Package ‘hiddenf’

March 24, 2015

Type Package

Title The all-configurations, maximum interaction F-test for hidden additivity.

Version 1.2

Date 2015-03-24

Author Jason A. Osborne, Christopher T. Franck and Bongseog Choi

Maintainer Jason A. Osborne <jaosborn@ncsu.edu>

Description Computes the F-test and Bonferroni-adjusted p-value for a test of interaction in two-factor studies. Reports corresponding interaction plot and analysis of variance table and p-values from several other tests of non-additivity.

License GPL-2

R topics documented:

  hiddenf-package ......................................................... 2
  additivityPvalues ..................................................... 3
  anova.hiddenf .......................................................... 4
  Boik.mtx ................................................................. 5
  cjejuni.mtx ........................................................... 5
  cnv1.mtx ............................................................... 6
  cnvall.mtx ............................................................. 6
  Graybill.mtx ........................................................... 7
  hiddenf ................................................................. 7
  KKSAPvalue ............................................................ 8
  Malikfunction ......................................................... 9
  MalikPvalue ........................................................... 10
  MalikTab .............................................................. 11
  MandelPvalue .......................................................... 12
  plot.hiddenf ........................................................... 13
  print.hiddenf .......................................................... 14
  summary.hiddenf ....................................................... 15
  TukeyPvalue ............................................................ 16

Index 17
hiddenf-package

Tests for nonadditivity using the hidden F test

Description

Fits a linear model to a (b-by-t) matrix of responses. Includes factorial effects of two factors, with matrix rows as one blocking/grouped factor with b levels and matrix columns as t levels of a treatment/other factor. Configurations formed by placing rows into two groups and creating a third grouping factor. Linear models are fit for all c=2^(b-1)-1 possible configurations. The resulting p-value for group-by-treatment interaction is reported, after Bonferroni correction for multiplicity of configurations. An object of class ‘hiddenf’ is returned than can be used as an argument for plot(), print(), summary() and anova() functions and to compute p-values from other tests of non-additivity, using other functions included in the package.

Details

<table>
<thead>
<tr>
<th>Package:</th>
<th>hiddenf</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type:</td>
<td>Package</td>
</tr>
<tr>
<td>Version:</td>
<td>1.2</td>
</tr>
<tr>
<td>Date:</td>
<td>2015-03-06</td>
</tr>
<tr>
<td>License:</td>
<td>GPL-2</td>
</tr>
</tbody>
</table>

Author(s)

Jason A. Osborne, Christopher T. Franck and Bongseog Choi
Maintainer: Jason A. Osborne <jaosborn@ncsu.edu>

References


Examples

data(cnvl mtx)
cnvl hfout <- hiddenf(cnvl mtx)
anova(cnvl hfout)
additivityPvalues

additivityPvalues  Non-additivity pvalues

Description


Usage

additivityPvalues(ymtx.out)

Arguments

ymtx.out  An object of class hiddenf created by the hiddenf function.

Value

A list with five component p-values.

Author(s)

Jason A. Osborne <jaosborn@ncsu.edu>, Christopher T. Franck and Bongseog Choi

References


Examples

library(hhiddenf)
data(cjejuni.mtx)
cjejuni.out <- hiddenf(cjejuni.mtx)
pvalues <- additivityPvalues(cjejuni.out)
print(pvalues)
anova.hiddenf

Anova function for the class 'hiddenf'

Description

Reproduces the analysis of variance table corresponding to the configuration of levels of a blocking/grouped factor into two groups such that interaction between group and the treatment/other factor is maximized

Usage

## S3 method for class 'hiddenf'
anova(object, ...)  

Arguments

object       An object of class "hiddenf"
...

Value

anova.out     An object of class ‘anova’

Author(s)

Jason A. Osborne, Bongseog Choi and Christopher T. Franck

References


See Also

anova, lm

Examples

data(cjejuni.mtx)
cjejuni.out <- hiddenf(cjejuni.mtx)
anova(cjejuni.out)
### Boik.mtx

#### Multi-headed Machine Data

**Description**

Performance of a multiple-headed machine used to fill bottles. Weights for six heads on five occasions were recorded.

**Usage**

```r
data(Boik.mtx)
```

**Source**


**Examples**

```r
data(Boik.mtx)
Boik.out <- hiddenf(Boik.mtx)
anova(Boik.out)
```

### cjejunimtx

#### Annual prevalence of C.jejuni strain of Campylobacter

**Description**

Data are courtesy of Dr. Sophia Kathariou and Yucan Liu, North Carolina State University. The entries in the matrix are fractions of campylobacter strains sampled that were classified as C.jejuni. Data were collected over 5 year period across four turkey plants in North Carolina. Rows are plants, columns are years 2008-2012.

**Usage**

```r
data(cjejunimtx)
```

**Value**

matrix of C.jejuni fractions

**Examples**

```r
data(cjejunimtx)
cjejunimtx.out <- hiddenf(cjejunimtx)
plot(cjejunimtx.out)
```
cnv1.mtx  

*Copy Number Dataset, Probe #1*

**Description**

Data from an experiment (courtesy of Matthew Breen, N.C. State University) to study copy number variation in dogs. Experiment included thousands of probes, one of which is included here.

**Usage**

data(cnv1.mtx)

**Value**

cnv1.mtx  

Matrix of copy number measurements for one specific probe. Measured for two types of tissue (columns) on each of six dogs (rows) with lymphoma.

**Examples**

data(cnv1.mtx)  
cnv1.out <- hiddenf(cnv1.mtx)  
summary(cnv1.out)

cnvall.mtx  

*Copy Number Variation*

**Description**

Data from an experiment (courtesy of Dr. Matthew Breen, N.C. State University) to study copy number variation in dogs. Experiment included thousands of probes, several of which are included here, and indexed by the variable called 'dataset'.

**Usage**

data(cnvall.mtx)

**Value**

cnvall.mtx  

Matrix of copy number measurements for several probes. Measured for two types of tissue (columns) on each of six dogs (rows) with lymphoma. Copy Number measurements are one column in the matrix and it is not formatted for functions in "hiddenf" that require matrix input.

**Examples**

data(cnvall.mtx)  
cnvall.mtx  
cnv3.mtx <- matrix(cnvall.mtx[25:36,3],byrow=TRUE,nrow=12,ncol=2)  
cnv3.out <- hiddenf(cnv3.mtx)  
print(cnv3.out$pvalue)  
anova(cnv3.out)
Graybill.mtx  Wheat Yields

Description
Wheat yields from four genotypes in randomized block design with 13 locations.

Usage
data(Graybill.mtx)

Value
Graybill.mtx  Matrix of wheat yields, rows are locations, columns are genotypes

Source

Examples
## Not run:
data(Graybill.mtx)
Graybill.out <- hiddenf(Graybill.mtx)
plot(Graybill.out)

## End(Not run)

hiddenf  Hiddenf test for matrix data

Description
Fits linear model to ymtx, a matrix of responses from two-factor layouts. Constructs all possible configurations of rows(=blocks) into two groups, then fits full factorial effects model with factors group, column(=treatment) and row-nested-within-group. Maximum F-ratio for group-by-treatment interaction is reported along with Bonferroni-corrected p-value.

Usage
hiddenf(ymtx)

Arguments
ymtx  A matrix of responses, with rows corresponding to levels of the blocking/grouped factor to be put into two groups and columns corresponding to levels of the treatment/other factor
Details

Method does not accommodate more than b=20 rows

Value

List-object of class ‘hiddenf’ with components

- pvalues: Vector of pvalues, one for each configuration
- pvalue: (Bonferroni-adjusted) pvalue from configuration with maximal hidden additivity
- config: Integer giving the number of the maximal configuration
- config.vector: Vector of group indicators for maximal configuration
- tall: List with components y, block, trt
- cc: Number of possible configurations

Author(s)

Jason A. Osborne <jaosborn@ncsu.edu>, Christopher T. Franck and Bongseog Choi

References


See Also

plot.hiddenf, anova.hiddenf, summary.hiddenf, print.hiddenf

Examples

data(cjejuni mtx)
cjejuni.out <- hiddenf(cjejuni mtx)
summary(cjejuni.out)

<table>
<thead>
<tr>
<th>KKSAPvalue</th>
<th>Kharrati-Kopaei and Sadooghi-Alvandi’s test for non-additivity</th>
</tr>
</thead>
</table>

Description

Reports the p-value from Kharrati-Kopaei and Sadooghi-Alvandi’s test for non-additivity. This procedure searches over all configurations of rows of the input matrix into two non-empty sets, each having at least two elements. Separate linear models in which row and column effects are additive are fit to each set, and the configuration with maximum ratio of error mean squares is reported, along with a p-value.

Usage

KKSAPvalue(hfobj)

Arguments

- hfobj: An object of class hiddenf created by the hiddenf function
Malikfunction

Details

Requires that data matrix has more than four rows (b > 4)

Value

A list containing the input data matrix converted to list form, a numeric p-value from a test of the hypothesis of additivity, and a vector giving the corresponding configuration of rows into two groups.

Author(s)

Jason A. Osborne, Christopher T. Franck and Bongseog Choi

References


See Also

hiddenf, additivityPvalues

Examples

```r
library(hiddenf)
data(cjejuni mtx)
cjejuni.out <- hiddenf(cjejuni mtx)
KKSOut <- KKSAPvalue(cjejuni.out)
print(KKSA.out$pvalue)
```

---

Malikfunction

Function for Malik’s test for non-additivity

Description

Computes the p-value and various other quantities of interest from Malik’s clustering-based test for non-additivity.

Usage

```r
Malikfunction(hfobj, N=1000)
```

Arguments

- `hfobj` An object of class hiddenf created by the hiddenf function
- `N` The number of Monte Carlo datasets used to determine critical thresholds for Malik’s test statistic. Default value is N=1000.
MalikPvalue

Value
A list containing data as named vectors, numbers of factor levels, vector of simulated test statistics, and corresponding Monte Carlo estimate of the p-value from Malik’s test of additivity. The standard error of this estimate is inversely proportional to the square root of N.

Author(s)
Jason A. Osborne, Christopher T. Franck and Bongseog Choi

References

See Also
hiddenf, additivityPvalues

Examples
```r
## not run:
library(hiddenf)
data(cjejuni.mtx)
cjejuni.out <- hiddenf(cjejuni.mtx)
cjejuni.Malikout <- Malikfunction(cjejuni.out)
## end(Not run)
```

MalikPvalue

Malik’s test for non-additivity

Description
Computes the p-value from the clustering-based test for non-additivity developed in Malik, et al. (2015).

Usage
MalikPvalue(hfobj, N=1000)

Arguments
- `hfobj`: An object of class `hiddenf` created by the `hiddenf` function
- `N`: The number of Monte Carlo datasets used to determine critical thresholds for Malik’s test statistic. Default value is N=1000.

Value
A Monte Carlo estimate of the p-value from the Malik et al (2015) test of non-additivity. The standard error of this estimate is inversely proportional to the square root of N.
MalikTab

Author(s)
Jason A. Osborne, Christopher T. Franck and Bongseog Choi

References

See Also
hiddenf, additivityPvalues

Examples
library(hiddenf)
data(cjejuni mtx)
cjejuni.out <- hiddenf(cjejuni mtx)
cjejuni.MalikPvalue <- MalikPvalue(cjejuni.out)

MalikTab
Malik’s critical values

Description
This function computes Monte Carlo estimates of critical values for Malik’s test for non-additivity at significance levels .01, .05 and .1

Usage
MalikTab(t, b, N)

Arguments
  t     Number of levels of column factor
  b     Number of levels of row factor
  N     Number of additive datasets to be generated for Monte Carlo estimation of critical values

Value
A list with several components:

  tcsim  a random sample of N test statistics from Malik’s procedure under the hypothesis of additivity
  q      a vector with first two elements equal to the number of levels of the row and column factors, along with the 99th, 95th and 90th quantiles from the random sample

Author(s)
Jason A. Osborne, Christopher T. Franck and Bongseog Choi
MandelPvalue

References

See Also
MalikPvalue

Examples

# get critical values to conduct Malik's test of additivity
# in an experiment with row and column factors with 4 and 5 levels,
# respectively
## not run:
data(cjejuni.mtx)
cjejuni.out <- hiddenf(cjejuni.mtx)
Malik.pvalue <- MalikPvalue(cjejuni.out)
cjejuni.Malikobj <- Malikt4,5,N=1000)
print(cjejuni.Malikobj$q)
## end(Not run)

---

MandelPvalue

*Mandel's rows-linear test for non-additivity*

Description
Computes the p-value from Mandel's rows-linear test for non-additivity. (The columns-linear test may be conducted by first transposing the input matrix argument.)

Usage
MandelPvalue(hfobj)

Arguments

hfobj An object of class hiddenf created by the hiddenf function

Value
A p-value from a test of the hypothesis of additivity, along with component sums of squares used to compute p-value.

Author(s)
Jason A. Osborne and Christopher T. Franck and Bongseog Choi

References
**plot.hiddenf**

### Description

Interaction plot with blocks colored according to configuration that maximizes hidden additivity.

### Usage

```r
## S3 method for class 'hiddenf'
plot(x, y = NULL, main = "Hidden Additivity Plot", tfactor = "Treatment Factor",
     bfactor = "Blocking Factor", colorvec = c("black", "red"), legendx = FALSE, center = FALSE, ...)
```

### Arguments

- **x**: Object of class `hiddenf`
- **y**: Deprecated variable not used in this version of plot
- **main**: Plot Title
- **tfactor**: Label of variable (treatment factor) on the horizontal axis
- **bfactor**: Label of trace variable (blocking factor) for optional legend of the interaction plot
- **colorvec**: Vector of colors for the two groups in interaction plot
- **legendx**: Graphical parameter that allows for an optional legend, whose location is determined by point-and-click interface
- **center**: Center the data about the row means
- **...**: Allows for the use of other graphical parameters for matplot or legend

### Author(s)

Jason A. Osborne, Christopher T. Franck and Bongseog Choi

### See Also

`hiddenf`
Examples

data(cjejuni.mtx)
cjejuni.out <- hiddenf(cjejuni.mtx)
plot(cjejuni.out)

print.hiddenf

Printing hiddenf objects

Description

‘print’ method for class ‘hiddenf’

Usage

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

Arguments

x
An object of class ‘hiddenf’

... further arguments

Value

Fratio The F-statistic for group-by-treatment interaction
adjpvalue The corresponding Bonferroni-adjusted p-value

Author(s)

Jason A. Osborne, Christopher T. Franck and Bongseog Choi

References


See Also

hiddenf

Examples

data(cnv1.mtx)
cnv1.out <- hiddenf(cnv1.mtx)
print(cnv1.out)
Summary function for the class "hiddenf"

Description

Summarize the results of the hidden F-test for nonadditivity, gives configuration of rows into two groups and their corresponding column means.

Usage

```r
## S3 method for class 'hiddenf'
summary(object, ...)
```

Arguments

- `object`: An object of class "hiddenf"
- `...`: other arguments

Value

- `group1`: Vector of levels of blocking/grouped factor in group 1
- `group2`: Vector of levels of blocking/grouped factor in group 2
- `grp1means`: Vector of column means among rows in group 1
- `grp2means`: Vector of column means among rows in group 2

Author(s)

Jason A. Osborne, Christopher T. Franck and Bongseog Choi

References


See Also

- `hiddenf`

Examples

```r
data(Boik.mtx)
Boik.out <- hiddenf(Boik.mtx)
summary(Boik.out)
```
TukeyPvalue

Tukey’s single degree of freedom test for nonadditivity

Description

Reports the p-value from Tukey’s single degree of freedom test for non-additivity

Usage

TukeyPvalue(hfobj)

Arguments

hfobj An object of class hiddenf created by the hiddenf function

Value

A list with two components: (1) a numeric p-value from Tukey’s single degree of freedom test of the hypothesis of additivity and (2) an object of class ‘lm’ corresponding to the linear model additive in row and column effects.

Author(s)

Jason A. Osborne, Christopher T. Franck and Bongseog Choi

References


See Also

additivityPvalues

Examples

library(hiddenf)
data(cjejuni.mtx)
cjejuni.out <- hiddenf(cjejuni.mtx)
tukey.pvalue <- TukeyPvalue(cjejuni.out)
Index

*Topic anova
  anova.hiddenf, 4

*Topic datasets
  Boik.mtx, 5
  cjejuni.mtx, 5
  cnv1.mtx, 6
  cnvall.mtx, 6
  Graybill.mtx, 7

*Topic hidden additivity
  anova.hiddenf, 4
  plot.hiddenf, 13
  summary.hiddenf, 15

*Topic interaction plot
  plot.hiddenf, 13

*Topic non-additivity
  additivityPvalues, 3
  anova.hiddenf, 4
  hiddenf, 7
  KKSAPvalue, 8
  Malikfunction, 9
  MalikPvalue, 10
  MalikTab, 11
  MandelPvalue, 12
  print.hiddenf, 14
  TukeyPvalue, 16

additivityPvalues, 3
anova, 4
anova(anova.hiddenf), 4
anova.hiddenf, 4
Boik.mtx, 5
cjejuni.mtx, 5
cnv1.mtx, 6
cnvall.mtx, 6
Graybill.mtx, 7
hiddenf, 7, 13
hiddenf-package, 2
KKSAPvalue, 8
lm, 4
Malikfunction, 9
MalikPvalue, 10
MalikTab, 11
MandelPvalue, 12
plot(plot.hiddenf), 13
plot.hiddenf, 13
print(print.hiddenf), 14
print.hiddenf, 14
summary(summary.hiddenf), 15
summary.hiddenf, 15
TukeyPvalue, 16