used by Venables and Ripley(1994 and later editions). They resulted from an experiment to study the toxicity of a pyrethroid insecticide to the tobacco budworm *Heliothis virescens* of different doses of the insecticide.

Usage

```
data(budworm)
```

Format

A data frame with 12 observations on the following 3 variables:

ldose the log of the dose of the insecticide

dead the number of budworms that were dead a day later

sex a factor with two levels: "F" and "M"

Source

Collett, D. 1991. Modelling Binary Data. Chapman and Hall, London.

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

Venables, W.N. and Ripley, B.D. 1994. Modern Applied Statistics with S-PLUS. Springer Verlag, New York.

Examples

```
data(budworm)
fit <- glm(cbind(dead, 20 - dead) ~ ldose, data=budworm,
family=binomial)
summary(fit)
```

Clin   *Made-up data to illustrate Simpson's paradox.*

Description

These made-up data illustrate the discrete form (contingency table form) of Simpson's paradox.

Usage

```
data(Clin)
```

Format

A three-dimensional array of frequencies with:

rows indicating "outcome" (either "death" or "cured"),

columns indicating "male" (either "Yes" or "No"), and

layers indicating "clinic" (either "A" or "B").

Source

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

Examples

```
data(Clin)
Clin[1,,]
prop.table(Clin[1,,], 2)
```

---

crickets   *Made-up data that are not unlike the actual data collected by Nespolo et al.(2003).*

Description

Nespolo et al.(2003) collected data on the metabolic rates (as measured by oxygen consumption) of crickets kept and acclimated at three different temperatures. Since the original data were not available and only a statistical summary was published, we simulated these data to approximately agree with the statistical summary.

Usage

```
data(crickets)
```

Format

A data frame with 292 observations on the following 3 variables:

VO2 oxygen consumption in μl/h (a measure of basal metabolic rate)

mass weight of the cricket in mg

temp temperature in degrees C.

Source

Nespolo et al., 2003.

References

Nespolo, R.F., Lardies, M.A., and Bozinovic, F. 2003. Intrapopulational variation in the standard metabolic rate of insects: repeatability, thermal dependence and sensitivity of (Q[10]) on oxygen consumption in a cricket. Journal of Experimental Biology 206, 4309–4315.

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

Examples

```
data(crickets)
crickets7 <- subset(crickets, crickets$temp==7)
with(crickets7, scatter.smooth(mass, VO2))
```

CTA   *Contingency Table Analysis in different ways*

Description

An n x n contingency table is analyzed in frequentist, information-theoretical, likelihood, and Bayesian ways. Note that for the Bayesian analysis package LearnBayes needs to be installed.

Usage

```
CTA(X, extBayes = FALSE)
```

Arguments

X	a matrix with non-negative integers representing the counts for the row-column levels
extBayes	should a Bayesian analysis with a near-independence prior (instead of only an independence prior) be done as well? Defaults to FALSE.

Value

none provided: the function is run for its graphical and numerical output

Author(s)

Robert van Hulst

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

See Also

[Bft2x2](Bft2x2)

Examples

```
data(Smoking)
CTA(Smoking)
```

---

darwin   *Charles Darwin's (1876) data on the fecundity of selfed and crossed corn plants.*

Description

Charles Darwin(1876) provided data on the difference in the heights attained by selfed and crossed mother plants.

Usage

```
data(darwin)
```

Format

A data frame with 15 observations on the following variable:

difference   the difference in height in inches between each paired pair of offspring of a selfed and a crossed mother plant

Source

Darwin, C.R. 1876. The effects of cross and self fertilisation in the vegetable kingdom. John Murray, London.

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

Examples

```
data(darwin)
with(darwin, qqnorm(difference) )
with(darwin, qqline(difference) )
```

Fat   *Human body fat and several covariates for calculating it.*

Description

Data from Johnson (1996) on human body fat: determined by under-water weight and several covariates to estimate it statistically.

Usage

```
data(Fat)
```

Format

A data frame with 252 observations on the following 19 variables:

Case case number

PBF.B percentage body fat estimated using Brozek's equation

PBF.S percentage body fat estimated using Siri's equation

Dens Density (gm/cm^3)

Age Age (yrs)

Weight Weight (lbs)

Height Height (inches)

AI Adiposity index = Weight/Height^2 (kg/m^2)

FFWt Fat Free Weight using Brozek's formula (lbs)

Neck Neck circumference (cm)

Chest Chest circumference (cm)

Abd Abdomen circumference (cm)

Hip Hip circumference (cm)

Thigh Thigh circumference (cm)

Knee Knee circumference (cm)

Ankle Ankle circumference (cm)

Biceps Extended biceps circumference (cm)

FArm Forearm circumference (cm)

Wrist Wrist circumference (cm)

Source

Johnson, R. 1996. Fitting percentage of body fat to simple body measurements. Journal of Statistics Education 2(1), 1–6.

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

Examples

```
data(Fat)
qqnorm(Fat$Height)
qqline(Fat$Height)
```

---

fev   *Data on lung capacity of 654 children and adolescents.*

Description

These data come from Rosner (2006), and represent forced expiratory volume (FEV) in l/s and several covariates.

Usage

```
data(fev)
```

Format

A data frame with 654 observations on the following 6 variables:

Id an identification code

Age age in years

FEV forced expiratory volume in l/s

Hgt height in inches

Sex gender: 0 for female, 1 for male

Smoke smokes (1) or not (0)

Source

Rosner, B. 2006. Fundamentals of Biostatistics. 6th ed. Duxbury Press.

Examples

```
data(fev)
splom(fev[c(3, 2, 4, 5, 6)], main="fev data")
```

| Glasses | *A contingency table of 16 British youths categorized as juvenile delinquents or not, and as wearing glasses or not.* |

Description

Data from Heidelberger and Holland(2004) categorizing a random sample of 16 British juveniles on the basis of whether they were juvenile delinquents or not, and whether wore glasses or not.

Usage

```
data(Glasses)
```

Format

A matrix with 16 counts cross-classified on Juvenile delinquency (rows) and the wearing of glasses (columns).

Source

Heiberger, R.M. and Holland, B.(2004) Statistical Analysis and Data Display: An Intermediate Course with Examples in S-PLUS, R, and SAS. Springer, New York.

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

Examples

```
data(Glasses)
Bft2x2(Glasses)
```

| HPDcrd | *generates the 100 * (1 - alpha)% most probable interval of a distribution of empirical values* |

Description

function used to produce a Bayesian credible interval of a unimodal distribution of empirical values using the Highest Posterior Probability approach

Usage

```
HPDcrd(x, alpha = 0.05)
```

Arguments

x	a vector of empirical values
alpha	1 - alpha is the desired level of credibility

Value

a vector of the lower and upper limits of the 95% credible interval calculated using a standard algorithm

Author(s)

Robert van Hulst

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

Examples

```
HPDcrd(rnorm(1000))
```

HSCrab   *Morphology of horseshoe crabs.*

Description

Data on horseshoe crab morphology collected by Brockman(1996) and used by Agresti(2012).

Usage

```
data(HSCrab)
```

Format

A data frame with 173 observations on the following 5 variables:

Col an indicator variable for the carapace color

spineW coded width of the spine

Width maximal width of the carapace (cm)

Satell number of satellite males

Weight weight in g

Source

Brockman, H.J.(1996) Satellite male groups in horseshoe crabs, *Limulus polyphemus* Ethology 102(1), 1–21.

References

Agresti, A.(2012) Categorical Data Analysis (3rd ed.) Wiley, New York.

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

Examples

```
data(HSCrab)
plot(Weight ~ Width, col = Col, data = HSCrab)
```

L1prop   *Likelihood analysis of the binomial parameter for one sample.*

Description

When given the number of "successes" and the sample size this function plots the normed likelihood of values of the binomial parameter π and calculates the likelihood ratio for a hypothesized value and the maximum likelihood value for the sample, as well as an approximate frequentist p-value.

Usage

```
L1prop(x, n, p.hypoth, pLset=0.05)
```

Arguments

x	the number of sampling units with the feature
n	the number of sampling units examined
p.hypoth	the hypothesized probability
pLset	the desired likelihood for the likelihood interval

Value

none, the normed likelihood for different values of the binomial probability is plotted with the likelihood interval, and some information is printed

Author(s)

Robert van Hulst

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

Pawitan, Y. 2001. In All Likelihood. Oxford University Press, Oxford.

See Also

B1prop

prop.test

Examples

```
L1prop(13, 78, 0.02)
```

L2prop   *Likelihood analysis of the binomial parameters for two samples.*

Description

When given the numbers of "successes" and the sample sizes for the two samples, this function plots the normed likelihoods of the two samples and calculates the likelihood ratio for two different models, one fitting two binomial parameters, and one fitting only one.

Usage

```
L2prop(x, n)
```

Arguments

x   a vector containing the 2 numbers of sampling units with the feature

n   a vector containing the 2 numbers of sampling units examined

Value

none, the inferred difference between the probabilities and its 95% credible interval are calculated and a plot is produced

Author(s)

Robert van Hulst

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

See Also

[B1prop](#)

[prop.test](#)

Examples

```
L2prop(c(13, 22), c(78, 92))
```

---

lightspeed   *Simon Newcomb's measurements of the speed of light*

Description

Simon Newcom's measured in the late 1900's the time it took light to cover a certain distance. The data are reported in Stigler(1977) and have been widely used since to illustrate statistical inference.

Usage

```
data(lightspeed)
```

Format

A vector with 66 observations of the travel time of light.

Source

Stigler, S.M. (1977) Do robust estimators work with real data? Annals of Statistics 5, 1055–1098.

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

Examples

```
data(lightspeed)
qqnorm(lightspeed)
qqline(lightspeed)
```

---

looicplot   *A dot plot is produced for several related models showing for each model its LOOIC-value with its credible interval.*

Description

The LOOIC-value (like the non-Bayesian AIC-value) is a useful measure of model performance for model prediction.

Usage

```
looicplot(looiclist, modnames, perc = 90)
```

Arguments

`looiclist`	a list of character-valued names of rstanarm model objects
`modnames`	a character-valued vector of model names for each of the models
`perc`	the percentage credibility for the credible intervals (defaults to 90%)

Value

None provided, but a printed list of looic-values, their standard errors, and credible intervals, and a dot plot with the same information are produced.

Author(s)

Robert van Hulst

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

See Also

dotchart

Examples

```
## Not run:
data(budworm)
Mbudworm1 <- stan_glm(formula = cbind(dead, 20 - dead) ~ ldose,
                      family = binomial, data = budworm,
                      prior = student_t(df = 7),
                      prior_intercept = student_t(df = 7))
Mbudworm2 <- stan_glm(formula = cbind(dead, 20 - dead) ~ ldose * sex,
                      family = binomial, data = budworm,
                      prior = student_t(df = 7),
                      prior_intercept = student_t(df = 7))
Mbudworm3 <- stan_glm(formula = cbind(dead, 20 - dead) ~ ldose + sex,
                      family = binomial, data = budworm,
                      prior = student_t(df = 7),
                      prior_intercept = student_t(df = 7))
looicplot(looiclist = list("Mbudworm1", "Mbudworm2", "Mbudworm3"),
          modnames = c("~ ldose", "~ ldose + sex", "~ ldose * sex") )

## End(Not run)
```

---

meansplot	*Plots a simple strip chart of the observations with group means and grand mean.*

Description

A strip chart of the first argument grouped by the second argument is produced. This function is useful for looking at experimental data with a numeric response and a factorial predictor.

Usage

```
meansplot(y, grp)
```

Arguments

y   a vector of observed values

grp   a factor of the same length as the observation vector indicating the treatment under which each observation was obtained

Value

none returned: the function is used for the plot it produces

Author(s)

Robert van Hulst

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

See Also

stripchart

Examples

```
data(PlantGrowth)
with(PlantGrowth, meansplot(weight, group))
```

MedDiagn	*Computes the posterior probability of having a certain disease from prevalence, sensitivity, and specificity data.*

Description

If experimental data on the sensitivity and the specificity of a diagnostic test are available, and the prevalence of the the condition is known with its raw data, then this function estimates the posterior probability of having the condition, with its 95% credible interval.

Usage

```
MedDiagn(x0, n0, x1, n1, x2, n2, N = 10000,
  alpha = 0.05, pdf = FALSE)
```

Arguments

x0	prevalence raw data: number of people with a certain condition
n0	number of people examined for that condition
x1	sensitivity data: number of people with the disease for whom this test was positive
n1	total number of people in the sensitivity sample
x2	specificity raw data: number of people who did not have the disease who tested negative
n2	total number of people in the specificity sample
N	number of cases to be simulated (best left at 10000 or greater
alpha	credibility required (default 95%)
pdf	set this to TRUE only if you want to keep a pdf-file of the posterior probability plot

Value

none returned: a plot and printed information are produced

Author(s)

Robert van Hulst

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

Examples

```
MedDiagn(105, 35000, 72, 80, 640, 800)
```

| nineplot | *produces a Normality plot for the argument surrounded by eight other Normality plots for Normal distributions having the same mean and standard deviation as the argument* |

Description

Normality plots can be hard to judge if one is not experienced. This function plots a Normality plot for the data surrounded by eight other Normality plots for samples with the same mean and standard deviation that were randomly generated. The eight plots provide an idea of the variability to be expected in Normally distributed data.

Usage

```
nineplot(x)
```

Arguments

x   a vector of observations to be examined for Normality

Value

none produced: the function is used for the plot it produces

Author(s)

Robert van Hulst

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

See Also

qqnorm

Examples

```
nineplot(rt(100, 2))
```

NPV   *computes the Negative Predictive Value.*

Description

The negative predictive value (NPV) of a diagnostic test is the probability that someone with a negative diagnostic test for a condition does not have the condition. The NPV can easily be calculated from the prevalence, the sensitivity, and the specificity, but this function automates the procedure.

Usage

```
NPV(sens, spec, prev)
```

Arguments

sens   the sensitivity of the test

spec   the specificity of the test

prev   the prevalence of the disease

Value

the negative predictive value

Author(s)

Robert van Hulst

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

See Also

PPV

Examples

```
NPV(0.9, 0.8, 0.003)
```

---

overdispersionCheck   *A robust comparison of the location and the scale of the input vector.*

Description

A large sample of Normal-distributed data with more than 10% of the observations further than 1.5 times the IQR from the median shows signs of overdispersion, as recommended in Gelman et al., 2014.

Usage

```
overdispersionCheck(x)
```

Arguments

x   an input vector of reals without missing values

Value

The function prints the approximate percentage of observations that are further from the median than would be expected in a normal distribution.

Author(s)

Robert van Hulst

References

Gelman, A., Carlin, J.B., Stern, H.S., Dunson, D.B., Vehtari, A., and Rubin, D.B. 2014. Bayesian Data Analysis. Third Ed.. CRC Press

Examples

```
overdispersionCheck(rt(100, 1))
```

---

p2BF   *Conversion of a frequentist p-value to the lower bound of the Bayes factor against the null hypothesis assuming equal odds of the null and the alternative*

Description

This function computes the approximate lower bound to the Bayes factor of the null hypothesis against the alternative, assuming equal odds of the null and the alternatIve.

Usage

```
p2BF(p)
```

Arguments

p   the frequentist p-value (which has to be less than 1/e or 0.37)

Value

the approximate lower bound of the Bayes factor of the null hypothesis against the alternative

Note

the p-value should be less than 1/e (= 0.37).

Author(s)

Robert van Hulst

References

Sellke, T., Bayarri, M.J., and Berger, J.O. 2001. Calibration of p Values for Testing Precise Hypotheses. Am. Statistician 55(1) pp 62–71.

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

See Also

[p2minpp](#)

Examples

```
p2BF(p = 0.05)
```

---

p2minpp   *Conversion of a frequentist p-value to a lower bound of the posterior*
                                          probability that the null hypothesis is true assuming equal odds of the
                                          null and the alternative

---

Description

This function computes the approximate lower bound to the posterior probability of the null hypothesis assuming equal odds of the null and the alternative. See Sellke et al.(2001) for the derivation, and note that the posterior probability of the null hypothesis is what many incorrectly assume the p-value is measuring.

Usage

```
p2minpp(p)
```

Arguments

p	the frequentist p-value (which has to be less than 1/e or 0.37)

Value

the approximate lower bound of the posterior probability of the null hypothesis

Note

the p-value should be less than 1/e (0.37).

Author(s)

Robert van Hulst

References

Sellke, T., Bayarri, M.J., and Berger, J.O. 2001. Calibration of p Values for Testing Precise Hypotheses. Am. Statistician 55(1) pp 62–71.

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

See Also

[p2BF](p2BF)

Examples

```
p2minpp(p=0.05)
```

PPV   *calculates the positive predictive value (PPV) of a diagnostic test.*

Description

The positive predictive value (PPV) of a dianostic test is the probability that someone with a positive diagnostic test for a condition does have the condition. The PPV can easily be calculated from the prevalence, the sensitivity, and the specificity, but this function automates the procedure.

Usage

```
PPV(sens, spec, prev)
```

Arguments

sens	the sensitivity of the test
spec	the specificity of the test
prev	the prevalence of the disease

Value

the positive predictive value of the test

Author(s)

Robert van Hulst

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

See Also

[NPV](#)

Examples

```
PPV(0.9, 0.8, 0.003)
```

---

rats	*Carcinogenesis data on rats exposed to a carcinogen.*

Description

Up to forty eight rats were exposed to the carcinogen retinyl acetate or to a placebo in their diet, after which the number of tumors they developed was evaluated.

Usage

```
data(rats)
```

Format

A data frame with 71 observations on the following 2 variables:

y number of rats that developed tumors

N number of rats in group

Source

Gail, M.H., Santner, T.J., and Brown, C.C. (1980) An analysis of comparative carcinogenesis experiments based on multiple times to tumor. Biometrics 36, 255–266.

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

---

sigtestCI   *Universal Fisherian significance test with confidence interval.*

Description

Given a critical value alpha, this function performs a Fisherian significance test of the null hypothesis at level p, reports the result of the test, as well as the lower and upper values of the corresponding confidence interval. See Kadane(2016) for the idea for this.

Usage

```
sigtestCI(p)
```

Arguments

p   the desired significance level

Details

Note that this function does not require any data: if a rare (as long as p is sufficiently small) event occurs, H[0] is deemed to be implausible, and rejected. If such an event does not occur, we can simply try to do the experiment again. A Neyman-Pearson hypothesis test does require data and also an alternative hypothesis. For a NP hypothesis test we can (and should) consider the power of the test (the probability of rejecting H[0] when H[a] is true).

Value

A message informing the user if H0 was rejected or not and the lower and upper boundaries of the corresponding confidence interval.

Author(s)

Robert van Hulst

References

Kadane, J.B. 2016. Beyond hypothesis testing. Entropy 18, 199.

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

Examples

```
sigtestCI(p=0.05)
```

Smoking   *Mortality due to heart infarct in smokers and non-smokers.*

Description

The data are from a retrospective study that compared mortality due to a heart infarct in people who smoked and sex-matched controls who did not.

Usage

```
data(Smoking)
```

Format

A matrix with 781 observations cross-classified on the following 2 factors: "Infarct" ("Yes" or "Control", rows), and "EverSmoked" ("Yes" or "No", columns).

Source

unknown

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

---

sn2ft2x2   *Conversion of 2 props input to 2x2 contingency table*

Description

This function converts the successes and totals vectors required as input for function B2props to a 2x2 contingency table for input to CTA or Bft2x2.

Usage

```
sn2ft2x2(s, n)
```

Arguments

s	a vector of length 2 of successes
n	a vector of length 2 of numbers of trials

Value

a 2 x 2 contingency table equivalent to the two arguments

Author(s)

Robert van Hulst

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

Examples

```
sn2ft2x2(c(47, 59), c(120, 125))
```

Snoring	*Data on the incidence of hypertension and three indicator variables.*

Description

A total of 433 persons were tested for hypertension and checked for whether they were smokers, obese, or snored. The data are in Altman(1991).

Usage

```
data(Snoring)
```

Format

A data frame with 8 observations on the following 5 variables:

smoking did the person smoke (1) or not (0)?

obese was the person obese (1) or not (0)?

snoring did the person snore (1) or not (0)?

n the number of persons observed with these covariates

hypert did the person suffer from hypertension (1) or not (0)?

Source

Altman, D.G. 1991. Practical Statistics for Medical Research. Chapman \& Hall, London.

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

Examples

```
data(Snoring)
fit <- glm(cbind(hypert, n - hypert) ~ smoking + obese + snoring,
  family=binomial, data=Snoring)
summary(fit)
```

SRb94   *Data of the growth of tissue cultures on five different media.*

Description

These data came from a designed experiment reported in Sokal and Rohlf(1995), box 9.4. The growth (in arbitrary units) of pea sections grown in tissue culture on five different sugars was replicated ten times.

Usage

```
data(SRb94)
```

Format

A data frame with 50 observations on the following 2 variables:

L length difference in mm

Treatm a factor with levels "Contr", "fruct.", "gluc.", "gluc&fruct.", and "sucr."

Source

Sokal, R.R., and Rohlf, F.J. Biometry. Freeman, New York.

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

Examples

```
data(SRb94)
with(SRb94, meansplot(L, Treatm))
```

SSQ   *A support function that calculates the sum of squares of a data vector.*

Description

The sum of squares of the input vector is returned.

Usage

```
SSQ(x)
```

Arguments

x   a vector of numbers without missing values

Value

the sum of squares of x

Author(s)

Robert van Hulst

Examples

```
SSQ(x = rnorm(n=100))
```

---

sumchart	*Plotting routine for dataframes of looic values.*

Description

Produces a dotchart with error bars as summary of a dataframe with model names ('modnames'), LOOIC-values ('looic'), standard errors ('se'), lower values ('lwr'), and upper values ('upr') .

Usage

```
sumchart(df, rownames, groups, perc)
```

Arguments

df	data.frame name
rownames	model names
groups	row names
perc	the percentage of credibility desired

Value

A plot is produced.

Author(s)

Robert van Hulst

References

van Hulst, R. 2018. Evaluating Scientific Evidence. ms.

See Also

dotchart

weightgain	*weight gain in rats*

Description

Rats were fed diets with different quantities of protein from either animal or plant sources. The weight gained at the end of the experiment was the response variable.

Usage

```
data("weightgain")
```

Format

A data frame with 40 observations on the following 3 variables

source source of protein given, a factor with levels Beef and Cereal

type amount of protein given, a factor with levels High and Low

weightgain weight gain in grams

Source

Hand, D.J., Daly, F., Lunn, A.D., McConway, K.J. and Ostrowski, E. 1994. A Handbook of Small Datasets, Chapman and Hall, London.

Examples

```
data("weightgain")
with(weightgain, table(source, type))
```

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