Package ‘SSRA’
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Description Takeya Semantic Structure Analysis (TSSA) and Sakai Sequential Relation Analysis (SSRA)
for polytomous items for examining whether each pair of items has a sequential or equal
relation. Package includes functions for generating a sequential relation table and a
treegram to visualize sequential or equal relations between pairs of items.
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Example data based on Takeya (1991)

Description

A dataset containing 10 observations on 5 items.

Usage

exdat

Format

A data frame with 10 rows and 5 variables

Plot ssra

Description

Function for plotting the ssra object

Usage

## S3 method for class 'ssra'
plot(x, r.crt = NULL, r.sig = TRUE, d.sq = NULL,
    m.sig = TRUE, sig.col = TRUE,
    col = c("red2", "green4", "blue3", "black"),
    pch = c(1, 2, 0, 4), mar = c(3.5, 3.5, 1.5, 1), ...)

Arguments

x requires the return object from the SSRA function
r.crt minimal absolute correlation to be judged 'sequential'
r.sig plot statistically significant correlations
d.sq minimal effect size Cohen’s d to be judged 'sequential'
m.sig plot statistically significant mean difference
sig.col significance in different colors
col color code or name
pch plotting character
mar number of lines of margin to be specified on the four sides of the plot
... further arguments passed to or from other methods
Details

Using this function, all item pairs are plotted on a graph by their correlation coefficients and their mean differences (Cohen’s d). This graph is useful for defining (or changing) criteria regarding correlation coefficient and mean difference to judge whether an item pair is 'sequential' or 'equal'.

Author(s)

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References


See Also

SSRA, treegram, scatterplot

Examples

# Example data based on Takeya (1991)
# Sakai Sequential Relation Analysis
# ordering assessed according to the correlation coefficient and mean difference
exdat.ssra <- SSRA(exdat, output = FALSE)
plot(exdat.ssra)

Description

print function for the ssra object

Usage

## S3 method for class 'ssra'
print(x, digits = 3, ...)

Arguments

x requires the result object of hssr function
digits integer indicating the number of decimal places to be used
... further arguments passed to or from other methods

Author(s)

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References


See Also

seqtable

Examples

# Example data based on Takeya (1991)

# Sakai Sequential Relation Analysis
# ordering assessed according to the correlation coefficient and mean difference
exdat.ssra <- SSRA(exdat, output = FALSE)
print(exdat.ssra)

print.tssa

**Semantric Structure Analysis Print**

**Description**

print function for the tssa object

**Usage**

```r
## S3 method for class 'tssa'
print(x, digits = 3, ...)
```

**Arguments**

- `x`: requires the result object of hssr function
- `digits`: integer indicating the number of decimal places to be used
- `...`: further arguments passed to or from other methods

**Author(s)**

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**References**


**See Also**

seqtable
Examples

# Example data based on Takeya (1991)

# Takeya Semantic Structure Analysis
# ordering assessed according to the ordering coefficient
exdat.tssa <- TSSA(exdat, m = 5, output = FALSE)
print(exdat.tssa)

# Takeya Semantic Structure Analysis including statistical testing
# ordering assessed according to the ordering coefficient and statistical significance
exdat.tssa <- TSSA(exdat, m = 5, sig = TRUE, output = FALSE)
print(exdat.tssa)

---

scatterplot Scatterplot Matrices

Description

This function produces a scatterplot matrix.

Usage

scatterplot(data, select = NULL, type = c("jitter", "size", "count", "sun"))

Arguments

data a data frame
select select items to be plotted
type type of plot, i.e., ‘jitter’, ‘size’, ‘count’, and ‘sun’

Details

Using a scatterplot matrix, an overview of the answer patterns for the pairs of items can be taken.

Author(s)

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References


See Also

TSSA, SSRA
Examples

# Example data based on Takeya (1991)

# Select items to be plotted
scatterplot(exdat, select = c("Item2", "Item3", "Item4"))

# Scatterplot matrix: jitter
scatterplot(exdat)

# Scatterplot matrix: size
scatterplot(exdat, type = "size")

# Scatterplot matrix: count
scatterplot(exdat, type = "count")

# Scatterplot matrix: sun
scatterplot(exdat, type = "sun")

---

seqtable | Sequential Relation Table

Description

This function builds a table for the tssa and ssra object used to create a treegram.

Usage

seqtable(object, order = c("no", "decreasing", "increasing"),
          digits = 3, output = TRUE)

Arguments

- **object**: requires the return object from the TSSA or SSRA function
- **order**: sort by item mean of j?
- **digits**: integer indicating the number of decimal places to be used
- **output**: print result table?

Details

In this table, we can see how many 'sequential' or 'equal' relations each of items has with the other items.

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SSRA

References


See Also

TSSA, SSRA, treegram, summary.seqtable

Examples

```r
# Example data based on Takeya (1991)

# Takeya Semantic Structure Analysis
# ordering assessed according to the correlation coefficient and mean difference
exdat.tssa <- TSSA(exdat, m = 5, output = FALSE)
seqtable(exdat.tssa)

# Sakai Sequential Relation Analysis
# ordering assessed according to the correlation coefficient and mean difference
exdat.ssra <- SSRA(exdat, output = FALSE)
seqtable(exdat.ssra)
```

SSRA

*Sakai Sequential Relation Analysis*

Description

This function conducts Sakai Sequential Relation Analysis (SSRA) based on Sakai 2016.

Usage

```r
SSRA(dat, r.crt = 0.3, mu.sq = 0, mu.eq = Inf, d.sq = 0.2, d.eq = 0.2,
pairwise = TRUE, method = c("pearson", "kendall", "spearman"), alpha = 0.05,
p.adjust.method = c("holm", "hochberg", "hommel",
"bonferroni", "BH", "BY", "fdr", "none"),
digits = 3, vnames = TRUE, order = c("no", "decreasing", "increasing"),
exclude = TRUE, output = TRUE)
```

Arguments

dat requires a data frame with polytomous data
r.crt correlation coefficient criterion to be judged 'sequential' or 'equivalent'
mu.sq Absolute mean difference criterion to be judged 'sequential'
mu.eq maximal absolute mean difference to be judged 'equivalent'
d.sq effect size for mean difference criterion to be judged 'sequential'
d.eq maximal effect size Cohen’s d to be judged 'equivalent'
pairwise deletion of missing data, if pairwise = FALSE listwise deletion is applied.

method character string indicating which correlation coefficient to be used, ‘pearson’ = Pearson’s product moment correlation coefficient ‘spearman’ = Spearman’s rho statistic ‘kendall’ = Kendall’s tau (default)

alpha significance level

p.adjust.method p-value correction method for multiple comparisons, see: ?p.adjust (default = holm)

digits integer indicating the number of decimal places to be used

vnames use variable names for labeling?

order sort by item mean of j and k?

exclude exclude paths with no relationship?

output print result table?

Details

In Sakai Sequential Relation Analysis (SSRA), a pair of items is judged ‘sequential’, if there is a higher correlation and a bigger mean difference than defined criterions between the two items. If there is a higher correlation and a smaller mean difference than defined criterions between the two items, the relation of the two items is judged ‘equal’.

Value

Returns an object of class ssra, to be used for the seqtable function. The object is a list with following entries: ‘dat’ (data frame), ‘call’ (function call), ‘args’ (specification of arguments), ‘time’ (time of analysis), ‘R’ (R version), ‘package’ (package version), and ‘restab’ (result table). The ‘restab’ entry has following entries:

j item j
k item k
n sample size
j.mean mean of item j
j.sd standard deviation of item j
k.mean mean of item k
k.sd standard deviation of item k
r correlation coefficient
r.t test statistic of the statistical significance test for the correlation coefficient
r.p statistical significance value of the correlation
r.sig statistical significance of the correlation (0 = not significant / 1 = significant)
r.crt correlation criterion for judging ‘sequential’ or ‘equal’: ‘r.p < alpha’ and ‘r > r.crt’ (0 = no / 1 = yes)
m.diff mean difference
sd.diff standard deviation difference
m.diff.eff effect size Cohen’s d for dependent samples
m.t test statistic of the statistical significance test for mean difference
m.p statistical significance value of the mean difference
m.sig statistical significance of the mean difference (0 = not significant / 1 = significant)
m.crt.sq  mean difference criteria for judging 'sequential': 'm.diff.p < alpha', 'm.diff > mu.sq' and 'm.diff.eff > d.sq' (0 = no
m.crt.eq  mean difference criteria for judging 'equivalence': statistical significant and 'm <= mu.eq' 'd <= d.sq' (0 = no
seq sequential relation of item pairs ("+", "-", "")
eq equivalence of item pairs ("=", "")
order order structure of item pairs ("=" or "")

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References

See Also
seqtable, TSSA, plot.ssra, scatterplot

Examples
# Example data based on Takeya (1991)
# Sakai Sequential Relation Analysis
# ordering assessed according to the correlation coefficient and mean difference
SSRA(exdat)

difference
summary(seqtable)

Description
summary function for the seqtab object

Usage
## S3 method for class 'seqtable'
summary(object, exclude = TRUE, ...)

Arguments
object requires the result object of seqtable function
exclude exclude lower-order paths (i.e., paths included in higher order paths)?
... additional arguments affecting the summary produced
Details

Summary function for the seqtab object.

In this function, the number of the sequences is counted. 'Sequence' means a range of items with sequential relations. Sequences are classified in their length and are counted.

Value

rel relationship: sq = sequential / eq = equal
var variables involved in the sequential/equal paths

Author(s)

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References


See Also

SSRA, TSSA

Examples

# Example data based on Takeya (1991)

# Sakai Sequential Relation Analysis
# ordering assessed according to the correlation coefficient and mean difference
exdat.ssra <- SSRA(exdat, output = FALSE)
exdat.seqtab <- seqtable(exdat.ssra, output = FALSE)
summary(exdat.seqtab)

Description

This function draws a treegram for the Takeya Semantic Structure Analysis (TSSA) and Sakai Sequential Relation Analysis (SSRA)
Usage

treegram(object, select = NULL, pos = NULL, col = NULL,
mai = c(0.2, 0, 0.2, 0.2), print.pos = TRUE, cex.text = 0.95,
x.factor = 1.7, x.digits = 0, y.digits = 2, y.intersp = 1.45,
cex.legend = 0.9)

Arguments

object requires the result object of seqtab function
select select items to be plotted
pos position of items on the x-axis
col color code or name for paths
mai numeric vector of the form c(bottom, left, top, right) which gives the margin size specified in inches
print.pos display x/y-position as legend
cex.text text expansion factor relative to current par("cex")
x.factor shift factor of legend position
x.digits decimal places of x-position
y.digits decimal places of y-position
y.intersp legend character interspacing factor for vertical (y) line distances
cex.legend legend character expansion factor relative to current par("cex")

Details

An item with lower item mean is located above, and an item with higher item mean is placed below in a treegram. An arrow is drawn between two items in sequential relation, namely, from the item with higher item mean to the item with lower item mean. And two items in equal relation are linked by a dashed line.

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References


See Also

seqtable
Examples

# Example data based on Takeya (1991)

# Sakai Sequential Relation Analysis
# ordering assessed according to the correlation coefficient and mean difference
exdat.ssra <- SSRA(exdat, output = FALSE)
exdat.seqtab <- seqtable(exdat.ssra, output = FALSE)
treegram(exdat.seqtab)

# Select items to be plotted
exdat.ssra <- SSRA(exdat, output = FALSE)
exdat.seqtab <- seqtable(exdat.ssra, output = FALSE)
treegram(exdat.seqtab, select = c("Item2", "Item3", "Item4"))

# Define position for each item on the x-axis
exdat.ssra <- SSRA(exdat, output = FALSE)
exdat.seqtab <- seqtable(exdat.ssra, output = FALSE)
treegram(exdat.seqtab, pos = c(Item5 = 1, Item4 = 3,
                                Item3 = 5, Item2 = 2, Item1 = 4))

# Change colors for each path of an item
exdat.ssra <- SSRA(exdat, output = FALSE)
exdat.seqtab <- seqtable(exdat.ssra, output = FALSE)
treegram(exdat.seqtab,
        col = c(Item5 = "red3", Item4 = "blue3",
                Item3 = "gray99", Item2 = "darkgreen", Item1 = "darkorange2"))

---

TSSA

Takeya Semantic Structure Analysis

Description

This function conducts Takeya Semantic Structure Analysis (TSSA) for polytomous items based on Takeya 1991.

Usage

TSSA(dat, m, crit = 0.93, pairwise = TRUE, sig = FALSE, exact = TRUE, alpha = 0.05,
     p.adjust.method = c("holm", "hochberg", "hommel",
                        "bonferroni", "BH", "BY", "fdr", "none"),
     digits = 3, vnames = TRUE, order = c("no", "decreasing", "increasing"),
     exclude = TRUE, output = TRUE)

Arguments

dat requires a data frame with polytomous data, all items need to have the same numbers of response categories

m requires the number of item response categories
crit criteria for ordering coefficient
pairwise pairwise deletion of missing data, if pairwise = FALSE listwise deletion if applied
sig if sig = TRUE, ordering will be assessed according to ordering coefficient and statistical significance
exact if exact = TRUE, exact binomial test will be applied otherwise single-sample proportion test will be applied
alpha significance level
p.adjust.method p-value correction method for multiple comparisons, see: ?p.adjust (default = holm)
digits integer indicating the number of decimal places to be used
vnames use variable names for labeling?
order sort by item mean of j and k?
exclude exclude paths with no relationship?
output print result table?

Details

In Takeya Semantic Structure Analysis (TSSA), a pair of items (e.g., Item1 and Item2) is judged 'sequential', if exceptional answer patterns are less than a defined criterion. If we suppose Item1 to be the item with higher item mean than Item2 (i.e., 'Item1 -> Item2' in the treegram), 'exceptional answer pattern' means that someone gets a lower score on Item1 and a higher score on Item2. If this kind of sequential relation is bi-directional (i.e., not only 'Item1 -> Item2' but also 'Item2 -> Item1'), the relation of the two items is judged 'equal'.

Value

Returns an object of class tssa, to be used for the seqtable function. The object is a list with following entries: 'dat' (data frame), 'call' (function call), 'args' (specification of arguments), 'time' (time of analysis), 'R' (R version), 'package' (package version), and 'restab' (result table). The 'restab' entry has following entries:

<table>
<thead>
<tr>
<th>j</th>
<th>item j</th>
</tr>
</thead>
<tbody>
<tr>
<td>k</td>
<td>item k</td>
</tr>
<tr>
<td>n</td>
<td>sample size</td>
</tr>
<tr>
<td>j.mean</td>
<td>mean of item j</td>
</tr>
<tr>
<td>j.sd</td>
<td>standard deviation of item j</td>
</tr>
<tr>
<td>k.mean</td>
<td>mean of item k</td>
</tr>
<tr>
<td>k.sd</td>
<td>standard deviation of item k</td>
</tr>
<tr>
<td>c.jk</td>
<td>ordering coefficient j -&gt; k</td>
</tr>
<tr>
<td>p.jk</td>
<td>p-value j -&gt; k (available if sig = TRUE)</td>
</tr>
<tr>
<td>sig.jk</td>
<td>statistical significance p-value j -&gt; k (0 = no / 1 = yes; available if sig = TRUE)</td>
</tr>
<tr>
<td>c.kj</td>
<td>ordering coefficient k -&gt; j</td>
</tr>
<tr>
<td>p.kj</td>
<td>p-value k -&gt; j (0 = no / 1 = yes; available if sig = TRUE)</td>
</tr>
<tr>
<td>sig.kj</td>
<td>statistical significance p-value k -&gt; j (available if sig = TRUE)</td>
</tr>
</tbody>
</table>
crt.jk  ordering j -> k

crt.kj  ordering k -> j

order  order structure of item pairs ("=", "+", "-")

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References

See Also
SSRA, seqtable, scatterplot

Examples

# Example data based on Takeya (1991)

# Takeya Semantic Structure Analysis
# ordering assessed according to the ordering coefficient
TSSA(exdat, m = 5)

# Takeya Semantic Structure Analysis including statistical testing
# ordering assessed according to the ordering coefficient and statistical significance
TSSA(exdat, m = 5, sig = TRUE)
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