Package ‘BayesGOF’

October 12, 2022

Type Package

Title Bayesian Modeling via Frequentist Goodness-of-Fit

Version 5.2

Date 2018-10-09

Author Subhadeep Mukhopadhyay, Douglas Fletcher

Maintainer Doug Fletcher <tug25070@temple.edu>

Description A Bayesian data modeling scheme that performs four interconnected tasks: (i) characterizes the uncertainty of the elicited parametric prior; (ii) provides exploratory diagnostic for checking prior-data conflict; (iii) computes the final statistical prior density estimate; and (iv) executes macro- and micro-inference. Primary reference is Mukhopadhyay, S. and Fletcher, D. 2018 paper `Generalized Empirical Bayes via Frequentist Goodness of Fit` (<https://www.nature.com/articles/s41598-018-28130-5 >).

Depends orthopolynom, VGAM, Bolstad2, nleqslv

Suggests knitr, rmarkdown

VignetteBuilder knitr

License GPL-2

NeedsCompilation no

Repository CRAN

Date/Publication 2018-10-09 21:50:09 UTC

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BayesGOF-package

Bayesian Modeling via Frequentist Goodness-of-Fit

Description

A Bayesian data modeling scheme that performs four interconnected tasks: (i) characterizes the uncertainty of the elicited parametric prior; (ii) provides exploratory diagnostic for checking prior-data conflict; (iii) computes the final statistical prior density estimate; and (iv) executes macro- and micro-inference.

References


arsenic

Arsenic levels in oyster tissue

Description

Results from an inter-laboratory study involving k = 28 measurements for the level of arsenic in oyster tissue. y is the mean level of arsenic from a lab and se is the standard error of the measurement.

Usage

data(“arsenic”)
AutoIns

**Format**

A data frame of \((y_i, se_i)\) for \(i = 1, \ldots, 28\).

- \(y\): mean level of arsenic in the tissue measured by the \(i^{th}\) lab
- \(se\): the standard error of the measurement by \(i^{th}\) lab

**Source**


<table>
<thead>
<tr>
<th>AutoIns</th>
<th>Number of claims on an insurance policy</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Description**

The number of claims on an automobile insurance policy made by \(k = 9461\) individuals during a single year.

**Usage**

```r
data("AutoIns")
```

**Format**

A vector of length 9461.

- value: number of auto insurance claims by the \(i^{th}\) person

**Source**


<table>
<thead>
<tr>
<th>ChildIll</th>
<th>Frequency of child illness</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Description**

Results of a study that followed \(k = 602\) pre-school children in north-east Thailand from June 1982 through September 1985. Researchers recorded the number of times a child became ill during every 2-week period.

**Usage**

```r
data("ChildIll")
```
**Format**

A vector of length \( k = 602 \).

\[ \text{value} \] number of times the \( i^{th} \) child became ill during the study

**Source**


---

<table>
<thead>
<tr>
<th>CorbBfly</th>
<th>Corbet's Butterfly data</th>
</tr>
</thead>
</table>

**Description**

The number of times Alexander Corbet captured a species of butterfly during a two-year period in Malaysia.

**Usage**

```r
data("CorbBfly")
```

**Format**

A vector of length \( k = 501 \).

\[ \text{value} \] number of times Corbet captured the \( i^{th} \) species

**Source**


**References**

Description

A function that calculates the full entropy of a DS(G,m) prior. For DS(G,m) with \( m > 0 \), also returns the excess entropy \( qLP \).

Usage

\[
\text{DS.entropy(DS.GF.obj)}
\]

Arguments

- **DS.GF.obj**: Object resulting from running DS.prior function on a data set.

Value

- **ent**: The total entropy of the DS(G,m) prior where \( m \geq 0 \).
- **qLP**: The excess entropy when \( m > 0 \).

Author(s)

Doug Fletcher

References


Examples

```r
data(rat)
rat.start <- gMLE.bb(rat$y, rat$n)$estimate
rat.ds <- DS.prior(rat, max.m = 4, rat.start, family = "Binomial")
DS.entropy(rat.ds)
```
DS.Finite.Bayes

Conduct Finite Bayes Inference on a DS object

Description

A function that generates the finite Bayes prior and posterior distribution, along with the Bayesian credible interval for the posterior mean.

Usage

```r
DS.Finite.Bayes(DS.GF.obj, y.0, n.0 = NULL,
                 cred.interval = 0.9, iters = 25)
```

Arguments

- **DS.GF.obj**: Object from `DS.prior`.
- **y.0**: For Binomial family, number of success $y_i$ for new study. In the Poisson family, it is the number of counts. Represents the study mean for the Normal family.
- **n.0**: For the Binomial family, the total number of trials for the new study. In the Normal family, $n.0$ is the standard error of $y.0$. Not used for the Poisson family.
- **cred.interval**: The desired probability for the credible interval of the posterior mean; the default is 0.90 (90%).
- **iters**: Integer value of total number of iterations.

Value

- **prior.fit**: Fitted values for the estimated parametric, DS, and finite Bayes prior distributions.
- **post.fit**: Dataframe with $\theta$, $\pi_G(\theta|y_0)$, and $\pi_{LP}(\theta|y_0)$.
- **interval**: The 100*cred.interval% Bayesian credible interval for the posterior mean.
- **post.vec**: Vector containing the PEB posterior mean (PEB.mean), DS posterior mean (DS.mean), PEB posterior mode (PEB.mode), and the DS posterior mode (DS.mode).

Author(s)

Doug Fletcher, Subhadeep Mukhopadhyay

References


Examples

```
## Not run:
### Finite Bayes: Rat with theta_71 (y_71 = 4, n_71 = 14)
data(rat)
rat.start <- gMLE.bb(rat$y, rat$n)$estimate
rat.ds <- DS.prior(rat, max.m = 4, rat.start, family = "Binomial")
rat.FB <- DS.FiniteBayes(rat.ds, y.0 = 4, n.0 = 14)
plot(rat.FB)
```

## End(Not run)

---

**DS.macro.inf**

Execute MacroInference (mean or mode) on a DS object

---

**Description**

A function that generates macro-estimates with their uncertainty (standard error).

**Usage**

```
DS.macro.inf(DS.GF.obj, num.modes = 1, 
method = c("mean", "mode"),
iters = 25, exposure = NULL)
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>DS.GF.obj</td>
<td>Object from DS.prior.</td>
</tr>
<tr>
<td>num.modes</td>
<td>The number of modes indicated by DS.prior object.</td>
</tr>
<tr>
<td>method</td>
<td>Returns mean or mode(s) (based on user choice) along with the associated standard error(s).</td>
</tr>
<tr>
<td>iters</td>
<td>Integer value of total number of iterations.</td>
</tr>
<tr>
<td>exposure</td>
<td>In the case where DS.GF.obj is from a Poisson family with exposure, exposure is the vector of exposures. Otherwise, the default is NULL.</td>
</tr>
</tbody>
</table>

**Value**

<table>
<thead>
<tr>
<th>Value</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>DS.GF.macro.obj</td>
<td>Object of class DS.GF.macro associated with either mean or mode.</td>
</tr>
<tr>
<td>model.modes</td>
<td>For method = &quot;mode&quot;, returns mode(s) of estimated DS prior.</td>
</tr>
<tr>
<td>mode.sd</td>
<td>For method = &quot;mode&quot;, provides the bootstrapped standard error for each mode.</td>
</tr>
<tr>
<td>boot.modes</td>
<td>For method = &quot;mode&quot;, returns all generated mode(s).</td>
</tr>
<tr>
<td>model.mean</td>
<td>For method = &quot;mean&quot;, returns mean of estimated DS prior.</td>
</tr>
<tr>
<td>mean.sd</td>
<td>For method = &quot;mean&quot;, provides the bootstrapped standard error for the mean.</td>
</tr>
<tr>
<td>boot.mean</td>
<td>For method = &quot;mean&quot;, returns all generated means.</td>
</tr>
<tr>
<td>prior.fit</td>
<td>Fitted values of estimated prior imported from the DS.prior object.</td>
</tr>
</tbody>
</table>
Author(s)

Doug Fletcher, Subhadeep Mukhopadhyay

References


Examples

```r
## Not run:
### MacroInference: Mode
data(rat)
rat.start <- gMLE.bb(rat$y, rat$n)$estimate
rat.ds <- DS.prior(rat, max.m = 4, rat.start, family = "Binomial")
rat.ds.macro <- DS.macro.inf(rat.ds, num.modes = 2, method = "mode", iters = 5)
rat.ds.macro
plot(rat.ds.macro)

### MacroInference: Mean
data(ulcer)
ulcer.start <- gMLE.nn(ulcer$y, ulcer$se)$estimate
ulcer.ds <- DS.prior(ulcer, max.m = 4, ulcer.start)
ulcer.ds.macro <- DS.macro.inf(ulcer.ds, num.modes = 1, method = "mean", iters = 5)
ulcer.ds.macro
plot(ulcer.ds.macro)
## End(Not run)
```

DS.micro.inf

MicroInference for DS Prior Objects

Description

Provides DS nonparametric adaptive Bayes and parametric estimate for a specific observation \(y_0\).

Usage

`DS.micro.inf(DS.GF.obj, y.0, n.0, e.0 = NULL)`

Arguments

- **DS.GF.obj**: Object resulting from running `DS.prior` function on a data set.
- **y.0**: For Binomial family, number of success \(y_i\) for new study. In the Poisson family, it is the number of counts. Represents the study mean for the Normal family.
- **n.0**: For the Binomial family, the total number of trials for the new study. In the Normal family, \(n.0\) is the standard error of \(y.0\). Not used for the Poisson family.
- **e.0**: In the case of the Poisson family with exposure, represents the exposure value for a given count value \(y.0\).
Details

Returns an object of class DS.GF.micro that can be used in conjunction with plot command to display the DS posterior distribution for the new study.

Value

- **DS.mean**: Posterior mean for $\pi_{LP}(\theta|y_0)$.
- **DS.mode**: Posterior mode for $\pi_{LP}(\theta|y_0)$.
- **PEB.mean**: Posterior mean for $\pi_G(\theta|y_0)$.
- **PEB.mode**: Posterior mode for $\pi_G(\theta|y_0)$.
- **post.vec**: Vector containing PEB.mean, DS.mean, PEB.mode, and DS.mode.
- **study**: User-provided $y_0$ and $n_0$.
- **post.fit**: Dataframe with $\theta$, $\pi_G(\theta|y_0)$, and $\pi_{LP}(\theta|y_0)$.

Author(s)

Doug Fletcher, Subhadeep Mukhopadhyay

References


Examples

```r
### MicroInference for Naval Shipyard Data: sample where y = 0 and n = 5
data(ship)
ship.ds <- DS.prior(ship, max.m = 2, c(.5,.5), family = "Binomial")
ship.ds.micro <- DS.micro.inf(ship.ds, y.0 = 0, n.0 = 5)
plot(ship.ds.micro)
```

---

**DS.posterior.reduce**  \hspace{1cm} *Posterior Expectation and Modes of DS object*

Description

A function that determines the posterior expectations $E(\theta_0|y_0)$ and posterior modes for a set of observed data.

Usage

```r
DS.posterior.reduce(DS.GF.obj, exposure)
```
Arguments

- **DS.GF.obj**: Object resulting from running DS.prior function on a data set.
- **exposure**: In the case of the Poisson family with exposure, represents the exposure values for the count data.

Value

Returns $k \times 4$ matrix with the columns indicating PEB mean, DS mean, PEB mode, and DS modes for $k$ observations in the data set.

Author(s)

Doug Fletcher

References


Examples

```r
data(rat)
rat.start <- gMLE.bb(rat$y, rat$n)$estimate
rat.ds <- DS.prior(rat, max.m = 4, rat.start, family = "Binomial")
DS.posterior.reduce(rat.ds)
```

Description

A function that generates the uncertainty diagnostic function (U-function) and estimates DS($G,m$) prior model.

Usage

```r
DS.prior(input, max.m = 8, g.par,
          family = c("Normal","Binomial", "Poisson"),
          LP.type = c("L2", "MaxEnt"),
          smooth.crit = "BIC", iters = 200, B = 1000,
          max.theta = NULL)
```
**Arguments**

- **input**: For "Binomial", a dataframe that contains the $k$ pairs of successes $y$ and the corresponding total number of trials $n$. For "Normal", a dataframe that has the $k$ means $y_i$ in the first column and their respective standard errors $s_i$ in the second. For the "Poisson", a vector of that includes the untabled count data.

- **max.m**: The truncation point $m$ reflects the concentration of true unknown $\pi$ around known $g$.

- **g.par**: Vector with estimated parameters for specified conjugate prior distribution $g$ (i.e beta prior: $\alpha$ and $\beta$; normal prior: $\mu$ and $\tau^2$; gamma prior: $\alpha$ and $\beta$).

- **family**: The distribution of $y_i$. Currently accommodates three families: Normal, Binomial, and Poisson.

- **LP.type**: User selects either "L2" for LP-orthogonal series representation of $U$-function or "MaxEnt" for the maximum entropy representation. Default is L2.

- **smooth.crit**: User selects either "BIC" or "AIC" as criteria to both determine optimal $m$ and smooth final LP parameters; default is "BIC".

- **iters**: Integer value that gives the maximum number of iterations allowed for convergence; default is 200.

- **B**: Integer value for number of grid points used for distribution output; default is 1000.

- **max.theta**: For "Poisson", user can provide a maximum theta value for prior; default is the maximum count value in input.

**Details**

Function can take $m = 0$ and will return the Bayes estimate with given starting parameters. Returns an object of class DS.GF.obj; this object can be used with plot command to plot the U-function (Ufunc), Deviance Plots (mDev), and DS-G comparison (DS_G).

**Value**

- **LP.par**: $m$ smoothed LP-Fourier coefficients, where $m$ is determined by maximum deviance.

- **g.par**: Parameters for $g$.

- **LP.max.uns**: Vector of all LP-Fourier coefficients prior to smoothing, where the length is the same as max.m.

- **LP.max.smt**: Vector of all smoothed LP-Fourier coefficients, where the length is the same as max.m.

- **prior.fit**: Fitted values for the estimated prior.

- **UF.data**: Dataframe that contains values required for plotting the U-function.

- **dev.df**: Dataframe that contains deviance values for values of $m$ up to max.m.

- **m.val**: The value of $m$ (less than or equal to the maximum $m$ from user) that has the maximum deviance and represents the appropriate number of LP-Fourier coefficients.

- **sm.crit**: Smoothing criteria; either "BIC" or "AIC".
The user-selected family.

User-selected representation of U-function.

The observed data provided by the user for input.

Author(s)

Doug Fletcher, Subhadeep Mukhopadhyay

References


Examples

```r
data(rat)
rat.start <- gMLE.bb(rat$y, rat$n)$estimate
rat.ds <- DS.prior(rat, max.m = 4, rat.start, family = "Binomial")
rat.ds
plot(rat.ds, plot.type = "Ufunc")
plot(rat.ds, plot.type = "DSg")
plot(rat.ds, plot.type = "mDev")
```

---

**DS.sampler**

Samples data from DS(G,m) distribution.

Description

Generates samples of size $k$ from DS(G, m) prior distribution.

Usage

```
DS.sampler(k, g.par, LP.par, con.prior, LP.type, B)
```

```
DS.sampler.post(k, g.par, LP.par, y.0, n.0, con.prior, LP.type, B)
```

Arguments

- **k**
  - Total number of samples requested.

- **g.par**
  - Estimated parameters for specified conjugate prior distribution (i.e beta prior: $\alpha$ and $\beta$; normal prior: $\mu$ and $\tau^2$; gamma prior: $\alpha$ and $\beta$).

- **LP.par**
  - LP coefficients for DS prior.

- **con.prior**
  - The distribution type of conjugate prior $g$; either "Beta", "Normal", or "Gamma".
LP.type  The type of LP means, either "L2" or "MaxEnt".

y.0  Depending on $g$, $y_0$ is either (i) the sample mean ("Normal"), (ii) the number of successes ("Beta"), or (iii) the specific count value ("Gamma") for desired posterior distribution (DS.sampler.post only).

n.0  Depending on $g$, $n_0$ is either (i) the sample standard error ("Normal"), or (ii) the total number of trials in the sample ("Beta"). Not used for "Gamma". (DS.sampler.post only).

B  The number of grid points, default is 250.

Details

DS.sampler.post uses the same type of sampling as DS.sampler to generate random values from a DS posterior distribution.

Value

Vector of length $k$ containing sampled values from DS prior or DS posterior.

Author(s)

Doug Fletcher, Subhadeep Mukhopadhyay

References


Examples

```r
# Extracted parameters from rat.ds object
rat.g.par <- c(2.3, 14.1)
rat.LP.par <- c(0, 0, -0.5)
samps.prior <- DS.sampler(25, rat.g.par, rat.LP.par, con.prior = "Beta")
hist(samps.prior, 15)

# Posterior for rat data
samps.post <- DS.sampler.post(25, rat.g.par, rat.LP.par, y.0 = 4, n.0 = 14, con.prior = "Beta")
hist(samps.post, 15)
```
The observed rotation velocities and their uncertainties of Low Surface Brightness (LSB) galaxies, along with the physical radius of the galaxy.

Usage

data("galaxy")

Format

A data frame of \((y_i, se_i, X_i)\) for \(i = 1, \ldots, 318\).

\(y\) actual observed (smoothed) velocity
\(se\) uncertainty of observed velocity
\(X\) physical radius of the galaxy

Source


gLP.basis

Determine LP basis functions for prior distribution \(g\)

Description

Determines the LP basis for a given parametric prior distribution.

Usage

gLP.basis(x, g.par, m, con.prior, ind)

Arguments

\(x\) x values (integer or vector) from 0 to 1.
\(g.par\) Estimated parameters for specified prior distribution (i.e beta prior: \(\alpha\) and \(\beta\); normal prior: \(\mu\) and \(\tau^2\); gamma prior: \(\alpha\) and \(\beta\)).
\(m\) Number of LP-Polynomial basis.
\(con.prior\) Specified conjugate prior distribution for basis functions. Options are "Beta", "Normal", and "Gamma".
\(ind\) Default is NULL which returns matrix with \(m\) columns that consists of LP-basis functions; user can provide a specific choice through \(ind\).
**Value**
Matrix with $m$ columns of values for the LP-Basis functions evaluated at $x$-values.

**Author(s)**
Subhadeep Mukhopadhyay, Doug Fletcher

**References**

---

**gMLE.bb**

- **Beta-Binomial Parameter Estimation**

**Description**
Computes type-II Maximum likelihood estimates $\hat{\alpha}$ and $\hat{\beta}$ for Beta prior $g \sim \text{Beta}(\alpha, \beta)$.

**Usage**
gMLE.bb(success, trials, start = NULL, optim.method = "default",
lower = 0, upper = Inf)

**Arguments**
- **success**: Vector containing the number of successes.
- **trials**: Vector containing the total number of trials that correspond to the successes.
- **start**: initial parameters; default is NULL which allows function to determine MoM estimates as initial parameters.
- **optim.method**: optimization method in optim(stats).
- **lower**: lower bound for parameters; default is 0.
- **upper**: upper bound for parameters; default is infinity.

**Value**
- **estimate**: MLE estimate for beta parameters.
- **convergence**: Convergence code from optim(); 0 means convergence.
- **loglik**: Loglikelihood that corresponds with MLE estimated parameters.
- **initial**: Initial parameters, either user-defined or determined from method of moments.
- **hessian**: Estimated Hessian matrix at the given solution.
gMLE.nn

Normal-Normal Parameter Estimation

Description

Computes type-II Maximum likelihood estimates \( \hat{\mu} \) and \( \hat{\tau}^2 \) for Normal prior \( g \sim \text{Normal}(\mu, \tau^2) \).

Usage

\[
\text{gMLE.nn}(\text{value, se, fixed = FALSE, method = c("DL","SJ","REML","MoM")})
\]

Arguments

- `value`: Vector of values.
- `se`: Standard error for each value.
- `fixed`: When FALSE, treats the input as if from a random effects model; otherwise, will treat it as if it a fixed effect.
- `method`: Determines the method to find \( \tau^2 \): "DL" uses Dersimonian and Lard technique, "SJ" uses Sidik-Jonkman, "REML" uses restricted maximum likelihood, and "MoM" uses a method of moments technique.

Value

- `estimate`: Vector with both estimated \( \hat{\mu} \) and \( \hat{\tau}^2 \).
- `mu.hat`: Estimated \( \hat{\mu} \).
- `tau.sq`: Estimated \( \hat{\tau}^2 \).
References

Examples
```r
data(ulcer)
### MLE estimate of alpha and beta
ulcer.mle <- gMLE.nn(ulcer$y, ulcer$se, method = "DL")$estimate
ulcer.mle
ulcer.reml <- gMLE.nn(ulcer$y, ulcer$se, method = "REML")$estimate
ulcer.reml
```

Description
Computes Type-II Maximum likelihood estimates $\hat{\alpha}$ and $\hat{\beta}$ for gamma prior $g \sim \Gamma(\alpha, \beta)$.

Usage
```r
gMLE.pg(cnt.vec, exposure = NULL, start.par = c(1,1))
```

Arguments
- `cnt.vec`: Vector containing Poisson counts.
- `exposure`: Vector containing exposures for each count. The default is no exposure, thus `exposure = NULL`.
- `start.par`: Initial values that will pass to optim.

Value
Returns a vector where the first component is $\hat{\alpha}$ and the second component is the scale parameter $\hat{\beta}$ for the gamma distribution: $\frac{1}{\Gamma(\alpha)\beta^\alpha} e^{-\frac{\theta}{\beta}}$. 
Author(s)
Doug Fletcher

References

Examples
### without exposure
```r
data(ChildIll)
ill.start <- gMLE.pg(ChildIll)
ill.start
```
### with exposure
```r
data(NorbergIns)
X <- NorbergIns$deaths
E <- NorbergIns$exposure/344
norb.start <- gMLE.pg(X, exposure = E)
norb.start
```

NorbergIns

**Norberg life insurance data**

Description
The number of claims $y_i$ on a life insurance policy for each of $k = 72$ Norwegian occupational categories and the total number of years the workers in each category were exposed to risk ($E_i$).

Usage
data("NorbergIns")

Format
A data frame of the occupational group number (group), the number of deaths (deaths), and the years of exposure (exposure) for $i = 1, \ldots, 72$.

- **group** Occupational group number
- **deaths** The number of deaths in the occupational group resulting in a claim on a life insurance policy.
- **exposure** The total number of years of exposure to risk for those who passed.

Source
rat

References


---

**rat**  
* Rat Tumor Data

**Description**

Incidence of endometrial stromal polyps in $k = 70$ studies of female rats in control group of a 1977 study on the carcinogenic effects of a diabetic drug phenformin. For each of the $k$ groups, $y$ represents the number of rats who developed the tumors out of $n$ total rats in the group.

**Usage**

data("rat")

**Format**

A data frame of $(y_i, n_i)$ for $i = 1, \ldots, 70$.

- $y$ number of female rats in the $i^{th}$ study who developed polyps/tumors
- $n$ total number of rats in the $i^{th}$ study

**Source**


**References**


Description
Data represents results of quality-control inspections executed by Portsmouth Naval Shipyard on lots of welding materials. The data has \( k = 5 \) observations of number of defects \( y \) out of the total number of tested \( n = 5 \).

Usage
data("ship")

Format
A data frame of \((y_i, n_i)\) for \( i = 1, \ldots, 5 \).

\( y \) number of defects found in the \( i^{th} \) inspection  
\( n \) total samples tested in the \( i^{th} \) inspection

Source

Description
The standardized mean difference \( y_i \) and standard errors \( se_i \) for seven randomised studies on the use of topical steroids in treatment of chronic rhinosinusitis with nasal polyps.

Usage
data("steroid")

Format
A data frame of \((y_i, se_i)\) for \( i = 1, \ldots, 7 \).

\( y \) standard mean difference of clinical trials for topical steroids found in the \( i^{th} \) study  
\( se \) standard error of the standard mean difference for the \( i^{th} \) study

Source
**surg**

*Intestinal surgery data*

**Description**

Data involves the number of malignant lymph nodes removed during intestinal surgery for $k = 844$ cancer patients. For each patient, $n$ is the total number of satellite nodes removed during surgery from a patient and $y$ is the number of malignant nodes.

**Usage**

```r
data("surg")
```

**Format**

A data frame of $(y_i, n_i)$ for $i = 1, \ldots, 844$.

- $y$ number of malignant lymph nodes removed from the $i^{th}$ patient
- $n$ total number of lymph nodes removed from the $i^{th}$ patient

**Source**


---

**tacks**

*Rolling Tacks Data*

**Description**

An experiment that requires a common thumbtack to be "flipped" $n = 9$ times. Out of these total number of flips, $y$ is the total number of times that the thumbtack landed point up.

**Usage**

```r
data("tacks")
```

**Format**

A data frame of $(y_i, n_i)$ for $i = 1, \ldots, 320$.

- $y$ number of times a thumbtack landed point up in the $i^{th}$ trial
- $n$ total number of flips for the thumbtack in the $i^{th}$ trial

**Source**

**terb**

Terbinafine trial data

**Description**

During several studies of the oral antifungal agent terbinafine, a proportion of the patients in the trial terminated treatment due to some adverse effects. In the data set, $y_i$ is the number of terminated treatments and $n_i$ is the total number of patients in the $i^{th}$ trial.

**Usage**

```r
data("terb")
```

**Format**

A data frame of $(y_i, n_i)$ for $i = 1, \ldots, 41$.

- $y$ number of patients who terminated treatment early in the $i^{th}$ trial
- $n$ total number of patients in the $i^{th}$ clinical trial

**Source**


---

**ulcer**

Recurrent Bleeding of Ulcers

**Description**

The data consist of $k = 40$ randomized trials between 1980 and 1989 of a surgical treatment for stomach ulcers. Each of the trials has an estimated log-odds ratio that measures the rate of occurrence of recurrent bleeding given the surgical treatment.

**Usage**

```r
data("ulcer")
```

**Format**

A data frame of $(y_i, se_i)$ for $i = 1, \ldots, 40$.

- $y$ log-odds of the occurrence of recurrent bleeding in the $i^{th}$ study
- $se$ standard error of the log-odds for the $i^{th}$ study
Source


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