

Package: GRCRegression (via r-universe)

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Type Package

Title Modified Poisson Regression of Grouped and Right-Censored Counts

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Depends MASS, pracma

Description Implement maximum likelihood estimation for Poisson generalized linear models with grouped and right-censored count data. Intended to be used for analyzing grouped and right-censored data, which is widely applied in many branches of social sciences. The algorithm implemented is described in Fu et al., (2021) <[doi:10.1111/rssa.12678](https://doi.org/10.1111/rssa.12678)>.

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NeedsCompilation no

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Repository <https://xguo20.r-universe.dev>

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 genData.P

Artificial Data Generation

Description

Generate artificial data for testing and verification.

Usage

```
genData.P(beta, data.size, scheme,
  scope.lambda = c(0.01, 100), link.lambda = link.log, seed = list(no = 1),
  y.lowRatio = -1)
```

Arguments

beta	Coefficients of modified Poisson regression.
data.size	The sample size of data to generate.
scheme	The grouped and right-censored grouping scheme. A sorted vector containing starting integers of all groups.
scope.lambda	A vector of length 2 specifying the range of λ .
link.lambda	The link function for λ .
seed	Random seed (optional).
y.lowRatio	The minimum proportion of groups in the sample distribution. This optional proportion is included to deal with imbalanced data.

Value

x	The design matrix.
y	The GRC outcome.
unused	An integer roughly describing the number of discarded sample observations in the generating process. If this number is too large, the generation of artificial data is not efficient and takes too much time.

Examples

```
set.seed(123)
tp <- genData.P(beta = c(0.5, -1, 1), data.size = 12, scheme = c(0:3, 5, 8))
```

GRCglm	<i>Maximum likelihood estimation for modified Poisson regression of GRC data</i>
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Description

This function implements maximum likelihood estimation of modified Poisson regression of grouped and right-censored counts.

Usage

```
GRCglm.P(y, x1, scheme, link.lambda = link.log, weights = rep(1, nrow(x1)),
  num.intercept = 1, xtol_rel = 1e-08, maxit = 100)
```

Arguments

y	A vector of the GRC outcome.
x1	The design matrix.
scheme	A vector (sorted) of the starting integers of all GRC groups.
link.lambda	The link function for λ
weights	The weight vector used to consider sampling weights.
num.intercept	Presence of the regression intercept. Can be set to 0 or 1. This is also used to calculate the null deviance.
xtol_rel, maxit	The tolerancethreshold and maximum number of iteration of the algorithm.

Value

coefficients	The inferred coefficients.
beta	An alias of coefficients.
fitting	The call.
log.likelihood	Value of the log likelihood function.
df.null	The residual degrees of freedom of the null model.
df.residual	The residual degrees of freedom.
null.deviance	Null deviance.
deviance	The deviance.
aic, bic	The AIC and BIC scores.
McFaddenR2, McFaddenAdjR2	The (rep. Adjusted) McFadden R-square.

Examples

```
set.seed(123)
tp <- genData.P(beta = c(0.5, -1, 1), data.size = 120, scheme = c(0:3, 5, 8),
  scope.lambda = c(1, 10))
a <- GRCglm.P(y = tp$y, x1 = tp$x, scheme = c(0:3, 5, 8))
```

 link.log

The log link

Description

The log link function

Usage

```
link.log()
```

Arguments

No arguments

Details

This implements the link function $g(x) = \log(x)$ on the domain $(0, \infty)$.

Value

class	A character "0Inf" denotes the domain $(0, \infty)$.
g	The link function g .
gInv	The inverse of the link function.
D.gInv	The derivative of the inverse link function.
DD.gInv	The second-order derivative of the link function.

Examples

```
a <- link.log()
```

 summary

Summary of estimates.

Description

A summary of estimates for the class GRCglm.P.

Usage

```
## S3 method for class 'GRCglm.P'
summary(object, level = 0.95, ...)
```

Arguments

object	An object of class "GRCglm.P".
level	Level of confidence.
...	Reserved parameter for matching other summary methods.

Value

FisherInfo	The observed Fisher information matrix.
stdErr	Estimated standard error.
ci	Confidence intervals of the estimated coefficients.
WOGRCStdErr	Estimated standard error for comparison, with Fisher information matrix computed using exact enumeration of counts.
zValue	Z-score of the estimated coefficients.
sigLevel	P-value of the estimated coefficients.

Examples

```
set.seed(123)
tp <- genData.P(beta = c(0.5, -1, 1), data.size = 120, scheme = c(0:3, 5, 8),
  scope.lambda = c(1, 10))
a <- GRCglm.P(y = tp$y, x1 = tp$x, scheme = c(0:3, 5, 8))
b <- summary(a)
```

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