

## Censored Poisson (version 2)

### Parametrisation

The Poisson distribution is

$$\text{Prob}(y) = \frac{\lambda^y}{y!} \exp(-\lambda)$$

for responses  $y = 0, 1, 2, \dots$ , where  $\lambda$  is the expected value. The censored version is that response in the interval  $L \leq y \leq H$  are censored (and reported as  $y = L$ , say), whereas other values are reported as is. This is often due to privacy issue, for example using  $L = 1$  and  $H = 5$ , for example.

The “cenpoisson” probability distribution is then, for  $y = 0, 1, \dots$ ,

$$\text{Prob}^*(y) = \begin{cases} \sum_{z=L}^H \frac{\lambda^z}{z!} \exp(-\lambda) & L \leq y \leq H \\ \frac{\lambda^y}{y!} \exp(-\lambda) & \text{otherwise} \end{cases}$$

### Link-function

The mean-parameter is  $\lambda$  and is linked to the linear predictor  $\eta$  by

$$\lambda = E \exp(\eta)$$

where  $E > 0$  is a known constant (or  $\log(E)$  is the offset of  $\eta$ ).

### Hyperparameters

None.

### Specification

- `family="cenpoisson2"`
- The `cenpoisson2` differ from `cenpoisson`, in that  $L$  and  $H$  are vectors and not scalars, hence different observations can have different censoring.
- Required arguments:  $y$ ,  $E$ ,  $L$  and  $H$ . The vector of the triplet  $(y_i, L_i, H_i)$  must be given as a `inla.mdata`-object.  $L$  and  $H$  are vectors of same length as  $y$  hence the censoring can be different for each observation.  $L$  and  $H$  must be integer valued or `Inf`.

$L[i] = \text{Inf}$  and/or  $H[i] = \text{Inf}$  are allowed, which is equivalent to  $L[i] = -1$  and/or  $H[i] = -1$ . See the example for details.

### Example

In the following example we estimate the parameters in a simulated example with Poisson responses.

```
n <- 300
a <- 0
b <- 1
x <- rnorm(n, sd = 0.3)
eta = a + b*x
low = sample(c(0, 1, 4, Inf), n, replace = TRUE)
high <- low + sample(c(0, 1, 2, Inf), n, replace = TRUE)

E = sample(1:10, n, replace=TRUE)
lambda = E*exp(eta)
```

```

y = rpois(n, lambda = lambda)

censored = which(y >= low & y <= high)
y[censored] = low[censored]

r <- inla(inla.mdata(cbind(y, low, high)) ~ 1 + x,
          family = "cenpoisson2",
          data = data.frame(y, low, high, x),
          E=E)
summary(r)

```

## Notes

For censored values, then  $y$  must be one arbitrary value in the interval; NA does not work!!!