

The Gamma-distribution

Parametrisation

The Gamma-distribution has the following density

$$\pi(y) = \frac{b^a}{\Gamma(a)} y^{a-1} \exp(-by), \quad a > 0, \quad b > 0, \quad y > 0,$$

where $E(y) = \mu = a/b$ and $\text{Var}(y) = 1/\tau = a/b^2$, where τ is the precision and μ is the mean. We will use the following parameterisation for the precision

$$\tau = (s\phi)/\mu^2$$

where ϕ is the precision parameter (or $1/\phi$ is the dispersion parameter) and $s > 0$ is a fixed scaling (for the regression model), which gives this density

$$\pi(y) = \frac{1}{\Gamma(s\phi)} \left(\frac{(s\phi)}{\mu} \right)^{(s\phi)} y^{(s\phi)-1} \exp \left(- (s\phi) \frac{y}{\mu} \right)$$

Link-function

The linear predictor η is linked to the mean μ using a default log-link

$$\mu = \exp(\eta)$$

Hyperparameter

The hyperparameter is the precision parameter ϕ , which is represented as

$$\phi = \exp(\theta)$$

and the prior is defined on θ .

Specification

- `family="gamma"` for regression models and `family="gamma.surv"` for survival models.
- Required arguments: for `gamma.surv`, y (to be given in a format by using `inla.surv()`), and for `gamma`, y and s (default value 1).

The scalings s is **not** used for `family="gamma.surv"`.

Hyperparameter spesification and default values

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`hyper`

`theta`

`hyperid` 58001

`name` precision parameter

`short.name` prec

`output.name` Precision-parameter for the Gamma observations

`output.name.intern` Intern precision-parameter for the Gamma observations

```

    initial 4.60517018598809
    fixed FALSE
    prior loggamma
    param 1 0.01
    to.theta function(x) log(x)
    from.theta function(x) exp(x)

survival FALSE

discrete FALSE

link default log quantile

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hyper
  theta1
    hyperid 58101
    name precision parameter
    short.name prec
    output.name Precision-parameter for the Gamma surv observations
    output.name.intern Intern precision-parameter for the Gamma surv observations
    initial 0
    fixed FALSE
    prior loggamma
    param 1 0.01
    to.theta function(x) log(x)
    from.theta function(x) exp(x)
  theta2
    hyperid 58102
    name beta1
    short.name beta1
    output.name beta1 for Gamma-Cure
    output.name.intern beta1 for Gamma-Cure
    initial -7
    fixed FALSE
    prior normal
    param -4 100
    to.theta function(x) x
    from.theta function(x) x
  theta3
    hyperid 58103
    name beta2
    short.name beta2
    output.name beta2 for Gamma-Cure

```

```

    output.name.intern beta2 for Gamma-Cure
    initial 0
    fixed FALSE
    prior normal
    param 0 100
    to.theta function(x) x
    from.theta function(x) x
theta4
    hyperid 58104
    name beta3
    short.name beta3
    output.name beta3 for Gamma-Cure
    output.name.intern beta3 for Gamma-Cure
    initial 0
    fixed FALSE
    prior normal
    param 0 100
    to.theta function(x) x
    from.theta function(x) x
theta5
    hyperid 58105
    name beta4
    short.name beta4
    output.name beta4 for Gamma-Cure
    output.name.intern beta4 for Gamma-Cure
    initial 0
    fixed FALSE
    prior normal
    param 0 100
    to.theta function(x) x
    from.theta function(x) x
theta6
    hyperid 58106
    name beta5
    short.name beta5
    output.name beta5 for Gamma-Cure
    output.name.intern beta5 for Gamma-Cure
    initial 0
    fixed FALSE
    prior normal
    param 0 100
    to.theta function(x) x
    from.theta function(x) x
theta7

```

```

hyperid 58107
name beta6
short.name beta6
output.name beta6 for Gamma-Cure
output.name.intern beta6 for Gamma-Cure
initial 0
fixed FALSE
prior normal
param 0 100
to.theta function(x) x
from.theta function(x) x
theta8
hyperid 58108
name beta7
short.name beta7
output.name beta7 for Gamma-Cure
output.name.intern beta7 for Gamma-Cure
initial 0
fixed FALSE
prior normal
param 0 100
to.theta function(x) x
from.theta function(x) x
theta9
hyperid 58109
name beta8
short.name beta8
output.name beta8 for Gamma-Cure
output.name.intern beta8 for Gamma-Cure
initial 0
fixed FALSE
prior normal
param 0 100
to.theta function(x) x
from.theta function(x) x
theta10
hyperid 58110
name beta9
short.name beta9
output.name beta9 for Gamma-Cure
output.name.intern beta9 for Gamma-Cure
initial 0
fixed FALSE
prior normal

```

```

    param 0 100
    to.theta function(x) x
    from.theta function(x) x
  theta11
    hyperid 58111
    name beta10
    short.name beta10
    output.name beta10 for Gamma-Cure
    output.name.intern beta10 for Gamma-Cure
    initial 0
    fixed FALSE
    prior normal
    param 0 100
    to.theta function(x) x
    from.theta function(x) x

survival TRUE

discrete FALSE

link default log neglog quantile

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```

Example 1

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

```

n = 1000
x = rnorm(n)
eta = 1 + x
mu = exp(eta)
prec.scale = runif(n, min = 0.5, max = 2)
prec.par = 1.2
a = prec.par * prec.scale
b = mu / (prec.par * prec.scale)
y = rgamma(n, shape = a, scale = b)
r = inla(y ~ 1 + x, data = data.frame(y, x),
        scale = prec.scale, family = "gamma")

```

Example 2

This is an example using the quantile link.

```

n <- 10^4
phi <- 3
a <- phi
## mu <- phi / rate
alpha <- 0.85
log.mu <- seq(-5, 5, by = 0.01)

```

```

## if exp(eta) is the alpha-quantile, what is then the mu?
log.q <- log(qgamma(alpha, shape = phi, rate = phi / exp(log.mu)))
fun <- splinefun(log.q, log.mu)

x <- rnorm(n, sd = 0.3)
eta <- 2 + x
mu <- exp(fun(eta))

## just a check
head(cbind(eta, log(qgamma(alpha, shape = phi, rate = phi / mu))))

y <- rgamma(n, shape = phi, rate = phi / mu)
r <- inla(y ~ 1 + x,
          family = "gamma",
          control.family = list(control.link = list(model = "quantile",
                                                    quantile = alpha)),
          data = data.frame(y, x),
          control.fixed = list(prec.intercept = 1, prec = 1),
          safe = FALSE,
          verbose = TRUE)
summary(r)

cbind(estimate = c(r$summary.fixed$mean, r$summary.hyperpar$mean),
      true = c(2, 1, phi))

```

Notes

None.