Fancy likelihood: "fl" (EXPERIMENTAL)

Parametrisation

This not a likelihood in the usual sense, but a artificial one to more easily be able add missing terms into the likelihood contribution due to various rewrites/reformulations. Obviously, it is only ment for special occations and to be used only for those who have spesific needs.

The "loglikelihood" is

$$\log f(y) = c_1 + c_2\eta - \frac{1}{2}c_3(c_4 - \eta)^2 - c_5 \exp(c_6 + c_7\eta) + c_8 \frac{\exp(c_9\eta) - \exp(c_{10}\eta)}{\eta}$$

for constants $c_1, \ldots, c_{10}$. In most cases, only a few of the c_i's will be non-zero. Note that there is no dependence on the reponse y, as y itself is not part of the spesification.

Link-function

The identity link is used.

Hyperparameters

None.

Specification

- `family="fl"`

- This family require the response to be a `inla.mdata`-object, where each row defines the vectorv $(c_1, \ldots, c_{10})$ for each likelihood contribution. Any `NA`'s in the c_i's will be converted to 0.

Hyperparameter spesification and default values

`family="fl"`

doc The fl likelihood

hyper

survival `FALSE`

discrete `TRUE`

link default `identity`

status experimental

pdf `fl`

Example

```
## example with Poisson likelihood in two ways
n <- 100
x <- rnorm(n)
eta <- 1 + 0.3 * x
y <- rpois(n, exp(eta))

## log-likelihood is in the fl-parameterisation:
```

```
## log(y!) + y * eta - 0.5 * 0 * (0 - eta)^2 - 1 * exp(0 + 1 *eta)
C <- cbind(-lfactorial(y), y, 0, 0, 1, 0, 1, 0, 0, 0)

r <- inla(inla.mdata(C) ~ 1 + x, family = "fl", data = list(C = C, x = x))
rr <- inla(y ~ 1 + x, family = "poisson", data = data.frame(y, x))

summary(rr)
summary(r)
r$mlik - rr$mlik
```

Notes

Since this is not a likelihood in the usual sense, it will not be used for CPO/GCPO calculations and not be influenced by the `control.inla=list(cmin=...)`-argument.

This likelihood is EXPERIMENTAL and only supported in using the (default) `compact`-mode for the moment.