

Package: PROreg (via r-universe)

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Description It offers a wide variety of techniques, such as graphics, recoding, or regression models, for a comprehensive analysis of patient-reported outcomes (PRO). Especially novel is the broad range of regression models based on the beta-binomial distribution useful for analyzing binomial data with over-dispersion in cross-sectional, longitudinal, or multidimensional response studies (see Najera-Zuloaga J., Lee D.-J. and Arostegui I. (2019) <[doi:10.1002/bimj.201700251](https://doi.org/10.1002/bimj.201700251)>).

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BB *The Beta-Binomial Distribution*

Description

Density and random generation for the beta-binomial distribution.

Usage

```
dBB(m, p, phi)
rBB(k, m, p, phi)
```

Arguments

k	number of simulations.
m	maximum score number in each beta-binomial observation..
p	probability parameter of the beta-binomial distribution.
phi	dispersion parameter of the beta-binomial distribution.

Details

The beta-binomial distribution consists of a finite sum of Bernoulli dependent variables whose probability parameter is random and follows a beta distribution. Assume that we have y_j a set of variables, $j = 1, \dots, m$, with m integer, that conditioned on a random variable u , are independent and follow a Bernoulli distribution with probability parameter u . On the other hand, the random variable u follows a beta distribution with parameter p/phi and $(1 - p)/phi$. Namely,

$$y_j \sim Ber(u), u \sim Beta(p/phi, (1 - p)/phi),$$

where $0 < p < 1$ and $phi > 0$. The first and second order marginal moments of this distribution are defined as

$$E[y_j] = p, Var[y_j] = p(1 - p),$$

and correlation between observations is defined as

$$Corr[y_j, y_k] = phi/(1 + phi),$$

where $j, k = 1, \dots, m$ are different. Consequently, phi can be considered as a dispersion parameter.

If we sum up all the variables we will define a new variable which follows a new distribution that is called beta-binomial distribution, and it is defined as follows. The variable y follows a beta-binomial distribution with parameters m, p and phi if

$$y|u \sim Bin(m, u), u \sim Beta(p/phi, (1 - p)/phi).$$

Value

`dBB` gives the density of a beta-binomial distribution with the defined m, p and phi parameters.

`rBB` generates k random observations based on a beta-binomial distribution with the defined m, p and phi parameters.

Author(s)

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D.-J. Lee

I. Arostegui

References

Arostegui I., Nunez-Anton V. & Quintana J. M. (2006): Analysis of short-form-36 (SF-36): The beta-binomial distribution approach, *Statistics in Medicine*, **26**, 1318-1342

See Also

The `rbeta` and `rbinom` functions of package `stats`.

Examples

```

set.seed(12)
# We define
m <- 10
p <- 0.4
phi <- 1.8

# We perform k beta-binomial simulations for those parameters.
k <- 100
bb <- rBB(k,m,p,phi)
bb
dd <- dBB(m,p,phi)

# We are going to plot the histogram of the created variable,
# and using dBB() function we are going to fit the distribution:
hist(bb,col="grey",breaks=seq(-0.5,m+0.5,1),probability=TRUE,
     main="Histogram",xlab="Beta-binomial random variable")
lines(seq(0,m),dd,col="red",lwd=4)

```

BBest

Estimation of the parameters of a beta-binomial distribution

Description

This function performs the estimation of the parameters of a beta-binomial distribution for the given data and maximum score number in each observation.

There are two different approaches available for performing the estimation of the parameters: (i) Method of moments, and, (ii) maximum likelihood approach.

Usage

```
BBest(y,m,method="MM")
```

Arguments

y	response variable which folloes a beta-binomial distribution.
m	maximum score number in each beta-binomial observation.
method	the method used for performing the estimation of the probability and dispersion parameters of a beta-binomial distribution, "MM" for the method of moments and "MLE" for maximum likelihood estimation. Default "MM".

Details

BBest function performs estimations in the parameters of a beta-binomial distribution for the given data. The estimations can be performed using two different approaches, the methods of moments and the maximum likelihood estimation approach.

The density function of a given observation y that follows a beta-binomial distribution with parameters m , p and ϕ is defined as

$$f(y) = [\Gamma(1/\phi) * \Gamma(p/\phi + m) * \Gamma((1-p)/\phi + m)] / [\Gamma(1/\phi + m) * \Gamma(p/\phi) * \Gamma((1-p)/\phi)].$$

The first and second order moments are defined as

$$E[y] = mp$$

$$Var[y] = mp(1-p)[1 + (n-1)\phi/(1+\phi)].$$

Hence, if $y = (y_1, \dots, y_n)$ is the given data, we can conclude the method of moments from the previous as

$$p = E/m,$$

$$\phi = [V - mp(1-p)] / [mp(1-p)m - V],$$

where E is the sample mean and V is the sample variance.

On the other hand, the maximum likelihood estimation of both parameters consists of solving the derivative of the log-likelihood defined by the density function with respect to each parameter and equaling them to zero. An iterative algorithm is needed for both parameter estimation as the score equations the parameters depend each other.

The variance of the estimation of the probability parameter of the beta-binomial distribution for the given data set is computed by the inverse of the Fisher information, i.e., the inverse of the negative second derivative of the log-likelihood replacing p by its estimation.

Value

BBest returns an object of class "BBest".

The function summary (i.e., `summary.BBest`) can be used to obtain or print a summary of the results.

<code>p</code>	estimated probability parameter of the beta-binomial distribution.
<code>phi</code>	estimated dispersion parameter of the beta-binomial distribution.
<code>pVar</code>	variance of the estimation of the probability parameter <code>p</code> .
<code>psi</code>	estimation of the logarithm of the dispersion parameter <code>phi</code> .
<code>psiVar</code>	variance of the estimation of the logarithm of the dispersion parameter <code>psi</code> .
<code>m</code>	maximum score number in each beta-binomial observation.
<code>balanced</code>	if the response variable is balanced it returns "yes", otherwise "no".
<code>method</code>	the used approach for performing the estimations.

Author(s)

J. Najera-Zuloaga

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I. Arostegui

References

Arostegui I., Nunez-Anton V. & Quintana J. M. (2006): Analysis of short-form-36 (SF-36): The beta-binomial distribution approach, *Statistics in Medicine*, **26**, 1318-1342

Examples

```
# We simulate 1000 observations of a beta-binomial distribution
# for the fixed paramters.
m <- 10
k <- 1000
p <- 0.7
phi <- 1.6

set.seed(5)
y <- rBB(k,m,p,phi)

# Performing the estimation of the parameters

# Method of moments:
MM <- BBest(y,m)
MM

# Maximum likelihood approach
MLE <- BBest(y,m,method="MLE")
MLE
```

BBmm

Beta-binomial mixed-effects model

Description

BBmm function performs beta-binomial mixed-effects models, i.e., it allows the inclusion of gaussian random effects in the linear predictor of a logistic beta-binomial regression model.

The structure of the random part of the model can be expecified by two different ways: (i) determining the random. formula argument, or (ii) especifying the model matrix of the random effects, Z, and determining the number of random effects in each random component, nRandComp.

For the estimation of the parameters the joint log-likelihood can be optimized by means of two different approaches: (i) BB-Delta, specific Delta algorithm developed for beta-binomial mixed-effect regression models, and (ii) usual Newton-Raphson method.

Usage

```
BBmm(fixed.formula,X,y,random.formula,Z=NULL,nRandComp=NULL,m,data,
      method="BB-Delta",maxiter=50,show=FALSE,nDim=1,tolerance=10^(-6))
```

Arguments

<code>fixed.formula</code>	an object of class "formula" (or one that can be coerced to that class): a symbolic description of the fixed part of the model to be fitted. It must be specified in cases where the model matrix of the fixed effects X and the outcome variable y are not specified.
<code>X</code>	a matrix class object containing the covariate structure of the fixed part of the model to be fitted. If the <code>fixed.formula</code> argument is specified this argument should not be defined, as we will be specifying twice the fixed structure of the model.
<code>y</code>	a vector containing the outcome variable(s). If joint analysis is expected, the outcome variables must be listed one after another in a vector.
<code>random.formula</code>	an object of class "formula" (or one that can be coerced to that class): a symbolic description of the random part of the model to be fitted. It must be specified in cases where the model matrix of the random effects Z is not determined.
<code>Z</code>	the design matrix of the random effects. If the <code>random.formula</code> argument is specified this argument should not be specified, as we will be specifying twice the random structure of the model.
<code>nRandComp</code>	the number of random effects in each random component of the model. It must be specified as a vector, where the i 'th value must correspond with the number of random effects of the i 'th random component. It must be only determined when we specify the random structure of the model by the model matrix of the random effects, Z .
<code>m</code>	maximum score number in each beta-binomial observation.
<code>data</code>	an optional data frame, list or environment (or object coercible by <code>as.data.frame</code> to a data frame) containing the variables in the model. If not found in data, the variables are taken from <code>environment(formula)</code> .
<code>method</code>	the methodology for performing the estimation of the parameters. Options "BB-Delta" or "NR". Default "BB-Delta".
<code>maxiter</code>	the maximum number of iterations in the parameters estimation algorithm. Default 50.
<code>show</code>	logical parameter. If TRUE, the step by step optimization process will be shown in the screen. FALSE by default.
<code>nDim</code>	number of response outcome variables involved in the multidimensional analysis. <code>nDim=1</code> by default.
<code>tolerance</code>	tolerance of the estimated linear predictor in the estimation process. <code>tolerance=10⁻⁶</code> by default.

Details

BBmm function performs beta-binomial mixed-effects regression models. It extends the beta-binomial regression model including gaussian random effects in the linear predictor. The model is defined as, conditional on some gaussian random effects u , the response variable y follows a beta-binomial distribution with parameters m , p and ϕ ,

$$y|u \sim BB(m, p, \phi), \text{ and } u \sim N(0, D)$$

where the regression model is defined as,

$$\log(p/(1-p)) = X * \beta + Z * u$$

and D is determined by some dispersion parameters included in the parameter vector θ .

The estimation of the regression parameters β and the prediction of the random effects u is done via the extended likelihood, where the marginal likelihood is approximated to the h-likelihood by a first order Laplace approximation,

$$h = f(y|\beta, u, \theta) + f(u|\theta).$$

The previous formula do not have a closed form and numerical methods are needed for the estimation procedure. Two approaches are available in the function in order to perform the fixed and random effects estimation: (i) A special case of the Delta algorithm developed for beta-binomial mixed-effects model estimations, and (ii) the general Newton-Raphson algorithm available in R-package `rootSolve`.

On the other hand, the estimation of dispersion parameters by the h-likelihood can be bias due to the previous estimation of the regression parameters. Consequently, a penalization of the h-likelihood must be performed to get unbiased estimations of the dispersion parameters. Lee and Nelder (1996) proposed the adjusted profile h-likelihood, where the following penalization is applied,

$$h(\theta) = h + (1/2) * \log[\det(2\pi H^{-1})],$$

being H the Hessian matrix of the model, replacing the terms β and u involved in the previous formula with their estimates.

The method iterates between both estimation processes until convergence is reached based on the pre-established tolerance of the linear predictor.

Value

BBmm returns an object of class "BBmm".

The function `summary` (i.e., `summary.BBmm`) can be used to obtain or print a summary of the results..

<code>fixed.coef</code>	estimated value of the fixed coefficients of the regression.
<code>fixed.vcov</code>	variance and covariance matrix of the estimated fixed coefficients of the regression.
<code>random.coef</code>	predicted random effects of the regression.
<code>sigma.coef</code>	estimated value of the random effects variance parameters.
<code>sigma.var</code>	variance of the estimated value of the random effects variance parameters.
<code>phi.coef</code>	estimated value of the dispersion parameter of the conditional beta-binomial distribution.
<code>psi.coef</code>	estimated value of the logarithm of the dispersion parameter of the conditional beta-binomial distribution.
<code>psi.var</code>	variance of the estimation of the logarithm of the conditional beta-binomial distribution.
<code>fitted.values</code>	the fitted mean values of the probability parameter of the conditional beta-binomial distribution.

conv	convergence of the methodology. If the method has converged it returns "yes", otherwise "no".
deviance	deviance of the model.
df	degrees of freedom of the model.
null.deviance	null-deviance, deviance of the null model. The null model will only include an intercept as the estimation of the probability parameter.
null.df	degrees of freedom of the null model.
nRand	number of random effects.
nComp	number of random components.
nRandComp	number of random effects in each random component of the model.
namesRand	names of the random components.
iter	number of iterations in the estimation method.
nObs	number of observations in the data.
y	dependent response variable in the model.
X	model matrix of the fixed effects.
Z	model matrix of the random effects.
D	variance and covariance matrix of the random effects.
balanced	if the response dependent variable is balanced it returns "yes", otherwise "no".
m	maximum score number in each beta-binomial observation.
call	the matched call.
formula	the formula supplied.

Author(s)

J. Najera-Zuloaga

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I. Arostegui

References

Najera-Zuloaga, J.; Lee, D.-J.; Esteban, C. & Arostegui, I. (2023): Multidimensional beta-binomial regression model: a joint analysis of patient-reported outcomes. *Statistical Modelling*, 0(0).

Najera-Zuloaga J., Lee D.-J. & Arostegui, I. (2019): A beta-binomial mixed effects model approach for analysing longitudinal discrete and bounded outcomes. *Biometrical Journal*, 61(3), 600-615.

Najera-Zuloaga J., Lee D.-J. & Arostegui I. (2018): Comparison of beta-binomial regression model approaches to analyze health related quality of life data. *Statistical Methods in Medical Research*, 27(10), 2989-3009.

Lee Y. & Nelder J. A. (1996): Hierarchical generalized linear models, *Journal of the Royal Statistical Society. Series B*, 58, 619-678

See Also

The [multroot](#) and [uniroot](#) functions of the R-package [rootSolve](#) for the general Newton-Raphson algorithm.

Examples

```

set.seed(7)

# Defining the parameters
k <- 100
m <- 10
phi <- 0.5
beta <- c(1.5,-1.1)
sigma <- 0.5

# Simulating the covariate and random effects
x <- runif(k,0,10)
X <- model.matrix(~x)
z <- as.factor(rBI(k,4,0.5,2))
Z <- model.matrix(~z-1)
u <- rnorm(5,0,sigma)

# The linear predictor and simulated response variable
eta <- beta[1]+beta[2]*x+crossprod(t(Z),u)
p <- 1/(1+exp(-eta))
y <- rBB(k,m,p,phi)
dat <- data.frame(cbind(y,x,z))
dat$z <- as.factor(dat$z)

# Apply the model
model <- BBmm(fixed.formula = y~x,random.formula = ~z,m=m,data=dat)
model

#-----#

# Multidimensional regression with 2 dimensions

set.seed(5)
nId <- 25

# Simulation

m <- 10
beta1 <- c(1,-0.5)
beta2 <- c(-1,0.5)
beta <- cbind(beta1,beta2)

x1 <- rnorm(nId, 1,2)
X1 <- model.matrix(~x1)
x2 <- rnorm(nId, -1,1)
X2 <- model.matrix(~x2)

```

```

sigma <- 0.6
u <- rnorm(nId,0,sigma)

eta1 <- beta1[1]+x1*beta1[2]+u
p1 <- 1/(1+exp(-eta1))
eta2 <- beta2[1]+x2*beta2[2]+u
p2 <- 1/(1+exp(-eta2))

phi1 <- 0.3
phi2 <- 1
phi <- c(phi1,phi2)

y1 <- rBB(nId,m,p1,phi1)
y2 <- rBB(nId,m,p2,phi2)
y <- c(y1,y2)

# Define matrices

X <- Matrix::bdiag(X1,X2)
X <- as.matrix(X)
Z <- diag(nId)
Z <- kronecker(rbind(1,1),Z.)

# Fit the model

Model.multi <- BBmm(X=X,y=y,Z=Z,nRandComp = nId,m=m,nDim=2)
Model.multi

```

BBreg

Fit a beta-binomial logistic regression model

Description

BBreg function fits a beta-binomial logistic regression model, i.e., it links the probability parameter of a beta-binomial distribution with the given covariates by means of a logistic link function. The estimation of the parameters in the model is done via maximum likelihood estimation.

Usage

```
BBreg(formula,m,data,maxiter=100)
```

Arguments

formula	an object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted.
m	maximum score number in each beta-binomial observation.

data	an optional data frame, list or environment (or object coercible by <code>as.data.frame</code> to a data frame) containing the variables in the model. If not found in data, the variables are taken from <code>environment(formula)</code> .
maxiter	the maximum number of iterations in the estimation process. Default 100.

Details

There are two different ways of defining a regression model based on the beta-binomial distribution: (i) the marginal regression approach, (ii) hierarchical generalized linear model approach. *Najera-Zuloaga et al. (2017)* proved that the first approach is more adequate when the interest consists of the interpretation of the regression coefficients. Consequently, this function is based on the first approach, i.e., the marginal regression approach.

Once the marginal density function of the beta-binomial distribution is explicitly calculated, we connect the probability parameter with the given covariates by means of a logistic link function:

$$\text{logit}(p) = \log(p/(1-p)) = X * \text{beta}$$

where X a model matrix composed by the given covariates and beta are the regression coefficients of the model.

Replacing the previous linear predictor in the marginal density function of the beta-binomial distribution, we can derive maximum likelihood estimations of both regression and dispersion parameters. Forcina and Franconi (1988) presented an estimation algorithm based on the Newton-Raphson approach. This function performs the estimation of the parameters following the presented methodology.

Value

BBreg returns an object of class "BBreg".

The function `summary` (i.e., `summary.BBreg`) can be used to obtain or print a summary of the results.

coefficients	the estimated value of the regression coefficients.
vcov	the variance-covariance matrix of the estimated coefficients of the regression.
phi	the estimation of the dispersion parameter of the beta-binomial distribution.
psi	the estimation of the logarithm of the dispersion parameter of the beta-binomial distribution.
psi.var	the variance of the estimated logarithm of the dispersion parameter of the beta-binomial distribution.
conv	convergence of the methodology. If the method has converged it returns "yes", otherwise "no".
fitted.values	the fitted mean values of the model.
deviance	the deviance of the model.
df	degrees of freedom of the model.
null.deviance	null-deviance, the deviance for the null model. The null model will only include an intercept as the estimation of the probability parameter.
null.df	the degrees of freedom for the null model.

iter	number of iterations in the estimation process.
X	the model matrix.
y	the dependent response variable in the model.
m	maximum score number in each beta-binomial observation.
balanced	if the response beta-binomial variable is balanced it returns "yes", otherwise "no".
nObs	number of observations.
call	the matched call.
formula	the formula supplied.

Author(s)

J. Najera-Zuloaga

D.-J. Lee

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References

Forcina A. & Franconi L. (1988): Regression analysis with Beta-Binomial distribution, *Revista di Statistica Applicata*, **21**, 7-12

Najera-Zuloaga J., Lee D.-J. & Arostegui I. (2017): Comparison of beta-binomial regression model approaches to analyze health related quality of life data, *Statistical Methods in Medical Research*, DOI: 10.1177/0962280217690413

Examples

```
# We simulate a covariate, fix the parameters of the beta-binomial
# distribution and simulate a response variable.

# Then we apply the model, and try to get the same values.
set.seed(18)
k <- 1000
m <- 10
x <- rnorm(k,5,3)

beta <- c(-10,2)
p <- 1/(1+exp(-(beta[1]+beta[2]*x)))
phi <- 1.2

y <- rBB(k,m,p,phi)

model <- BBreg(y~x,m)
model
```

Description

Density and random generation for the binomial distribution with optional dispersion parameter.

Usage

```
dBI(m,p,phi)
rBI(k,m,p,phi)
```

Arguments

k	number of simulations.
m	number of trials in each binomial observation.
p	probability parameter of the binomial distribution.
phi	dispersion parameter of the binomial distribution. If phi=1, the binomial distribution without dispersion parameter will be considered. Default 1.

Details

The binomial distribution belongs to the exponential family of distributions. Consequently, although the usual binomial distribution only consists of two parameters, an additional dispersion parameter can be included. The inclusion of a dispersion parameter softens the relationship between the expectation and variance that the binomial distribution keeps, i.e. the model allows overdispersion to be included,

$$E[y] = mp, Var[y] = phi * mp(1 - p).$$

The density function of the binomial distribution with dispersion parameter is based on the exponential family approach and it is defined as

$$f(y) = exp\{[y * log(p/(1 - p)) + m * log(1 - p)]/phi + c(y, phi)\},$$

where $c()$ is a function that it is approximated with the deviance of the model by quadratic approximations of the log-likelihood function.

Value

dBI gives the density of the binomial distribution for those m, p and phi parameters.

rBI generates k random observations based on a binomial distribution for those m, p and phi parameters.

Author(s)

J. Najera-Zuloaga
D.-J. Lee
I. Arostegui

References

Pawitan Y. (2001): *In All Likelihood: Statistical Modelling and Inference Using Likelihood*. Oxford University Press

See Also

The `rbinom` functions of package `stats`. This function performs simulations based on a binomial distribution without dispersion parameter.

Examples

```
k <- 1000
m <- 10
p <- 0.765
phi <- 4.35

#simulating
y <- rBI(k,m,p,phi)
y

#density function
d <- dBI(m,p,phi)
d

#plot the simulated variable and fit the density
hist(y,col="lightgrey")
lines(seq(0,m),k*d,col="blue",lwd=2)
```

BIest

Estimation of the parameters of a binomial distribution with optional dispersion parameter.

Description

BIest function estimates the probability parameter of a binomial distribution for the given data and number of trials. It is possible to include a dispersion parameter in the binomial distribution and get the estimation by the method of moments or maximum quasi-likelihood approach. This function also returns the standard deviation of the estimated probability parameter and the upper and lower bounds of the 95% confidence interval.

Usage

```
BIest(y,m,disp=FALSE,method="MM")
```

Arguments

<code>y</code>	response variable which follows a binomial distribution.
<code>m</code>	number of trials in each binomial observation.
<code>disp</code>	dispersion parameter of the binomial distribution. If <code>phi=FALSE</code> , then the binomial distribution without dispersion parameter will be considered for estimation. Default <code>FALSE</code> .
<code>method</code>	the method used for estimating the parameters, "MM" for the method of moments and "MLE" for maximum quasi-likelihood. Default "MM".

Details

This function performs the estimation of the parameters involved in a binomial distribution for a given data.

The estimation of the probability parameter is done by either maximum likelihood approach or method of moments due to the fact that both approaches give the same estimation,

$$p = \text{sum}(y)/(m * n),$$

where m is the number of trials and n is the number of observations.

If the dispersion parameter is included in the model, `BIest` function performs its estimation by the method of moments or maximum quasi-likelihood methodology. The method of moments is based on the variance equation of a binomial distribution with dispersion parameter

$$\text{Var}[y] = \text{phi} * mp(1 - p).$$

The maximum quasi-likelihood approach is based on the quadratic approximation of the log-likelihood function of a binomial distribution with dispersion parameter, where the unknown term involving phi is estimated with the deviance of the model.

The standard deviation of the estimated probability parameter is calculated by the Fisher information, i.e., the negative of the second derivative of the log-likelihood (log-quasi-likelihood) function.

Value

`BIest` returns an object of class "BIest".

<code>p</code>	estimation of the probability parameter. Both estimating approaches, the method of moments and the maximum likelihood estimation, perform the same estimation.
<code>pVar</code>	the variance of the estimated probability parameter.
<code>pIC.low</code>	the lower bound of the 95% confidence interval of the estimated probability parameter.
<code>pIC.up</code>	the upper bound of the 95% confidence interval of the estimated probability parameter.
<code>phi</code>	if the <code>disp</code> option is <code>TRUE</code> , it returns the estimated value of the dispersion parameter. Default <code>FALSE</code> .
<code>m</code>	number of trials in each binomial observation.
<code>balanced</code>	if the data is balanced it returns "yes", otherwise "no".
<code>method</code>	the used methodology for performing the estimation of the parameters.

Author(s)

J. Najera-Zuloaga

D.-J. Lee

I. Arostegui

References

Pawitan Y. (2001): *In All Likelihood: Statistical Modelling and Inference Using Likelihood*, Oxford University Press

See Also

The [rBI](#) and [dBI](#) functions of package HRQoL. The functions perform simulations and estimate the density of a binomial distribution with optional dispersion parameter for a given set of parameters.

Examples

```
set.seed(9)
# We simulate the binomial data with some fixed parameters and
# then try to reach the same estimations.
m <- 10
k <- 100
p <- 0.654
y <- rBI(k,m,p) #Simulations

# without dispersion parameter
BIest(y,m)

# with dispersion parameter
# estimation by method of moments.
BIest(y,m,disp=TRUE,method="MM")
# estimation by maximum quasi-likelihood.
BIest(y,m,disp=TRUE,method="MLE")
```

EDpro

Eating Disorders patient-reported outcome data.

Description

A prospective study of patients diagnosed with an eating disorder who were followed up for two years in the Eating Disorders Outpatient Clinic of the Psychiatric Service at Galdakao Hospital in Bizkaia, Basque Country.

Usage

```
data(EDpro)
```

Format

The EDpro data frame has 525 rows and 18 columns. The variables included in the data frame are the following:

- id: Patient identifier.
- visit: Visit number.
- bmi: Body Mass Index.
- age: Age.
- duration: Duration of the illness in years.
- diagnosis: Diagnosis of the eating disorder (1: Anorexia Nervosa, 2: Bulimic Anorexia, 3: Bulimia Nervosa/Binge Eating).
- severity: Severity of the disease, using the Eating Attitudes Test (1: Mild, 2: Moderate, 3: Severe).
- anxiety: Level of anxiety using the Hospital Anxiety and Depression Scale (0: No, 1: Yes).
- depression: Level of depression using the Hospital Anxiety and Depression Scale (0: No, 1: Yes).
- pf: Physical Function dimension measured by the SF-36 questionnaire.
- rp: Role Physical dimension measured by the SF-36 questionnaire.
- bp: Body Pain dimension measured by the SF-36 questionnaire.
- gh: General Health dimension measured by the SF-36 questionnaire.
- vt: Vitality dimension measured by the SF-36 questionnaire.
- sf: Social Functioning dimension measured by the SF-36 questionnaire.
- re: Role Emotional dimension measured by the SF-36 questionnaire.
- mh: Mental Health dimension measured by the SF-36 questionnaire.
- time: Years elapsed since the beginning of the study.

Details

All consecutive patients seen at the Eating Disorders Outpatient Clinic of the Psychiatric Service at Galdakao Hospital between October 1996 and October 1997 were eligible for the study. Patients were included if they were ambulatory; had received a diagnosis of anorexia nervosa or bulimia nervosa based on criteria in the Diagnostic and Statistical Manual of Mental Disorders, 4th edition (DSM-IV); and were between the ages of 14 and 65 years.

Throughout the 2-year study period, each of the 193 patient received a psychopharmacologic and psychotherapeutic treatment program consisting of cognitive-behavioural treatment; nutritional orientation and counselling; psychoeducation; motivationaltherapy; social skills training; and therapy to modify distorted perception of body image. These interventions were adjusted to each patient's needs by a multidisciplinary team.

At most, 3 measurements were obtained from each of the 193 patients: at baseline, at one year, and at two years from the start of the study. Clinical measurements and Health-Related Quality of Life (HQRoL) data were recorded at each visit using the Short Form-36 (SF-36) and the Hospital Anxiety and Depression (HAD) Scale health questionnaires.

More information about the study can be found in Padierna et al. (2002) and Arostegui et al. (2007).

References

Arostegui I., Nunez-Anton V. & Quintana J. M. (2007): Analysis of short-form-36 (SF-36): The beta-binomial distribution approach, *Statistics in Medicine*, **26**, 1318-1342.

Padierna A., Quintana J.M., Arostegui I., Gonzalez N. & Horcajo M.J.(2002): Changes in health related quality of life among patients treated for eating disorders, *Quality of Life Research*, **11**, 545-552.

 HRQoLplot

Spider plot of the dimensions of the Short Form-36 Health Survey

Description

This function creates a spider plot with the 8 health related quality of life dimensions provided by the Short Form-36 Health Survey.

Usage

```
HRQoLplot(data,legend=FALSE,title="Short Form-36 Health Survey",
           dimlabel.cex=NULL,legend.cex=1,linewidth=3,title.cex=1,lty=1)
```

Arguments

<code>data</code>	a data frame with each column relative to the observations of each SF-36 dimension. The columns of the data frame must be introduced in the following order: <ol style="list-style-type: none"> 1. column -> Physical Functioning 2. column -> Role Physical 3. column -> Body Pain 4. column -> General Health 5. column -> Vitality 6. column -> Social Functioning 7. column -> Role Emotional 8. column -> Mental Health
<code>legend</code>	logical parameter, if TRUE the legend with the name of the rows of the data will appear. Default FALSE.
<code>title</code>	the title of the plot. Default "Short Form-36 Health Survey".
<code>dimlabel.cex</code>	font size magnification for the labels of the dimension in the plot. If NULL, the font size is fixed at text()'s default. Default NULL.
<code>legend.cex</code>	font size of legend text(). Default 1.
<code>linewidth</code>	the width of the lines of the plot. Default 3.
<code>title.cex</code>	the font size of the title. Default 1.
<code>lty</code>	the line type of the plot and the legend. Default 1.

Details

The Short Form-36 Health Survey is a commonly used technique to measure the Health Related Quality of Life (HRQoL) in chronic diseases. It was developed within the Medical Outcomes Study (Ware *et al.* (1993)). It measures generic HRQoL concepts and provides an objective way to measure HRQoL from the patients point of view by scoring standardized responses to standardized questions. The validity and reliability of this instrument has been broadly tested (Stansfeld *et al.* (1997)). The SF-36 has 36 items, with different answer options. It was constructed to represent eight health dimensions, which are *physical functioning* (PF), *role physical* (RP), *body pain* (BP), *general health* (GH), *vitality* (VT), *social functioning* (SF), *role emotional* (RE) and *mental health* (MH). Each item is assigned to a unique health dimension. Each of the multi-item dimensions contains two to ten items. The first four dimensions are mainly physical, whereas the last four measure mental aspects of HRQoL. The resulting raw scores are typically transformed to standardized scale scores from 0 to 100, where a higher score indicates a better health status.

Arostegui *et al.* (2013) proposed a recoding methodology for the Short Form-36 Health Survey (SF-36) dimensions in order to apply a beta-binomial distribution. The HRQoLplot function plots the SF-36 dimensions scores in a spider plot. Each axis of the plot refers to an specific SF-36 dimension. Hence, the order of the dimensions in the data frame object of the function has been established as it has been explained in Arguments section. Each observation of the data frame, the value of each observation in all the dimensions, is drawn with a line of a different color in the plot. The plot shows the name of each dimension and the maximum number of scores each dimension can obtain in each axis of the plot.

Author(s)

J. Najera-Zuloaga

D.-J. Lee

I. Arostegui

This function depends on the function [radarchart](#) of the package fmsb created by Minato Nakazawa.

References

Arostegui I., Nunez-Anton V. & Quintana J. M. (2013): On the recoding of continuous and bounded indexes to a binomial form: an application to quality-of-life scores, *Journal of Applied Statistics*, **40**, 563-583

See Also

As it is said in the author section, the function depends on the function [radarchart](#) of the package fmsb

Examples

```
set.seed(5)
# We insert the columns in the order that has been determined:
n <- c(20,4,9,20,20,8,3,13)
k=3
p=runif(8,0,1)
phi <- runif(8,1,3)
```

```
dat <- data.frame(
  PF=rBB(k,n[1],p[1],phi[1]),
  RP=rBB(k,n[2],p[2],phi[2]),
  BP=rBB(k,n[3],p[3],phi[3]),
  GH=rBB(k,n[4],p[4],phi[4]),
  VT=rBB(k,n[5],p[5],phi[5]),
  SF=rBB(k,n[6],p[6],phi[6]),
  RE=rBB(k,n[7],p[7],phi[7]),
  MH=rBB(k,n[8],p[8],phi[8]))

rownames(dat) <- c("ID1", "ID2", "ID3")
HRQoLplot(dat,TRUE)
```

print.BBest *Print a BBest class model.*

Description

print.BBest is the BBest specific method for the generic function print which prints objects returned by modelling functions.

Usage

```
## S3 method for class 'BBest'
print(x, ...)
```

Arguments

x a BBest class model.
... for extra arguments.

Value

Prints a BBest object.

Author(s)

J. Najera-Zuloaga
D.-J. Lee
I. Arostegui

References

Arostegui I., Nunez-Anton V. & Quintana J. M. (2006): Analysis of short-form-36 (SF-36): The beta-binomial distribution approach, *Statistics in Medicine*, **26**, 1318-1342

See Also

[BBest](#)

Examples

```
set.seed(9)
# Simulate a binomial distribution
y <- rBB(100,10,0.5,2)

# Apply the model
model <- BBest(y,10)
print(model) # or just model
```

print.BBmm *Print a BBmm class model.*

Description

print.BBmm is the BBmm specific method for the generic function print which prints objects returned by modelling functions.

Usage

```
## S3 method for class 'BBmm'
print(x, ...)
```

Arguments

x a BBmm class model.
... for extra arguments.

Value

Prints a BBmm object.

Author(s)

J. Najera-Zuloaga
D.-J. Lee
I. Arostegui

References

Breslow N. E. & Calyton D. G. (1993): Approximate Inference in Generalized Linear Mixed Models, *Journal of the American Statistical Association*, **88**, 9-25

Lee Y. & Nelder J. A. (1996): Hierarchical generalized linear models, *Journal of the Royal Statistical Society. Series B*, **58**, 619-678

Najera-Zuloaga J., Lee D.-J. & Arostegui I. (2017): Comparison of beta-binomial regression model approaches to analyze health related quality of life data, *Statistical Methods in Medical Research*, DOI: 10.1177/0962280217690413

See Also[BBmm](#)**Examples**

```

set.seed(14)

# Defining the parameters
k <- 100
m <- 10
phi <- 0.5
beta <- c(1.5,-1.1)
sigma <- 0.5

# Simulating the covariate and random effects
x <- runif(k,0,10)
X <- model.matrix(~x)
z <- as.factor(rBI(k,4,0.5,2))
Z <- model.matrix(~z-1)
u <- rnorm(5,0,sigma)

# The linear predictor and simulated response variable
eta <- beta[1]+beta[2]*x+crossprod(t(Z),u)
p <- 1/(1+exp(-eta))
y <- rBB(k,m,p,phi)
dat <- data.frame(cbind(y,x,z))
dat$z <- as.factor(dat$z)

# Apply the model
model <- BBmm(fixed.formula = y~x,random.formula = ~z,m=m,data=dat)
print(model) # or just model

```

```
print.BBreg          Print a BBreg class model.
```

Description

print.BBreg is the BBreg specific method for the generic function print which prints objects returned by modelling functions.

Usage

```
## S3 method for class 'BBreg'
print(x, ...)
```

Arguments

```
x          a BBreg class model.
...        for extra arguments.
```

Value

Prints a BBreg object.

Author(s)

J. Najera-Zuloaga

D.-J. Lee

I. Arostegui

References

Forcina A. & Franconi L. (1988): Regression analysis with Beta-Binomial distribution, *Revista di Statistica Applicata*, **21**, 7-12

Najera-Zuloaga J., Lee D.-J. & Arostegui I. (2017): Comparison of beta-binomial regression model approaches to analyze health related quality of life data, *Statistical Methods in Medical Research*, DOI: 10.1177/0962280217690413

See Also

[BBreg](#)

Examples

```
# We simulate a covariate, fix the paramters of the beta-binomial
# distribution and simulate a response variable.

# Then we apply the model, and try to get the same values.
set.seed(18)
k <- 1000
m <- 10
x <- rnorm(k,5,3)

beta <- c(-10,2)
p <- 1/(1+exp(-(beta[1]+beta[2]*x)))
phi <- 1.2

y <- rBB(k,m,p,phi)

model <- BBreg(y~x,m)
print(model) # or just model
```

print.summary.BBest *Print a summary.BBest class model.*

Description

print.summary.BBest is the summary.BBest specific method for the generic function print which prints objects returned by modelling functions.

Usage

```
## S3 method for class 'summary.BBest'  
print(x, ...)
```

Arguments

x a summary.BBest class model.
... for extra arguments.

Value

Prints a summary.BBest object.

Author(s)

J. Najera-Zuloaga
D.-J. Lee
I. Arostegui

References

Arostegui I., Nunez-Anton V. & Quintana J. M. (2006): Analysis of short-form-36 (SF-36): The beta-binomial distribution approach, *Statistics in Medicine*, **26**, 1318-1342

See Also

[BBest,summary.BBest](#)

Examples

```
set.seed(9)  
# Simulate a binomial distribution  
y <- rBB(100,10,0.5,2)  
  
# Apply the model  
model <- BBest(y,10)  
sum.model <- summary(model)  
print(sum.model) # or just sum.model
```

print.summary.BBmm *Print a summary.BBmm class model.*

Description

print.summary.BBmm is the summary.BBmm specific method for the generic function print which prints objects returned by modelling functions.

Usage

```
## S3 method for class 'summary.BBmm'  
print(x, ...)
```

Arguments

x a summary.BBmm class model.
... for extra arguments.

Value

Prints a summary.BBmm object.

Author(s)

J. Najera-Zuloaga
D.-J. Lee
I. Arostegui

References

Breslow N. E. & Calyton D. G. (1993): Approximate Inference in Generalized Linear Mixed Models, *Journal of the American Statistical Association*, **88**, 9-25

Lee Y. & Nelder J. A. (1996): Hierarchical generalized linear models, *Journal of the Royal Statistical Society. Series B*, **58**, 619-678

Najera-Zuloaga J., Lee D.-J. & Arostegui I. (2017): Comparison of beta-binomial regression model approaches to analyze health related quality of life data, *Statistical Methods in Medical Research*, DOI: 10.1177/0962280217690413

See Also

[BBmm](#), [summary.BBmm](#)

Examples

```

set.seed(14)

# Defining the parameters
k <- 100
m <- 10
phi <- 0.5
beta <- c(1.5,-1.1)
sigma <- 0.5

# Simulating the covariate and random effects
x <- runif(k,0,10)
X <- model.matrix(~x)
z <- as.factor(rBI(k,4,0.5,2))
Z <- model.matrix(~z-1)
u <- rnorm(5,0,sigma)

# The linear predictor and simulated response variable
eta <- beta[1]+beta[2]*x+crossprod(t(Z),u)
p <- 1/(1+exp(-eta))
y <- rBB(k,m,p,phi)
dat <- data.frame(cbind(y,x,z))
dat$z <- as.factor(dat$z)

# Apply the model
model <- BBmm(fixed.formula = y~x,random.formula = ~z,m=m,data=dat)
sum.model <- summary(model)
print(sum.model) # or just sum.model

```

```
print.summary.BBreg Print a summary.BBreg class model.
```

Description

print.summary.BBreg is the summary.BBreg specific method for the generic function print which prints objects returned by modelling functions.

Usage

```
## S3 method for class 'summary.BBreg'
print(x, ...)
```

Arguments

```
x          a summary.BBreg class model.
...        for extra arguments.
```

Value

Prints a summary.BBreg object.

Author(s)

J. Najera-Zuloaga

D.-J. Lee

I. Arostegui

References

Forcina A. & Franconi L. (1988): Regression analysis with Beta-Binomial distribution, *Revista di Statistica Applicata*, **21**, 7-12

Najera-Zuloaga J., Lee D.-J. & Arostegui I. (2017): Comparison of beta-binomial regression model approaches to analyze health related quality of life data, *Statistical Methods in Medical Research*, DOI: 10.1177/0962280217690413

See Also

[BBreg.summary.BBreg](#)

Examples

```
# We simulate a covariate, fix the parameters of the beta-binomial
# distribution and simulate a response variable.

# Then we apply the model, and try to get the same values.
set.seed(18)
k <- 1000
m <- 10
x <- rnorm(k,5,3)

beta <- c(-10,2)
p <- 1/(1+exp(-(beta[1]+beta[2]*x)))
phi <- 1.2

y <- rBB(k,m,p,phi)

model <- BBreg(y~x,m)
sum.model <- summary(model)
print(sum.model) # or just sum.model
```

SF36rec

*Short Form-36 Health Survey recode***Description**

The SF36rec function recodes to a binomial form the 0-100 original standardized scores of the dimensions provided by the Short Form-36 Health Survey (SF-36) based on *Arostegui et al. (2013)*.

Usage

SF36rec(x, k)

Arguments

- | | |
|---|--|
| x | the 0-100 scale standardized dimension of the SF-36. It must be numeric and bounded between 0 and 100. |
| k | an integer from 1 to 8 that defines which SF-36 dimension belongs x. These are the dimensions depending on the k value:
k=1 -> Physical functioning
k=2 -> Role physical
k=3 -> Body pain
k=4 -> General health
k=5 -> Vitality
k=6 -> Social functioning
k=7 -> Role emotional
k=8 -> Mental health |

Details

The Short Form-36 Health Survey is a commonly used technique to measure the Health Related Quality of Life (HRQoL) in chronic diseases. It was developed within the Medical Outcomes Study (*Ware et al. (1993)*). It measures generic HRQoL concepts and provides an objective way to measure HRQoL from the patients point of view by scoring standardized responses to standardized questions. The validity and reliability of this instrument has been broadly tested (*Stansfeld et al. (1997)*). The SF-36 has 36 items, with different answer options. It was constructed to represent eight health dimensions, which are *physical functioning* (PF), *role physical* (RP), *body pain* (BP), *general health* (GH), *vitality* (VT), *social functioning* (SF), *role emotional* (RE) and *mental health* (MH). Each item is assigned to a unique health dimension. Each of the multi-item dimensions contains two to ten items. The first four dimensions are mainly physical, whereas the last four measure mental aspects of HRQoL. The resulting raw scores are typically transformed to standardized scale scores from 0 to 100, where a higher score indicates a better health status.

Arostegui et al. (2013) proposed a recoding methodology of the SF-36 standardized scores to a binomial form in order to apply the beta-binomial distribution. The method was mainly based on the possible number of values each dimension can obtain, which comes from the number of items related with the construction of each dimension.

The SF36rec function performs the cited recoding methodology to the specified SF-36 dimension. It has two inputs. The first one is the dimension that will be recoded, and the second one identifies which SF-36 dimension is.

Value

The score values of the recoded dimension.

Author(s)

J. Najera-Zuloaga

D.-J. Lee

I. Arostegui

References

Arostegui I., Nunez-Anton V. & Quintana J. M. (2013): On the recoding of continuous and bounded indexes to a binomial form: an application to quality-of-life scores, *Journal of Applied Statistics*, **40**, 563-583

Ware J. E., Snow K. K., Kosinski M. A. & Gandek B. (1993): *SF-36 Health Survey, Manual and Interpretation Guides*. The Health Institute, New England Medical Center.

Stansfeld S. A., Roberts R. & Foot S. P. (1997): Assessing the validity of the SF-36 general health survey. *Quality of Life Research*, **6**, 217-224.

Examples

```
set.seed(2)
# We simulate a variable bounded between 0 and 100.
BodyPain <- runif(1000,0,100)

# We specify that the simulated dimension corresponds
# with body pain dimension.
k <- 3

# We perform the recoding.
BodyPain.rec <- SF36rec(BodyPain,k)
```

summary.BBest

Summarizes a BBest class model.

Description

summary.BBest is the BBest specific method for the generic function summary which summarizes objects returned by modelling functions.

Usage

```
## S3 method for class 'BBest'  
summary(object, ...)
```

Arguments

object a BBest class model.
... for extra arguments.

Details

summary.BBest summarizes all the relevant information about the estimation of the parameters in a BBest class model.

Value

summary.BBest returns an object of class "summary.BBest".

coefficients a table with the estimated parameters is in the BBest class model.
p.coefficients a summarized table of the estimation of the probability parameter of the beta-binomial distribution. The table contents the estimation of the probability parameter and the standard errors of the estimations.
psi.coefficients a summarized table of the estimation of the logarithm of the dispersion parameter of the beta-binomial distribution. The table contents the estimation of the logarithm of the dispersion parameter and the standard errors of the estimations.
m the maximum score number in each beta-binomial observation.

Author(s)

J. Najera-Zuloaga
D.-J. Lee
I. Arostegui

References

Arostegui I., Nunez-Anton V. & Quintana J. M. (2006): Analysis of short-form-36 (SF-36): The beta-binomial distribution approach, *Statistics in Medicine*, **26**, 1318-1342

See Also

[BBest](#)

Examples

```

set.seed(9)
# Simulate a binomial distribution
y <- rBB(100,10,0.5,2)

# Apply the model
model <- BBest(y,10)
sum.model <- summary(model)

```

summary.BBmm	<i>Summarizes a BBmm class model.</i>
--------------	---------------------------------------

Description

summary.BBmm is the BBmm specific method for the generic function summary which summarizes objects returned by modelling functions.

Usage

```

## S3 method for class 'BBmm'
summary(object, ...)

```

Arguments

object	a BBmm class model.
...	for extra arguments.

Details

summary.BBmm summarizes all the relevant information about the estimation of the parameters in a BBmm class model.

The function performs statistical significance hypothesis about the estimated fixed parameters based on the normal distribution of the estimates. It also performs a goodness of fit test based on the difference between the calculated deviance of the model and the null deviance or deviance of the null model, which it is supposed to follow a Chi-square distribution with degrees of freedom equal to the difference in degrees of freedom of the models.

Value

summary.BBmm returns an object of class "summary.BBmm".

fixed.coefficients

a table with all the relevant information about the significance of the fixed effects estimates in the model. It includes the estimates, the standard errors of the estimates, the test-statistics and the p-values.

sigma.table

a table which includes the estimates and the standard errors of the estimates of the random effects variance parameters.

psi.table	a table which includes the estimate and the standard errors of the estimate of the logarithm of the dispersion parameter of the conditional beta-binomial distribution.
random.coef	predicted random effects of the regression.
iter	number of iterations in the estimation method.
nObs	number of observations in the data.
nRand	number of random effects.
nComp	number of random components.
nRandComp	number of random effects in each random component of the model.
namesRand	names of the random components.
deviance	deviance of the model.
df	degrees of freedom of the model.
null.deviance	null-deviance, deviance of the null model. The null model will only include an intercept as the estimation of the probability parameter of the conditional beta-binomial distribution.
null.df	degrees of freedom of the null model.
Goodness.of.fit	p-value of the goodness of fit test.
balanced	if the conditional beta-binomial response variable is balanced it returns "yes", otherwise "no".
m	maximum score number in each beta-binomial observation.
conv	convergence of the methodology. If the algorithm has converged it returns "yes", otherwise "no".

Author(s)

J. Najera-Zuloaga

D.-J. Lee

I. Arostegui

References

Breslow N. E. & Calyton D. G. (1993): Approximate Inference in Generalized Linear Mixed Models, *Journal of the American Statistical Association*, **88**, 9-25

Lee Y. & Nelder J. A. (1996): Hierarchical generalized linear models, *Journal of the Royal Statistical Society. Series B*, **58**, 619-678

Najera-Zuloaga J., Lee D.-J. & Arostegui I. (2017): Comparison of beta-binomial regression model approaches to analyze health related quality of life data, *Statistical Methods in Medical Research*, DOI: 10.1177/0962280217690413

See Also

The [multroot](#) and [uniroot](#) functions of the R-package rootSolve for the general Newton-Raphson algorithm.

[BBmm](#).

Examples

```

set.seed(14)

# Defining the parameters
k <- 100
m <- 10
phi <- 0.5
beta <- c(1.5,-1.1)
sigma <- 0.5

# Simulating the covariate and random effects
x <- runif(k,0,10)
X <- model.matrix(~x)
z <- as.factor(rBI(k,4,0.5,2))
Z <- model.matrix(~z-1)
u <- rnorm(5,0,sigma)

# The linear predictor and simulated response variable
eta <- beta[1]+beta[2]*x+crossprod(t(Z),u)
p <- 1/(1+exp(-eta))
y <- rBB(k,m,p,phi)
dat <- data.frame(cbind(y,x,z))
dat$z <- as.factor(dat$z)

# Apply the model
model <- BBmm(fixed.formula = y~x,random.formula = ~z,m=m,data=dat)
sum.model <- summary(model)

```

summary.BBreg

Summarizes a BBreg class model.

Description

summary.BBreg is the BBreg specific method for the generic function summary which summarizes objects returned by modelling functions.

Usage

```

## S3 method for class 'BBreg'
summary(object, ...)

```

Arguments

object	a BBreg class model.
...	for extra arguments.

Details

summary.BBreg summarizes all the relevant information about the estimation of the parameters in a BBreg class model.

The function performs statistical significance hypothesis about the estimated regression parameters based on the normal distribution of the estimates. It also performs a goodness of fit test based on the difference between the calculated deviance of the model and the null deviance or deviance of the null model, which it is suppose to follow a Chi-square distribution with degrees of freedom equal to the difference in degrees of freedom of the models.

Value

summary.BBreg returns an object of class "summary.BBreg".

coefficients	a table with all the relevant information about the significance of the regression coefficients of the model. It includes the estimations, the standard errors of the estimations, the test-statistics and the p-values.
psi.table	a table which includes the estimation and standard errors of the logarithm of the dispersion parameter of the conditional beta-binomial distribution.
deviance	deviance of the model.
df	degrees of freedom of the model.
null.deviance	null-deviance, deviance of the null model.
null.df	degrees of freedom of the null model.
Goodness.of.fit	p-value of the goodness of fit test.
iter	number of iterations in the estimation method.
X	the model matrix.
y	the dependent variable in the model.
balanced	if the response variable is balanced it returns "yes", otherwise "no".
m	number of trials in each binomial observation.
nObs	number of observations.
m	number of trials in each observation.
balanced	if the response beta-binomial variable is balanced it returns "yes", otherwise "no".
conv	convergence of the methodology. If the algorithm has converged it returns "yes", otherwise "no".

Author(s)

J. Najera-Zuloaga

D.-J. Lee

I. Arostegui

References

Forcina A. & Franconi L. (1988): Regression analysis with Beta-Binomial distribution, *Revista di Statistica Applicata*, **21**, 7-12

Najera-Zuloaga J., Lee D.-J. & Arostegui I. (2017): Comparison of beta-binomial regression model approaches to analyze health related quality of life data, *Statistical Methods in Medical Research*, DOI: 10.1177/0962280217690413

Examples

```
# We simulate a covariate, fix the parameters of the beta-binomial
# distribution and simulate a response variable.

# Then we apply the model, and try to get the same values.
set.seed(18)
k <- 1000
m <- 10
x <- rnorm(k,5,3)

beta <- c(-10,2)
p <- 1/(1+exp(-(beta[1]+beta[2]*x)))
phi <- 1.2

y <- rBB(k,m,p,phi)

model <- BBreg(y~x,m)
sum.model <- summary(model)
```

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