Package 'MultiResponseR'

March 23, 2026

Title Analysis of Data from Multiple-Response Questionnaires

Version 1.4.1

Description Provides a multiple-response chi-square framework for the analysis of contingency tables arising from multiple-response questionnaires, such as check-all-that-apply tasks, where response options are crossed with a known grouping factor. The framework accommodates within-block (e.g., within-subject) designs, as commonly encountered in sensory evaluation. It comprises a multiple-response chi-square test of homogeneity with an associated dimensionality test, a multiple-response Correspondence Analysis (CA), and per-cell multiple-response hypergeometric tests. These methods extend their classical counterparts by grounding inference in a null model that properly accounts for the multiple-response nature of the data, treating evaluations, rather than individual citations, as the experimental units, yielding more statistically valid conclusions than standard contingency table analyses. Details may be found in Mahieu, Schlich, Visalli, and Cardot (2021). <doi:10.1016/j.foodqual.2021.104256>.

License GPL (>= 3)

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RoxygenNote 7.3.3

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Contents

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milkchoc   *Check-All-That-Apply data*

Description

Data coming from a Check-All-That-Apply experiment on milk chocolates. This dataset corresponds to the flavor data used as examples and described more precisely in Mahieu, Schlich, Visalli, and Cardot (2021)

Usage

```
data(milkchoc)
```

Format

An object of class data.frame with 280 rows and 8 columns.

References

Mahieu, B., Schlich, P., Visalli, M., & Cardot, H. (2021). A multiple-response chi-square framework for the analysis of Free-Comment and Check-All-That-Apply data. Food Quality and Preference, 93.

Examples

```
data(milkchoc)
```

---

mr.chisq.test   *Multiple-response chi-square test*

Description

Performs a multiple-response chi-square test as defined in Loughin and Scherer (1998) using random permutations to estimate the null distribution.

Usage

```
mr.chisq.test(data, nperm = 300)
```

Arguments

data
: A data.frame of observations in rows whose first column is a factor (the categories) and subsequent columns are binary numeric or integer, each column being a response option.

nperm
: Number of permuted datasets to estimate the distribution of the statistic under the null hypothesis. See details.

Details

- **nperm**: The distribution of the statistic under the null hypothesis of no associations between categories and response options is estimated using *nperm* datasets generated thanks to random permutations of the response vectors along observations. Note that this differs from the original proposition of Loughin and Scherer (1998) who used a parametric bootstrap to do so.

Value

A list with the following elements:

statistic Observed multiple-response chi-square statistic

p.value p-value of the test

References

Loughin, T. M., & Scherer, P. N. (1998). Testing for Association in Contingency Tables with Multiple Column Responses. Biometrics, 54(2), 630-637.

Mahieu, B., Schlich, P., Visalli, M., & Cardot, H. (2021). A multiple-response chi-square framework for the analysis of Free-Comment and Check-All-That-Apply data. Food Quality and Preference, 93.

Examples

```
nb.obs=200
nb.response=5
nb.category=5
vec.category=paste("C",1:nb.category,sep="")
right=matrix(rbinom(nb.response*nb.obs,1,0.25),nb.obs,nb.response)
category=sample(vec.category,nb.obs,replace = TRUE)
dset=cbind.data.frame(category,right)
dset$category=as.factor(dset$category)


mr.chisq.test(dset)
```

```
mr.dimensionality.test
```
Multiple-response dimensionality test

Description

Performs a multiple-response dimensionality test as defined in Mahieu, Schlich, Visalli, and Cardot (2021) using random permutations to estimate the null distribution.

Usage

```
mr.dimensionality.test(data, nperm = 300, alpha = 0.05)
```

Arguments

data	A data.frame of observations in rows whose first column is a factor (the categories) and subsequent columns are binary numeric or integer, each column being a response option.
nperm	Number of permuted datasets to estimate the distribution of the statistic under the null hypothesis. See details.
alpha	The alpha risk of the test

Details

- **nperm**: The distribution of the statistic under the null hypothesis of no associations between categories and response options is estimated using *nperm* datasets generated thanks to random permutations of the response vectors along observations.

Value

A list with the following elements:

dim.sig The number of significant dimensions

statistics Observed multiple-response chi-square statistic of each dimension

p.values P-value of the test of each dimension adjusted for closed testing procedure

References

Loughin, T. M., & Scherer, P. N. (1998). Testing for Association in Contingency Tables with Multiple Column Responses. Biometrics, 54(2), 630-637.

Mahieu, B., Schlich, P., Visalli, M., & Cardot, H. (2021). A multiple-response chi-square framework for the analysis of Free-Comment and Check-All-That-Apply data. Food Quality and Preference, 93.

Examples

```
nb.obs=200
nb.response=5
nb.category=5
vec.category=paste("C",1:nb.category,sep="")
right=matrix(rbinom(nb.response*nb.obs,1,0.25),nb.obs,nb.response)
category=sample(vec.category,nb.obs,replace = TRUE)
dset=cbind.data.frame(category,right)
dset$category=as.factor(dset$category)


mr.dimensionality.test(dset)
```

---

mr.sig.cell	*Multiple-response tests per cell*

Description

This function performs for each pair of category and response option a multiple-response hypergeometric test as defined in Mahieu, Schlich, Visalli, and Cardot (2021) using random hypergeometric samplings to estimate the null distribution.

Usage

```
mr.sig.cell(data, nsample = 300, nbaxes.sig = Inf, two.sided = TRUE)
```

Arguments

data	A data.frame of observations in rows whose first column is a factor (the categories) and subsequent columns are binary numeric or integer, each column being a response option.
nsample	Number of randomly sampled datasets to estimate the distribution of the value under the null hypothesis. See details
nbaxes.sig	The number of significant axes retuned by `mr.dimensionality.test`. By default, all axes are considered significant. See details.
two.sided	Logical. Should the tests be two-sided or not?

Details

- **nsample**: The distribution of the value under the null hypothesis of no associations between categories and response options is estimated using *nsample* datasets generated thanks to random hypergeometric samplings of the response vectors along observations.

- **nbaxes.sig**: If *nbaxes.sig* is lower than the total number of axes then the tests are performed on the derived contingency table corresponding to significant axes (Mahieu, Schlich, Visalli, & Cardot, 2021). This table is obtained by using the reconstitution formula of MR-CA on the first *nbaxes.sig* axes.

Value

A list with the following elements:

original.cont Observed number of times each category chosen each response option

percent.cont Within each category, percentage of observations where the response options were chosen

null.cont Expected number of times each category chosen each response option under the null hypothesis

p.values P-values of the tests per cell fdr adjusted by response option

derived.cont The derived contingency table corresponding to *nbaxes.sig* axes

percent.derived.cont Within each category, percentage of observations where the response options were chosen in the derived contingency table corresponding to *nbaxes.sig* axes

References

Loughin, T. M., & Scherer, P. N. (1998). Testing for Association in Contingency Tables with Multiple Column Responses. Biometrics, 54(2), 630-637.

Mahieu, B., Schlich, P., Visalli, M., & Cardot, H. (2021). A multiple-response chi-square framework for the analysis of Free-Comment and Check-All-That-Apply data. Food Quality and Preference, 93.

Examples

```
nb.obs=200
nb.response=5
nb.category=5
vec.category=paste("C",1:nb.category,sep="")
right=matrix(rbinom(nb.response*nb.obs,1,0.25),nb.obs,nb.response)
category=sample(vec.category,nb.obs,replace = TRUE)
dset=cbind.data.frame(category,right)
dset$category=as.factor(dset$category)

res=mr.sig.cell(dset)

plot(res)
```

---

mrCA   *Multiple-response Correspondence Analysis (MR-CA)*

Description

This functions performs a multiple-response Correspondence Analysis (MR-CA) as defined in Mahieu, Schlich, Visalli, and Cardot (2021).

Usage

```
mrCA(
  data,
  proj.row = NULL,
  proj.row.obs = NULL,
  proj.col = NULL,
  ellipse = FALSE,
  nboot = 300,
  nbaxes.sig = Inf
)
```

Arguments

data	A data.frame of observations in rows whose first column is a factor (the categories) and subsequent columns are binary numeric or integer, each column being a response option.
proj.row	Optional. A contingency table with new categories to be projected as supplementary rows within the MR-CA space in rows and the same response options as data in columns.
proj.row.obs	A numeric vector whose length equals nrow(proj.row) and giving the number of observations within each projected rows. Useless if proj.row=NULL.
proj.col	Optional. A contingency table with new response options to be projected as supplementary columns within the MR-CA space in columns and the same categories as data in rows.
ellipse	Logical. Are confidence ellipses for the categories to be computed? Default is FALSE. See details.
nboot	Number of virtual datasets used in the total bootsrap procedure. Useless when ellipse=FALSE. See details.
nbaxes.sig	The number of significant axes retuned by mr.dimensionality.test. By default, all axes are considered significant. Useless when ellipse=FALSE. See details.

Details

- **ellipse**: When ellipse=TRUE, confidence ellipses for the categories are computed using a total bootstrap procedure (Cadoret & Husson, 2013). **nboot** virtual datasets are generated by

randomly sampling with replacement response vectors within each category. A MR-CA is then performed on these virtual dataset and the resulting virtual configurations are adjusted to the actual configuration using Procrustes rotations accounting for **nbaxes.sig** axes (Mahieu, Schlich, Visalli, & Cardot, 2021). Finally, for each category, a confidence ellipse is constructed using the position of its bootstrap replicates. The ellipses are plotted when using plot.mrCA Pairwise total bootstrap tests as proposed in Castura et al. (2023) are also performed between the categories.

Value

A list with the following elements:

eigen Eigenvalues and their corresponding percentages of inertia

row.coord Rows coordinates

col.coord Columns coordinates

proj.row.coord Projected rows coordinates

proj.col.coord Projected columns coordinates

svd Results of the singular value decomposition

bootstrap.replicate.coord Coordinates of the rotated bootstrap replicates

total.bootstrap.test.pvalues P-values of the pairwise total bootstrap tests

References

Mahieu, B., Schlich, P., Visalli, M., & Cardot, H. (2021). A multiple-response chi-square framework for the analysis of Free-Comment and Check-All-That-Apply data. Food Quality and Preference, 93.

Loughin, T. M., & Scherer, P. N. (1998). Testing for Association in Contingency Tables with Multiple Column Responses. Biometrics, 54(2), 630-637.

Cadoret, M., & Husson, F. (2013). Construction and evaluation of confidence ellipses applied at sensory data. Food Quality and Preference, 28(1), 106-115.

Castura, J. C., Varela, P., & Næs, T. (2023). Evaluation of complementary numerical and visual approaches for investigating pairwise comparisons after principal component analysis. Food Quality and Preference, 107.

Examples

```
nb.obs=200
nb.response=5
nb.category=5
vec.category=paste("C",1:nb.category,sep="")
right=matrix(rbinom(nb.response*nb.obs,1,0.25),nb.obs,nb.response)
category=sample(vec.category,nb.obs,replace = TRUE)
dset=cbind.data.frame(category,right)
dset$category=as.factor(dset$category)

res=mrCA(dset)

plot(res)
```

---

plot.mr.sig.cell *Plot significant cells*

Description

This function plots the results coming from mr.sig.cell.

Usage

```
## S3 method for class 'mr.sig.cell'
plot(
  x,
  alpha.1 = 0.05,
  alpha.2 = 0,
  choice = "percent.derived.cont",
  col.greater.1 = "green3",
  col.lower.1 = "orangered",
  col.greater.2 = "lightgreen",
  col.lower.2 = "lightsalmon",
  ...
)
```

Arguments

x	A list returned by mr.sig.cell.
alpha.1	The alpha risk to consider the tests as significant.
alpha.2	The alpha risk to consider the tests as showing a trend. If trends are not to be considered, *alpha.2* can be set to 0 (Default).
choice	Which table from *res* should be plotted? Default is percent.derived.cont.
col.greater.1	The color used to highlight significant positive associations.
col.lower.1	The color used to highlight significant negative associations.
col.greater.2	The color used to highlight positive associations showing a trend.
col.lower.2	The color used to highlight negative associations showing a trend.
...	further arguments passed to or from other methods.

Value

A table with cells highlighted.

Examples

```
nb.obs=200
nb.response=5
nb.category=5
vec.category=paste("C",1:nb.category,sep="")
```

```
right=matrix(rbinom(nb.response*nb.obs,1,0.25),nb.obs,nb.response)
category=sample(vec.category,nb.obs,replace = TRUE)
dset=cbind.data.frame(category,right)
dset$category=as.factor(dset$category)

res=mr.sig.cell(dset)

plot(res)
```

---

plot.mrCA	*Plot factor plan resulting from multiple-response Correspondence Analysis (MR-CA).*

Description

This function plots the results coming from [mrCA](#).

Usage

```
## S3 method for class 'mrCA'
plot(
  x,
  axes = c(1, 2),
  alpha.total.bootstrap.test = 0.05,
  alpha.ellipse = alpha.total.bootstrap.test,
  select.rep = rownames(x$col.coord),
  rev.x = FALSE,
  rev.y = FALSE,
  size.points = 3.5,
  size.lab = 6,
  size.head.arrow = 0.4,
  expansion = 1.25,
  title = NULL,
  ...
)
```

Arguments

x	A list returned by [mrCA](#).
axes	Which dimensions of the MR-CA should be plotted?
alpha.total.bootstrap.test	
	The alpha risk of the total bootstrap tests. Only useful if the MR-CA was computed using [mrCA](#) and ellipse=TRUE. See details.
alpha.ellipse	The alpha risk of the confidence ellipses. Only useful if the MR-CA was computed using [mrCA](#) and ellipse=TRUE.
select.rep	A character vector specifying the response options to plot. By default, all response options are plotted.

rev.x	Should the horizontal plotted dimension be reversed? Useful in case of map comparisons to align categories.
rev.y	Should the vertical plotted dimension be reversed? Useful in case of map comparisons to align categories.
size.points	The size of the points used to represent the categories on the map.
size.lab	The size of the label on the map.
size.head.arrow	
	The size of the head of the arrows used to represent the response options on the map.
expansion	The factor of expansion applied to response options coordinates to increase readability.
title	An optional title to be added to the plot.
...	further arguments passed to or from other methods.

Details

- **alpha.total.bootstrap.test**: Categories non-significantly different at the alpha risk of *alpha.total.bootstrap.test* according to the total bootstrap test are linked by a line on the plot. If these links are not required, *alpha.total.bootstrap.test* can be set to 1.

Value

A MR-CA factor map.

Examples

```
nb.obs=200
nb.response=5
nb.category=5
vec.category=paste("C",1:nb.category,sep="")
right=matrix(rbinom(nb.response*nb.obs,1,0.25),nb.obs,nb.response)
category=sample(vec.category,nb.obs,replace = TRUE)
dset=cbind.data.frame(category,right)
dset$category=as.factor(dset$category)

res=mrCA(dset)

plot(res)
```

---

plot.sensory.mr.sig.cell

Plot significant cells

Description

This function plots the results coming from sensory.mr.sig.cell.

Usage

```
## S3 method for class 'sensory.mr.sig.cell'
plot(
  x,
  alpha.1 = 0.05,
  alpha.2 = 0,
  choice = "percent.derived.cont",
  col.greater.1 = "green3",
  col.lower.1 = "orangered",
  col.greater.2 = "lightgreen",
  col.lower.2 = "lightsalmon",
  ...
)
```

Arguments

x	A list returned by `sensory.mr.sig.cell`.
alpha.1	The alpha risk to consider the tests as significant.
alpha.2	The alpha risk to consider the tests as showing a trend. If trends are not to be considered, *alpha.2* can be set to 0 (Default).
choice	Which table from *res* should be plotted? Default is percent.derived.cont.
col.greater.1	The color used to highlight significant positive associations.
col.lower.1	The color used to highlight significant negative associations.
col.greater.2	The color used to highlight positive associations showing a trend.
col.lower.2	The color used to highlight negative associations showing a trend.
...	further arguments passed to or from other methods.

Value

A table with cells highlighted.

Examples

```
data(milkchoc)

dim.sig=sensory.mr.dimensionality.test(milkchoc)$dim.sig

res=sensory.mr.sig.cell(milkchoc,nbaxes.sig=dim.sig)

plot(res)
```

---

plot.sensory.mrCA	*Plot factor plan resulting from multiple-response Correspondence Analysis (MR-CA) applied on sensory data*

Description

This function plots the results coming from sensory.mrCA.

Usage

```
## S3 method for class 'sensory.mrCA'
plot(
  x,
  axes = c(1, 2),
  alpha.total.bootstrap.test = 0.05,
  alpha.ellipse = alpha.total.bootstrap.test,
  select.desc = rownames(x$desc.coord),
  rev.x = FALSE,
  rev.y = FALSE,
  size.points = 3.5,
  size.lab = 6,
  size.head.arrow = 0.4,
  expansion = 1.25,
  title = NULL,
  ...
)
```

Arguments

x	A list returned by sensory.mrCA.
axes	Which dimensions of the MR-CA should be plotted?
alpha.total.bootstrap.test	
	The alpha risk of the total bootstrap tests. See details.
alpha.ellipse	The alpha risk of the confidence ellipses.
select.desc	A character vector specifying the descriptors to plot. By default, all descriptors are plotted.
rev.x	Should the horizontal plotted dimension be reversed? Useful in case of map comparisons to align products.
rev.y	Should the vertical plotted dimension be reversed? Useful in case of map comparisons to align products.
size.points	The size of the points used to represent the products on the map.
size.lab	The size of the label on the map.
size.head.arrow	
	The size of the head of the arrows used to represent the descriptors on the map.

expansion	The factor of expansion applied to descriptors coordinates to increase readability.
title	An optional title to be added to the plot.
...	further arguments passed to or from other methods.

Details

- **alpha.total.bootstrap.test**: products non-significantly different at the alpha risk of *alpha.total.bootstrap.test* according to the total bootstrap test are linked by a line on the plot. If these links are not required, *alpha.total.bootstrap.test* can be set to 1.

Value

A MR-CA factor map

Examples

```
data(milkchoc)

dim.sig=sensory.mr.dimensionality.test(milkchoc)$dim.sig

res=sensory.mrCA(milkchoc,nbaxes.sig=dim.sig)

plot(res)
```

---

sensory.mr.dimensionality.test

Multiple-response dimensionality test for sensory data

Description

Performs a multiple-response dimensionality test as defined in Mahieu, Schlich, Visalli, and Cardot (2021) using random permutations to estimate the null distribution. The difference with `mr.dimensionality.test` is that random permutations are performed within subjects rather than along all evaluations.

Usage

```
sensory.mr.dimensionality.test(data, nperm = 300, alpha = 0.05)
```

Arguments

data	A data.frame of evaluations in rows whose first two columns are factors (subject and product) and subsequent columns are binary numeric or integer, each column being a descriptor.
nperm	Number of permuted datasets to estimate the distribution of the statistic under the null hypothesis. See details.
alpha	The alpha risk of the test.

Details

- **nperm**: The distribution of the statistic under the null hypothesis of no associations between products and descriptors is estimated using *nperm* datasets generated thanks to random permutations of the response vectors along products within subjects.

Value

A list with the following elements:

dim.sig The number of significant dimensions

statistics Observed multiple-response chi-square statistic of each dimension

p.values P-value of the test of each dimension adjusted for closed testing procedure

References

Loughin, T. M., & Scherer, P. N. (1998). Testing for Association in Contingency Tables with Multiple Column Responses. Biometrics, 54(2), 630-637.

Mahieu, B., Schlich, P., Visalli, M., & Cardot, H. (2021). A multiple-response chi-square framework for the analysis of Free-Comment and Check-All-That-Apply data. Food Quality and Preference, 93.

Examples

```
data(milkchoc)

sensory.mr.dimensionality.test(milkchoc)
```

---

sensory.mr.sig.cell *Multiple-response tests per cell for sensory data*

Description

This function performs for each pair of product and descriptor a multiple-response hypergeometric test as defined in Mahieu, Schlich, Visalli, and Cardot (2021) using random hypergeometric samplings to estimate the null distribution. The difference with `mr.sig.cell` is that random hypergeometric samplings are performed within subjects in `sensory.mr.sig.cell`.

Usage

```
sensory.mr.sig.cell(data, nsample = 300, nbaxes.sig = Inf, two.sided = TRUE)
```

Arguments

data	A data.frame of evaluations in rows whose first two columns are factors (subject and product) and subsequent columns are binary numeric or integer, each column being a descriptor.
nsample	Number of randomly sampled datasets to estimate the distribution of the value under the null hypothesis. See details.
nbaxes.sig	The number of significant axes retuned by `sensory.mr.dimensionality.test`. By default, all axes are considered significant. See details.
two.sided	Logical. Should the tests be two-sided or not?

Details

- **nsample**: The distribution of the value under the null hypothesis of no associations between products and descriptors is estimated using *nsample* datasets generated thanks to random hypergeometric samplings of the response vectors along products within subjects.

- **nbaxes.sig**: If *nbaxes.sig* is lower than the total number of axes then the tests are performed on the derived contingency table corresponding to significant axes (Mahieu, Schlich, Visalli, & Cardot, 2021) This table is obtained by using the reconstitution formula of MR-CA on the first *nbaxes.sig* axes.

Value

A list with the following elements:

original.cont Observed number of times each product was described by each descriptor

percent.cont For each product, percentage of evaluations where each descriptor was cited for this product

null.cont Expected number of times each product was described by each descriptor under the null hypothesis

p.values P-values of the tests per cell fdr adjusted by descriptor

derived.cont The derived contingency table corresponding to *nbaxes.sig* axes

percent.derived.cont For each product, percentage of evaluations where each descriptor was cited for this product in the derived contingency table corresponding to *nbaxes.sig* axes

References

Loughin, T. M., & Scherer, P. N. (1998). Testing for Association in Contingency Tables with Multiple Column Responses. Biometrics, 54(2), 630-637.

Mahieu, B., Schlich, P., Visalli, M., & Cardot, H. (2021). A multiple-response chi-square framework for the analysis of Free-Comment and Check-All-That-Apply data. Food Quality and Preference, 93.

Examples

```
data(milkchoc)

dim.sig=sensory.mr.dimensionality.test(milkchoc)$dim.sig

res=sensory.mr.sig.cell(milkchoc,nbaxes.sig=dim.sig)

plot(res)
```

---

sensory.mrCA	*Multiple-response Correspondence Analysis (MR-CA) for sensory data*

Description

This function performs the MR-CA of the data as well as the total bootstrap procedure (Cadoret & Husson, 2013) and the pairwise total bootstrap tests as proposed in Castura et al. (2023). The difference with mrCA used with ellipse=TRUE is that the total bootstrap procedure is stratified with respect to subjects in sensory.mrCA.

Usage

```
sensory.mrCA(data, nboot = 300, nbaxes.sig = Inf)
```

Arguments

data	A data.frame of evaluations in rows whose first two columns are factors (subject and product) and subsequent columns are binary numeric or integer, each column being a descriptor.
nboot	The number of bootstrapped panel of the total bootstrap procedure.
nbaxes.sig	The number of significant axes returned by sensory.mr.dimensionality.test. By default, all axes are considered significant. See details.

Details

- **nbaxes.sig**: The number of significant axes determines the number of axes accounted for while performing the Procrustes rotations of the total bootstrap procedure (Mahieu, Schlich, Visalli, & Cardot, 2021). These same axes are accounted for the pairwise total bootstrap tests.

Value

A list with the following elements:

eigen Eigenvalues of the MR-CA and their corresponding percentages of inertia

prod.coord Products coordinates

desc.coord Descriptors coordinates

svd Results of the singular value decomposition

bootstrap.replicate.coord Coordinates of the rotated bootstrap replicates

total.bootstrap.test.pvalues P-values of the pairwise total bootstrap tests

References

Cadoret, M., & Husson, F. (2013). Construction and evaluation of confidence ellipses applied at sensory data. Food Quality and Preference, 28(1), 106-115.

Castura, J. C., Varela, P., & Næs, T. (2023). Evaluation of complementary numerical and visual approaches for investigating pairwise comparisons after principal component analysis. Food Quality and Preference, 107.

Mahieu, B., Schlich, P., Visalli, M., & Cardot, H. (2021). A multiple-response chi-square framework for the analysis of Free-Comment and Check-All-That-Apply data. Food Quality and Preference, 93.

Examples

```
data(milkchoc)

dim.sig=sensory.mr.dimensionality.test(milkchoc)$dim.sig

res=sensory.mrCA(milkchoc,nbaxes.sig=dim.sig)

plot(res)
```

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