Package: prevalence (via r-universe)

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Type Package

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BugReports https://github.com/brechtdv/prevalence/issues

Description The prevalence package provides Frequentist and Bayesian methods for prevalence assessment studies. IMPORTANT: the truePrev functions in the prevalence package call on JAGS (Just Another Gibbs Sampler), which therefore has to be available on the user's system. JAGS can be downloaded from <https://mcmc-jags.sourceforge.io/>.

Depends R (>= 4.0.0)

Imports methods, utils, stats, graphics, grDevices, coda, rjags

SystemRequirements JAGS (>= 4.0.0) (see https://mcmc-jags.sourceforge.io/)

License GPL (>= 2)

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`prevalence-package` *Tools for prevalence assessment studies*

Description

The **prevalence** package provides Frequentist and Bayesian methods useful in prevalence assessment studies. Visit `http://prevalence.cbra.be/` for more information and tutorials.

Details

Package:	prevalence
Type:	Package
Version:	0.4.1
Date:	2022-06-03
BugReports:	`https://github.com/brechtdv/prevalence/issues`
Depends:	R (>= 4.0.0), rjags, coda, methods
SystemRequirements:	JAGS (>= 3.2.0) (see `https://mcmc-jags.sourceforge.io/`)
License:	GNU >= 2

Available functions in the **prevalence** package:

`propCI`	Derive confidence intervals for an apparent prevalence estimate
`truePrev`	Estimate TP from AP obtained by testing individual samples with a single test
`truePrevMulti`	Estimate TP from AP obtained by testing individual samples with multiple tests, using a conditional proba
`truePrevMulti2`	Estimate TP from AP obtained by testing individual samples with multiple tests, using a covariance schem

truePrevPools	Estimate TP from AP obtained by testing pooled samples
betaPERT	Calculate the parameters of a Beta-PERT distribution
betaExpert	Calculate the parameters of a Beta distribution based on expert opinion

IMPORTANT: the truePrev functions in the **prevalence** package call on **JAGS (Just Another Gibbs Sampler)**, through the **rjags** package. Therefore, JAGS has to be installed on the user's system.

JAGS can be downloaded from https://mcmc-jags.sourceforge.io/

Author(s)

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betaExpert *Calculate the parameters of a Beta distribution based on expert information*

Description

The betaExpert function fits a (standard) Beta distribution to expert opinion. The expert provides information on a best-guess estimate (mode or mean), and an uncertainty range:

- The parameter value is with 100*p% certainty greater than lower
- The parameter value is with 100*p% certainty smaller than upper
- The parameter value lies with 100*p% in between lower and upper

Usage

```
betaExpert(best, lower, upper, p = 0.95, method = "mode")

## S3 method for class 'betaExpert'
print(x, conf.level = .95, ...)
## S3 method for class 'betaExpert'
plot(x, y, ...)
```

Arguments

best	Best-guess estimate; see argument method
lower	Lower uncertainty limit
upper	Upper uncertainty limit

p	Expert's certainty level
method	Does best-guess estimate correspond to the mode or to the mean? Defaults to mode
x	Object of class betaExpert
y	Currently not implemented
conf.level	Confidence level used in printing quantiles of resulting Beta distribution
...	Other arguments to pass to function print and plot

Details

The methodology behind the betaExpert function is presented by Branscum et al. (2005) and implemented in the *BetaBuster* software, written by Chun-Lung Su.

The parameters of a standard Beta distribution are calculated based on a best-guess estimate and a $100(p)\%$ uncertainty range, defined by a lower and/or upper limit. The betaExpert function uses minimization (optimize) to derive α and β from this best guess and lower and/or upper limit. The resulting distribution is a standard 2-parameter Beta distribution: Beta(α, β).

Value

A list of class "betaExpert":

alpha	Parameter α (shape1) of the Beta distribution
beta	Parameter β (shape2) of the Beta distribution

The print method for "betaExpert" additionally calculates the mean, median, mode, variance and range of the corresponding Beta distribution.

Author(s)

Brecht Devleesschauwer <<brechtdv@gmail.com>>

References

Branscum AJ, Gardner IA, Johnson WO (2005) Estimation of diagnostic-test sensitivity and specificity through Bayesian modeling. *Prev Vet Med* **68**:145-163.

See Also

Package **rriskDistributions**, which provides a collection of functions for fitting distributions to given data or by known quantiles.

betaPERT, for modelling a generalized Beta distribution based on expert opinion

Examples

```
## Most likely value (mode) is 90%
## Expert states with 95% certainty that true value is larger than 70%
betaExpert(best = 0.90, lower = 0.70, p = 0.95)

## Most likely value (mode) is 0%
## Expert states with 95% certainty that true value is smaller than 40%
betaExpert(best = 0, upper = 0.40, p = 0.95)

## Most likely value (mode) is 80%
## Expert states with 90% certainty that true value lies in between 40% and 90%
betaExpert(best = 0.80, lower = 0.40, upper = 0.90, p = 0.90)

## Mean value is assumed to be 80%
## Expert states with 90% certainty that true value lies in between 40% and 90%
betaExpert(best = 0.80, lower = 0.40, upper = 0.90, p = 0.90, method = "mean")
```

---

betaPERT *Calculate the parameters of a Beta-PERT distribution*

Description

The Beta-PERT methodology allows to parametrize a generalized Beta distribution based on expert opinion regarding a pessimistic estimate (minimum value), a most likely estimate (mode), and an optimistic estimate (maximum value). The `betaPERT` function incorporates two methods of calculating the parameters of a Beta-PERT distribution, designated `"classic"` and `"vose"`.

Usage

```
betaPERT(a, m, b, k = 4, method = c("classic", "vose"))

## S3 method for class 'betaPERT'
print(x, conf.level = .95, ...)
## S3 method for class 'betaPERT'
plot(x, y, ...)
```

Arguments

`a`	Pessimistic estimate (Minimum value)
`m`	Most likely estimate (Mode)
`b`	Optimistic estimate (Maximum value)
`k`	Scale parameter
`method`	`"classic"` or `"vose"`; see details below
`x`	Object of class `betaPERT`
`y`	Currently ignored
`conf.level`	Confidence level used in printing quantiles of resulting Beta-PERT distribution
`...`	Other arguments to pass to function `print` and `plot`

Details

The Beta-PERT methodology was developed in the context of Program Evaluation and Review Technique (PERT). Based on a pessimistic estimate (minimum value), a most likely estimate (mode), and an optimistic estimate (maximum value), typically derived through expert elicitation, the parameters of a Beta distribution can be calculated. The Beta-PERT distribution is used in stochastic modeling and risk assessment studies to reflect uncertainty regarding specific parameters.

Different methods exist in literature for defining the parameters of a Beta distribution based on PERT. The two most common methods are included in the `BetaPERT` function:

Classic: The standard formulas for mean, standard deviation, α and β, are as follows:

$$mean = \frac{a + k * m + b}{k + 2}$$

$$sd = \frac{b - a}{k + 2}$$

$$\alpha = \frac{mean - a}{b - a} * \left\{ (mean - a) * \frac{b - mean}{sd^2} - 1 \right\}$$

$$\beta = \alpha * \frac{b - mean}{mean - a}$$

The resulting distribution is a 4-parameter Beta distribution: Beta(α, β, a, b).

Vose: Vose (2000) describes a different formula for α:

$$(mean - a) * \frac{2 * m - a - b}{(m - mean) * (b - a)}$$

Mean and β are calculated using the standard formulas; as for the classical PERT, the resulting distribution is a 4-parameter Beta distribution: Beta(α, β, a, b).

Note: If $m = mean$, α is calculated as $1 + k/2$, in accordance with the **mc2d** package (see 'Note').

Value

A list of class `"betaPERT"`:

`alpha`	Parameter α (shape1) of the Beta distribution
`beta`	Parameter β (shape2) of the Beta distribution
`a`	Pessimistic estimate (Minimum value)
`m`	Most likely estimate (Mode)
`b`	Optimistic estimate (Maximum value)
`method`	Applied method

Available generic functions for class `"betaPERT"` are `print` and `plot`.

Note

The **mc2d** package provides the probability density function, cumulative distribution function, quantile function and random number generation function for the PERT distribution, parametrized by the "vose" method.

Author(s)

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References

Classic: Malcolm DG, Roseboom JH, Clark CE, Fazar W (1959) Application of a technique for research and development program evaluation. *Oper Res* **7**(5):646-669.

Vose: David Vose. *Risk analysis, a quantitative guide, 2nd edition.* Wiley and Sons, 2000. PERT distribution in *ModelRisk* (Vose software)

See Also

betaExpert, for modelling a standard Beta distribution based on expert opinion

Examples

```
## The value of a parameter of interest is believed to lie between 0 and 50
## The most likely value is believed to be 10

# Classical PERT
betaPERT(a = 0, m = 10, b = 50, method = "classic")

# Vose parametrization
betaPERT(a = 0, m = 10, b = 50, method = "vose")
```

---

convert-methods *Methods for Function* as.matrix *in Package* **prevalence**

Description

Convert objects of class prev to matrix

Usage

```
## S4 method for signature 'prev'
as.matrix(x, iters = FALSE, chains = FALSE)
```

Arguments

x	An object of class prev
iters	Logical flag, indicating whether a column should be added for iteration number; defaults to FALSE
chains	Logical flag, indicating whether a column should be added for chain number; defaults to FALSE

Methods

signature(x = "prev") Convert objects of class prev to matrix

See Also

prev-class

Examples

```
## Not run:

## Taenia solium cysticercosis 1-test model
cysti <-
truePrev(x = 142, n = 742,
         SE = ~dunif(0.60, 1.00), SP = ~dunif(0.75, 1.00))

head(as.matrix(cysti))


## Campylobacter 2-test model
campy <-
truePrevMulti(
  x = c(113, 46, 156, 341),
  n = 656,
  prior = {
    theta[1] ~ dunif(0.45, 0.80)
    theta[2] ~ dunif(0.24, 0.50)
    theta[3] <- 1
    theta[4] ~ dbeta(30, 12)
    theta[5] ~ dbeta(1, 1)
    theta[6] <- 1
    theta[7] <- 1
  }
)

head(as.matrix(campy, iters = TRUE, chains = TRUE))

## End(Not run)
```

define *Definition of* truePrevMulti *and* truePrevMulti2 *model*

Description

These utility functions generate definitions for the test results and priors used by truePrevMulti and truePrevMulti2.

Usage

```
define_x(h)
define_prior(h)
define_prior2(h)
```

Arguments

h	Number of tests

Details

The vector of apparent tests results, x, must contain the number of samples corresponding to each combination of test results. The models assume that the first value corresponds to the number of samples that tested positive on all tests and that the last value corresponds to the number of samples that tested negative on all tests.

Function truePrevMulti estimates true prevalence from individual samples tested with h tests, using the approach of Berkvens et al. (2006). The prior in the multinomial model consists of a vector theta, which holds values for the true prevalence (TP), the sensitivity and specificity of the first test (SE1, SP1), and the conditional dependencies between the results of the subsequent tests and the preceding one(s). define_prior generates the definition of prior for h tests.

Function truePrevMulti2 implements and extends the approach described by Dendukuri and Joseph (2001), which uses a multinomial distribution to model observed test results, and in which conditional dependence between tests is modelled through covariances. Argument prior consists of prior distributions for:

- True Prevalence: TP
- SEnsitivity of each individual test: vector SE
- SPecificity of each individual test: vector SP
- Conditional covariance of all possible test combinations given a truly positive disease status: vector a
- Conditional covariance of all possible test combinations given a truly negative disease status: vector b

define_prior2 generates the definition of prior for h tests.

Author(s)

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References

- Berkvens D, Speybroeck N, Praet N, Adel A, Lesaffre E (2006) Estimating disease prevalence in a Bayesian framework using probabilistic constraints. *Epidemiology* **17**:145-153
- Dendukuri N, Joseph L (2001) Bayesian approaches to modeling the conditional dependence between multiple diagnostic tests. *Biometrics* **57**:158-167

See Also

truePrevMulti, truePrevMulti2

Examples

```
## how is a 2-test model defined?

define_x(2)
# Definition of the apparent test results, 'x', for 2 tests:
# x[1] : T1-,T2-
# x[2] : T1-,T2+
# x[3] : T1+,T2-
# x[4] : T1+,T2+

define_prior(2)
# Conditional probability scheme
# Definition of the prior, 'theta', for 2 tests:
# theta[1] : P(D+) = TP
# theta[2] : P(T1+|D+) = SE1
# theta[3] : P(T1-|D-) = SP1
# theta[4] : P(T2+|D+,T1+)
# theta[5] : P(T2+|D+,T1-)
# theta[6] : P(T2-|D-,T1-)
# theta[7] : P(T2-|D-,T1+)

define_prior2(2)
# Covariance scheme
# Definition of the prior for 2 tests:
# TP :    True Prevalence
# SE[1] : Sensitity T1
# SE[2] : Sensitity T2
# SP[1] : Specificity T1
# SP[2] : Specificity T2
# a[1] :  Covariance(T1,T2|D+)
# b[1] :  Covariance(T1,T2|D-)

## how is a 3-test model defined?

define_x(3)
# Definition of the apparent test results, 'x', for 3 tests:
```

```
# x[1] : T1-,T2-,T3-
# x[2] : T1-,T2-,T3+
# x[3] : T1-,T2+,T3-
# x[4] : T1-,T2+,T3+
# x[5] : T1+,T2-,T3-
# x[6] : T1+,T2-,T3+
# x[7] : T1+,T2+,T3-
# x[8] : T1+,T2+,T3+

define_prior(3)
# Conditional probability scheme
# Definition of the prior, 'theta', for 3 tests:
# theta[1] : P(D+) = TP
# theta[2] : P(T1+|D+) = SE1
# theta[3] : P(T1-|D-) = SP1
# theta[4] : P(T2+|D+,T1+)
# theta[5] : P(T2+|D+,T1-)
# theta[6] : P(T2-|D-,T1-)
# theta[7] : P(T2-|D-,T1+)
# theta[8] : P(T3+|D+,T1+,T2+)
# theta[9] : P(T3+|D+,T1+,T2-)
# theta[10] : P(T3+|D+,T1-,T2+)
# theta[11] : P(T3+|D+,T1-,T2-)
# theta[12] : P(T3-|D-,T1-,T2-)
# theta[13] : P(T3-|D-,T1-,T2+)
# theta[14] : P(T3-|D-,T1+,T2-)
# theta[15] : P(T3-|D-,T1+,T2+)

define_prior2(3)
# Covariance scheme
# Definition of the prior for 3 tests:
# TP :    True Prevalence
# SE[1] : Sensitity T1
# SE[2] : Sensitity T2
# SE[3] : Sensitity T3
# SP[1] : Specificity T1
# SP[2] : Specificity T2
# SP[3] : Specificity T3
# a[1] :  Covariance(T1,T2|D+)
# a[2] :  Covariance(T1,T3|D+)
# a[3] :  Covariance(T2,T3|D+)
# a[4] :  Covariance(T1,T2,T3|D+)
# b[1] :  Covariance(T1,T2|D-)
# b[2] :  Covariance(T1,T3|D-)
# b[3] :  Covariance(T2,T3|D-)
# b[4] :  Covariance(T1,T2,T3|D-)
```

---

plot-methods *Methods for Function* plot *in Package* **prevalence**

Description

Plot objects of class prev

Usage

```
## S4 method for signature 'prev,ANY'
plot(x, y = NULL, ...)
```

Arguments

x	An object of class prev
y	Which parameter to plot? Defaults to NULL, in which case TP will be used
...	Other arguments to pass to the plot function

Methods

signature(x = "prev", y = "ANY") Show density, trace, Brooks-Gelman-Rubin and autocorrelation plots.

See Also

prev-class
densplot-methods, traceplot-methods, gelman.plot-methods, autocorr.plot-methods

---

plot-methods-coda *Plotting functions from package* **coda**

Description

Different plotting functions from package **coda** have been made available as method to class prev

Usage

```
## S4 method for signature 'prev'
densplot(x, exclude_fixed = TRUE, ...)

## S4 method for signature 'prev'
traceplot(x, exclude_fixed = TRUE, ...)

## S4 method for signature 'prev'
autocorr.plot(x, exclude_fixed = TRUE, chain = 1, ...)
```

Arguments

x	An object of class prev
exclude_fixed	Should fixed parameters be excluded from plotting? defaults to TRUE
chain	Which chain to plot in autocorr.plot; defaults to 1
...	Other arguments to pass to the specific plot function.

Methods

`signature(x = "prev")` Show density, trace, Brooks-Gelman-Rubin and autocorrelation plots.

See Also

`prev-class`
`plot-methods`
`densplot`, `traceplot`, `gelman.plot`, `autocorr.plot`

---

prev-class *Class* "prev"

Description

The "prev" class represents output from Bayesian true prevalence estimation models.

Objects from the Class

Objects of class "prev" are created by `truePrev`, `truePrevMulti`, `truePrevMulti2` and `truePrevPools`.

Slots

Objects of class "prev" contain the following four slots:

par: A list of input parameters

model: The fitted Bayesian model, in BUGS language (S3 class "prevModel")

mcmc: A list, with one element per chain, of the simulated true prevalences, sensitivities and specificities

diagnostics: A list with elements for the Deviance Information Criterion (`$DIC`), the Brooks-Gelman-Rubin statistic (`$BGR`), and in the case of `truePrevMulti` and `truePrevMulti2`, the Bayes-P statistic (`$bayesP`)

Author(s)

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See Also

`truePrev`, `truePrevMulti`, `truePrevMulti2`, `truePrevPools`
`show-methods`, `print-methods`, `summary-methods`, `convert-methods`, `plot-methods`, `plot-methods-coda`

Examples

```
## Taenia solium cysticercosis in Nepal
SE <- list(dist = "uniform", min = 0.60, max = 1.00)
SP <- list(dist = "uniform", min = 0.75, max = 1.00)
TP <- truePrev(x = 142, n = 742, SE = SE, SP = SP)

## Summarize estimates per chain
summary(TP)

## Diagnostic plots
par(mfrow = c(2, 2))
plot(TP)

## Generic plots from package coda
par(mfrow = c(1, 1))
densplot(TP)
traceplot(TP)
gelman.plot(TP)
autocorr.plot(TP)

## Use 'slotNames()' to see the slots of object TP
slotNames(TP)

## Every slot can be accessed using the '@' operator
## Use 'str()' to see the structure of each object
str(TP@par)          # input parameters
str(TP@model)        # fitted model
str(TP@mcmc)         # simulated TP, SE, SP
str(TP@diagnostics)  # DIC and BGR (and bayesP)

## Each element of TP@mcmc inherits from coda class 'mcmc.list'
## List all available methods for this class
methods(class = "mcmc.list")
## List all available functions in the coda package
library(help = "coda")

## Highest Posterior Density interval, from coda package
coda::HPDinterval(TP@mcmc$TP)
```

`print-methods` *Methods for Function* `print` *in Package* **prevalence**

Description

Print objects of class `prev`

Usage

```
## S4 method for signature 'prev'
print(x, conf.level = 0.95, dig = 3, ...)
```

Arguments

x	An object of class prev
conf.level	Confidence level to be used in credibility interval
dig	Number of decimal digits to print
...	Other arguments to pass to the print function

Methods

signature(x = "prev") Print mean, median, mode, standard deviation and credibility interval of estimated true prevalence, sensitivities and specificities. In addition, print multivariate Brooks-Gelman-Rubin statistic (or univariate BGR statistic with corresponding upper confidence limit in case of a single stochastic node). BGR values substantially above 1 indicate lack of convergence. For prev objects created by truePrevMulti, the Bayes-P statistic is also printed. Bayes-P should be as close to 0.5 as possible.

See Also

prev-class
gelman.diag

---

propCI *Calculate confidence intervals for prevalences and other proportions*

Description

The propCI function calculates five types of confidence intervals for proportions:

- Wald interval (= Normal approximation interval, asymptotic interval)
- Agresti-Coull interval (= adjusted Wald interval)
- Exact interval (= Clopper-Pearson interval)
- Jeffreys interval (= Bayesian interval)
- Wilson score interval

Usage

```
propCI(x, n, method = "all", level = 0.95, sortby = "level")
```

Arguments

x	Number of successes (positive samples)
n	Number of trials (sample size)
method	Confidence interval calculation method; see details
level	Confidence level for confidence intervals
sortby	Sort results by "level" or "method"

Details

Five methods are available for calculating confidence intervals. For convenience, synonyms are allowed. Please refer to the PDF version of the manual for proper formatting of the below formulas.

`"agresti.coull"`, `"agresti-coull"`, `"ac"`

$$\tilde{n} = n + z^2_{1-\frac{\alpha}{2}}$$

$$\tilde{p} = \frac{1}{\tilde{n}}(x + \frac{1}{2}z^2_{1-\frac{\alpha}{2}})$$

$$\tilde{p} \pm z_{1-\frac{\alpha}{2}}\sqrt{\frac{\tilde{p}(1-\tilde{p})}{\tilde{n}}}$$

`"exact"`, `"clopper-pearson"`, `"cp"`

$$(Beta(\frac{\alpha}{2}; x, n-x+1), Beta(1-\frac{\alpha}{2}; x+1, n-x))$$

`"jeffreys"`, `"bayes"`

$$(Beta(\frac{\alpha}{2}; x+0.5, n-x+0.5), Beta(1-\frac{\alpha}{2}; x+0.5, n-x+0.5))$$

`"wald"`, `"asymptotic"`, `"normal"`

$$p \pm z_{1-\frac{\alpha}{2}}\sqrt{\frac{p(1-p)}{n}}$$

`"wilson"`

$$\frac{p + \frac{z^2_{1-\frac{\alpha}{2}}}{2n} \pm z_{1-\frac{\alpha}{2}}\sqrt{\frac{p(1-p)}{n} + \frac{z^2_{1-\frac{\alpha}{2}}}{4n^2}}}{1 + \frac{z^2_{1-\frac{\alpha}{2}}}{n}}$$

Value

Data frame with seven columns:

`x`	Number of successes (positive samples)
`n`	Number of trials (sample size)
`p`	Proportion of successes (prevalence)
`method`	Confidence interval calculation method
`level`	Confidence level
`lower`	Lower confidence limit
`upper`	Upper confidence limit

Note

In case the observed prevalence equals 0% (ie, `x == 0`), an upper one-sided confidence interval is returned. In case the observed prevalence equals 100% (ie, `x == n`), a lower one-sided confidence interval is returned. In all other cases, two-sided confidence intervals are returned.

Author(s)

Brecht Devleesschauwer <<brechtdv@gmail.com>>

Examples

```
## All methods, 95% confidence intervals
propCI(x = 142, n = 742)

## Wald-type 90%, 95% and 99% confidence intervals
propCI(x = 142, n = 742, method = "wald", level = c(0.90, 0.95, 0.99))
```

---

show-methods *Methods for Function* show *in Package* **prevalence**

Description

Show objects of class prev

Usage

```
## S4 method for signature 'prev'
show(object)
```

Arguments

object	An object of class prev

Methods

signature(object = "prev") Corresponds to print(object)

See Also

prev-class

summary-methods *Methods for Function* summary *in Package* **prevalence**

Description

Summarize objects of class prev

Usage

```
## S4 method for signature 'prev'
summary(object, conf.level)
```

Arguments

object	An object of class prev
conf.level	Confidence level to be used in credibility intervals

Methods

signature(object = "prev") Obtain mean, median, mode, standard deviation, variance, credibility interval and number of samples for each chain separately and for all chains combined.

See Also

prev-class

truePrev *Estimate true prevalence from individuals samples*

Description

Bayesian estimation of true prevalence from apparent prevalence obtained by testing *individual* samples.

Usage

```
truePrev(x, n, SE = 1, SP = 1, prior = c(1, 1),
         nchains = 2, burnin = 10000, update = 10000,
         verbose = FALSE)
```

Arguments

x	The apparent number of positive samples
n	The sample size
SE, SP	The prior distribution for sensitivity (SE) and specificity SP); see 'Details' below for specification of these distributions
prior	The parameters of the prior Beta distribution for true prevalence; defaults to c(1, 1)
nchains	The number of chains used in the estimation process; 'n' must be ≥ 2
burnin	The number of discarded model iterations; defaults to 10,000
update	The number of withheld model iterations; defaults to 10,000
verbose	Logical flag, indicating if JAGS process output should be printed to the R console; defaults to FALSE

Details

truePrev calls on **JAGS/rjags** to estimate the true prevalence from the apparent prevalence in a Bayesian framework. The default model, in BUGS language, is given below. To see the actual fitted model, see the model slot of the prev-object.

```
model {
  x ~ dbin(AP, n)
  AP <- SE * TP + (1 - SP) * (1 - TP)
  # SE ~ user-defined (see below)
  # SP ~ user-defined (see below)
  TP ~ dbeta(prior[1], prior[2])
}
```

The test sensitivity (SE) and specificity (SP) can be specified, independently, as one of "fixed", "uniform", "beta", "pert", or "beta-expert", with "fixed" as the default.

Distribution parameters can be specified in a *named* list() as follows:

- **Fixed:** list(dist = "fixed", par)
- **Uniform:** list(dist = "uniform", min, max)
- **Beta:** list(dist = "beta", alpha, beta)
- **Beta-PERT:** list(dist = "pert", method, a, m, b, k)
  'method' must be "classic" or "vose";
  'a' denotes the pessimistic (minimum) estimate, 'm' the most likely estimate, and 'b' the optimistic (maximum) estimate;
  'k' denotes the scale parameter.
  See betaPERT for more information on Beta-PERT parametrization.

- **Beta-Expert:** `list(dist = "beta-expert", mode, mean, lower, upper, p)`
  `'mode'` denotes the most likely estimate, `'mean'` the mean estimate;
  `'lower'` denotes the lower bound, `'upper'` the upper bound;
  `'p'` denotes the confidence level of the expert.
  Only `mode` or `mean` should be specified; `lower` and `upper` can be specified together or alone.
  See `betaExpert` for more information on Beta-Expert parametrization.

For Uniform, Beta and Beta-PERT distributions, BUGS-style short-hand notation is also allowed:

- **Uniform:** `~dunif(min, max)`
- **Beta:** `~dbeta(alpha, beta)`
- **Beta-PERT:** `~dpert(min, mode, max)`

Value

An object of class `prev`.

Note

Markov chain Monte Carlo sampling in `truePrev` is performed by **JAGS (Just Another Gibbs Sampler)** through the **rjags** package. JAGS can be downloaded from `https://mcmc-jags.sourceforge.io/`.

Author(s)

Brecht Devleesschauwer <<brechtdv@gmail.com>>

References

- Speybroeck N, Devleesschauwer B, Joseph L, Berkvens D (2013) Misclassification errors in prevalence estimation: Bayesian handling with care. *Int J Public Health* **58**:791-795
- Online Shiny application: `https://cbra.shinyapps.io/truePrev/`

See Also

coda for various functions that can be applied to the `prev@mcmc` object
`truePrevMulti`: estimate true prevalence from apparent prevalence obtained by testing *individual* samples with multiple tests, using a conditional probability scheme
`truePrevMulti2`: estimate true prevalence from apparent prevalence obtained by testing *individual* samples with multiple tests, using a covariance scheme
`truePrevPools`: estimate true prevalence from apparent prevalence obtained by testing *pooled* samples
`betaPERT`: calculate the parameters of a Beta-PERT distribution
`betaExpert`: calculate the parameters of a Beta distribution based on expert opinion

Examples

```
## Taenia solium cysticercosis in Nepal
## 142 positives out of 742 pigs sampled

## Model SE and SP based on literature data
## Sensitivity ranges uniformly between 60% and 100%
## Specificity ranges uniformly between 75% and 100%
#> BUGS-style:
truePrev(x = 142, n = 742,
         SE = ~dunif(0.60, 1.00), SP = ~dunif(0.75, 1.00))

#> list-style:
SE <- list(dist = "uniform", min = 0.60, max = 1.00)
SP <- list(dist = "uniform", min = 0.75, max = 1.00)
truePrev(x = 142, n = 742, SE = SE, SP = SP)

## Model SE and SP based on expert opinions
## Sensitivity lies in between 60% and 100%; most likely value is 90%
## Specificity is with 95% confidence larger than 75%; most likely value is 90%
SE <- list(dist = "pert", a = 0.60, m = 0.90, b = 1.00)
SP <- list(dist = "beta-expert", mode = 0.90, lower = 0.75, p = 0.95)
truePrev(x = 142, n = 742, SE = SE, SP = SP)

## Model SE and SP as fixed values (each 90%)
truePrev(x = 142, n = 742, SE = 0.90, SP = 0.90)
```

`truePrevMulti` *Estimate true prevalence from individuals samples using multiple tests – conditional probability scheme*

Description

Bayesian estimation of true prevalence from apparent prevalence obtained by applying *multiple* tests to *individual* samples. `truePrevMulti` implements the approach described by Berkvens et al. (2006), which uses a multinomial distribution to model observed test results, and in which conditional dependence between tests is modelled through conditional probabilities.

Usage

```
truePrevMulti(x, n, prior, nchains = 2, burnin = 10000, update = 10000,
              verbose = FALSE)
```

Arguments

`x`	Vector of apparent test results; see 'Details' below
`n`	The total sample size
`prior`	The prior distribution for `theta`; see 'Details' below
`nchains`	The number of chains used in the estimation process; must be ≥ 2

burnin	The number of discarded model iterations; defaults to 10,000
update	The number of withheld model iterations; defaults to 10,000
verbose	Logical flag, indicating if JAGS process output should be printed to the R console; defaults to FALSE

Details

truePrevMulti calls on **JAGS** via the **rjags** package to estimate true prevalence from apparent prevalence in a Bayesian framework. truePrevMulti fits a multinomial model to the apparent test results obtained by testing individual samples with a given number of tests. To see the actual fitted model, see the model slot of the prev-object.

The vector of apparent tests results, x, must contain the number of samples corresponding to each combination of test results. To see how this vector is defined for the number of tests h at hand, use define_x.

The prior in the multinomial model consists of a vector theta, which holds values for the true prevalence (TP), the sensitivity and specificity of the first test (SE1, SP1), and the conditional dependencies between the results of the subsequent tests and the preceding one(s). To see how this vector is defined for the number of tests n at hand, use define_prior.

The values of prior can be specified in two ways, referred to as BUGS-style and list-style, respectively. See also below for some examples.

For BUGS-style specification, the values of theta should be given between curly brackets (i.e., {}), separated by line breaks. theta values can be specified to be deterministic (i.e., fixed), using the <- operator, or stochastic, using the ~ operator. In the latter case, the following distributions can be used:

- **Uniform:** dunif(min, max)
- **Beta:** dbeta(alpha, beta)
- **Beta-PERT:** dpert(min, mode, max)

Alternatively, theta values can be specified in a *named* list() as follows:

- **Fixed:** list(dist = "fixed", par)
- **Uniform:** list(dist = "uniform", min, max)
- **Beta:** list(dist = "beta", alpha, beta)
- **Beta-PERT:** list(dist = "pert", method, a, m, b, k)
  'method' must be "classic" or "vose";
  'a' denotes the pessimistic (minimum) estimate, 'm' the most likely estimate, and 'b' the optimistic (maximum) estimate;
  'k' denotes the scale parameter.
  See betaPERT for more information on Beta-PERT parameterization.

- **Beta-Expert:** `list(dist = "beta-expert", mode, mean, lower, upper, p)`
  `'mode'` denotes the most likely estimate, `'mean'` the mean estimate;
  `'lower'` denotes the lower bound, `'upper'` the upper bound;
  `'p'` denotes the confidence level of the expert.
  Only `mode` or `mean` should be specified; `lower` and `upper` can be specified together or alone.
  See `betaExpert` for more information on Beta-Expert parameterization.

Value

An object of class `prev`.

Note

Markov chain Monte Carlo sampling in `truePrevMulti` is performed by **JAGS (Just Another Gibbs Sampler)** through the **rjags** package. JAGS can be downloaded from `https://mcmc-jags.sourceforge.io/`.

Author(s)

Brecht Devleesschauwer `<<brechtdv@gmail.com>>`

References

- Berkvens D, Speybroeck N, Praet N, Adel A, Lesaffre E (2006) Estimating disease prevalence in a Bayesian framework using probabilistic constraints. *Epidemiology* **17**:145-153
- Habib I, Sampers I, Uyttendaele M, De Zutter L, Berkvens D (2008) A Bayesian modelling framework to estimate *Campylobacter* prevalence and culture methods sensitivity: application to a chicken meat survey in Belgium. *J Appl Microbiol* **105**:2002-2008
- Geurden T, Berkvens D, Casaert S, Vercruysse J, Claerebout E (2008) A Bayesian evaluation of three diagnostic assays for the detection of *Giardia duodenalis* in symptomatic and asymptomatic dogs. *Vet Parasitol* **157**:14-20

See Also

`define_x`: how to define the vector of apparent test results `x`
`define_prior`: how to define the vector of `theta` values in `prior`

coda for various functions that can be applied to the `prev@mcmc` object
`truePrevMulti2`: estimate true prevalence from apparent prevalence obtained by testing *individual* samples with multiple tests, using a covariance scheme
`truePrev`: estimate true prevalence from apparent prevalence obtained by testing *individual* samples with a single test
`truePrevPools`: estimate true prevalence from apparent prevalence obtained by testing *pooled* samples
`betaPERT`: calculate the parameters of a Beta-PERT distribution
`betaExpert`: calculate the parameters of a Beta distribution based on expert opinion

Examples

```
## Not run:
## ================================================== ##
## 2-TEST EXAMPLE: Campylobacter                      ##
## -------------------------------------------------- ##
## Two tests were performed on 656 chicken meat samples  ##
## -> T1 = enrichment culture                         ##
## -> T2 = direct plating                             ##
## The following assumption were made:                ##
## -> TP is larger than 45% and smaller than 80%      ##
## -> SE1 must lie within 24% and 50%                 ##
## -> SP1 and SP2 both equal 100%                     ##
## -> beta(30, 12) describes P(T2+|D+,T1+)            ##
## The following results were obtained:               ##
## -> 113 samples T1+,T2+                             ##
## ->  46 samples T1+,T2-                             ##
## -> 156 samples T1-,T2+                             ##
## -> 341 samples T1-,T2-                             ##
## ================================================== ##

## how is the 2-test model defined?
define_x(2)
define_prior(2)

## fit campylobacter 2-test model
campy <-
truePrevMulti(
  x = c(113, 46, 156, 341),
  n = 656,
  prior = {
    theta[1] ~ dunif(0.45, 0.80)
    theta[2] ~ dunif(0.24, 0.50)
    theta[3] <- 1
    theta[4] ~ dbeta(30, 12)
    theta[5] ~ dbeta(1, 1)
    theta[6] <- 1
    theta[7] <- 1
  }
)

## fit same model using 'list-style'
campy <-
truePrevMulti(
  x = c(113, 46, 156, 341),
  n = 656,
  prior =
    list(
      theta1 = list(dist = "uniform", min = 0.45, max = 0.80),
      theta2 = list(dist = "uniform", min = 0.24, max = 0.50),
      theta3 = 1,
      theta4 = list(dist = "beta", alpha = 30, beta = 12),
      theta5 = list(dist = "beta", alpha = 1, beta = 1),
```

```
      theta6 = 1,
      theta7 = 1
    )
)

## show model results
campy

## explore model structure
str(campy)         # overall structure
str(campy@par)     # structure of slot 'par'
str(campy@mcmc)    # structure of slot 'mcmc'
campy@model        # fitted model
campy@diagnostics  # DIC, BGR and Bayes-P values

## standard methods
print(campy)
summary(campy)
par(mfrow = c(2, 2))
plot(campy)         # shows plots of TP by default
plot(campy, "SE1")  # same plots for SE1
plot(campy, "SE2")  # same plots for SE2

## coda plots of TP, SE1, SE2
par(mfrow = c(1, 3))
densplot(campy, col = "red")
traceplot(campy)
gelman.plot(campy)
autocorr.plot(campy)


## ======================================================= ##
## 3-TEST EXAMPLE: Giardia                                 ##
## ------------------------------------------------------- ##
## Three tests were performed on stools from 272 dogs      ##
## -> T1 = immunofluorescence assay                        ##
## -> T2 = direct microscopy                               ##
## -> T3 = SNAP immunochromatography                       ##
## The following assumption were made:                     ##
## -> TP is smaller than 20%                               ##
## -> SE1 must be higher than 80%                          ##
## -> SP1 must be higher than 90%                          ##
## The following results were obtained:                    ##
## ->   6 samples T1+,T2+,T3+                              ##
## ->   4 samples T1+,T2+,T3-                              ##
## ->  12 samples T1+,T2-,T3+                              ##
## ->  12 samples T1+,T2-,T3-                              ##
## ->   1 sample  T1-,T2+,T3+                              ##
## ->  14 samples T1-,T2+,T3-                              ##
## ->   3 samples T1-,T2-,T3+                              ##
## -> 220 samples T1-,T2-,T3-                              ##
## ======================================================= ##
```

```
## how is the 3-test model defined?
define_x(3)
define_prior(3)

## fit giardia 3-test model
giardia <-
truePrevMulti(
  x = c(6, 4, 12, 12, 1, 14, 3, 220),
  n = 272,
  prior = {
    theta[1] ~ dunif(0.00, 0.20)
    theta[2] ~ dunif(0.90, 1.00)
    theta[3] ~ dunif(0.80, 1.00)
    theta[4] ~ dbeta(1, 1)
    theta[5] ~ dbeta(1, 1)
    theta[6] ~ dbeta(1, 1)
    theta[7] ~ dbeta(1, 1)
    theta[8] ~ dbeta(1, 1)
    theta[9] ~ dbeta(1, 1)
    theta[10] ~ dbeta(1, 1)
    theta[11] ~ dbeta(1, 1)
    theta[12] ~ dbeta(1, 1)
    theta[13] ~ dbeta(1, 1)
    theta[14] ~ dbeta(1, 1)
    theta[15] ~ dbeta(1, 1)
  }
)

## show model results
giardia

## coda densplots
par(mfcol = c(2, 4))
densplot(giardia, col = "red")

## End(Not run)
```

`truePrevMulti2` *Estimate true prevalence from individuals samples using multiple tests – covariance scheme*

Description

Bayesian estimation of true prevalence from apparent prevalence obtained by applying *multiple* tests to *individual* samples. `truePrevMulti2` implements and extends the approach described by Dendukuri and Joseph (2001), which uses a multinomial distribution to model observed test results, and in which conditional dependence between tests is modelled through covariances.

Usage

```
truePrevMulti2(x, n, prior, nchains = 2, burnin = 10000, update = 10000,
               verbose = FALSE)
```

Arguments

x	Vector of apparent test results; see 'Details' below
n	The total sample size
prior	The prior distributions; see 'Details' below
nchains	The number of chains used in the estimation process; must be ≥ 2
burnin	The number of discarded model iterations; defaults to 10,000
update	The number of withheld model iterations; defaults to 10,000
verbose	Logical flag, indicating if JAGS process output should be printed to the R console; defaults to FALSE

Details

truePrevMulti2 calls on **JAGS** via the **rjags** package to estimate true prevalence from apparent prevalence in a Bayesian framework. truePrevMulti2 fits a multinomial model to the apparent test results obtained by testing individual samples with a given number of tests. To see the actual fitted model, see the model slot of the prev-object.

The vector of apparent tests results, x, must contain the number of samples corresponding to each combination of test results. To see how this vector is defined for the number of tests h at hand, use define_x.

Argument prior consists of prior distributions for:

- True Prevalence: TP
- SEnsitivity of each individual test: vector SE
- SPecificity of each individual test: vector SP
- Conditional covariance of all possible test combinations given a truly positive disease status: vector a
- Conditional covariance of all possible test combinations given a truly negative disease status: vector b

To see how prior is defined for the number of tests h at hand, use define_prior2.

The values of prior can be specified in two ways, referred to as BUGS-style and list-style, respectively. See also below for some examples.

For BUGS-style specification, the values of prior should be given between curly brackets (i.e., {}), separated by line breaks. Priors can be specified to be deterministic (i.e., fixed), using the <- operator, or stochastic, using the ~ operator. In the latter case, the following distributions can be used:

- **Uniform:** `dunif(min, max)`
- **Beta:** `dbeta(alpha, beta)`
- **Beta-PERT:** `dpert(min, mode, max)`

Alternatively, priors can be specified in a *named* `list()` as follows:

- **Fixed:** `list(dist = "fixed", par)`
- **Uniform:** `list(dist = "uniform", min, max)`
- **Beta:** `list(dist = "beta", alpha, beta)`
- **Beta-PERT:** `list(dist = "pert", method, a, m, b, k)`
  `'method'` must be `"classic"` or `"vose"`;
  `'a'` denotes the pessimistic (minimum) estimate, `'m'` the most likely estimate, and `'b'` the optimistic (maximum) estimate;
  `'k'` denotes the scale parameter.
  See `betaPERT` for more information on Beta-PERT parameterization.
- **Beta-Expert:** `list(dist = "beta-expert", mode, mean, lower, upper, p)`
  `'mode'` denotes the most likely estimate, `'mean'` the mean estimate;
  `'lower'` denotes the lower bound, `'upper'` the upper bound;
  `'p'` denotes the confidence level of the expert.
  Only `mode` or `mean` should be specified; `lower` and `upper` can be specified together or alone.
  See `betaExpert` for more information on Beta-Expert parameterization.

Value

An object of class `prev`.

Note

Markov chain Monte Carlo sampling in `truePrevMulti2` is performed by **JAGS (Just Another Gibbs Sampler)** through the **rjags** package. JAGS can be downloaded from `https://mcmc-jags.sourceforge.io/`.

Author(s)

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References

- Dendukuri N, Joseph L (2001) Bayesian approaches to modeling the conditional dependence between multiple diagnostic tests. *Biometrics* **57**:158-167

See Also

`define_x`: how to define the vector of apparent test results `x`
`define_prior2`: how to define `prior`

coda for various functions that can be applied to the `prev@mcmc` object
`truePrevMulti`: estimate true prevalence from apparent prevalence obtained by testing *individual*

samples with multiple tests, using a conditional probability scheme
truePrev: estimate true prevalence from apparent prevalence obtained by testing *individual* samples with a single test
truePrevPools: estimate true prevalence from apparent prevalence obtained by testing *pooled* samples
betaPERT: calculate the parameters of a Beta-PERT distribution
betaExpert: calculate the parameters of a Beta distribution based on expert opinion

Examples

```
## Not run:
## ======================================================== ##
## 2-TEST EXAMPLE: Strongyloides                            ##
## -------------------------------------------------------- ##
## Two tests were performed on 162 humans                   ##
## -> T1 = stool examination                                ##
## -> T2 = serology test                                    ##
## Expert opinion generated the following priors:           ##
## -> SE1 ~ dbeta( 4.44, 13.31)                             ##
## -> SP1 ~ dbeta(71.25,  3.75)                             ##
## -> SE2 ~ dbeta(21.96,  5.49)                             ##
## -> SP2 ~ dbeta( 4.10,  1.76)                             ##
## The following results were obtained:                     ##
## -> 38 samples T1+,T2+                                    ##
## ->  2 samples T1+,T2-                                    ##
## -> 87 samples T1-,T2+                                    ##
## -> 35 samples T1-,T2-                                    ##
## ======================================================== ##

## how is the 2-test model defined?
define_x(2)
define_prior2(2)

## fit Strongyloides 2-test model
## a first model assumes conditional independence
## -> set covariance terms to zero
strongy_indep <-
truePrevMulti2(
  x = c(38, 2, 87, 35),
  n = 162,
  prior = {
    TP ~ dbeta(1, 1)
    SE[1] ~ dbeta( 4.44, 13.31)
    SP[1] ~ dbeta(71.25,  3.75)
    SE[2] ~ dbeta(21.96,  5.49)
    SP[2] ~ dbeta( 4.10,  1.76)
    a[1] <- 0
    b[1] <- 0
  })

## show model results
strongy_indep
```

```
## fit same model using 'list-style'
strongy_indep <-
truePrevMulti2(
  x = c(38, 2, 87, 35),
  n = 162,
  prior =
    list(
      TP = list(dist = "beta", alpha = 1, beta = 1),
      SE1 = list(dist = "beta", alpha = 4.44, beta = 13.31),
      SP1 = list(dist = "beta", alpha = 71.25, beta = 3.75),
      SE2 = list(dist = "beta", alpha = 21.96, beta = 5.49),
      SP2 = list(dist = "beta", alpha = 4.10, beta = 1.76),
      a1 = 0,
      b1 = 0
    )
  )

## show model results
strongy_indep

## fit Strongyloides 2-test model
## a second model allows for conditional dependence
## -> a[1] is the covariance between T1 and T2, given D+
## -> b[1] is the covariance between T1 and T2, given D-
## -> a[1] and b[1] can range between +/- 2^-h, ie, (-.25, .25)
strongy <-
truePrevMulti2(
  x = c(38, 2, 87, 35),
  n = 162,
  prior = {
    TP ~ dbeta(1, 1)
    SE[1] ~ dbeta( 4.44, 13.31)
    SP[1] ~ dbeta(71.25,  3.75)
    SE[2] ~ dbeta(21.96,  5.49)
    SP[2] ~ dbeta( 4.10,  1.76)
    a[1] ~ dunif(-0.25, 0.25)
    b[1] ~ dunif(-0.25, 0.25)
  })

## explore model structure
str(strongy)         # overall structure
str(strongy@par)     # structure of slot 'par'
str(strongy@mcmc)    # structure of slot 'mcmc'
strongy@model        # fitted model
strongy@diagnostics  # DIC, BGR and Bayes-P values

## standard methods
print(strongy)
summary(strongy)
par(mfrow = c(2, 2))
plot(strongy)           # shows plots of TP by default
plot(strongy, "SE[1]")  # same plots for SE1
```

```
plot(strongy, "SE[2]")  # same plots for SE2
plot(strongy, "SP[1]")  # same plots for SP1
plot(strongy, "SP[2]")  # same plots for SP2
plot(strongy, "a[1]")   # same plots for a[1]
plot(strongy, "b[1]")   # same plots for b[1]

## coda plots of all parameters
par(mfrow = c(2, 4)); densplot(strongy, col = "red")
par(mfrow = c(2, 4)); traceplot(strongy)
par(mfrow = c(2, 4)); gelman.plot(strongy)
par(mfrow = c(2, 4)); autocorr.plot(strongy)

## End(Not run)
```

`truePrevPools` *Estimate true prevalence from pooled samples*

Description

Bayesian estimation of true prevalence from apparent prevalence obtained by testing *pooled* samples.

Usage

```
truePrevPools(x, n, SE = 1, SP = 1, prior = c(1, 1),
              nchains = 2, burnin = 10000, update = 10000,
              verbose = FALSE)
```

Arguments

`x`	The vector of indicator variables, indicating whether a pool was positive (`"1"`) or negative (`"0"`)
`n`	The vector of pool sizes
`SE`, `SP`	The prior distribution for sensitivity (SE) and specificity (SP); see 'Details' below for specification of these distributions
`prior`	The parameters of the prior Beta distribution for true prevalence; defaults to `c(1, 1)`
`nchains`	The number of chains used in the estimation process; `nchains` must be ≥ 2
`burnin`	The number of discarded model iterations; defaults to 10,000
`update`	The number of withheld model iterations; defaults to 10,000
`verbose`	Logical flag, indicating if JAGS process output should be printed to the R console; defaults to `FALSE`

Details

truePrevPools calls on **JAGS/rjags** to estimate the true prevalence from the apparent prevalence in a Bayesian framework. The default model, in BUGS language, is given below. To see the actual fitted model, see the model slot of the prev-object.

```
model {
  for (i in 1:N) {
    x[i] ~ dbern(AP[i])
  AP[i] <- SEpool[i] * (1 - pow(1 - TP, n[i])) + (1 - SPpool[i]) * pow(1 - TP, n[i])
    SEpool[i] <- 1 - (pow(1 - SE, n[i] * TP) * pow(SP, n[i] * (1 - TP)))
    SPpool[i] <- pow(SP, n[i])
  }
# SE ~ user-defined (see below)
# SP ~ user-defined (see below)
TP ~ dbeta(prior[1], prior[2])
}
```

The test sensitivity (SE) and specificity (SP) can be specified by the user, independently, as one of "fixed", "uniform", "beta", "pert", or "beta-expert", with "fixed" as the default. Note that SE and SP must correspond to the test characteristics for testing individual samples; truePrevPools will calculate SEpool and SPpool, the sensitivity and specificitiy for testing pooled samples, based on Boelaert et al. (2000).

Distribution parameters can be specified in a *named* list() as follows:

- **Fixed:** list(dist = "fixed", par)
- **Uniform:** list(dist = "uniform", min, max)
- **Beta:** list(dist = "beta", alpha, beta)
- **PERT:** list(dist = "pert", method, a, m, b, k)
  'method' must be "classic" or "vose";
  'a' denotes the pessimistic (minimum) estimate, 'm' the most likely estimate, and 'b' the optimistic (maximum) estimate;
  'k' denotes the scale parameter.
  See betaPERT for more information on Beta-PERT parametrization.
- **Beta-Expert:** list(dist = "beta-expert", mode, mean, lower, upper, p)
  'mode' denotes the most likely estimate, 'mean' the mean estimate;
  'lower' denotes the lower bound, 'upper' the upper bound;
  'p' denotes the confidence level of the expert.
  Only mode or mean should be specified; lower and upper can be specified together or alone.
  See betaExpert for more information on Beta-Expert parameterization.

For Uniform, Beta and Beta-PERT distributions, BUGS-style short-hand notation is also allowed:

- **Uniform:** ~dunif(min, max)
- **Beta:** ~dbeta(alpha, beta)
- **Beta-PERT:** ~dpert(min, mode, max)

Value

An object of class prev.

Note

Markov chain Monte Carlo sampling in truePrevPools is performed by **JAGS (Just Another Gibbs Sampler)** through the **rjags** package. JAGS can be downloaded from https://mcmc-jags.sourceforge.io/.

Author(s)

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References

- Speybroeck N, Williams CJ, Lafia KB, Devleesschauwer B, Berkvens D (2012) Estimating the prevalence of infections in vector populations using pools of samples. *Med Vet Entomol* **26**:361-371
- Boelaert F, Walravens K, Biront P, Vermeersch JP, Berkvens D, Godfroid J (2000) Prevalence of paratuberculosis (Johne's disease) in the Belgian cattle population. *Vet Microbiol* **77**:269-281

See Also

coda for various functions that can be applied to the prev@mcmc object
truePrev: estimate true prevalence from apparent prevalence obtained by testing *individual* samples with a single test
truePrevMulti: estimate true prevalence from apparent prevalence obtained by testing *individual* samples with multiple tests, using a conditional probability scheme
truePrevMulti2: estimate true prevalence from apparent prevalence obtained by testing *individual* samples with multiple tests, using a covariance scheme
betaPERT: calculate the parameters of a Beta-PERT distribution
betaExpert: calculate the parameters of a Beta distribution based on expert opinion

Examples

```
## Sandflies in Aurabani, Nepal, 2007
pool_results <- c(0, 0, 0, 0, 0, 0, 0, 0, 1, 0)
pool_sizes <- c(2, 1, 6, 10, 1, 7, 1, 4, 1, 3)

## Sensitivity ranges uniformly between 60% and 95%
## Specificity is considered to be 100%

#> BUGS-style:
truePrevPools(x = pool_results, n = pool_sizes,
              SE = ~dunif(0.60, 0.95), SP = 1)

#> list-style:
SE <- list(dist = "uniform", min = 0.60, max = 0.95)
truePrevPools(x = pool_results, n = pool_sizes,
```

```
                SE = SE, SP = 1)
```

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