

# GaussianJW

## Parametrisation

The GaussianJW likelihood is a two-part likelihood for  $\{(y, v)_i\}$ . First a Gaussian observation  $y$

$$y | \dots \sim \mathcal{N}(p, V(p, n))$$

with mean (probability)  $p$  and a variance function

$$V(p, n) = \exp(\beta_1 + \beta_2 \log(p(1-p)) + \beta_3 \log(n))$$

and then an (conditional independent) observed variance  $v$ , where

$$\nu \frac{v}{V(p, n)} | \dots \sim \chi^2_\nu.$$

The case  $\beta_1 = 0, \beta_2 = 1, \beta_3 = -1$  resembles the case where a Binomial is approximated with a Normal.  $(n, \nu)$  is considered as fixed.

## Link-function

The probability  $p$  is linked to the linear predictor  $\eta$  with a (default) logit link

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

but other links are also possible.

## Hyperparameters

The hyperparameters are

$$\theta_1 = \beta_1$$

$$\theta_2 = \beta_2$$

$$\theta_3 = \beta_3$$

and the prior is defined on  $(\theta_1, \theta_2, \theta_3)$ .

## Specification

- family = `gaussianjw`
- Required arguments:  $y$ ,  $n$  and  $\nu$  (all vectors of the same length) as an `inla.mdata()`-object with this spesific ordering, see the example.

## Hyperparameter spesification and default values

**doc** The GaussianJW likelihoood

**hyper**

**theta1**

**hyperid** 65101

**name** beta1

**short.name** beta1

**initial** 0

```

    fixed FALSE
    prior normal
    param 0 100
    to.theta function(x) x
    from.theta function(x) x
  theta2
    hyperid 65102
    name beta2
    short.name beta2
    initial 1
    fixed FALSE
    prior normal
    param 1 100
    to.theta function(x) x
    from.theta function(x) x
  theta3
    hyperid 65103
    name beta3
    short.name beta3
    initial -1
    fixed FALSE
    prior normal
    param -1 100
    to.theta function(x) x
    from.theta function(x) x

status experimental

survival FALSE

discrete FALSE

link default logit probit

pdf gaussianjw

```

### Example

```

n <- 300
x <- rnorm(n, sd = 0.5)
eta <- 1 + x
p <- 1/(1 + exp(-eta))
df <- sample(10:100, n, replace = TRUE)
size <- df
va <- p * (1.0 - p) / size
v <- rchisq(n, df = df) * va / df
phat <- rnorm(n, mean = p, sd = sqrt(v))
Y <- inla.mdata(phat, v, size, df)

```

```
r <- inla( Y ~ 1 + x,  
          data = list(Y = Y, x = x),  
          family = "gaussianjw",  
          ## this might be needed  
          control.inla = list(cmin = 0))  
summary(r)
```