

# Package ‘CloNcaSe’

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**Type** Package

**Title** Estimation of Effective Size and Sex Rate of a Partially Clonal Population

**Version** 2.0

**Date** 2015-07-07

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## Description

Nc (effective size) and s (sex rate) estimator. Code to estimate effective size and sex rate of a partially clonal population sampled at two different times. The samples are supposed to be separated by several clonal cycles and one mixed (i.e. sexual-clonal) cycle.

**License** GPL-3

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CloNcaSe-package	<i>Estimation of effective size and sex rate of a partially clonal population</i>
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## Description

CloNcaSe: Nc (effective size) and s (sex rate) estimator. Code to estimate effective size (Nc) and sex rate (s) of a partially clonal population sampled at two different times. The samples are supposed to be separated by several clonal cycles and one mixed (i.e. sexual-clonal) cycle.

## Details

Package: CloNcaSe  
Type: Package  
Version: 2.0  
Date: 2015-07-07  
License: GPL-3

The main function of this package is the function [ncase](#).

## Author(s)

Samuel Soubeyrand

Maintainer: Samuel Soubeyrand <Samuel.Soubeyrand@avignon.inra.fr>

## References

Ali S, Soubeyrand S, Gladieux P, Giraud T, Leconte M, Gautier A, Mboup M, de Vallavieille-Pope C and Enjalbert J (2015). CloNcaSe: Estimation of sex frequency and effective population size by clonemate re-sampling in partially clonal organisms. Research Report.

## See Also

[ncase](#), [simul](#), [ncase4simul](#).

## Examples

```
## Yellow rust data
data(yellowrust)

## Point estimates
ncase(yellowrust, nb1ClonalCycles=17, nb2ClonalCycles=7,
start=expand.grid(c(100, 1000), c(0.2, 0.8)))
```

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ncase

*Function for estimating effective size (Nc) and sex rate (s)*

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## Description

This function computes point estimates of  $N_c$  and  $s$  for a partially clonal population, confidence intervals (using parametric bootstrap) and the coverage rates of the intervals. The parametric bootstrap is also used to propose a bias correction of the point estimates and their confidence intervals.

## Usage

```
ncase(counts, nb1ClonalCycles, nb2ClonalCycles, start.param, maxit = 500,
nbBootstrap = 0, conf.level = 0.95, nbCoverage = 0, trace = TRUE)
```

**Arguments**

<code>counts</code>	2-column matrix whose 1st (resp. 2nd) column gives the counts of strains in sample 1 (resp. 2).
<code>nb1ClonalCycles</code>	Non-negative integer indicating the number of clonal cycles separating the 1st sample and the mixed (i.e. clonal-sexual) cycle.
<code>nb2ClonalCycles</code>	Non-negative integer indicating the number of clonal cycles separating the mixed (i.e. clonal-sexual) cycle and the 2nd sample.
<code>start.param</code>	2-column matrix whose rows give initial values for the effective size ( $N_c$ ) and the sex rate ( $s$ ) that are used in the optimization of the contrast.
<code>maxit</code>	Maximum number (non-negative integer) of iterations in the optimization of the contrast. Default to 500.
<code>nbBootstrap</code>	Number (non-negative integer) of bootstrap replications to assess confidence intervals (based on a normal approximation) and to carry out a bias correction. Default to 0 (no bootstrap procedure).
<code>conf.level</code>	Confidence level (between 0 and 1) of the marginal confidence intervals for $N_c$ and $s$ . Default to 0.95. Used if <code>nbBootstrap</code> >0.
<code>nbCoverage</code>	Number of (non-negative integer) iterations to assess the coverage rates of the marginal confidence intervals. Default to 0 (no coverage assessment). Used if <code>nbBootstrap</code> >0.
<code>trace</code>	Logical indicating if tracing information are displayed (TRUE) or not displayed (FALSE). Default to TRUE. Tracing information consist of a message every 100 iterations in the bootstrap procedure and in the assessment of the coverage rates of the confidence intervals.

**Details**

The optimization method that is used is the Nelder and Mead (1965) method implemented in the `optim` function (stats package).

**Value**

A list whose items are:

<code>bootstrap.estim</code>	(if <code>nbBootstrap</code> >0) Estimates of $N_c$ (1st col.) and $s$ (2nd col.) obtained for bootstrap replications.
<code>cover</code>	(if <code>nbCoverage</code> >0) Coverage rates of the marginal intervals for $N_c$ and $s$ when no bias correction is applied (1st col.) and when bias correction is applied (2nd col.).
<code>optim.output</code>	A list consisted of (i) the output of the <code>optim</code> function ( <code>optim</code> is applied to the logarithm of $N_c$ and the logit of $s$ ) and (ii) the optimal values of $N_c$ and $s$ (transformed back to the original units of $N_c$ and $s$ ).
<code>estimates</code>	A numeric vector providing the estimates of $N_c$ and $s$ (if <code>nbBootstrap</code> =0) or a matrix providing the estimates of $N_c$ and $s$ , their bias-corrected versions, and the associated confidence intervals (if <code>nbBootstrap</code> >0).

**Author(s)**

Samuel Soubeyrand

## References

Ali S, Soubeyrand S, Gladioux P, Giraud T, Leconte M, Gautier A, Mboup M, de Vallavieille-Pope C and Enjalbert J (2015). CloNcaSe: Estimation of sex frequency and effective population size by clonemate re-sampling in partially clonal organisms. Research Report.

## See Also

[simul](#), [ncase4simul](#).

## Examples

```
## Yellow rust data
data(yellowrust)

## Point estimates
ncase(yellowrust,nb1ClonalCycles=17,nb2ClonalCycles=7,
start=expand.grid(c(100,1000),c(0.2,0.8)))

## Point estimates, Parametric bootstrap, Bias correction
## and confidence intervals

ncase(yellowrust,nb1ClonalCycles=17,nb2ClonalCycles=7,
start=expand.grid(c(100,1000),c(0.2,0.8)),
nbBootstrap=5000,conf.level=0.95)

## Point estimates, Parametric bootstrap, Bias correction
## and confidence intervals and their coverage

ncase(yellowrust,nb1ClonalCycles=17,nb2ClonalCycles=7,
start=expand.grid(c(100,1000),c(0.2,0.8)),
nbBootstrap=5000,conf.level=0.95,nbCoverage=100)
```

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ncase4simul	<i>Function estimating effective size (Nc) and sex rate (s) for simulated data</i>
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## Description

This function simulates the evolution and the sampling of a partially clonal population, and computes raw point estimates of  $N_c$  and  $s$  for each simulated data set.

## Usage

```
ncase4simul(param, nb1ClonalCycles, nb2ClonalCycles, nb1Sample, nb2Sample,
start.counts, nbPrelCycles, nbSimul, start.param, maxit = 500, trace = TRUE)
```

## Arguments

`param` 2-component numeric vector with the values of  $N_c$  and  $s$  used for the simulations.

<code>nb1ClonalCycles</code>	Non-negative integer indicating the number of clonal cycles separating the 1st sample and the mixed (i.e. clonal-sexual) cycle.
<code>nb2ClonalCycles</code>	Non-negative integer indicating the number of clonal cycles separating the mixed (i.e. clonal-sexual) cycle and the 2nd sample.
<code>nb1Sample</code>	Non-negative integer indicating the size of the 1st sample.
<code>nb2Sample</code>	Non-negative integer indicating the size of the 2nd sample.
<code>start.counts</code>	Vectors of non-negative integers providing counts of strains used to initialize the simulations.
<code>nbPrelCycles</code>	Number of preliminary series of cycles (one series consists of <code>nb1ClonalCycles</code> clonal cycles, 1 mixed cycle and <code>nb2ClonalCycles</code> clonal cycles) performed before the collection of the 1st sample.
<code>nbSimul</code>	Non-negative integer giving the number of simulated data sets that are generated and for which <code>Nc</code> and <code>s</code> are estimated.
<code>start.param</code>	2-column matrix whose rows give initial values for <code>Nc</code> and <code>s</code> that are used in the optimization of the contrast.
<code>maxit</code>	Maximum number (non-negative integer) of iterations in the optimization of the contrast. Default to 500.
<code>trace</code>	Logical indicating if tracing information are displayed (TRUE) or not displayed (FALSE). Default to TRUE.

### Details

The optimization method that is used is the Nelder and Mead (1965) method implemented in the `optim` function (stats package).

### Value

A 4-column matrix with true `Nc` (1st col.), true `s` (2nd col.), the raw estimate of `Nc` (3rd col.) and the raw estimate of `s` (4th col.). The raw estimates are the estimates of `Nc` and `s` without bias correction. The matrix contains as many lines as the number of simulations requested by the argument `nbSimul`.

### Author(s)

Samuel Soubeyrand

### References

Ali S, Soubeyrand S, Gladieux P, Giraud T, Leconte M, Gautier A, Mboup M, de Vallavieille-Pope C and Enjalbert J (2015). CloNcaSe: Estimation of sex frequency and effective population size by clonemate re-sampling in partially clonal organisms. Research Report.

Nelder J A and Mead R (1965). A simplex algorithm for function minimization. *Computer Journal* 7: 308-313.

### See Also

[simul](#), [ncase](#).

**Examples**

```
## count data used to initialize the simulations
counts1=c(20,10,5,1,1,1,1,1)

## simulation and raw estimation
ncase4simul(param=c(1000,0.5),nb1ClonalCycles=17,nb2ClonalCycles=7,
            nb1Sample=200,nb2Sample=200,start.counts=counts1,nbPrelCycles=5,
            nbSimul=100,start.param=expand.grid(c(100,1000),c(0.2,0.8)))
```

simul

*Function simulating data sets***Description**

This function simulates the evolution and the sampling of a partially clonal population.

**Usage**

```
simul(start.counts, param, nb1ClonalCycles, nb2ClonalCycles, nb1Sample, nb2Sample,
      nbPrelCycles)
```

**Arguments**

<code>start.counts</code>	Vectors of non-negative integers providing counts of strains used to initialize the simulations.
<code>param</code>	2-component numeric vector with the values of $N_c$ and $s$ used for the simulations.
<code>nb1ClonalCycles</code>	Non-negative integer indicating the number of clonal cycles separating the 1st sample and the mixed (i.e. clonal-sexual) cycle.
<code>nb2ClonalCycles</code>	Non-negative integer indicating the number of clonal cycles separating the mixed (i.e. clonal-sexual) cycle and the 2nd sample.
<code>nb1Sample</code>	Non-negative integer indicating the size of the 1st sample.
<code>nb2Sample</code>	Non-negative integer indicating the size of the 2nd sample.
<code>nbPrelCycles</code>	Number of preliminary series of cycles (one series consists of <code>nb1ClonalCycles</code> clonal cycles, 1 mixed cycle and <code>nb2ClonalCycles</code> clonal cycles) performed before the collection of the 1st sample.

**Value**

A list consisted of:

<code>population</code>	Counts of strains in the population at the 1st and 2nd sampling dates.
<code>samples</code>	Counts of sampled strains in the population at the 1st and 2nd sampling dates.
<code>statistics</code>	Numeric vector providing the following statistics: the empirical probabilities of sampling two clonemates at the 1st and 2nd sampling dates (1st and 2nd components of the vector), and the empirical probability that two random isolates, the 1st one being collected at the 1st sampling date and the 2nd one being collected at the 2nd sampling date, are clonemates (5th component of the vector). The 3rd and 4th components of the vector can be ignored.

**Author(s)**

Samuel Soubeyrand

**References**

Ali S, Soubeyrand S, Gladieux P, Giraud T, Leconte M, Gautier A, Mboup M, de Vallavieille-Pope C and Enjalbert J (2015). CloNcaSe: Estimation of sex frequency and effective population size by clonemate re-sampling in partially clonal organisms. Research Report.

**See Also**

[ncase4simul](#).

**Examples**

```
## count data used to initialize the simulation
counts1=c(20,10,5,1,1,1,1,1)

## simulated data set
simul(start.counts=counts1,param=c(1000,0.8),nb1ClonalCycles=17,nb2ClonalCycles=7,
nb1Sample=100,nb2Sample=100,nbPrelCycles=5)
```

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yellowrust

*Yellow rust data set*

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**Description**

Counts of strains of yellow rust disease collected at two different sampling dates.

**Usage**

```
data("yellowrust")
```

**Format**

The format is: num [1:436, 1:2] 18 0 1 7 6 0 3 3 1 0 ... - attr(\*, "dimnames")=List of 2 ..\$ : NULL  
..\$ : chr [1:2] "counts1" "counts2"

**Details**

yellowrust is a 2-column matrix whose 1st column gives the counts of strains of yellow rust disease collected at 1st sampling date and 2nd column gives the counts of strains of yellow rust disease collected at 2nd sampling date.

**Source**

Ali S, Soubeyrand S, Gladieux P, Giraud T, Leconte M, Gautier A, Mboup M, de Vallavieille-Pope C and Enjalbert J (2015). CloNcaSe: Estimation of sex frequency and effective population size by clonemate re-sampling in partially clonal organisms. Research Report.

**References**

Ali S, Soubeyrand S, Gladioux P, Giraud T, Leconte M, Gautier A, Mboup M, de Vallavieille-Pope C and Enjalbert J (2015). CloNcaSe: Estimation of sex frequency and effective population size by clonemate re-sampling in partially clonal organisms. Research Report.

**Examples**

```
data(yellowrust)  
yellowrust
```



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