

# Package ‘Rcapture’

April 28, 2009

**Type** Package

**Title** Loglinear Models for Capture-Recapture Experiments

**Version** 1.2-0

**Date** 2009-04-28

**Author** Sophie Baillargeon <Sophie.Baillargeon@mat.ulaval.ca> and Louis-Paul Rivest  
<Louis-Paul.Rivest@mat.ulaval.ca>

**Maintainer** Sophie Baillargeon <Sophie.Baillargeon@mat.ulaval.ca>

**Description** Estimation of abundance and other demographic parameters for closed populations, open populations and the robust design in capture-recapture experiments using loglinear models.

**Imports** stats, graphics

**License** GPL-2

**Repository** CRAN

**Date/Publication** 2009-04-28 18:31:20

## R topics documented:

Rcapture-package . . . . .	2
BBS2001 . . . . .	4
bunting . . . . .	5
catb . . . . .	7
closedp . . . . .	8
closedp.bc . . . . .	11
closedp.custom . . . . .	14
closedp.Mtb . . . . .	16
closedpCI . . . . .	17
descriptive . . . . .	20
duck . . . . .	23
hare . . . . .	24
histpos . . . . .	25

HIV	27
mvole	28
openp	30
periodhist	32
profileCI	34
rbvole	36
robustd	37
uifit	40

<b>Index</b>	<b>42</b>
--------------	-----------

---

Rcapture-package      *Loglinear Models for Capture-Recapture Experiments*

---

## Description

Estimation of abundance and other demographic parameters for closed populations, open populations and the robust design in capture-recapture experiments using loglinear models.

## Details

Package: Rcapture  
 Type: Package  
 Version: 1.2-0  
 Date: 2009-04-27  
 License: GPL

### DESCRIPTION OF THE ACCEPTED DATA SET FORMATS

A capture-recapture data set is given to the various **Rcapture** functions through the `X` argument. `X` must be a numeric matrix. The arguments `dfreq` and `dtype` indicate the format of the matrix. Each have two possible values, meaning that a total of four data set formats are possible with **Rcapture**.

1- If `dfreq=FALSE` and `dtype="hist"`, the default, `X` has one row per unit captured in the experiment. Each row is an observed capture history. It must contain only zeros and ones; the number one indicates a capture. In this case, the number of columns in the table represents the number of capture occasions in the experiment (noted  $t$ ). Here is a fictive example of a data set of this type for  $t = 2$ :

```
1 1
1 1
1 0
1 0
1 0
1 0
0 1
```

2- If `dfreq=TRUE` and `dtype="hist"`, `X` contains one row per capture history followed by

its frequency. In that case,  $X$  has  $t+1$  columns. As for the format presented previously, the first  $t$  columns of  $X$ , identifying the capture histories, must contain only zeros and ones. The number one indicates a capture. In this format, the example data set is represented by the following matrix:

```
1 1 2
1 0 4
0 1 1
```

3- If `dfreq=FALSE` and `dtype="nbcap"`,  $X$  is simply a vector of numbers of captures. The length of the vector is  $n$ , the number of captured units. In this format, the example data set looks like:

```
2 2 1 1 1 1 1
```

4- If `dfreq=TRUE` and `dtype="nbcap"`,  $X$  is a 2 columns matrix. The first column contains the numbers of captures, the second column contains the observed frequencies. In this format, the example data is:

```
2 2
1 5
```

Only few functions have the `dtype` argument. Functions without `dtype` argument accept only a data matrix  $X$  of the form `dtype="hist"`. So the first two formats listed above are the most common.

Formats with `dtype="nbcap"` are useful for experiments with a large number of capture occasions  $t$ . Often, no units will be caught a large number of times, and the data set will contain no observations for  $t$  captures. Therefore, the number of capture occasions  $t$  cannot be deduced from  $X$  as it can be when `dtype="hist"`. So if one gives a data matrix  $X$  with `dtype="nbcap"`, one must also provide  $t$ , the number of capture occasions, as an additional argument.

For now, the data formats with `dtype="nbcap"` are not generalized to the robust design. So `dtype` is not an argument of the `robustd.0` function.

### Author(s)

Sophie Baillargeon (Sophie.Baillargeon@mat.ulaval.ca) and  
Louis-Paul Rivest (Louis-Paul.Rivest@mat.ulaval.ca)

### References

- Baillargeon, S. and Rivest, L.P. (2007) Rcapture: Loglinear models for capture-recapture in *R. Journal of Statistical Software*, **19**(5), <http://www.jstatsoft.org/v19/i05>.
- Chao, A. (1987) Estimating the population size for capture-recapture data with unequal catchability. *Biometrics*, **43**(4), 783–791.
- Cormack, R. M. (1985) Example of the use of glim to analyze capture-recapture studies. In *Lecture Notes in Statistics 29: Statistics in Ornithology*, Morgan, B. et North, P. editors, New York,: Springer-Verlag, 242–274.
- Cormack, R. M. (1989) Log-linear models for capture-recapture. *Biometrics*, **45**, 395–413.
- Cormack, R. M. (1992) Interval estimation for mark-recapture studies of closed populations. *Biometrics*, **48**, 567–576.

- Cormack, R. M. (1993) Variances of mark-recapture estimates. *Biometrics*, **49**, 1188–1193.
- Cormack, R. M. and Jupp, P. E. (1991) Inference for Poisson and multinomial models for capture-recapture experiments. *Biometrika*, **78**(4), 911–916.
- Rivest, L.P. and Levesque, T. (2001) Improved log-linear model estimators of abundance in capture-recapture experiments. *Canadian Journal of Statistics*, **29**, 555–572.
- Rivest, L.P. and Daigle, G. (2004) Loglinear models for the robust design in mark-recapture experiments. *Biometrics*, **60**, 100–107.
- Rivest, L.P. and Baillargeon, S. (2007) Applications and extensions of Chao’s moment estimator for the size of a closed population. *Biometrics*, **63**(4), 999–1006.
- Rivest, L.P. (2008) Why a time effect often has a limited impact on capture-recapture estimates in closed populations. *Canadian Journal of Statistics*, **36**(1), 75–84.

---

 BBS2001

*Species Richness Data from the North American Breeding Bird Survey (BBS) in 2001*


---

### Description

This data set contains species richness data from the North American Breeding Bird Survey (BBS) in 2001. The number of capture occasions  $t$  is 50.

### Usage

```
data(BBS2001)
```

### Format

36 by 2 numeric matrix, with the following columns:

**nbcap** Numbers of captures

**freq** Observed frequencies for each number of captures

### Details

This data set is presented in Dorazio and Royle (2003). It comes from the North American Breeding Bird Survey (BBS). This survey includes more than 4000 39.4 km survey routes throughout North America. Along each survey route an observer stops at 50 equidistant locations and records the species identity and number of all birds heard or seen within a 3-minute period.

The data in BBS2001 was collected along Route 123, in Maryland, in 2001. In this data set a capture occasion is in fact a location and the frequencies represent the number of species detected at  $i$  locations out of the 50 locations on that route. The frequencies for  $i = 37, \dots, 50$  are null and do not appear in the data set.

### Source

Dorazio, R. M. and Royle, A. J. (2003) Mixture models for estimating the size of a closed population when capture rates vary among individuals. *Biometrics*, **59**, 351–364

**Examples**

```

data(BBS2001)
desc<-descriptive(BBS2001,dfreq=TRUE,dtype="nbcap",t=50)
plot(desc)
  # Note in this plot the convex shape typical of model Mh.

cp<-closedp.0(BBS2001,dfreq=TRUE,dtype="nbcap",t=50,t0=20)
cp
plot(cp)
  # The Gamma estimator has the smallest deviance and the all
  # its residuals are small.

  # Let's calculate a profile confidence interval for the gamma
  # estimator:
closedpCI.0(BBS2001,dfreq=TRUE,dtype="nbcap",t=50,t0=20,
            m="Mh",h="Gamma",theta=3.5)

  # One can also calculate a profile confidence interval for Chao's
  # lower bound:
closedpCI.0(BBS2001,dfreq=TRUE,dtype="nbcap",t=50,t0=20,
            m="Mh",h="Chao")

```

---

bunting

*Lazuli Bunting Data*


---

**Description**

This data set contains frequencies of capture histories for 8 years of observation of lazuli buntings.

**Usage**

```
data(bunting)
```

**Format**

255 by 9 numeric matrix, with the following columns:

**p1, p2, p3, p4, p5, p6, p7, p8** Capture histories for eight periods

**freq** Observed frequencies for each capture history

**Details**

The data come from an eight-year (1973 to 1980) study by Allen W. Stokes of lazuli buntings wintering in Logan, Utah. This data set is analysed in Burnham and al. (1987) and in Cormack (1993).

Each row of this data set represents an observed capture history followed by its frequency.

## References

Baillargeon, S. and Rivest, L.P. (2007) Rcapture: Loglinear models for capture-recapture in R. *Journal of Statistical Software*, **19**(5), <http://www.jstatsoft.org/v19/i05>.

Burnham, K.P., Anderson, D.R., White, G.C., Brownie, C. and Pollock, K.H. (1987) Design and analysis methods for fish survival experiments based on release-recapture. *American Fisheries Society Monographs* 5. Bethesda, Maryland.

Cormack, R. M. (1993) The flexibility of GLIM analyses of multiple recapture or resighting data. In J.D. Lebreton and P. North editors: *Marked Individuals in the Study of Bird Population*. Basel, Switzerland: Birkhauser Verlag, 39–49.

## Examples

```
data(bunting)
descriptive(bunting,dfreq=TRUE)
# 1430 birds of a total of 1681 birds seen (85%) were caught only once.
# This suggests the presence of transient birds at each capture occasion.

op.m1<-openp(bunting,dfreq=TRUE)
op.m1$model.fit
plot(op.m1)
# The residuals plot shows large residuals for the birds caught twice or
# more while the residuals are small for birds caught once. The Jolly-Seber
# model does not fit well and the likely presence of transients might
# cause that. Let's remove the birds caught only once from the analysis.

keep2<-apply(histpos.t(8),1,sum)>1
op.m2<- openp(bunting,dfreq=TRUE,keep=keep2)
op.m2$model.fit
# The deviance drop of 94 for 6 degrees of freedom is highly significant.
plot(op.m2)
# The residual plot still shows Pearson residuals larger than 4. We redo
# the analysis without the transient birds and without the large residuals.

keep3p<-residuals(op.m2$glm,type="pearson")<4
num3<-((1:255)[keep2])[keep3p]
keep3<-rep(FALSE,255)
keep3[num3]<-TRUE
op.m3<- openp(bunting,dfreq=TRUE,keep=keep3)
cbind(op.m2$survivals,op.m3$survivals)
# These changes have little impact on the survival estimates.

# We now test the equality of the survival probabilities and estimate its
# common value phi. Least squares estimates of phi and its standard error:
siginv<-solve(op.m2$cov[8:12,8:12])
phi<-t(rep(1,5))%*%siginv%*%op.m2$survivals[2:6,1] /
(t(rep(1,5))%*%siginv%*%rep(1,5))
se<-1/sqrt(t(rep(1,5))%*%siginv%*%rep(1,5))
cbind(estimate=phi,stderr=se)
# The chi-square goodness of fit statistic for a constant survival
# and its pvalue are:
chisq4<-t(op.m2$survivals[2:6,1]-phi*rep(1,5))%*%siginv %*%
```

```
(op.m2$survivals[2:6,1]-phi*rep(1,5))
cbind(chi2stat=chisq4,pvalue=1-pchisq(chisq4,df=4))
# The hypothesis of a constant survival is accepted.
```

---

catb *Catbird Site Occupancy Data*

---

## Description

This data set contains site occupancy data for catbirds. The number of capture occasions  $t$  is 11.

## Usage

```
data(catb)
```

## Format

6 by 2 numeric matrix, with the following columns:

**nbcap** Numbers of captures

**freq** Observed frequencies for each number of captures

## Details

This data set is presented in Royle (2006). It comes from an experiment in which 50 locations have been visited 11 times. The presence or absence of catbirds was noted at each visit. The experiment aims at estimating the number of locations ( $\leq 50$ ) at which catbirds are present.

In the data set `catb`, the frequencies represent the number of locations at which catbirds have been detected  $i$  times, out of  $t = 11$  visits. The frequencies for  $i = 7, \dots, 11$  are null and do not appear in the data set.

## Source

Royle, A. J. (2006) Site occupancy models with heterogeneous detection probabilities. *Biometrics*, **62**, 97–102

## Examples

```
data(catb)
desc<-descriptive(catb,dfreq=TRUE,dtype="nbcap",t=11)
plot(desc)
# The heterogeneity graph is mildly convex, mostly because of
# 2 sites where the catbirds have been seen six times.

closedp.0(catb,dfreq=TRUE,dtype="nbcap",t=11)
# The residuals are OK. The occupancy rate (N/50) estimates
# varies between 40.6% for M0 and 49.4% for Mh Gamma.
# One could also try fitting M0 removing the 2 unusual sites:
closedp.0(catb,dfreq=TRUE,dtype="nbcap",t=11,t0=5)
# M0 fits very well and the occupancy rate estimate is 42.6%.
```

closedp

*Loglinear Models for Closed Population Capture-Recapture Experiments***Description**

The functions `closedp.t` and `closedp.0` fit various loglinear models for closed populations in capture-recapture experiments. For back compatibility, `closedp.t` is also named `closedp`.

`closedp.t` fits more models than `closedp.0` but for data set with more than 20 capture occasions, the function might fail. However, `closedp.0` works with fairly large data sets (see Details).

**Usage**

```
closedp(X, dfreq=FALSE, neg=TRUE, trace=FALSE)
closedp.t(X, dfreq=FALSE, neg=TRUE, trace=FALSE)

closedp.0(X, dfreq=FALSE, dtype=c("hist", "nbcap"), t, t0=t,
          neg=TRUE, trace=FALSE)

## S3 method for class 'closedp':
print(x, ...)

## S3 method for class 'closedp':
boxplot(x, main="Boxplots of Pearson Residuals", ...)

## S3 method for class 'closedp':
plot(x, main="Residual plots for some heterogeneity models", ...)
```

**Arguments**

<code>X</code>	The matrix of the observed capture histories (see <a href="#">Rcapture-package</a> for a description of the accepted formats).
<code>dfreq</code>	A logical. By default FALSE, which means that <code>X</code> has one row per unit. If TRUE, it indicates that the matrix <code>X</code> contains frequencies in its last column.
<code>dtype</code>	A characters string, either "hist" or "nbcap", to specify the type of data. "hist", the default, means that <code>X</code> contains complete observed capture histories. "nbcap" means that <code>X</code> contains numbers of captures (see <a href="#">Rcapture-package</a> for details on data formats).
<code>t</code>	Requested only if <code>dtype="nbcap"</code> . A numeric specifying the total number of capture occasions in the experiment.
<code>t0</code>	A numeric. Models are fitted considering only the frequencies of units captured 1 to <code>t0</code> times. By default <code>t0=t</code> .
<code>neg</code>	If this option is set to TRUE, negative eta parameters in Chao's models are set to zero.

<code>trace</code>	A logical, by default FALSE. If set to TRUE, a note is printed for each model while the function runs. It is useful to identify which model is associated to a warning.
<code>x</code>	An object, produced by a <code>closedp</code> function, to print or to plot.
<code>main</code>	A main title for the plot
<code>...</code>	Further arguments to be passed to methods (see <code>print.default</code> , <code>boxplot.default</code> and <code>plot.default</code> ).

## Details

`closedp.t` fits models M0, Mt, Mh Chao, Mh Poisson2, Mh Darroch, Mh Gamma3.5, Mth Chao, Mth Poisson2, Mth Darroch, Mth Gamma3.5, Mb and Mbh. `closedp.0` fits only models M0, Mh Chao, Mh Poisson2, Mh Darroch and Mh Gamma3.5. However, `closedp.0` can be used with larger data sets than `closedp.t`. This is explained by the fact that `closedp.t` fits models using the frequencies of the observable capture histories (vector of size  $2^t - 1$ ), whereas `closedp.0` uses the numbers of units captured  $i$  times, for  $i = 1, \dots, t$  (vector of size  $t$ ).

`closedp.0` has an additional argument `t0` which gives to the numbers of units caught more than  $t_0$  times their own parameters in the loglinear model. For example, the model for Mh Gamma3.5 has  $3+t-t_0$  parameters. This means that `closedp.0` fits models considering only the frequencies of units captured 1 to  $t_0$  times.

Chao's models estimate a lower bound for the abundance, both with a time effect (Mth Chao) and without (Mh Chao). The estimate obtained under Mh Chao is Chao's (1987) moment estimator. Rivest and Baillargeon (2007) exhibit a loglinear model underlying this estimator and provide a generalization to Mth. For these two models, a small deviance means that there is an heterogeneity in capture probabilities; it does not mean that the lower bound estimates are unbiased.

Other models for heterogeneity are defined as follows :

Model	Column for heterogeneity in the design matrix
Poisson2	$2^k - 1$
Darroch	$k^2/2$
Gamma3.5	$-\log(3.5 + k) + \log(3.5)$

where  $k$  is the number of captures. Poisson and Gamma models with parameter values different than 2 and 3.5 respectively can be fitted with the `closedpCI.t` and `closedpCI.0` functions.

Darroch's models for Mh and Mth are considered by Darroch et al. (1993) and Agresti (1994). Poisson and Gamma models are discussed in Rivest and Baillargeon (2007). Poisson models typically yield smaller corrections for heterogeneity than Darroch's model since the capture probabilities are bounded from below under these models. On the other hand, Gamma models can lead to very large estimators of abundance. We suggest considering this estimator in experiments where very small capture probabilities are likely.

When the variance of an abundance estimate is large, it is useful to use the `closedpCI.t` or `closedpCI.0` function to construct a profile confidence interval for this abundance.

The `boxplot.closedp` function produces boxplots of the Pearson residuals of the fitted loglinear models that converged.

The `plot.closedp` function produces scatterplots of the Pearson residuals in terms of  $f_i$  (number of units captured  $i$  times) for the heterogeneous models Mh Poisson2, Mh Darroch and Mh Gamma3.5 if they converged.

To calculate bias corrected abundance estimates, use the `closedp.bc` function.

### Value

<code>n</code>	The number of captured units.										
<code>t</code>	The total number of capture occasions in the experiment.										
<code>results</code>	A table containing, for every fitted model, the estimated population size, the standard error of estimation, the deviance, the number of degrees of freedom and the Akaike criteria.										
<code>converge</code>	A logical vector indicating whether or not the fitted models converged.										
<code>glm</code>	A list of the 'glm' objects obtained from fitting models.										
<code>parameters</code>	Capture-recapture parameters estimates. It contains N, the estimated population size, and $p$ or $p_1$ to $p_t$ defined as follows for the different models : <table style="margin-left: 2em;"> <tr> <td>M0</td> <td>the capture probability at any capture occasion</td> </tr> <tr> <td>Mt</td> <td>the capture probabilities for each capture occasion</td> </tr> <tr> <td>Mh models</td> <td>the average probability of capture</td> </tr> <tr> <td>Mth models</td> <td>the average probabilities of capture for each occasion</td> </tr> <tr> <td>Mb and Mbh</td> <td>the probability of first capture at any capture occasion</td> </tr> </table> <p>For models Mb and Mbh, it also contains <math>c</math>, the recapture probability at any capture occasion.</p>	M0	the capture probability at any capture occasion	Mt	the capture probabilities for each capture occasion	Mh models	the average probability of capture	Mth models	the average probabilities of capture for each occasion	Mb and Mbh	the probability of first capture at any capture occasion
M0	the capture probability at any capture occasion										
Mt	the capture probabilities for each capture occasion										
Mh models	the average probability of capture										
Mth models	the average probabilities of capture for each occasion										
Mb and Mbh	the probability of first capture at any capture occasion										
<code>neg.eta</code>	The position of the eta parameters set to zero in the loglinear parameter vector of model MhC and MthC.										
<code>x</code>	A copy of the data given as input in the function call.										
<code>dfreq</code>	A copy of the <code>dfreq</code> argument given in the function call.										
<code>t0</code>	For <code>closedp.0</code> only, a copy of the <code>t0</code> argument given in the function call.										

### Note

This function uses the `glm` function of the `stats` package.

### Author(s)

Sophie Baillargeon (Sophie.Baillargeon@mat.ulaval.ca) and  
Louis-Paul Rivest (Louis-Paul.Rivest@mat.ulaval.ca)

### References

- Agresti, A. (1994) Simple capture-recapture models permitting unequal catchability and variable sampling effort. *Biometrics*, **50**, 494–500.
- Baillargeon, S. and Rivest, L.P. (2007) Rcapture: Loglinear models for capture-recapture in R. *Journal of Statistical Software*, **19**(5), <http://www.jstatsoft.org/v19/i05>.

Chao, A. (1987) Estimating the population size for capture-recapture data with unequal catchability. *Biometrics*, **45**, 427–438.

Darroch, S.E., Fienberg, G., Glonek, B. and Junker, B. (1993) A three sample multiple capture-recapture approach to the census population estimation with heterogeneous catchability. *Journal of the American Statistical Association*, **88**, 1137–1148.

Rivest, L.P. and Levesque, T. (2001) Improved log-linear model estimators of abundance in capture-recapture experiments. *Canadian Journal of Statistics*, **29**, 555–572.

Rivest, L.P. and Baillargeon, S. (2007) Applications and extensions of Chao's moment estimator for the size of a closed population. *Biometrics*, **63**(4), 999–1006.

Seber, G.A.F. (1982) *The Estimation of Animal Abundance and Related Parameters*, 2nd edition, New York: Macmillan.

### See Also

[closedpCI.t](#), [closedpCI.0](#), [closedp.bc](#), [closedp.Mtb](#), [uifit](#).

### Examples

```
data(hare)
hare.closedp<-closedp.t(hare)
hare.closedp
boxplot(hare.closedp)

data(mvole)
period3<-mvole[,11:15]
closedp.t(period3)

data(BBS2001)
BBS.closedp<-closedp.0(BBS2001,dfreq=TRUE,dtype="nbcap",t=50,t0=20)
BBS.closedp
plot(BBS.closedp)

# Seber (1982) p.107
# When there is 2 capture occasions, the heterogeneity models cannot be fitted
X <- matrix(c(1,1,167,1,0,781,0,1,254),byrow=TRUE,ncol=3)
closedp.t(X,dfreq=TRUE)
```

### Description

This function applies a bias correction to the abundance estimations obtained by closed population models.

**Usage**

```
closedp.bc(X, dfreq=FALSE, dtype=c("hist", "nbcap"), t, t0=t,
           m=c("M0", "Mt", "Mh", "Mth", "Mb", "Mbh"),
           h=c("Chao", "Poisson", "Darroch", "Gamma"), theta=2)

## S3 method for class 'closedp.bc':
print(x, ...)
```

**Arguments**

X	The matrix of the observed capture histories (see <a href="#">Rcapture-package</a> for a description of the accepted formats).
dfreq	A logical. By default FALSE, which means that X has one row per unit. If TRUE, it indicates that the matrix X contains frequencies in its last column.
dtype	A characters string, either "hist" or "nbcap", to specify the type of data. "hist", the default, means that X contains complete observed capture histories. "nbcap" means that X contains numbers of captures (see <a href="#">Rcapture-package</a> for details on data formats). If m is "Mt", "Mth", "Mb" or "Mbh", dtype must be "hist".
t	Requested only if dtype="nbcap". A numeric specifying the total number of capture occasions in the experiment.
t0	A numeric. Models are fitted considering only the frequencies of units captured 1 to t0 times. By default t0=t.
m	A character string indicating the model to fit, either "M0"=M0 model, "Mt"=Mt model, "Mh"=Mh model, "Mth"=Mth model, "Mb"=Mb model, "Mbh"=Mbh model.
h	A character string ("Chao", "Poisson", "Darroch" or "Gamma") or a numerical R function specifying the form of the column for heterogeneity in the design matrix. "Chao" represents Chao's model, "Poisson" represents the function $f(k) = \theta^k - 1$ , where $k$ is the number of captures, "Darroch" represents the function $f(k) = k^2/2$ , and "Gamma" represents the function $f(k) = -\log(\theta + k) + \log(\theta)$ . If an R function is given, it is the implementation of any convex mathematical function $f(k)$ . It has only one argument.
theta	The value of the parameter for a Poisson or Gamma model.
x	An object, produced by the closedp.bc function, to print.
...	Further arguments to be passed to print.default.

**Details**

The abundance estimate for the Mt model when  $t=2$  has Chapman bias correction and a standard error derived from Seber and Wittes variance estimate. For  $t>2$ , closedp.bc() implements the bias correction of Rivest and Levesque (2001). The estimate for N and its variance are calculated by solving an estimating equation as proposed in Seber (1982), not by fitting a Poisson regression. This approach works for large values of t.

For other models, the bias correction is done through frequency modifications in Poisson regression as described in Rivest and Levesque (2001). The variances calculated with the modified frequencies

are less biased than the standard ones, but they can overestimate the mean squared errors, especially when the data is sparse.

This function works with fairly large data set, except if an "Mth" model is requested. In this case, only heterogeneity of the form "Chao", "Poisson" with `theta=2` or "Darroch" is accepted.

### Value

<code>n</code>	The number of captured units
<code>results</code>	A table containing, for every fitted model, the corrected population size estimation and its standard error.
<code>converge</code>	A logical vector indicating whether or not the fitted models converged.

### Note

This function uses the `glm` function of the `stats` package.

### Author(s)

Sophie Baillargeon (Sophie.Baillargeon@mat.ulaval.ca) and  
Louis-Paul Rivest (Louis-Paul.Rivest@mat.ulaval.ca)

### References

Baillargeon, S. and Rivest, L.P. (2007) Rcapture: Loglinear models for capture-recapture in R. *Journal of Statistical Software*, **19**(5), <http://www.jstatsoft.org/v19/i05>.

Rivest, L.P. and Levesque, T. (2001) Improved log-linear model estimators of abundance in capture-recapture experiments. *Canadian Journal of Statistics*, **29**, 555–572.

Seber, G.A.F. (1982) *The Estimation of Animal Abundance and Related Parameters*, 2nd edition, New York: Macmillan.

### See Also

[closedp](#)

### Examples

```
data(mvole)
period3<-mvole[,11:15]
closedp.bc(period3,m="Mh",h="Darroch")
closedp.bc(period3,m="Mh",h="Gamma",theta=3.5)

data(BBS2001)
closedp.bc(BBS2001,dfreq=TRUE,dtype="nbcap",t=50,t0=20,
           m="Mh",h="Gamma",theta=3.5)

# Seber (1982) p.107
# When there is 2 capture occasions, only models M0 and Mt can be fitted
X <- matrix(c(1,1,167,1,0,781,0,1,254),byrow=TRUE,ncol=3)
closedp.bc(X,dfreq=TRUE, m="M0")
closedp.bc(X,dfreq=TRUE, m="Mt")
```

---

closedp.custom	<i>Customization of a Loglinear Model for Closed Populations Capture-Recapture Experiments</i>
----------------	--

---

## Description

This function is deprecated, please use `closedpCI.t` instead.

The `closedp.mX` function fits a loglinear model given a design matrix `mX`. The `closedp.h` function fits Mh or Mth models for which the form of the column for heterogeneity in the design matrix is determined by the user.

## Usage

```
closedp.mX(X, dfreq=FALSE, mX, mname="Customized model")

closedp.h(X, dfreq=FALSE, m="Mh", h="Poisson", a=2)

## S3 method for class 'closedp.custom':
print(x, ...)

## S3 method for class 'closedp.custom':
boxplot(x, ...)
```

## Arguments

<code>X</code>	The matrix of the observed capture histories (see <a href="#">Rcapture-package</a> for a description of the accepted formats).
<code>dfreq</code>	A logical. By default FALSE, which means that <code>X</code> has one row per unit. If TRUE, it indicates that the matrix <code>X</code> contains frequencies in its last column.
<code>mX</code>	The design matrix of the loglinear model. In this matrix, the order of the capture histories is as defined in the <code>histpos.t</code> function.
<code>mname</code>	A character string specifying the name of the customized model.
<code>m</code>	A character string indicating the model to fit, either "Mh"=Mh model or "Mth"=Mth model
<code>h</code>	The character string "Poisson" ( $2^k - 1$ ) or a numerical function taking only one argument specifying the form of the column for heterogeneity in the design matrix.
<code>a</code>	The value of the exponent's base for a Poisson model.
<code>x</code>	An object, produced by the <code>closedp.mX</code> or the <code>closedp.h</code> function, to print or to plot.
<code>...</code>	Further arguments passed to or from other methods.

**Details**

An intercept is added to the model. Therefore, the  $mX$  matrix must not contain a column of ones.

The abundance estimation is calculated as the number of captured units plus the exponential of the intercept. Therefore, these functions are not suited for models with a behavioral effect.

In `closedp.h`, the argument `h` cannot take the value "Chao" or "Darroch" because these models are already fitted by the `closedp` function.

The `boxplot.closedp.custom` function produces a boxplot of the pearson residuals of the customized model.

**Value**

<code>n</code>	The number of captured units
<code>results</code>	A table containing the estimated population size, the standard error of estimation, the deviance, the number of degrees of freedom and the Akaike criteria.
<code>glm</code>	The 'glm' object obtained from fitting the model.

**Note**

These functions use the `glm` function of the `stats` package.

**Author(s)**

Sophie Baillargeon (sbaillar@mat.ulaval.ca) and Louis-Paul Rivest (lpr@mat.ulaval.ca)

**References**

Rivest, L.P. and Baillargeon, S. (2007) Applications and extensions of Chao's moment estimator for the size of a closed population. *Biometrics*, **63**(4), 999–1006.

**See Also**

[closedp](#), [closedp.Mtb](#)

**Examples**

```
data(HIV)
mat<-histpos.t(4)
mX2<-cbind(mat,mat[,1]*mat[,2])
closedp.mX(HIV,dfreq=TRUE,mX=mX2)

data(mvole)
period3<-mvole[,11:15]
psi <- function(x) { -log(3.5 + x) + log(3.5) }
closedp.h(period3, h = psi)
```

closedp.Mtb

*Closed Population Capture-Recapture Model Mtb***Description**

This function fits model Mtb for closed populations in capture-recapture experiments.

**Usage**

```
closedp.Mtb(X, dfreq=FALSE)

## S3 method for class 'closedp.Mtb':
print(x, ...)
```

**Arguments**

X	The matrix of the observed capture histories (see <a href="#">Rcapture-package</a> for a description of the accepted formats).
dfreq	A logical. By default FALSE, which means that X has one row per unit. If TRUE, it indicates that the matrix X contains frequencies in its last column.
x	An object, produced by the closedp.Mtb function, to print.
...	Further arguments to be passed to print.default.

**Details**

The Mtb model is non-linear. It is fitted with the `optim` function instead of the `glm` fonction. Therefore, the abundance estimate can be unstable.

For the model to be identifiable, the parameters are constrained in the following way:  $\text{logit}(c_i) = \text{logit}(p_i) + b$  for  $i$  in  $2, \dots, l$ .

**Value**

n	The number of captured units
results	A table containing the estimated population size, the standard error of estimation, the deviance, the number of degrees of freedom and the Akaike criteria.
parMtb	Capture-recapture parameters estimates for model Mtb : the abundance N, $p_1$ to $p_t$ , the probabilities of first capture for each capture occasion, and $c_2$ to $c_t$ , the recapture probabilities for each capture occasion.

**Author(s)**

Sophie Baillargeon (Sophie.Baillargeon@mat.ulaval.ca) and  
Louis-Paul Rivest (Louis-Paul.Rivest@mat.ulaval.ca)

## References

Baillargeon, S. and Rivest, L.P. (2007) Rcapture: Loglinear models for capture-recapture in R. *Journal of Statistical Software*, **19**(5), <http://www.jstatsoft.org/v19/i05>.

## See Also

`closedp`, `closedpCI.t`

## Examples

```
data(hare)
closedp.Mtb(hare)

## Example producing an unstable estimate
data(mvole)
period4<-mvole[,16:20]
closedp.Mtb(period4)
```

---

closedpCI	<i>Customization of a Loglinear Model and profile Likelihood Confidence Interval for Abundance Estimation in Closed Population Capture-Recapture Experiments</i>
-----------	--

---

## Description

The `closedpCI.t` and `closedpCI.0` functions fit a loglinear model specified by the user and computes the multinomial profile likelihood confidence interval for the abundance estimation. The model can be given as a design matrix `mX` or identified trough arguments `m`, `h` and `theta`. These functions extend `closedp.t` and `closedp.0` as they broaden the range of model one can fit and they computes confidence interval. Unlike the `closedp` functions, it fits only one model at a time.

## Usage

```
closedpCI.t(X, dfreq=FALSE, m=c("M0", "Mt", "Mh", "Mth"),
            h=c("Chao", "Poisson", "Darroch", "Gamma"), theta=2,
            mX=NULL, mname, neg=TRUE, alpha=0.05)

closedpCI.0(X, dfreq=FALSE, dtype=c("hist", "nbcap"), t, t0=t,
            m=c("M0", "Mh"), h=c("Chao", "Poisson", "Darroch", "Gamma"),
            theta=2, mX=NULL, mname, neg=TRUE, alpha=0.05)

## S3 method for class 'closedpCI':
print(x, ...)

plotCI(x, ...)
## S3 method for class 'closedpCI':
plotCI(x, main="Profile Likelihood Confidence Interval", ...)
```

```
## S3 method for class 'closedpCI':
boxplot(x, main="Boxplots of Pearson Residuals", ...)

## S3 method for class 'closedpCI':
plot(x, main="Scatterplot of Pearson Residuals", ...)
```

## Arguments

<code>x</code>	The matrix of the observed capture histories (see <a href="#">Rcapture-package</a> for a description of the accepted formats).
<code>dfreq</code>	A logical. By default FALSE, which means that <code>x</code> has one row per unit. If TRUE, it indicates that the matrix <code>x</code> contains frequencies in its last column.
<code>dtype</code>	A characters string, either "hist" or "nbcap", to specify the type of data. "hist", the default, means that <code>x</code> contains complete observed capture histories. "nbcap" means that <code>x</code> contains numbers of captures (see <a href="#">Rcapture-package</a> for details on data formats).
<code>t</code>	Requested only if <code>dtype="nbcap"</code> . A numeric specifying the total number of capture occasions in the experiment.
<code>t0</code>	A numeric. Models are fitted considering only the frequencies of units captured 1 to <code>t0</code> times. By default <code>t0=t</code> .
<code>m</code>	A character string indicating the model to fit. For <code>closedpCI.0</code> it can be either "M0"=M0 model or "Mh"=Mh model. For <code>closedpCI.t</code> it can also be "Mt"=Mt model or "Mth"=Mth model.
<code>h</code>	A character string ("Chao", "Poisson", "Darroch" or "Gamma") or a numerical R function specifying the form of the column for heterogeneity in the design matrix. "Chao" represents Chao's model, "Poisson" represents the function $f(k) = \theta^k - 1$ , where $k$ is the number of captures, "Darroch" represents the function $f(k) = k^2/2$ , and "Gamma" represents the function $f(k) = -\log(\theta + k) + \log(\theta)$ . If an R function is given, it is the implementation of any convex mathematical function $f(k)$ . It has only one argument.
<code>theta</code>	The value of the parameter for a Poisson or Gamma model.
<code>mX</code>	The design matrix of the loglinear model. In this matrix, the order of the capture histories is as defined in the <code>histpos.t</code> or <code>histpos.0</code> function.
<code>mname</code>	A character string specifying the name of the customized model.
<code>neg</code>	If this option is set to TRUE, negative eta parameters in Chao's models are set to zero.
<code>alpha</code>	A confidence interval with confidence level $1-\alpha$ is constructed. The value of <code>alpha</code> must be between 0 and 1; the default is 0.05.
<code>x</code>	An object, produced by the <code>closedpCI.t</code> function, to print.
<code>main</code>	A main title for the plot
<code>...</code>	Further arguments to be passed to methods (see <code>print.default</code> , <code>plot.default</code> or <code>boxplot.default</code> ).

**Details**

The `closedpCI.t` function fits models using the frequencies of the observable capture histories (vector of size  $2^t - 1$ ), whereas `closedp.0` uses the number of units capture  $i$  times, for  $i = 1, \dots, t$  (vector of size  $t$ ). Thus, `closedpCI.0` can be used with data sets larger than those for `closedpCI.t`.

This function does not work for closed population models featuring a behavioral effect, such as Mb and Mbh. The abundance estimation is calculated as the number of captured units plus the exponential of the Poisson regression intercept. However, models with a behavioral effect can be fitted with `closedp.t` (Mb and Mbh), `closedp.Mtb` and `closedp.bc`.

An intercept is added to the model. Therefore, the `mX` matrix must not contain a column of ones.

The `plotCI.closedpCI` function produces a plot of the multinomial profile likelihood for  $N$ . The value of  $N$  maximizing the profile likelihood and the bounds of the confidence interval are identified.

The `boxplot.closedpCI` function produces a boxplot of the Pearson residuals of the customized model.

The `plot.closedpCI` function traces the scatterplot of the Pearson residuals in terms of  $f_i$  (number of units captured  $i$  times) for the customized model.

**Value**

<code>n</code>	The number of captured units
<code>t</code>	The number of capture occasions in the data matrix $X$
<code>results</code>	A table containing the estimated population size, the standard error of estimation, the deviance, the number of degrees of freedom and the Akaike criteria.
<code>glm</code>	The 'glm' object obtained from fitting the model.
<code>CI</code>	A table containing the abundance estimation and its confidence interval.
<code>alpha</code>	1-the confidence level of the interval.
<code>NCI</code>	The x-coordinates for <code>plot.closedpCI.t</code>
<code>loglikCI</code>	The y-coordinates for <code>plot.closedpCI.t</code>
<code>t0</code>	A copy of the <code>t0</code> argument given in the function call.

**Note**

This function uses the `optimize` and the `uniroot` functions of the `stats` package.

**Author(s)**

Sophie Baillargeon (Sophie.Baillargeon@mat.ulaval.ca) and  
Louis-Paul Rivest (Louis-Paul.Rivest@mat.ulaval.ca)

## References

- Baillargeon, S. and Rivest, L.P. (2007) Rcapture: Loglinear models for capture-recapture in R. *Journal of Statistical Software*, **19**(5), <http://www.jstatsoft.org/v19/i05>.
- Rivest, L.P. and Baillargeon, S. (2007) Applications and extensions of Chao's moment estimator for the size of a closed population. *Biometrics*, **63**(4), 999–1006.
- Cormack, R. M. (1992) Interval estimation for mark-recapture studies of closed populations. *Biometrics*, **48**, 567–576.

## See Also

[closedp](#), [closedp.Mtb](#)

## Examples

```
data(hare)
CI<-closedpCI.t(hare, m = "Mth", h = "Poisson", theta = 2)
CI
plotCI(CI)

data(HIV)
mat<-histpos.t(4)
mX2<-cbind(mat,mat[,1]*mat[,2])
closedpCI.t(HIV,dfreq=TRUE,mX=mX2,mname="Mt interaction 1,2")

data(BBS2001)
CI0<-closedpCI.0(BBS2001,dfreq=TRUE,dtype="nbcap",t=50,t0=20,
                 m="Mh",h="Gamma",theta=3.5)
CI0
plot(CI0)
plotCI(CI0)

### As an alternative to a gamma model, one can fit a negative Poisson model.
### It is appropriate in experiments where very small capture probabilities
### are likely. It can lead to very large estimators of abundance.
data(mvole)
period3<-mvole[,11:15]
psi <- function(x) { 0.5^x - 1 }
closedpCI.t(period3, m = "Mh", h = psi)
```

## Description

This function produces descriptive statistics for capture-recapture data.

**Usage**

```
descriptive(X, dfreq=FALSE, dtype=c("hist", "nbcap"), t)

## S3 method for class 'descriptive':
print(x, ...)

## S3 method for class 'descriptive':
plot(x, main="Exploratory Heterogeneity Graph", ...)
```

**Arguments**

<code>X</code>	The matrix of the observed capture histories (see <a href="#">Rcapture-package</a> for a description of the accepted formats).
<code>dfreq</code>	A logical. By default FALSE, which means that <code>X</code> has one row per unit. If TRUE, it indicates that the matrix <code>X</code> contains frequencies in its last column.
<code>dtype</code>	A characters string, either "hist" or "nbcap", to specify the type of data. "hist", the default, means that <code>X</code> contains complete observed capture histories. "nbcap" means that <code>X</code> contains numbers of captures (see <a href="#">Rcapture-package</a> for details on data formats).
<code>t</code>	Requested only if <code>dtype="nbcap"</code> . A numeric specifying the total number of capture occasions in the experiment.
<code>x</code>	An object, produced by the <code>descriptive</code> function, to print or to plot.
<code>main</code>	A main title for the plot
<code>...</code>	Further arguments to be passed to methods (see <code>print.default</code> and <code>plot.default</code> ).

**Details**

The `plot.descriptive` function produces an exploratory heterogeneity graph. In the absence of heterogeneity, the relation(s) presented in the graph should be almost linear. Convex functions indicate heterogeneity.

If `dtype="nbcap"`, only the the number of units captured  $i$  times,  $f_i$ , can be computed.

**Value**

<code>n</code>	The total number of captured units.
<code>base.freq</code>	A table of basic descriptive statistics. For $i = 1, \dots, t$ : $f_i$ : the number of units captured $i$ times $u_i$ : the number of units captured for the first time on occasion $i$ $v_i$ : the number of units captured for the last time on occasion $i$ $n_i$ : the number of units captured on occasion $i$
<code>m.array</code>	A $t$ by $t$ matrix containing recapture statistics for units released on occasion $i$ , for $i = 1, \dots, t$ : $n_i$ : the number of units released on occasion $i$ ; $c_2$ : the number of units released on occasion $i$ and recaptured for the first time on occasion 2; ...

ct: the number of units released on occasion  $i$  and recaptured for the first time on occasion  $t$ ;

not recapt: the number of units released on occasion  $i$  and never recaptured again.

The `m.array` matrix is used in `Mark` (see White and Burnham 1999; White 2005) and `MSurge` (see Choquet, Reboulet, Pradel, Gimenez, and Lebreton 2004) to fit open population models to the data.

### Author(s)

Sophie Baillargeon (Sophie.Baillargeon@mat.ulaval.ca) and  
Louis-Paul Rivest (Louis-Paul.Rivest@mat.ulaval.ca)

### References

Baillargeon, S. and Rivest, L.P. (2007) Rcapture: Loglinear models for capture-recapture in R. *Journal of Statistical Software*, **19**(5), <http://www.jstatsoft.org/v19/i05>.

Choquet, R., Reboulet, A.M., Pradel, R., Gimenez, O. and Lebreton, J.D. (2004). M-Surge: New Software Specifically Designed for Multistate Capture-Recapture Models. *Animal Biodiversity and Conservation*, **27.1**, 207–215.

Lindsay, B. G. (1986) Exponential family mixture models (with least-squares estimators). *Annals of Statistics*, **14**, 124–137.

Rivest, L.P. (2008) Why a time effect often has a limited impact on capture-recapture estimates in closed populations. *Canadian Journal of Statistics*, **36**(1), 75–84.

White, G. (2005) *Software Developed by Department of Fishery and Wildlife Biology and Colorado Coop. Fish and Wildlife Unit, Colorado State University*. <http://www.warnercnr.colostate.edu/~gwhite/software.html>.

White, G. and Burnham, K.P. (1999) Program Mark: Survival Estimation from Populations of Marked Animals. *Bird Study*, **46** (Supplement), 120–138.

### Examples

```
data(hare)
hare.desc<-descriptive(hare)
hare.desc
plot(hare.desc)
```

```
data(catb)
catb.desc<-descriptive(catb,dfreq=TRUE,dtype="nbcap",t=11)
plot(catb.desc)
```

---

 duck

*Eider Duck Data*


---

### Description

This data set contains capture-recapture data for eider ducks.

### Usage

```
data(duck)
```

### Format

63 by 7 numeric matrix, with the following columns:

**p1, p2, p3, p4, p5, p6** Capture histories for six periods

**freq** Observed frequencies for each capture history

### Details

The data points are extracted from a 25-year study by Coulson (1984). The capture periods are six consecutive years : years 19-24. This data set is analysed in Cormack (1989).

Each row of this data set represents an observed capture history followed by its frequency.

### Source

Coulson, J. C. (1984) The population dynamics of the Eider Duck *Somateria mollissima* and evidence of extensive non breeding by adults ducks. *Ibis*, **126**, 525–543.

### References

Baillargeon, S. and Rivest, L.P. (2007) Rcapture: Loglinear models for capture-recapture in R. *Journal of Statistical Software*, **19**(5), <http://www.jstatsoft.org/v19/i05>.

Cormack, R. M. (1989) Log-linear models for capture-recapture. *Biometrics*, **45**, 395–413.

### Examples

```
data(duck)
op.m1<-openp(duck,dfreq=TRUE)
op.m1$model.fit
# The pvalue of the goodness of fit test based on the deviance is
1-pchisq(op.m1$model.fit[1,1],df=49)
plot(op.m1)
# The residual plot shows a large residual for the 13 individuals
# captured all the times. We redo the analysis without them.

keep2<-apply(histpos.t(6),1,sum)!=6
op.m2<-openp(duck,dfreq=TRUE,keep=keep2)
```

```

op.m2$model.fit
1-pchisq(op.m2$model.fit[1,1],df=48)
  # The fit is still not satisfactory.
plot(op.m2)
  # The residual plot has the convex shape characteristic of
  # heterogeneity in the capture probabilities. We also remove the
  # individuals caught at 5 periods out of 6.

keep3<-apply(histpos.t(6),1,sum)<5
op.m3<-openp(duck,dfreq=TRUE,keep=keep3)
op.m3$model.fit
1-pchisq(op.m3$model.fit[1,1],df=42)
  # The fit is better but there is still heterogeneity in the data.

  # To investigate whether the capture probabilities are homogeneous,
  # one can fit a model with equal capture probabilities.
op.m4<-openp(duck,dfreq=TRUE,m="ep",keep=keep3)
op.m4$model.fit
  # It gives a much larger deviance; this model is not considered anymore.

  # We now investigate models for the growth rate  $N[i+1]/N[i]$  of this
  # population using the multivariate normal distribution for the
  # abundance estimates. The growth rates and their standard errors are
growth<-op.m3$N[3:5]/op.m3$N[2:4]
partial<-matrix(c(-op.m3$N[3]/op.m3$N[2]^2,1/op.m3$N[2],0,0,0,
                 -op.m3$N[4]/op.m3$N[3]^2,1/op.m3$N[3],0,0,0,
                 -op.m3$N[5]/op.m3$N[4]^2,1/op.m3$N[4]),3,4,byrow=TRUE)
sig<-partial%*%op.m3$cov[9:12,9:12]%*%t(partial)
cbind(estimate=growth,stderr=sqrt(diag(sig)))
  # An estimate for the common growth rate is
siginv<-solve(sig)
growth.e<-t(rep(1,3))%*%siginv%*%growth/(t(rep(1,3))%*%siginv%*%rep(1,3))
se<-1/sqrt(t(rep(1,3))%*%siginv%*%rep(1,3))
cbind(estimate=growth.e,stderr=se)
  # A chi-square statistics for testing the equality of the growth rates
  # and its pvalue
chisq2<-t(growth-growth.e*rep(1,3))%*%siginv%*%(growth-growth.e*rep(1,3))
c(chi2stat=chisq2,pvalue=1-pchisq(chisq2,df=2))
  # The hypothesis of a common growth rate is rejected

```

---

hare

*Snowshoe Hare Data*

---

### Description

This data set contains capture-recapture data for snowshoe hares.

### Usage

data(hare)

**Format**

68 by 6 numeric matrix, with the following columns:

**c1, c2, c3, c4, c5, c6** Capture histories for the six capture occasions

**Details**

This data set is analysed in Cormack (1989) and Agresti (1994).

Each row of this data set represents the capture history of one animal.

**References**

Agresti, A. (1994) Simple capture-recapture models permitting unequal catchability and variable sampling effort. *Biometrics*, **50**, 494–500.

Baillargeon, S. and Rivest, L.P. (2007) Rcapture: Loglinear models for capture-recapture in R. *Journal of Statistical Software*, **19**(5), <http://www.jstatsoft.org/v19/i05>.

Cormack, R. M. (1989) Log-linear models for capture-recapture. *Biometrics*, **45**, 395–413.

**Examples**

```
data(hare)
desc<-descriptive(hare)
plot(desc)
# The fi plot shows that the two animals caught on all occasions create
# some heterogeneity in the capture probabilities.

closedp(hare)
# The best fitting model Mth Poisson2(N = 81.1, s.e.=5.7) has an AIC of 146.
closedpCI.t(hare,m="Mth",h="Poisson",theta=2)

# One can compare the fit of this model with that obtained by removing the
# 2 hares caught 6 times. This can be done by adding a column to the design
# matrix for Mt taking the value 1 for the capture history (1,1,1,1,1,1).
col<-rep(0,2^6-1)
mat<-histpos.t(6)
col[apply(mat,1,sum)==6]<-1
closedpCI.t(hare,mX=cbind(mat,col),mname="Mt without 111111")
# This gives N = 76.8 (s.e.=3.9) with an AIC of 146.
```

---

histpos

*Possible Capture Histories*

---

**Description**

`histpos.t` builds the matrix of observable capture histories in terms of captures and misses for a capture-recapture experiment with `t` capture occasions.

`histpos.0` builds the matrix of observable capture histories in terms of number of captures for each primary period of a robust design with `vt` capture occasions. For `closedp` populations, `vt=t` and `histpos.0` simply returns `t:1`.

**Usage**

```
histpos.t(t)
histpos.0(vt)
```

**Arguments**

t	The number of capture occasions.
vt	A vector containing the numbers of capture occasions for each primary sampling period of a robust design. The length of this vector equals the number of primary sampling periods (noted $I$ ).

**Value**

`histpos.t` gives a  $2^t - 1$  by  $t$  matrix with rows representing capture histories. This matrix contains only zeros and ones.

`histpos.0` gives a  $(t_1 + 1) \times (t_2 + 1) \times \dots \times (t_I + 1) - 1$  by  $I$  matrix with rows representing possible capture histories in terms of number of captures. This matrix elements are integers between 0 and  $t_i$  inclusively.

**Note**

The `histpos.t` function is called by [descriptive](#), [closedp](#), [closedp.bc](#), [closedp.Mtb](#), [openp](#), [robustd.t](#).

The `histpos.0` function is called by [robustd.0](#).

**Author(s)**

Sophie Baillargeon (Sophie.Baillargeon@mat.ulaval.ca) and  
Louis-Paul Rivest (Louis-Paul.Rivest@mat.ulaval.ca)

**References**

Baillargeon, S. and Rivest, L.P. (2007) Rcapture: Loglinear models for capture-recapture in R. *Journal of Statistical Software*, **19**(5), <http://www.jstatsoft.org/v19/i05>.

**See Also**

[periodhist](#), [descriptive](#)

**Examples**

```
histpos.t(5)
histpos.0(5)

histpos.0(rep(5, 3))
```

**Description**

Epidemiological capture-recapture data on HIV from four reporting centers in Rome, Italy.

**Usage**

```
data(HIV)
```

**Format**

15 by 5 numeric matrix, with the following columns:

**c1, c2, c3, c4** Capture histories for the four capture occasions

**freq** Observed frequencies for each capture history

**Details**

The capture histories are obtained by linking the records of the four reporting centers.

Each row of this data set represents an observed capture history followed by its frequency.

**Source**

Abeni, D.A., Brancato, G. and Perucci, C. A. (1994) Capture-recapture to estimate the size of the population with human immunodeficiency virus type 1 infection. *Epidemiology*, **5**, 410–414.

**References**

Baillargeon, S. and Rivest, L.P. (2007) Rcapture: Loglinear models for capture-recapture in R. *Journal of Statistical Software*, **19**(5), <http://www.jstatsoft.org/v19/i05>.

**Examples**

```
data(HIV)
desc<-descriptive(HIV,dfreq=TRUE)
desc
# 1774 out of 1896 individuals (94%) appear on one list only.

plot(desc)
# The fi plot is linear showing that heterogeneity is not a problem.
# Models with a time (or list) effect and possible pairwise dependencies
# between lists will be considered.

mat<-histpos.t(4)
mX1<-cbind(mat,mat[,1]*mat[,2],mat[,1]*mat[,3],mat[,1]*mat[,4],
           mat[,2]*mat[,3],mat[,2]*mat[,4],mat[,3]*mat[,4])
cp.m1<-closedpCI.t(HIV,dfreq=TRUE,mX=mX1,mname="Mt double interaction")
```

```

cp.m1
# The model fits well. Let's find out which interactions are important.
summary(cp.m1$glm)$coefficients
# Eliminating the non significant interactions stepwise shows that only
# the [1,2] interaction is important.

mX2<-cbind(mat,mat[,1]*mat[,2])
closedpCI.t(HIV,dfreq=TRUE,mX=mX2,mname="Mt interaction 1,2")

```

---

mvole

---

*Robust Design Data for Adult Male Meadow Voles*


---

### Description

This data set contains robust design capture history data for adult male meadow voles.

### Usage

```
data(mvole)
```

### Format

171 by 30 numeric matrix, with the following columns:

**c11, c12, c13, c14, c15** Capture histories for the 5 capture occasions within primary period 1  
**c21, c22, c23, c24, c25** Capture histories for the 5 capture occasions within primary period 2  
**c31, c32, c33, c34, c35** Capture histories for the 5 capture occasions within primary period 3  
**c41, c42, c43, c44, c45** Capture histories for the 5 capture occasions within primary period 4  
**c51, c52, c53, c54, c55** Capture histories for the 5 capture occasions within primary period 5  
**c61, c62, c63, c64, c65** Capture histories for the 5 capture occasions within primary period 6

### Details

The data set is extracted from Table 19.1 of Williams, Nichols and Conroy (2002). The capture occasions represent five consecutive days of trapping each month from June to December 1981 at Patuxent Wildlife Research Center, Laurel, Maryland.

Each row of this data set represents the capture history of one animal.

### Note

In this data set, ten animals are in fact not released after capture. These trap deaths are not identified.

### Source

Williams, B.K., Nichols, J.D., and Conroy, M.J. (2002) *Analysis and Management of Animal Populations*, San Diego: Academic Press.

## References

Baillargeon, S. and Rivest, L.P. (2007) Rcapture: Loglinear models for capture-recapture in R. *Journal of Statistical Software*, **19**(5), <http://www.jstatsoft.org/v19/i05>.

## Examples

```
# First, a between primary period Jolly-Seber analysis is obtained.
data(mvole)
mvole.pp<-periodhist(mvole,vt=rep(5,6))
op.m1<-openp(mvole.pp,dfreq=TRUE)
plot(op.m1)
# There is one large residual, removing the corresponding capture history
# from the analysis does not change the results. The model fits well.
keep2<-residuals(op.m1$glm,type="pearson")<4
op.m2<-openp(mvole.pp,dfreq=TRUE,keep=keep2)
op.m2$model.fit

# To find a suitable model within each primary period, the function closedp
# can be used repeatedly. Heterogeneity is detected in all periods except
# the second one where the data collection was perturbed (the last capture
# occasion doesn't have any new capture and is taken out of the analysis).

# In a robust design, we use Mh models for all primary periods bearing in
# mind the questionable fit in the second one. Since there is no time effect
# within primary periods, we use the function robustd.0 to fit the model.
### The following command might take a few minutes to run.
rd.m1<-robustd.0(mvole[,-10], vt=c(5,4,rep(5,4)),vm="Mh",vh="Chao")
rd.m1$model.fit
rd.m1$emig.fit
# The test for temporary immigration is not significant meaning that capture
# probabilities estimated with the Jolly-Seber model are not different from
# those estimated with the individual closed population models. The
# differences, on the logit scale, of the Jolly-Seber minus the closed
# population models capture probabilities are
rd.m1$emig.param
# Even in period 2, where the closed population model does not fit well, the
# difference on the logit scale is non significant (estimate=.59, s.e.=1.12).

# The following command allows to fit a robust design that does not specify
# any model for the second period.
### The following command might take a few minutes to run.
rd.m3<-robustd.0(mvole[,-10], vt=c(5,4,rep(5,4)),vm=c("Mh","none","Mh","Mh",
"Mh","Mh"),vh="Chao")

# With Darroch's model, the closed population estimates of the capture
# probabilities are significantly smaller than those obtained from the
# Jolly-Seber model. This cannot be interpreted as indicating temporary
# immigration. This suggests that Darroch's model is not appropriate within
# primary sessions.

# The smallest AIC is obtained with the Poisson model, with parameter a=1.5
# within sessions.
```

```
rd.m4<-robustd.0(mvole[,-10], vt=c(5,4,rep(5,4)),vm="Mh",vh="Poisson",vtheta=1.5)
# The estimators of the demographic parameters obtained with the robust design
# are similar to those obtained with the Jolly-Seber model applied to the
# between primary period data.
cbind(op.m1$survivals,rd.m4$survivals)
cbind(op.m1$N,rd.m4$N)
cbind(op.m1$birth,rd.m4$birth)
cbind(op.m1$Ntot,rd.m4$Ntot)
```

---

openp

*Loglinear Models for Open Population Capture-Recapture Experiments*


---

### Description

This function computes various demographic parameters using a loglinear model for open populations in capture-recapture experiments.

### Usage

```
openp(X, dfreq=FALSE, m=c("up","ep"), neg=TRUE, keep=rep(TRUE,2^I-1))

## S3 method for class 'openp':
print(x, ...)

## S3 method for class 'openp':
plot(x, main="Scatterplot of Pearson Residuals", ...)
```

### Arguments

X	The matrix of the observed capture histories (see <a href="#">Rcapture-package</a> for a description of the accepted formats).
dfreq	A logical. By default FALSE, which means that X has one row per unit. If TRUE, it indicates that the matrix X contains frequencies in its last column.
m	This argument is a character string taking the value "up" (up = unconstrained probabilities) or "ep" (ep = equal probabilities). If m is set to "up" (the default), no constraint is fixed on the loglinear parameters. Therefore some loglinear and demographic parameters are not estimable. On the other hand, when m takes the value "ep", the capture probabilities are set to a common value; this enables the estimation of all the parameters.
keep	This option is useful to fit the model on a subset of the possible capture histories. keep is a logical vector of length $2^I - 1$ taking the value TRUE for a history kept and FALSE for a history put aside. In this vector, the order of the capture histories is as defined in the <code>histpos.t</code> function. By default, every capture history is kept.

<code>neg</code>	If this option is set to TRUE, relevant negative gamma parameters are set to zero. This insures that the estimated survival probabilities belong to [0, 1] and that the births are positive.
<code>x</code>	An object, produced by the <code>openp</code> function, to print or to plot.
<code>main</code>	A main title for the plot
<code>...</code>	Further arguments to be passed to methods (see <code>print.default</code> and <code>plot.default</code> ).

### Details

The function `openp` generates statistics to test the presence of a trap effect.

The `plot.openp` function produces a scatterplot of the Pearson residuals of the model versus the frequencies of capture.

If the data matrix  $X$  was obtained through the `periodhist` function, the `dfreq` argument must be set to TRUE.

Standard errors are calculated by linearization.

### Value

<code>n</code>	The number of captured units
<code>model.fit</code>	A table containing the deviance, degrees of freedom and AIC of the fitted model.
<code>trap.fit</code>	A table containing, for the models with an added trap effect, the deviance, degrees of freedom and AIC.
<code>trap.param</code>	The estimated trap effect parameters and their standard errors. For <code>m="up"</code> , the $I-3$ first rows of <code>trap.param</code> are estimations of the differences $\text{logit}(\text{capture probability after a capture}) - \text{logit}(\text{capture probability after a miss})$ for periods 3 to $I-1$ . The last row gives a pooled estimate of these differences calculated under the assumption that they are homogenous.
<code>capture.prob</code>	The estimated capture probabilities per period and their standard errors.
<code>survivals</code>	The estimated survival probabilities between periods and their standard errors.
<code>N</code>	The estimated population sizes per period and their standard errors.
<code>birth</code>	The estimated number of new arrivals in the population between periods and their standard errors.
<code>Ntot</code>	The estimated total number of units who ever inhabited the survey area and its standard error.
<code>glm</code>	The 'glm' object obtained from fitting the loglinear model
<code>loglin.param</code>	The loglinear model parameters estimations and their standard errors, calculated by the <code>glm</code> function.
<code>u.vector</code>	The $U_i$ statistics, useful for the survival probabilities calculation, and their standard errors
<code>v.vector</code>	The $V_i$ statistics, useful for the population sizes estimation, and their standard errors
<code>cov</code>	The covariance matrix of all the demographic parameters estimates.
<code>neg</code>	The position of the gamma parameters set to zero in the loglinear parameter vector.

**Note**

If your data contains more than one capture occasion within primary periods, use the `periodhist` function to create the input data matrix  $X$  needed by the `openp` function.

This function uses the `glm` function of the `stats` package.

**Author(s)**

Sophie Baillargeon (Sophie.Baillargeon@mat.ulaval.ca) and  
Louis-Paul Rivest (Louis-Paul.Rivest@mat.ulaval.ca)

**References**

Baillargeon, S. and Rivest, L.P. (2007) Rcapture: Loglinear models for capture-recapture in R. *Journal of Statistical Software*, **19**(5), <http://www.jstatsoft.org/v19/i05>.

Rivest, L.P. and Daigle, G. (2004) Loglinear models for the robust design in mark-recapture experiments. *Biometrics*, **60**, 100–107.

**See Also**

`closedp`, `periodhist`, `robustd`

**Examples**

```
data(duck)
op.m1 <- openp(duck, dfreq=TRUE)
plot(op.m1)

# To remove the capture history 111111.
keep2 <- apply(histpos.t(6), 1, sum) != 6
op.m2 <- openp(duck, dfreq=TRUE, keep=keep2)
op.m2

# To remove the capture histories with 5 captures or more
keep3 <- apply(histpos.t(6), 1, sum) < 5
op.m3 <- openp(duck, dfreq=TRUE, keep=keep3)
op.m3

data(mvole)
mvole.op <- periodhist(mvole, vt=rep(5, 6))
openp(mvole.op, dfreq=TRUE)
```

**Description**

This function produces a reduced matrix of capture histories from a complete one by merging together some capture occasions.

It can also be used to change the format of a capture-recapture data set with complete capture histories: it transforms a data set with one row per captured unit to a data set with one row per capture history followed by its frequency.

**Usage**

```
periodhist(X, dfreq=FALSE, vt, drop=TRUE)
```

**Arguments**

X	The matrix of the observed capture histories (see <a href="#">Rcapture-package</a> for a description of the accepted formats).
dfreq	A logical. By default FALSE, which means that X has one row per unit. If TRUE, it indicates that the matrix X contains frequencies in its last column.
vt	A vector containing the numbers of capture occasions for each pooled capture occasions. The length of this vector equals the number of capture occasions in the reduced matrix (noted $I$ ).
drop	A logical, by default TRUE, meaning that in the output matrix the unobserved capture histories having a frequency of 0 are omitted. To keep them, drop must be set to FALSE.

**Details**

This function is useful when using an open population model to analyse a robust design data set. It can be used to reduce the data set to one observation per primary period. The observation is one for a unit caught at least once during the period and zero for a unit never caught.

It is also useful for experiments with a large number of capture occasions but a limited number of catches, especially when there is no capture on some occasions. In such cases, one can pool together some capture occasions with the `periodhist` function.

If a data matrix produced by the `periodhist` function is given in argument to an model fitting function, the `dfreq` argument must be set to TRUE.

**Value**

A  $2^I - 1$  by  $I + 1$  matrix of all the pooled capture histories, with their observed frequencies.

**Author(s)**

Sophie Baillargeon <Sophie.Baillargeon@mat.ulaval.ca> and  
Louis-Paul Rivest <Louis-Paul.Rivest@mat.ulaval.ca>

**References**

Baillargeon, S. and Rivest, L.P. (2007) Rcapture: Loglinear models for capture-recapture in R. *Journal of Statistical Software*, **19**(5), <http://www.jstatsoft.org/v19/i05>.

**See Also**[openp](#)**Examples**

```
data(mvole)
mvole.op<-periodhist(mvole,vt=rep(5,6))
openp(mvole.op, dfreq=TRUE)
```

profileCI

---

*Profile Likelihood Confidence Interval for Abundance Estimation in Closed Populations Capture-Recapture Experiments*

---

**Description**

This function is deprecated, please use `closedpCI.t` instead.

The `profileCI` function computes the multinomial profile likelihood for the abundance of some closed population capture-recapture models.

**Usage**

```
profileCI(X, dfreq=FALSE, m="M0", h="Chao", a=2, mX=NULL,
          mname="Customized model", neg=TRUE, alpha=0.05)

## S3 method for class 'profileCI':
print(x, ...)
```

**Arguments**

- |       |  |
|-------|--|
| X     | The table of the observed capture histories in one of the two accepted formats. In the default format, it has one row per unit captured in the experiment. In this case, the number of columns in the table represents the number of capture occasions in the experiment (noted $t$ ). In the alternative format, it contains one row per capture history followed by its frequency. In that case, X has $t+1$ columns. The first $t$ columns of X, identifying the capture histories, must contain only zeros and ones. The number one indicates a capture. |
| dfreq | This argument specifies the format of the data matrix X. By default, it is set to "FALSE", which means that X has one row per unit. If it is set to TRUE, then the matrix X contains frequencies in its last column.   |
| m     | A character string identifying the model, either "M0"=M0 model, "Mt"=Mt model, "Mh"=Mh model or "Mth"=Mth model.   |
| h     | A character string ("Chao" = Chao model, "Poisson" = $2^k - 1$ ), "Darroch" = $(k^2)/2$ or a numerical function taking only one argument specifying the form of the column for heterogeneity in the design matrix.   |
| a     | The value of the exponent's base for a Poisson model.  |

mX	The design matrix of the loglinear model. In this matrix, the order of the capture histories is as defined in the <code>histpos.t</code> function.
mname	A character string specifying the name of the customized model.
neg	If this option is set to TRUE, negative eta parameters in Chao models are set to zero.
alpha	A confidence interval with confidence level $1-\alpha$ is constructed. The value of alpha must be between 0 and 1; the default is 0.05.
x	An object, produced by the <code>profileCI</code> function, to print.
...	Further arguments passed to or from other methods.

### Details

This function does not work for closed population models featuring a behavioral effect, such as Mb and Mbh.

### Value

This function produces a plot of the multinomial profile likelihood for N. The value of N maximizing the profile likelihood and the bounds of the confidence interval are identified. It also produces the following objects :

n	The number of captured units
results	A table containing the abundance estimation and its confidence interval.
alpha	1-the confidence level of the interval.

### Author(s)

Sophie Baillargeon (sbailar@mat.ulaval.ca) and Louis-Paul Rivest (lpr@mat.ulaval.ca)

### References

- Baillargeon, S. and Rivest, L.P. (2007) Rcapture: Loglinear models for capture-recapture in R. *Journal of Statistical Software*, **19**(5), <http://www.jstatsoft.org/v19/i05>.
- Cormack, R. M. (1992) Interval estimation for mark-recapture studies of closed populations. *Biometrics*, **48**, 567–576.

### See Also

[closedp](#), [closedp.mX](#), [closedp.h](#)

### Examples

```
data(hare)
profileCI(hare, m = "Mth", h = "Poisson", a = 2)

data(HIV)
mat<-histpos.t(4)
mX2<-cbind(mat,mat[,1]*mat[,2])
```

```
profileCI(hare,m="Mh",h="Chao")
```

---

rbvole

*Robust Design Data for Red-Back Voles*

---

### Description

This data set contains robust design capture history data for red-back voles.

### Usage

```
data(rbvole)
```

### Format

66 by 19 numeric matrix, with the following columns:

**c11, c12, c13** Capture histories for the three capture occasions within primary period 1

**c21, c22, c23** Capture histories for the three capture occasions within primary period 2

**c31, c32, c33** Capture histories for the three capture occasions within primary period 3

**c41, c42, c43** Capture histories for the three capture occasions within primary period 4

**c51, c52, c53** Capture histories for the three capture occasions within primary period 5

**c61, c62, c63** Capture histories for the three capture occasions within primary period 6

**freq** Observed frequencies for each capture history

### Details

Data collection was carried out by Etcheverry and al.. The capture occasions represent three consecutive days of trapping in May 1999, July 1999, August 1999, May 2000, July 2000 and August 2000 in the Duchénier conservation area in southeastern Quebec. This data set is analysed in Rivest and Daigle (2004).

Each row of this data set represents an observed capture history followed by its frequency.

### References

Rivest, L.P. and Daigle, G. (2004) Loglinear models for the robust design in mark-recapture experiments. *Biometrics*, **60**, 100–107.

## Examples

```
# According to Rivest and Daigle (2004), a good robust design model
# for this data set is formed of an Mth Chao model for each period.
# This model can be fitted as follows.

### data(rbvole)
### memory.limit(size=2000)
### rd<-robustd.t(rbvole,dfreq=TRUE,vt=rep(3,6),vm="Mth",vh="Chao")

# WARNING : Because the data has 18 capture occasions, fitting this
# model uses a lot of memory. Its runtime is several minutes long.
```

---

robustd	<i>Loglinear Models for Capture-Recapture Experiments Carried Out According to a Robust Design</i>
---------	--

---

## Description

These functions compute various demographic parameters and capture probabilities per period using loglinear robust design models in capture-recapture experiments.

`robustd.t` and `robustd.0` fit the model using different response variable. `robustd.t` uses the frequencies of the observable capture histories in terms of capture success or failure for each capture occasions of each primary period. `robustd.0` uses the frequencies of the observable capture histories in terms of number of captures per primary period.

## Usage

```
robustd.t(X, dfreq = FALSE, vt, vm = "M0", vh = list("Chao"),
          vtheta = 2, neg = TRUE)

robustd.0(X, dfreq = FALSE, vt, vm = "M0", vh = list("Chao"),
          vtheta = 2, neg = TRUE)

## S3 method for class 'robustd':
print(x, ...)
```

## Arguments

<code>X</code>	The matrix of the observed capture histories (see <a href="#">Rcapture-package</a> for a description of the accepted formats).
<code>dfreq</code>	A logical. By default FALSE, which means that <code>X</code> has one row per unit. If TRUE, it indicates that the matrix <code>X</code> contains frequencies in its last column.
<code>vt</code>	A vector containing the numbers of capture occasions for each primary sampling period. The length of this vector equals the number of primary sampling periods (noted $I$ ).

<code>vm</code>	A vector indicating the closed population model for each primary period. The elements of <code>vm</code> can be "none"=no model, "M0"=M0 model, "Mt"=Mt model, "Mh"=Mh model or "Mth"=Mth model for <code>robustd.t</code> . For <code>robustd.0</code> , models with time effect are not allowed. So <code>vm</code> can than be "none"=no model, "M0"=M0 model, or "Mh"=Mh model. The 'no model' cannot be selected for the first or the last period. If a single character string is given for <code>vm</code> , the corresponding model is used for all periods. The default value for <code>vm</code> is "M0" for all period.
<code>vh</code>	A list indicating, for each primary period with a heterogeneity model, the form of the columns for heterogeneity in the design matrix. The elements of <code>vh</code> can be "Chao", "Poisson", "Darroch" or any numerical R function created beforehand by the user. "Chao" represents Chao's model, "Poisson" represents the function $f(k) = \theta^k - 1$ , where $k$ is the number of captures, "Darroch" represents the function $f(k) = k^2/2$ , and "Gamma" represents the function $f(k) = -\log(\theta + k) + \log(\theta)$ . If an R function is given, it is the implementation of any convex mathematical function $f(k)$ . It has only one argument. For the Poisson or Gamma model, the parameter <code>theta</code> is specified in the argument <code>vtheta</code> .
<code>vtheta</code>	A vector indicating, for each primary period with a Poisson or Gamma heterogeneity model, the value of the parameter. If <code>vtheta</code> consists of a single number, this number is used for all the periods with a Poisson or Gamma model. The default value for <code>vtheta</code> is 2 for all the periods with a Poisson or Gamma model.
<code>neg</code>	If this option is set to TRUE, negative gamma parameters and negative eta parameters in Chao's models are set to zero. This insures that the estimated survival probabilities belong to $[0, 1]$ and that the births are positive.
<code>x</code>	An object, produced by the <code>robustd.t</code> or the <code>robustd.0</code> function, to print.
<code>...</code>	Further arguments to be passed to <code>print.default</code> .

### Details

These functions also generate statistics to test the presence of temporary emigration.

The Poisson regression used to fit a robust design model has one entry for each possible capture history, including those that are unobserved. The size of the dependent vector is therefore  $2^{\text{sum}(vt)} - 1$  for `robustd.t`. Models with a large `sum(vt)` are hard to fit with `robustd.t`. `robustd.0` uses a more parsimonious coding for the capture histories and can fit larger models.

Standard errors are calculated by linearization.

### Value

<code>n</code>	The number of captured units
<code>models</code>	A vector of length $I$ identifying the closed population models chosen for each period.
<code>model.fit</code>	A table containing the deviance, degrees of freedom and AIC of the fitted model.
<code>emig.fit</code>	A table containing, for the model with an added temporary emigration effect, the deviance, degrees of freedom and AIC.

emig.param	The estimated temporary emigration parameters and their standards errors. The $I - 1$ first rows are estimations of the differences $\text{logit}(p^b) - \text{logit}(p^w)$ for periods 2 to $I - 1$ ( $p^b$ represents a between primary period and $p^w$ a within primary period estimate of the capture probability). The last row gives a pooled estimate of these differences calculated under the assumption that they are homogenous. Negative estimates are associated with a temporary emigration.
capture.prob	The estimated capture probabilities per period and their standard errors.
survivals	The estimated survival probabilities between periods and their standard errors.
N	The estimated population sizes per period and their standard errors.
birth	The estimated number of new arrivals in the population between periods and their standard errors.
Ntot	The estimated total number of units who ever inhabited the survey area and its standard error.
loglin.param	The loglinear model parameters estimations and their standard errors, calculated by the <code>glm</code> function.
u.vector	The $U_i$ statistics, useful for the survival probabilities calculation, and their standard errors
v.vector	The $V_i$ statistics, useful for the population sizes estimation, and their standard errors
cov	The covariance matrix of all the demographic parameters estimates.
neg	The position of the gamma and eta parameters set to zero in the loglinear parameter vector.

**Note**

This function uses the `glm` function of the `stats` package.

**Author(s)**

Sophie Baillargeon (Sophie.Baillargeon@mat.ulaval.ca) and  
Louis-Paul Rivest (Louis-Paul.Rivest@mat.ulaval.ca)

**References**

- Baillargeon, S. and Rivest, L.P. (2007) Rcapture: Loglinear models for capture-recapture in R. *Journal of Statistical Software*, **19**(5), <http://www.jstatsoft.org/v19/i05>.
- Rivest, L.P. and Daigle, G. (2004) Loglinear models for the robust design in mark-recapture experiments. *Biometrics*, **60**, 100–107.

**See Also**

[closedp](#), [openp](#)

**Examples**

```

data(mvole)

# The mvole data set contains a total of 30 capture occasions (the
# tenth capture occasion doesn't have any new capture and is taken
# out of the analysis). This number being large, we can only use
# the robustd.0 function to fit a robust design model.
robustd.0(mvole[, -10], vt=c(5, 4, rep(5, 4)), vm="Mh", vh="Poisson", vtheta=1.5)
# Not run:
# robustd.t(mvole[, -10], vt=c(5, 4, rep(5, 4)), vm="Mh", vh="Poisson", vtheta=1.5)
# should fail

# Considering only the first 3 periods of the data set, we can use the
# robustd.t function to fit a model with a temporal effect.
robustd.t(mvole[, c(1:9, 11:15)], vt=c(5, 4, 5), vm="Mth", vh="Poisson", vtheta=1.5)

```

---

uifit

*Closed Population Models Fit Statistics Concerning the  $u_i$* 


---

**Description**

This function produces fit statistics concerning the  $u_i$ , i.e. the numbers of first captures on each capture occasion, for closed population models. It also forecasts, for some models, the number of additional units that would be captured if the experiment was continued for five more occasions.

**Usage**

```
uifit(x.closedp)
```

**Arguments**

`x.closedp` An object produced by the `closedp.t` function.

**Value**

`predicted` The observed and predicted values of the  $u_i$  frequencies,  $i = 1, \dots, t$ , for each model in `closedp`. For models M0, Mh Poisson2, Mh Darroch and Mb, predicted values are also extrapolated for  $i = t + 1, \dots, t + 5$ .

`fit.stat` Chi-square fit statistics for each model in `closedp` ( $\sum_{i=1}^t \frac{(\text{observed}_i - \text{predicted}_i)^2}{\text{predicted}_i}$ ).

`day.first.capt` The mean and variance of the day of first capture, calculated with the observed and predicted  $u_i$ , for each model in `closedp`.

**Author(s)**

Sophie Baillargeon (Sophie.Baillargeon@mat.ulaval.ca) and  
Louis-Paul Rivest (Louis-Paul.Rivest@mat.ulaval.ca)

**References**

Baillargeon, S. and Rivest, L.P. (2007) Rcapture: Loglinear models for capture-recapture in R. *Journal of Statistical Software*, **19**(5), <http://www.jstatsoft.org/v19/i05>.

**See Also**

[closedp](#)

**Examples**

```
data(mvole)
period3<-mvole[,11:15]
cp <- closedp(period3)
uifit(cp)
```

# Index

## \*Topic **datasets**

BBS2001, 4  
bunting, 5  
catb, 6  
duck, 22  
hare, 24  
HIV, 26  
mvole, 27  
rbvole, 35

## \*Topic **manip**

histpos, 25  
periodhist, 32

## \*Topic **models**

closedp, 7  
closedp.bc, 11  
closedp.custom, 13  
closedp.Mtb, 15  
closedpCI, 16  
openp, 29  
profileCI, 33  
robustd, 36

## \*Topic **package**

Rcapture-package, 1

## \*Topic **univar**

descriptive, 20  
uifit, 39

BBS2001, 4

boxplot.closedp (*closedp*), 7

boxplot.closedp.custom  
(*closedp.custom*), 13

boxplot.closedpCI (*closedpCI*), 16

bunting, 5

catb, 6

closedp, 7, 13, 15, 16, 19, 25, 31, 35, 39, 40

closedp.bc, 9, 10, 11, 18, 25

closedp.custom, 13

closedp.h, 35

closedp.h (*closedp.custom*), 13

closedp.Mtb, 10, 15, 15, 18, 19, 25

closedp.mX, 35

closedp.mX (*closedp.custom*), 13

closedp.t, 18

closedpCI, 16

closedpCI.0, 9, 10

closedpCI.t, 9, 10, 16

descriptive, 20, 25, 26

duck, 22

hare, 24

histpos, 25

HIV, 26

mvole, 27

openp, 25, 29, 33, 39

periodhist, 26, 31, 32

plot.closedp (*closedp*), 7

plot.closedpCI (*closedpCI*), 16

plot.descriptive (*descriptive*), 20

plot.openp (*openp*), 29

plotCI (*closedpCI*), 16

print.closedp (*closedp*), 7

print.closedp.bc (*closedp.bc*), 11

print.closedp.custom  
(*closedp.custom*), 13

print.closedp.Mtb (*closedp.Mtb*),  
15

print.closedpCI (*closedpCI*), 16

print.descriptive (*descriptive*),  
20

print.openp (*openp*), 29

print.profileCI (*profileCI*), 33

print.robustd (*robustd*), 36

profileCI, 33

rbvole, 35

Rcapture (*Rcapture-package*), 1

Rcapture-package, 8, 11, 14, 15, 17, 20,  
29, 32, 37

Rcapture-package, 1

robustd, 31, 36

robustd.0, 25

robustd.t, 25

uifit, 10, 39