

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

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

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

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

Hyperparameter specification and default values

`doc` NegBinomial-Poisson mixture

`hyper`

`theta1`

`hyperid` 101121

`name` beta1

`short.name` beta1

`output.name` beta[1] for NMixNB observations

`output.name.intern` beta[1] for NMixNB observations

`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
    output.name beta[2] for NMixNB observations
    output.name.intern beta[2] for NMixNB observations
    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
    output.name beta[3] for NMixNB observations
    output.name.intern beta[3] for NMixNB observations
    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
    output.name beta[4] for NMixNB observations
    output.name.intern beta[4] for NMixNB observations
    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
    output.name beta[5] for NMixNB observations
    output.name.intern beta[5] for NMixNB observations

```

```

    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
    output.name beta[6] for NMixNB observations
    output.name.intern beta[6] for NMixNB observations
    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
    output.name beta[7] for NMixNB observations
    output.name.intern beta[7] for NMixNB observations
    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
    output.name beta[8] for NMixNB observations
    output.name.intern beta[8] for NMixNB observations
    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
output.name beta[9] for NMixNB observations
output.name.intern beta[9] for NMixNB observations
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
  output.name beta[10] for NMixNB observations
  output.name.intern beta[10] for NMixNB observations
  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
  output.name beta[11] for NMixNB observations
  output.name.intern beta[11] for NMixNB observations
  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
  output.name beta[12] for NMixNB observations
  output.name.intern beta[12] for NMixNB observations
  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
  output.name beta[13] for NMixNB observations
  output.name.intern beta[13] for NMixNB observations
  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
  output.name beta[14] for NMixNB observations
  output.name.intern beta[14] for NMixNB observations
  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
  output.name beta[15] for NMixNB observations
  output.name.intern beta[15] for NMixNB observations
  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
  output.name overdispersion for NMixNB observations
  output.name.intern log_overdispersion for NMixNB observations

```

```

initial 0
fixed FALSE
prior pc.gamma
param 7
to.theta function(x) log(x)
from.theta function(x) exp(x)

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 $(x_{i1}, x_{i2}, \dots, x_{im})$ defines the covariates used for the i 'th response(s) (the i 'th row of Y). Note that $\beta_{m+1}, \dots, \beta_{15}$ 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 = rbinom(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