

Package: cotram (via r-universe)

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Title Count Transformation Models

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Description Count transformation models featuring parameters interpretable as discrete hazard ratios, odds ratios, reverse-time discrete hazard ratios, or transformed expectations. An appropriate data transformation for a count outcome and regression coefficients are simultaneously estimated by maximising the exact discrete log-likelihood using the computational framework provided in package 'mlt', technical details are given in Siegfried & Hothorn (2020) <[DOI:10.1111/2041-210X.13383](https://doi.org/10.1111/2041-210X.13383)>. The package also features joint count transformation models with covariate-dependent correlations applied to a species community of three aquatic birds <[DOI:10.48550/arXiv.2201.13095](https://doi.org/10.48550/arXiv.2201.13095)>.

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confband	<i>Confidence Bands</i>
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Description

Confidence bands for transformation, distribution, survivor or cumulative hazard functions

Usage

```
## S3 method for class 'cotram'
confband(object, newdata, level = 0.95,
         type = c("trafo", "distribution", "survivor", "cumhazard"),
         smooth = FALSE, q = NULL, K = 20, cheat = K, ...)
```

Arguments

object	an object of class cotram .
newdata	a data frame of observations.
level	the confidence level.
type	the function to compute the confidence band for.
smooth	logical; if TRUE a smoothed function of type is returned.
q	quantiles at which to evaluate the model.
K	number of grid points the function is evaluated at (in the absence of q and smooth = TRUE).
cheat	number of grid points the function is evaluated at when using the quantile obtained for K grid points (in the absence of q and smooth = TRUE).
...	additional arguments to confint.glm .

Details

The function is evaluated at the count response or at K grid points and simultaneous confidence intervals are then interpolated in order to construct the band.

Value

For each row in newdata the function and corresponding confidence band evaluated at the count response (or K or cheat grid points) is returned.

Examples

```
op <- options(digits = 4)

data("birds", package = "TH.data")

### fit count transformation model with cloglog link
m_birds <- cotram(SG5 ~ AOT + AFS + GST + DBH + DWC + LOG, data = birds,
                 method = "cloglog")

### compute asymptotic confidence bands for the distribution function
### for the first observation
confband(m_birds, newdata = birds[1, ], type = "distribution")

options(op)
```

cotram

Count Transformation Models

Description

Likelihood-based count transformation models for fully parameterised discrete conditional distribution functions. The link function governing the interpretation of the predictor can be chosen and results in discrete hazard ratios, odds ratios, reverse time hazard ratios or conditional expectation of transformed counts.

Usage

```
cotram(formula, data, method = c("logit", "cloglog", "loglog", "probit"),
       log_first = TRUE, prob = 0.9, subset, weights, offset, cluster,
       na.action = na.omit, ...)
```

Arguments

formula an object of class "formula": a symbolic description of the model structure to be fitted. The details of model specification are given under [tram](#) and in the package vignette.

data	an optional data frame, list or environment (or object coercible by <code>as.data.frame</code> to a data frame) containing the variables in the model. If not found in data, the variables are taken from <code>environment(formula)</code> .
method	character specifying the choice of the link function, mapping the transformation function into probabilities. Available choices include the logit, complementary log-log, log-log or probit link. The different link functions govern the interpretation of the linear predictor. Details of the interpretation can be found in the package vignette.
prob	probability giving the quantile of the response defining the upper limit of the support of a smooth Bernstein polynomial (with the lower limit being set to 0). If a vector of two probabilities is specified, the corresponding quantiles of the response define the lower and upper limit of the support, respectively. Note, that the support is rounded to integer values.
log_first	logical; if TRUE, a Bernstein polynomial is defined on the log-scale for $(y + 1)$.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
weights	an optional vector of weights to be used in the fitting process. Should be NULL or a numeric vector. If present, the weighted log-likelihood is maximised.
offset	this can be used to specify an <code>_a priori_</code> known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases.
cluster	optional factor with a cluster ID employed for computing clustered covariances.
na.action	a function which indicates what should happen when the data contain NAs. The default is set to <code>na.omit</code> .
...	additional arguments to <code>tram</code> .

Details

Likelihood-based estimation of a fully parameterised conditional discrete distribution function for count data, while ensuring interpretability of the linear predictors. The models are defined with a negative shift term relating positive predictors to larger values of the conditional mean. For the model with logistic or cloglog link `exp(-coef())` is the multiplicative change of discrete odds-ratios or hazard ratios. For the model with loglog link `exp(coef())` is the multiplicative change of the reverse time hazard ratios. Applying a transformation model with probit link `coef()` gives the conditional expectation of the transformed counts, with transformation function estimated from data.

Value

An object of class `cotram` and `tram`, with corresponding `coef`, `vcov`, `logLik`, `summary`, `print`, `plot` and `predict` methods.

References

Sandra Siegfried, Torsten Hothorn (2020), Count Transformation Models, *Methods in Ecology and Evolution*, **11**(7), 818–827, doi:[10.1111/2041210X.13383](https://doi.org/10.1111/2041210X.13383).

Torsten Hothorn, Lisa Möst, Peter Bühlmann (2018), Most Likely Transformations, *Scandinavian Journal of Statistics*, **45**(1), 110–134, doi:10.1111/sjos.12291.

Torsten Hothorn (2020), Most Likely Transformations: The mlt Package, *Journal of Statistical Software*, **92**(1), 1–68, doi:10.18637/jss.v092.i01.

Examples

```
op <- options(digits = 2)

data("birds", package = "TH.data")
cotram(SG5 ~ AOT + AFS + GST + DBH + DWC + LOG, data = birds)

options(op)
```

cotram-methods

Methods for Count Transformation Models

Description

Methods for objects inheriting from class cotram

Usage

```
## S3 method for class 'cotram'
predict(object, newdata = model.frame(object),
        type = c("lp", "trafo", "distribution", "survivor", "density",
                 "logdensity", "hazard", "loghazard", "cumhazard",
                 "logcumhazard", "odds", "logodds", "quantile"),
        smooth = FALSE, q = NULL, K = 20, prob = 1:(10-1)/10, ...)
## S3 method for class 'cotram'
plot(x, newdata, type = c("distribution", "survivor", "density",
                          "logdensity", "cumhazard", "quantile", "trafo"),
     confidence = c("none", "band"), level = 0.95,
     smooth = FALSE, q = NULL, K = 20, cheat = K, prob = 1:(10-1)/10,
     col = "black", fill = "lightgrey",
     lty = 1, lwd = 1, add = FALSE, ...)
## S3 method for class 'cotram'
as.mlt(object)
## S3 method for class 'cotram'
logLik(object, parm = coef(as.mlt(object)), fixed = FALSE, newdata, ...)
```

Arguments

object, x	a fitted linear count transformation model inheriting from class cotram.
newdata	an optional data frame of observations.
parm	model parameters.

type	type of prediction, current options include linear predictors ("lp", of x variables in the formula $y \sim x$), transformation functions ("trafo") or distribution functions on the scale of the cdf ("distribution"), survivor function, density function, log-density function, cumulative hazard function or quantile function.
confidence	whether to plot a confidence band (see confband).
level	the confidence level.
smooth	logical; if TRUE a smoothed function of type is returned.
q	quantiles at which to evaluate the model.
prob	probabilities for the evaluation of the quantile function (type = "quantile").
K	number of grid points the function is evaluated at (for smooth = TRUE and in absence of q).
cheat	number of grid points the function is evaluated at when using the quantile obtained for K grid points (in the absence of q and smooth = TRUE).
col	color for the lines to plot.
fill	color for the confidence band.
lty	line type for the lines to plot.
lwd	line width.
add	logical; indicating if a new plot shall be generated (the default).
...	additional arguments to the underlying methods for predict.

Details

predict and plot can be used to inspect the model on different scales.

See Also

[predict.cotram](#), [confband.cotram](#), [tram-methods](#), [mlt-methods](#), [plot.ctm](#)

Examples

```
op <- options(digits = 4)

data("birds", package = "TH.data")

### fit count transformation model with cloglog link
m_birds <- cotram(SG5 ~ AOT + AFS + GST + DBH + DWC + LOG, data = birds,
                 method = "cloglog")
logLik(m_birds)

### classical likelihood inference
summary(m_birds)

### coefficients of the linear predictor (discrete hazard ratios)
exp(-coef(m_birds))

### compute predicted median along with 10% and 90% quantile for the first
```

```

### three observations
nd <- birds[1:3,]
round(predict(m_birds, newdata = nd, type = "quantile", prob = c(.1, .5, .9),
             smooth = TRUE), 3)

### plot the predicted distribution for these observations
plot(m_birds, newdata = nd, type = "distribution",
     col = c("skyblue", "grey", "seagreen"))

options(op)

```

mcotram

*Multivariate Count Conditional Transformation Models***Description**

A proof-of-concept implementation of multivariate conditional transformation models for count data.

Usage

```

mcotram(..., formula = ~ 1, data, conditional = FALSE, theta = NULL,
        fixed = NULL, scale = FALSE, optim = mltoptim(hessian = TRUE),
        M = 1000, dofit = TRUE, domargins = TRUE)

```

Arguments

...	marginal count transformation models, one for each response
formula	a model formula describing a model for the dependency structure via the lambda parameters. The default is set to ~ 1 for constant lambdas.
data	a data.frame.
conditional	logical; parameters are defined conditionally (only possible when all models are probit models). This is the default as described by Klein et al. (2022). If FALSE, parameters can be directly interpreted marginally, this is explained in Section 2.6 by Klein et al. (2022). Using conditional = FALSE with probit-only models gives the same likelihood but different parameter estimates.
theta	an optional vector of starting values.
fixed	an optional named numeric vector of predefined parameter values.
scale	a logical indicating if (internal) scaling shall be applied to the model coefficients.
optim	a list of optimisers as returned by <code>mltoptim</code>
M	number of Halton sequences used to approximate the log-likelihood in <code>lpmvnorm</code> .
dofit	logical; parameters are fitted by default, otherwise a list with log-likelihood and score function is returned.
domargins	logical; all model parameters are fitted by default, including the parameters of marginal models.

Details

The function implements multivariate count conditional transformation models. The response is assumed to be a vector of counts.

Value

An object of class `mmlt` with `coef` and `predict` methods.

References

Luisa Barbani, Roland Brandl, Torsten Hothorn (2022), Multi-species Count Transformation Models, [doi:10.48550/arXiv.2201.13095](https://doi.org/10.48550/arXiv.2201.13095).

Nadja Klein, Torsten Hothorn, Luisa Barbanti, Thomas Kneib (2020), Multivariate Conditional Transformation Models. *Scandinavian Journal of Statistics*, [doi:10.1111/sjos.12501](https://doi.org/10.1111/sjos.12501).

Examples

```
library("cotram")
data("spiders", package = "cotram")

### for illustration only
OR <- 1      ### order of transformation function
             ### OR = 1 means log-linear, use OR ~ 6
M <- 50     ### number of Halton sequences, seem sufficient here
fastopt <- mltoptim(abstol = 1e-3, reltol = 1e-3)
             ### faster convergence

## fit conditional marginal count transformation models
## one for each species
m_PF <- cotram(Pardosa_ferruginea ~ Elevation + Canopy_openess,
              data = spiders, method = "probit", order = OR)
m_HL <- cotram(Harpactea_lepida ~ Elevation + Canopy_openess,
              data = spiders, method = "probit", order = OR)
m_CC <- cotram(Callobius_claustrarius ~ Elevation + Canopy_openess,
              data = spiders, method = "probit", order = OR)
m_CT <- cotram(Coelotes_terrestris ~ Elevation + Canopy_openess,
              data = spiders, method = "probit", order = OR)
m_PL <- cotram(Pardosa_lugubris ~ Elevation + Canopy_openess,
              data = spiders, method = "probit", order = OR)
m_PR <- cotram(Pardosa_riparia ~ Elevation + Canopy_openess,
              data = spiders, method = "probit", order = OR)

### fit dependence parameters
mm <- mcotram(m_PF, m_HL, m_CC, m_CT, m_PL, m_PR, data = spiders,
            M = M, scale = TRUE, optim = fastopt)
logLik(mm)

### Kendall's tau: Dependence of species after accounting
### for elevation and canopy openess in marginal models
coef(mm, type = "Kendall")
```

```

### regress dependencies on elevation and canopy openness
mmc <- mcotram(m_PF, m_HL, m_CC, m_CT, m_PL, m_PR, data = spiders,
              formula = ~ Elevation + Canopy_openess, M = M,
              scale = TRUE, optim = fastopt)
logLik(mmc)

### weak evidence for such effects
pchisq(2 * (logLik(mmc) - logLik(mm)), df = 30, lower.tail = FALSE)

### plot Kendall's tau for different elevations / openness levels
nd <- expand.grid(Elevation = 80:120 * 10, Canopy_openess = 1:10 * 10)
KD <- Lower_tri(coef(mmc, newdata = nd, type = "Kendall"))
f <- factor(rownames(KD))
nd <- cbind(f = rep(f, nrow(nd)), nd[rep(1:nrow(nd), each = nlevels(f)),])
nd$KD <- c(KD)

if (require("lattice"))
  contourplot(KD ~ Elevation + Canopy_openess | f, data = nd,
              cuts = 18, xlab = "Elevation", ylab = "Canopy openness")

### for example:
### => constant negative dependence of Pardosa_lugubris and Coelotes_terrestris
### => weak dependence of Harpactea_lepida and Pardosa_ferruginea
###   for low elevations, negative dependence increasing with elevation

```

spiders

Bavarian Forest Spider Data

Description

Abundance of six spider species on 190 plots in the Bavarian Forest National Park

Usage

```
data("spiders")
```

Format

A data frame with 190 observations on the following 9 variables.

Plot experimental plot id

Elevation elevation of the plot

Canopy_openess openness of canopy at plot

Pardosa_ferruginea number of Pardosa ferruginea observed

Harpactea_lepida number of Harpactea lepida observed
Callobius_claustrarius number of Callobius claustrarius observed
Coelotes_terrestris number of Coelotes terrestris observed
Pardosa_lugubris number of Pardosa lugubris observed
Pardosa_riparia number of Pardosa riparia observed

Details

To untangle effects of dead-wood addition and canopy openness on non-saproxyllic epigeal arthropods, Seibold et al (2016) exposed different amounts of logs and branches on 190 0.1-ha plots located in sunny or shady mixed montane forests and sampled epigeal arthropods over three years. The data contain abundances of six spider species for all 190 plots, along with plot elevation and canopy openness.

Source

Sebastian Seibold, Claus Bässler, Petr Baldrian, Lena Reinhard, Simon Thorn, Michael D. Ulyshen, Ingmar Weiß and Jörg Müller (2016). Dead-wood addition promotes non-saproxyllic epigeal arthropods but effects are mediated by canopy openness. *Biological Conservation*, **204**, 181–188, doi:[10.1016/j.biocon.2016.09.031](https://doi.org/10.1016/j.biocon.2016.09.031).

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