Package ‘parsec’

November 2, 2018

Version 1.2.1
Date 2018-11-02
Title Partial Orders in Socio-Economics
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Depends igraph
License GPL (>= 2)
NeedsCompilation yes
Repository CRAN
Date/Publication 2018-11-02 13:10:03 UTC
RoxygenNote 6.1.0

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Description

The package implements tools for the analysis of partially ordered data, with a particular focus on the evaluation of multidimensional systems of indicators and on the analysis of poverty.

Its main objective is to provide socio-economic scholars with an integrated set of elementary functions for multidimensional evaluation, based on ordinal information. In particular, it provides functions for data management and basic analysis of partial orders as well as other functions for the evaluation and application of both the poset-based approach and a more classic counting method.

Details

Package: parsec
Type: Package
Version: 1.2.0
Date: 2018-04-01
License: GPL (>= 2)

Author(s)

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Maintainer: A, Arcagni <alberto.arcagni@unimib.it>

Examples

# a simple example of package application
# definition of the variables by their number of grades
variables <- c(2, 2, 2)

# definition of the threshold
threshold <- c("112", "211")

# extraction of all of the possible profiles from variables; the
# function returns an object of class "wprof", weighted profiles: by default,
# weights/frequencies are set equal to 1
profiles <- var2prof(varlen = variables)

# the following function creates matrices describing the poset, and
# provides all the results related to it
eval <- evaluation(profiles, threshold, nit = 10^5, maxint = 10^3)

# The results can then be summarized
summary(summary(eval))

# a method of the plot function returns the Hasse diagram, a frequency
# distribution of the threshold, the identification function, the rank
# distribution of each profile through a barplot, and the relative gap.
plot(eval)

# definition of the variables and of the corresponding profiles
v1 <- as.ordered(c("a", "b", "c", "d"))
v2 <- 1:3
prof <- var2prof(varmod = list(v1 = as.ordered(c("a", "b", "c", "d")), v2 = 1:3))
np <- nrow(prof$profiles)

# definition of different distributions over the set of profiles
k <- 10 # number of populations
set.seed(0)
populations <- as.data.frame(lapply(1:k, function(x) round(runif(np)*100)))ownames(populations) <- rownames(prof$profiles)
names(populations) <- paste0("P", 1:k)

prof
populations

# evaluation of the fuzzy first order dominance
res <- FFOD(profiles = prof, distributions = populations)
res

# rank stablity analysis
res <- rank_stability(res)
res

# graphical representation
plot(res)

---

**OPHI counting approach**

**Description**

The function implements the OPHI counting approach, in a single call. The implementation is limited to ordinal attributes.
Usage

\[ \text{AF}(y, \ldots) \]

## Default S3 method:

\[ \text{AF}(y, z, w=\text{rep}(1, \text{ncol}(y)), k=\text{sum}(w), \text{freq}=\text{rep}(1, \text{nrow}(y)), \ldots) \]

## S3 method for class 'wprof'

\[ \text{AF}(y, \ldots) \]

Arguments

- \( y \): matrix of profiles, possibly substituted by an object of class `wprof`.
- \( z \): vector of attribute cutoffs.
- \( w \): variables' weights.
- \( k \): overall cutoff.
- \( \text{freq} \): profiles' frequencies; the argument can be omitted if \( y \) is an object of class `wprof`.
- \( \ldots \): any of the above.

Value

An object of S3 class `ophi` containing all the outputs related to the OPHI counting approach. The object is a list comprising:

- \( y \): matrix of profiles,
- \( \text{freq} \): profiles' frequencies,
- \( d \): number of variables
- \( n \): number of observations (sum of frequencies),
- \( z \): vector of cutoffs,
- \( k \): overall cutoff,
- \( \text{rho} \): function comparing profiles to the vector of cutoffs,
- \( \text{rho}_k \): function comparing profiles to the overall cutoff, by weighting variables,
- \( g\theta \): profile-variable matrix reporting the output of function `rho`,
- \( c \): censored vector of deprivation counts,
- \( Z_k \): boolean vector identifying deprived profiles, according to the specified cutoffs,
- \( q \): number of poor statistical units in the population,
- \( H \): headcount ratio, i.e. \( q/n \), where \( n \) is the number of statistical units in the population,
- \( A \): average deprivation share,
- \( \lambda \): adjusted headcount ratio.

References

AF2threshold

Poset threshold making the poset approach equivalent to the AF counting approach

Description
The function computes the threshold in the profile poset, which makes the poset approach equivalent to the AF counting approach, described in argument mpi.

Usage
AF2threshold(mpi, prof, zeta = NULL)

Arguments
mpi an object of class ophi, see AF for details.
prof an object of class wprof.
zeta an object of class incidence.

See Also
AF

Examples
vl <- c(2, 3, 3, 2)
prof <- var2prof(varlen = vl)
res <- AF(prof, z = c(1, 2, 1), k = 1)
res

thr <- AF2threshold(res, prof)

plot(prof, col = 1 + thr, lwd = 1 + res$c,
     main = "Comparison between OPHI and parsec",
     sub = "bold: deprived profiles identified by OPHI, red: parsec threshold")

eval <- evaluation(prof, thr, maxint = 10^4, nit = 10^7)
ord <- order(eval$idn_f, res$c)
plot(eval$idn_f[ord], col = "red", lwd=2, type = "l", xlab="",


Description

The function checks whether boolean square matrix \( m \) represents an antisymmetric binary relation.

Usage

\[
\text{antisymmetry}(m)
\]

Arguments

\( m \)  
a square matrix.

See Also

\( \text{transitivity}, \text{binary}, \text{reflexivity}, \text{is.preorder}, \text{is.partialorder}, \text{validate.partialorderDIC} \)

Examples

```r
M <- c(TRUE, FALSE, FALSE, FALSE, TRUE, TRUE, FALSE, TRUE, FALSE, TRUE, TRUE, TRUE, FALSE, TRUE, TRUE, TRUE)
M <- matrix(M, 4, 4)
rownames(M) <- colnames(M) <- LETTERS[1:4]
antisymmetry(M)
```
average_ranks

### Description

The function evaluates the average rank, and other distribution details, for each element of the poset.

### Usage

```r
average_ranks(x, ...)  # S3 method for class 'cover'
average_ranks(x, level = 0.9, error = 10^-5, ...)  # S3 method for class 'incidence'
```

### Arguments

- `x`: an incidence or cover matrix representing a partial order.
- `level`: coverage probability of the rank intervals.
- `error`: the "distance" from uniformity in the sampling distribution of linear extensions used to evaluate the average ranks. See `idn` for details.
- `...`: any of above.

### Details

The function computes the rank distribution for each element of the poset, through function `idn`. Next, it checks whether there are any equivalent profiles, using function `equivalences`, and makes their rank distribution equal. Finally it provides a dataframe comprising, for each element of the poset: the average rank `avrg`, the extremes `inf` and `sup` of the rank interval, the effective coverage probability of the rank interval `prob`, the estimated minimum and maximum rank values (`min` and `max`) and the rank `range`.

The output is a dataframe of class `average_ranks` for which a method of function `plot` is available. See `plot.average_ranks` for details.

### Value

A dataframe of class `average_ranks` whose columns are:

- `avrg`: the average rank;
- `inf`: the lower extreme of the rank interval;
- `sup`: the upper extreme of the rank interval;
- `prob`: the effective coverage probability of the rank interval;
- `min`: the minimum rank;
- `max`: the maximum rank;
- `range`: the rank range.
The function checks whether square matrix \( m \) represents a binary relation.

**Usage**

```r
binary(m)
```

**Arguments**

- \( m \)  
  
  A square matrix.

**See Also**

- `transitivity`
- `reflexivity`
- `antisymmetry`
- `is.preorder`
- `is.partialorder`
- `validate.partialorder.incidence`

**Examples**

```r
M <- c(TRUE, FALSE, FALSE, FALSE, TRUE, TRUE, FALSE, FALSE, TRUE, FALSE, TRUE, TRUE, TRUE, TRUE, TRUE, TRUE, FALSE, TRUE, FALSE, TRUE, TRUE, TRUE, TRUE, TRUE)
M <- matrix(M, 4, 4)
rownames(M) <- colnames(M) <- LETTERS[1:4]

binary(M)
```
colevels  
**Colevels of a poset**

**Description**

The function returns colevels associated to poset elements.

**Usage**

```r
colevels(y)
```

**Arguments**

- `y` an object of class `cover` or `incidence`.

**Examples**

```r
vl <- c(3, 2, 4)
prof <- var2prof(varlen = vl)
Z <- getzeta(prof)
colevels(Z)
```

---

**Description**

The function computes the incidence matrix of a poset from its cover matrix.

**Usage**

```r
cover2incidence(g)
```

**Arguments**

- `g` a cover matrix, an object of class `cover`

**Value**

The function returns the corresponding incidence matrix, an object of class `incidence`.

**See Also**

`incidence2cover`
**depths**

**Description**

The function computes the depths of poset elements.

**Usage**

```
depths(z)
```

**Arguments**

- `z` an object of class `cover` or `incidence`.

**Examples**

```r
vl <- c(3, 2, 4)
prof <- var2prof(varlen = vl)
Z <- getzeta(prof)
depths(Z)
```

---

**downset**

**Description**

The function computes a boolean vector identifying the poset elements below (or equal to) at least one element of the input subset `Q`.

**Usage**

```
downset(z, ...) # S3 method for class 'cover'
downset(z, ...) # S3 method for class 'incidence'
```

**Arguments**

- `z` a cover, or an incidence, matrix of S3 class `cover` or `incidence` respectively
- `Q` vector of indices identifying a subset of poset profiles
- `...` any of the above.
**Examples**

```r
z <- getzeta(var2prof(varlen = c(2, 2, 2)))
plot(z, col = 1 + c(1, 1, 0, 0, 0, 0, 0, 0) + c(0, 0, 0, 2, 0, 0, 2, 2), lwd = 2)
Q <- c(4, 7, 8)
rownames(z)[Q]
downset(z, Q)
Q <- c("211", "112", "111")
downset(z, Q)
```

**drawedges**

**Description**

Graphical function called by `plot.cover` to draw the edges of the Hasse diagram representing the input cover matrix `C`.

**Usage**

`drawedges(C, vertices, ...)`

**Arguments**

- `C` cover matrix.
- `vertices` coordinates of the vertices obtained by function `vertices`.
- `...` line parameters, see `graphics{lines}`.

**See Also**

`plot.cover, vertices, graphics{lines}`

**equivalences**

**Equivalence classes in a poset.**

**Description**

The function computes the set of poset elements sharing the same upset and downset.

**Usage**

`equivalences(x)`
**evaluation**

Arguments

x an object of class incidence or cover.

Value

The function computes a vector assigning an equivalence class to each profile. The vector is of class factor.

Author(s)

Arcagni A.

Examples

```r
Lmbd <- getlambda(A > B, A > C, B > D, A > E, B > E, C > F, C > G)
res <- equivalences(Lmbd)
equivalence_classes <- levels(res)
colrs <- sapply(res, function(x) which(equivalence_classes == x)) + 1
plot(Lmbd, col = colrs, lwd = 2)
```

---

**Multidimensional evaluation on posets**

Description

Given a partial order (arguments profiles and/or zeta) and a selected threshold, the function returns an object of S3 class parsec, comprising the identification function and different severity measures, computed by uniform sampling of the linear extensions of the poset, through a C implementation of the Bubley - Dyer (1999) algorithm.

Usage

```r
evaluation(
  profiles = NULL,
  threshold,  # or error = 10^-3,
  zeta = getzeta(profiles),
  weights = {
    if (!is.null(profiles))
      profiles$freq
    else rep(1, nrow(zeta))
  },
  distances = {
    n <- nrow(zeta)
    matrix(1, n, n) - diag(1, n)
  },
```


linext = lingen(zeta),
nit = floor(
    n <- nrow(zeta)
    n^5 * log(n) + n^4 * log(error^(-1))
),
maxint = 2^31 - 1
)

Arguments

profiles an object of S3 class wprof.
threshold a vector identifying the threshold. It can be a vector of indexes (numeric), a vector of profile names (character) or a boolean vector of length equal to the number of profiles.
error the "distance" from uniformity in the sampling distribution of linear extensions.
zeta the incidence matrix of the poset. An object of S3 class incidence. By default, extracted from profiles.
weights weights assigned to profiles. If the argument profiles is not NULL, weights are by default set equal to profile frequencies, otherwise they are set equal to 1.
distances matrix of distances between pairs of profiles. The matrix must be square, with dimensions equal to the number of profiles. Even if the poset is complete, the distance between two profiles is computed only if one profile covers the other.
linext the linear extension initializing the sampling algorithm. By default, it is generated by lingen(zeta). Alternatively, it can be provided by the user through a vector of profile positions.
nit Number of iterations in the Bubley-Dyer algorithm, by default evaluated from a formula of Karzanov and Khachiyan based on the number of profiles and the argument error (see Bubley and Dyer, 1999).
maxint Maximum integer. By default the maximum integer obtainable in a 32bit system. This argument is used to group iterations and run the compiled C code more times, so as to avoid memory indexing problems. Users can set a lower value to maxint in case of low RAM availability.

Value

profiles an object of S3 class wprof reporting poset profiles and their associated frequencies (number of statistical units in each profile).
number_of_profiles number of profiles.
number_of_variables number of variables.
incidence S3 class incidence, incidence matrix of the poset.
cover S3 class cover, cover matrix of the poset.
threshold boolean vector specifying whether a profile belongs to the threshold.
number_of_iterations
number of iterations performed by the Bubley-Dyer algorithm.

rank_dist
matrix reporting by rows the relative frequency distributions of the ranks of each profile, over the set of sampled linear extensions.

thr_dist
vector reporting the relative frequency a profile is used as threshold in the sampled linear extensions.

prof_w
vector of weights assigned to each profile.

edg_w
matrix of distances between profiles, used to evaluate the gap measures.

idn_f
vector reporting the identification function, computed as the fraction of sampled linear extensions where a profile is in the downset of the threshold.

svr_abs
vector reporting, for each profile, the average graph distance from the first profile above all threshold elements, over the sampled linear extensions. In each linear extension, the distance is set equal to 0 for profiles above the threshold.

svr_rel
equal to svr_abs divided by its maximum, that is svr_abs of the minimal element in the linear extension.

wea_abs
vector reporting, for each profile, the average graph distance from the maximum threshold element, over the sampled linear extensions. In each linear extension, the distance is set equal to 0 for profiles in the downset of threshold elements.

wea_rel
the previous absolute distance is divided by its maximum possible value, that is the absolute distance of the threshold from the maximal element in the linear extension.

poverty_gap
Population mean of svr_rel

wealth_gap
Population mean of wea_rel

References


Examples

profiles <- var2prof(varlen = c(3, 2, 2))
threshold <- c("311", "112")

res <- evaluation(profiles, threshold, maxint = 10^5)

summary(res)
plot(res)
**FOD**

*Fuzzy First Order Dominance analysis on partial orders*

**Description**

The function FOD performs the Fuzzy First Order Dominance analysis described in Fattore and Arcagni (forthcoming).

**Usage**

```r
FFOD(profiles, ...) 
## S3 method for class 'wprof'
FFOD(profiles,
    distributions = as.data.frame(profiles$freq),
    lambda = do.call(
        getlambda, as.list(names(profiles$profiles))
    ), ...)
```

**Arguments**

- `profiles` an object of class wprof.
- `distributions` a data.frame of frequencies/weights where the columns correspond to the different distributions and the rows to the profiles. The profiles in the rows have to be ordered as in profiles.
- `lambda` object of class incidence representing the partial order of the relative importance of the indicators. By default, the lambda poset is an antichain (i.e. all the indicators are considered equi-important).
- `...` any of above.

**Details**

The function requires the set of profiles, through the object profiles of class wprof, and the corresponding frequencies, which can be defined by the argument distributions of class data.frame. Notice that a warning is provided if the rownames of the distributions do not match the rownames of the profiles.

Through poset lambda, it is possible to provide (ordinal) information on the relative importance of the indicators in the multi-indicator system.

**Value**

An object of class FODposet containing:

- `delta` matrix of the overall dominance degrees.
- `minr.delta` matrix of the min-transitive closure of matrix delta.
- `global.approx` L1 distance between delta and minr.delta, divided by the L1 norm of delta.
global.approx.corr
L1 distance between delta and mintr.delta, divided by the L1 norm of delta after removing its diagonal.

cell.approx
matrix of absolute differences between the elements of delta and the elements of mintr.delta.

posets.ind
data.frame with indicators describing the partial orders obtained as alpha-cuts of the min-transitive closure mintr.delta. For each poset, the data frame provides: its cardinality, the number of comparabilities, the number of incomparabilities and their ratio (ci.ratio).

eqv.classes
list of boolean matrices specifying, for each alpha-cut, the equivalence classes of the input distributions. Equivalence classes are reported by rows and the initial distributions by columns. If element ij of the matrix is TRUE, then distribution j belongs to the i-th equivalence class.

covers
list of objects of class cover comprising the cover matrices of the poset generated by each alpha-cut of mintr.delta.

Author(s)
Fattore M., Arcagni A.

References

Examples
v1 <- as.ordered(c("a", "b", "c", "d"))
v2 <- 1:3
prof <- var2prof(varmod = list(v1 = as.ordered(c("a", "b", "c", "d")), v2 = 1:3))
np <- nrow(prof$profiles)
k <- 10 # number of populations
set.seed(0)
populations <- as.data.frame(lapply(1:k, function(x) round(runif(np)*100)))
rownames(populations) <- rownames(prof$profiles)
names(populations) <- paste0("P", 1:k)

res <- FFOD(profiles = prof, distributions = populations)
res
Description

The function returns the antichain generating the input downset \( Q \), given the incidence matrix \( z \) of the poset.

Usage

```r
gen.downset(z, Q = 1)
```

Arguments

- \( z \): an incidence matrix.
- \( Q \): a vector (boolean, numeric indexing elements, or character with elements’ names) identifying the input downset.

Value

A boolean vector.

See Also

- `gen.upset`

Examples

```r
lv <- c(2, 3, 2)
prof <- var2prof(varlen = lv)

z <- getzeta(prof)
down <- c("111", "211", "112", "212")
gen <- gen.downset(z, down)

plot(z, lwd = 1 + (rownames(prof$profiles) %in% down), col = 1 + gen, sub = "bold = the downset, red = the antichain generating the downset")
```
**Description**

The function returns the antichain generating the input upset \( Q \), given the incidence matrix \( z \) of the poset.

**Usage**

\[
\text{gen.upset}(z, Q = 1)
\]

**Arguments**

- \( z \) an incidence matrix.
- \( Q \) a vector (boolean, numeric indexing elements, or character with elements' names) identifying the input upset.

**Value**

A boolean vector.

**See Also**

- `gen.downset`

**Examples**

```r
lv <- c(2, 3, 2)
prof <- var2prof(varlen = lv)

z <- getzeta(prof)
up <- c("221", "131", "231", "222", "132", "232")
gen <- gen.upset(z, up)

plot(z, lwd = 1 + (rownames(prof$profiles) %in% up), col = 1 + gen, sub = "bold = the upset, red = the antichain generating the upset")
```
getlambda

**Object constructor for the incidence matrix representing a partial order on variables.**

**Description**

The function creates an object of class `incidence` representing a partial order on the set of variables.

**Usage**

```
getlambda(...)
```

**Arguments**

... Cover relations between variable pairs.

**Details**

Cover relations between pair of variables are defined by the names of the two variables and the symbols `<` and `^`. For instance, if variable A is covered by variable B, write the cover relation as `A < B` or `B ^ A`. If a variable is not comparable to the others, write the name of the variable alone.

**Value**

an object of class `incidence`.

**Author(s)**

Alberto Arcagni

**See Also**

`plot.cover`

**Examples**

```
Lambda <- getlambda(BOTTOM < A, B > BOTTOM, INCOMP)
plot(Lambda)
```
getzeta

**Incidence matrix generation**

**Description**

The function computes the incidence matrix from the set of input profiles \( y \). The output is a boolean matrix of S3 class `incidence`.

**Usage**

```r
getzeta(y)
# S3 method for class 'wprof'
getzeta(y)
```

**Arguments**

- \( y \) the set of profiles, an object of S3 class `wprof`.

**Examples**

```r
prf <- var2prof(varlen = c(2, 3))
getzeta(prf)
```

---

**Heights**

**Description**

The function computes the vector of heights of poset elements.

**Usage**

```r
heights(z)
```

**Arguments**

- \( z \) an object of class `cover`, `incidence` or `poset`.

**Examples**

```r
vl <- c(3, 2, 4)
prof <- var2prof(varlen = vl)
Z <- getzeta(prof)
heights(Z)
```
idn

Description

Given a partial order (arguments profiles and/or zeta) and a selected threshold, the function computes the identification function, as a S3 class object parsec. The identification function is computed by uniform sampling of the linear extensions of the input poset, through a C implementation of the Bubley - Dyer (1999) algorithm. idn is a simplified and faster version of evaluation, computing just the identification function.

Usage

```r
idn(
  profiles = NULL,
  threshold, 
  error = 10^(-3),
  zeta = getzeta(profiles),
  weights = {
    if (!is.null(profiles))
      profiles$freq
    else rep(1, nrow(zeta))
  },
  linext = lingen(zeta),
  nit = floor({
    n <- nrow(zeta)
    n^5 * log(n) + n^4 * log(error^(-1))
  }),
  maxint = 2^31 - 1
)
```

Arguments

- **profiles**: an object of S3 class wprof.
- **threshold**: a vector identifying the threshold. It can be a vector of indexes (numeric), a vector of poset element names (character) or a boolean vector of length equal to the number of elements.
- **error**: the "distance" from uniformity in the sampling distribution of linear extensions.
- **zeta**: the incidence matrix of the poset. An object of S3 class incidence. By default, extracted from profiles.
- **weights**: weights assigned to profiles. If the argument profiles is not NULL, weights are by default set equal to profile frequencies, otherwise they are set equal to 1.
- **linext**: the linear extension initializing the sampling algorithm. By default, it is generated by lingen(zeta). Alternatively, it can be provided by the user through a vector of elements positions.
<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>nit</td>
<td>Number of iterations in the Bubley-Dyer algorithm, by default evaluated using a formula of Karzanov and Khachiyan based on the number of poset elements and the argument <code>error</code> (see Bubley and Dyer, 1999).</td>
</tr>
<tr>
<td>maxint</td>
<td>Maximum integer. By default the maximum integer obtainable in a 32bit system. This argument is used to group iterations and run the compiled C code more times, so as to avoid memory indexing problems. User can set a lower value to <code>maxint</code> in case of lower RAM availability.</td>
</tr>
</tbody>
</table>

**Value**

- **profiles**: an object of S3 class `wprof` reporting poset profiles and their associated frequencies (number of statistical units in each profile).
- **number_of_profiles**: number of profiles.
- **number_of_variables**: number of variables.
- **incidence**: S3 class `incidence`, incidence matrix of the poset.
- **cover**: S3 class `cover`, cover matrix of the poset.
- **threshold**: boolean vector specifying whether a profile belongs to the threshold.
- **number_of_iterations**: number of iterations performed by the Bubley Dyer algorithm.
- **rank_dist**: matrix reporting by rows the relative frequency distribution of the poverty ranks of each profile, over the set of sampled linear extensions.
- **thr_dist**: vector reporting the relative frequency a profile is used as threshold in the sampled linear extensions. This result is useful for a posteriori valuation of the poset threshold.
- **prof_w**: vector of weights assigned to each profile.
- **edges_weights**: matrix of distances between profiles, used to evaluate the measures of gap.
- **idn_f**: vector reporting the identification function, computed as the fraction of sampled linear extensions where a profile is in the downset of the threshold.

<table>
<thead>
<tr>
<th>Value</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td><code>svr_abs</code></td>
<td>NA use <code>evaluation</code> to obtain this result.</td>
</tr>
<tr>
<td><code>svr_rel</code></td>
<td>NA use <code>evaluation</code> to obtain this result.</td>
</tr>
<tr>
<td><code>wea_abs</code></td>
<td>NA use <code>evaluation</code> to obtain this result.</td>
</tr>
<tr>
<td><code>wea_rel</code></td>
<td>NA use <code>evaluation</code> to obtain this result.</td>
</tr>
<tr>
<td><code>poverty_gap</code></td>
<td>NA use <code>evaluation</code> to obtain this result.</td>
</tr>
<tr>
<td><code>wealth_gap</code></td>
<td>NA use <code>evaluation</code> to obtain this result.</td>
</tr>
<tr>
<td><code>inequality</code></td>
<td>NA use <code>evaluation</code> to obtain this result.</td>
</tr>
</tbody>
</table>

**References**


Examples

```r
profiles <- var2prof(varlen = c(3, 2, 4))
threshold <- c("311", "112")

res <- idn(profiles, threshold, maxint = 10^5)
summary(res)
plot(res)
```

Description

The function computes the cover matrix associated to the input incidence matrix (i.e. the cover matrix whose transitive closure is the input incidence matrix).

Usage

```r
incidence2cover(z)
```

Arguments

- `z` an incidence matrix, an object of class `incidence`.

Value

Cover matrix, an object of class `cover`.

See Also

- `cover2incidence`

Description

Incomparability between profiles

The function computes the set of pairwise incomparabilities between poset elements.

Usage

```r
incomp(z)
```

Arguments

- `z` an incidence matrix.
Value

A boolean matrix whose element \(ij\) is TRUE when profiles \(i\) and \(j\) are incomparable.

See Also

getzeta

Examples

\[
vl <- \text{c}(2, 2, 2) \\
pr <- \text{var2prof}(\text{varlen} = vl) \\
Z <- \text{getzeta}(pr) \\
\text{incomp}(Z)
\]

\[
\text{is.downset(z, Q = 1)}
\]

Arguments

\[
z \quad \text{incidence matrix}
\]

\[
Q \quad \text{vector identifying the input set of profiles.}
\]

Examples

\[
z <- \text{getzeta(\text{var2prof}(\text{varlen} = \text{c}(2, 2, 2))))}
\]

\[
\text{plot(z, col = 1 + \text{c}(1, 1, 0, 1, 0, 0, 0) + \text{c}(0, 0, 0, 2, 0, 0, 2), \text{lwd} = 2)}
\]

\[
Q <- \text{c}(4, 7, 8) \\
\text{rownames(z)[Q]} \\
\text{is.downset(z, Q)}
\]

\[
Q <- \text{c("211", "112", "111")} \\
\text{is.downset(z, Q)}
\]
is.linext
is.linext

Description

The function checks whether the input argument order is a linear extension of the poset represented by the incidence matrix z.

Usage

is.linext(order, z)

Arguments

order  indexes of the poset elements (as rows and columns of z matrix) specifying the candidate linear order.

z  incidence matrix.

Examples

```r
Z <- getzeta(var2prof(varlen = c(3, 3)))
ranks <- c(1, 4, 2, 3, 5, 7, 6, 8, 9)
names(ranks) <- rownames(Z)
ranks
is.linext(order = ranks, z = Z)
```

is.partialorder

Description

The function checks whether the input boolean square matrix m represents a partial order.

Usage

is.partialorder(m)

Arguments

m  a boolean square matrix.

See Also

transitivity, binary, reflexivity, antisymmetry, is.preorder, validate.partialorder.incidence
The function checks whether the input boolean square matrix \( m \) represents a preorder.

**Usage**

\[ \text{is.preorder}(m) \]

**Arguments**

\( m \) a boolean square matrix.

**See Also**

* transitivity.binary, reflexivity.
* antisymmetry.is.partialorder.
* validate.partialorder.incidence

**Examples**

\[ M \leftarrow \text{c(TRUE, FALSE, FALSE, FALSE, TRUE, TRUE, FALSE, FALSE, TRUE, TRUE, TRUE, FALSE, TRUE, TRUE, TRUE, TRUE)} \]
\[ M \leftarrow \text{matrix}(M, 4, 4) \]
\[ \text{rownames}(M) \leftarrow \text{colnames}(M) \leftarrow \text{LETTERS}[1:4] \]
\[ \text{is.preorder}(M) \]
Description
The function checks whether the input set of elements Q is an upset of the poset represented by the incidence matrix z.

Usage
is.\upset(z, Q = 1)

Arguments
- \( z \) an incidence matrix.
- \( Q \) vector specifying the input set of poset elements.

Examples
\begin{verbatim}
z <- getzeta(var2prof(varlen = c(2, 2, 2)))
plot(z, col = 1 + c(1, 1, 0, 0, 1, 0, 0) + c(0, 0, 0, 2, 0, 0, 2), lwd = 2)

Q <- c(4, 7, 8)
rownames(z)[Q]
is.\upset(z, Q)
\end{verbatim}

Description
The function returns the LaTeX code to create a tikz figure representing the Hasse diagram drawn from a set of profiles (\texttt{prof}), an incidence matrix (\texttt{Z}) or a cover matrix (\texttt{C}). The code can be copied and pasted into a LaTeX file. The LaTeX source requires the \texttt{tikz} package.

Usage
\begin{verbatim}
l\atex(y, \ldots)
## S3 method for class 'wprof'
l\atex(y, label = "", caption = "", scale = c(1, 1), \ldots)
## S3 method for class 'incidence'
l\atex(y, label = "", caption = "", scale = c(1, 1), \ldots)
## S3 method for class 'cover'
l\atex(y, label = "", caption = "", scale = c(1, 1), \ldots)
\end{verbatim}
Arguments

- `y`: an object of S3 class `wprof`, an object of S3 class `incidence` or an object of S3 class `cover`.
- `label`: the label of the LaTeX figure.
- `caption`: the caption of the LaTeX figure.
- `scale`: a vector of two elements to control the scale of the X-axis and the scale of the Y-axis in the LaTeX output.
- ... any of above.

Examples

```r
prof <- var2prof(varlen = c(2, 3))
latex(prof, label="fg:hasse", caption="Hasse diagram", scale = c(2, 2))
```

---

Description

The function generates all of the linear extensions of the partial order defined by the incidence matrix `Lambda`.

Usage

```r
LE(Lambda)
```

Arguments

- `Lambda`: incidence matrix.

Value

a list of vectors representing all linear orders compatible with the `Lambda` incidence matrix.

Author(s)

Alberto Arcagni

See Also

`getlambda`

Examples

```r
Lambda <- getlambda(A < B, A < C, D < C)
LE(Lambda)
```
**Description**

The function generates the incidence matrices of the lexicographic linear extensions of a profile poset, given the variables (argument `varmod` or `varlen`) and a list of complete orders on them (argument `lst`).

**Usage**

```r
LE2incidence(
  lst,
  varmod = lapply(as.list(varlen), function(lst) 1:1st),
  varlen = sapply(varmod, length)
)
```

```r
## Default S3 method:
LE2incidence(
  lst,
  varmod = lapply(as.list(varlen), function(lst) 1:1st),
  varlen = sapply(varmod, length)
)
```

```r
## S3 method for class 'list'
LE2incidence(
  lst,
  varmod = lapply(as.list(varlen), function(x) 1:x),
  varlen = sapply(varmod, length)
)
```

**Arguments**

- `lst`  
  a vector of characters, or a list of specifies the names of the variables in increasing order. See details.

- `varmod`  
  list of variables and their grades. See details.

- `varlen`  
  a vector with the number of grades of each variable. See details.

**Details**

Argument `lst` is a list of character vectors. Each vector lists variable names in increasing order.

List `varmod` and vector `varlen` must be named so as to identify the variables they refer to. Profiles are generated as combinations of the variables’ grades. The names of the profiles are the grades of the variables concatenated, after the variables order in `varmod/varlen`. See `var2prof` for more details about these arguments.
Levels of a poset

Description

The methods return a vector associating each profile with the corresponding level. The behaviour of these methods for objects of classes incidence and cover is different from the behaviour of function `levels` for factors.

Usage

```r
## S3 method for class 'incidence'
levels(x)
## S3 method for class 'cover'
levels(x)
```

Arguments

- `x` an object of class cover or incidence.

See Also

the function `levels` for objects of type factor
Examples

vl <- c(3, 2, 4)
prof <- var2prof(varlen = vl)
Z <- getzeta(prof)

levels(Z)

logen
logen

Description

The function computes a vector of ranks, defining a linear extension of the poset represented by incidence matrix z.

Usage

lingen(z)

Arguments

z an incidence matrix.

Examples

Z <- getzeta(var2prof(varlen = c(3, 3)))
lingen(Z)

linzeta
linzeta

Description

The function computes the incidence matrix of the linear order defined by the rank vector lin. It returns an object of S3 class incidence.

Usage

linzeta(lin)

Arguments

lin a vector of elements’ ranks.
maximal

Examples

```r
ranks <- c(5, 3, 4, 2, 1)
names(ranks) <- LETTERS[1:5]
linzeta(ranks)
plot(linzeta(ranks))
```

maximal  

Maximal elements of a poset.

Description

The function returns a boolean vector identifying the maximal elements of the poset.

Usage

```r
maximal(z)
```

Arguments

z  
an object of class cover or incidence.

Examples

```r
vl <- c(3, 2, 4)
prof <- var2prof(varlen = vl)
Z <- getzeta(prof)
maximal(Z)
```

merge.wprof  

Merge two sets of profiles.

Description

Method of the function merge of package base to merge two objects of class wprof generated through functions var2prof or pop2prof.

Usage

```r
## S3 method for class 'wprof'
merge(x, y, support = FALSE, FUN = "+", all = TRUE, ...)
```
Arguments

x, y  
objects of class wprof to be coerced to one.

support  
boolean variables specifying whether y is the support of x (FALSE by default).

FUN  
function to be applied to the profiles’ frequencies (by default, FUN = sum). It is ignored if support is TRUE.

all  
same argument of function merge, by default set to TRUE, to get all possible profiles. If a profile is not observed in the data, its frequency is set to 0.

...  
additional arguments to be passed to method merge.data.frame of the package base.

Details

Objects of class wprof are composed of a data.frame of profiles and a vector of frequencies. This method applies method merge.data.frame to the profiles and applies function FUN to the frequencies.

If support is TRUE, function merge.data.frame is not used and the output corresponds to the object y, but with its frequencies modified. These are set equal to the frequencies of the corresponding profiles in x, or to 0 for profiles not contained in x.

Author(s)

Arcagni A.

See Also

merge, var2prof, pop2prof

Examples

n <- 5
v1 <- as.ordered(c("a", "b", "c", "d"))
v2 <- 1:3
set.seed(0)
pop <- data.frame(v1 = sample(v1, n, replace = TRUE),
v2 = sample(v2, n, replace = TRUE))

survey_weights <- round(runif(5)*10)

prof1 <- pop2prof(pop, weights = survey_weights)
prof2 <- var2prof(varmod = list(v1 = as.ordered(c("a", "b", "c", "d")), v2 = 1:3))

# prof2 is the support of prof1
merge(prof1, prof2, support = TRUE)

# union between the two sets of profiles and their frequencies are added
merge(prof1, prof2)
# intersection of the sets of profiles with the assumption
# that the minimum number of observations is shared
# between the two distributions
merge(prof1, prof2, all = FALSE, FUN = min)

prof2$freq <- prof2$freq*10
# to remove from prof2 the observations in prof1
distribution <- merge(prof2, prof1, FUN = "-")); distribution

---

**minimal**

*Minimal elements of a poset*

**Description**

The function returns a boolean vector identifying the minimal elements of the poset.

**Usage**

```r
minimal(z)
```

**Arguments**

- `z` an object of class `cover` or `incidence`.

**Examples**

```r
v1 <- c(3, 2, 4)
prof <- var2prof(varlen = v1)
z <- getzeta(prof)
minimal(z)
```

---

**mrg**

*Merge posets*

**Description**

The function merges posets defined through a list of incidence matrices or a list of complete orders between the variables (argument `lst`). In the second case the variables must be defined (argument `varmod` or `varlen`).

Usage

```r
mrg(
  lst,
  varmod = lapply(as.list(varlen), function(x) 1:x),
  varlen = sapply(varmod, length)
)
```

Arguments

- `lst`: a list of incidence matrices (class `incidence`) or list of vectors of characters. See details.
- `varmod`: list of variables and their grades. See details.
- `varlen`: a vector of number of grades of each variable. See details.

Details

For efficiency reasons, the argument `lst` can be also a list of vectors of characters. In this case, each vector lists the names of the variables in increasing order.

The list `varmod` and the vector `varlen` must be named, so as to identify the variables they refer to. The profiles are generated by the combinations of the variables grades. The names of the profiles are the grades of the variables concatenated, according to variables order in `varmod`/`varlen`. See `var2prof` for more details about these arguments.

Value

an object of S3 class `incidence`.

Author(s)

Alberto Arcagni

See Also

- `var2prof`, `LE2incidence`

Examples

```r
# Example with lst as list of incidence matrices
Lambda <- getLambda(A < B, C < D)
plot(Lambda)
lst <- LE(Lambda)
```
obsprof

Remove unobserved profiles.

Description

The function removes, from the set of possible profiles prof derived from the multi-indicator system, those unobserved in the input dataset (i.e. profiles with associated frequency equal to zero). It returns an object of class S3 wprof comprising the observed profiles and their frequencies.

Usage

obsprof(prof)

## S3 method for class 'wprof'
obsprof(prof)

Arguments

prof object of S3 class wprof.

Examples

prf <- var2prof(varlen = c(3, 3, 3))
prf$freq <- sample(c(0, 1), 3*3*3, replace = TRUE)
prf <- obsprof(prf)
plot(prf, shape = "equispaced")

vl <- c(A = 2, B = 2, C = 2, D = 2)
lstZeta <- L2zincidence(lst, varlen = vl)
for (x in lstZeta)
  plot(x)
mrg(lstZeta)

# Example with lst as list of characters
Lambda <- getlambda(A < B, C < D)
lst <- L(E(Lambda))
v1 <- c(A = 2, B = 2, C = 2, D = 2)
Zeta <- mrg(lst, varlen = vl)
plot(Zeta)
parse2igraph  

Converting a partial order to an object of the package igraph.

Description

The function turns a cover matrix to an igraph object, so as to allow using the graphical power of igraph to plot Hasse diagrams. Objects of class cover are boolean matrices where element ij is equal to 1 if element i is covered by element j. This makes the cover matrix the transpose of the adjacency matrix of a graph, describing the cover relation in igraph.

Usage

parse2igraph(p, ...)
## S3 method for class 'cover'
parse2igraph(p, ...)
## S3 method for class 'incidence'
parse2igraph(p, ...)

Arguments

p  an object of class cover or incidence.
... additional arguments of the function vertices.

Value

The function returns an object of class igraph, representing the directed graph defined by the cover relation.

The function adds to the graph a layout generated through function vertices, so as to plot the graph according to the conventions used for Hasse diagrams.

Author(s)

Arcagni, A.

References


See Also

igraph, vertices
plot.average_ranks

Examples

```r
example(merge.wprof)
poset <- getzeta(distribution)
incidence2cover(poset)

G <- parsec2igraph(poset, noise = TRUE)
get.adjacency(G)
# tkplot(G, vertex.size = distribution$freq, vertex.color = "white")

G <- parsec2igraph(poset, noise = 10)
# tkplot(G, vertex.size = distribution$freq, vertex.color = "white")
```

---

plot.average_ranks  Method of function plot for objects of class average_ranks

Description

From the output of the function average_ranks, the function plots the average rank and the associated rank interval, for each element of the poset.

Usage

```r
## S3 method for class 'average_ranks'
plot(x,
    range.first = TRUE, range.col = "black", range.lty = 1,
    range.lwd = 1, type = "p", ylim = c(max(x$sup), 1),
    xlab = "", ylab = "Average rank", pch = c(16, 3, 3),
    col = "black", cex = c(1, 1, 1), ...
)
```

Arguments

- `x`  
  An object of class average_ranks.
- `range.first`  
  A boolean attribute to specify whether the interval is plotted in background (TRUE) or in foreground (FALSE).
- `range.col`  
  Color of the interval.
- `range.lty`  
  The line type to represent the range; the values are the same of the attribute lty in the `plot.default` function.
- `range.lwd`  
  Width of the lines representing the range.
- `type`  
  Attribute of the function `plot.default`, here "p" by default.
- `ylim`  
  Attribute of function `plot.default`, here c(max(x$sup), 1) by default (this way, the Y-axis is reversed, so that rank 1 corresponds to "best").
- `xlab`  
  Attribute of the function `plot.default`, here "" by default.
- `ylab`  
  Attribute of the function `plot.default`, here "Average rank" by default.
Attribute of the function `plot.default`, here `c(16, 3, 3)` by default. This method uses the `matplot` function to plot the average ranks and their range. The first value refers to the point character of the average rank, the other two to the point characters of the range.

`col` Attribute of the function `plot.default`, here "black" by default. The average ranks and their ranges are of the same color, but similarly to `pch`, users can provide a vector of different colors.

`cex` Attribute of the function `plot.default`, here `c(1, 1, 1)` by default.

Other arguments of the function `plot.default`.

### See Also

`average_ranks`, `plot.default`, `matplot`

### Examples

```r
profiles <- var2prof(varlen = c(3, 2, 4))
Z <- getzeta(profiles)
res <- average_ranks(Z)
plot(res)
```

---

### Description

plot methods to draw Hasse diagrams, for objects of S3 classes `wprof`, `incidence`, `cover`,

### Usage

```r
## S3 method for class 'wprof'
plot(x, shape = c("square", "circle", "equispaced"), noise = FALSE, ...)
## S3 method for class 'incidence'
plot(x, shape = c("square", "circle", "equispaced"), noise = FALSE, ...)
## S3 method for class 'cover'
plot(x, shape = c("square", "circle", "equispaced"), noise = FALSE,
     pch = 21, cex = max(nchar(rownames(x))) + 2, bg = "white", ...)
```

### Arguments

- `x` an object of S3 class `wprof`, an object of S3 class `incidence` or an object of S3 class `cover`.
- `shape` shape of the Hasse diagram. See `vertices`.
- `noise` jittering in the shape of the Hasse diagram. See `vertices`.
- `pch` graphical parameter. See `plot.default`.
- `cex` graphical parameter. See `plot.default`.
- `bg` graphical parameter. See `plot.default`.
- `...` further optional graphical parameters. See `plot.default`.

---

### Hasse diagram

plot methods to draw Hasse diagrams, for objects of S3 classes `wprof`, `incidence`, `cover`,

```r
## S3 method for class 'wprof'
plot(x, shape = c("square", "circle", "equispaced"), noise = FALSE, ...)
## S3 method for class 'incidence'
plot(x, shape = c("square", "circle", "equispaced"), noise = FALSE, ...)
## S3 method for class 'cover'
plot(x, shape = c("square", "circle", "equispaced"), noise = FALSE,
     pch = 21, cex = max(nchar(rownames(x))) + 2, bg = "white", ...)
```

### Arguments

- `x` an object of S3 class `wprof`, an object of S3 class `incidence` or an object of S3 class `cover`.
- `shape` shape of the Hasse diagram. See `vertices`.
- `noise` jittering in the shape of the Hasse diagram. See `vertices`.
- `pch` graphical parameter. See `plot.default`.
- `cex` graphical parameter. See `plot.default`.
- `bg` graphical parameter. See `plot.default`.
- `...` further optional graphical parameters. See `plot.default`.
Examples

```r
prf <- var2prof(varlen = c(5, 5, 5))
prf$freq <- sample(c(rep(0, 20), 1, 2, 3), 5*5*5, replace = TRUE)
prf <- obsprof(prf)

z <- getzeta(prf)

plot(z, shape = "equispaced", col = prf$freq, lwd = 2)
```

Description

Several representations of the results provided by the evaluation function.

Usage

```r
## S3 method for class 'parsec'
plot(
  x,
  which = c("Hasse", "threshold", "identification", "rank", "gap"),
  ask = dev.interactive(),
  shape = c("square", "circle", "equispaced"),
  noise = FALSE,
  ...
)
```

Arguments

- `x`: an object of S3 class `parsec`, output of the `evaluation` function.
- `which`: the names of the graphs to be plotted (all, by default); the user can choose among:
  - Hasse, the Hasse diagram of the poset, see `plot.cover` for details,
  - threshold, the relative frequencies of the times a profile is used as threshold in the sampled linear extensions.
  - rank, barplot providing the rank distribution of each profile (X-axis). The heights of the blocks represent relative frequencies (the sum of the heights over profiles is equal to 1) and the color represents the rank: white for rank one, black for the highest rank and a gray scale for intermediate ranks.
  - gap, a unified representation of the relative (e.g. poverty) gap and of the relative (e.g. wealth) gap. The horizontal lines represent the average (e.g. poverty) gap and the average (e.g. wealth gap). The darker vertical dashed lines represent the threshold profiles.
- `ask`: boolean value indicating whether the system has to ask users before changing the plot.
shape the shape of the Hasse diagram, see `plot.cover` for details.
noise jittering in the shape of the Hasse diagram. See `vertices`.
... further arguments for the `plot.cover` function.

See Also

`evaluation, plot.cover`

Examples

```r
profiles <- var2prof(varlen = c(3, 2, 4))
threshold <- c("311", "112")
res <- evaluation(profiles, threshold, nit = 10^3)
plot(res)
```

Description

The function generates four plots, to reproduce the sequence of the average ranks and of the positions of the elements, in the rankings associated to the alpha-cut posets.

Rankings and average ranks have to be evaluated with the function `rank_stability`.

First and third plots show the sequence of average ranks, second and fourth show the sequence of rankings. Sequences in first and second plots are shown against the sequence of alpha-cuts, in third and fourth plots as a function of alpha values.

Usage

```r
## S3 method for class 'rank_stability'
plot(x,
     which = 1:4, legend = TRUE, legend.x = "bottomleft",
     legend.y = NULL, legend.bg = "white", grid = TRUE,
     grid.lty = 2, grid.col = rgb(0, 0, 0, 1/7),
     grid.lwd = 1, y_axis = "reversed", ask = dev.interactive(),
     type = "l", col = gray(1:ncol(x$ranking)/ncol(x$ranking)/1.3),
     lwd = 3, lty = 1, ...)
```

Arguments

- `x` object of class `rank_stability` generated by function `rank_stability`.
- `which` select a subset of the numbers 1:4, to specify the desired plots. See caption below (and the 'Details').
pop2prof

legend
boolean argument to choose whether to show the legend in the plots.
legend.x, legend.y, legend.bg
arguments x, y and bg of the function legend defining the coordinates and the
background color of the legend.

grid
boolean argument to choose whether to show the grid in the plots.
grid.lty, grid.col, grid.lwd
arguments defining the line type, color and width of the grid.

y_axis
if it is set equal to "reversed" plots show the y axis reversed.

ask
boolean argument indicating whether the system has to ask users before chang-
ing plots.

type
1-character string giving the desired type of plot. See plot.default for details.

col
vector of colors. See matplot for details.
lwd
vector of line widths. See matplot for details.
lty
vector of line types. See matplot for details.
...
other arguments of function matplot.

See Also
rank_stability, legend, plot.default, matplot

Examples

v1 <- as.ordered(c("a", "b", "c", "d"))
v2 <- 1:3
prof <- var2prof(varmod = list(v1 = as.ordered(c("a", "b", "c", "d")), v2 = 1:3))
np <- nrow(prof$profiles)
k <- 10 # number of populations
set.seed(0)
populations <- as.data.frame(lapply(1:k, function(x) round(runif(np)*100)))
rownames(populations) <- rownames(prof$profiles)
names(populations) <- paste0("P", 1:k)

x <- FFOD(profiles = prof, distributions = populations)

res <- rank_stability(x)
plot(res)

pop2prof

Population to profiles

Description

Extract the observed profiles and the corresponding frequencies, out of the statistical population.
Usage

```r
pop2prof(y, labtype = c("profiles", "progressive"), sep = "", weights = rep(1, nrow(y)))
```

Arguments

- `y`: a dataset, used to count profile frequencies. See details.
- `labtype`: users can choose the type of labels to assign to profiles. See details.
- `sep`: variables separator in the profiles labels.
- `weights`: a vector of length equal to the number of observations in `y`, representing the survey weights of each observation.

Details

`y` is a data.frame of observations on the ordinal or numeric variables. The partial order must be defined within the object type, so as to build the incidence matrix of the order relation (see `getzeta`).

The function extracts variables and their observed modalities from the population; it builds all possible profiles and assigns to them the corresponding frequency. If some modalities are not observed in the population, they will not be used to build the profiles. If one is interested in the set of all possible profiles from a given set of variables, function `var2prof` is to be used.

Users can choose the label type to assign to profiles. When the names of modalities are too long, it is suggested to choose `progressive`.

Value

The function returns a S3 class object `wprof`, "weighted profiles", containing the data.frame named `profiles` and the frequency vector `freq`.

See Also

`var2prof`, `getzeta`

Examples

```r
n <- 5
v1 <- as.ordered(c("a", "b", "c", "d"))
v2 <- 1:3
pop <- data.frame(
  v1 = sample(v1, n, replace = TRUE),
  v2 = sample(v2, n, replace = TRUE)
)
pop2prof(pop)
```
Description

The function identifies in a matrix \( y \), profiles in \( \text{prof} \). For each row of matrix \( y \), the function returns the location of the corresponding profile in object \( \text{prof} \).

Usage

\[
popelem(\text{prof}, \ldots)
\]

\#\# S3 method for class 'wprof'

\[
popelem(\text{prof}, y, \ldots)
\]

Arguments

- \( \text{prof} \): an object of S3 class \( \text{wprof} \).
- \( y \): a matrix or data.frame representing a set of observations with variables (the same contained in \( \text{prof} \)) by columns.
- \( \ldots \): any of the above.

Examples

\[
v1 <- \text{c}(2, 3, 2)
prf <- \text{var2prof}(\text{varlen} = v1)
pop <- \text{matrix}(\text{c}(2, 1, 1, 2, 1, 2, 3, 1, 3, 3), \text{byrow} = \text{FALSE})
rownames(pop) <- \text{LETTERS}[1:3]
\]

\[
v <- popelem(\text{prof} = prf, y = pop)
v
\]

\[
\text{prf$profiles[v,]}
\]

proFreq

\begin{center}
\textbf{Observed profile frequencies}
\end{center}

Description

The function computes profile frequencies, by counting the number of times a profile appears in the population.

Usage

\[
\text{proFreq(profiles, population)}
\]
Arguments

- profiles: an object of S3 class wprof.
- population: a matrix or data.frame representing a set of observations with variables (the same contained in prof) by columns.

Value

An object of class wprof with the same profiles of the argument but with different frequencies.

Author(s)

Alberto Arcagni

See Also

popelem

Examples

```r
vl <- c(2, 3, 2)
prf <- var2prof(varlen = vl)
pop <- matrix(c(2, 1, 1, 1, 2, 1, 2, 3, 1), 3, 3)
rownames(pop) <- LETTERS[1:3]

profreq(profiles = prf, population = pop)
```

---

**rank_stability**

*Rank stability analysis in posetic FOD*

Description

The function computes the average ranks and the positions in the ranking of the elements of the alpha-cuts.

Usage

```r
rank_stability(x, ...)
## S3 method for class 'FODposet'
rank_stability(x,
    selection = 1:length(x$covers),
    coverage_probability = 0.9,
    error = 10^-5, ...)
```
Arguments

- **x**: object of class `FODposet` generated by function `FOD`.
- **selection**: numeric vector or a vector of names to select the cover matrices in argument `x`.
- **coverage_probability**: least coverage probability of the rank intervals with extremes `lower_ranks` and `upper_ranks`.
- **error**: the "distance" from uniformity in the sampling distribution of linear extensions used to evaluate the average ranks. See `idn` for details.
- **...**: any of above.

Value

- **alpha**: vector of the alpha values defining the alpha-cuts.
- **average_ranks**: data frame of average ranks of the poset elements (by columns) at different alpha values (by rows).
- **lower_ranks**: data frame of the lower bounds of the rank interval, of each poset element (by columns) at different alpha values (by rows).
- **upper_ranks**: data frame of the upper bounds of the rank interval, of each poset element (by columns) at different alpha values (by rows).
- **ranking**: data frame of the positions of poset elements (by columns), in the ranking extracted from the posets associated to alpha-cuts (by rows).
- **resolution**: number of elements of the posets associated to the alpha-cuts.

Author(s)

Fattore M., Arcagni A.

See Also

`FFOD`, `idn`

Examples

```r
v1 <- as.ordered(c("a", "b", "c", "d"))
v2 <- 1:3
prof <- var2prof(varmod = list(v1 = as.ordered(c("a", "b", "c", "d")), v2 = 1:3))
np <- nrow(prof$profiles)
k <- 10 # number of populations
set.seed(0)
populations <- as.data.frame(lapply(1:k, function(x) round(runif(np)*100)))
rownames(populations) <- rownames(prof$profiles)
names(populations) <- paste0("P", 1:k)

x <- FFOD(profiles = prof, distributions = populations)
res <- rank_stability(x)
res
```
Description

The function checks whether the input boolean square matrix \( m \) represents a reflexive binary relation.

Usage

```r
reflexivity(m)
```

Arguments

- \( m \) a boolean square matrix.

See Also

- `transitivity`, `binary`, `antisymmetry`
- `is.preorder`, `is.partialorder`
- `validate.partialorder.inheritance`

Examples

```r
M <- c(TRUE, FALSE, FALSE, FALSE, TRUE, TRUE, FALSE, FALSE, TRUE, FALSE, TRUE, TRUE, TRUE, FALSE, TRUE, TRUE, TRUE, TRUE, FALSE, TRUE, TRUE, TRUE, TRUE)
M <- matrix(M, 4, 4)
rownames(M) <- colnames(M) <- LETTERS[1:4]
reflexivity(M)
```

Description

Function to remove profiles from an object of class \( wprof \).

Usage

```r
rmProfiles(y, ...)
```

# S3 method for class 'wprof'
```r
rnProfiles(y, v, ...)
```
Arguments

\( \text{y} \)  
object of class wprof.

\( \text{v} \)  
a vector pointing to the profiles to be removed. The vector can be of type:

- numeric whose components refer to the positions of profiles in \( \text{y} \);
- logical of the same length as the number of profiles in \( \text{y} \);
- character, referring to profile names in \( \text{y} \).

...  
any of the above.

Value

The function returns an wprof object equal to \( \text{y} \) but without the profiles in \( \text{v} \).

Examples

\[ \begin{align*}
\text{vl} & \leftarrow \text{c}(3, 3, 3) \\
\text{prof} & \leftarrow \text{var2prof(varlen = vl)} \\
\text{rownames(prof$profiles)} & \\
\text{prof} & \leftarrow \text{rmProfiles(prof, c("123", "321"))} \\
\text{plot(prof)}
\end{align*} \]

summary.cover  
Summary method for cover and incidence objects.

Description

The function computes a summary of cover and incidence S3 objects. Currently, the function returns just the number of profiles and the number of comparabilities.

Usage

\[ \begin{align*}
\# \text{S3 method for class 'cover'} \\
\text{summary(object, ...)}
\end{align*} \]

\[ \begin{align*}
\# \text{S3 method for class 'incidence'} \\
\text{summary(object, ...)}
\end{align*} \]

Arguments

\( \text{object} \)  
a cover matrix or an incidence matrix.

...  
added for consistency with the generic method.
Examples

```r
vl <- c(2, 3, 3)
prf <- var2prof(varlen = vl)
Z <- getzetaprfrf
summary(Z)
C <- incidence2cover(Z)
summary(C)
```

summary.parsen  Summary of outputs of the evaluation function.

Description

S3 method of function `summary` reporting main information for an object of class `parsen`, obtained from function `evaluation`. In particular, the function computes a table showing, for each profile:

- the variables’ grades identifying the profile (if these are returned by `evaluation`.
- the assigned weight.
- whether or not it belongs to the threshold.
- the corresponding value of the identification function.
- the average poverty rank.
- the different gap measures (see `evaluation` for details).

If the number of profiles is higher than ten, the shown table gets cut, but the method returns a `data.frame` providing the complete output.

Usage

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

Arguments

- `object` an object of S3 class `parsen`, output of the `evaluation` function.
- `...` added for consistency with the generic method.

See Also

`evaluation`

Examples

```r
profiles <- var2prof(varlen = c(3, 2, 4))
threshold <- c("311", "112")

res <- evaluation(profiles, threshold, nit = 10^3)

sm <- summary(res)
summary(sm)
```
transitiveClosure

### Description
The function computes the transitive closure of a reflexive and antisymmetric binary relation.

### Usage
```
transitiveClosure(m)
```

### Arguments
- `m` - a generic square boolean matrix representing a reflexive and antisymmetric binary relation, an object of class `cover` or an object of class `incidence`.

### Value
Incidence matrix of the transitive closure of the input matrix `m`.

### See Also
- `is.partialorder`

### Examples
```
m <- c(1, 0, 0, 1, 0, 1, 0, 1, 0, 1, 0, 1, 0, 1, 0, 1)
m <- matrix(m, 4, 4)
transitiveClosure(m)
```

---

transitivity

### Description
The function checks whether the boolean square matrix `m` represents a transitive binary relation.

### Usage
```
transitivity(m)
```

### Arguments
- `m` - a boolean square matrix.
See Also

binary, reflexivity, antisymmetry.

is.preorder, is.partialorder,

validate.partialorder.incidence

Examples

M <- c(TRUE, FALSE, FALSE, FALSE, TRUE, TRUE, FALSE, FALSE, TRUE, FALSE, TRUE, TRUE, FALSE, TRUE, TRUE, TRUE, TRUE, FALSE, TRUE, TRUE, TRUE)
M <- matrix(M, 4, 4)
rownames(M) <- colnames(M) <- LETTERS[1:4]

transitivity(M)

upset

Description

The function computes a boolean vector specifying which poset elements belong to the downset generated by subposet Q.

Usage

upset(z, ...)

## S3 method for class 'cover'
upset(z, ...)

## S3 method for class 'incidence'
upset(z, Q = NULL, ...)

Arguments

z a cover or an incidence matrix, of S3 classes cover or incidence, respectively.
Q vector specifying a subposet of the poset represented by z.
... any of the above.

Examples

z <- getzeta(var2prof(varlen = c(2, 2, 2)))

plot(z, col = 1 + c(1, 1, 0, 0, 1, 0, 0, 0) + c(0, 0, 0, 2, 0, 0, 2, 2), lwd = 2)

Q <- c(4, 7, 8)
rownames(z)[Q]
upset(z, Q)

Q <- c("211", "112", "111")
upset(z, Q)
validate.partialorder.incidence

Description

The function checks whether the boolean square matrix \( m \) represents a partial order. If yes, the function returns the same input matrix as a S3 class object incidence. Otherwise, the unfulfilled partial order properties of matrix \( m \) are returned.

Usage

validate.partialorder.incidence(m)

Arguments

\( m \)  
a boolean square matrix.

See Also

transitivity, binary, reflexivity,
antisymmetry, is.preorder, is.partialorder

Examples

\[
M <- c(TRUE, FALSE, FALSE, FALSE, TRUE, TRUE, FALSE, TRUE, FALSE, TRUE,
FALSE, TRUE, TRUE, TRUE, TRUE)
\]
\[
M <- matrix(M, 4, 4)
\]
\[
rownames(M) <- colnames(M) <- LETTERS[1:4]
\]
\[
M <- validate.partialorder.incidence(M)
\]
\[
plot(M)
\]

---

var2prof

Variables to profiles

Description

The function computes the list of all of the profiles from a list of input ordinal variables. See details for how to define variables.

Usage

var2prof(varmod = lapply(as.list(varlen), function(x) 1:x),
varlen = sapply(varmod, length), freq = NULL,
labtype = c("profiles", "progressive"), y=NULL)
Arguments

- **varmod**: list of variables and their grades. See details.
- **varlen**: a vector of number of grades of each variable. See details.
- **freq**: profiles frequency distribution. By default, the frequencies are set equal to 1.
- **labtype**: type of labels to assign to profiles. See details.
- **y**: a matrix of observations, used to count profiles frequencies. See details.

Details

Variables can be defined through their names and grades, using a list as argument `varmod`. The names of the objects in the list are taken as variable names. The objects in the list must be ordered vectors or numeric vectors.

A faster way to define variables is through a vector with the number of grades of each variable, as argument `varlen`. This way, variables and their grades are assigned arbitrary names. In particular, grades are identified by their ranks in the variable definition.

The user can choose the type of label to assign to profiles. Profiles is the combination of grades identifying the profiles. When the names of the grades are too long, it is suggested to choose `progressive`.

`y` is a matrix of observations on the ordinal variables (observations by rows and variables by columns). Variables must be ordered as defined in the previous arguments. The names of variable grades must match their definition. By this argument, the function counts the number of times a profile is observed in the population, assigning the result to the `freq` output. This method should be used when the variables and their grades are known, otherwise the function `pop2prof` is available.

Value

The function returns a S3 class object `wprof`, "weighted profiles", comprising the data.frame profiles and the vector of frequencies `freq`.

See Also

- `pop2prof`, `getzeta`

Examples

```r
# 2 variables with 2 modalities, frequencies detected from population
pop <- matrix(sample(1:2, 200, replace=TRUE), 50, 2)
var2prof(varlen=c(2, 2))

# 2 variables:
# - mood: 2 modalities
# - weather: 3 modalities
# 2x3 profiles and frequencies sampled from a Binomial distribution n = 10, p = 0.5
var <- list(
  mood = ordered(c("bad", "good"), levels = c("bad", "good")),
  weather = ordered(c("rainy", "cloudy", "sunny"), levels = c("rainy", "cloudy", "sunny"))
)
var2prof(var, freq = rbinom(2*3, 10, 0.5), labtype = "progressive")
```
coordinates of the vertices of the Hasse diagram, representing the input cover relation.

Description

The function computes the coordinates of the vertices of the Hasse diagram.

Usage

vertices(C, shape = c("square", "circle", "equispaced"), noise = FALSE)

Arguments

- C: cover matrix, an object of class S3 cover.
- shape: shape of the diagram. See details.
- noise: some jittering on the x axis, so as to improve readability. Values can be boolean or positive values, to get different jittering intensities.

Details

Possible Hasse diagram shapes: square; circle; equispaced. The last option is suggested when the poset has more than one maximal or minimal elements. The function is used by the plot methods defined in the package (see plot.cover).

See Also

plot.cover
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