Package 'cdnbcr'

May 8, 2026

Type Package

Title Correlated Destructive Negative Binomial Cure Rate Model

Version 1.1.1

Maintainer Rodrigo M. R. de Medeiros <rodrigo.matheus@ufrn.br>

Description Provides tools for modeling time-to-event data with a cure fraction under correlated destructive negative binomial cure rate models. The models assume multiple latent competing causes with possible dependence and allow for elimination (inactivation) of some initial causes. Estimation is performed via an Expectation-Maximization algorithm, and diagnostic tools based on Cox-Snell residuals are provided.

Encoding UTF-8

LazyData true

URL https://github.com/rdmatheus/cdnbcr

BugReports https://github.com/rdmatheus/cdnbcr/issues

Suggests survival, testthat (>= 3.0.0)

Config/testthat/edition 3

RoxygenNote 7.3.2

Imports Formula (>= 1.2.4), pracma (>= 2.3.3)

Depends R (>= 3.5)

License GPL (>= 3)

NeedsCompilation no

Author Rodrigo M. R. de Medeiros [aut, cre, cph] (ORCID: <https://orcid.org/0000-0001-8101-3038>), Diego Gallardo [aut] (ORCID: <https://orcid.org/0000-0001-8184-7403>)

Repository CRAN

Date/Publication 2026-03-09 11:10:02 UTC

Contents

`cdnbcr` *Correlated Destructive Negative Binomial Cure Rate Model*

Description

Fits the correlated destructive negative binomial cure rate (CDNBCR) model to right-censored survival data using maximum likelihood estimation via the expectation–maximization (EM) algorithm.

Usage

```
cdnbcr(
  formula,
  data,
  subset,
  na.action,
  theta.link = "log",
  p.link = "logit",
  alpha = TRUE,
  control = control_EM(...),
  y = TRUE,
  x = TRUE,
  ...
)

## S3 method for class 'cdnbcr'
print(x, digits = getOption("digits"), ...)
```

Arguments

`formula`	A model formula following the syntax of the `Formula` package. The left-hand side must be a `Surv` object specifying the observed follow-up time and censoring indicator. The right-hand side may contain two regression components separated by the `|` operator: the first for `theta` (expected number of initial competing causes) and the second for `p` (activation probability of an initial competing cause). If only one component is provided, it is used for `theta` and `p` is modeled with an intercept only.

`data`	A data frame containing the variables used in the model.
`subset`	An optional vector specifying a subset of observations to be used in the model.
`na.action`	A function indicating how to handle missing values. See `model.frame`.
`theta.link`, `p.link`	Link functions for the regression submodels of `theta` and `p`. Defaults are `"log"` for `theta.link` and `"logit"` for `p.link`. Alternative links can be specified using `make.link`.
`alpha`	Logical; if `TRUE` (default), the correlation parameter `alpha` is estimated. If `FALSE`, `alpha` is fixed at zero, yielding the uncorrelated destructive model.
`control`	A list of control parameters for the EM algorithm, as returned by `control_EM`.
`y`	Logical; if `TRUE` (default), the response vector is returned.
`x`	Logical; if `TRUE` (default), the model matrices are returned. For `print()`, `x` is a fitted model object of class `"cdnbcr"`.
`...`	Additional arguments passed to `control_EM`.
`digits`	a non-null value for digits specifies the minimum number of significant digits to be printed in values.

Details

The CDNBCR model assumes that the number of initial competing causes follows a negative binomial distribution with mean $\theta > 0$ and dispersion parameter $\phi > 0$. Each initial cause may remain active with probability $p \in (0, 1)$, and the activation indicators may be correlated through the parameter $\alpha \in [0, 1]$. The event time is defined as the minimum of the latent failure times associated with the remaining active causes. Individuals with no active causes are considered cured and will never experience the event of interest. Regression structures can be specified for both the expected number of initial competing causes (θ) and the activation probability (p).

The CDNBCR model reduces to the (uncorrelated) destructive negative binomial cure rate model (Rodrigues et al., 2011) when $\alpha = 0$. In practice, this is obtained by setting `alpha = FALSE` in `cdnbcr()`.

The response must be specified using `Surv(time, status)`, where `time` is the observed follow-up time and `status` is the event indicator (1 = event, 0 = right-censored). Regression structures can be specified separately for θ and p using the `|` operator. For example,

```
Surv(time, status) ~ x1 + x2 | z1 + z2
```

specifies a model in which θ depends on covariates `x1` and `x2`, while p depends on covariates `z1` and `z2`.

Value

An object of class `"cdnbcr"` with components:

coefficients A list with the estimated regression coefficients for the `theta` and `p` submodels.

phi, alpha, mu, sigma Maximum likelihood estimates of the additional model parameters.

fitted Fitted values of `theta` and `p` for each observation.

links A named list with the link functions used in the `theta` and `p` regression submodels.

vcov Estimated covariance matrix associated with the parameter estimates.

logLik Log-likelihood of the fitted model.

nobs Number of observations used in the fit.

df.null Residual degrees of freedom of the null model.

df.residual Residual degrees of freedom of the fitted model.

convergence Convergence code of the EM algorithm (0 = successful, 1 = maximum iterations reached).

inits Initial values used in the EM algorithm.

control Control parameters used in the EM algorithm.

iterations Number of EM iterations.

latent A list with components `M`, `D`, and `Y` containing posterior expectations of the latent variables used in the EM algorithm. Here, `M` denotes the initial number of competing causes, `D` is the number of remaining active competing causes, and `Y` is a latent Bernoulli variable that governs the activation regime of the destructive mechanism (and induces dependence through `alpha`).

call Matched function call.

formula Model formula.

terms Terms objects for the regression submodels.

y Response vector (if `y = TRUE`).

x Model matrices (if `x = TRUE`).

Author(s)

Diego I. Gallardo <diego.gallardo.mateluna@gmail.com>

Rodrigo M. R. de Medeiros <rodrigo.matheus@ufrn.br>

References

Cox, D. R., and Snell, E. J. (1968). A general definition of residuals. *Journal of the Royal Statistical Society B*, **30**, 248–265.

De Medeiros, R. M. R., Bourguignon, M., Gómez, Y. M., and Gallardo, D. I. (2026). A correlated approach to cancer cell counting in cure rate models.

Rodrigues, J., De Castro, M., Balakrishnan, N., and Cancho, V. G. (2011). Destructive weighted Poisson cure rate models. *Lifetime Data Analysis*, **17**, 333–346

See Also

`summary.cdnbcr` for detailed model summaries, `residuals.cdnbcr` to extract Cox–Snell residuals (Cox and Snell, 1968), `plot.cdnbcr` for diagnostic plots based on Cox–Snell residuals, and `predict.cdnbcr` for prediction under the CDNBCR model. Additional methods for `"cdnbcr"` objects are documented in `cdnbcr-methods`.

Examples

```
## Loading survival package
library(survival)

## Dataset: e1690 (see ?e1690)
head(e1690)

## Correlated destructive fit
fit <- cdnbcr(formula = Surv(time, status) ~ nodeII + nodeIII + nodeIV - 1 |
                sex + trt + thickness + age, data = e1690)
fit

## Uncorrelated destructive fit
fit0 <- cdnbcr(formula = Surv(time, status) ~ nodeII + nodeIII + nodeIV - 1 |
                 sex + trt + thickness + age, data = e1690, alpha = FALSE)
fit0
```

---

cdnbcr-methods *Extract Information From a CDNBCR Fit*

Description

Methods for "cdnbcr" objects.

Usage

```
## S3 method for class 'cdnbcr'
model.frame(formula, ...)

## S3 method for class 'cdnbcr'
model.matrix(object, parm = c("full", "theta", "p"), ...)

## S3 method for class 'cdnbcr'
coef(object, parm = c("full", "theta", "p"), ...)

## S3 method for class 'cdnbcr'
vcov(object, parm = c("full", "theta", "p"), ...)

## S3 method for class 'cdnbcr'
residuals(object, ...)

## S3 method for class 'cdnbcr'
logLik(object, ...)

## S3 method for class 'cdnbcr'
AIC(object, ..., k = 2)
```

Arguments

formula	A model Formula or terms object or an "cdnbcr" object.
...	Additional arguments passed to or from other methods.
object	An object of class "cdnbcr".
parm	A character indicating which regression structure should be used. It can be "theta" for the expected initial competing causes regression structure, "p" for the activation probability of an initial competing cause regression submodel, or "full" for both regression structures.
k	Numeric, the penalty per parameter to be used; the default k = 2 is the classical AIC. See AIC.

Value

- model.frame returns a data.frame containing the variables required by formula and any additional arguments provided via ....
- model.matrix returns the design matrix used in the regression structure, as specified by the parm argument.
- coef returns a numeric vector of estimated regression coefficients, based on the parm argument. If parm = "full", it returns a list with the components "theta" and "p", each containing the corresponding coefficient estimates.
- vcov returns the asymptotic covariance matrix of the regression coefficients, based on the parm argument.
- residuals returnas a "Surv" object with the Cox-Snell residuals (Cox and Snell, 1968). If the model is well fitted to the data, the Cox-Snell residuals are expected to be distributed as a censored random sample from the exponential distribution with mean 1.
- logLik returns the log-likelihood value of the fitted model.
- AIC returns a numeric value representing the Akaike Information Criterion (AIC), Bayesian Information Criterion, or another criterion, depending on k.

Author(s)

Rodrigo M. R. de Medeiros <<rodrigo.matheus@ufrn.br>>

References

Cox, D. R., and Snell, E. J. (1968). A general definition of residuals. *Journal of the Royal Statistical Society B*, **30**, 248–265.

De Medeiros, R. M. R., Bourguignon, M., Gómez, Y. M., and Gallardo, D. I. (2026). A correlated approach to cancer cell counting in cure rate models.

Rodrigues, J., De Castro, M., Balakrishnan, N., and Cancho, V. G. (2011). Destructive weighted Poisson cure rate models. *Lifetime Data Analysis*, **17**, 333–346

Examples

```
## Loading survival package
library(survival)

## Dataset: e1690 (see ?e1690)
head(e1690)

## Correlated destructive fit
fit <- cdnbcr(formula = Surv(time, status) ~ nodeII + nodeIII + nodeIV - 1 |
                sex + trt + thickness + age, data = e1690)

# Model frame
mf <- model.frame(fit)
mf

# Model matrices
model.matrix(fit, parm = "theta")
model.matrix(fit, parm = "p")

# Coef
coef(fit)
coef(fit, parm = "theta")
coef(fit, parm = "p")

# vcov
vcov(fit)
vcov(fit, parm = "theta")
vcov(fit, parm = "p")

# residuals
residuals(fit)

# Log-likelihood value
logLik(fit)

# AIC and BIC
AIC(fit)
AIC(fit, k = log(fit$nobs))
```

`cdnbcr-model` *The Correlated Destructive Negative Binomial Cure Rate Model*

Description

Provides the main distributional components of the correlated destructive negative binomial cure rate (CDNBCR) model, including the probability density function, cumulative distribution function, cure fraction, and random number generation.

Usage

```
dcdnbcr(x, theta, phi, p, alpha, mu, sigma, log.p = FALSE)

pcdnbcr(q, theta, phi, p, alpha, mu, sigma, lower.tail = TRUE, log.p = FALSE)

rcdnbcr(n, theta, phi, p, alpha, mu, sigma)

cure_rate(theta, phi, p, alpha)
```

Arguments

x	Vector of positive event times.
theta, phi	Positive parameters related to the expected initial number of competing causes and their dispersion.
p, alpha	Parameters controlling the probability that a cause remains active. The dependence among active causes is governed by alpha. Both p and alpha are restricted to the closed unit interval [0, 1]. When alpha = 0, activations are assumed to be independent.
mu, sigma	Strictly positive parameters of the Weibull distribution assumed for the time-to-event of active competing causes.
log.p	Logical; if TRUE, probabilities p are returned as log(p).
q	Vector of quantiles.
lower.tail	Logical; if TRUE (default), probabilities are P(X <= x); otherwise, P(X > x).
n	Number of random values to generate.

Details

The CDNBCR model describes the time until the occurrence of an event while accounting for a cure fraction, assuming multiple initial competing causes with possible dependence. The model is termed *destructive* because some of the initial competing causes contributing to the occurrence of the event may be eliminated or inactivated. This formulation is particularly useful in applications where interventions (e.g., treatments) may remove or deactivate some competing causes.

The number of initial competing causes is modeled by a negative binomial random variable with mean theta and variance theta * (1 + phi * theta). Each initial competing cause remains active with probability p. Dependence in the activation mechanism is introduced through the parameter alpha. Let Y_j denote the survival time associated with the jth remaining competing cause, $j = 1, \ldots, D$, where D is a latent random variable. We assume that Y_j follows a Weibull distribution with mean mu and variance mu^2 * (Gamma(2/sigma + 1) / Gamma(1/sigma + 1)^2 - 1). The observed uncensored survival time is given by $T = \min(Y_1, \ldots, Y_D)$.

Value

dcdnbcr returns the probability density function, pcdnbcr returns the distribution function, cure_rate returns the cure fraction of the model, and rcdnbcr generates random observations.

Author(s)

Diego I. Gallardo <<diego.gallardo.mateluna@gmail.com>>

Rodrigo M. R. de Medeiros <<rodrigo.matheus@ufrn.br>>

See Also

cdnbcr for parameter estimation in the CDNBCR model.

Examples

```
# Parameters
theta <- 1.5
phi <- 1.2
p <- 0.6
alpha <- 0.3
mu <- 5
sigma <- 1.5

n <- 1000
tobs <- rcdnbcr(n, theta, phi, p, alpha, mu, sigma)

# Censoring
Cens <- 10
delta <- ifelse(tobs <= Cens, 1, 0)
tobs[delta == 0] <- Cens

op <- par()$mfrow
par(mfrow = c(1, 2))
# Histogram
hist(tobs, prob = TRUE, main = " ", xlab = expression(T[obs]))
curve(dcdnbcr(x, theta, phi, p, alpha, mu, sigma), add = TRUE, col = 2, lwd = 2)
points(Cens, mean(1 - delta), pch = 16, col = 2, lwd = 2)

# Survival function
plot(survival::survfit(survival::Surv(tobs, delta) ~ 1, se.fit = FALSE),
     xlab = expression(T[obs]), ylab = "Survival function")
curve(1 - pcdnbcr(x, theta, phi, p, alpha, mu, sigma), add = TRUE, col = 2, lwd = 2)

# Cure rate
abline(h = cure_rate(theta, phi, p, alpha), col = 4)
legend("bottomleft", c("Empirical", "Theoretical", "Cure rate"),
        col = c(1, 2, 4), bty = "n", lty = 1)
par(mfrow = op)
```

---

control_EM *Auxiliary for Controlling a CDNBCR Fit via EM Algorithm*

Description

Optimization parameters that control the fitting of the correlated destructive negative binomial cure rate model (CDNBCR) via Expectation-Maximization (EM) algorithm.

Usage

```
control_EM(method = "BFGS", maxit = 10000, start = NULL, prec = 5e-05, ...)
```

Arguments

`method`	Optimization method for the "M" steps, specifying the `method` argument passed to `optim`.
`maxit`	Maximum number of EM algorithm iterations. The default is `10.000` iterations. If this limit is reached, a warning message is displayed.
`start`	An optional vector of initial values for the algorithm. The expected order of the parameters is `(beta1, phi, beta2, alpha, mu, sigma)`, where `beta1` and `beta2` are vectors of coefficients associated with the regression structures of `theta` and `p`, respectively.
`prec`	Numeric tolerance for convergence in the EM iterations.
`...`	Additional arguments passed to `optim`.

Value

A list with components named as the arguments.

Author(s)

Rodrigo M. R. de Medeiros <<rodrigo.matheus@ufrn.br>>

See Also

`cdnbcr` for parameter estimation in the CDNBCR model via EM algorithm.

Examples

```
## Loading the survival package
library(survival)

## Dataset:  (see ?e1690)
head(e1690)

## Correlated destructive fit (default fit)
fit1 <- cdnbcr(Surv(time, status) ~ nodeII + nodeIII + nodeIV - 1 |
                trt + thickness, data = e1690)

## Changing the initial values
beta1 <- c(1, 1.5, 2)
phi <- 2
beta2 <- c(0.5, -0.5, 0.5)
```

```
alpha <- 0.5
mu <- 3
sigma <- 2

fit2 <- cdnbcr(Surv(time, status) ~ nodeII + nodeIII + nodeIV - 1 |
                trt + thickness, data = e1690,
               start = c(beta1, phi, beta2, alpha, mu, sigma))

## Compare the fits:
fit1
fit2
```

---

e1690 *Phase III cutaneous melanoma clinical trial*

Description

A well-known dataset from a Phase III cutaneous melanoma clinical trial (Ibrahim et al., 2001). The study was conducted by the Eastern Cooperative Oncology Group (ECOG) and aimed to evaluate the effectiveness of the Interferon alpha-2b chemotherapy in preventing recurrence after surgery. After eliminating missing data, the observations include 417 patients from 1991 to 1995, with follow-up until 1998.

Usage

```
e1690
```

Format

A data frame with 417 rows and 9 columns:

trt Indicates whether the patient was treated with Interferon alpha-2b chemotherapy (chemotherapy) or not (control).

time Post-surgery survival or censoring time, in years.

status Censoring status.

age Age, in years.

sex Sex of the patient.

thickness Tumor thickness, in mm.

nodeII, nodeIII, nodeIV Binary variables indicating the nodal category.

References

Ibrahim, J. G., Chen, M., Sinha, D. (2001). *Bayesian Survival Analysis*. Springer.

Examples

```
data(e1690)
plot(time ~ trt, e1690, xlab = "Treatment", ylab = "Time")
```

`plot.cdnbcr` *Diagnostic Plots for the CDNBCR Model*

Description

Produces two diagnostic plots to assess the goodness-of-fit of a Correlated Destructive Negative Binomial Cure Rate model fit based on the Cox-Snell residuals. Available plots include the Kaplan-Meier estimate and the cumulative hazard plot.

Usage

```
## S3 method for class 'cdnbcr'
plot(
  x,
  which = 1:2,
 ask = prod(graphics::par("mfcol")) < length(which) && grDevices::dev.interactive(),
  col.lines = c("black", "#56B4E9"),
  lwd = 2,
  pch = 16,
  cex = 0.8,
  ...
)
```

Arguments

`x`	An object of class `"cdnbcr"`, a result of a call to `cdnbcr`.
`which`	Numeric; if a subset of the plots is required, specify a subset of the numbers `1:2`.
`ask`	Logical; if `TRUE`, the user is asked before each plot.
`col.lines`	A vector with dimension two with the color for empirical and expected lines.
`pch, cex, lwd, ...`	Graphical parameters (see `par`).

Details

The function produces two diagnostic plots for assessing model fit:

- The Kaplan-Meier estimate for Cox-Snell residuals, compared to the expected survival function of an exponential distribution with mean 1;
- The cumulative hazard function against the Cox-Snell residuals, which should align approximately with the identity line if the model is well-fitted.

Value

`plot` method for `"cdnbcr"` objects returns two types of diagnostic plots based on the Cox-Snell residuals.

Author(s)

Diego I. Gallardo <<diego.gallardo.mateluna@gmail.com>>

Rodrigo M. R. de Medeiros <<rodrigo.matheus@ufrn.br>>

References

Cox, D. R., and Snell, E. J. (1968). A general definition of residuals. *Journal of the Royal Statistical Society B*, **30**, 248–265.

De Medeiros, R. M. R., Bourguignon, M., Gómez, Y. M., and Gallardo, D. I. (2026). A correlated approach to cancer cell counting in cure rate models.

Rodrigues, J., De Castro, M., Balakrishnan, N., and Cancho, V. G. (2011). Destructive weighted Poisson cure rate models. *Lifetime Data Analysis*, **17**, 333–346

Examples

```
## Loading survival package
library(survival)

## Dataset: e1690 (see ?e1690)
head(e1690)

## Correlated destructive fit
fit <- cdnbcr(formula = Surv(time, status) ~ nodeII + nodeIII + nodeIV - 1 |
              sex + trt + thickness + age, data = e1690)

## Plot of the Cox-Snell residuals
oldpar <- par(mfrow = c(1, 2))
plot(fit, ask = FALSE)
par(oldpar)
```

---

predict.cdnbcr *Prediction Method for CDNBCR Models*

Description

Computes fitted values and predictions from a correlated destructive negative binomial cure rate (CDNBCR) model fitted with cdnbcr. Predictions may include the survival function, cure rate, expected number of initial competing causes, or the activation probability of competing causes.

Usage

```
## S3 method for class 'cdnbcr'
predict(
  object,
  newdata = NULL,
  type = c("survival", "cure", "theta", "p"),
  time,
```

```
  na.action = stats::na.pass,
  ...
)
```

Arguments

`object`	An object of class `"cdnbcr"`, as returned by `cdnbcr`.
`newdata`	An optional data frame containing covariate values for which predictions are required. If omitted, predictions are computed for the data used in the model fit.
`type`	Character string indicating the type of prediction. Possible values are: `"survival"` Predicted survival function evaluated at the values supplied in `time`. `"cure"` Predicted cure fraction (probability of being cured). `"theta"` Predicted expected number of initial competing causes. `"p"` Predicted activation probability of an initial competing cause.
`time`	Numeric vector of time points at which the survival function is evaluated. Only used when `type = "survival"`.
`na.action`	A function specifying how missing values in `newdata` should be handled. The default is to return `NA` for predictions involving incomplete cases.
`...`	Further arguments passed to or from other methods.

Value

A numeric vector or matrix of predicted values. The structure of the output depends on the selected `type`:

`"survival"` A matrix of survival probabilities with rows corresponding to observations in `newdata` (or the original data) and columns corresponding to the values in `time`.

`"cure"` A numeric vector with the predicted cure fractions.

`"theta"` A numeric vector with the predicted expected numbers of initial competing causes.

`"p"` A numeric vector with the predicted activation probabilities.

Author(s)

Diego I. Gallardo <<diego.gallardo.mateluna@gmail.com>>

Rodrigo M. R. de Medeiros <<rodrigo.matheus@ufrn.br>>

References

Cox, D. R., and Snell, E. J. (1968). A general definition of residuals. *Journal of the Royal Statistical Society, Series B*, **30**, 248–265.

De Medeiros, R. M. R., Bourguignon, M., Gómez, Y. M., and Gallardo, D. I. (2026). A correlated approach to cancer cell counting in cure rate models.

Rodrigues, J., De Castro, M., Balakrishnan, N., and Cancho, V. G. (2011). Destructive weighted Poisson cure rate models. *Lifetime Data Analysis*, **17**, 333–346.

Examples

```
## Loading survival package
library(survival)

## Dataset: e1690 (see ?e1690)
head(e1690)

## Correlated destructive fit
fit <- cdnbcr(formula = Surv(time, status) ~ nodeII + nodeIII + nodeIV - 1 |
                sex + trt + thickness + age, data = e1690)

## New data for predictions
newdata <- data.frame(trt = c("Control", "Control", "Chemotherapy", "Chemotherapy"),
                      age = median(e1690$age),
                      sex = c("Male", "Female", "Male", "Female"),
                      thickness = median(e1690$thickness),
                      nodeII = c(0, 0, 0, 0),
                      nodeIII = c(0, 0, 0, 0),
                      nodeIV = c(1, 1, 1, 1))
newdata

## Fitted survival curves
pred <- predict(fit, newdata)

plot(pred[1, ], type = "l", ylim = c(0, 1), xlab = "Time", ylab = "Survival")
lines(pred[2, ], col = 2, lty = 2)
lines(pred[3, ], col = 3, lty = 3)
lines(pred[4, ], col = 4, lty = 4)
legend("topright", legend = c("trt: Control, sex: Male",
                              "trt: Control, sex: Female",
                              "trt: Chemotherapy, sex: Male",
                              "trt: Chemotherapy, sex: Female"),
       col = 1:4, lty = 1:4)

## Predicted cure rates
predict(fit, newdata, type = "cure")

## Predicted expected number of initial competing causes
predict(fit, newdata, type = "theta")

## Predicted activation probability of an initial competing cause
predict(fit, newdata, type = "p")
```

---

summary.cdnbcr *Summarizing a CDNBCR Fit*

Description

summary method for class "cdnbcr".

Usage

```
## S3 method for class 'cdnbcr'
summary(object, ...)

## S3 method for class 'summary.cdnbcr'
print(x, digits = getOption("digits"), ...)
```

Arguments

object	An object of class "cdnbcr", a result of a call to cdnbcr.
...	Further arguments passed to or from other methods.
x	An object of class "summary.cdnbcr", a result of a call to summary.cdnbcr.
digits	A non-null value for digits specifies the minimum number of significant digits to be printed in values.

Value

The function summary.cdnbcr returns an object of class "summary.cdnbcr", a list with the following components:

call The original function call.

theta Summary of the regression coefficients for the theta submodel.

p Summary of the regression coefficients for the p submodel.

par Estimates and standard errors for the additional model parameters: phi (dispersion of the initial number of competing causes), alpha (dependence parameter, when estimated), and the baseline parameters mu and sigma (reparameterized Weibull).

links Named list with the link functions used in the theta and p regression submodels.

residuals A "Surv" object with the Cox-Snell residuals (Cox and Snell, 1968). If the model is well fitted to the data, the Cox-Snell residuals are expected to be distributed as a censored random sample from the exponential distribution with mean 1.

iterations Number of EM iterations.

logLik Log-likelihood of the fitted model.

AIC, BIC Akaike and Bayesian information criteria.

Author(s)

Diego I. Gallardo <diego.gallardo.mateluna@gmail.com>

Rodrigo M. R. de Medeiros <rodrigo.matheus@ufrn.br>

References

Cox, D. R., and Snell, E. J. (1968). A general definition of residuals. *Journal of the Royal Statistical Society B*, **30**, 248–265.

De Medeiros, R. M. R., Bourguignon, M., Gómez, Y. M., and Gallardo, D. I. (2026). A correlated approach to cancer cell counting in cure rate models.

Rodrigues, J., De Castro, M., Balakrishnan, N., and Cancho, V. G. (2011). Destructive weighted Poisson cure rate models. *Lifetime Data Analysis*, **17**, 333–346

Examples

```
## Loading survival package
library(survival)

## Dataset: e1690 (see ?e1690)
head(e1690)

## Correlated destructive fit
fit <- cdnbcr(formula = Surv(time, status) ~ nodeII + nodeIII + nodeIV - 1 |
                sex + trt + thickness + age, data = e1690)
out <- summary(fit)
out

### Summary table for the regression coefficients
out$theta
out$p

### Summary table for the additional parameters
out$par

### Cox-Snell residuals
out$residuals
class(out$residuals)
plot(out$residuals)
curve(pexp(x, 1, lower.tail = FALSE), add = TRUE, col = "blue")

## Uncorrelated destructive fit
fit0 <- cdnbcr(formula = Surv(time, status) ~ nodeII + nodeIII + nodeIV - 1 |
                 sex + trt + thickness + age, data = e1690, alpha = FALSE)
summary(fit0)
```

Index