

Gompertz

Parametrisation

The Gompertz distribution has log survival function

$$\log S(y) = -\frac{\mu}{\alpha} (\exp(\alpha y) - 1)$$

for response $y \geq 0$, $\mu > 0$ and $\alpha > 0$. The cumulative distribution function and the density then follows as

$$F(y) = 1 - \exp \left[-\frac{\mu}{\alpha} (\exp(\alpha y) - 1) \right]$$

and

$$f(y) = \mu \exp \left[\alpha y - \frac{\mu}{\alpha} (\exp(\alpha y) - 1) \right].$$

Link-function

The parameter μ is linked to the linear predictor η as:

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

Hyperparameters

The shape parameter α is represented as

$$\alpha = \exp(S\theta)$$

and the prior is defined on θ . The constant S currently set to 0.1 to avoid numerical instabilities in the optimization, since small changes of α can make a huge difference.

Specification

- `family="gompertz"` for regression models and `family="gompertz.surv"` for survival models.
- Required arguments: y (to be given in a format by using `inla.surv()` for survival models)

Hyperparameter spesification and default values

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hyper

theta

hyperid 105101

name shape

short.name alpha

initial -1

fixed FALSE

prior normal

param 0 1

to.theta function(x, sc = 0.1) log(x) / sc

from.theta function(x, sc = 0.1) exp(sc * x)

status experimental

survival FALSE

discrete FALSE

link default log neglog

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hyper

theta1

hyperid 106101

name shape

short.name alpha

initial -10

fixed FALSE

prior normal

param 0 1

to.theta function(x, sc = 0.1) log(x) / sc

from.theta function(x, sc = 0.1) exp(sc * x)

theta2

hyperid 106102

name beta1

short.name beta1

initial -5

fixed FALSE

prior normal

param -4 100

to.theta function(x) x

from.theta function(x) x

theta3

hyperid 106103

name beta2

short.name beta2

initial 0

fixed FALSE

prior normal

param 0 100

to.theta function(x) x

from.theta function(x) x

theta4

hyperid 106104

name beta3

short.name beta3

initial 0

```

    fixed FALSE
    prior normal
    param 0 100
    to.theta function(x) x
    from.theta function(x) x
theta5
    hyperid 106105
    name beta4
    short.name beta4
    initial 0
    fixed FALSE
    prior normal
    param 0 100
    to.theta function(x) x
    from.theta function(x) x
theta6
    hyperid 106106
    name beta5
    short.name beta5
    initial 0
    fixed FALSE
    prior normal
    param 0 100
    to.theta function(x) x
    from.theta function(x) x
theta7
    hyperid 106107
    name beta6
    short.name beta6
    initial 0
    fixed FALSE
    prior normal
    param 0 100
    to.theta function(x) x
    from.theta function(x) x
theta8
    hyperid 106108
    name beta7
    short.name beta7
    initial 0
    fixed FALSE
    prior normal
    param 0 100
    to.theta function(x) x

```

```

    from.theta function(x) x
theta9
  hyperid 106109
  name beta8
  short.name beta8
  initial 0
  fixed FALSE
  prior normal
  param 0 100
  to.theta function(x) x
  from.theta function(x) x
theta10
  hyperid 106110
  name beta9
  short.name beta9
  initial 0
  fixed FALSE
  prior normal
  param 0 100
  to.theta function(x) x
  from.theta function(x) x
theta11
  hyperid 106111
  name beta10
  short.name beta10
  initial 0
  fixed FALSE
  prior normal
  param 0 100
  to.theta function(x) x
  from.theta function(x) x

```

status experimental

survival TRUE

discrete FALSE

link default log neglog

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Example

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

```

library(flexsurv)
library(INLA)

n <- 1000
alpha <- 1.0
intercept <- 1.1
beta <- 1.2
x <- rnorm(n, sd = 0.2)
eta <- intercept + beta*x
mu <- exp(eta)
event <- rep(1,n)
y <- rgompertz(n, rate = mu, shape = alpha)

r <- inla(y ~ 1 + x,
          family = "gompertz", data=data.frame(y, x))
r.surv <- inla(inla.surv(y, event) ~ 1 + x,
               family = "gompertzsurv", data=data.frame(y, event, x))

## should be 'small'
print(r$mlik - r.surv$mlik)

```

Notes