Negative Binomial

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 $y = 0, 1, 2, \ldots$, 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.

Link-function

The mean and variance of y are given as

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

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 knows constant and $\log(E)$ is the offset of η.

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 θ.

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

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

and the prior is defined on θ.

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 θ.

Specification

- family $=$ `nbinomial`

- Required arguments: y 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)`.

Hyperparameter spesification and default values

doc The negBinomial likelihood

hyper

> **theta**
>> **hyperid** 63001
>> **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)

survival FALSE

discrete TRUE

link default log logoffset quantile

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Example

In the following example we estimate the parameters in a simulated example with negative binomial responses and assign the hyperparameter θ a Gaussian prior with mean 0 and precision 0.01

```
n = 1000
x = rnorm(n,  sd = 0.2)
eta = 1 + x
E = runif(n, min = 0, max=10)

mu = E * exp(eta)
size = 3
y = rnbinom(n, size=size, mu=mu)
r = inla(y ~ 1 + x, data = data.frame(y, x, E),
    family = "nbinomial", E=E)

mu = E * exp(eta)
size = E*3
y = rnbinom(n, size=size, mu=mu)
rr = inla(y ~ 1 + x, data = data.frame(y, x, E),
    family = "nbinomial",
    control.family = list(variant = 1),
    E=E)
```

Notes

As $n \to \infty$, the negative Binomial converges to the Poisson distribution. For numerical reasons, if n is too large:

$$\frac{\mu}{n} < 10^{-4},$$

then the Poisson limit is used.

The PC-prior is available for `variant=1`, see `inla.doc("pc.gamma")`.

The `nbinomial2` distribution

The negative Binomial distribution is also available in its "pure form", as the number of excess experiments to get n successes with a success in the last experiment,

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

for $y = 0, 1, 2, \ldots$, where

n: the (fixed) number of successes before stopping, $n = 1, 2, \ldots$,

p: the probability of success in each independent trial.

Link-function

The probability p is (by default) linked to the linear predictor η as

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

Hyperparameters

None.

Specification

- family $=$ `nbinomial2`
- Required arguments: y and *Ntrials*

The argument `Ntrials` gives the value of n for each observation.

Hyperparameter spesification and default values

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hyper

survival FALSE

discrete TRUE

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Example

```
n = 300
x = rnorm(n, sd = 0.2)
eta = 1 + 1.1*x
p = exp(eta)/(1 + exp(eta))
size = sample(1:5, n, replace=TRUE)
y = rnbinom(n, size = size, prob = p)
r = inla(y ~ 1 + x, family = "nbinomial2", Ntrials = size,
         data = data.frame(y, x, size))
summary(r)
```