

# Binomial-mixture likelihood

## Parametrisation

### Details

This likelihood is a mixture of three binomials, where two of them are simple predictors and one is general. The probability for success is

$$p = w_1 p_1 + w_2 p_2 + w_3 p_3$$

where  $w_1 + w_2 + w_3 = 1$  are the positive weights, and

$$\text{logit}(p_3) = \eta$$

where the linear predictor  $\eta$  is defined in the formula. Further,

$$\text{logit}(p_1) = \beta_1 z_1 + \beta_2 z_2 + \beta_3 z_3$$

and

$$\text{logit}(p_2) = \beta_4 z_4 + \beta_5 z_5 + \beta_6 z_6$$

for fixed covariates  $z_i$ .

### Link-function

The link-function is given as usual, and they are all equal.

### Hyperparameters

The six regression coefficients  $\beta_i$  are treated as hyperparameters.

### Specification

- `family="binomialmix"`
- Required arguments: A  $n \times 2$  matrix  $Y$  with the observations and the number of trials  $s$ ,  $Y = (y, s)$ , a  $n \times 6$  matrix  $Z$  with the covariates  $Z = c(z_1, \dots, z_6)$ , and a  $n \times 2$  matrix  $W$  with weights  $W = (w_1, w_2)$ . The `inla.mdata` is used as

```
inla.mdata(Y, Z, W) ~ ...
```

## Hyperparameter specification and default values

doc Binomial mixture

hyper

theta1

hyperid 56551  
name beta1  
short.name beta1  
output.name beta1 for binomialmix observations  
output.name.intern beta1 for binomialmix observations  
initial 0  
fixed FALSE  
prior normal  
param 0 100  
to.theta function(x) x  
from.theta function(x) x

theta2

hyperid 56552  
name beta2  
short.name beta2  
output.name beta2 for binomialmix observations  
output.name.intern beta2 for binomialmix observations  
initial 0  
fixed FALSE  
prior normal  
param 0 100  
to.theta function(x) x  
from.theta function(x) x

theta3

hyperid 56553  
name beta3  
short.name beta3  
output.name beta3 for binomialmix observations  
output.name.intern beta3 for binomialmix observations  
initial 0  
fixed FALSE  
prior normal  
param 0 100  
to.theta function(x) x  
from.theta function(x) x

theta4

hyperid 56554  
name beta4  
short.name beta4  
output.name beta4 for binomialmix observations  
output.name.intern beta4 for binomialmix observations  
initial 0  
fixed FALSE  
prior normal

```

param 0 100
to.theta function(x) x
from.theta function(x) x
theta5
  hyperid 56555
  name beta5
  short.name beta5
  output.name beta5 for binomialmix observations
  output.name.intern beta5 for binomialmix observations
  initial 0
  fixed FALSE
  prior normal
  param 0 100
  to.theta function(x) x
  from.theta function(x) x
theta6
  hyperid 56556
  name beta6
  short.name beta6
  output.name beta6 for binomialmix observations
  output.name.intern beta6 for binomialmix observations
  initial 0
  fixed FALSE
  prior normal
  param 0 100
  to.theta function(x) x
  from.theta function(x) x
status experimental
survival FALSE
discrete TRUE
link default logit probit
pdf binomialmix

```

## Example

Here is a simple example.

```
n <- 30000

## this makes it to easy to its just to check the likelihood
## implementation
size <- sample(10:20, n, replace = TRUE)

beta1 <- rnorm(3, sd = 0.2)
beta2 <- rnorm(3, sd = 0.2)
beta <- c(beta1, beta2)
Z <- matrix(NA, n, 6)
W <- matrix(NA, n, 2)
Y <- matrix(NA, n, 2)

x <- rnorm(n, sd = 0.1)
xx <- rnorm(n, sd = 0.4)
eta <- 1 + x + xx

for (i in 1:n) {
  Z[i, ] <- rnorm(6)
  w <- c(rbeta(2, 1, 10), rbeta(1, 10, 1))
  w <- w/sum(w)
  W[i, ] <- w[1:2]

  p1 <- inla.link.invlogit(sum(beta1 * Z[i, 1:3]))
  p2 <- inla.link.invlogit(sum(beta2 * Z[i, 3 + 1:3]))
  p3 <- inla.link.invlogit(eta[i])
  p <- w[1] * p1 + w[2] * p2 + w[3] * p3
  Y[i, ] <- c(rbinom(1, size = size[i], prob = p), size[i])
}

r <- inla(inla.mdata(Y, Z, W) ~ 1 + x + xx,
  family = "binomialmix",
  data = list(Y = Y, Z = Z, W = W, x = x, xx = xx),
  verbose = TRUE)

cbind(estimate = r$summary.fixed["mean"], true = 1)
cbind(estimate = r$summary.hyperpar["mean"], true = beta)
```