Package ‘QCA’

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Description An extensive set of functions to perform Qualitative Comparative Analysis: crisp sets ('csQCA'), temporal ('tQCA'), multi-value ('mvQCA') and fuzzy sets ('fsQCA'), using a GUI - graphical user interface. 'QCA' is a methodology that bridges the qualitative and quantitative divide in social science research. It uses a Boolean algorithm that results in a minimal causal combination which explains a given phenomenon.
License GPL (>= 2)
NeedsCompilation yes
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Description

The package QCA contains functions to perform Qualitative Comparative Analysis, complemented with a graphical user interface. It implements the comparative method as first described by Ragin (1987), and extended by Cronqvist and Berg-Schlosser (2009) and Ragin (2000, 2008). QCA is a bridge between the qualitative and quantitative research methodologies, making use of the qualitative procedures in a systematic, algorithmic way (therefore increasing the “confidence” in the results, as understood by quantitative researchers).

The Quine-McCluskey minimization algorithms implemented in this package are mathematically exact, as described by Dusa (2007b), Dusa (2010), Dusa and Thiem (2015) and Dusa (2017). They all return the same, relevant set of prime implicants for csQCA (binary crisp sets QCA), mvQCA (multi-value QCA) and fsQCA (fuzzy-sets QCA).

Between versions 1.0-0 and up to version 1.1-3, the package welcomed a second co-author Alrik Thiem, responsible with the manual testing and documentation of functions, while the main author Adrian Dusa developed this software. The package gained new functionality and also other types of
QCA-like tsQCA (temporal QCA), see Caren and Panofsky (2005), Ragin and Strand (2008) and more recently also causal chains similar to those from the package cna (see Ambuehl et al. 2015).

The results of the QCA package are consistent with (and sometimes better than) the results of the other software packages for QCA, most notably fs/QCA by Ragin and Davey (2014) and Tosmana by Cronqvist and Berg-Schlosser (2009). A comparison of several such software is provided by Thiem and Dusa (2013).

From version 2.0, this package uses a new graphical user interface based on the package shiny. In order to avoid developing different interfaces for different operating systems, the current GUI was designed to work into a webpage. It uses a combination of HTML, CSS, jQuery for the user interface, a custom development framework using vector graphics based on the Raphael library, and extensive Javascript code to bind these altogether. A first version of this user interface was presented by Dusa (2007a), but users should be aware the current version is much more advanced. Starting with version 2.5, the user interface gained a web-based command console to offer a complete experience of available functionality.

Version 3.0 brings major improvements and additions, most notably the implementation of a new minimization algorithm called CCubes (Consistency Cubes), that is hundreds of times faster than the previous eQMC.

Details

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Type: Package
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References


calibrate

Calibrate raw data to crisp or fuzzy sets

description

This function transforms (calibrates) the raw data to either crisp or fuzzy sets values, using both the direct and the indirect methods of calibration.

usage

calibrate(x, type = "fuzzy", method = "direct", thresholds = NA,
          logistic = TRUE, idm = 0.95, ecdf = FALSE, below = 1, above = 1, ...)

Trier: University of Trier.
URL: http://www.tosmana.net

vol.60, no.5, pp.576-586, DOI: 10.1016/j.jbusres.2007.01.002


Quantity vol.44, no.1, pp.99-113, DOI: 10.1007/s11135-008-9183-x

Dusa, A.; Thiem, A. (2015) “Enhancing the Minimization of Boolean and Multivalue Output Func-
tions With eQMC” Journal of Mathematical Sociology vol.39, no.2, pp.92-108,
DOI: 10.1080/0022250X.2014.897949

lished working paper on ResearchGate, DOI: RG.2.2.36359.19361/1

Ragin, C.C. (1987) The Comparative Method: Moving beyond Qualitative and Quantitative Strate-


Chicago Press.

Comment on Caren and Panofsky (2005)”. Sociological Methods & Research vol.36, no.4, pp.431-
441.

[Computer Program]. Irvine: Department of Sociology, University of California.

Current Software for Qualitative Comparative Analysis (QCA).” Social Science Computer Review
vol.31, no.4, pp.505-521, DOI 10.1177/0894439313478999
**Arguments**

- **x**: A numerical causal condition.
- **type**: Calibration type, either "crisp" or "fuzzy".
- **method**: Calibration method, either "direct" or "indirect".
- **thresholds**: A vector of (named) thresholds.
- **logistic**: Calibrate to fuzzy sets using the logistic function.
- **idm**: The set inclusion degree of membership for the logistic function.
- **ecdf**: Calibrate to fuzzy sets using the empirical cumulative distribution function of the raw data.
- **below**: Numeric (non-negative), determines the shape below crossover.
- **above**: Numeric (non-negative), determines the shape above crossover.
- **...**: Additional parameters, mainly for backwards compatibility.

**Details**

Calibration is a transformational process from raw numerical data (interval or ratio level of measurement) to set membership scores, based on a certain number of qualitative anchors.

When **type** = "crisp", the process is similar to recoding the original values to a number of categories defined by the number of thresholds. For one threshold, the calibration produces two categories (intervals): 0 if below, 1 if above. For two thresholds, the calibration produces three categories: 0 if below the first threshold, 1 if in the interval between the thresholds and 2 if above the second threshold etc.

When **type** = "fuzzy", calibration produces fuzzy set membership scores, using three anchors for the increasing or decreasing s-shaped distributions (including the logistic function), and six anchors for the increasing or decreasing bell-shaped distributions.

The argument **thresholds** can be specified either as a simple numeric vector, or as a named numeric vector. If used as a named vector, for the first category of s-shaped distributions, the names of the thresholds should be:

- "e" for the full set exclusion
- "c" for the set crossover
- "i" for the full set inclusion

For the second category of bell-shaped distributions, the names of the thresholds should be:

- "e1" for the first (left) threshold for full set exclusion
- "c1" for the first (left) threshold for set crossover
- "i1" for the first (left) threshold for full set inclusion
- "i2" for the second (right) threshold for full set inclusion
- "c2" for the second (right) threshold for set crossover
- "e2" for the second (right) threshold for full set exclusion
If used as a simple numerical vector, the order of the values matter.

If \( e < c < i \), then the membership function is increasing from \( e \) to \( i \). If \( i < c < e \), then the membership function is decreasing from \( i \) to \( e \).

Same for the bell-shaped distribution, if \( e_1 < c_1 < i_1 \leq i_2 < c_2 < e_2 \), then the membership function is first increasing from \( e_1 \) to \( i_1 \), then flat between \( i_1 \) and \( i_2 \), and then decreasing from \( i_2 \) to \( e_2 \). In contrast, if \( i_1 < c_1 < e_1 \leq e_2 < c_2 < i_1 \), then the membership function is first decreasing from \( i_1 \) to \( e_1 \), then flat between \( e_1 \) and \( e_2 \), and finally increasing from \( e_2 \) to \( i_2 \).

When logistic = TRUE (the default), the argument idm specifies the inclusion degree of membership for the logistic function. If logistic = FALSE, the function returns linear s-shaped or bell-shaped distributions (curved using the arguments below and above), unless activating the argument ecdf.

If there is no prior knowledge on the shape of the distribution, the argument ecdf asks the computer to determine the underlying distribution of the empirical, observed points, and the calibrated measures are found along that distribution.

Both logistic and ecdf arguments can be used only for s-shaped distributions (using 3 thresholds), and they are mutually exclusive.

The parameters below and above (active only when both logistic and ecdf are deactivated, establish the degree of concentration and dilation (convex or concave shape) between the threshold and crossover:

\[
\begin{align*}
0 < \text{below} < 1 & \quad \text{dilates in a concave shape below the crossover} \\
\text{below} = 1 & \quad \text{produces a linear shape (neither convex, nor concave)} \\
\text{below} > 1 & \quad \text{concentrates in a convex shape below the crossover} \\
0 < \text{above} < 1 & \quad \text{dilates in a concave shape above the crossover} \\
\text{above} = 1 & \quad \text{produces a linear shape (neither convex, nor concave)} \\
\text{above} > 1 & \quad \text{concentrates in a convex shape above the crossover}
\end{align*}
\]

Usually, below and above have equal values, unless specific reasons exist to make them different.

For the type = "fuzzy" it is also possible to use the "indirect" method to calibrate the data, using a procedure first introduced by Ragin (2008). The indirect method assumes a vector of thresholds to cut the original data into equal intervals, then it applies a (quasi)binomial logistic regression with a fractional polynomial equation.

The results are also fuzzy between 0 and 1, but the method is entirely different: it has no anchors (specific to the direct method), and it doesn’t need to specify a calibration function to calculate the scores along with.

**Value**

A numeric vector of set membership scores, either crisp (starting from 0 with increments of 1), or fuzzy numeric values between 0 and 1.

**Author(s)**

Adrian Dusa
References


Examples

```r
# generate heights for 100 people
# with an average of 175cm and a standard deviation of 10cm
set.seed(12345)
x <- rnorm(n = 100, mean = 175, sd = 10)

cx <- calibrate(x, type = "crisp", thresholds = 175)
plot(x, cx, main="Binary crisp set using 1 threshold",
     xlab = "Raw data", ylab = "Calibrated data", yaxt="n")
axis(2, at = 0:1)

cx <- calibrate(x, type = "crisp", thresholds = c(170, 180))
plot(x, cx, main="3 value crisp set using 2 thresholds",
     xlab = "Raw data", ylab = "Calibrated data", yaxt="n")
axis(2, at = 0:2)

# calibrate to a increasing, s-shaped fuzzy-set
# calibrate to an decreasing, s-shaped fuzzy-set
# when not using the logistic function, linear increase
# tweaking the parameters "below" and "above" the crossover,
# at value 3.5 approximates a logistic distribution, when e=155 and i=195
```
xlab = "Raw data", ylab = "Calibrated data")

# calibrate to a bell-shaped fuzzy set
cx <- calibrate(x, thresholds = "e1=155, c1=165, i1=175, i2=175, c2=185, e2=195",
                 below = 3, above = 3)
plot(x, cx, main = "Membership scores in the set of average height",
     xlab = "Raw data", ylab = "Calibrated data")

# calibrate to an inverse bell-shaped fuzzy set
cx <- calibrate(x, thresholds = "i1=155, c1=165, e1=175, e2=175, c2=185, i2=195",
                 below = 3, above = 3)
plot(x, cx, main = "Membership scores in the set of non-average height",
     xlab = "Raw data", ylab = "Calibrated data")

# the default values of "below" and "above" will produce a triangular shape
cx <- calibrate(x, thresholds = "e1=155, c1=165, i1=175, i2=175, c2=185, e2=195")
plot(x, cx, main = "Membership scores in the set of average height",
     xlab = "Raw data", ylab = "Calibrated data")

# different thresholds to produce a linear trapezoidal shape
cx <- calibrate(x, thresholds = "e1=155, c1=165, i1=172, i2=179, c2=187, e2=195")
plot(x, cx, main = "Membership scores in the set of average height",
     xlab = "Raw data", ylab = "Calibrated data")

# larger values of above and below will increase membership in or out of the set
cx <- calibrate(x, thresholds = "e1=155, c1=165, i1=175, i2=175, c2=185, e2=195",
                 below = 10, above = 10)
plot(x, cx, main = "Membership scores in the set of average height",
     xlab = "Raw data", ylab = "Calibrated data")

# while extremely large values will produce virtually crisp results
cx <- calibrate(x, thresholds = "e1=155, c1=165, i1=175, i2=175, c2=185, e2=195",
                 below = 10000, above = 10000)
plot(x, cx, main = "Binary crisp scores in the set of average height",
     xlab = "Raw data", ylab = "Calibrated data", yaxt="n")
axis(2, at = 0:1)
abline(v = c(165, 185), col = "red", lty = 2)

# check if crisp
round(cx, 0)

# using the empirical cumulative distribution function
# require manually setting logistic to FALSE
cx <- calibrate(x, thresholds = "e=155, c=175, i=195", logistic = FALSE, 
                 ecdf = TRUE)
plot(x, cx, main = "Membership scores in the set of tall people", 
     xlab = "Raw data", ylab = "Calibrated data")
The `causalChain` function performs coincidence analysis using QCA. It mimics the functionality in the `cna` package, finding all possible necessary and sufficient solutions for all possible outcomes in a specific dataset.

### Usage

```r
causalChain(data, ordering = NULL, strict = FALSE, ...)
```

### Arguments

- **data**: A data frame containing calibrated causal conditions.
- **ordering**: A character string, or a list of character vectors specifying the causal ordering of the causal conditions.
- **strict**: Logical, prevents causal conditions on the same temporal level to act as outcomes for each other.
- **...**: Other arguments to be passed to functions `minimize()` and `truthTable()`.

### Details

Although claiming to be a novel technique, coincidence analysis is yet another form of Boolean minimization. What it does is very similar and results in the same set of solutions as performing separate QCA analyses where every causal condition from the data is considered an outcome.

This function aims to demonstrate this affirmation and show that results from package `cna` can be obtained with package `QCA`. It is not intended to offer a complete replacement for the function `cna()`, but only to replicate its so called “asf” - atomic solution formulas.

The three most important arguments from function `cna()` have direct correspondents in function `minimize()`:

```r
calc <- c(40110, 34400, 25200, 24920, 20660, 17090, 15320, 13680, 11720, 11290, 10940, 9800, 7470, 4670, 4100, 4070, 3740, 3690, 3590, 2980, 1000, 650, 450, 110)
inc <- calibrate(calc, method = "indirect",
thresholds = "1000, 4000, 5000, 10000, 20000")
```
Two other arguments from function `cna()` have been directly imported in this function, to complete the list of arguments that generate the same results.

The argument `ordering` splits the causal conditions in different temporal levels, where prior arguments can act as causal conditions, but not as outcomes for the subsequent temporal conditions. One simple way to split conditions is to use a list object, where different components act as different temporal levels, in the order of their index in the list: conditions from the first component act as the oldest causal factors, while those from the last and the last component are part of the most recent temporal level.

Another, perhaps simpler way to express the same thing is to use a single character, where factors on the same level are separated with a comma, and temporal levels are separated by the sign `<`. A possible example is: "A, B, C < D, E < F".

Here, there are three temporal levels and conditions A, B and C can act as causal factors for the conditions D, E and F, while the reverse is not possible. Given that D, E and F happen in a subsequent temporal levels, they cannot act as causal conditions for A, B or C. The same thing is valid with D and E, which can act as causal conditions for F, whereas F cannot act as a causal condition for D or E, and certainly not for A, B or C.

The argument `strict` controls whether causal conditions from the same temporal level may be outcomes for each other. If activated, none of A, B and C can act as causal conditions for the other two, and the same thing happens in the next temporal level where neither D nor E can be causally related to each other.

Although the two functions reach the same results, they follow different methods. The input for the minimization behind the function `cna()` is a coincidence list, while in package `QCA` the input for the minimization procedure is a truth table. The difference is subtle but important, with the most important difference that package `cna` is not exhaustive.

To find a set of solutions in a reasonable time, the formal choice in package `cna` is to deliberately stop the search at certain (default) depths of complexity. Users are free to experiment with these depths from the argument `maxstep`, but there is no guarantee the results will be exhaustive.

On the other hand, the function `causalChain()` and generally all related functions from package `QCA` are spending more time to make sure the search is exhaustive. Depths can be set via the arguments `pi.depth` and `sol.depth` from the arguments in function `minimize()`, but unlike package `cna` these are not mandatory.

Exhaustiveness is guaranteed in package `QCA` precisely because it uses a truth table as an input for the minimization procedure. The only exception is the option of finding solutions based on their consistency, with the argument `sol.cons`: for large PI charts, time can quickly increase to infinity. If not otherwise specified in the argument `sol.depth` the function `causalChain()` silently sets a complexity level of 5 prime implicants per solution.

**Value**

A list of length equal to the number of columns in the data. Each component contains the result of the QCA minimization for that specific column acting as an outcome.
### causalChain

**Author(s)**

Adrian Dusa

**See Also**

minimize, truthTable

**Examples**

```r
## Not run:
# The following examples assume the package cna is installed

library(cna)
data(d.educate)
cna(d.educate, what = "a")

# same results with
c <- causalChain(d.educate)
c

# inclusion and coverage scores can be inspected for each outcome
c$E$IC

# another example, function cna() requires specific complexity depths
data(d.women)
cna(d.women, maxstep = c(3, 4, 9), what = "a")

# same results with, no specific depths are required
causalChain(d.women)

# multivalue data require a different function in package cna
data(d.pban)
mvcna(d.pban, ordering = list(c("C", "F", "T", "V"), "PB"),
   cov = 0.95, maxstep = c(6, 6, 10), what = "a")

# same results again, simpler command
causalChain(d.pban, ordering = "C, F, T, V < PB", sol.cov = 0.95)

# specifying a lower consistency threshold for the solutions
mvcna(d.pban, ordering = list(c("C", "F", "T", "V"), "PB"), con = .95,
   maxstep = c(6, 6, 10), what = "a")

# same thing with
causalChain(d.pban, ordering = "C, F, T, V < PB", pi.cons = 0.95, sol.cons = 0.95)

# setting consistency thresholds for the PIs, solutions and also
# a coverage threshold for the solution (note that an yet another
export C function for fuzzy sets is needed in package cnaI
data(d autonomy)
dat2 <- d autonomy[15:30, c("AU", "RE", "CN", "DE")]
fscna(dat2, ordering = list("AU"), con = .9, con.msc = .85, cov = .85,
what = "a")

# again, the same results using the same function:
causalChain(dat2, ordering = "AU", sol.cons = 0.9, pi.cons = 0.85,
sol.cov = 0.85)

## End(Not run)

---

**export**  
*Export a dataframe to a file or a connection*

---

**Description**

This function is a wrapper to `write.table()`, to overcome possible issues with the row names.

**Usage**

```r
export(x, file = "", ...)```

**Arguments**

- `x` The object to be written (matrix or dataframe)
- `file` A character string containing the path to the file to be created
- `...` Same arguments that are used in `write.table()`

**Details**

The default convention for `write.table()` is to add a blank column name for the row names, but (despite it is a standard used for CSV files) that doesn’t work with all spreadsheets or other programs that attempt to import the result of `write.table()`.

This function acts as if `write.table()` was called, with only one difference: if row names are present in the dataframe (i.e. any of them should be different from the default row numbers), the final result will display a new column called `cases` in the first position, except the situation that another column called `cases` already exists in the data, when the row names will be completely ignored.

If not otherwise specified, an argument `sep = "", "` is added by default.

The argument `row.names` is always set to `FALSE`, a new column being added anyways (if possible).

Since this function pipes everything to `write.table()`, the argument `file` can also be a connection open for writing, and "" indicates output to the console.
factorize

Author(s)
Adrian Dusa

See Also
The “R Data Import/Export” manual.

write.table

factorize  Factorize Boolean expressions

Description
This function finds all combinations of common factors in a Boolean expression written in SOP -
Sum Of Products form.

Usage
factorize(input, snames = "", noflevels, pos = FALSE, tilde, ...)

Arguments
input
A string containing the SOP expression, or an object of class "qca".
snames
A string containing the sets’ names, separated by commas.
noflevels
Numerical vector containing the number of levels for each set.
poss
Logical, if possible factorize using product(s) of sums.
tilde
Logical, use a tilde to negate the sets.
...
Other arguments (mainly for backwards compatibility).

Details
Factorization is a process of finding common factors in a Boolean expression, written in a SOP -
sum of products (or DNF - disjunctive normal form). Whenever possible, the factorization can also
be performed in a POS - product of sums form.

Conjunctions should preferably be indicated with a star * sign, but this is not necessary when
conditions have single letters or when the expression is expressed in multi-value notation.

The argument snames is only needed when conjunctions are not indicated by any sign, and the set
names have more than one letter each (see function translate() for more details).

The number of levels in noflevels is needed only when negating multivalue conditions, and it
should complement the snames argument.

If input is an object of class "qca" (the result of the minimize() function), a factorization is
performed for each of the minimized solutions.

Value
A list with two components:
The input expression.

All possible factorizations of the input expression.

Author(s)
Adrian Dusa

References

See Also
translate

Examples

# typical example with redundant conditions
factorize("AbcD + AbCd + AbCD + ABCd")

# results presented in alphabetical order
factorize("one*TWo*four + one*THREE + THREE*four")

# to preserve a certain order of the set names
factorize("one*TWo*four + one*THREE + THREE*four", snames = "ONE, TWO, THREE, FOUR")

factorize("~one*TWo*~FOUr + ~one*THREE + THREE*~FOUr", snames = "ONE, TWO, THREE, FOUR")

# using pos - products of sums
factorize("ac + aD + bc + bD", pos = TRUE)

# using an object of class "qca" produced with minimize()
data(CVF)
pCVF <- minimize(CVF, outcome = "PROTEST", incl.cut = 0.8, include = "?", use.letters = TRUE)
factorize(pCVF)

# using an object of class "deMorgan" produced with negate()
factorize(negate(pCVF))
Description

This function takes a truth table as the input, and finds various types of untenable assumptions that are usually used in function `minimize()` when excluding certain remainders or some observed configurations from the minimization process.

Usage

```
findRows(expression = '', obj, remainders = TRUE, type = 1)
```

Arguments

- **expression**: String: a QCA expression written in sum of products form.
- **obj**: A truth table (an object of class 'tt') or an equivalent numerical matrix.
- **remainders**: Logical: find remainders only or also observed configurations, when `obj` is a truth table.
- **type**: Numeric vector, specifying the type(s) of untenable configurations

Details

The primary purpose is to find untenable assumptions to be excluded from the Boolean minimization process. For this reason, the input is most of the times a truth table, but for demonstration purposes it can also be a simple matrix having column names.

It started as a function to find rows that are subsets of a given SOP expression, and it developed to cover even more untenable assumptions.

Subset rows can be anything, from remainders to the observed configurations (positive output, negative output and contradictions), but the function returns only the subset configurations which do not have a positive output.

It might occasionally find negative output configurations or contradictions, but that doesn’t have any side effect because they are going to be excluded from the minimization anyways, unless contradictions are included in the minimization. The only category that really matters if they are identified or not, are the positive output configurations.

The contradictory simplifying assumptions (CSAs) are those which are used for both the presence and the absence of the outcome, while simultaneous subset relations (SSRs) when observed configurations are sufficient for both the presence and the absence of the outcome. CSAs and SSRs are incoherent counterfactuals, part of a category called Untenable Assumptions.

This function takes does what is normally done with a series of commands, in a more integrated and systematic way.

Providing a truth table is sufficient to perform all these tasks, because a truth table already contains all necessary information of how it was produced, most importantly the inclusion cut-off(s). It uses the same options to produce a truth table for the negation of the outcome (if the input truth table was
created for its presence, or the other way round), and minimizes both to inspect their simplifying assumptions to detect which are contradictory.

If there are such simplifying assumptions in both parsimonious solutions, it means these are contradictory, and if there are observed configurations that are sufficient for both the presence and the absence of the outcome, these are also incoherent because of the simultaneous subset relations problem.

The following types of untenable assumptions can be searched for:

- 0 all of them
- 1 subsets of a given expression (default)
- 2 contradictory simplifying assumptions
- 3 simultaneous subset relations

**Value**

A numeric vector of row numbers from the truth table.

**Author(s)**

Adrian Dusa

**See Also**

`truthtable, minimize`

**Examples**

```r
# Lipset's binary crisp version
data(LC)
ttLC <- truthtable(LC, "SURV", show.cases = TRUE)
findRows("DEV*ind*STB", ttLC)

## all subset rows from the truth table, not only the remainders
findRows("DEV*ind*STB", ttLC, remainders = FALSE)

# Lipset's fuzzy version
data(LF)
ttLF <- truthtable(LF, outcome = "SURV", incl.cut = 0.8)
findRows(obj = ttLF, type = 2) # contradictory simplifying assumptions
```
Description

The purpose of this function is to automatically find calibration thresholds for a numerical causal condition, to be split into separate groups.

Usage

```r
findTh(x, n = 1, hclustm = "complete", distm = "euclidean", ...)
```

Arguments

- `x` A numerical causal condition.
- `n` The number of thresholds to find.
- `hclustm` The agglomeration (clustering) method to be used.
- `distm` The distance measure to be used.
- `...` Other arguments (mainly for backwards compatibility).

Details

The process of calibration into crisp sets assumes expert knowledge about the best threshold(s) that separate the raw data into the most meaningful groups.

In the absence of such knowledge, an automatic procedure might help grouping the raw data according to statistical clustering techniques.

The number of groups to split depends on the number of thresholds: one thresholds splits into two groups, two thresholds splits into three groups etc.

For more details about how many groups can be formed with how many thresholds, see `?cutree`.

More details about the clustering techniques used in this function are found using `?hclust`, and also more details about different distance measures can be found with `?dist`. This function uses their default values.

Value

A numeric vector of length `n`.

Author(s)

Adrian Dusa

See Also

`cutree`, `hclust`, `dist`
Examples

# hypothetical list of country GDPs
gdp <- c(460, 500, 900, 2000, 2100, 2400, 15000, 16000, 20000)

# find one threshold to separate into two groups
findTh(gdp)
# 8700

# find two thresholds to separate into two groups
findTh(gdp, n = 2)
# 8700 18000

# using different clustering methods
findTh(gdp, n = 2, hclustm = "ward.D2", distm = "canberra")
# 1450 8700

---

**fuzzyand, fuzzyor**  
*Logical operations*

Description

These functions perform logical operations AND and OR, for binary crisp or fuzzy set membership scores.

Usage

```
fuzzyand(..., na.rm = FALSE, use.tilde = FALSE)
fuzzyor(..., na.rm = FALSE, use.tilde = FALSE)
```

Arguments

- `...`: Two or more numerical (calibrated) objects containing membership scores, or a matrix/data frame of calibrated columns.
- `na.rm`: Logical, indicating whether missing values should be removed.
- `use.tilde`: Logical, construct the expression in the name attribute using a tilde to signal a negation.

Value

A numerical vector of class "fuzzy", with a name attribute expression.
Author(s)
Adrian Dusa

Examples

```r
# ------
# Cebotari & Vink (2013, 2015)
data(CVF)

# DEMOC*GEOCON*NATPRIDE
with(CVF, fuzzyand(DEMOC, GEOCON, NATPRIDE))

# same thing with
fuzzyand(CVF[, c(1,3,5)])

# DEMOC*geocon*NATPRIDE
fa <- with(CVF, fuzzyand(DEMOC, 1 - GEOCON, NATPRIDE))
fa

attr(fa, "name")

# ETHFRACT + POLDIS
with(CVF, fuzzyor(ETHFRACT, POLDIS))

# same thing with
fuzzyor(CVF[, c(2,4)])

# ETHFRACT + poldis
fo <- with(CVF, fuzzyor(ETHFRACT, 1 - POLDIS))
fo

attr(fo, "name")

# ETHFRACT + ~POLDIS
fo <- with(CVF, fuzzyor(ETHFRACT, 1 - POLDIS, use.tilde = TRUE))
attr(fo, "name")
```

Description
This is a set of functions dedicated to the implicant matrix, a space where all causal configurations and their minimized solutions are found.
Implicant matrix functions: `allExpressions`, `createMatrix`, `getRow`

They can produce all possible implicants and prime implicants, or all possible combinations for a specific number of causal conditions and their number of values (either binary or multi-value).

**Usage**

```r
allExpressions(noflevels, arrange = FALSE, depth = NULL, raw = FALSE, ...)
createMatrix(noflevels, ...)
getRow(row.no, noflevels, zerobased = FALSE)
```

**Arguments**

- `noflevels` The number of levels (values) for each causal condition.
- `arrange` Logical, if TRUE the result matrix is arranged for visual inspection.
- `depth` Integer, an upper number of causal conditions to form expressions with.
- `raw` Logical, if TRUE it returns the matrix indicating which conditions have been minimized, using -1.
- `row.no` A vector, the desired row numbers.
- `zerobased` Logical, if TRUE the first row number is zero.
- `...` Other arguments.

**Details**

A truth table for binary crisp conditions is a matrix with $2^k$ rows, where $k$ is the number of causal conditions.

For multi-value causal conditions, the same equation can be generalised to:

$$v_1 \cdot v_2 \cdot ... \cdot v_k$$

where $v$ is the number of values (levels) for every causal condition from 1 to $k$.

Implicant matrices contain all rows from the truth table, plus all of their supersets, (all implicants and prime implicants), including the empty set (Dusa 2007, 2010).

For a binary crisp set procedure, there are $3^k - 1$ possible expressions (groupings), see Ragin (2010). Including the empty set (the situation when all causal conditions have been minimized), the implicant matrix consists of exactly $3^k$ rows, including the truth table configurations.

In fact, $3^k$ is also obtained by the product:

$$(2 + 1) \cdot (2 + 1) \cdot ... \cdot (2 + 1)$$

For multi-value causal conditions, the same equation can be generalised to:

$$(v_1 + 1) \cdot (v_2 + 1) \cdot ... \cdot (v_k + 1)$$

where every number of levels in each causal conditions is incremented with 1, to allow coding the minimization of literals in each (prime) implicant (see examples).

The function `allExpressions()` creates a matrix which contains all possible implicants and prime implicants, displayed in the original values form using the code -1 to point the minimized literals, while the other functions use the code 0, all other values being incremented with 1.

Specifying a smaller `depth` automatically activates the argument `arrange`.
When the argument `arrange` is activated, the output is arranged in the increasing order of the number of conditions which form conjunctions, up to the maximum number specified by the argument `depth` (which if `NULL`, it is considered equal to the number of columns in the matrix).

The function `createMatrix()` creates a base matrix for truth tables and implicant matrices.

The function `getRow()` takes the number of a row in the truth table or implicant matrix (in its decimal form), and transforms it into its binary (or multi-base) representation, as a configuration of binary or multi-values for each causal condition.

Note that \( R \) is a 1-based language (all numbers start from 1), and similarly positions in vectors and matrices start with 1. For this reason, although (mathematically) the binary representation of the decimal number 0 (for example, at three causal conditions) is 0 0 0, in \( R \) that would be the “first” line in the implicant matrix, therefore 0 0 0 is translated into the number 1, unless the argument `zerobased` is activated.

**Value**

A matrix with \( k \) columns and:
- \( v_1 \cdot v_2 \cdot \ldots \cdot v_k \) rows if a truth table;
- \((v_1 + 1) \cdot (v_2 + 1) \cdot \ldots \cdot (v_k + 1)\) rows if an implicant matrix;
- \( x \) rows, equal to the length of `row.no`.

**Author(s)**

Adrian Dusa

**References**


**See Also**

`expand.grid`

**Examples**

```r
# three binary causal conditions, having two levels each: 0 and 1
noflevels <- c(2, 2, 2)

# for three binary causal conditions
allExpressions(noflevels)

# the same matrix, this time arranged better
# (last rows represent the truth table)
allExpressions(noflevels, arrange = TRUE)
```
# show only the implicants (excluding the truth table)
allExpressions(noflevels, arrange = TRUE, depth = 2)

# using the raw form
allExpressions(noflevels, raw = TRUE)

# create a base truth table for 3 binary conditions
createMatrix(noflevels)

# its implicant matrix
createMatrix(noflevels + 1)

# create a base truth table where the second condition has three levels
createMatrix(c(2, 3, 2))

# deriving rows
rows <- c(2, 4, 5, 7, 8, 10, 11, 13, 14, 16, 17)
mat <- getRow(rows, noflevels + 1) # note the +1
rownames(mat) <- rows
colnames(mat) <- c("A", "B", "C")
mat

# implicant matrix normal values
#
# | A B C | A B C |
# | 2 0 0 1 | 2 - - 0 c |
# | 4 0 1 0 | 4 - 0 - b |
# | 5 0 1 1 | 5 - 0 0 bc |
# | 7 0 2 0 | 7 - 1 - B |
# | 8 0 2 1 | 8 - 1 0 Bc |
# | 10 1 0 0 | 10 0 - - a |
# | 11 1 0 1 | 11 0 - 0 ac |
# | 13 1 1 0 | 13 0 0 - ab |
# | 14 1 1 1 | 14 0 0 0 abc |
# | 16 1 2 0 | 16 0 1 - aB |
# | 17 1 2 1 | 17 0 1 0 aBc

Interpret SOP expressions: translate, compute, sop

*Functions to interpret or create a SOP expression*

**Description**

These functions interpret an expression written in a SOP (sum of products) form, for both crisp and multivalue QCA. The function `translate()` translates the expression into a standard (canonical) SOP form using a matrix of implicants, while `compute()` uses the first to compute the scores based on a particular data input.
For crisp sets notation, upper case letters are considered the presence of that causal condition, and lower case letters are considered the absence of the respective causal condition. Tilde is recognized as a negation, even in combination with upper/lower letters.

Functions similar to `translate()` and `compute()` have initially been written by Lewandowski (2015) but the actual code in these functions has been completely re-written and expanded with more extensive functionality (see details and examples below).

The function `sop()` transforms any expression (most notably a POS - product of sums) into a sum of products, minimizing it to the simplest equivalent logical expression. It provides a software implementation of the intersection examples presented by Ragin (1987: 144-147), and extended to multi-value sets.

**Usage**

```r
translate(expression = "", snames = "", noflevels, data)
compute(expression = "", data, separate = FALSE)
sop(expression = "", snames = "", use.tilde = FALSE, noflevels)
```

**Arguments**

- `expression`: String: a QCA expression written in sum of products form.
- `snames`: A string containing the sets’ names, separated by commas.
- `use.tilde`: Logical, use tilde to negate bivalent conditions.
- `noflevels`: Numerical vector containing the number of levels for each set.
- `data`: A dataset with binary cs, mv and fs data.
- `separate`: Logical, perform computations on individual, separate paths.

**Details**

A SOP - sum of products is also known as a DNF - disjunctive normal form, or in other words a "union of intersections", for example $A \cdot D + B \cdot C$.

The same expression can be written in multivalue notation: $A(1) \cdot D(1) + B(1) \cdot C(0)$. Both types of expressions are valid, and yield the same result on the same dataset.

For multivalue notation, causal conditions are expected as upper case letters, and they will be converted to upper case by default. Expressions can contain multiple values to translate, separated by a comma. If $B$ was a multivalue causal condition, an expression could be: $A(1) + B(1,2) \cdot C(0)$.

In this example, all values in $B$ equal to either 1 or 2 will be converted to 1, and the rest of the (multi)values will be converted to 0.

These functions automatically detects the use of tilde "~" as a negation for a particular causal condition. ~A does two things: it identifies the presence of causal condition A (because it was specified as upper case) and it recognizes that it must be negated, because of the tilde. It works even combined with lower case names: ~a, which is interpreted as A.

To negate a multivalue condition using a tilde, the number of levels should be supplied (see examples below). Improvements in version 2.5 allow for intersections between multiple levels of
the same condition. For a causal condition with 3 levels (0, 1 and 2) the following expression
~A(0, 2)*A(1, 2) is equivalent with A(1), while A(0)*A(1) results in the empty set.
The number of levels, as well as the set names can be automatically detected from a dataset via the argument data. Arguments snames and noflevels have precedence over data, when specified.
The use of the product operator * is redundant when the set names are single letters (for example AD + Bc), and is also redundant for multivalue data, where product terms can be separated by using the curly brackets notation.
When conditions are binary and their names have multiple letters (for example AA + CC*bb), the use of the product operator * is preferable but the function manages to translate an expression even without it (AA + CCbb) by searching deep in the space of the conditions' names, at the cost of slowing down for a high number of causal conditions. For this reason, an arbitrary limit of 7 causal snames is imposed, to write an expression.
For the function sop(), if a tilde is present in the expression, the argument use.tilde is automatically activated.

Value

For the function translate(), a matrix containing the implicants on the rows and the set names on the columns, with the following codes:

<table>
<thead>
<tr>
<th>Code</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>absence of a causal condition</td>
</tr>
<tr>
<td>1</td>
<td>presence of a causal condition</td>
</tr>
<tr>
<td>-1</td>
<td>causal condition was eliminated</td>
</tr>
</tbody>
</table>

The matrix was also assigned a class "translate", to avoid printing the -1 codes when signaling a minimized condition. The mode of this matrix is character, to allow printing multiple levels in the same cell, such as "1,2".

Author(s)

Adrian Dusa

References


Examples

```r
translate("A + B*C")
# same thing in multivalue notation
translate("A{1} + B{1}*C{1}")
# using upper/lower letters
translate("A + b*C")
```
Interpret SOP expressions: translate, compute, sop

# the negation with tilde is recognised
translate("~A + b*C")

# even in combination of upper/lower letters
translate("~A + ~b*C")

# and even for multivalue variables
# in multivalue notation, the product sign * is redundant
translate("C(1) + T(2) + T(1)V(0) + C(0)")

# negation of multivalue sets requires the number of levels
translate("~A(1) + ~B(0)*C(1)", snames = "A, B, C", noflevels = c(2,2,2))

# multiple values can be specified
translate("C(1) + T(1,2) + T(1)V(0) + C(0)")

# or even negated
translate("C(1) + ~T(1,2) + T(1)V(0) + C(0)", snames = "C, T, V", noflevels = c(2,3,2))

# if the expression does not contain the product sign *
# snames are required to complete the translation
translate("AB + cD", snames = "A, B, C, D")

# otherwise snames are not required
translate("PER*FECT + string")

# snames are required
translate("PERFECT + string", snames = "PER, FECT, STR, ING")

# it works even with overlapping columns
# SU overlaps with SUB in SUBER, but the result is still correct
translate("SUBER + subset", "SU, BER, SUB, SET")

## Not run:
# error because combinations of condition names clash
translate("SUPER + subset", "SUP, ER, SU, PER, SUB, SET")

## End(Not run)

# to print _all_ codes from the standard output matrix
(obj <- translate("A + b*C"))
print(obj, original = TRUE) # also prints the -1 code

# -----# for compute()
data(LF)
compute("DEV*ind + URB*STB", data = LF)

# calculating individual paths
compute("DEV*ind + URB*STB", data = LF, separate = TRUE)

# -----  
# for sop()
sop("(A + B)(A + ~B")") # result is "A"

# to force a certain order of the set names
sop("(URB + LIT*DEV)(~LIT + "DEV")", snames = "DEV, URB, LIT")

# multilevel conditions can also be specified (and negated)
sop("(A(0) + B(0))(B(1) + C(0))", snames = "A, B, C", nolevels = c(2, 3, 2))

# in Ragin's (1987) book, the equation E = SG + LW is the result  
# of the Boolean minimization for the ethnic political mobilization.

# intersecting the reactive ethnicity perspective (R = lw)  
# with the equation E (page 144)
sop("lw(SG + LW)", snames = "S, L, W, G")  
# [1] "SlwG"

# resources for size and wealth (C = SW) with E (page 145)  
sop("SW(SG + LW)", snames = "S, L, W, G")  
# [1] "SWG + SLW"

# and factorized
factorize(sop("SW(SG + LW)", snames = "S, L, W, G"))

# F1: SW(G + L)

# developmental perspective (D = Lg) and E (page 146)  
sop("Lg(SG + LW)", snames = "S, L, W, G", use.tilde = TRUE)  
# [1] "LW-G"

---

**intersection**

**Intersect expressions**

**Description**

This function takes two or more QCA expressions (combinations of conjunctions and disjunctions) or even entire minimization objects, and finds their intersection.
Usage

intersection(..., snames = "", use.tilde = FALSE, noflevels)

Arguments

... One or more expressions, combined with / or minimization objects of class "qca".

snames A string containing the sets’ names, separated by commas.

use.tilde Logical, use tilde to negate bivalent conditions.

noflevels Numerical vector containing the number of levels for each set.

Details

The initial aim of this function was to provide a software implementation of the intersection examples presented by Ragin (1987: 144-147). That type of example can also be performed with the function sop(), while this function is now mainly used in conjunction with the modelfit function, to assess the intersection between theory and a QCA model.

Irrespective of the input type (character expressions and / or minimiation objects), this function is now a wrapper to the main sop() function (which only accepts character expressions).

It can deal with any kind of expressions, but multivalent crisp conditions need additional information about their number of levels, via the argument noflevels.

The expressions can be formulated in terms of either lower case - upper case notation for the absence and the presence of the causal condition, or use the tilde notation (see examples below). Usage of either of these is automatically detected, as long as all expressions use the same notation.

If the snames argument is provided, the result is sorted according to the order of the causal conditions (set names) in the original dataset, otherwise it sorts the causal conditions in alphabetical order.

For minimzation objects of class "qca", the number of levels, and the set names are automatically detected.

Author(s)

Adrian Dusa

References


Examples

# using minimization objects
data(LF)
ttLF <- truthTable(LF, outcome = "SURV", incl.cut = 0.8)
pLF <- minimize(ttLF, include = "?")
# for example the intersection between the parsimonious model and
# a theoretical expectation

intersection(pLF, "DEV*STB")

# E1: (DEV*ind + URB*STB)*DEV*STB
# I1: DEV*ind*STB + DEV*URB*STB

# negating the model
intersection(negate(pLF), "DEV*STB")

# E1: (dev*urb + dev*stb + urb*IND + IND*stb)*DEV*STB
# I1: DEV*IND*STB*urb

# -----  
# in Ragin's (1987) book, the equation E = SG + LW is the result
# of the Boolean minimization for the ethnic political mobilization.

# intersecting the reactive ethnicity perspective (R = lw)
# with the equation E (page 144)
intersection("lw", "SG + LW", snames = "S, L, W, G")

# E1: lw(SG + LW)
# I1: SlwG

# resources for size and wealth (C = SW) with E (page 145)
intersection("SW", "SG + LW", snames = "S, L, W, G")

# E1: SW(SG + LW)
# I1: SWG + SLW

# and factorized
factorize(intersection("SW", "SG + LW", snames = "S, L, W, G"))

# M1: SWG + SLW
# F1: SW(G + L)

# developmental perspective (D = Lg) and E (page 146)
intersection("Lg", "SG + LW", snames = "S, L, W, G")

# E1: Lg(SG + LW)
# I1: Lwg
minimize

Description

This function performs the QCA minimization of an input truth table, or if the input is a dataset the minimization it minimizes a set of causal conditions with respect to an outcome. Three minimization methods are available: the classical Quine-McCluskey, the enhanced Quine-McCluskey and the latest Consistency Cubes algorithm that is built for performance.

All algorithms return the same, exact solutions, see Dusa (2017) and Dusa and Thiem (2015).

Usage

minimize(input, include = "", exclude = NULL, dir.exp = "", pi.cons = 0, pi.depth = 0, sol.cons = 0, sol.cov = 1, sol.depth = 0, min.pin = TRUE, row.dom = FALSE, all.sol = FALSE, details = FALSE, use.tilde = FALSE, method = "CCubes", ...)

Arguments

input A truth table object (preferred) or a data frame containing calibrated causal conditions and an outcome.
include A vector of other output values to include in the minimization process.
exclude A vector of row numbers from the truth table, or a matrix of causal combinations to exclude from the minimization process.
dir.exp A vector of directional expectations to derive intermediate solutions.
pi.cons Numerical fuzzy value between 0 and 1, minimal consistency threshold for a prime implicant to be declared as sufficient.
pi.depth Integer, a maximum number of causal conditions to be used when searching for conjunctive prime implicants.
sol.cons Numerical fuzzy value between 0 and 1, minimal consistency threshold for a model to be declared as sufficient.
sol.cov Numerical fuzzy value between 0 and 1, minimal coverage threshold for a model to be declared as necessary.
sol.depth Integer, a maximum number of prime implicants to be used when searching for disjunctive solutions.
min.pin Logical, terminate the search at the depth where newly found prime implicants do not contribute to minimally solving the PI chart.
row.dom Logical, perform row dominance in the prime implicants’ chart to eliminate redundant prime implicants.
all.sol Logical, search for all possible solutions even of not minimal.
details Logical, print more details about the solution.
use.tilde Logical, use tilde to signal the absence of conditions.
method Minimization method, one of "CCubes" (default), or "QMC" the classical Quine-McCluskey, or "eQMC" the enhanced Quine-McCluskey.
...
Other arguments to be passed to function truthTable.
Details

Most of the times, this function takes a truth table object as the input for the minimization procedure, but the same argument can refer to a data frame containing calibrated columns.

For the later case, the function `minimize()` originally had some additional formal arguments which were sent to the function `truthTable()`: `outcome`, `conditions`, `n.cut`, `incl.cut`, `show.cases`, `use.letters` and `inf.test`.

All of these parameters are still possible with function `minimize()`, but since they are sent to the `truthTable()` function anyway, it is unnecessary to duplicate their explanation here. The only situation which does need an additional description relates to the argument `outcome`, where unlike `truthTable()` which accepts a single one, the function `minimize()` accepts multiple outcomes and performs a minimization for each of them (a situation when all columns are considered causal conditions).

The argument `include` specifies which other truth table rows are included in the minimization process. Most often, the remainders are included but any value accepted in the argument `exclude` is also accepted in the argument `include`.

The argument `exclude` is used to exclude truth table rows from the minimization process, from the positive configurations and/or from the remainders. It can be specified as a vector of truth table line numbers, or as a matrix of causal combinations.

The argument `dir.exp` is used to specify directional expectations, as described by Ragin (2003). They can be specified as a single string, with values separated by commas. For multi-value directional expectations, they are specified together, separated by semicolons. The total length of the directional expectations must match the number of causal conditions specified in the analysis, using a dash "-" if there are no particular expectations for a specific causal condition.

Activating the `details` argument has the effect of printing parameters of fit for each prime implicant and each overall solution, the essential prime implicants being listed in the top part of the table. It also prints the truth table, in case the argument `input` has been provided as a data frame instead of a truth table object.

The argument `use.tilde` signals the absence of a causal condition, in a sufficiency relation with the outcome, using a tilde sign "~". It is ignored if the data is multivalent.

By default, the package QCA employs a different search algorithm based on Consistency Cubes (Dusa, 2017), analysing all possible combinations of causal conditions and all possible combinations of their respective levels. The structure of the input dataset (number of causal conditions, number of levels, number of unique rows in the truth table) has a direct implication on the search time, as all of those characteristics become entry parameters when calculating all possible combinations.

Consequently, two kinds of depth arguments are provided:

- `pi.depth` the maximum number of causal conditions needed to construct a prime implicant, the complexity level where the search can be stopped, as long as the PI chart can be solved.
- `sol.depth` the maximum number of prime implicants needed to find a solution (to cover all initial positive output configurations)

These arguments introduce a possible new way of deriving prime implicants and solutions, that can lead to different results (i.e. even more parsimonious) compared to the classical Quine-McCluskey.
When either of them is modified from the default value of 0, the minimization method is automatically set to "CCubes" and the remainders are automatically included in the minimization.

The search time is larger the higher these depths, or inversely the search time can be significantly shorter if these depths are smaller. Irrespective of how large \texttt{pi.depth} is, the algorithm will always stop at a maximum complexity level where no new, non-redundant prime implicants are found. The argument \texttt{sol.depth} is relevant only when activating the argument \texttt{all.sol} to solve the PI chart.

The default method (when \texttt{all.sol = FALSE}), is to find the minimal number (k) of prime implicants needed to cover all initial positive output configurations, then it exhaustively searches through all possible disjunctions of k prime implicants which do cover those configurations.

The argument \texttt{min.pin} introduces an additional parameter to control when to stop the search for prime implicants. It is based on the observation by Dusa (2017) that out of the entire set of non-redundant prime implicants, only a subset actually contribute to solving the chart with disjunctions of k PIs. The search depth can be shortened at the level where the next subset of PIs do not contribute to solving the PI chart, thus avoiding to spend unnecessary time on finding the maximal number of non-redundant PIs. Instead, it finds the set of minimal ("min") number of PIs ("pin") necessary to obtain exactly the same solutions, with a dramatically improved overall performance.

Once the PI chart is constructed using the prime implicants found in the previous stages, the argument \texttt{row.dom} can be used to further eliminate irrelevant prime implicants when solving the PI chart, applying the principle of row dominance: if a prime implicant A covers the same (initial) positive output configurations as another prime implicant B and in the same time covers other configurations which B does not cover, then B is irrelevant and eliminated.

The argument \texttt{all.sol} automatically deactivates the argument \texttt{min.pin}, because it aims to exhaustively identify all possible non-redundant disjunctions of n prime implicants that solve the PI chart, where n >= k, with an inflated number of possible solutions. Depending on the complexity of the PI chart, sometimes it may take a very long time to identify all possible non-redundant (disjunctions that are not subsets of previously found) disjunctive solutions. In such a situation, the number of combinations of all possible numbers of prime implicants is potentially too large to be solved in a polynomial time and if not otherwise specified, the depth for the disjunctive solutions is automatically bounded to 5 prime implicants.

The task of solving the PI chart depends on its size, with prime implicants on the rows and the positive output configurations on the columns. Since the columns are fixed, another possible way to reduce the solving time is to eliminate redundant rows, by activating the argument \texttt{row.dom}.

If minimizing a dataset instead of a truth table, unless otherwise specified the argument \texttt{incl.cut} is automatically set to the minimum value between \texttt{pi.cons} and \texttt{sol.cons}, then passed to the function \texttt{truthtableHI}.

The argument \texttt{sol.cons} introduces another possibility to change the method of solving the PI chart. Normally, once the solutions are found among all possible combinations of k prime implicants, consistencies and coverages are subsequently calculated. When \texttt{sol.cons} is lower than 1, then solutions are searched based on their consistencies, which should be at least equal to this threshold.

### Value

An object of class "qca" when using a single outcomes, or class "mqca" when using multiple outcomes. These objects are lists having the following components:

- \texttt{tt} The truth table object.
options Values for the various options used in the function (including defaults).

negatives The line number(s) of the negative configuration(s).

initials The initial positive configuration(s).

PIchart A list containing the PI chart(s).

primes The prime implicant(s).

solution A list of solution(s).

essential A list of essential PI(s).

pims A list of PI membership scores.

IC The matrix containing the inclusion and coverage scores for the solution(s).

SA A list of simplifying assumptions.

i.sol A list of components specific to intermediate solution(s), each having a PI chart, prime implicant membership scores, (non-simplifying) easy counterfactuals and difficult counterfactuals.

call The user’s command which produced all these objects and result(s).

Author(s)

Adrian Dusa

References


See Also

truthTable, factorize

Examples

# -----
# Lipset binary crisp data
data(LC)

data(LC)

ttLC <- truthTable(LC, "SURV", sort.by = "incl, n")
ttLC

cLC <- minimize(ttLC)
cLC

# view the Venn diagram for the associated truth table
library(venn)
venn(cLC)

# add details and case names
minimize(ttLC, details = TRUE, show.cases = TRUE)

# negating the outcome

ttLCn <- truthTable(LC, "~SURV", sort.by = "incl, n")
minimize(ttLCn)

# using a tilde instead of upper/lower case names
minimize(ttLCn, use.tilde = TRUE)

# parsimonious solution, positive output

pLC <- minimize(ttLC, include = "?", details = TRUE, show.cases = TRUE)
pLC

# the associated simplifying assumptions
pLC$SA

# parsimonious solution, negative output

pLCn <- minimize(ttLCn, include = "?", details = TRUE, show.cases = TRUE)
pLCn

# -----
# Lipset multi-value crisp data (Cronqvist & Berg-Schlosser 2009, p.80)
data(LM)

data(LM)

ttLM <- truthTable(LM, "SURV", conditions = "DEV, URB, LIT, IND",
sort.by = "incl", show.cases = TRUE)
# conservative solution, positive output
minimize(ttlM, details = TRUE, show.cases = TRUE)

# parsimonious solution, positive output
minimize(ttlM, include = "?", details = TRUE, show.cases = TRUE)

# negate the outcome
ttlMn <- truthTable(LM, "SURV", conditions = "DEV, URB, LIT, IND",
                   sort.by = "incl", show.cases = TRUE)

# conservative solution, negative output
minimize(ttlMn, details = TRUE, show.cases = TRUE)

# parsimonious solution, positive output
minimize(ttlMn, include = "?", details = TRUE, show.cases = TRUE)

# ------
# Lipset fuzzy sets data (Ragin 2009, p.112)
data(lf)
# truth table using a very low inclusion cutoff
ttlF <- truthTable(lf, "SURV", incl.cut = 0.7,
                   show.cases = TRUE, sort.by="incl")

# conservative solution
minimize(ttlF, details = TRUE, show.cases = TRUE)

# parsimonious solution
minimize(ttlF, include = "?", details = TRUE, show.cases = TRUE)

# intermediate solution using directional expectations
iLF <- minimize(ttlF, include = "?", details = TRUE, show.cases = TRUE,
                dir.exp = "1,1,1,1,1")
iLF

# ------
# Cebotari & Vink (2013, 2015)
data(cvf)
ttcvf <- truthTable(cvf, outcome = "PROTEST", incl.cut = 0.8,
                    show.cases = TRUE, sort.by = "incl, n")

pcvf <- minimize(ttcvf, include = "?", details = TRUE, show.cases = TRUE)

# inspect the PI chart
pcvf$pichart

# DEMOC*ETHFRACT*poldis is dominated by DEMOC*ETHFRACT*GEOCON
# using row dominance to solve the PI chart
pcvfrd <- minimize(ttcvf, include = "?", row.dom = TRUE,
```r
modelFit

   details = TRUE, show.cases = TRUE)

   # plot the prime implicants on the outcome
   pims <- pCVFrD$pims

   par(mfrow = c(2, 2))
   for(i in 1:4) {
     XYplot(pims[, i], CVF$PROTEST, cex.axis = 0.6)
   }

   # ------
   # temporal QCA (Ragin & Strand 2008) serving the input as a dataset,
   # which will automatically be passed to truthTable() as an intermediary
   # step before the minimization

   data(RS)
   minimize(RS, outcome = "REC", details = TRUE, show.cases = TRUE)
```

---

### Description

Function to enable theory evaluation, as introduced by Ragin (1987, p.118) and extended Schneider & Wageman (2012, p.295), by producing parameters of fit for all possible intersections between a given theoretical statement (a SOP expression) and the solutions found by function `minimize()`.

### Usage

```r
modelFit(model, theory)
```

### Arguments

- **model**: A minimization object of class "qca".
- **theory**: Character, a SOP expression.

### Details

Following Ragin’s (1987) original work, theory evaluation amounts to intersecting a theoretical expectation with a model resulting from a minimization process.

There are in fact four intersections: presence - presence, presence - absence, absence - presence and absence - absence, where by “absence” is actually meant a negation of an expression using the function `negate()`.

When multiple models exist, all of them are automatically detected, negated and intersection with the theory. Intersections and parameters of fit are going to be produced using a single theoretical expression.
Value
A list containing objects of class "pof" with the parameters of fit. For a single theoretical expression and a single model, the object is a simple "pof" object.

Author(s)
Adrian Dusa

References

See Also
intersection, negate, pof

Examples
# Lipset fuzzy version data
data(LF)
ttlLF <- truthTable(LF, outcome = "SURV", incl.cut = 0.8)

# parsimonious solution
plLF <- minimize(ttlLF, include = "?")
modelFit(model = plLF, theory = "DEV*STB")

# hypothetical exploration of intermediate solutions
ilLF <- minimize(ttlLF, include = "?", dir.exp = "1,0,0,0,0")
modelFit(ilLF, "DEV*STB")

Description
Function to negate a SOP expression.

Usage
negate(expression, snames = "", nolevels, use.tilde = FALSE)
negate

Arguments

- **expression**: A string representing a SOP expression, or a minimization object of class "qca".
- **snames**: A string containing the sets’ names, separated by commas.
- **noflevels**: Numerical vector containing the number of levels for each set.
- **use.tilde**: Logical, use tilde for negation with bivalent variables.

Details

In Boolean algebra, there are two transformation rules named after the British mathematician Augustus De Morgan. These rules state that:

1. The complement of the union of two sets is the intersection of their complements.
2. The complement of the intersection of two sets is the union of their complements.

In "normal" language, these would be written as:

1. \( \text{not } (A \text{ and } B) = (\text{not } A) \text{ or } (\text{not } B) \)
2. \( \text{not } (A \text{ or } B) = (\text{not } A) \text{ and } (\text{not } B) \)

Based on these two laws, any Boolean expression written in disjunctive normal form can be transformed into its negation.

It is also possible to negate all models and solutions from the result of a Boolean minimization from function `minimize()`. The resulting object, of class "qca", is automatically recognised by this function.

In a SOP expression, the products should normally be split by using a star * sign, otherwise the sets’ names will be considered the individual letters in alphabetical order, unless they are specified via `snames`.

To negate multilevel expressions, the argument `noflevels` is required.

Value

A list with the following two components:

- **initial**: The initial expression.
- **negated**: The negation of the initial expression.

If `expression` is an object of type "qca", the result is a list of solutions.

Author(s)

Adrian Dusa

References

PI chart functions: makeChart, findmin, solveChart

See Also

minimize

Examples

# example from Ragin (1987, p.99)
negate("AC + B\cdot C")

# with different intersection operators
negate("AB\cdot EF + \neg CD\cdot EF")

# using an object of class "qca" produced with minimize()
data(LC)
cLC <- minimize(LC, outcome = "SURV")
negate(cLC)

# parsimonious solution
pLC <- minimize(LC, outcome = "SURV", include = ")
negate(pLC)

PI chart functions: makeChart, findmin, solveChart

Create and solve a prime implicants chart

Description

These functions help creating a demo for a prime implicant chart, and also show how to solve it using a minimum number of prime implicants.

Usage

makeChart(primes = ",", configs = ",", snames = ",", mv = FALSE,
use.tilde = FALSE, collapse = ",", ...)

findmin(chart)

solveChart(chart, row.dom = FALSE, all.sol = FALSE, depth = NULL, ...)

Arguments

primes A string containing prime implicants, separated by commas, or a matrix of implicants.
**PI chart functions:** makeChart, findmin, solveChart

```r
configs
```
A string containing causal configurations, separated by commas, or a matrix of causal configurations in the implicants space.

```r
snames
```
A string containing the sets’ names, separated by commas.

```r
mv
```
Logical, row and column names in multi-value notation.

```r
use.tilde
```
Logical, row and column names indicating absence with a tilde.

```r
collapse
```
Scalar character, how to collapse different parts of the row or column names.

```r
chart
```
An object of class "bicp" or a logical matrix.

```r
row.dom
```
Logical, apply row dominance to eliminate redundant prime implicants.

```r
all.sol
```
Derive all possible solutions, irrespective if the disjunctive number of prime implicants is minimal or not.

```r
depth
```
A maximum number of prime implicants for any disjunctive solution.

... Other arguments (mainly for backwards compatibility).

**Details**

A PI chart, in this package, is a logical matrix (with TRUE/FALSE values), containing the prime implicants on the rows and the observed positive output configurations on the columns. Such a chart is produced by `makeChart()`, and it is useful to visually determine which prime implicants (if any) are essential.

When `primes` and `configs` are character, the individual sets are identified using the function `translate()`, using the SOP - Sum Of Products form, which needs the set names in the absence of any other information. If products are formed using the standard * operator, specifying the set names is not mandatory.

When `primes` and `configs` are matrices, they have to be specified at implicants level, where the value \( \emptyset \) is interpreted as a minimized literal.

The chart is subsequently processed algorithmically by `solveChart()` to find the absolute minimal number \( M \) of rows (prime implicants) necessary to cover all columns, then searches through all possible combinations of \( M \) rows, to find those which actually cover the columns.

The number of all possible combinations of \( M \) rows increases exponentially with the number of prime implicants generated by the Quine-McCluskey minimization procedure, and the solving time quickly grows towards infinity for large PI charts.

To solve the chart in a minimal time, the redundant prime implicants need to first be eliminated. This is the purpose of the argument `row.dom`. When activated, it eliminates the dominated rows (those which cover a smaller number of columns than another, dominant prime implicant).

The identification of the full model space (including the non-minimal solutions) requires the entire PI chart and is guaranteed to consume a lot of time (towards infinity for very large PI charts). This is done by activating the argument `all.sol`, which automatically deactivates the argument `row.dom`.

The argument `depth` is relevant only when the argument `all.sol` is activated, and it is automatically increased if the minimal number of rows \( M \) needed to cover all columns is larger. By default, it bounds the disjunctive solutions to at most 5 prime implicants, but this number can be increased to widen the search space, with a cost of increasing the search time.
PI chart functions: makeChart, findmin, solveChart

Value

For makeChart: a logical matrix of class "pic".

For findmin: a numerical scalar.

For solveChart: a matrix containing all possible combinations of PI chart rows necessary to cover all its columns.

Author(s)

Adrian Dusa

References


Examples

# non-standard products, it needs the set names
chart <- makeChart("A, B, c", "ABC, Abc, AbC, aBc", snames = "A,B,C")

chart
#   ABC  Abc  AbC  aBc
# A  x   x   x   -
# B  x   -   -   x
# c  -   x   -   x

findmin(chart)
# 2

solveChart(chart)
# first and second rows (A + B)
# and first and third rows (A + c)
# A is an essential prime implicant
#   A + B  A + c
# [1] 1 1
# [2] 2 3

# Quine's example, page 528
rows <- "AB, BC, Ac, aC, abd, bcd"
cols <- "ABCD, ABCd, ABcD, ABDc, AbCD, aBcd, ABdC, aBCD, abCD, abCd, abCD, abcd"

chart <- makeChart(rows, cols, "A,B,C,D")

chart
#   ABCD  ABCd  ABCd  ABCd  AbCD  AbcD  aBCD  aBcd  abCD  abCd  abCD  abcd
# AB  x   x   x   x   -   -   -   -   -   -   -   -
# BC  x   x   -   -   -   x   x   -   -   -   -   -
# Ac  -  -  x  x  x  x  -  -  -  -  -  -  -  -  -  
# aC  -  -  -  -  -  -  -  -  -  x  x  x  x  -  
# abd -  -  -  -  -  -  -  -  -  -  -  -  x  x  
# bcd -  -  -  -  -  -  -  -  -  -  -  -  x

findmin(chart)
# 4

solveChart(chart)
# [1,] 1 1 2 2
# [2,] 3 3 3 3
# [3,] 4 4 4 4
# [4,] 5 6 5 6

# using SOP standard product sign
rows <- "EF, ¬GH, IJ"
cols <- "¬EF¬GH¬IJ, EF¬GH¬IJ, ¬EF¬GH¬IJ, EF¬GH¬IJ"
chart <- makeChart(rows, cols)
chart
#  ¬EF¬GH¬IJ EF¬GH¬IJ ¬EF¬GH¬IJ EF¬GH¬IJ
#  EF  -  x  -  x
#  ¬GH  x  -  -  x
#  IJ  x  -  x  -

solveChart(chart)
# ¬GH is redundant
#  EF + IJ
#  [1,]
# [1,]  1
# [2,]  3

# using implicant matrices
primes <- matrix(c(2,2,1,0,2,2,0,2,2,2), nrow = 2)
configs <- matrix(c(2,2,2,1,1,2,2,2,1,2,2,2,2,2,2,2), nrow = 3)
colnames(primes) <- colnames(configs) <- LETTERS[1:5]

# the prime implicants: AbCE and ACDE
primes
#  A  B  C  D  E
# [1,] 2 1 2 0 2
# [2,] 2 0 2 2 2

# the initial causal combinations: AbCdE, AbCE and ABCDE
configs
#  A  B  C  D  E
# [1,] 2 1 2 1 2
# [2,] 2 1 2 2 2
# [3,] 2 2 2 2 2

chartLC <- makeChart(primes, configs)
pof

Calculate parameters of fit

Description

This function returns inclusion (consistency) and coverage, plus PRI for sufficiency and RoN for necessity.

Usage

pof(setms, outcome, data, relation = "necessity", inf.test = "", incl.cut = c(0.75, 0.5), add = NULL, ...)

Arguments

setms A data frame of (calibrated) set memberships, or a matrix of implicants, or a vector of row numbers from the implicant matrix, or a character expression
outcome The name of the outcome column from a calibrated data frame, or the actual numerical column from the data frame, representing the outcome.
data The calibrated data frame, in case the outcome is a name.
relation The set relation to outcome, either "necessity" or "sufficiency", partial words like "suf" being accepted (see examples).
inf.test Specifies the statistical inference test to be performed (currently only "binom") and the critical significance level. It can be either a vector of length 2, or a single string containing both, separated by a comma.
incl.cut The inclusion cutoff(s): either a single value for the presence of the output, or a vector of length 2, the second for the absence of the output.
add A function, or a list containing functions, to add more parameters of fit.
... Other arguments (mainly for backward compatibility).

Details

This is one of the most flexible functions in the QCA package. Depending on particular situations, its arguments can be provided in various formats which are automatically recognized and treated accordingly.

When specified as a data frame, the argument setms contains any kind of set membership scores:
- calibrated causal conditions from the original data,
- membership scores from the resulting combinations (component coms) of function superSubset().
- prime implicant membership scores (component `pims`) from function `minimize()`,
- any other, custom created combinations of set memberships.

When specified as a matrix, `setms` contains the crisp causal combinations similar to those found in the truth table. If some of the causal conditions have been minimized, they can be replaced by the numerical value \(-1\) (see examples section). The number of columns in the matrix should be equal to the number of causal conditions in the original data.

More generally, `setms` can be a numerical vector of line numbers from the implicant matrix (see function `createMatrix()`), which are automatically transformed into their corresponding set membership scores.

The argument `setms` can also be a string expression, written in sum of products (SOP) form.

For all situations when `setms` is something else than a data frame, it requires the original data to generate the set memberships.

If character, the argument `outcome` is the name of the column from the original data, to be explained (it is a good practice advice to specify it using upper case letters, although it will nevertheless be converted to upper case, by default).

If the outcome column is multi-value, the argument `outcome` should use the standard curly-bracket notation `X{value}`. Multiple values are allowed, separated by a comma (for example `X{1,2}`). Negation of the outcome can also be performed using the tilde \(\sim\) operator, for example \(~X{1,2}\), which is interpreted as: “all values in X except 1 and 2” and it becomes the new outcome to be explained.

The argument `outcome` can also be a numerical vector of set membership values, either directly from the original data frame, or a recoded version (if originally multi-value).

The argument `inf.test` provides the possibility to perform statistical inference tests, comparing the calculated inclusion score with a pair of thresholds (ic1 and ic0) specified in the argument `incl.cut`. Currently, it can only perform binomial tests (“`binom`”), which means that data should only be provided as binary crisp (not multivalue, not fuzzy).

If the critical significance level is not provided, the default level of \(0.05\) is taken.

The resulting object will contain the calculated p-values (pval1 and pval0) from two separate, one-tailed tests with the alternative hypothesis that the true inclusion score is:
- greater than ic1 (the inclusion cut-off for an output value of 1)
- greater than ic0 (the inclusion cut-off for an output value of 0)

It should be noted that statistical tests are performing well only when the number of cases is large, otherwise they are usually not significant.

For the necessity relation, the standard measures of inclusion and coverage are supplemented with the Ron (Relevance of Necessity) measure, as suggested by Schneider & Wagemann’s (2012).

The negation of both `setms` and `outcome` is accepted and recognized using the Boolean subtraction from 1. If the names of the conditions are provided via an optional (undocumented) argument `conditions`, the column names of the `setms` object are negated using the function `negate()`.

The logical argument `neg.out` is deprecated, but backwards compatible. `neg.out` = TRUE and a tilde \(\sim\) in the outcome name don’t cancel each other out, either one (or even both) signaling if the outcome should be negated.

When argument `setms` is a SOP expression, it is the only situation when everything (including the `outcome`) can be negated using lower case letters, with or without a tilde. Lower case letters and a tilde do cancel each other out, for example \(\sim x\) is interpreted as \(x\), while \(\sim x\) is interpreted as \(x\).
Author(s)

Adrian Dusa

References


See Also

minimize, superSubset, translate

Examples

```r
# -----
# Cebotari & Vink (2013) fuzzy data
data(CVF)

conds <- CVF[, 1:5]
PROTEST <- CVF$PROTEST

# parameters of fit (default is necessity)
pof(conds, PROTEST)

# parameters of fit negating the conditions
pof(1 - conds, PROTEST)

# negating the outcome
pof(conds, 1 - PROTEST)

# parameters of fit for sufficiency
pof(conds, PROTEST, relation = "suf")

# also negating the outcome
pof(conds, 1 - PROTEST, relation = "suf")

# -----
# standard analysis of necessity
# using the "coms" component from superSubset()
nCVF <- superSubset(CVF, outcome = "PROTEST", incl.cut = 0.90, cov.cut = 0.6)

# also checking their necessity inclusion score in the negated outcome
pof(nCVF$coms, 1 - PROTEST)

# -----
# standard analysis of sufficiency
```
# using the "pims" component from minimize()

# conservative solution
cCVF <- minimize(CVF, outcome = "PROTEST", incl.cut = 0.8, details = TRUE)

# verify if their negations are also sufficient for the outcome
pof(1 - cCVF$pims, PROTEST, relation = "sufficiency")

# -----  
# using a SOP expression, translated using the function translate()

# notice that lower case letters mean the absence of a causal condition
pof("natpride + GEOCON => PROTEST", data = CVF)

# same for the negation of the outcome
pof("natpride + GEOCON => ~PROTEST", data = CVF)

# same using lower letters for the negation
pof("natpride + GEOCON => protest", data = CVF)

# necessity is indicated by the reverse arrow
pof("natpride + GEOCON <= PROTEST", data = CVF)

# -----  
# more parameters of fit, for instance Haesebrouck' consistency

inclH <- function(x, y) {
  sum(fuzzyand(x, y)) /  
  sum(fuzzyand(x, y) + sqrt(fuzzyor(x - y, 0)*x))
}

pof("natpride + GEOCON => protest", data = CVF, add = inclH)

---

### recode

**Recode a variable**

**Description**

Recodes a vector (numeric, character or factor) according to a set of rules. Similar to the `recode()` function in package `car`, but more flexible. It is also similar to function `findInterval()` from package `base`.

**Usage**

```r
recode(x, rules, cuts, values, ...)
```
Arguments

- **x**: A vector of mode numeric, character or factor.
- **rules**: Character string or a vector of character strings for recoding specifications.
- **cuts**: A vector of one or more unique cut points.
- **values**: A vector of output values.
- **...**: Other parameters, for compatibility with other functions such as `recode()` in package `car` but also `factor()` in package `base`.

Details

Similar to the `recode()` function in package `car`, the recoding rules are separated by semicolons, of the form `input = output`, and allow for:

- a single value: `1 = 0`
- a range of values: `2:5 = 1`
- a set of values: `c(6,7,10) = 2`
- else: everything that is not covered by the previously specified rules

Contrary to the `recode()` function in package `car`, this function allows the : sequence operator (even for factors), so that a rule such as `c(1,3,5:7)`, or `c(a,d,f:h)` would be valid.

Actually, since all rules are specified in a string, it really doesn’t matter if the `c()` function is used or not. For compatibility reasons it accepts it, but a more simple way to specify a set of rules is "1,3,5:7=A; else=B"

Special values `lo` and `hi` may also appear in the range of values, while `else` can be used with `else=copy` to copy all values which were not specified in the recoding rules.

In the package `car`, a character output would have to be quoted, like "1:2='A'", but that is not mandatory in this function, "1:2=A" would do just as well. Output values such as "NA" or "missing" are converted to NA.

Another difference from the `car` package: the output is not automatically converted to a factor even if the original variable is a factor. That option is left to the user’s decision to specify `as.factor.result`, defaulted to FALSE.

A capital difference is the treatment of the values not present in the recoding rules. By default, package `car` copies all those values in the new object, whereas in this package the default values are NA and new values are added only if they are found in the rules. Users can choose to copy all other values not present in the recoding rules, by specifically adding `else=copy` in the rules.

Since the two functions have the same name, it is possible that users loading both packages to use one instead of the other (depending which package is loaded first). In order to preserve functionality, special efforts have been made to ensure this function performs exactly as the other one (plus more).

In order to minimize possible namespace collisions with package `car`, special efforts have been invested to ensure perfect compatibility with the other `recode()` function. The argument ... allows for more arguments specific to the `car` package, such as `as.factor.result`, `as.numeric.result` and `levels`. In addition, it also accepts labels and ordered specific to function `factor()` in package `base`.

Blank spaces outside category labels are ignored, see the last example.
It is possible to use recode() in a similar way to function cut(), by specifying a vector of cuts which work for both numeric and character/factor objects. For any number of c cuts, there should be \(c + 1\) values, and if not otherwise specified the argument values is automatically constructed as a sequence of numbers from 1 to \(c + 1\).

Unlike the function cut(), arguments such as include.lowest or right are not necessary because the final outcome can be changed by tweaking the cut values.

**Author(s)**

Adrian Dusa

**Examples**

```r
x <- rep(1:3, 3)
x
# [1] 1 2 3 1 2 3 1 2 3
recode(x, "1:2 = A; else = B")
# [1] "A" "A" "B" "A" "A" "B" "A" "A" "B"
recode(x, "1:2 = 0; else = copy")
# [1] 0 0 3 0 3 0 3 0 3
set.seed(1234)
x <- factor(sample(letters[1:10], 20, replace = TRUE),
    levels = letters[1:10])
x
# [1] b g g i g a c g f g c j c i c c b c
# Levels: a b c d e f g h i j
recode(x, "b:d = 1; g:hi = 2; else = NA") # note the "hi" special value
# [1] 1 2 2 2 2 NA 1 2 NA 2 NA 1 2 1 1 1 1
recode(x, "a, c:f = A; g:hi = B; else = C", as.factor.result = TRUE)
# Levels: A B C
recode(x, "a, c:f = 1; g:hi = 2; else = 3", as.factor.result = TRUE,
    labels = c("one", "two", "three"), ordered = TRUE)
# [1] three two two two two one one two one one one three one
# Levels: one < two < three
set.seed(1234)
categories <- c("An", "example", "that has", "spaces")
x <- factor(sample(categories, 20, replace = TRUE),
    levels = categories, ordered = TRUE)
sort(x)
# [1] An  An  An  An  An  example
# [7] example example example that has that has that
# [13] has that has that has that has has spaces
# [19] spaces spaces
# Levels: An < example < that has < spaces

recode(sort(x), "An : 'that has' = 1; spaces = 2")

# [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

# same thing with

recode(sort(x), "An : that has = 1; spaces = 2")

# [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

# same using cut values

recode(sort(x), cuts = "that has")

# [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

# modifying the output values

recode(sort(x), cuts = "that has", values = 0:1)

# [1] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1

# more treatment of "else" values

x <- 10:20

# recoding rules don't overlap all existing values, the rest are empty

recode(x, "8:15=1")

# all other values are copied

recode(x, "8:15=1; else=copy")

---

**retention**

*Compute the retention probability of a csQCA solution*

**Description**

This function computes the retention probability for a csQCA solution, under various perturbation scenarios. It only works with bivalent crisp-set data, containing the binary values 0 or 1.

**Usage**

```
retention(data, outcome = "", conditions = "", incl.cut = 1, n.cut = 1, 
           type = "corruption", dependent = TRUE, p.pert = 0.5, n.pert = 1)
```

**Arguments**

- **data**
  A dataset of bivalent crisp-set factors.

- **outcome**
  The name of the outcome.

- **conditions**
  A string containing the condition variables’ names, separated by commas.

- **incl.cut**
  The minimum sufficiency inclusion score for an output function value of "1".

- **n.cut**
  The minimum number of cases for a causal combination with a set membership score above 0.5, for an output function value of "0" or "1".
type  Simulate corruptions of values in the conditions ("corruption"), or cases deleted entirely ("deletion").
dependent  Logical, if TRUE indicating DPA - Dependent Perturbations Assumption and if FALSE indicating IPA - Independent Perturbations Assumption.
p.pert  Probability of perturbation under independent (IPA) assumption.
n.pert  Number of perturbations under dependent (DPA) assumption.

Details

The argument data requires a suitable data set, in the form of a data frame. with the following structure: values of 0 and 1 for bivalent crisp-set variables.
The argument outcome specifies the outcome to be explained, in upper-case notation (e.g. X).
The argument conditions specifies the names of the condition variables. If omitted, all variables in data are used except outcome.
The argument type controls which type of perturbations should be simulated to calculate the retention probability. When type = "corruption", it simulates changes of values in the conditions (values of 0 become 1, and values of 1 become 0). When type = "deletion", it calculates the probability of retaining the same solution if a number of cases are deleted from the original data.
The argument dependent is a logical which choses between two categories of assumptions. If dependent = TRUE (the default) it indicates DPA - Dependent Perturbations Assumption, when perturbations depend on each other and are tied to a fixed number of cases, ex-ante (see Thiem, Spohel and Dusa, 2016). If dependent = FALSE, it indicates IPA - Independent Perturbations Assumption, when perturbations are assumed to occur independently of each other.
The argument n.cut is one of the factors that decide which configurations are coded as logical remainders or not, in conjunction with argument incl.cut. Those configurations that contain fewer than n.cut cases with membership scores above 0.5 are coded as logical remainders (OUT = "?"), if the number of such cases is at least n.cut, configurations with an inclusion score of at least incl.cut are coded positive (OUT = "1"), while configurations with an inclusion score below incl.cut are coded negative (OUT = "0").
The argument p.pert specifies the probability of perturbation under the IPA - independent perturbations assumption (when dependent = FALSE).
The argument n.pert specifies the number of perturbations under the DPA - dependent perturbations assumption (when dependent = TRUE). At least one perturbation is needed to possibly change a csQCA solution, otherwise the solution will remain the same (retention equal to 100%) if zero perturbations occur under this argument.

Author(s)
Adrian Dusa

References

Examples

```r
data <- data.frame(matrix(c(
  rep(1,25), rep(0,20), rep(c(0,0,1,0,0),3),
  0,0,0,1,0,0,0,0, rep(1,7),0,1),
nrow = 16, byrow = TRUE, dimnames = list(
c("AT","DK","FI","NO","SE","AU","CA","FR",
  "US","DE","NL","CH","JP","NZ","IE","BE"),
c("P","U","C","S","W"))
))

# calculate the retention probability, for 2.5% probability of data corruption
# under the IPA - independent perturbation assuption
retention(dat, outcome = "W", incl.cut = 1, type = "corruption",
  dependent = FALSE, p.pert = 0.025)

# the probability that a csQCA solution will change
1 - retention(dat, outcome = "W", incl.cut = 1, type = "corruption",
  dependent = FALSE, p.pert = 0.025)
```

---

**runGUI**

**run the GUI shiny app for the QCA package**

**Description**

Runs the graphical user interface app based on the *shiny* package.

**Usage**

```r
runGUI(x)
```

**Arguments**

- `x` Path to the shiny app.

**Details**

This function is a wrapper to the `runApp()` function in package *shiny*. If `x` is not provided, it automatically locates the gui directory in the path where the QCA package has been installed, and runs it.

The user interface has an interactive R console in the webpage. Commands are parsed and evaluated into a dedicated environment, with efforts to capture errors and warnings.

**Author(s)**

Adrian Dusa
Functions to find subsets or supersets

Description

Functions to find a list of implicants that satisfy some restrictions (see details), or to find the corresponding row numbers in the implicant matrix, for all subsets, or supersets, of a (prime) implicant or an initial causal configuration.

Usage

```r
superSubset(data, outcome = "", conditions = "", relation = "necessity", incl.cut = 1, cov.cut = 0, ron.cut = 0, pri.cut = 0, use.tilde = FALSE, use.letters = FALSE, depth = NULL, add = NULL, ...)
```

```r
findSubsets(input, noflevels, stop, ...)
```

```r
findSupersets(input, noflevels, ...)
```

Arguments

data A data frame with crisp (binary and multi-value) or fuzzy causal conditions
outcome The name of the outcome.
conditions A string containing the conditions’ names, separated by commas.
relation The set relation to outcome, either "necessity", "sufficiency", "necsuf" or "sufnec". Partial words like "suf" are accepted.
incl.cut The minimal inclusion score of the set relation.
cov.cut The minimal coverage score of the set relation.
ron.cut The minimal score for the RoN - relevance of necessity.
pri.cut The minimal score for the PRI - proportional reduction in inconsistency.
use.tilde Logical, use tilde for negation with bivalent variables.
use.letters Logical, use simple letters instead of original conditions’ names.
noflevels A vector containing the number of levels for each causal condition plus 1 (all subsets are located in the higher dimension, implicant matrix)
input A vector of row numbers where the (prime) implicants are located, or a matrix of configurations (only for supersets).
stop The maximum line number (subset) to stop at, and return
depth Integer, an upper number of causal conditions to form expressions with.
add A function, or a list containing functions, to add more parameters of fit.
... Other arguments, mainly for backward compatibility.
Details

The function `superSubset()` finds a list of implicants that satisfy some restrictions referring to the inclusion and coverage with respect to the outcome, under given assumptions of necessity and/or sufficiency.

Ragin (2000) posits that under the necessity relation, instances of the outcome constitute a subset of the instances of the cause(s). Conversely, under the sufficiency relation, instances of the outcome constitute a superset of the instances of the cause(s).

When `relation = "necessity"` the function finds all implicants which are supersets of the outcome, then eliminates the redundant ones and returns the surviving (minimal) supersets, provided they pass the inclusion and coverage thresholds. If none of the surviving supersets pass these thresholds, the function will find disjunctions of causal conditions, instead of conjunctions.

When `relation = "sufficiency"` it finds all implicants which are subsets of the outcome, and similarly eliminates the redundant ones and return the surviving (minimal) subsets.

When `relation = "necsuf"`, the relation is interpreted as necessity, and `cov.cut` is automatically set equal to the inclusion cutoff `incl.cut`. The same automatic equality is made for `relation = "sufnec"`, when relation is interpreted as sufficiency.

The argument `outcome` specifies the name of the outcome, and if multi-value the argument can also specify the level to explain, using curly brackets notation.

Outcomes can be negated using a tilde operator `~x`. The logical argument `neg.out` is now deprecated, but still backwards compatible. Replaced by the tilde in front of the outcome name, it controls whether `outcome` is to be explained or its negation. If `outcome` is from a multivalent variable, it has the effect that the disjunction of all remaining values becomes the new outcome to be explained. `neg.out = TRUE` and a tilde `~` in the outcome name don’t cancel each other out, either one (or even both) signaling if the outcome should be negated.

If the argument `conditions` is not specified, all other columns in `data` are used.

Along with the standard measures of inclusion and coverage, the function also returns PRI for sufficiency and RoN (relevance of necessity, see Schneider & Wagemann, 2012) for the necessity relation.

A subset is a conjunction (an intersection) of causal conditions, with respect to a larger (super)set, which is another (but more parsimonious) conjunction of causal conditions.

All subsets of a given set can be found in the so called “implicant matrix”, which is a $n^k$ space, understood as all possible combinations of values in any combination of bases $n$, each causal condition having three or more levels (Dusa, 2007, 2010).

For every two levels of a binary causal conditions (values 0 and 1), there are three levels in the implicants matrix:

- 0 to mark a minimized literal
- 1 to replace the value of 0 in the original binary condition
- -1 to replace the value of 1 in the original binary condition

A prime implicant is a superset of an initial combination of causal conditions, and the reverse is also true: the initial combination is a subset of a prime implicant.

Any normal implicant (not prime) is a subset of a prime implicant, and in the same time a superset of some initial causal combinations.
Functions `findSubsets()` and `findSupersets()` find:

- all possible such subsets for a given (prime) implicant, or
- all possible supersets of an implicant or initial causal combination

in the implicant matrix.

The argument depth can be used to impose an upper number of causal conditions to form expressions with, it is the complexity level where the search is stopped. Depth is set to a maximum by default, and the algorithm will always stop at the maximum complexity level where no new, non-redundant prime implicants are found. Reducing the depth below that maximum will also reduce computation time.

For examples on how to add more parameters of fit via argument `add`, see the function `pof()`.

**Value**

The result of the `superSubset()` function is an object of class "ss", which is a list with the following components:

- `incl.cov` A data frame with the parameters of fit.
- `coms` A data frame with the (m)embership (s)cores of the resulting (co)mbinations.

For `findSubsets()` and `findSupersets()`, a vector with the row numbers corresponding to all possible subsets, or supersets, of a (prime) implicant.

**Author(s)**

Adrian Dusa

**References**


**See Also**

`createMatrix`, `getRow`
Examples

```r
# Lipset binary crisp sets
data(LC)
ssLC <- superSubset(LC, "SURV")

require(venn)
x = list("SURV" = which(LC$SURV == 1),
         "STB" = which(ssLC$coms[, 1] == 1),
         "LIT" = which(ssLC$coms[, 2] == 1))
venn(x, cexil = 0.7)

# Lipset multi-value sets
data(LM)
superSubset(LM, "SURV")

# Cebotari & Vink (2013) fuzzy data
data(CVF)

# all necessary combinations with at least 0.9 inclusion and 0.6 coverage cut-offs
ssCVF <- superSubset(CVF, outcome = "PROTEST", incl.cut = 0.90, cov.cut = 0.6)

# the membership scores for the first minimal combination (GEOCON)
ssCVF$coms$GEOCON

# same restrictions, for the negation of the outcome
superSubset(CVF, outcome = "~PROTEST", incl.cut = 0.90, cov.cut = 0.6)

# to find supersets or supersets, a hypothetical example using
# three binary causal conditions, having two levels each: 0 and 1
noflevels <- c(2, 2, 2)

# second row of the implicant matrix: 0 0 1
# which in the "normal" base is: - - 0
# the prime implicant being: ~C
(sub <- findSubsets(input = 2, noflevels + 1))
# 5 8 11 14 17 20 23 26

getRow(sub, noflevels + 1)

# implicant matrix      normal values
#   A B C          A B C
# 5 0 1 1         5 - 0 0  bc
# 8 0 2 1         8 - 1 0  Bc
# 11 1 0 1        11 0 - 0  ac
# 14 1 1 1        14 0 0 0  abc
# 17 1 2 1        17 0 1 0  aBc
# 20 2 0 1        20 1 - 0  Ac
# 23 2 1 1        23 1 0 0  Abc
# 26 2 2 1        26 1 1 0  Abc
```
### Truth Table

Create a truth table

**Description**

Function to create a truth table from all types of calibrated data (binary crisp, multi-value crisp and fuzzy). For fuzzy data, an improved version of Ragin’s (2008) procedure is applied to assign cases.
to the vector space corners (the truth table rows).

Usage

```r
truthTable(data, outcome = "", conditions = "", incl.cut = 1, n.cut = 1,
    complete = FALSE, use.letters = FALSE, show.cases = FALSE,
    dcc = FALSE, sort.by = "", inf.test = "", ...)```

Arguments

- **data**: A data frame containing calibrated causal conditions and an outcome.
- **outcome**: String, the name of the outcome.
- **conditions**: A single string containing the conditions’ (columns) names separated by commas, or a character vector of conditions’ names.
- **incl.cut**: The inclusion cut-off(s): either a single value for the presence of the output, or a vector of length 2, the second for the absence of the output.
- **n.cut**: The minimum number of cases under which a truth table row is declared as a remainder.
- **complete**: Logical, print complete truth table.
- **use.letters**: Logical, use letters instead of causal conditions’ names.
- **show.cases**: Logical, print case names.
- **dcc**: Logical, if show.cases = TRUE, the cases being displayed are the deviant cases consistency in kind.
- **sort.by**: Sort the truth table according to various columns.
- **inf.test**: Specifies the statistical inference test to be performed (currently only "binom") and the critical significance level. It can be either a vector of length 2, or a single string containing both, separated by a comma.
- ... Other arguments (mainly for backward compatibility).

Details

The `data` should always be provided as a data frame, with calibrated columns. Calibration can be either crisp, with 2 or more values starting from 0, or fuzzy with continuous scores from 0 to 1. Raw data containing relative frequencies can also be continuous between 0 and 1, but these are not calibrated, fuzzy data.

Some columns can contain the placeholder "-" indicating a “don’t care”, which is used to indicate the temporal order between other columns in tQCA. These special columns are not causal conditions, hence no parameters of fit will be calculated for them.

The argument `outcome` specifies the column name to be explained. If the outcome is a multivalued column, it can be specified in curly bracket notation, indicating the value to be explained (the others being automatically converted to zero).

The outcome can be negated using a tilde operator `~`. The logical argument `neg.out` is now deprecated, but still backwards compatible. Replaced by the tilde in front of the outcome name, it controls whether outcome is to be explained or its negation.
If the outcome column is multi-value, the argument `outcome` should use the standard curly-bracket notation \( X(\text{value}) \). Multiple values are allowed, separated by a comma (for example \( X(1,2) \)). Negation of the outcome can also be performed using the tilde \( \sim \) operator, for example \( \sim X(1,2) \), which is interpreted as: "all values in \( X \) except 1 and 2" and it becomes the new outcome to be explained.

Using both `neg.out = TRUE` and a tilde \( \sim \) in the outcome name don’t cancel each other out, either one (or even both) signaling if the outcome should be negated.

The argument `conditions` specifies the causal conditions’ names among the other columns in the data. When this argument is not specified, all other columns except for the outcome are taken as causal conditions.

A good practice advice is to specify both `outcome` and `conditions` as upper case letters. It is possible, in a next version, to negate outcomes using lower case letters, a situation where it really does matter how the outcome and/or conditions are specified.

The argument `incl.cut` replaces the (deprecated, but still backwards compatible) former arguments `incl.cut1` and `incl.cut0`. Most of the analyses use the inclusion cutoff for the presence of the output (code "1"). When users need both inclusion cutoffs (see below), `incl.cut` can be specified as a vector of length 2, in the form: \( c(\text{ic1}, \text{ic0}) \) where:

- `ic1` is the inclusion cutoff for the presence of the output,
  a minimum sufficiency inclusion score above which the output value is coded with "1".

- `ic0` is the inclusion cutoff for the absence of the output,
  a maximum sufficiency inclusion score below which the output value is coded with "0".

If not specifically declared, the argument `ic0` is automatically set equal to `ic1`, but otherwise `ic0` should always be lower than `ic1`.

Using these two cutoffs, the observed combinations are coded with:

- "1" if they have an inclusion score above `ic1`
- "C" if they have an inclusion score below `ic1` and above `ic0` (contradiction)
- "0" if they have an inclusion score below `ic0`

The argument `n.cut` specifies the frequency threshold under which a truth table row is coded as a remainder, irrespective of its inclusion score.

When argument `show.cases` is set to `TRUE`, the case names will be printed at their corresponding row in the truth table. The resulting object always contains the cases for each causal combination, even if not printed on the screen (the print function can later be used to print them).

The `sort.by` argument orders all configurations by any of the columns present in the truth table. Typically, sorting occurs by their outcome value, and/or by their inclusion score, and/or by their frequency, in any order.

Sorting decreasingly (the default) or increasingly can be specified adding the signs `-` or `+`, next after
the column name in argument sort.by (see examples). Note that – is redundant because it is the default anyways.

The order specified in this vector is the order in which the configurations will be sorted. When sorting based on the OUTput column, remainders will always be sorted last.

The argument use.letters controls using the original names of the causal conditions, or replace them by single letters in alphabetical order. If the causal conditions are already named with single letters, the original letters will be used.

The argument inf.test combines the inclusion score with a statistical inference test, in order to assign values in the output column OUT. For the moment, it is only the binomial test, which needs crisp data (it doesn’t work with fuzzy sets). Following a similar logic as above, for a given (specified) critical significance level, the output for a truth table row will be coded as:

"1" if the true inclusion score is significantly higher than ic1,

"C" contradiction, if the true inclusion score is not significantly higher than ic1 but significantly higher than ic0,

"0" if the true inclusion score is not significantly higher than ic0.

It should be noted that statistical tests perform well only when the number of cases is large, otherwise they are usually not significant. For a low number of cases, depending on the inclusion cutoff value(s), it will be harder to code a value of "1" in the output, and also harder to obtain contradictions if the true inclusion is not significantly higher than ic0.

The argument complete controls how to print the table on the screen, either complete (when set to TRUE), or just the observed combinations (default). For up to 7 causal conditions, the resulting object will always contain the complete truth table, even if it’s not printed on the screen. This is useful for multiple reasons: researchers like to manually change output values in the truth table (sometimes including in this way a remainder, for example), and it is also useful to plot Venn diagrams, each truth table row having a correspondent intersection in the diagram.

Value

An object of class "tt", a list containing the following components:

- tt The truth table itself.
- indexes The line numbers for the observed causal configurations.
- nolevels A vector with the number of values for each causal condition.
- initial.data The initial data.
- recoded.data The crisp version of the initial.data, if fuzzy.
- cases The cases for each observed causal configuration.
- options The command options used.
- rowsorder The order of the rows after sorting, if using sort.by.
- minmat The membership scores matrix of cases in the observed truth table combinations.
Author(s)

Adrian Dusa

References


See Also

minimize

Examples

```r
# -----
# Lipset binary crisp data
data(LC)
ttlLC <- truthTable(LC, "SURV")

# inspect the truth table
ttlLC

# print the cases too, even if not specifically asked for
print(ttlLC, show.cases = TRUE)

# the printing function also supports the complete version
print(ttlLC, show.cases = TRUE, complete = TRUE)

# formally asking the complete version
truthTable(LC, "SURV", complete = TRUE)

# sorting by multiple columns, decreasing by default
truthTable(LC, "SURV", complete = TRUE, sort.by = "incl, n")
```
# sort the truth table decreasing for inclusion, and increasing for n
# note that "-" is redundant, sorting is decreasing by default
thruthTable(LC, "SURV", complete = TRUE, sort.by = "incl", n="")

# -----  
# Lipset multi-value crisp data (Cronqvist & Berg-Schlosser 2009, p.80)
data(LM)
thruthTable(LM, "SURV", sort.by = "incl")

# using a frequency cutoff equal to 2 cases
ttLM <- truthTable(LM, "SURV", n.cut = 2, sort.by = "incl")
ttLM

# the observed combinations coded as remainders
	ttLM$excluded

# -----  
# Cebotari & Vink fuzzy data
data(CVF)
ttCFV <- truthTable(CVF, "PROTEST", incl.cut = 0.8, sort.by = "incl")

# view the Venn diagram for this truth table
library(venn)
venn(tttCFV)

# each intersection transparent by its inclusion score
venn(tttCFV, transparency = tttCFV$t$t$incl)

# the truth table negating the outcome
truthTable(CVF, "~PROTEST", incl.cut = 0.8, sort.by = "incl")

# allow contradictions
truthTable(CVF, "PROTEST", incl.cut = c(0.8, 0.75), sort.by = "incl")

# -----  
# Ragin and Strand data with temporal QCA
ndata(RS)

# truth table containing the "-" placeholder as a "don't care"
thruthTable(RS, "REC")
Description

This function creates a plot for a single vector of numerical values, arranging them horizontally on the X axis from minimum to maximum.

Usage

\texttt{Xplot(x, jitter = FALSE, at = NULL, ...)}

Arguments

- \texttt{x} \hspace{1cm} A numeric vector.
- \texttt{jitter} \hspace{1cm} Logical, vertically jitter the points.
- \texttt{at} \hspace{1cm} The points at which tick-marks are to be drawn. Non-finite (infinite, NaN or NA) values are omitted. By default (when NULL) tickmark locations are automatically computed, see the help file for \texttt{axis}.
- \texttt{...} \hspace{1cm} Other graphical parameters from \texttt{par}

Details

This is a special type of (scatter)plot, with points being arranged only on the horizontal axis (it has no vertical axis). Useful when inspecting if points are grouped into naturally occurring clusters, mainly for crisp calibration purposes.

The argument \texttt{...} is used to pass arguments to the various graphical parameters from \texttt{par}, and also to the settings from \texttt{jitter}.

The points have a default \texttt{cex} (character expansion) value of 1, and a default \texttt{pch} value of 1 (empty points), which can be modified accordingly (for instance value 21 for filled points). When \texttt{pch} = 21, the color for the margins of the points can be specified via the argument \texttt{col}, while the argument \texttt{bg} will determine the fill color of the points.

The axis labels have a default \texttt{cex.axis} value of 0.8, which affects both the tickmarks labels and the axis labels.

When jittering the points, default values of 0.5 are used for the parameters \texttt{factor} and \texttt{amount}, on the horizontal axis. More details can be found in the base function \texttt{jitter}().

Although the points are displayed in a single dimension, on the horizontal axis, the R graphical window will still have the default squared shape, with a lot of empty space on the vertical axis. Users are free to create their custom code to determine the size of the graphics window, or simply resize it to a suitable height.

Author(s)

Adrian Dusa

See Also

\texttt{par, text, jitter}
Examples

```r
# Lipset's raw data
data(LR)

# plot the DEV (level of development) causal condition
xplot(LR$DEV)

# jitter the points vertically
xplot(LR$DEV, jitter = TRUE)

# make the x axis large enough to accommodate all values
xplot(LR$DEV, jitter = TRUE, at = pretty(LR$DEV))

# clip plotting between the range of min and max
xplot(LR$DEV, jitter = TRUE, at = range(LR$DEV))
```

---

**XYplot**

Create an XY plot

**Description**

This function creates an XY plot from the first two columns of a dataframe/matrix, or from two separate vectors of numeric values.

**Usage**

```r
XYplot(x, y, data, relation = "sufficiency", mguides = TRUE, 
jitter = FALSE, clabels = NULL, enhance = FALSE, model = FALSE, ...)
```

**Arguments**

- `x`: Character, the name of the column from the data for the X axis, or the coordinates of points in the plot (either a matrix/dataframe with at least two columns, or a vector of numerical values for the X axis), or a valid SOP expression.
- `y`: Character, the name of the column from the data for the Y axis, or the Y coordinates of points in the plot, optional if `x` is a matrix/dataframe.
- `data`: A calibrated dataset, only if `x` and `y` are names.
- `relation`: The set relation to Y, either "sufficiency" (default) or "necessity".
- `mguides`: Logical, print the middle guides.
- `jitter`: Logical, jitter the points.
- `clabels`: A vector of case labels with the same length as `x` and `y`, or a logical vector of the same length as the number of rows in the data (if provided).
- `enhance`: Logical, if TRUE print the points using different characters for each of the five significant regions for process tracing.
model Logical, for an enhanced plot specify if the SOP expression in argument x is a solution model.

... Other graphical parameters from ?par

Details

If x is a dataframe or a matrix, the axes labels will be taken from the column names of x, otherwise they will be inferred from the names of the x and y objects that are passed to this function.

x can also be a string containing either the name of the column for the X axis, or two column names separated by a comma, referring to the X and Y axis respectively. When x contains both X and Y column names, the next argument will be considered as the data.

If data is provided, and the names of the X and Y columns are valid R statements, quoting them is not even necessary and they can be negated using either a tilde "~" or "1 - ".

The numeric values should be restricted between 0 and 1, otherwise an error is generated.

The XY plot will also provide inclusion and coverage scores for a sufficiency (along with PRI) or a necessity relation (along with RoN).

The argument x can also be a SOP - sum of products expression, in which case the relation is determined by the usual forward arrow "=>" for sufficiency and backward arrow "<=" for necessity.

The argument ... is used to pass arguments to the various graphical parameters from ?par, and also to the settings from ?jitter.

The points have a default cex (character expansion) value of 0.8, and a default pch value of 21 (filled points), which can be modified accordingly (for example with value 1 of empty points). When pch = 21, the color for the margins of the points can be specified via the argument col, while the argument bg will determine the fill color of the points.

The axes' labels have a default cex.axis value of 0.8, which affects both the tickmarks labels and the axis labels.

When jittering the points, default values of 0.01 are used for the parameters factor and amount, on both horizontal and vertical axes.

The argument enhance does all the work for the shape of the points and their colors, according to the five regions specified by Schneider & Rohlfing (2016), who augmented the classical XY plot with process tracing.

The default enhanced XY plot has even more settings when the input SOP expression is a minimization model (different colors, different regions where to place the labels etc.), available by activating the argument model. The model is automatically detected if the input for x is a minimization object.

Value

A list of x and y values, especially useful when the points are jittered.

Author(s)

Adrian Dusa
References


See Also

par, text, jitter

Examples

```r
# Cebotari & Vink (2013)
data(CVF)

# necessity relation between NATPRIDE and PROTEST
XYplot(CVF[, 5:6])

# same using two numeric vectors
XYplot(CVF$NATPRIDE, CVF$PROTEST)

# same using two column names
XYplot("NATPRIDE", "PROTEST", data = CVF)

# or using one string containing both
XYplot("NATPRIDE, PROTEST", data = CVF)

# since they are valid R statements, it works even without quotes
# (this only works in normal R console, not in the GUI version)
XYplot(NATPRIDE, PROTEST, data = CVF)

# negating the X axis, using numeric vectors
XYplot(1 - CVF$NATPRIDE, CVF$PROTEST)

# same thing using quotes
XYplot("1 - NATPRIDE, PROTEST", data = CVF)

# using tilde for negation
XYplot("~NATPRIDE, PROTEST", data = CVF)

# different color for the points
XYplot("~NATPRIDE, PROTEST", data = CVF, col = "blue")

# using a different character expansion for the axes
XYplot("~NATPRIDE, PROTEST", data = CVF, cex.axis = 0.9)

# custom axis labels
```
Description

This data set was used by Cebotari and Vink (2013), and it was taken here from the associated replication file Cebotari and Vink (2015).
Usage

data(CVR)
data(CVF)

Format

A data frame containing 29 cases (ethnic minorities) and the following 6 columns:

**DEMOC** Level of democracy: (contextual factor), based on a democracy index ranking countries on a scale from strong autocracies (0) to strong democracies (10). The fuzzy scores were calibrated using an exclusion threshold of 2, a crossover of 7 and an inclusion threshold of 9.5.

**ETHFRACT** Degree of ethnic fractionalization: (contextual factor), with raw scores ranging from a homogenous society (0) to a highly fragmented country (1). The fuzzy scores were calibrated using an exclusion threshold of 0, a crossover of 0.495 and an inclusion threshold of 0.8.

**GEOCON** Territorial concentration: (group-related factor) with raw data coded as: widely dispersed (0) and primarily urban minorities (1) considered territorially dispersed minorities, and ethnic communities majoritary in a region (2) and entirely concentrated in one region (3) considered as territorially concentrated minorities. The fuzzy scores were calibrated using an exclusion threshold of 0, a crossover of 1.25 and an inclusion threshold of 3.

**POLDIS** Political discrimination: (group-related factor) captures discrimination practices toward minority groups that vary from no discrimination (0) to exclusive and repressive policies toward a minority group (4). The fuzzy scores were calibrated using an exclusion threshold of 0, a crossover of 0.75 and an inclusion threshold of 3.

**NATPRIDE** National pride: (group-related factor) with raw scores ranging from ‘not at all proud’ (0) to ‘very proud’ (3). The fuzzy scores were calibrated using an exclusion threshold of 0.5, a crossover of 1.5 and an inclusion threshold of 2.5.

**PROTEST** Outcome, ethno-political protest: measured on a range from 0 to 5 with higher values indicating more intense protest actions. The fuzzy scores were calibrated using an exclusion threshold of 0.5, a crossover of 1.5 and an inclusion threshold of 3.

Details

There are two different versions of the Cebotari and Vink data: CVR contains the raw data, and CVF contains the data calibrated to fuzzy-sets.

References


Description

This data set was used by Hino (2009), to demonstrate the Time-Difference QCA.

Usage

data(Hc)

Format

A data frame containing 15 cases (countries) and the following 5 columns:

- FOREIGN Percentage of foreign population.
- UNEMP Percentage of unemployed population.
- CONV Party system convergence.
- PRES80 Presence of extreme-right parties in 1980s.
- VOTE Outcome, vote share of extreme-right parties.

Details

For all columns in the data, a value of 1 means a positive difference between 1990 and 1980, and a value of 0 means negative or zero difference, except for the condition CONV, which is the inverse of the condition DIVERT in the raw data. The condition PRES80 does not have a time difference, it represents a simple presence / absence of extreme-right parties in the 1980s.

References


Legacy datasets

The following datasets are no longer part of this package in the formal documentation, but have been added to ensure backwards compatibility with prior publications.
Usage

```r
data(d.AS)
data(d.Bas)
data(d.biodiversity)
data(d.BWB)
data(d.CS)
data(d.CZH)
data(d.education)
data(d.Emm)
data(d.graduate)
data(d.health)
data(d.HK)
data(d.HMN)
data(d.homeless)
data(d.jobsecurity)
data(d.Kil)
data(d.Kro)
data(d.napoleon)
data(d.partybans)
data(d.represent)
data(d.RS)
data(d.SA)
data(d.socialsecurity)
data(d.SS)
data(d.stakeholder)
data(d.transport)
data(d.urban)
data(Emme)
data(HarKem)
data(Krook)
data(RagStr)
data(Rokkan)
```

---

_Lipset_  
Lipset’s indicators for the survival of democracy during the inter-war period.

Description

This dataset is taken from Lipset (1959), as used by Rihoux and De Meur (2009), Cronqvist and Berg-Schlosser (2009) and Ragin (2009).

Usage

```r
data(LR)
data(LC)
```
data(LM)
data(LF)

**Format**

A data frame containing 18 rows and the following 6 columns:

- **DEV** Level of development: it is the GDP per capita (USD) in the raw data, calibrated in the binary crisp version to 0 if below 550 USD and 1 otherwise. For the multi-value crisp version, two thresholds were used: 550 and 850 USD.
- **URB** Level of urbanization: percent of the population in towns with 20000 or more inhabitants, calibrated in the crisp versions to 0 if below 50% and 1 if above.
- **LIT** Level of literacy: percent of the literate population, calibrated in the crisp versions to 0 if below 75% and 1 if above.
- **IND** Level of industrialization: percent of the industrial labor force, calibrated in the crisp versions to 0 if below 30% and 1 if above.
- **STB** Government stability: a “political-institutional” condition added to the previous four “socioeconomic” ones. The raw data has the number of cabinets which governed in the period under study, calibrated in the crisp versions to 0 if 10 or above and to 1 if below 10.
- **SURV** Outcome: survival of democracy during the inter-war period: calibrated to 0 if negative, and 1 if positive raw data.

**Details**

There are four different versions of the Lipset data:

- **LR** contains the raw data
- **LC** is the same data calibrated to binary crisp sets
- **LM** is calibrated to multi-value sets
- **LF** is calibrated to fuzzy-sets

**References**


Description

This fuzzy dataset is an adaptation from Ragin (2005, 2008), the data itself being attributed to Nieuwbeerta (1995).

Usage

data(NF)

Format

A data frame containing 12 cases (countries) and the following 5 columns:

- A: degree of membership in the set of highly affluent countries
- I: degree of membership in the set of countries with substantial levels of income inequality
- M: degree of membership in the set of countries with a high percentage of workers employed in manufacturing
- U: degree of membership in the set of countries with strong unions
- W: outcome: degree of membership in the set of countries with weak class voting

Details

All fuzzy sets in this data are constructed on a six-values scale, for demonstrative purposes.

In the original dataset, the outcome W is presented as the first column.

References


Description

Original data used by Caren and Panofsky (2005), and reanalysed by Ragin and Strand (2008).
Usage
data(RS)

Format

A data frame containing 17 cases and the following 6 columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>P</td>
<td>Public university</td>
</tr>
<tr>
<td>E</td>
<td>Support of elite allies</td>
</tr>
<tr>
<td>A</td>
<td>National union affiliation</td>
</tr>
<tr>
<td>S</td>
<td>Strike or a strike threat</td>
</tr>
<tr>
<td>EBA</td>
<td>E happens before A</td>
</tr>
<tr>
<td>REC</td>
<td>Union recognition</td>
</tr>
</tbody>
</table>

Details

The causal conditions are P, E, A and S. All of them are binary crisp with two values: 0 = No and 1 = Yes.

The column EBA is not a causal condition, specifying in which case the causal condition E happens before the causal condition A. It has two values (0 = No and 1 = Yes) plus the placeholder "-" to signal a “don’t care”.

The outcome is the union recognition EBA, also binary crisp with two values: 0 = No and 1 = Yes.

Source


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