Package ‘SPAS’

December 2, 2019

Type Package

Title Stratified-Petersen Analysis System

Version 2020.1.1

Date 2020-01-01

Author Carl James Schwarz

Maintainer Carl James Schwarz <cschwarz.stat.sfu.ca@gmail.com>

LinkingTo TMB, RcppEigen

Imports BB, MASS, Matrix, msm, numDeriv, plyr, TMB (>= 1.7.15)

Description The Stratified-Petersen Analysis System (SPAS) is designed to estimate abundance in two-sample capture-recapture experiments where the capture and recaptures are stratified. This is a generalization of the simple Lincoln-Petersen estimator. Strata may be defined in time or in space or both, and the s strata in which marking takes place may differ from the t strata in which recoveries take place. When s=t, SPAS reduces to the method described by Darroch (1961) <https://www.jstor.org/stable/2332748>. When s<t, SPAS implements the methods described in Plante, Rivest, and Tremblay (1988) <https://www.jstor.org/stable/2533994>. Schwarz and Taylor (1998) <doi:10.1139/f97-238> describe the use of SPAS in estimating return of salmon stratified by time and geography. A related package, BTSPAS, deals with temporal stratification where a spline is used to model the distribution of the population over time as it passes the second capture location. This is the R-version of the (now obsolete) standalone Windows program available at <http://www.cs.umanitoba.ca/~popan/spas/spas_home.html>.

License GPL (>= 2)

RoxygenNote 7.0.1

Suggests knitr, rmarkdown

VignetteBuilder knitr
Description

This function fits a Stratified-Petersen (Plante, 1996) to data and specify which rows/columns of the data should be pooled. The number of rows after pooling should be <= number of columns after pooling.

Usage

```r
SPAS.fit.model(
  model.id = "Stratified Petersen Estimator",
  rawdata,
  row.pool.in,
  col.pool.in,
  row.physical.pool = TRUE,
  theta.pool = FALSE,
  CJSpool = FALSE,
  optMethod = c("nlminb"),
  optMethod.control = list(maxit = 50000),
  svd.cutoff = 1e-04,
  chisq.cutoff = 0.1
)
```

Arguments

- `model.id`: Character string identifying the name of the model including any pooling.
- `rawdata`: An (s+1) x (t+1) of the raw data BEFORE pooling. The s x t upper left matrix is the number of animals released in row stratum i and recovered in column stratum j. Row s+1 contains the total number of UNMARKED animals recovered in column stratum j. Column t+1 contains the number of animals marked in each row stratum but not recovered in any column stratum. The rawdata[s+1, t+1] is
not used and can be set to 0 or NA. The sum of the entries in each of the first
s rows is then the number of animals marked in each row stratum. The sum of
the entries in each of the first t columns is then the number of animals captured
(marked and unmarked) in each column stratum. The row/column names of the
matrix may be set to identify the entries in the output.

row.pool.in, col.pool.in
Vectors (character/numeric) of length s and t respectively. These identify the
rows/columns to be pooled before the analysis is done. The vectors consists of
entries where pooling takes place if the entries are the same. For example, if s=4,
then row.pool.in = c(1,2,3,4) implies no pooling because all entries are distinct;
row.pool.in=c("a","a","b","b") implies that the first two rows will be pooled and
the last two rows will be pooled. It is not necessary that row/columns be con-
tinuous to be pooled, but this is seldom sensible. A careful choice of pooling labels
helps to remember what as done, e.g. row.pool.in=c("123","123","123","4") in-
dicates that the first 3 rows are pooled and the 4th row is not pooled. Character
entries ensure that the resulting matrix is sorted properly (e.g. if row.pool.in=c(123,123,123,4),
then the same pooling is done, but the matrix rows are sorted rather strangely.

row.physical.pool
Should physical pooling be done (default) or should logical pooling be done. For
example, if there are 3 rows in the data matrix and row.pool.in=c(1,1,3), then in
physical pooling, the entries in rows 1 and 2 are physically added together to
create 2 rows in the data matrix before fitting. Because the data has changed,
you cannot compare physical pooling using AIC. In logical pooling, the data
matrix is unchanged, but row parameters p1=p2 but the movement parameters
for the rest of the matrix are not forced equal.

theta.pool, CJSpool
NOT YET IMPLEMENTED. DO NOT CHANGE.

optMethod
What optimization method is used. Defaults is the nlminb() function..

optMethod.control
Control parameters for optimization method. See the documentation on the dif-
ferent optimization methods for details.

svd.cutoff
When finding the variance-covariance matrix, a singular value decomposition is
used. This identifies the smallest singular value to retain.

chisq.cutoff
When finding a goodness of fit statistic using (obs-exp)^2/exp, all cell whose
Exp < gof.cutoff are ignored to try and remove structural zero cells.

Value
A list with many entries. Refer to the vignettes for more details.

Examples

```r
conne.data.csv <- textConnection(" 9 , 21 , 0 , 0 , 0 , 0 , 171 0 , 101 , 22 , 1 , 0 , 0 , 763 0 , 0 , 128 , 49 , 0 , 0 , 934 0 , 0 , 48 , 12 , 0 , 0 , 434 0 , 0 , 0 , 7 , 0 , 0 , 49")
```

SPAS.fit.model.legacy

SPAS.fit.model.legacy

`SPAS.fit.model.legacy`  
*Fit a Stratified-Petersen (SP) model using the legacy method without TMB. The preferred method is to use the `SPAS.fit.model()` function that used TMB.*

**Description**

This function fits a Stratified-Petersen (Plante, 1996) to data and specify which rows/columns of the data should be pooled. The number of rows after pooling should be <= number of columns after pooling.

**Usage**

```r
SPAS.fit.model.legacy(  
  model.id = "Stratified Petersen Estimator",  
  rawdata,  
  row.pool.in,  
  col.pool.in,  
  row.physical.pool = TRUE,  
  theta.pool = FALSE,  
  CJSpool = FALSE,  
  sd.noise.init.est = 0,  
  optMethod = c("BBoptim", "optim"),  
  optMethod.control = list(maxit = 50000, ftol = 1e-09, gtol = 1e-05),  
  svd.cutoff = 1e-04,  
  chisq.cutoff = 0.1  
)
```

**Arguments**

- `model.id`  
  Character string identifying the name of the model including any pooling.

- `rawdata`  
  An (s+1) x (t+1) of the raw data BEFORE pooling. The s x t upper left matrix is the number of animals released in row stratum i and recovered in column stratum j. Row s+1 contains the total number of UNMARKED animals recovered in column stratum j. Column t+1 contains the number of animals marked in each row stratum but not recovered in any column stratum. The rawdata[s+1, t+1] is not used and can be set to 0 or NA. The sum of the entries in each of the first s rows is then the number of animals marked in each row stratum. The sum of

```r
corne.data <- as.matrix(read.csv(corne.data.csv, header=FALSE))
close(corne.data.csv)
mod1 <- SPAS.fit.model(corne.data, model.id="Pooling rows 1/2, 5/6; pooling columns 5/6",  
  row.pool.in=c("12", "12", "3", "4", "56", "56"),  
  col.pool.in=c(1,2,3,4,56,56))
```
the entries in each of the first t columns is then the number of animals captured (marked and unmarked) in each column stratum. The row/column names of the matrix may be set to identify the entries in the output.

row.pool.in, col.pool.in
Vectors (character/numeric) of length s and t respectively. These identify the rows/columns to be pooled before the analysis is done. The vectors consists of entries where pooling takes place if the entries are the same. For example, if s=4, then row.pool.in = c(1,2,3,4) implies no pooling because all entries are distinct; row.pool.in=c("a","a","b","b") implies that the first two rows will be pooled and the last two rows will be pooled. It is not necessary that row/columns be continuous to be pooled, but this is seldom sensible. A careful choice of pooling labels helps to remember what as done, e.g. row.pool.in=c("123","123","123","4") indicates that the first 3 rows are pooled and the 4th row is not pooled. Character entrie ensure that the resulting matrix is sorted properly (e.g. if row.pool.in=c(123,123,123,4), then the same pooling is done, but the matrix rows are sorted rather strangely.

row.physical.pool
Should physical pooling be done (default) or should logical pooling be done. For example, if there are 3 rows in the data matrix and row.pool.in=c(1,1,3), then in physical pooling, the entries in rows 1 and 2 are physically added together to create 2 rows in the data matrix before fitting. Because the data has changed, you cannot compare physical pooling using AIC. In logical pooling, the data matrix is unchanged, but now parameters p1=p2 but the movement parameters for the rest of the matrix are not forced equal.

theta.pool, CJSpool
NOT YET IMPLEMENTED. DO NOT CHANGE.

sd.noise.init.est
How much random noise should be added to the initial (least squares) estimates. Normally only used with severe convergence problems.

optMethod
What optimization method is used. Defaults is the BBoptim function from the BB package.

optMethod.control
Control parameters for optimization method. See spg() function in BB package or optim() function for details. For BBoptim, a suggest control parameter for debugging is optMethod.control=list(M=20, trace=TRUE , maxit = 50000, ftol=10^-5).

svd.cutoff
When finding the variance-covariance matrix, a singular value decomposition is used. This identifies the smallest singular value to retain.

chisq.cutoff
When finding a goodness of fit statistic using (obs-exp)^2/exp, all cell whose Exp < gof.cutoff are ignored to try and remove structural zero cells.

Value
A list with many entries. Refer to the vignettes for more details.

Examples
conne.data.csv <- textConnection("

SPAS.print.model

Print the results from a fit of a Stratified-Petersen (SP) model when using the TMB optimizer

Description

This function makes a report of the results of the model fitting.

Usage

SPAS.print.model(x)

Arguments

x

A result from the model fitting. See SPAS.fit.model.

Value

A report to the console. Refer to the vignettes.

Examples

conne.data.csv <- textConnection("9 , 21 , 0 , 0 , 0 , 0 , 171
0 , 101 , 22 , 1 , 0 , 0 , 763
0 , 0 , 128 , 49 , 0 , 0 , 934
0 , 0 , 0 , 48 , 12 , 0 , 434
0 , 0 , 0 , 7 , 0 , 0 , 49
0 , 0 , 0 , 0 , 0 , 0 , 4
351 , 2736 , 3847 , 1818 , 543 , 191 , 0")
conne.data <- as.matrix(read.csv(conne.data.csv, header=FALSE))
close(conne.data.csv)

mod1 <- SPAS.fit.model.legacy(conne.data, model.id="Pooling rows 1/2, 5/6; pooling columns 5/6",
   row.pool.in=c("12","12","3","4","56","56"),
   col.pool.in=c(1,2,3,4,56,56),
   optMethod.control=list(ftol=.0001))

conne.data <- as.matrix(read.csv(conne.data.csv, header=FALSE))
close(conne.data.csv)

mod1 <- SPAS.fit.model(conne.data, model.id="Pooling rows 1/2, 5/6; pooling columns 5/6",
   row.pool.in=c("12","12","3","4","56","56"),
   col.pool.in=c(1,2,3,4,56,56),
   optMethod.control=list(ftol=.0001))
SPAS.print.model.legacy

Print the results from a fit of a Stratified-Petersen (SP) model from the legacy (i.e. pre using TMB) code

Description

This function makes a report of the results of the model fitting.

Usage

SPAS.print.model.legacy(x)

Arguments

x

A result from the model fitting. See SPAS.fit.model.

Value

A report to the console. Refer to the vignettes.

Examples

conne.data.csv <- textConnection("  9 ,  21 ,  0 ,  0 ,  0 ,  0 ,  0 ,  171  0 ,  101 ,  22 ,  1 ,  0 ,  0 ,  763  0 ,  0 ,  128 ,  49 ,  0 ,  0 ,  934  0 ,  0 ,  0 ,  48 ,  12 ,  0 ,  434  0 ,  0 ,  0 ,  0 ,  7 ,  0 ,  49  0 ,  0 ,  0 ,  0 ,  0 ,  0 ,  4  351,  2736 ,  3847 ,  1818 ,  543 ,  191 ,  0")  conne.data <- as.matrix(read.csv(conne.data.csv, header=FALSE))  close(conne.data.csv)

mod1 <- SPAS.fit.model.legacy(conne.data, model.id="Pooling rows 1/2, 5/6; pooling columns 5/6",  row.pool.in=c("12","12","3","4","56","56"),  col.pool.in=c(1,2,3,4,56,56),  optMethod.control=list(ftol=.0001))

SPAS.print.model.legacy(mod1)
Index

SPAS.fit.model, 2
SPAS.fit.model.legacy, 4
SPAS.print.model, 6
SPAS.print.model.legacy, 7