

## Linkmodel: gevit and cgevit

This is work in progress.

### Parametrization

### Hyperparameters

### Specification

### Hyperparameter spesification and default values

doc GEVIT link

hyper

theta1

hyperid 49033

name gev tail

short.name tail

initial 0.1

fixed FALSE

prior pc.egptail

param 5 -0.5 0.5

to.theta function(x, interval = c(REPLACE.ME.low, REPLACE.ME.high)) log(-(interval[1]

from.theta function(x, interval = c(REPLACE.ME.low, REPLACE.ME.high)) interval[1] + (

theta2

hyperid 49034

name gev p0

short.name p0

initial 0

fixed FALSE

prior normal

param 0 1

to.theta function(x) log(x / (1 - x))

from.theta function(x) 1 / (1 + exp(-x))

pdf gevit

doc Complement GEVIT link

hyper

theta1

hyperid 49035

name gev tail

short.name tail

initial -3

fixed FALSE

prior pc.gevtail

param 7 0 0.5

```

to.theta function(x, interval = c(REPLACE.ME.low, REPLACE.ME.high)) log(-(interval[1]
from.theta function(x, interval = c(REPLACE.ME.low, REPLACE.ME.high)) interval[1] + (
theta2
  hyperid 49036
  name gev p0
  short.name p0
  initial 0
  fixed FALSE
  prior normal
  param 0 1
  to.theta function(x) log(x / (1 - x))
  from.theta function(x) 1 / (1 + exp(-x))

```

pdf gevit

## Example

```

n <- 3000
x <- rnorm(n, sd = .5)
intercept <- runif(1)
beta.x <- runif(1, 0.5, 1.5)
eta <- intercept + beta.x * x

xi <- -0.3
p.intercept <- inla.link.invgevit(intercept, tail = xi)
prob <- inla.link.invgevit(eta, tail = xi)
size <- 2
y <- rbinom(n, size = size, prob = prob)

r <- inla(y ~ 1 + x,
  data = data.frame(y, x),
  family = "binomial",
  Ntrials = size,
  control.inla = list(cmin = 0, int.strategy = "eb"),
  control.fixed = list(remove.names = "(Intercept)"),
  control.family = list(
    control.link =
      list(model = "gevit",
        hyper = list(tail = list(prior = "pcegptail",
          param = c(7, -0.5, 0.5)),
        intercept = list(initial = 0, param = c(0, 1))))),
  verbose = !TRUE)

summary(r)

round(dig = 3,
  cbind(true = c(p.intercept = p.intercept, beta.x = beta.x, xi = xi),
    estimate = c(p.intercept = r$summary.hyperpar[2,"mean"],
      beta.x = r$summary.fixed["x", "mean"],

```

```

xi = r$summary.hyperpar[1, "mean"])))

## this shows that the intercept is not part of the linear predictor, then also, not the fitted
## values
plot(eta, r$summary.linear.predictor$mean +
      inla.link.gevit(r$summary.hyperpar[2,"mean"],
                     r$summary.hyperpar[1,"mean"]),
      lwd = 3, col = "red", type = "l")
abline(a = 0, b = 1, lwd = 1, col = "blue")

##### same check for 'cgevit' link
##p.intercept <- 1 - inla.link.invgevit(intercept, tail = xi)
##prob <- 1 - inla.link.invgevit(eta, tail = xi)
p.intercept <- inla.link.invcgevit(intercept, tail = xi)
prob <- inla.link.invcgevit(eta, tail = xi)
## to get the same data
y <- size - y

rc <- inla(y ~ -1 + x,
           data = data.frame(y, x),
           family = "binomial",
           Ntrials = size,
           control.inla = list(cmin = 0, int.strategy = "eb"),
           control.family = list(
             control.link =
               list(model = "cgevit",
                    hyper = list(tail = list(prior = "pcegptail",
                                              param = c(7, -0.5, 0.5)),
                                intercept = list(initial = 0, param = c(0, 1)))))
print(round(dig = 3,
           cbind(true = c(p.intercept = p.intercept, beta.x = beta.x, xi = xi),
                        estimate = c(p.intercept = rc$summary.hyperpar[2,"mean"],
                                    beta.x = rc$summary.fixed["x", "mean"],
                                    xi = rc$summary.hyperpar[1, "mean"])))

```