NMixNB

Parametrisation

The N-MixtureNB distribution is a negative Binomial mixture of the Binomials, as

$$\text{Prob}(y) = \sum_{n=y}^{\infty} \binom{n}{y} p^n (1-p)^{n-y} \times \frac{\Gamma(n+\delta)}{\Gamma(\delta) n!} q^{\delta} (1-q)^n$$

for responses $y = 0, 1, 2, \ldots, n$, where n is Poisson number of trials, and p is probability of success. For δ and q, see below. Replicated reponses $y_1, y_2, \ldots, y_r$, are iid from the Binomial with the same p, conditioned on the same n from the negative Binomial,

$$\text{Prob}(y_1, \ldots, y_r) = \sum_{n=\max\{y_1,\ldots,y_r\}}^{\infty} \left\{ \prod_{i=1}^{r} \binom{n}{y_i} p^n (1-p)^{n-y_i} \right\} \times \frac{\Gamma(n+\delta)}{\Gamma(\delta) n!} q^{\delta} (1-q)^n$$

The negative binomial is parameterisized in terms of the mean λ and overdispersion $1/\delta$, where $q = \delta/(\delta + \mu)$; see the `R` documentation `?dnbinom` for this parameterisation (where $\delta =$ `size`).

Link-function

The probability p is linked to the linear predictor by

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

for the default logit link, while λ depends on fixed covariates

$$\log(\lambda) = \sum_{j=1}^{m} \beta_j x_j$$

with one vector of covariates for each observation. m can be maximum 15 and minimum 1.

Hyperparameters

The parameters $\theta_1 = \beta_1, \theta_2 = \beta_2, \ldots, \theta_m = \beta_m$, and overdispersion $\theta_{16} = \log(1/\delta)$.

Hyperparameter spesification and default values

doc NegBinomial-Poisson mixture

hyper

theta1

hyperid 101121
name beta1
short.name beta1
initial 2.30258509299405
fixed FALSE
prior normal
param 0 0.5
to.theta `function(x) x`
from.theta `function(x) x`

theta2

hyperid 101122
name beta2
short.name beta2
initial 0
fixed FALSE
prior normal
param 0 1
to.theta `function(x) x`
from.theta `function(x) x`

theta3

hyperid 101123
name beta3
short.name beta3
initial 0
fixed FALSE
prior normal
param 0 1
to.theta `function(x) x`
from.theta `function(x) x`

theta4

hyperid 101124
name beta4
short.name beta4
initial 0
fixed FALSE
prior normal
param 0 1
to.theta `function(x) x`
from.theta `function(x) x`

theta5

hyperid 101125
name beta5
short.name beta5
initial 0
fixed FALSE
prior normal
param 0 1
to.theta `function(x) x`
from.theta `function(x) x`

theta6

hyperid 101126
name beta6
short.name beta6

initial 0
fixed FALSE
prior normal
param 0 1
to.theta `function(x) x`
from.theta `function(x) x`

theta7

hyperid 101127
name beta7
short.name beta7
initial 0
fixed FALSE
prior normal
param 0 1
to.theta `function(x) x`
from.theta `function(x) x`

theta8

hyperid 101128
name beta8
short.name beta8
initial 0
fixed FALSE
prior normal
param 0 1
to.theta `function(x) x`
from.theta `function(x) x`

theta9

hyperid 101129
name beta9
short.name beta9
initial 0
fixed FALSE
prior normal
param 0 1
to.theta `function(x) x`
from.theta `function(x) x`

theta10

hyperid 101130
name beta10
short.name beta10
initial 0
fixed FALSE
prior normal
param 0 1

to.theta `function(x) x`
from.theta `function(x) x`

theta11
hyperid 101131
name beta11
short.name beta11
initial 0
fixed FALSE
prior normal
param 0 1
to.theta `function(x) x`
from.theta `function(x) x`

theta12
hyperid 101132
name beta12
short.name beta12
initial 0
fixed FALSE
prior normal
param 0 1
to.theta `function(x) x`
from.theta `function(x) x`

theta13
hyperid 101133
name beta13
short.name beta13
initial 0
fixed FALSE
prior normal
param 0 1
to.theta `function(x) x`
from.theta `function(x) x`

theta14
hyperid 101134
name beta14
short.name beta14
initial 0
fixed FALSE
prior normal
param 0 1
to.theta `function(x) x`
from.theta `function(x) x`

theta15
hyperid 101135

name beta15
short.name beta15
initial 0
fixed FALSE
prior normal
param 0 1
to.theta `function(x) x`
from.theta `function(x) x`

theta16

hyperid 101136
name overdispersion
short.name overdispersion
initial 0
fixed FALSE
prior pc.gamma
param 7
to.theta `function(x) log(x)`
from.theta `function(x) exp(x)`

status experimental

survival FALSE

discrete TRUE

link default logit loga probit

pdf nmixnb

Specification

- `family="nmixnb"`
- Required arguments: the response Y and covariates X as `inla.mdata(Y, X [, additional.covariates])`

The response is a matrix where each row are replicates, where responses that are `NA`'s are ignored. The covariates is one or many vectors, matrices or data.frames. Each row of the covariates $(x_{i1}, x_{i2}, \ldots, x_{im})$ defines the covariates used for the i'th response(s) (the i'th row of `Y`). Note that $\beta_{m+1}, \ldots, \beta_{15}$ are fixed to zero.

Example

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

```
nrep.max = 5
n = 50
y = matrix(NA, n, nrep.max)
x = c()
xx = c()
size = 3
```

```
overdispersion = 1/size
intercept = 1

for(i in 1:n) {
    local.x = runif(1) - 0.5
    lambda = exp(2 + local.x)
    N = rnbinom(1, mu=lambda, size=size)
    local.xx = runif(1) - 0.5
    eta = intercept + local.xx
    p = exp(eta)/(exp(eta) + 1)
    ## sample the number of replications
    nr = sample(1:nrep.max, 1)
    ## and sample these. note that 'y' is initialized with NA's,
    ## so if nr < nrep.max, then
    ## y[i,(nr+1):nrep.max]  would be NA.
    y[i, 1:nr]= rbinom(nr, size = N, prob = p)
    x = c(x, local.x)
    xx = c(xx, local.xx)
}

Y = inla.mdata(y, 1, x)
r = inla(Y ~ 1 + xx,
         data = list(Y=Y, xx=xx),
         family = "nmixnb",
         control.fixed = list(prec.intercept=1,  prec=1))
```

Notes