Package ‘spiders’

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spiders-package

Fits predator preferences model.

Description
Models predator preferences over an array of time and prey species

Details

Package: spiders
Type: Package
Version: 1.0
Date: 2014-04-30
License: GPL

Author(s)
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References
Reliability Estimates for Ivlev’s Electivity Index, the Forage Ratio, and a Proposed Linear Index of Food Selection Richard E. Strauss Transactions of the American Fisheries Society Vol. 108, Iss. 4, 1979

Examples

```r
## make up some numbers
Predators <- 20
Traps <- 20
PreySpecies <- 3
Times <- 12
ST <- Times*PreySpecies
```
calcHypotheses

calculate hypotheses

description

calculates hypotheses, given a user specified null and alternative

usage

calcHypotheses(hyp, Xdst, Ydst, J, I, balanced, EM, em_maxiter)

arguments

hyp a 2-tuple specifying the null and alternative hypotheses, respectively
Xdst matrix of sums of number of eaten prey species s during occurrence t; rows
indexed by time, and cols indexed by prey species, TxS
Ydst matrix sum of number of caught prey species s during occurrence t; rows indi-
exted by time, and cols indexed by prey species, TxS
J vector of predators caught in each time period
I vector of number of days all traps were left out in a given time period
balanced boolean specifying balanced data or not
EM boolean specifying if EM algorithm should be used
em_maxiter maximum number of iterations allowed for EM algorithm

checkHypotheses

description

function to check user specified hypotheses

usage

checkHypotheses(hyp)

arguments

hyp a 2-tuple specifying the null and alternative hypotheses, respectively
**Description**

checks convergence of the parameters for the estimation functions

**Usage**

\[
\text{converged}(\theta, \theta_{old}, \text{eps} = 1e^{-05})
\]

**Arguments**

- **theta**: an object, convertible to a matrix, of current parameter values
- **theta_old**: an object, convertible to a matrix, of old parameter values
- **eps**: tolerance to determine convergence

**est1**

*estimate hypothesis c_{st} = 1*

**Description**

estimates parameters from hypothesis lambda = gamma

**Usage**

\[
est1(X_{dst}, Y_{dst}, J, I, \text{EM}, \text{em_maxiter}, \text{BALANCED})\]

**Arguments**

- **X_{dst}**: matrix of sums of number of eaten prey species s during occurrence t; rows indexed by time, and cols indexed by prey species, TxS
- **Y_{dst}**: matrix sum of number of caught prey species s during occurrence t; rows indexed by time, and cols indexed by prey species, TxS
- **J**: vector of predators caught in each time period
- **I**: vector of number of days all traps were left out in a given time period
- **EM**: boolean; whether or not EM algorithm is used
- **em_maxiter**: integer specifying max number of EM iterations
- **BALANCED**: boolean; whether or not data are BALANCED

**Details**

There are S*T free parameters under this hypothesis.
estC

**Description**

estimate parameters from hypothesis $\lambda = c^{\ast}\gamma$

**Usage**

`estC(Xdst, Ydst, J, I, EM, em_maxiter, BALANCED)`

**Arguments**

- **Xdst**: matrix of sums of number of eaten prey species $s$ during occurrence $t$; rows indexed by time, and cols indexed by prey species, $T \times S$
- **Ydst**: matrix sum of number of caught prey species $s$ during occurrence $t$; rows indexed by time, and cols indexed by prey species, $T \times S$
- **J**: vector of predators caught in each time period
- **I**: vector of number of days all traps were left out in a given time period
- **EM**: boolean; whether or not EM algorithm is used
- **em_maxiter**: integer specifying max number of EM iterations
- **BALANCED**: boolean; whether or not data are BALANCED

**Details**

There are $S \times T + 1$ free parameters under this hypothesis.

---

estCs

**Description**

estimates parameters from hypothesis $\lambda_s = c_s \times \gamma_s$

**Usage**

`estCs(Xdst, Ydst, J, I, EM, em_maxiter, BALANCED)`

**Arguments**

- **Xdst**: matrix of sums of number of eaten prey species $s$ during occurrence $t$; rows indexed by time, and cols indexed by prey species, $T \times S$
- **Ydst**: matrix sum of number of caught prey species $s$ during occurrence $t$; rows indexed by time, and cols indexed by prey species, $T \times S$
- **J**: vector of predators caught in each time period
- **I**: vector of number of days all traps were left out in a given time period
- **EM**: boolean; whether or not EM algorithm is used
- **em_maxiter**: integer specifying max number of EM iterations
- **BALANCED**: boolean; whether or not data are BALANCED
**Arguments**

- **Xdst**: matrix of sums of number of eaten prey species \( s \) during occurrence \( t \); rows indexed by time, and cols indexed by prey species, \( T \times S \)
- **Ydst**: matrix sum of number of caught prey species \( s \) during occurrence \( t \); rows indexed by time, and cols indexed by prey species, \( T \times S \)
- **J**: vector of predators caught in each time period
- **I**: vector of number of days all traps were left out in a given time period
- **EM**: boolean; whether or not EM algorithm is used
- **em_maxiter**: integer specifying max number of EM iterations
- **BALANCED**: boolean; whether or not data are BALANCED

**Details**

There are \( S \times T + S \) free parameters under this hypothesis.

---

**estCst**

*estimate hypothesis c_st*

---

**Description**

estimates parameters from hypothesis \( \lambda = c_{st} \times \gamma \)

**Usage**

```r
estCst(Xdst, Ydst, J, I, EM, em_maxiter, BALANCED)
```

**Arguments**

- **Xdst**: matrix of sums of number of eaten prey species \( s \) during occurrence \( t \); rows indexed by time, and cols indexed by prey species, \( T \times S \)
- **Ydst**: matrix sum of number of caught prey species \( s \) during occurrence \( t \); rows indexed by time, and cols indexed by prey species, \( T \times S \)
- **J**: vector of predators caught in each time period
- **I**: vector of number of days all traps were left out in a given time period
- **EM**: boolean; whether or not EM algorithm is used
- **em_maxiter**: integer specifying max number of EM iterations
- **BALANCED**: boolean; whether or not data are BALANCED

**Details**

There are \( 2 \times S \times T \) free parameters under this hypothesis.
estCt

**Description**

estimates parameters from hypothesis \( \lambda_t = c_t \cdot \gamma_t \)

**Usage**

\[ \text{estCt}(X_{dst}, Y_{dst}, J, I, EM, \text{em\_maxiter}, \text{BALANCED}) \]

**Arguments**

- \( X_{dst} \) matrix of sums of number of eaten prey species \( s \) during occurrence \( t \); rows indexed by time, and cols indexed by prey species, \( T \times S \)
- \( Y_{dst} \) matrix sum of number of caught prey species \( s \) during occurrence \( t \); rows indexed by time, and cols indexed by prey species, \( T \times S \)
- \( J \) vector of predators caught in each time period
- \( I \) vector of number of days all traps were left out in a given time period
- \( \text{EM} \) boolean; whether or not EM algorithm is used
- \( \text{em\_maxiter} \) integer specifying max number of EM iterations
- \( \text{BALANCED} \) boolean; whether or not data are BALANCED

**Details**

There are \( S \times T + T \) free parameters under this hypothesis.

estGen

**Description**

estimate a reparameterization of the hypothesis \( c_{st} \)

**Usage**

\[ \text{estGen}(X_{dst}, Y_{dst}, J, I, EM, \text{em\_maxiter}, \text{BALANCED}) \]

**Description**

estimates parameters from hypothesis \( \lambda \neq \gamma \), where \( \lambda \) is independent of \( \gamma \)

**Usage**

\[ \text{estGen}(X_{dst}, Y_{dst}, J, I, EM, \text{em\_maxiter}, \text{BALANCED}) \]
Arguments

Xdst  matrix of sums of number of eaten prey species s during occurrence t; rows indexed by time, and cols indexed by prey species, TxS
Ydst  matrix sum of number of caught prey species s during occurrence t; rows indexed by time, and cols indexed by prey species, TxS
J     vector of predators caught in each time period
I     vector of number of days all traps were left out in a given time period
EM    boolean; whether or not EM algorithm is used
em_maxiter integer specifying max number of EM iterations
BALANCED boolean; whether or not data are BALANCED

Details

There are $2*S*T$ free parameters under this hypothesis.

---

getTimeCounts  sum specified columns by time

---

Description

sum specified columns by time

Usage

g getTimeCounts(data, vars)

Arguments

data  a dataframe
vars  column variables in data to sum over

---

ll  observed count log-likelihood of predator preferences model

---

Description

log-likelihood of fully observed count data predator preferences model

Usage

ll(Xdst, Ydst, lambda, gamma, J, I, c = NULL)
Arguments

\( X_{dst} \) matrix of sums of number of eaten prey species \( s \) during occurrence \( t \); rows indexed by time and cols indexed by prey species, \( T \times S \)

\( Y_{dst} \) matrix sum of number of caught prey species \( s \) during occurrence \( t \); rows indexed by time and cols indexed by prey species, \( T \times S \)

\( \lambda \) matrix of parameters representing rates predator ate prey species \( s \) in time period \( t \); \( T \times S \)

\( \gamma \) matrix of parameters representing rates traps caught prey species \( s \) in time period \( t \); \( T \times S \)

\( J \) vector of predators caught in each time period

\( I \) vector of number of days all traps were left out in a given time period

\( c \) scalar in null hypotheses

\texttt{llem} \quad \textit{non-observed count log-likelihood of predators preferences}

Description

log-likelihood for non-observed count data; model with EM

Usage

\texttt{llem}(Z_{dst}, Y_{dst}, \lambda, \gamma, J, I, c = \text{NULL})

Arguments

\( Z_{dst} \) matrix of sums of indicators whether or not predator ate prey species \( s \) during occurrence \( t \); \( T \times S \)

\( Y_{dst} \) matrix sum of number of caught prey species \( s \) during occurrence \( t \); \( T \times S \)

\( \lambda \) matrix of parameters representing rates predator ate prey species \( s \) in time period \( t \); \( T \times S \)

\( \gamma \) matrix of parameters representing rates traps caught prey species \( s \) in time period \( t \); \( T \times S \)

\( J \) vector of predators caught in each time period

\( I \) vector of number of days all traps were left out in a given time period

\( c \) scalar in null hypotheses
Description

Estimates parameters of predator preferences model and calculates LRT. Eaten and caught dataframes are indexed with rows across time points and columns of prey species.

Usage

```
predPref(eaten, caught, hypotheses = c("c", "Ct"), alpha = 0.05, em_maxiter = 1000)
```

Arguments

- `eaten`: a dataframes of eatings preferences; TxS
- `caught`: a dataframes of caught prey species; TxS
- `hypotheses`: a 2-tuple specifying the null and alternative hypotheses, respectively
- `alpha`: LRT level of significance
- `em_maxiter`: maximum number of iterations allowed for EM algorithm

Value

A list of class ’predPref’ with the following elements:
- `null`: parameters as estimated under the specified null hypothesis.
- `alt`: parameters as estimated under the specified alternative hypothesis.
- `loglikH0`: the null hypothesis log-likelihood, with constants not accounted for.
- `loglikH1`: the alternative hypothesis log-likelihood, with constants not accounted for.
- `J`: a column vector of dimension T containing the number of predators in each time period.
- `I`: a column vector of dimension T containing the number of traps in each time period.
- `LRT`: the likelihood ratio test statistics.
- `hypotheses`: a 2-tuple of the user specified hypotheses.
- `data.name`: a character string giving the names of the data.

See Also

`simPref` `summary.predPref`
Examples

# set parameters
Predators <- Traps <- 100
PreySpecies <- 2
Times <- 5
g <- matrix(sqrt(2), nrow=Times, ncol=PreySpecies)  # gamma
l <- matrix(seq(0.4,1.8,length.out=5)*sqrt(2), nrow=Times, ncol=PreySpecies)  # ct

# fit model
## Not run:
 fdata <- simPref(PreySpecies, Times, Predators, Traps, l, g, EM=FALSE)
predPref(fdata$eaten, fdata$caught, hypotheses=c('ct', 'cst'))

## End(Not run)

Description

printing method for the summary function for class predPref

Usage

## S3 method for class 'summary.predPref'
print(x, ...)

Arguments

x  object of class predPref
...
  additional arguments

simPref       simulate data

Description

simulate data for predator preferences model

Usage

simPref(S, T, J, I, lambda, gamma, EM = F)
Arguments

S  number of prey species
T  number of time periods
J  scalar or vector (of length T) number of predators caught at each time
I  scalar or vector (of length T) effective number of traps at each time
lambda  matrix of rates at which predator eats prey species; TxS
gamma  matrix of rates at which prey species is seen in habitat; TxS
EM  boolean specifying test of EM algorithm

Details

Both lambda and gamma must be specified as a matrix with rows indexing time and columns indexing the number of species.

Value

A list consisting of two dataframes, eaten and caught, made specifically for the function predPref.

See Also

predPref

summary method for predPref objects as returned by the function predPref

Usage

# S3 method for class 'predPref'
summary(object, ..., sig.level = 0.05)

Arguments

object  predPref object as returned from predPref()
...  additional arguments
sig.level  significance level used in hypothesis test
sumSp

**Description**

sum over species to get a vector of values for each time period

**Usage**

```r
sumSp(mat)
```

**Arguments**

- `mat`: a matrix of values with columns indexing species

sumT

**Description**

sum over times to get a vector of values for each species

**Usage**

```r
sumT(mat)
```

**Arguments**

- `mat`: a matrix of values with rows indexing time

testC

**Description**

estimates linear contrasts of the elements of c, c_s, c_t, or c_st from a `predPref` object

**Usage**

```r
testC(x, b, mu = 0, alternative = c("two.sided", "less", "greater"), conf.level = 0.95, sig.level = 0.05)
```
Arguments

- **x**: a `predPref` object as fit by the eponymous function
- **b**: a vector to linearly transform `c_st`
- **mu**: a number to test the linear contrast against in the null
- **alternative**: string to specify alternative hypothesis
- **conf.level**: confidence level of the interval
- **sig.level**: determines null/alternative hypothesis value of `c_st` from `predPref`

Details

The input vector `b` performs the linear transformation `t(b) %*% matrix(c_st)`, so that `c_st` becomes a column vector by indexing `t` first and then `s`. Hence there is no requirement of a linear contrast, any linear transformation such that `t(b) %*% matrix(1, nrow=length(b)) != 0` is allowed.

Of the two estimated hypotheses in the underlying call to `predPref`, the linear transformation `b` is applied to the hypothesis that is determined by the choice of `sig.level`.

Value

A list with class '"htest"' containing the following components:
- **statistic**: the value of the t-statistic.
- **parameter**: the degrees of freedom for the t-statistic.
- **p.value**: the p-value for the test.
- **conf.int**: a confidence interval for the mean appropriate to the specified alternative hypothesis.
- **estimate**: the estimated mean or difference in means depending on whether it was a one-sample test or a two-sample test.
- **null.value**: the specified hypothesized value of the mean or mean difference depending on whether it was a one-sample test or a two-sample test.
- **alternative**: a character string describing the alternative hypothesis.
- **method**: a character string indicating what type of t-test was performed.
- **data.name**: a character string giving the names of the data.

Examples

```r
# set parameters
Predators <- Traps <- 100
PreySpecies <- 2
Times <- 5
g <- matrix(sqrt(2), nrow=Times, ncol=PreySpecies)  # gamma
l <- matrix(seq(0.4,1.8,length.out=5)*sqrt(2), nrow=Times, ncol=PreySpecies)  # ct

# fit model and contrast
## Not run:
set.seed(0)
ndata <- simPref(PreySpecies, Times, Predators, Traps, l, g, EM=FALSE) # p-value=0.305
pref <- predPref(ndata$eaten, ndata$caught, hypotheses=c('ct', 'cst'))
```
testC(pref, b = c(0, 1, -1, 0, 0)) # p-value > sig.level => ct is used, not cst

## End(Not run)
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