

NMix

Parametrisation

The N-Mixture distribution is a Poisson mixture of the Binomials, as

$$\text{Prob}(y) = \sum_{n=y}^{\infty} \binom{n}{y} p^n (1-p)^{n-y} \times \frac{\lambda^n}{n!} \exp(-\lambda)$$

for responses $y = 0, 1, 2, \dots, n$, where n is Poisson number of trials, and p is probability of success. 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 Poisson,

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

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 $\theta_1 = \beta_1, \theta_2 = \beta_2, \dots, \theta_m = \beta_m$.

Hyperparameter specification and default values

doc Binomial-Poisson mixture

hyper

theta1

hyperid 101101

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 101102

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 101103
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 101104
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 101105
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 101106
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 101107
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 101108
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 101109
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 101110
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 101111
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 101112
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 101113
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 101114
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 101115
name beta15
short.name beta15

```

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

```

status experimental

survival FALSE

discrete TRUE

link default logit loga probit

pdf nmix

Specification

- family = nmix
- 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()
intercept = 1

for(i in 1:n) {
  local.x = runif(1) - 0.5
  lambda = exp(2 + local.x)
  N = rpois(1, lambda)
  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 = "nmix",
        control.fixed = list(prec.intercept=1, prec=1))
```

Notes