

# Censored Negative Binomial (version2)

## Parametrisation

The negative Binomial distribution is

$$\text{Prob}(y) = \frac{\Gamma(y+n)}{\Gamma(n)\Gamma(y+1)} p^n (1-p)^y$$

for responses  $y = 0, 1, 2, \dots$ , where

$n$ : number of successful trials (*size*), or dispersion parameter. Must be strictly positive, need not be integer.

$p$ : probability of success in each trial.

The censoring is that response values in the interval  $L \leq y \leq H$  are censored (and reported as a value in the interval, like  $y = L$ , say), whereas other values are reported as is.

This function is the nbinoial version of `cenpoisson2`.

## Link-function

The mean and variance of (the uncensored)  $y$  are given as

$$\mu = n \frac{1-p}{p} \quad \text{and} \quad \sigma^2 = \mu \left(1 + \frac{\mu}{n}\right)$$

and the mean is linked to the linear predictor by

$$\mu = E \exp(\eta)$$

where the hyperparameter  $n$  (*size*) plays the role of an dispersion parameter.  $E$  represents known constant and  $\log(E)$  is the offset of  $\eta$ .

## Hyperparameters

The default parameterization (`variant=0`) is that the dispersion parameter  $n$  (*size*) is represented as

$$n = \exp(\theta)$$

and the prior is defined on  $\theta$ .

If `variant=1`, then dispersion parameter  $n$  (*size*) is represented as

$$n = E \exp(\theta)$$

and the prior is defined on  $\theta$ .

If `variant=2`, then dispersion parameter  $n$  (*size*) is represented as

$$n = S \exp(\theta)$$

where  $S$  is `scale`, and the prior is defined on  $\theta$ .

## Specification

- `family="nbinomial"`
- Required arguments:  $(y, L, H)$  [see below] and  $E$  (default  $E = 1$ ) and `scale` (default `scale=1`)
- Chose variant with either `control.family = list(variant=0)` (default) or `control.family = list(variant=1)` or `control.family = list(variant=2)`.
- Data and censoring information is given by the triplet:  $y$ ,  $L$  and  $H$ , and must be defined as a `inla.mdata`-object.  $L$  and  $H$  are vectors of same length as  $y$  giving the censoring information for each observation.  $L$  and  $H$  must be integer valued or `Inf`.

If  $y[i]$  is not in the interval, then the observation is not censored.

$L[i] = \text{Inf}$  and/or  $H[i] = \text{Inf}$  is equivalent to  $L[i] = -1$  and/or  $H[i] = -1$ .

$L[i] = \text{Inf}$  implies no interval censoring.  $H[i] = \text{Inf}$  and  $0 \leq L[i] < \infty$  implies right censoring.

## Hyperparameter spesification and default values

**doc** The CenNegBinomial2 likelihood (similar to `cenpoisson2`)

**hyper**

**theta**

**hyperid** 63101  
**name** size  
**short.name** size  
**initial** 2.30258509299405  
**fixed** FALSE  
**prior** pc.mgamma  
**param** 7  
**to.theta** function(x) log(x)  
**from.theta** function(x) exp(x)

**status** experimental

**survival** FALSE

**discrete** TRUE

**link** default log logoffset quantile

**pdf** `cennbinomial2`

## Example

In the following example we estimate the parameters in a simulated example.

```
n = 300
x = rnorm(n, sd = 0.2)
eta = 1 + x
E = runif(n, min = 0.5, max=2)
S = runif(n, min = 0.5, max=2)

## variant 0
mu = E * exp(eta)
```

```

size = 1
prob = size/(size + mu)
y = rnbino(n, size, mu=mu)

y.low <- sample(c(1:4, Inf), n, replace = TRUE)
y.high <- y.low + sample(c(1:5, Inf), n, replace = TRUE)

Y <- inla.mdata(cbind(y, y.low, y.high))
r = inla(Y ~ 1 + x,
        data = list(Y = Y, x = x, E = E),
        family = "cennbinomial2",
        control.family = list(variant = 0),
        E=E, scale = S)
summary(r)
censored = which(y >= y.low & y <= y.high)
print(length(censored)/ n)

## variant 1
mu = E * exp(eta)
size = 1 * E
prob = size/(size + mu)
y = rnbino(n, size, mu=mu)

y.low <- sample(c(1:4, Inf), n, replace = TRUE)
y.high <- y.low + sample(c(1:5, Inf), n, replace = TRUE)

Y <- inla.mdata(cbind(y, y.low, y.high))
r = inla(Y ~ 1 + x,
        data = list(Y = Y, x = x, E = E),
        family = "cennbinomial2",
        control.family = list(variant = 1),
        E=E)

summary(r)
censored = which(y >= y.low & y <= y.high)
print(length(censored)/ n)

## variant 2
mu = E * exp(eta)
size = 1 * S
prob = size/(size + mu)
y = rnbino(n, size, mu=mu)

y.low <- sample(c(1:4, Inf), n, replace = TRUE)
y.high <- y.low + sample(c(1:5, Inf), n, replace = TRUE)

Y <- inla.mdata(cbind(y, y.low, y.high))
r = inla(Y ~ 1 + x,
        data = list(Y = Y, x = x, E = E, S = S),
        family = "cennbinomial2",
        control.family = list(variant = 2),
        E=E, scale = S)

summary(r)
censored = which(y >= y.low & y <= y.high)
print(length(censored)/ n)

```

## Notes