

## Binomial and negative binomial distribution

### Parametrisation

The Binomial distribution is

$$\text{Prob}(y) = \binom{n}{y} p^y (1-p)^{n-y}$$

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

$n$ : number of trials.

$p$ : probability of success in each trial.

The negative binomial distribution is

$$\text{Prob}(n) = \binom{n-1}{y-1} p^y (1-p)^{n-y}$$

for given  $y = 1, 2, \dots$  and response  $n - y = 0, 1, 2, \dots$

### Link-function

The mean and variance of  $y$  are given in the binomial case as

$$\mu = np \quad \text{and} \quad \sigma^2 = np(1-p)$$

and the probability  $p$  is linked to the linear predictor by

$$p(\eta) = \frac{\exp(\eta)}{1 + \exp(\eta)}$$

### Hyperparameters

None.

### Hyperparameter specification and default values

**doc** The Binomial likelihood

**hyper**

**survival** FALSE

**discrete** TRUE

**link** default logit loga cauchit probit cloglog ccloglog loglog log sslogit logitoffset quantil

**pdf** binomial

### Specification

- `family="binomial"`
- Required arguments:  $y$  and  $n$  (keyword `Ntrials`)
- Optional argument: `variant=0` for binomial (default), and `variant=1` for the negative binomial.

## Expert version

There is also an “expert” version where you are supposed to know what you are doing. Here, we allow  $y$  and  $n$  to be non-integers (whatever that means), however, the condition  $0 \leq y \leq n$  apply. The normalizing constant is computed as above using the integer part of  $y$  and  $n$ . This is similar to using `floor(y)` and `floor(n)` in R. The marginal likelihood estimate will in this case make less sense.

- `family="xbinomial"`
- Required arguments:  $y$  and  $n$  (keyword `Ntrials`)
- Optional argument: `scale=q`, which scales the probability with  $0 < q \leq 1$  into  $p'$ , where

$$p' = qp(\eta).$$

By default,  $q = 1$ . Note that “fitted values” will still be  $p(\eta)$ .

**doc** The Binomial likelihood (expert version)

**hyper**

**survival** FALSE

**discrete** TRUE

**link** default logit loga cauchit probit cloglog ccloglog loglog log sslogit logitoffset quantil

**pdf** binomial

**status** experimental

## Examples

In the following example we estimate the parameters in a simulated example with binomial responses.

```
## binomial
n=100
a = 1
b = 1
z = rnorm(n)
eta = a + b*z
formula <- y ~ 1 + z
prob = exp(eta)/(1 + exp(eta))

Ntrials = sample(1:10, size=n, replace=TRUE)
y = rbinom(n, size = Ntrials, prob = prob)
data = data.frame(y, z, Ntrials)
r = inla(formula, family = "binomial", data = data, Ntrials=Ntrials)
summary(r)

## negative binomial
y = sample(1:3, size=n, replace=TRUE)
Ntrials = y + rnbino(n, size = y, prob = prob)
r = inla(formula,
          family = "binomial",
          control.family = list(variant = 1),
```

```

      Ntrials = Ntrials,
      data = data.frame(y, z, Ntrials))
summary(r)

```

In the following example we estimate the parameters in a simulated example with binomial responses using the `scale`-argument as well. This requires the use of the expert-version “`xbinomial`”.

```

n <- 10000
x <- rnorm(n, sd = 1)
q <- runif(n)
eta <- 0.88 + 0.77*x
p <- q * 1.0/(1+exp(-eta))
ntrials <- sample(1:25, size=n, replace=TRUE)
y <- rbinom(n = n, size=ntrials, prob = p)
r <- inla(y ~ 1 + x,
          family = "xbinomial",
          Ntrials = ntrials,
          scale = q,
          data = data.frame(y, x, q, ntrials))
summary(r)

```

## Notes

- If the response is a **factor** it must be converted to  $\{0,1\}$  before calling `inla()`, as this conversion is not done automatically (as for example in `glm()`).
- This version of the negative binomial mimics the binomial distribution, and the “data” kind of enter in the `Ntrials` argument (as `y` is pre-determined) which both can appear, and should appear, strange. There is also an alternative implementation, `family="nbinomial"`, which mimics the Poisson distribution.