

# Package ‘Countr’

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**Type** Package

**Title** Flexible Univariate Count Models Based on Renewal Processes

**Version** 3.5.7

**Description** Flexible univariate count models based on renewal processes. The models may include covariates and can be specified with familiar formula syntax as in `glm()` and package 'flexsurv'. The methodology is described by Kharrat et al (2019) <[doi:10.18637/jss.v090.i13](https://doi.org/10.18637/jss.v090.i13)> (included as vignette 'Countr\_guide' in the package).

**License** GPL (>= 2)

**URL** <https://geobosh.github.io/Countr/> (doc),  
<https://github.com/GeoBosh/Countr> (devel)

**BugReports** <https://github.com/GeoBosh/Countr/issues>

**Depends** R (>= 3.3.0)

**Imports** Matrix, Rcpp (>= 0.11.3), flexsurv, Formula, VGAM, optimx,  
numDeriv, boot, MASS, car, utils, Rdpack (>= 0.7-0), lattice,  
RColorBrewer, dplyr, standardize, pscl, lmtest, xtable

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'convCount\_loglik.R' 'convCount\_moments.R' 'convCount\_probs.R'  
'dWeibull.R' 'dWeibullgamma.R' 'data.R' 'renewal\_IV.R'  
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'renewal\_methods.R'

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Countr-package

*Flexible Univariate Count Models Based on Renewal Processes*

---

### Description

Flexible univariate count models based on renewal processes. The models may include covariates and can be specified with familiar formula syntax as in `glm()` and `'flexsurv'`.

## Details

The methodology is described in the forthcoming paper (Kharrat et al. 2019) in the Journal of Statistical Software (included in the package as vignette `vignette('Countr_guide_paper', package = "Countr")`).

The main function is `renewalCount`, see its documentation for examples.

Goodness of fit chi-square (likelihood ratio and Pearson) tests for glm and count renewal models are implemented in `chiSq_gof` and `chiSq_pearson`.

## References

Kharrat T, Boshnakov GN, McHale I, Baker R (2019). “Flexible Regression Models for Count Data Based on Renewal Processes: The Countr Package.” *Journal of Statistical Software*, **90**(13), 1–35. doi:10.18637/jss.v090.i13.

Baker R, Kharrat T (2017). “Event count distributions from renewal processes: fast computation.” *IMA Journal of Management Mathematics*.

Boshnakov G, Kharrat T, McHale IG (2017). “A bivariate Weibull count model for forecasting association football scores.” *International Journal of Forecasting*, **33**(2), 458–466.

Cameron AC, Trivedi PK (2013). *Regression analysis of count data*, volume 53. Cambridge university press.

Kharrat T, Boshnakov GN, McHale IG, Baker R (2018). “Flexible regression models for count data based on renewal processes: the Countr package.” *Journal of Statistical Software (to appear)*.

McShane B, Adrian M, Bradlow ET, Fader PS (2008). “Count models based on Weibull interarrival times.” *Journal of Business & Economic Statistics*, **26**(3), 369–378.

Winkelmann R (1995). “Duration dependence and dispersion in count-data models.” *Journal of Business & Economic Statistics*, **13**(4), 467–474.

---

`addBootSampleObject`    *Create a bootstrap sample for coefficient estimates*

---

## Description

Create a bootstrap sample from coefficient estimates.

## Usage

```
addBootSampleObject(object, ...)
```

## Arguments

<code>object</code>	an object to add boot object to
<code>...</code>	extra parameters to be passed to the <code>boot::boot()</code> function other than data and statistic.

**Details**

The information in `object` is used to prepare the arguments and then `boot` is called to generate the bootstrap sample. The bootstrap sample is stored in `object` as component "boot". Arguments in "... " can be used to customise the `boot()` call.

**Value**

object with additional component "boot"

**See Also**

[renewal\\_methods](#)

**Examples**

```
## see renewal_methods
```

---

chiSq\_gof

*Formal Chi-square goodness-of-fit test*

---

**Description**

Carry out the formal chi-square goodness-of-fit test described by Cameron (2013).

**Usage**

```
chiSq_gof(object, breaks, ...)

## S3 method for class 'renewal'
chiSq_gof(object, breaks, ...)

## S3 method for class 'negbin'
chiSq_gof(object, breaks, ...)

## S3 method for class 'glm'
chiSq_gof(object, breaks, ...)
```

**Arguments**

<code>object</code>	an object from class <code>renewal</code>
<code>breaks</code>	integer values at which the breaks should happen. The function will compute the observed frequencies in the intervals <code>[breaks[i], breaks[i + 1])</code> .
<code>...</code>	currently not used

**Details**

The test is a conditional moment test described in details in Cameron (2013, Section 5.3.4). We compute the asymptotically equivalent outer product of the gradient version which is justified for renewal models (fully parametric + parameters based on MLE).

**Value**

data.frame

**References**

Cameron AC, Trivedi PK (2013). *Regression analysis of count data*, volume 53. Cambridge university press.

**See Also**

[chiSq\\_pearson](#)

---

chiSq_pearson	<i>Pearson Chi-Square test</i>
---------------	--------------------------------

---

**Description**

Carry out Pearson Chi-Square test and compute the Pearson statistic.

**Usage**

```
chiSq_pearson(object, ...)

## S3 method for class 'renewal'
chiSq_pearson(object, ...)

## S3 method for class 'glm'
chiSq_pearson(object, ...)
```

**Arguments**

object	an object from class renewal
...	currently not used

**Details**

The computation is inspired from Cameron(2013) Chapter 5.3.4. Observed and fitted frequencies are computed and the contribution of every observed cell to the Pearson's chi-square test statistic is reported. The idea is to check if the fitted model has a tendency to over or under predict some ranges of data

**Value**

data.frame with 5 columns given the count values (Counts), observed frequencies (Actual), model's prediction (Predicted), the difference (Diff) and the contribution to the Pearson's statistic (Pearson).

**References**

Cameron AC, Trivedi PK (2013). *Regression analysis of count data*, volume 53. Cambridge university press.

**See Also**

[chiSq\\_gof](#)

---

compareToGLM

*Compare renewals fit to glm models fit*

---

**Description**

Compare renewals fit to glm models fit on the same data.

**Usage**

```
compareToGLM(poisson_model, breaks, nbinom_model, ...)
```

**Arguments**

poisson_model	fitted Poisson glm model
breaks	integer values at which the breaks should happen. The function will compute the observed frequencies in the intervals [breaks[i],breaks[i + 1]).
nbinom_model	fitted negative binomial (fitted using MASS::glm.nb()). This argument is optional.
...	renewal models to be considered.

**Details**

This function computes a data.frame similar to Table 5.6 in Cameron(2013), using the observed frequencies and predictions from different models. Supported models accepted are Poisson and negative binomial (fitted using MASS::glm.nb()) from the glm family and any model from the renewal family (passed in ...).

**Value**

data.frame with columns Counts, Actual (observed probability) and then 2 columns per model passed (predicted probability and pearson statistic) for the associated count value.

**References**

Cameron AC, Trivedi PK (2013). *Regression analysis of count data*, volume 53. Cambridge university press.

---

CountrFormula	<i>Create a formula for renewalCount</i>
---------------	--

---

**Description**

Create a formula for renewalCount

**Usage**

```
CountrFormula(response, ...)
```

**Arguments**

response	the formula for the "main" parameter. It also specifies the response variable.
...	additional arguments for the ancilliary parameters.

**Value**

a Formula object suitable for argument formula of renewalCount().

---

count_table	<i>Summary of a count variable</i>
-------------	------------------------------------

---

**Description**

Summary of a count variable.

**Usage**

```
count_table(count, breaks, formatChar = FALSE)
```

**Arguments**

count	integer, observed count value for every individual in the sample.
breaks	integer, values at which the breaks should happen. The function will compute the observed frequency in $[breaks[i], breaks[i + 1])$ .
formatChar	logical, should the values be converted to character and formatted?

## Details

The function does a similar job to `table()` with more flexibility introduced by the argument `breaks`. The user can decide how to break the count values and decide to merge some cells if needed.

## Value

matrix with 2 rows and `length(breaks)` columns. The column names are the cells names. The rows are the observed frequencies and relative frequencies (probabilities).

---

dCount_conv_bi	<i>Compute count probabilities using convolution</i>
----------------	--

---

## Description

Compute count probabilities using one of several convolution methods. `dCount_conv_bi` does the computations for the distributions with builtin support in this package.

`dCount_conv_user` does the same using a user defined survival function.

## Usage

```
dCount_conv_bi(  
  x,  
  distPars,  
  dist = c("weibull", "gamma", "gengamma", "burr"),  
  method = c("dePril", "direct", "naive"),  
  nsteps = 100,  
  time = 1,  
  extrap = TRUE,  
  log = FALSE  
)
```

```
dCount_conv_user(  
  x,  
  distPars,  
  extrapolPars,  
  survR,  
  method = c("dePril", "direct", "naive"),  
  nsteps = 100,  
  time = 1,  
  extrap = TRUE,  
  log = FALSE  
)
```



**Arguments**

x	integer (vector), the desired count values.
distPars	Rcpp::List with distribution specific slots, see details.
dist	character name of the built-in distribution, see details.
method	character string, the method to use, see Details.
nsteps	unsigned integer, number of steps used to compute the integral.
time	double, time at which to compute the probabilities. Set to 1 by default.
extrap	logical, if TRUE, Richardson extrapolation will be applied to improve accuracy.
log	logical, if TRUE the log-probability will be returned.
extrapolPars	vector of length 2, the extrapolation values.
survR	function, user supplied survival function; should have signature <code>function(t, distPars)</code> , where <code>t</code> is a positive real number (the time where the survival function is evaluated) and <code>distPars</code> is a list of distribution parameters. It should return a double value.

**Details**

dCount\_conv\_bi computes count probabilities using one of several convolution methods for the distributions with builtin support in this package.

The following convolution methods are implemented: "dePril", "direct", and "naive".

The builtin distributions currently are Weibull, gamma, generalised gamma and Burr.

**Value**

vector of probabilities  $P(x(i), i = 1, \dots, n)$  where  $n$  is the length of  $x$ .

**Examples**

```
x <- 0:10
lambda <- 2.56
p0 <- dpois(x, lambda)
ll <- sum(dpois(x, lambda, TRUE))

err <- 1e-6
## all-probs convolution approach
distPars <- list(scale = lambda, shape = 1)
pmat_bi <- dCount_conv_bi(x, distPars, "weibull", "direct",
                          nsteps = 200)

## user pwei
pwei_user <- function(tt, distP) {
  alpha <- exp(-log(distP[["scale"]])) / distP[["shape"]]
  pweibull(q = tt, scale = alpha, shape = distP[["shape"]],
          lower.tail = FALSE)
}

pmat_user <- dCount_conv_user(x, distPars, c(1, 2), pwei_user, "direct",
```

```

                                nsteps = 200)
max((pmat_bi - p0)^2 / p0)
max((pmat_user - p0)^2 / p0)

## naive convolution approach
pmat_bi <- dCount_conv_bi(x, distPars, "weibull", "naive",
                          nsteps = 200)
pmat_user <- dCount_conv_user(x, distPars, c(1, 2), pwei_user, "naive",
                              nsteps = 200)

max((pmat_bi- p0)^2 / p0)
max((pmat_user- p0)^2 / p0)

## dePril conv approach
pmat_bi <- dCount_conv_bi(x, distPars, "weibull", "dePril",
                          nsteps = 200)
pmat_user <- dCount_conv_user(x, distPars, c(1, 2), pwei_user, "dePril",
                              nsteps = 200)

max((pmat_bi- p0)^2 / p0)
max((pmat_user- p0)^2 / p0)

```

---

dCount\_conv\_loglik\_bi *Log-likelihood of a count probability computed by convolution (bi)*

---

### Description

Compute the log-likelihood of a count model using convolution methods to compute the probabilities. `dCount_conv_loglik_bi` is for the builtin distributions. `dCount_conv_loglik_user` is for user defined survival functions.

### Usage

```

dCount_conv_loglik_bi(
  x,
  distPars,
  dist = c("weibull", "gamma", "gengamma", "burr"),
  method = c("dePril", "direct", "naive"),
  nsteps = 100,
  time = 1,
  extrap = TRUE,
  na.rm = TRUE,
  weights = NULL
)

dCount_conv_loglik_user(
  x,
  distPars,
  extrapolPars,
  survR,

```

```

method = c("dePril", "direct", "naive"),
nsteps = 100,
time = 1,
extrap = TRUE,
na.rm = TRUE,
weights = NULL
)

```

### Arguments

x	integer (vector), the desired count values.
distPars	list of the same length as x with each slot being itself a named list containing the distribution parameters corresponding to x[i].
dist	character name of the built-in distribution, see details.
method	character, convolution method to be used; choices are "dePril" (section 3.2), "direct" (section 2) or "naive" (section 3.1).
nsteps	unsigned integer number of steps used to compute the integral.
time	double time at which to compute the probabilities. Set to 1 by default.
extrap	logical if TRUE, Richardson extrapolation will be applied to improve accuracy.
na.rm	logical, if TRUE, NAs (produced by taking the log of very small probabilities) will be replaced by the smallest allowed probability; default is TRUE.
weights	numeric, vector of weights to apply. If NULL, a vector of ones.
extrapolPars	list of same length as x where each slot is a vector of length 2 (the extrapolation values to be used) corresponding to x[i].
survR	a user defined survival function; should have the signature function(t, distPars) where t is a real number (>0) where the survival function is evaluated and distPars is a list of distribution parameters. It should return a double value.

### Value

numeric, the log-likelihood of the count process

### Examples

```

x <- 0:10
lambda <- 2.56
distPars <- list(scale = lambda, shape = 1)
distParsList <- lapply(seq(along = x), function(ind) distPars)
extrapolParsList <- lapply(seq(along = x), function(ind) c(2, 1))
## user pwei
pwei_user <- function(tt, distP) {
  alpha <- exp(-log(distP[["scale"]])) / distP[["shape"]]
  pweibull(q = tt, scale = alpha, shape = distP[["shape"]],
    lower.tail = FALSE)
}
## log-likelihood allProbs Poisson

```

```

dCount_conv_loglik_bi(x, distParsList,
                      "weibull", "direct", nsteps = 400)

dCount_conv_loglik_user(x, distParsList, extrapolParsList,
                        pwei_user, "direct", nsteps = 400)

## log-likelihood naive Poisson
dCount_conv_loglik_bi(x, distParsList,
                      "weibull", "naive", nsteps = 400)

dCount_conv_loglik_user(x, distParsList, extrapolParsList,
                        pwei_user, "naive", nsteps = 400)

## log-likelihood dePril Poisson
dCount_conv_loglik_bi(x, distParsList,
                      "weibull", "dePril", nsteps = 400)

dCount_conv_loglik_user(x, distParsList, extrapolParsList,
                        pwei_user, "dePril", nsteps = 400)
## see dCount_conv_loglik_bi()

```

---

dmodifiedCount_bi	<i>Compute count probabilities based on modified renewal process (bi)</i>
-------------------	---

---

### Description

Compute count probabilities based on modified renewal process using dePril algorithm. dmodifiedCount\_bi does it for the builtin distributions.

dmodifiedCount\_user does the same for a user specified distribution.

### Usage

```

dmodifiedCount_bi(
  x,
  distPars,
  dist,
  distPars0,
  dist0,
  nsteps = 100L,
  time = 1,
  extrap = TRUE,
  cdfout = FALSE,
  logFlag = FALSE
)

dmodifiedCount_user(
  x,
  distPars,

```

```

    survR,
    distPars0,
    survR0,
    extrapolPars,
    nsteps = 100L,
    time = 1,
    extrap = TRUE,
    cdfout = FALSE,
    logFlag = FALSE
)

```

### Arguments

<code>x</code>	integer (vector), the desired count values.
<code>distPars0, distPars</code>	Rcpp: :List with distribution specific slots for the first arrival and the rest of the process respectively.
<code>dist0, dist</code>	character, name of the first and following survival distributions.
<code>nsteps</code>	unsigned integer number of steps used to compute the integral.
<code>time</code>	double time at which to compute the probabilities. Set to 1 by default.
<code>extrap</code>	logical if TRUE, Richardson extrapolation will be applied to improve accuracy.
<code>cdfout</code>	TODO
<code>logFlag</code>	logical if TRUE the log-probability will be returned.
<code>survR0, survR</code>	user supplied survival function; should have signature <code>function(t, distPars)</code> , where <code>t</code> is a positive real number (the time at which the survival function is evaluated) and <code>distPars</code> is a list of distribution parameters. It should return a double value (first arrival and following arrivals respectively).
<code>extrapolPars</code>	list of same length as <code>x</code> , where each slot is a vector of length 2 (the extrapolation values to be used) corresponding to <code>x[i]</code> .

### Details

For the modified renewal process the first arrival is allowed to have a different distribution from the time between subsequent arrivals. The renewal assumption is kept.

### Value

vector of probabilities  $P(x(i))$  for  $i = 1, \dots, n$  where  $n$  is the length of `x`.

---

`dWeibullCount`*Probability calculations for Weibull count models*

---

**Description**

Probability computations for the univariate Weibull count process. Several methods are provided. `dWeibullCount` computes probabilities.

`dWeibullCount_loglik` computes the log-likelihood.

`evWeibullCount` computes the expected value and variance.

**Usage**

```
dWeibullCount(  
  x,  
  shape,  
  scale,  
  method = c("series_acc", "series_mat", "conv_direct", "conv_naive", "conv_dePril"),  
  time = 1,  
  log = FALSE,  
  conv_steps = 100,  
  conv_extrap = TRUE,  
  series_terms = 50,  
  series_acc_niter = 300,  
  series_acc_eps = 1e-10  
)
```

```
dWeibullCount_loglik(  
  x,  
  shape,  
  scale,  
  method = c("series_acc", "series_mat", "conv_direct", "conv_naive", "conv_dePril"),  
  time = 1,  
  na.rm = TRUE,  
  conv_steps = 100,  
  conv_extrap = TRUE,  
  series_terms = 50,  
  series_acc_niter = 300,  
  series_acc_eps = 1e-10,  
  weights = NULL  
)
```

```
evWeibullCount(  
  xmax,  
  shape,  
  scale,  
  method = c("series_acc", "series_mat", "conv_direct", "conv_naive", "conv_dePril"),
```

```

    time = 1,
    conv_steps = 100,
    conv_extrap = TRUE,
    series_terms = 50,
    series_acc_niter = 300,
    series_acc_eps = 1e-10
  )

```

### Arguments

x	integer (vector), the desired count values.
shape	numeric (length 1), shape parameter of the Weibull count.
scale	numeric (length 1), scale parameter of the Weibull count.
method	character, one of the available methods, see details.
time	double, length of the observation window (defaults to 1).
log	logical, if TRUE, the log of the probability will be returned.
conv_steps	numeric, number of steps used for the extrapolation.
conv_extrap	logical, should Richardson extrappolation be applied ?
series_terms	numeric, number of terms in the series expansion.
series_acc_niter	numeric, number of iterations in the Euler-van Wijngaarden algorithm.
series_acc_eps	numeric, tolerance of convergence in the Euler-van Wijngaarden algorithm.
na.rm	logical, if TRUE NA's (produced by taking the log of very small probabilities) will be replaced by the smallest allowed probaility; default is TRUE.
weights	numeric, vector of weights to apply. If NULL, a vector of one's will be applied.
xmax	unsigned integer, maximum count to be used.

### Details

Argument method can be used to specify the desired method, as follows:

```

"series_mat" - series expansion using matrix techniques,
"series_acc" - Euler-van Wijngaarden accelerated series expansion (default),
"conv_direct" - direct convolution method of section 2,
"conv_naive" - naive convolurion described in section 3.1,
"conv_dePril" - dePril convolution described in section 3.2.

```

The arguments have sensible default values.

### Value

for dWeibullCount, a vector of probabilities  $P(x(i)), i = 1, \dots, n$ , where  $n = \text{length}(x)$ .

for dWeibullCount\_loglik, a double, the log-likelihood of the count process.

for evWeibullCount, a list with components:

ExpectedValue	expected value,
Variance	variance.

---

dWeibullgammaCount\_mat\_Covariates

*Univariate Weibull Count Probability with gamma and covariate heterogeneity*

---

### Description

Univariate Weibull Count Probability with gamma and covariate heterogeneity

### Usage

```
dWeibullgammaCount_mat_Covariates(
  x,
  cc,
  r,
  alpha,
  Xcovar,
  beta,
  t = 1,
  logFlag = FALSE,
  jmax = 100L
)
```

### Arguments

x, cc, t, logFlag, jmax	TODO keywords internal
r	numeric shape of the gamma distribution
alpha	numeric rate of the gamma distribution
Xcovar	matrix covariates value
beta	numeric vector of slopes

---

evCount\_conv\_bi

*Expected value and variance of renewal count process*

---

### Description

Compute numerically expected values and variances of renewal count processes.



**Usage**

```

evCount_conv_bi(
  xmax,
  distPars,
  dist = c("weibull", "gamma", "gengamma", "burr"),
  method = c("dePril", "direct", "naive"),
  nsteps = 100,
  time = 1,
  extrap = TRUE
)

evCount_conv_user(
  xmax,
  distPars,
  extrapolPars,
  survR,
  method = c("dePril", "direct", "naive"),
  nsteps = 100,
  time = 1,
  extrap = TRUE
)

```

**Arguments**

xmax	unsigned integer maximum count to be used.
distPars	TODO
dist	TODO
method	TODO
nsteps	unsigned integer, number of steps used to compute the integral.
time	double, time at which to compute the probabilities. Set to 1 by default.
extrap	logical, if TRUE, Richardson extrapolation will be applied to improve accuracy.
extrapolPars	ma::vec of length 2. The extrapolation values.
survR	function, user supplied survival function; should have signature function(t, distPars), where t is a positive real number (the time where the survival function is evaluated) and distPars is a list of distribution parameters. It should return a double value.

**Details**

evCount\_conv\_bi computes the expected value and variance of renewal count processes for the builtin distributions of inter-arrival times.

evCount\_conv\_user computes the expected value and variance for a user specified distribution of the inter-arrival times.

**Value**

a named list with components "ExpectedValue" and "Variance".

**Examples**

```

pwei_user <- function(tt, distP) {
  alpha <- exp(-log(distP[["scale"]]) / distP[["shape"]])
  pweibull(q = tt, scale = alpha, shape = distP[["shape"]],
    lower.tail = FALSE)
}

## ev convolution Poisson count
lambda <- 2.56
beta <- 1
distPars <- list(scale = lambda, shape = beta)

evbi <- evCount_conv_bi(20, distPars, dist = "weibull")
evu <- evCount_conv_user(20, distPars, c(2, 2), pwei_user, "dePril")

c(evbi[["ExpectedValue"]], lambda)
c(evu[["ExpectedValue"]], lambda )
c(evbi[["Variance"]], lambda    )
c(evu[["Variance"]], lambda    )

## ev convolution weibull count
lambda <- 2.56
beta <- 1.35
distPars <- list(scale = lambda, shape = beta)

evbi <- evCount_conv_bi(20, distPars, dist = "weibull")
evu <- evCount_conv_user(20, distPars, c(2.35, 2), pwei_user, "dePril")

x <- 1:20
px <- dCount_conv_bi(x, distPars, "weibull", "dePril",
  nsteps = 100)
ev <- sum(x * px)
var <- sum(x^2 * px) - ev^2

c(evbi[["ExpectedValue"]], ev)
c(evu[["ExpectedValue"]], ev )
c(evbi[["Variance"]], var    )
c(evu[["Variance"]], var    )

```

---

fertility

*Fertility data*


---

**Description**

Fertility data analysed by Winkelmann(1995). The data comes from the second (1985) wave of German Socio-Economic Panel. The sample is formed by 1,243 women aged 44 or older in 1985. The response variable is the number of children per woman and explanatory variables are described in more details below.

**Usage**

fertility

**Format**

A data frame with 9 variables (5 factors, 4 integers) and 1243 observations:

children integer; response variable: number of children per woman (integer).

german factor; is the mother German? (yes or no).

years\_school integer; education measured as years of schooling.

voc\_train factor; vocational training ? (yes or no)

university factor; university education ? (yes or no)

religion factor; mother's religion: Catholic, Protestant, Muslim or Others (reference).

rural factor; rural (yes or no ?)

year\_birth integer; year of birth (last 2 digits)

age\_marriage integer; age at marriage

For further details, see Winlemann(1995).

**References**

Winkelmann R (1995). "Duration dependence and dispersion in count-data models." *Journal of Business & Economic Statistics*, **13**(4), 467–474.

---

football

*Football data*

---

**Description**

Final scores of all matches in the English Premier League from seasons 2009/2010 to 2016/2017.

**Usage**

football

**Format**

a data.frame with 6 columns and 1104 observations:

seasonId integer season identifier (year of the first month of competition).

gameDate POSIXct game date and time.

homeTeam, awayTeam character home and away team name.

homeTeamGoals, awayTeamGoals integer number of goals scored by the home and the away team.

**Details**

The data were collected from <https://www.football-data.co.uk/> and slightly formatted and simplified.

---

frequency_plot	<i>Plot a frequency chart</i>
----------------	-------------------------------

---

**Description**

Plot a frequency chart to compare actual and predicted values.

**Usage**

```
frequency_plot(count_labels, actual, pred, colours)
```

**Arguments**

count_labels	character, labels to be used.
actual	numeric, the observed probabilities for the different count specified in count_labels.
pred	data.frame of predicted values. Should have the same number of rows as actual and one column per model. The columns' names will be used as labels for the different models.
colours	character vector of colour codes with length ncol(pred) + 2.

**Details**

In order to compare actual and fitted values, a barchart plot is created. It is the user's responsibility to provide the count, observed and fitted values.

---

getParNames	<i>Return the names of distribution parameters</i>
-------------	--

---

**Description**

Return the names of the parameters of a count distribution.

**Usage**

```
getParNames(dist, ...)
```

**Arguments**

dist	character, name of the distribution.
...	parameters to pass when dist == "custom".

**Value**

character vector with the names of the distribution parameters.

---

predict.renewal      *Predict method for renewal objects*

---

### Description

Compute predictions from renewal objects.

### Usage

```
## S3 method for class 'renewal'
predict(
  object,
  newdata = NULL,
  type = c("response", "prob"),
  se.fit = FALSE,
  terms = NULL,
  na.action = na.pass,
  time = 1,
  ...
)
```

### Arguments

object	Object of class inheriting from "lm"
newdata	An optional data frame in which to look for variables with which to predict. If omitted, the fitted values are used.
type	type of prediction. If equal to "response", give the mean probability associated with the individual covariates. If "prob", give the probability of the observed count.
se.fit	A switch indicating if standard errors are required.
terms	If type = "terms", which terms (default is all terms), a <a href="#">character</a> vector.
na.action	function determining what should be done with missing values in newdata. The default is to predict NA.
time	TODO
...	further arguments passed to or from other methods.

### Examples

```
fn <- system.file("extdata", "McShane_Wei_results_boot.RDS", package = "Countr")
object <- readRDS(fn)
data <- object$data
## old data
predOld.response <- predict(object, type = "response", se.fit = TRUE)
predOld.prob <- predict(object, type = "prob", se.fit = TRUE)

## newData (extracted from old Data)
```

```

newData <- head(data)
predNew.response <- predict(object, newdata = newData,
                             type = "response", se.fit = TRUE)
predNew.prob <- predict(object, newdata = newData,
                        type = "prob", se.fit = TRUE)

cbind(head(predOld.response$values),
       head(predOld.response$se$scale),
       head(predOld.response$se$shape),
       predNew.response$values,
       predNew.response$se$scale,
       predNew.response$se$shape)

cbind(head(predOld.prob$values),
       head(predOld.prob$se$scale),
       head(predOld.prob$se$shape),
       predNew.prob$values,
       predNew.prob$se$scale,
       predNew.prob$se$shape)

```

---

renewalCoef

*Get named vector of coefficients for renewal objects*


---

### Description

Get named vector of coefficients for renewal objects.

### Usage

```
renewalCoef(object, ...)
```

### Arguments

object	an object, there are methods for several classes, see Details.
...	further arguments to be passed to <code>renewalNames</code> , usually something like <code>target = "weibull"</code> .

### Details

This is a convenience function for constructing named vector of coefficients for renewal count models. Such vectors are needed, for example, for starting values in the model fitting procedures. The simplest way to get a suitably named vector is to take the coefficients of a fitted model but if the fitting procedure requires initial values, this is seemingly a circular situation.

The overall idea is to take coefficients specified by `object` and transform them to coefficients suitable for a renewal count model as specified by the arguments "...". The provided methods eliminate the need for tedious manual preparation of such vectors and in the most common cases allow the user to do this in a single line.

The default method extracts the coefficients of `object` using

`co <- coef(object)` (an error is raised if this fails). It prepares a named numeric vector with names requested by the arguments in `"..."` and assigns `co` to the first `length(co)` elements of the prepared vector. The net effect is that the coefficients of a model can be initialised from the coefficients of a nested model. For example a Poisson regression model can be used to initialise a Weibull count model. Of course the non-zero shape parameter(s) of the Weibull model need to be set separately.

If `object` is from class `glm`, the method is identical to the default method.

If `object` is from class `renewalCoefList`, its elements are simply concatenated in one long vector.

## References

Kharrat T, Boshnakov GN, McHale I, Baker R (2019). "Flexible Regression Models for Count Data Based on Renewal Processes: The Countr Package." *Journal of Statistical Software*, **90**(13), 1–35. [doi:10.18637/jss.v090.i13](https://doi.org/10.18637/jss.v090.i13).

## See Also

`renewalNames`

---

<code>renewalCoefList</code>	<i>Split a vector using the prefixes of the names for grouping</i>
------------------------------	--

---

## Description

Split a vector using the prefixes of the names for grouping.

## Usage

```
renewalCoefList(coef)
```

## Arguments

`coef`                    a named vector

## Details

The names of the coefficients of renewal regression models are prefixed with the names of the parameters to which they refer. This function splits such vectors into a list with one component for each parameter. For example, for a Weibull renewal regression model this will create a list with components `"scale"` and `"shape"`.

This is a convenience function allowing users to manipulate the coefficients related to a parameter more easily. `renewalCoef` can convert this list back to a vector.

---

renewalCount

*Fit renewal count processes regression models*


---

### Description

Fit renewal regression models for count data via maximum likelihood.

### Usage

```
renewalCount(
  formula,
  data,
  subset,
  na.action,
  weights,
  offset,
  dist = c("weibull", "weibullgam", "custom", "gamma", "gengamma"),
  anc = NULL,
  convPars = NULL,
  link = NULL,
  time = 1,
  control = renewal.control(...),
  customPars = NULL,
  seriesPars = NULL,
  weiMethod = NULL,
  computeHessian = TRUE,
  standardise = FALSE,
  standardise_scale = 1,
  model = TRUE,
  y = TRUE,
  x = FALSE,
  ...
)
```

### Arguments

formula	a formula object. If it is a standard formula object, the left hand side specifies the response variable and the right hand sides specifies the regression equation for the first parameter of the conditional distribution. formula can also be used to specify the ancilliary regressions, using the operator 'l', see Details.
data, subset, na.action,	arguments controlling formula processing via model.frame.
weights	optional numeric vector of weights.
offset	optional numeric vector with an a priori known component to be included in the linear predictor of the count model. Currently not used.



<code>dist</code>	character, built-in distribution to be used as the inter-arrival time distribution or "custom" for a user defined distribution, see Details. Currently the built-in distributions are "weibull", "weibullgam", "gamma", "gengamma" (generalized-gamma) and "burr".
<code>anc</code>	a named list of formulas for ancillary regressions, if any, otherwise NULL. The formulas associated with the (exact) parameter names are used. The left-hand sides of the formulas in <code>anc</code> are ignored.
<code>convPars</code>	a list of convolution parameters arguments with slots <code>nsteps</code> , <code>extrap</code> and <code>convMethod</code> , see <code>dCount_conv_bi</code> . If NULL, default parameters will be applied.
<code>link</code>	named list of character strings specifying the name of the link functions to be used in the regression. If NULL, the canonical link function will be used, i.e, log if the parameter is supposed to be positive, identity otherwise.
<code>time</code>	numeric, time at which the count is observed; default to unity (1).
<code>control</code>	a list of control arguments specified via <code>renewal.control</code> .
<code>customPars</code>	list, user inputs if <code>dist = "custom"</code> , see details.
<code>seriesPars</code>	list, series expansion input parameters with slots <code>terms</code> (number of terms in the series expansion), <code>iter</code> (number of iteration in the accelerated series expansion algorithm) and <code>eps</code> (tolerance in the accelerated series expansion algorithm), Only used if <code>dist = "weibull"</code> and <code>weiMethod = c("series_mat", "series_acc")</code> .
<code>weiMethod</code>	character, computation method to be used if <code>dist = "weibull"</code> or <code>"weibullgam"</code> , see <code>dWeibullCount</code> and <code>dWeibullgammaCount</code> .
<code>computeHessian</code>	logical, should the hessian (and hence the covariance matrix) be computed numerically at the fitted values.
<code>standardise</code>	logical should the covariates be standardised using <code>standardize::standardize()</code> function.
<code>standardise_scale</code>	numeric the desired scale for the covariates; default to 1
<code>model, y, x</code>	logicals. If TRUE the corresponding components of the fit (model frame, response, model matrix) are returned.
<code>...</code>	arguments passed to <code>renewal.control</code> in the default setup.

## Details

`renewal` re-uses design and functionality of the basic R tools for fitting regression model (`lm`, `glm`) and is highly inspired by `hurdle()` and `zeroinfl()` from package `pscl`. Package `Formula` is used to handle formulas.

Argument `formula` is a formula object. In the simplest case its left-hand side (lhs) designates the response variable and the right-hand side the covariates for the first parameter of the distribution (as reported by `getParNames`). In this case, covariates for the ancillary parameters are specified using argument `anc`.

The ancillary regressions, can also be specified in argument `formula` by adding them to the right-hand side, separated by the operator `'|'`. For example `Y | shape ~ x + y | z` can be used in place of the pair `Y ~ x + y` and `anc = list(shape = ~z)`. In most cases, the name of the second parameter

can be omitted, which for this example gives the equivalent  $Y \sim x + y \mid z$ . The actual rule is that if the parameter is missing from the left-hand side, it is inferred from the default parameter list of the distribution.

As another convenience, if the parameters are to have the same covariates, it is not necessary to repeat the rhs. For example,  $Y \mid \text{shape} \sim x + y$  is equivalent to  $Y \mid \text{shape} \sim x + y \mid x + y$ . Note that this is applied only to parameters listed on the lhs, so  $Y \sim x + y$  specifies covariates only for the response variable and not any other parameters.

Distributions for inter-arrival times supported internally by this package can be chosen by setting argument "dist" to a suitable character string. Currently the built-in distributions are "weibull", "weibullgam", "gamma", "gengamma" (generalized-gamma) and "burr".

Users can also provide their own inter-arrival distribution. This is done by setting argument "dist" to "custom", specifying the initial values and giving argument customPars as a list with the following components:

**parNames** character, the names of the parameters of the distribution. The location parameter should be the first one.

**survivalFct** function object containing the survival function. It should have signature `function(t, distPars)` where `t` is the point where the survival function is evaluated and `distPars` is the list of the distribution parameters. It should return a double value.

**extrapolFct** function object computing the extrapolation values (numeric of length 2) from the value of the distribution parameters (in `distPars`). It should have signature `function(distPars)` and return a numeric vector of length 2. Only required if the extrapolation is set to TRUE in `convPars`.

Some checks are done to validate `customPars` but it is user's responsibility to make sure the functions have the appropriate signatures.

**Note:** The Weibull-gamma distribution is an experimental version and should be used with care! It is very sensitive to initial values and there is no guarantee of convergence. It has also been reparameterized in terms of  $(1/r, 1/\alpha, c)$  instead of  $(r, \alpha, c)$ , where  $r$  and  $\alpha$  are the shape and scale of the gamma distribution and  $c$  is the shape of the Weibull distribution.

**(2017-08-04(Georgi) experimental feature:** probability residuals in component 'probResiduals'. I also added type 'prob' to the method for residuals() to extract them.

`probResiduals[i]` is currently  $1 - \text{Prob}(Y[i] \text{ given the covariates})$ . "one minus", so that values close to zero are "good". On its own this is probably not very useful but when comparing two models, if one of them has mostly smaller values than the other, there is some reason to claim that the former is superior. For example (see below), `gamModel < poisModel` in 3:1

## Value

An S3 object of class "renewal", which is a list with components including:

**coefficients** values of the fitted coefficients.

**residuals** vector of weighted residuals  $\omega * (\text{observed} - \text{fitted})$ .

**fitted.values** vector of fitted means.

**optim** data.frame output of `optimx`.

**method** optimisation algorithm.



---

renewalNames	<i>Get names of parameters of renewal regression models</i>
--------------	---

---

**Description**

Get names of parameters of renewal regression models

**Usage**

```
renewalNames(object, ...)
```

**Arguments**

object	an object.
...	further arguments.

**Details**

renewalNames gives the a character vector of names of parameters for renewal regression models. There are two main use scenarios: `renewalNames(object, target = "dist")` and `renewalNames(object, ...)`. In the first scenario `target` can be a count distribution, such as "weibull" or a parameter name, such as `shape`. In this case `renewalNames` transforms coefficient names of `object` to those specified by `target`. In the second scenario the argument list is the same that would be used to call `renewalCount`. In this case `renewalNames` returns the names that would be used by `renewalCount` for the coefficients of the fitted model.

---

renewal_methods	<i>Methods for renewal objects</i>
-----------------	------------------------------------

---

**Description**

Methods for renewal objects.

**Usage**

```
## S3 method for class 'renewal'
coef(object, ...)

## S3 method for class 'renewal'
vcov(object, ...)

## S3 method for class 'renewal'
residuals(object, type = c("pearson", "response", "prob"), ...)

## S3 method for class 'renewal'
```

```
residuals_plot(object, type = c("pearson", "response", "prob"), ...)  
  
## S3 method for class 'renewal'  
fitted(object, ...)  
  
## S3 method for class 'renewal'  
confint(  
  object,  
  parm,  
  level = 0.95,  
  type = c("asymptotic", "boot"),  
  bootType = c("norm", "bca", "basic", "perc"),  
  ...  
)  
  
## S3 method for class 'renewal'  
summary(object, ...)  
  
## S3 method for class 'renewal'  
print(x, digits = max(3, getOption("digits") - 3), ...)  
  
## S3 method for class 'summary.renewal'  
print(  
  x,  
  digits = max(3, getOption("digits") - 3),  
  width = getOption("width"),  
  ...  
)  
  
## S3 method for class 'renewal'  
model.matrix(object, ...)  
  
## S3 method for class 'renewal'  
logLik(object, ...)  
  
## S3 method for class 'renewal'  
nobs(object, ...)  
  
## S3 method for class 'renewal'  
extractAIC(fit, scale, k = 2, ...)  
  
## S3 method for class 'renewal'  
addBootSampleObject(object, ...)  
  
## S3 method for class 'renewal'  
df.residual(object, ...)
```

**Arguments**

object            an object from class "renewal".  
 ...                further arguments for methods  
 type, parm, level, bootType, x, digits  
                   see the corresponding generics and section Details.  
 width             numeric width length  
 fit, scale, k     same as in the generic.

**Details**

Objects from class "renewal" represent fitted count renewal models and are created by calls to "renewalCount()". There are methods for this class for many of the familiar functions for interacting with fitted models.

**Examples**

```

fn <- system.file("extdata", "McShane_Wei_results_boot.RDS", package = "Countr")
object <- readRDS(fn)
class(object) # "renewal"

coef(object)
vcov(object)

## Pearson residuals: rescaled by sd
head(residuals(object, "pearson"))
## response residuals: not rescaled
head(residuals(object, "response"))

head(fitted(object))

## loglik, nobs, AIC, BIC
c(loglik = as.numeric(logLik(object)), nobs = nobs(object),
  AIC = AIC(object), BIC = BIC(object))

asym <- se.coef(object, , "asymptotic")
boot <- se.coef(object, , "boot")
cbind(asym, boot)
## CI for coefficients
asym <- confint(object, type = "asymptotic")
## Commenting out for now, see the nite in the code of confint.renewal():
## boot <- confint(object, type = "boot", bootType = "norm")
## list(asym = asym, boot = boot)
summary(object)
print(object)
## see renewal_methods
## see renewal_methods

```

---

residuals_plot	<i>Method to visualise the residuals</i>
----------------	--

---

**Description**

A method to visualise the residuals

**Usage**

```
residuals_plot(object, type, ...)
```

**Arguments**

object	object returned by one of the count-modeling functions
type	character type of residuals to be used.
...	further arguments for methods.

---

se.coef	<i>Extract Standard Errors of Model Coefficients</i>
---------	--

---

**Description**

Extract standard errors of model coefficients from objects returned by count-modeling functions.

**Usage**

```
se.coef(object, parm, type, ...)

## S3 method for class 'renewal'
se.coef(object, parm, type = c("asymptotic", "boot"), ...)
```

**Arguments**

object	object returned by one of the count-modeling functions
parm	parameter's name or index
type	type of standard error: asymptotic normal standard errors ("asymptotic") or bootstrap ("boot").
...	further arguments for methods.

**Details**

The method for class "renewal" extracts standard errors of model coefficients from objects returned by renewal. When bootstrap standard error are requested, the function checks for the bootstrap sample in object. If it is not found, the bootstrap sample is created and a warning is issued. Users can choose between asymptotic normal standard errors (asymptotic) or bootstrap (boot).

**Value**

a named numeric vector

**Examples**

```
## see examples for renewal_methods
```

---

surv

*Wrapper to built in survival functions*

---

**Description**

Wrapper to built in survival functions

**Usage**

```
surv(t, distPars, dist)
```

**Arguments**

<code>t</code>	double, time point where the survival is to be evaluated at.
<code>distPars</code>	Rcpp::List with distribution specific slots, see details.
<code>dist</code>	character name of the built-in distribution, see details.

**Details**

The function wraps all builtin-survival distributions. User can choose between the `weibull`, `gamma`, `gengamma` (generalized gamma) and `burr` (Burr type XII distribution). It is the user responsibility to pass the appropriate list of parameters as follows:

**weibull** scale (the scale) and shape (the shape) parameters.

**burr** scale (the scale) and shape1 (the shape1) and shape2 (the shape2) parameters.

**gamma** scale (the scale) and shape (the shape) parameter.

**gengamma** mu (location), sigma (scale) and Q (shape) parameters.

**Value**

a double giving the value of the survival function at time point `t` at the parameters' values.



**Examples**

```
tt <- 2.5
## weibull

distP <- list(scale = 1.2, shape = 1.16)
alpha <- exp(-log(distP[["scale"]]) / distP[["shape"]])
pweibull(q = tt, scale = alpha, shape = distP[["shape"]],
        lower.tail = FALSE)
surv(tt, distP, "weibull") ## (almost) same

## gamma
distP <- list(shape = 0.5, rate = 1.0 / 0.7)
pgamma(q = tt, rate = distP[["rate"]], shape = distP[["shape"]],
       lower.tail = FALSE)
surv(tt, distP, "gamma") ## (almost) same

## generalized gamma
distP <- list(mu = 0.5, sigma = 0.7, Q = 0.7)
flexsurv::pgengamma(q = tt, mu = distP[["mu"]],
                   sigma = distP[["sigma"]],
                   Q = distP[["Q"]],
                   lower.tail = FALSE)
surv(tt, distP, "gengamma") ## (almost) same
```

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