Package ‘QCA’

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LazyData yes
Imports admisc (> 0.1), fastdigest, methods, shiny, venn (>= 1.2)
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 that explains a given phenomenon.
License GPL (>= 2)
NeedsCompilation yes
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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 (2018). 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. Starting with version 3.5, it is possible to specify conjunctural directional expectations in the minimization function.

Details

Package: QCA
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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

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


Arguments

x  A numerical causal condition.
type Calibration type, either "crisp" or "fuzzy".
method Calibration method, either "direct", "indirect" or "TFR".
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 measure-
ment) 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 nu-
meric 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 \( e_l < c_1 < i_1 \leq i_2 < c_2 < e_2 \), 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 \( i_1 \).

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

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

Both \( \text{logistic} \) and \( \text{ecdf} \) 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 \( \text{logistic} \) and \( \text{ecdf} \) 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, \( \text{below} \) and \( \text{above} \) 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 with.

The third method applied to fuzzy calibrations is called "TFR" and calibrates categorical data (such as Likert type response scales) to fuzzy values using the Totally Fuzzy and Relative method (Chelli and Lemmi, 1995).

**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

# 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)

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

px <- calibrate(x, type = "crisp", thresholds = c(170, 180))
plot(x, px, 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
px <- calibrate(x, thresholds = "e=165, c=175, i=185")
plot(x, px, main = "Membership scores in the set of tall people",
    xlab = "Raw data", ylab = "Calibrated data")

# calibrate to a decreasing, s-shaped fuzzy-set
px <- calibrate(x, thresholds = "i=165, c=175, e=185")
plot(x, px, main = "Membership scores in the set of short people",
    xlab = "Raw data", ylab = "Calibrated data")

# when not using the logistic function, linear increase
px <- calibrate(x, thresholds = "e=165, c=175, i=185", logistic = FALSE)
plot(x, px, main = "Membership scores in the set of tall people",
    xlab = "Raw data", ylab = "Calibrated data")
# tweaking the parameters "below" and "above" the crossover, 
# at value 3.5 approximates a logistic distribution, when e=155 and i=195
cx <- calibrate(x, thresholds = "e1=155, c1=165, i1=175, i2=175, c2=185, e2=195", 
               below = 3.5, above = 3.5)
plot(x, cx, main = "Membership scores in the set of tall people",
     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)
```r
# 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 indirect method, per capita income data from Ragin (2008)
inc <- c(40110, 34400, 25200, 24920, 20060, 17090, 15320, 13680, 11720,
         11290, 10940, 9800, 7470, 4670, 4100, 4070, 3740, 3690, 3590,
         2980, 1000, 650, 450, 110)
cinc <- calibrate(inc, method = "indirect",
                  thresholds = "1000, 4000, 5000, 10000, 20000")
plot(inc, cinc, main = "Membership scores in the set of high income",
     xlab = "Raw data", ylab = "Calibrated data")

# calibrating categorical data
set.seed(12345)
values <- sample(1:7, 100, replace = TRUE)
TFR <- calibrate(values, method = "TFR")
table(round(TFR, 3))
```

---

**causalChain**

Perform CNA - coincidence analysis using QCA

**Description**

This function mimics the functionality in the package `cna`, 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():

- con corresponds to sol.cons.
- con.msc corresponds to pi.cons.
- cov corresponds to sol.cov.

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 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.

Author(s)

Adrian Dusa

See Also

minimize, truthTable

Examples

```r
## Not run:
# The following examples assume the package cna is installed
library(cna)
cna(d.educate, what = "a")
## End(Not run)

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

# inclusion and coverage scores can be inspected for each outcome
c <- causalChain(d.educate)
cc$E$IC

## Not run:
# another example, function cna() requires specific complexity depths
cna(d.women, maxstep = c(3, 4, 9), what = "a")
## End(Not run)

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

## Not run:
# multivalue data require a different function in package cna
mvcna(d.pban, ordering = list(c("C", "F", "T", "V"), "PB"),
    cov = 0.95, maxstep = c(6, 6, 10), what = "a")
## End(Not run)

# same results again, simpler command
causalChain(d.pban, ordering = "C, F, T, V < PB", sol.cov = 0.95)
```
## Not run:
# specifying a lower consistency threshold for the solutions
mvca(d.pban, ordering = list(c("C", "F", "T", "V"), "PB"), con = .93,
maxstep = c(6, 5, 10), what = "a")
## End(Not run)

# same thing with
causalChain(d.pban, ordering = "C, F, T, V < PB", pi.cons = 0.93,
sol.cons = 0.95)

# setting consistency thresholds for the PIs, solutions and also
# a coverage threshold for the solution (note that an yet another
# function for fuzzy sets is needed in package cna)
dat2 <- d.autonomy[15:30, c("AU", "RE", "CN", "DE")]
## Not run:
fscna(dat2, ordering = list("AU"), con = .9, con.msc = .85, cov = .85,
what = "a")
## End(Not run)

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

---

**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()`
factorize

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.

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.

Usage

```r
factorize(input, snames = "\", noflevels = NULL, pos = FALSE, use.tilde = FALSE, ...)```

Arguments

- `input`  
  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.

- `pos`  
  Logical, if possible factorize using product(s) of sums.

- `use.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 SOP - sum of products. 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 nollevels 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.

The argument use. tilde is automatically activated if the input contains a tilde to negate conditions.

Value

A named list, each component containing all possible factorizations of the input expression(s), found in the name(s).

Author(s)

Adrian Dusa

References


See Also

`translate`

Examples

```r
# 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)

## Not run:
# using an object of class "qca" produced with function minimize()
# in package QCA
library(QCA)

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))

## End(Not run)

---

**findRows**

**Find untenable configurations**

**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**

```r
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.
- **...** Additional arguments to be passed to function `truthTable()`, for the negation of the outcome.

**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). By default, 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.

Identical simplifying assumptions that found in both parsimonious solutions are declared as contradictory. Observed configurations that are sufficient for both the presence and the absence of the outcome are 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

To find contradictory simplifying assumptions, a truth table for the negated outcome is constructed, using the \texttt{incl.cut} argument from the \texttt{obj} input object. If the inclusion cut-off has a single value, the same is used for the negated outcome, and if it has two values the second is used.

If very specific cutoff values are needed for the negation of the outcome, these can be provided via the \texttt{...} argument, that will be passed to function \texttt{truthTable()}.  

\textbf{Value}  
A numeric vector of row numbers from the truth table.

\textbf{Author(s)}  
Adrian Dusa

\textbf{See Also}  
\texttt{truthTable}, \texttt{minimize}
findTh

Examples

# Lipset's binary crisp version
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
ttlF <- truthTable(LF, outcome = "SURV", incl.cut = 0.8)

findRows(obj = ttlF, type = 2) # contradictory simplifying assumptions

# Contradictory simplifying assumptions using different cutoff values
# for the _negation_ of the outcome
findRows(obj = ttlF, type = 2, incl.cut = 0.9, pri.cut = 0.7)

---

findTh  Find calibration thresholds

Description

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

Usage

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**

```r
# 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

# -----  
# Cebotari & Vink (2013, 2015)

# 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")

---

Implicant matrix functions: allExpressions, createMatrix, getRow

**Functions Related to the Implicant Matrix**

**Description**

This is a set of functions dedicated to the implicant matrix, a space where all causal configurations and their minimized solutions are found.

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:

$$v_1 \cdot v_2 \cdot \ldots \cdot v_k$$

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:

\[
(2 + 1) \cdot (2 + 1) \cdot \ldots \cdot (2 + 1)
\]

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

\[
(v_1 + 1) \cdot (v_2 + 1) \cdot \ldots \cdot (v_k + 1)
\]

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:

\(v_1 \cdot v_2 \ldots \cdot v_k\) 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**


Implicant matrix functions: allExpressions, createMatrix, getRow

See Also

expand.grid

Examples

# 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
Interpret SOP/DNF expressions: compute, simplify

Functions to interpret a SOP/DNF expression

Description

These functions interpret an expression written in a SOP - sum of products (or in canonical DNF - disjunctive normal form), for both crisp and multivalue QCA. The function `compute()` calculates set membership scores based on a SOP expression applied to a calibrated data set.

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.

A function similar to `compute()` was initially 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 `simplify()` transforms any expression (most notably a POS - product of sums) into a simpler 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
compute(expression = "", data, separate = FALSE)
```

```r
simplify(expression = "", snames = "", noflevels, use.tilde = FALSE, ...)
```

Arguments

- **expression** String: a QCA expression written in sum of products form.
- **data** A dataset with binary cs, mv and fs data.
- **separate** Logical, perform computations on individual, separate paths.
- **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 to negate bivalent conditions.
- **...** Other arguments, mainly for backwards compatibility.
Interpret SOP/DNF expressions: compute, simplify

Details

An expression written in SOP - sum of products, is a “union of intersections”, for example \(A \cdot B + B \cdot C\). The DNF - disjunctive normal form is also a sum of products, with the restriction that each product has to contain all literals. The equivalent expression is: \(A \cdot B \cdot C + A \cdot B \cdot C + A \cdot B \cdot C\).

The same expression can be written in multivalue notation: \(A(1) \cdot B(1) + B(1) \cdot C(0)\). 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 “\(^\sim\)” as a negation for a particular causal condition. \(^\sim\)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: \(^\sim\)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 \(^\sim\)A(0,2) \cdot A(1,2) is equivalent with A(1), while A(0) \cdot 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 nolvels have precedence over data, when specified.

The use of the product operator \(\cdot\) 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 \(\cdot\) 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 simplify(), if a tilde is present in the expression, the argument use.tilde is automatically activated. For Boolean expressions, the simplest equivalent logical expression can result in the empty set, if the conditions cancel each other out.

Value

For the function compute(), a vector of set membership values.

For function simplify(), a character expression.

Author(s)

Adrian Dusa
Interpret SOP/DNF expressions: compute, simplify

References


Examples

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

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

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

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

# multilevel conditions can also be specified (and negated)
simplify("(A(1) + ~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)
simplify("lw(SG + LW)", snames = "S, L, W, G")

# SLwG

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

# SLW + SWG

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

# SW(G + L)

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

# subnations that exhibit ethnic political mobilization (E) but were
# not hypothesized by any of the three theories (page 147)
# \( \neg H = \neg (l_w + S + \neg L_g) = G_lS + G_Lw + G_SW + 1Sw \)

simplify("(G_lS + G_Lw + G_SW + 1Sw)(S + Lw)", snames = "S, L, W, G")

# sLWG + SLwG

---

### 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 = NULL)
```

### 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 `simplify()`, 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 `simplify()` 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 minimization objects of class "qca", the number of levels, and the set names are automatically detected.

Author(s)

Adrian Dusa

References


Examples

```r
# using minimization objects
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")

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

# 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")

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

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

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

# subnations that exhibit ethnic political mobilization (E) but were


# not hypothesized by any of the three theories (page 147)

\[
-\mathbf{H} = \neg(\mathbf{LW} + \mathbf{SW} + \mathbf{Lg})
\]

intersection(negate("LW + SW + Lg"), "SG + LW", snames = "S, L, W, G")

---

**minimize**

*Minimize a truth table*

**Description**

This function performs the QCA minimization of an input truth table, or if the input is a dataset 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 (2018) 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 = FALSE, 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.
\textbf{minimize}

- \texttt{all.sol} Logical, search for all possible solutions even of not minimal.
- \texttt{details} Logical, print more details about the solution.
- \texttt{use.tilde} Logical, use tilde to signal the absence of conditions.
- \texttt{method} Minimization method, one of \texttt{"CCubes"} (default), or \texttt{"QMC"} the classical Quine-McCluskey, or \texttt{"eQMC"} the enhanced Quine-McCluskey.
- ... Other arguments to be passed to function \texttt{truthTable}.

\textbf{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 \texttt{minimize()} originally had some additional formal arguments which were sent to the function \texttt{truthTable()}: outcome, conditions, n.cut, incl.cut, show.cases, use.letters and inf.test.

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

The argument \texttt{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 \texttt{explain} is also accepted in the argument \texttt{include}.

The argument \texttt{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 \texttt{dir.exp} is used to specify directional expectations, as described by Ragin (2003). They can be specified using SOP (sum of products) expressions, which opens up the possibility to experiment with conjunctural directional expectations. Don’t care conditions are simply left unspecified.

Activating the \texttt{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 \texttt{input} has been provided as a data frame instead of a truth table object.

The argument \texttt{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 \texttt{QCA} employs a different search algorithm based on Consistency Cubes (Dusa, 2018), 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:

- \texttt{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 pi.depth is, the algorithm will always stop at a maximum complexity level where no new, non-redundant prime implicants are found. The argument sol.depth is relevant only when activating the argument all.sol to solve the PI chart.

The default method (when 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 min.pin introduces an additional parameter to control when to stop the search for prime implicants. It is based on the observation by Dusa (2018) 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 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 all.sol automatically deactivates the argument 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 row.dom.

If minimizing a dataset instead of a truth table, unless otherwise specified the argument incl.cut is automatically set to the minimum value between pi.cons and sol.cons, then passed to the function truthTable().

The argument 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 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 outcome, or class "mqca" when using multiple outcomes. These objects are lists having the following components:

- **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

```r
# -----
# Lipset binary crisp data

# the associated truth table
tttLC <- truthTable(LC, "SURV", sort.by = "incl, n", show.cases = TRUE)
tttLC

# conservative solution (Rihoux & De Meur 2009, p.57)
cLC <- minimize(tttLC)
cLC

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

# add details and case names
minimize(tttLC, details = TRUE)

# negating the outcome
tttLn <- truthTable(LC, "~SURV", sort.by = "incl, n", show.cases = TRUE)
minimize(tttLn)

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

# parsimonious solution, positive output
pltC <- minimize(tttLC, include = "?", details = TRUE)
pltC

# the associated simplifying assumptions
pltC$SA

# parsimonious solution, negative output
pltLn <- minimize(tttLn, include = "?", details = TRUE)
```
# Lipset multi-value crisp data (Cronqvist & Berg-Schlosser 2009, p.80)

# truth table
```
TtLM <- truthTable(LM, "SURV", conditions = "DEV, URB, LIT, IND",
                   sort.by = "incl", show.cases = TRUE)
```

# conservative solution, positive output
```
minimize(TtLM, details = TRUE)
```

# parsimonious solution, positive output
```
minimize(TtLM, include = "?", details = 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)
```

# parsimonious solution, positive output
```
minimize(TtLMn, include = "?", details = TRUE)
```

# Lipset fuzzy sets data (Ragin 2009, p.112)

# truth table using a very low inclusion cutoff
```
TtLF <- truthTable(LF, "SURV", incl.cut = 0.8,
                    sort.by = "incl", show.cases = TRUE)
```

# conservative solution
```
minimize(TtLF, details = TRUE)
```

# parsimonious solution
```
minimize(TtLF, include = "?", details = TRUE)
```

# intermediate solution using directional expectations
```
minimize(TtLF, include = "?", details = TRUE,
         dir.exp = "DEV, URB, LIT, IND, STB")
```

# URB as a don't care condition (left unspecified) and
# experimentally, conjunctural directional expectations
```
minimize(TtLF, include = "?", details = TRUE,
         dir.exp = "DEV, STB, ~LITxIND")
```

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

pCVF <- minimize(ttCVF, include = "?", details = TRUE)
pCVF

# 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, details = 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
minimize(RS, outcome = "REC", details = TRUE)

---

**modelFit**

*Theory evaluation*

**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**

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

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

# parsimonious solution
pLF <- minimize(ttlF, include = "?"

modelFit(model = pLF, theory = "DEV*STB")

# hypothetical exploration of intermediate solutions
iLF <- minimize(ttlF, include = "?", dir.exp = "1,0,0,0,0"

modelFit(iLF, "DEV*STB")
```
Negate Boolean expressions

Description

Function to negate a SOP expression.

Usage

\texttt{negate(input, snames = ",", noflevels = NULL, use.tilde = FALSE)}

Arguments

- \texttt{input}: A string representing a SOP expression, or a minimization object of class "qca".
- \texttt{snames}: A string containing the sets' names, separated by commas.
- \texttt{noflevels}: Numerical vector containing the number of levels for each set.
- \texttt{use.tilde}: Logical, use a tilde to negate the sets.

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. $\neg (A \lor B) = (\neg A) \land (\neg B)$
2. $\neg (A \land B) = (\neg A) \lor (\neg B)$

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 \texttt{minimize()} in package QCA. 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 \texttt{snames}.

To negate multilevel expressions, the argument \texttt{noflevels} is required.

It is entirely possible to obtain multiple negations of a single expression, since the result of the negation is passed to function \texttt{simplify()}.

Value

A character vector when the input is a SOP expresison, or a named list for minimization input objects, each component containing all possible negations of the model(s).
Parameters of fit

Author(s)
Adrian Dusa

References

See Also
minimize

Examples

# example from Ragin (1987, p.99)

negate("AC + B-\sim C")

# with different intersection operators

negate("AB\times EF + \neg CD\times EF")

# using an object of class "qca" produced with minimize()

cLC <- minimize(LC, outcome = "SURV")

negate(cLC)

# parsimonious solution

pLC <- minimize(LC, outcome = "SURV", include = "?")

negate(pLC)

Description

These functions returns inclusion (consistency) and coverage, plus PRI for sufficiency and RoN for necessity. The function pofind() is a stripped down version of the pof() function, to calculate parameters of fit for single conditions.

Usage

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

pofind(data, outcome, conditions, relation = "necessity", use.tilde = FALSE, ...)
Parameters of fit

Arguments

setms  A data frame or a single vector of (calibrated) set memberships, or an expression written in sum of products form.
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  A calibrated data frame.
conditions  A single string containing the conditions' (columns) names separated by commas, or a character vector of conditions' names.
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. Used only in conjunction with the argument inf.test
add  A function, or a list containing functions, to add more parameters of fit.
use.tilde  Logical, use tilde to signal the absence of conditions.
...  Other arguments to be passed to the main function.

Details

The function pof() 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. The number of columns in the matrix should be equal to the number of causal conditions in the original data. If some of them are minimized, they can be replaced by the numerical value -1 (see examples section).

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 SOP - sum of products form.

For all situation 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 `~` 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 `infNtest` provides the possibility to perform statistical inference tests, comparing the calculated inclusion score with a pair of thresholds (`icQ` and `icP`) specified in the argument `inclNcut`. 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` (`pvalQ` and `pvalP`) 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 `negNout` is deprecated, but backwards compatible. `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.

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 `~X` is interpreted as `X`, while `~x` is interpreted as `x`.

The arguments from function `pofind()` are passed to the main function `pof()` to calculate parameters of fit.

**Author(s)**

Adrian Dusa

**References**


**See Also**

`minimize`, `superSubset`, `translate`
Examples

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

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)
```
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.
- **configs**: A string containing causal configurations, separated by commas, or a matrix of causal configurations in the implicants space.
- **snames**: A string containing the sets’ names, separated by commas.
- **mv**: Logical, row and column names in multi-value notation.
- **use.tilde**: Logical, row and column names indicating absence with a tilde.
- **collapse**: Scalar character, how to collapse different parts of the row or column names.
- **chart**: An object of class "pic" or a logical matrix.
row.dom Logical, apply row dominance to eliminate redundant prime implicants.
all.sol Derive all possible solutions, irrespective if the disjunctive number of prime implicants is minimal or not.
depth A maximum number of prime implicants for any disjunctive solution.
...

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 P 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 deactivated 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.

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]  [,2]
  # [1,]  1    1
  # [2,]  2    3

# Quine's example, page 528
rows <- "AB, BC, Ac, aC, abd, bcd"
cols <- "ABCD, ABCd, ABD, ABcd, ABCD, aBCD, aBcd, abCd, abCd, 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  x  x  x  x  -  -  -  -
  #  BC  x  x  -  -  -  x  x  -  -  -  -
  #  Ac  -  x  x  x  x  -  -  -  -  -  -
  #  aC  -  -  -  -  -  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
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 (\text{OUT} = "1"), while configurations with an inclusion score below incl.cut are coded negative (\text{OUT} = "0").

The argument \texttt{p.pert} specifies the probability of perturbation under the IPA - independent perturbations assumption (when dependent = FALSE).

The argument \texttt{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.

\section*{Author(s)}
Adrian Dusa

\section*{References}


\section*{Examples}
\begin{verbatim}
# the replication data, see Thiem, Spoehel and Dusa (2015)
dat <- data.frame(matrix(c(  
rep(1,25), rep(0,20), rep(c(0,0,1,0,0),3),  
0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),  
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 assumption
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)
\end{verbatim}
runGUI

run the GUI shiny app for the QCA package

Description

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

Usage

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

superset, findSubsets, findSupersets

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

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, ...)

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

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.
prl.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 ~. 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, un-
derstood 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 expres-
sions 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
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, cex.l = 0.7)

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

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

# 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

ggetRow(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

# stopping at maximum row number 20
findSubsets(input = 2, noflevels + 1, stop = 20)
# 5 8 11 14 17 20

# -----
# for supersets
findSupersets(input = 14, noflevels + 1)
# 2 4 5 10 11 13 14

findSupersets(input = 17, noflevels + 1)
# 2 7 8 10 11 16 17

# input as a matrix
(im <- getRow(c(14, 17), noflevels + 1))

# implicant matrix normal values
#   A  B  C |   A  B  C
# 14 1 1 1 | 14  0  0  abc
# 17 1 2 1 | 17  0  1  aBc

sup <- findSupersets(input = im, noflevels + 1)
sup
# 2 4 5 7 8 10 11 13 14 16 17

ggetRow(sup, noflevels + 1)
# 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  bc
# 7 0 2 0 |  7  -  1  B
# 8 0 2 1 |  8  -  1  Bc
# 10 1 0 0 | 10  0  -  a
# 11 1 0 1 | 11  0  -  ac
# 13 1 1 0 | 13  0  -  ab
# 14 1 1 1 | 14  0  0  abc
# 16 1 2 0 | 16  0  1  aB
# 17 1 2 1 | 17  0  1  aBc

```
# truthTable  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
truthTable(data, outcome = "", conditions = "", incl.cut = 1, n.cut = 1, pri.cut = 0, 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.
pri.cut The minimal score for the PRI - proportional reduction in inconsistency, under which a truth table row is declared as negative.
complete Logical, print complete truth table.
use.letters Logical, use letters instead of causal conditions’ names.
show.cases Logical, print case names.
**truthTable**

- **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 multivalue 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. Note that using both `neg.out = TRUE` and a tilde `~` in the outcome name cancel each other out.

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 `~` 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 `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 both (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(ic1, 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 \( \text{ic0} \) is automatically set equal to \( \text{ic1} \), but otherwise \( \text{ic0} \) should always be lower than \( \text{ic1} \).

Using these two cutoffs, as well as \( \text{pri.cut} \) the observed combinations are coded with:

- \( "1" \) if they have an inclusion score of at least \( \text{ic1} \) and a PRI score of at least \( \text{pri.cut} \)
- \( "c" \) if they have an inclusion score below \( \text{ic1} \) and at least \( \text{ic0} \) (contradiction)
- \( "0" \) if they have an inclusion score below \( \text{ic0} \) or a PRI score below \( \text{pri.cut} \)

The argument \( \text{n.cut} \) specifies the frequency threshold under which a truth table row is coded as a remainder, irrespective of its inclusion score.

When argument \( \text{show.cases} \) is set to \( \text{TRUE} \), 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 \( \text{sort.by} \) 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 \( \text{sort.by} \) (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 \( \text{use.letters} \) 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 \( \text{inf.test} \) combines the inclusion score with a statistical inference test, in order to assign values in the output column \( \text{OUT} \). 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 \( \text{ic1} \),
- \( "c" \) contradiction, if the true inclusion score is not significantly higher than \( \text{ic1} \) but significantly higher than \( \text{ic0} \),
- \( "0" \) if the true inclusion score is not significantly higher than \( \text{ic0} \).

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 \( \text{ic0} \).

The argument \( \text{complete} \) 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.
- **noflevels** 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

# -----  
# Lipset binary crisp data
ttlC <- truthTable(LC, "SURV")

# inspect the truth table
ttlC

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

# the printing function also supports the complete version print(ttlC, 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 truthTable(LC, "SURV", complete = TRUE, sort.by = "incl-, n+")

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

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

# the observed combinations coded as remainders ttlLM$excluded

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

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

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

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

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

# -----
# Ragin and Strand data with temporal QCA
# truth table containing the "-" placeholder as a "don't care"
trueTable(RS, "REC")

Xplot  Display the distribution of points for a single condition

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
Xplot(x, jitter = FALSE, at = NULL, ...)

Arguments
  x       A numeric vector.
  jitter  Logical, vertically jitter the points.
  at      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 auto-
           matically computed, see the help file for ?axis.
  ...     Other graphical parameters from ?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 occuring clusters,
mainly for crisp calibration purposes.

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 1, and a default pch value of 1 (empty
points), which can be modified accordingly (for instance value 21 for filled 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 axis 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 0.5 are used for the parameters factor and amount, on
the horizontal axis. More details can be found in the base function 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

par, text, jitter

Examples

# Lipset's raw data
# plot the DEV (level of developent) 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

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.
XYplot  

**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 & Rohlffing (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)
# 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
xyplot("~NATPRIDE, PROTEST", data = CVF, xlab = "Negation of NATPRIDE", ylab = "Outcome: PROTEST")

# necessity relation
xyplot("~NATPRIDE, PROTEST", data = CVF, relation = "necessity")

# jitter the points
xyplot("~NATPRIDE, PROTEST", data = CVF, jitter = TRUE)

# jitter with more amount
xyplot("~NATPRIDE, PROTEST", data = CVF, jitter = TRUE, amount = 0.02)

# adding labels to points
xyplot("~NATPRIDE, PROTEST", data = CVF, jitter = TRUE, cex = 0.8, clabels = rownames(CVF))

# or just the row numbers, since the row names are too long
xyplot("~NATPRIDE, PROTEST", data = CVF, jitter = TRUE, cex = 0.8, clabels = seq(nrow(CVF)))

# using a SOP expression (necessity relation)
xyplot("NATPRIDE <= ~PROTEST", data = CVF, jitter = TRUE, cex = 0.8, clabels = seq(nrow(CVF)))

#----
# enhanced XY plot for process tracing
xyplot("~NATPRIDE, PROTEST", data = CVF, enhance = TRUE, jitter = TRUE)

# enhanced XY plot for a solution model
sol <- "natpride + DEMOC*GEOCON+POLDIS + DEMOC*ETHFRACT*GEOCON"
xyplot("~NATPRIDE, PROTEST", data = CVF, enhance = TRUE, model = TRUE)

# same plot, automatically detected from object pCVF
ttCVF <- truthTable(CVF, "PROTEST", incl.cut = 0.85)
pCVF <- minimize(ttCVF, include = "?"
xyplot(pCVF$solution[1], "PROTEST", data = CVF, enhance = TRUE)
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, ethnopolitical 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


_Hino

*Ethnic protest in Europe*

**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

*Legacy datasets*

**Description**

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

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

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:

- **P**: Public university  
- **E**: Support of elite allies  
- **A**: National union affiliation  
- **S**: Strike or a strike threat  
- **eba**: E happens before A  
- **REC**: Union recognition

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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