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Item Type	Journal article
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DOI	10.32614/rj-2018-031
Publisher	The R Foundation
Rights	CC BY 4.0
Download date	2025-01-02 21:46:59
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Link to Item	http://hdl.handle.net/20.500.14018/14154

SetMethods: an Add-on R Package for Advanced QCA

by Ioana-Elena Oana and Carsten Q. Schneider

Abstract This article presents the functionalities of the R package **SetMethods**, aimed at performing advanced set-theoretic analyses. This includes functions for performing set-theoretic multi-method research, set-theoretic theory evaluation, Enhanced Standard Analysis, diagnosing the impact of temporal, spatial, or substantive clusterings of the data on the results obtained via Qualitative Comparative Analysis (QCA), indirect calibration, and visualising QCA results via XY plots or radar charts. Each functionality is presented in turn, the conceptual idea and the logic behind the procedure being first summarized, and afterwards illustrated with data from Schneider et al. (2010).

Introduction

Set-theoretic methods, in general (Goertz and Mahoney, 2012), and Qualitative Comparative Analysis, in particular, are becoming increasingly popular within different disciplines in the social sciences and neighboring fields (Rihoux et al., 2013). Parallel to conceptual developments and increasing numbers of applied studies, accelerating progress in terms of software development can be witnessed. While less than a decade ago only two functioning software packages were available to users (*fsQCA* Ragin et al. (2006) and *Tosmana Cronqvist* (2011)), there are now over a dozen different software solutions offered (see <http://compasss.org/software.htm>). Many of them are developed within the R software environment, with R package **QCA** (Dusa, 2007) being not only the one with the longest history, but also the most complete and complex.

In this paper, we discuss the different functionalities of the R package **SetMethods** (Medzihorsky et al., 2016). It is best perceived of as an add-on tool to package **QCA** and allows applied researchers to perform advanced set-theoretic analyses. More precisely, **SetMethods** enables researchers to perform Set-Theoretic Multi-Method Research, the Enhanced Standard Analysis (ESA), Set-Analytic Theory Evaluation, to run diagnostics in the presence of clustered data structures, and to display their results in various ways.

We proceed as follows. Each of the different functionalities within **SetMethods** is presented in a separate section. Within each section, we first briefly summarize the conceptual idea behind the analysis in question, then describe the computational logic of the function for performing the analysis, after which we demonstrate the use of the function by displaying the R syntax and selected output by using an example from published research.

Even though the main purpose is to present the functionality of R package **SetMethods**, this article is also useful for researchers who perform their QCA in software environments other than R because we present the logic of several of the main advanced set-analytic procedures in a concise and transparent manner.

The empirical example

In order to illustrate the use of the different functions in **SetMethods**, we use the empirical example by Schneider et al. (2010) which uses fuzzy-sets for explaining capitalist variety and export performance in high-tech industries. More precisely, the research question focuses on the institutional determinants of export performance in high-tech industries. The outcome consists of the export performance in high-tech industries (EXPORT). The conditions used are: employment protection (EMP), collective bargaining (BARGAIN), university training (UNI), occupational training (OCCUP), stock market size (STOCK), and mergers and acquisitions (MA). The authors analyze 76 cases, representing 19 countries at four time points.

For the sake of simplicity, we use the same data for illustrating all the functions. Our goal is not, of course, to contribute to the substantive discussion on varieties of capitalism or institutional context. This is why we will take the liberty to alter the analytic setup if needed for demonstration purposes, by, for instance, dropping cases or conditions or by changing the outcome to be explained.

```
# We load the SetMethods package:
```

```
library(SetMethods)

# First rows of the Schneider et al.(2010) data called SCHF from package
# SetMethods:

data(SCHF)
head(SCHF)

##           EMP BARGAIN  UNI OCCUP STOCK  MA EXPORT
## Australia_90 0.07    0.90 1.00  0.68  0.45 0.33  0.19
## Austria_90   0.70    0.98 0.01  0.91  0.01 0.05  0.25
## Belgium_90   0.94    0.95 0.14  0.37  0.26 0.14  0.14
## Canada_90    0.04    0.21 0.99  0.11  0.62 0.31  0.28
## Denmark_90   0.59    0.78 0.10  0.55  0.53 0.10  0.34
## Finland_90   0.70    0.97 0.20  0.95  0.02 0.13  0.17
```

Set-theoretic multi-method research (MMR)

The term Set-Theoretic Multi-Method Research (MMR) captures all those empirical approaches for combining cross-case analyses with within-case studies in which both levels of analysis follow the goal of investigating sets and their relations. At the cross-case level the most common methodological tool is Qualitative Comparative Analysis (QCA) and at the within-case level, process tracing. Both tools can be rooted in (fuzzy) set theory (see, e.g. [Ragin \(2008\)](#) for QCA and [Mikkelsen \(2017\)](#) for process tracing). In principle and practice any sequence of analyses can and is performed in the applied literature. In the following, we focus on the sequence 'cross-case QCA first, followed by within-case analyses'. This sequence may or may not be continued by another QCA. As any decent QCA, it is certainly preceded by a thorough accumulation of case knowledge in order to select and calibrate conditions. These crucial research steps, however, fall outside of the definitional scope of set-theoretic MMR.¹

In the following, we limit our discussion to set-theoretic MMR after a cross-case analysis of sufficiency, as discussed in [Schneider and Rohlfing \(2013, 2016\)](#), [Schneider and Rohlfing \(manuscript\)](#), and [Rohlfing and Schneider \(2018\)](#).² We first briefly summarize the different types of cases and the purpose of their within-case analysis (Section 2.3.1). After this, we discuss the four different feasible comparative within-case analyses in Figure 1 and their analytic purposes (Section 2.3.2). For each form of within-case analysis, we explain the use of the `mmr` function and the formula used for finding cases ([Schneider and Rohlfing, manuscript](#))³. The general structure of function `mmr` is illustrated in Figure 1. Users need to specify whether they want to perform single or comparative within-case analysis and then on which cases the analysis is performed.

Identifying types of cases

Key for combining QCA with process tracing is the sorting of cases to different case types based on the QCA solution formula. The literature identifies five different types ([Schneider and Rohlfing, 2013](#)). Membership in a type is defined by the membership scores of a case in the outcome Y , on the one hand, and the sufficient term T or the solution formula S , on the other hand. Table 1 summarizes the definition of each case type and the analytic purpose of the within-case analysis in single cases. Figure 2 visualizes the location of each case type in an XY plot.

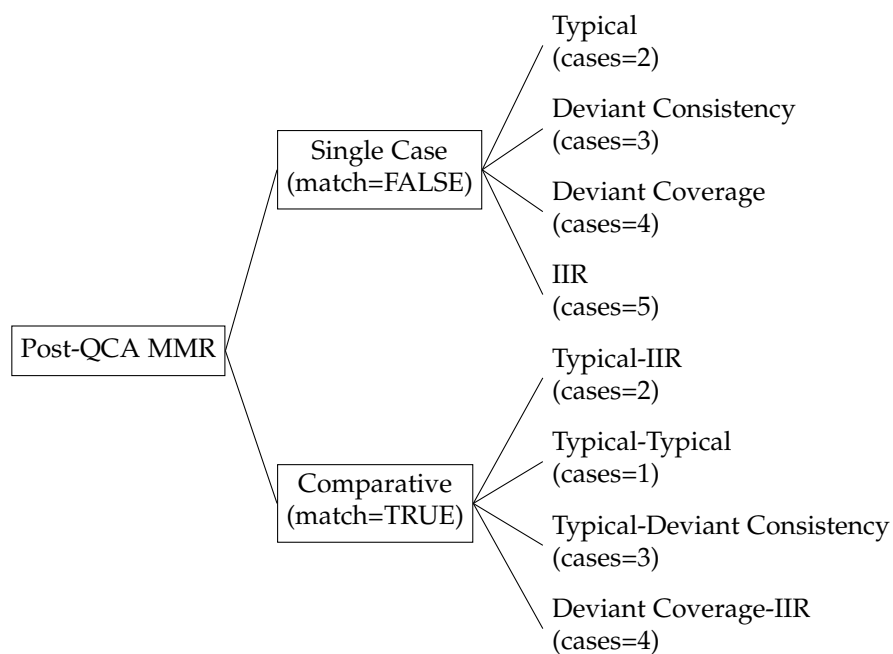
Typical cases and deviant cases consistency are defined based on their membership in a sufficient term T , whereas deviant cases coverage and IIR cases are defined based on their membership solution formula S . Deviant cases consistency are subdivided into deviant in degree and deviant in kind. The latter are always preferable for within-case analysis. IIR cases are not useful for single-case studies, but they play an important role for comparative within-case analyses (see Section 2.3.2).

Table 1 is adapted from Schneider and Rohlfing (manuscript).

¹For a systematic discussion of the pre-QCA case studies, see [Rihoux and Lobe \(2009\)](#).

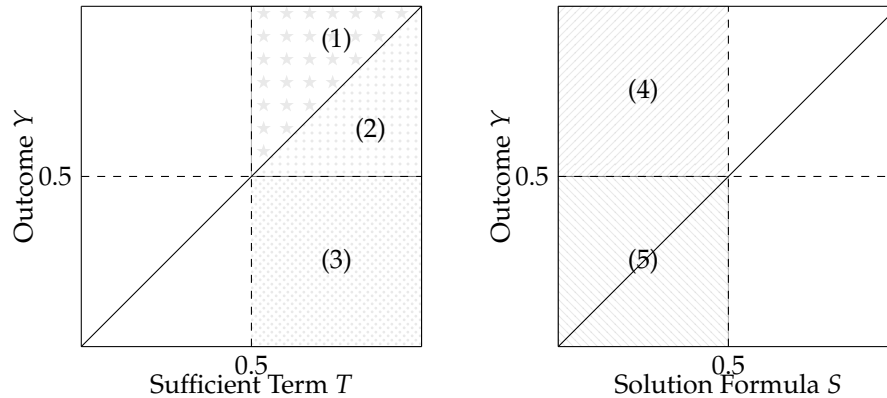
²For MMR after an analysis of necessity, see [Rohlfing and Schneider \(2013\)](#).

³For a systematic test of the mathematical formulas used for selecting single cases or pairs of cases for set-theoretic MMR see the Appendix of this paper.

Figure 1: Types of Post-QCA Case Studies**Table 1:** Types of cases in fsQCA of sufficiency

Type of case	Membership in			Goal of within-case analysis
	<i>T</i>	<i>Y</i>		
(1) Typical	>.5	>.5	$T \leq Y$	identify mechanism <i>M</i>
(2) Deviant consistency (degree)	>.5	>.5	$T \geq Y$	not recommended
(3) Deviant consistency (kind)	>.5	<.5		identify missing INUS
	<i>S</i>			
(4) Deviant coverage	<.5	>.5		identify missing conjunction
(5) IIR	<.5	<.5		not useful

Figure 2: Types of Cases, XY Plot



Typical cases

Process tracing in typical cases aims at empirically probing the causal mechanism(s) linking the sufficient term S to outcome Y . For conjunction S to be causal, each conjunct C of S must be causal, i.e. they must make a difference to outcome Y by making a difference to mechanism M . This requires as many within-case analyses of typical cases as there are conjuncts in the sufficient conjunction. For each analysis, one is the focal conjunct FC and the others are the complementary conjuncts CC . The focal conjunct FC is the conjunct for which we want to find out whether it makes a difference for the mechanism M , while the complementary conjuncts CC represent the other conjuncts of the sufficient term S (Schneider and Rohlfing, manuscript). For causal inference on the configuration we proceed by taking each conjunct at a time as the focal conjunct FC . Additionally, we also apply the *test severity principle*. With fuzzy-sets the membership in mechanism M can only vary within the corridor established by the membership in FC (the lowest value M can take) and Y (the highest value M can take) for preserving the causal chain $FC \rightarrow M \rightarrow Y$ (Schneider and Rohlfing, manuscript). The smaller the corridor, the smaller the range of membership values M can take. Therefore, the most *severe test* for M is the one in which $FC = S = Y$ because the only consistent membership score in M equals $FC = S = Y$.

The *best-available* typical case fulfills the following criteria: a) the focal conjunct is the one that defines the membership of the typical case in the term ($FC \leq CC$); b) the corridor for mechanism M as defined by the sufficient term S (from a) we also have $S = FC$) and Y is small; c) membership in the sufficient term S is high; d) the case is uniquely covered by the sufficient term S .

Figure 3 visualizes the test severity principle in two different ways. The XY plot in the upper panel shows that for cases closer to the diagonal, test severity increases. The length of the vertical and horizontal arrows, respectively, visualizes the range of fuzzy set membership scores for M that would still be consistent. The larger this range, the less severe the test. The Euler diagram in the lower panel visualizes the same by contrasting S_1 almost as big as Y with S_2 being much smaller than Y . The former leaves little and the latter a lot of room for M .

The ideal typical case is located in the upper-right corner of the XY plot in Figure 3 with $FC = S = Y = 1$. In applied QCA, such cases usually do not exist in the data at hand. Function `mmr()` identifies the best available typical case in a given data set.

Function `mmr()` first sorts each typical case based on whether $FC \leq CC$ (rank 1) or $FC > CC$ (rank 2). Cases in each rank are then further sorted according to Formula 1. Smaller values indicate better suitable cases.⁴

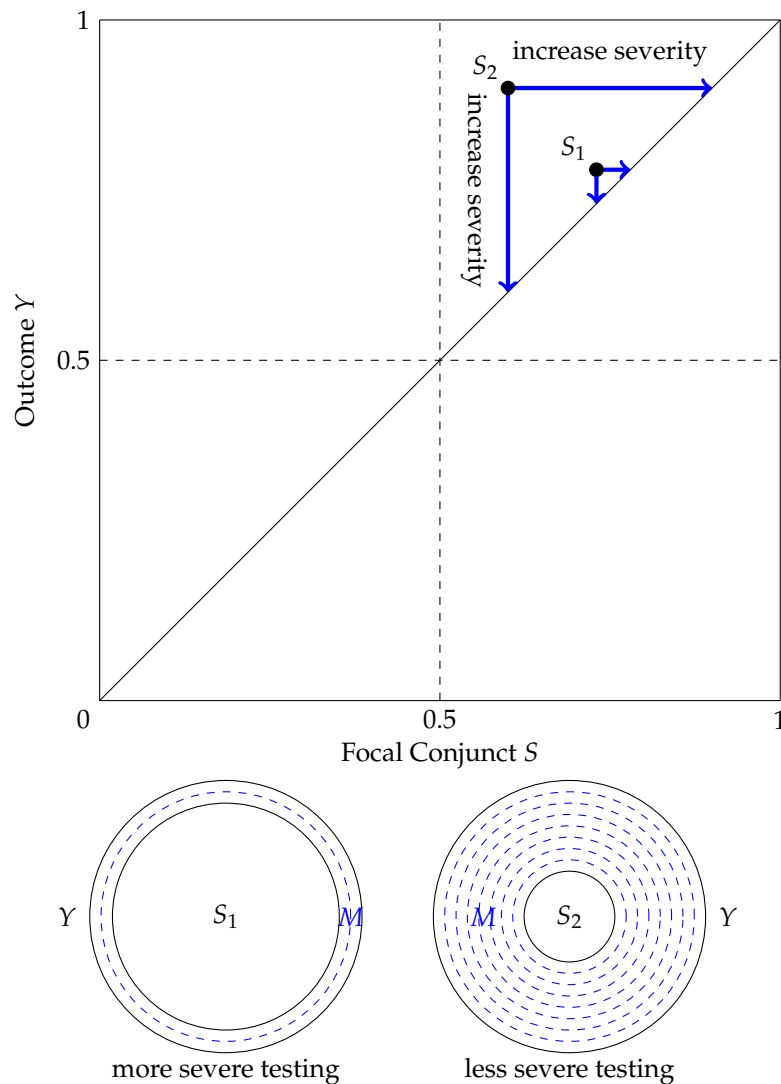
$$TYP = (Y - S) \quad \text{small corridor for mechanism} \\ + (1 - S) \quad \text{large membership in the sufficient term} \quad (1)$$

where Y = outcome, S = sufficient term

Applied to our example, function `mmr()` works as follows. After minimizing the truth table `TT_y` and producing the parsimonious and intermediate solutions `sol_yp` and `sol_yi` using package **QCA**, we input these solutions⁵ into the `mmr()` function while setting arguments `match` to `FALSE` and `cases`

⁴This holds for all `mmr()` formulas: the smaller the value, the more suitable the case (pair) is.

⁵For inputting solutions that have model ambiguity, argument `sol` can be used to specify which solution the user wants to work with. If a single number is used, this number indicates which model of the conservative or

Figure 3: Two visualizations of test severity

to 2. As argument term is set to 1 the output shows the typical cases for each focal condition in the first sufficient term, together with some additional information. The information included in the output comprises of membership values of the typical cases in the focal conjunct, complementary conjuncts, the whole sufficient term, and the outcome (in this case *EXPORT*), formula values St , whether the case is the most typical according to the formula, which rank does the case sit in, and whether the case is uniquely covered by the sufficient term. The order of the information that users should look for in this output is whether the case is uniquely covered, what rank is the case in (the smaller, the better), and what formula value St does the case have (the smaller, the better). For example, for focal conjunct *emp* in sufficient term *emp * bargain * OCCUP*, Switzerland_03 appears to be the *best available* typical case, being uniquely covered, being in Rank 1, and having the smallest formula value ($St=0.59$).

We create the truth table:

```
TT_y <- truthTable(SCHF, outcome = "EXPORT",
  conditions = c("EMP", "BARGAIN", "UNI",
    "OCCUP", "STOCK", "MA"),
```

parsimonious solution according to the order in the "qca" object the user wants to work with. However, since QCA solutions (conservative, parsimonious, intermediate) are in a subset relationship with each other, they tend to have more complicated structures in which model ambiguity is tied from one solution to the other. For this cases the argument *sol* allows users to specify the models they want to choose by using a character string of the form "c1p3i2" where c = conservative solution, p = parsimonious solution and i = intermediate solution.

```

      incl.cut = .9,
      complete = TRUE,
      PRI = TRUE,
      sort.by = c("out", "incl", "n"))

# Get the parsimonious solution:

sol_yp <- minimize(TT_y, include = "?", details = TRUE,
                  show.cases = TRUE)

# Get the intermediate solution:

sol_yi <- minimize(TT_y, include = "?", details = TRUE,
                  show.cases = TRUE, dir.exp = c(0,0,0,0,0,0))

# Get typical cases for the first term of the second intermediate solution:

mmr (results = sol_yi, outcome = "EXPORT", neg.out = FALSE,
      sol = "c1p1i2", match = FALSE, cases = 2, term = 1)

## Typical Cases - Focal Conjunct emp :
## -----
##               Focal Conjunct Comp. Conjunct Term Membership EXPORT  St
## Switzerland_03          0.70          0.71          0.70  0.99 0.59
## Switzerland_99          0.75          0.54          0.54  0.98 0.69
##               most_typical Rank uniquely_cov
## Switzerland_03          TRUE      1          TRUE
## Switzerland_99          FALSE     2          TRUE
##
## Typical Cases - Focal Conjunct bargain :
## -----
##               Focal Conjunct Comp. Conjunct Term Membership EXPORT  St
## Switzerland_99          0.54          0.74          0.54  0.98 0.90
## Switzerland_03          0.76          0.70          0.70  0.99 0.53
##               most_typical Rank uniquely_cov
## Switzerland_99          FALSE     1          TRUE
## Switzerland_03          TRUE      2          TRUE
##
## Typical Cases - Focal Conjunct OCCUP :
## -----
##               Focal Conjunct Comp. Conjunct Term Membership EXPORT  St
## Switzerland_03          0.71          0.70          0.70  0.99 0.58
## Switzerland_99          0.74          0.54          0.54  0.98 0.70
##               most_typical Rank uniquely_cov
## Switzerland_03          TRUE      2          TRUE
## Switzerland_99          FALSE     2          TRUE

```

Deviant cases consistency

Deviant cases consistency are puzzling because their membership in the sufficient term S exceeds that in the outcome Y , i.e. $S > Y$. This becomes even more puzzling if $S > 0.5$ & $Y < 0.5$, that is, if we have deviant cases consistency in kind rather than just in degree (see Table 1). The more S exceeds Y , the bigger the empirical puzzle, especially if membership in S is high. Within-case analysis of a deviant case consistency aims at identifying the reasons why mechanism M either absent or prevented from producing Y . The reason must be an INUS condition omitted from S . Formula 2 identifies the best available deviant case consistency in a data set.

$$DCN = [1 - (S - Y)] \quad \text{far from to the diagonal} \\ + (1 - S) \quad \text{large membership in the sufficient term} \quad (2)$$

where Y = outcome, S = sufficient term

Using the same data from [Schneider et al. \(2010\)](#) and focusing on the parsimonious solution, function `mmr()` identifies the deviant consistency cases for each sufficient term. For obtaining this we need to keep argument `match` set to `FALSE`, as we are doing single case identification, but set argument `cases` to 3, the identifier for deviant cases consistency (see Figure 1). The output shows the deviant consistency cases (first column) grouped by sufficient term (second column) together with term membership, outcome membership, formula value *Sd*, and whether the case is the most deviant for a particular term. In the output we see that, for example, for term *emp * OCCUP* the most deviant case consistency is *Switzerland_90* with the smallest formula value (*Sd*=0.67). Figure 4 shows all the deviant cases consistency (cases in the lower right corner) for the first sufficient path *emp * OCCUP* of the parsimonious solution.

```
# Get deviant cases consistency for the parsimonious solution:
```

```
mmr (results = sol_yp, outcome = "EXPORT", neg.out = FALSE,
     sol = 1, match = FALSE, cases = 3)

## Deviant Consistency Cases :
## -----
##          cases          term term_membership EXPORT  Sd
## 2  Switzerland_90      emp*OCCUP          0.82  0.31 0.67
## 1   Australia_90      emp*OCCUP          0.68  0.19 0.83
## 3   Australia_95      emp*OCCUP          0.68  0.31 0.95
## 4   Australia_99      emp*OCCUP          0.68  0.38 1.02
## 14  Australia_95 BARGAIN*UNI*STOCK        0.90  0.31 0.51
## 7   Australia_03 BARGAIN*UNI*STOCK        0.90  0.35 0.55
## 6    Spain_99    BARGAIN*UNI*STOCK        0.79  0.27 0.69
## 8    Norway_03   BARGAIN*UNI*STOCK        0.79  0.32 0.74
## 41  Australia_99 BARGAIN*UNI*STOCK        0.79  0.38 0.80
## 21   Denmark_95 BARGAIN*UNI*STOCK        0.76  0.40 0.88
## 5    Belgium_99 BARGAIN*UNI*STOCK        0.72  0.40 0.96
## 31   Finland_95 BARGAIN*UNI*STOCK        0.73  0.49 1.03
## 42    Spain_03   occup*STOCK*ma         0.74  0.30 0.82
## 32   Denmark_95   occup*STOCK*ma         0.73  0.40 0.94
## 15   Canada_90   occup*STOCK*ma         0.62  0.28 1.04
## 22   Canada_95   occup*STOCK*ma         0.60  0.30 1.10
##  most_deviant
## 2          TRUE
## 1          FALSE
## 3          FALSE
## 4          FALSE
## 14         TRUE
## 7          FALSE
## 6          FALSE
## 8          FALSE
## 41         FALSE
## 21         FALSE
## 5          FALSE
## 31         FALSE
## 42         TRUE
## 32         FALSE
## 15         FALSE
## 22         FALSE
```

```
# Plot each sufficient path of the parsimonious solution:
```

```
pimplot(data = SCHF, results = sol_yp, outcome = "EXPORT", case_labels = FALSE)
```

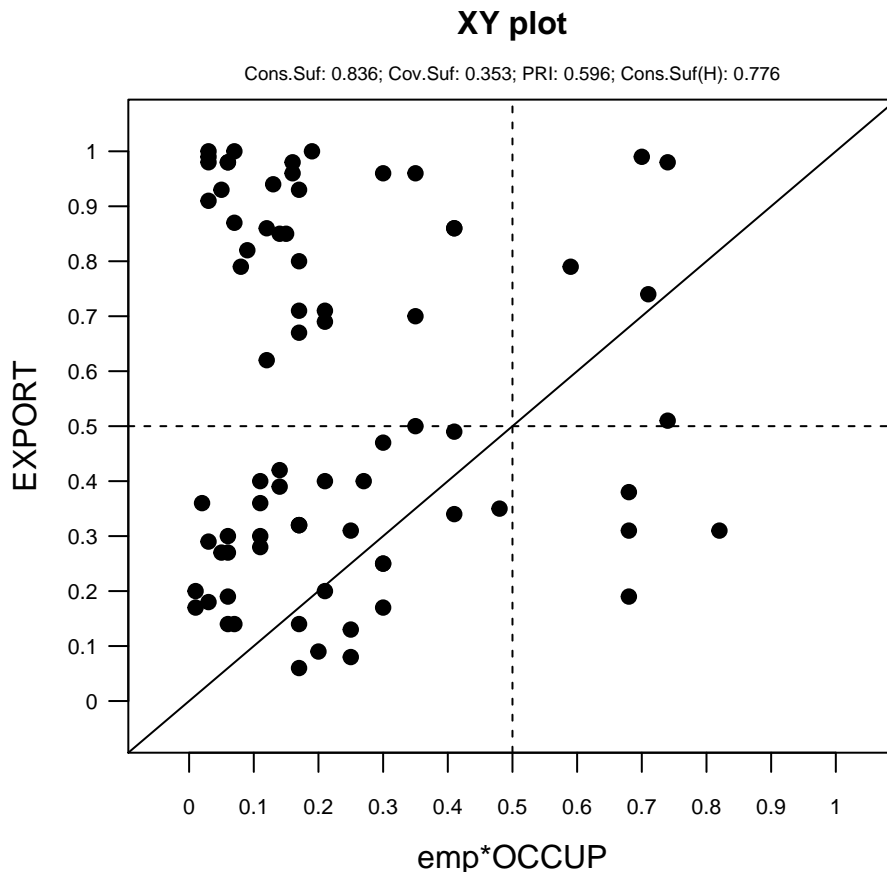



Figure 4: Deviant Cases Consistency

Deviant cases coverage

Deviant cases coverage are puzzling because they are members of the outcome without, however, being members of any known sufficient term. Within-case analysis aims at identifying sufficient term S_+ omitted from the solution formula, which triggers mechanism M and outcome Y .

Since deviant cases coverage are defined by what they are *not* - members of the solution formula (see Table 1) - this solution formula is not a good place to start selecting the best available deviant cases coverage. Instead, this type of case is selected based on their membership in their truth table row TT . For each TT with at least one deviant case coverage, a within-case analysis can be performed. If more than one deviant case coverage populates the same TT , Formula 3 identifies the best available case for within-case analysis.

$$DCV = |Y - TT| \quad \text{small corridor for mechanism} \\ + (1 - TT) \quad \text{large membership in the truth table row} \quad (3)$$

where Y = outcome, TT = membership in the Truth Table row

Similar to the Formula 1 for identifying the best available typical case, the goal is to minimize the difference between the membership scores in Y and TT and to prefer higher membership in TT . This is achieved by formula 3. Since the primary goal in this within-case analysis is not to draw causal inference but to identify a missing conjunction, there is no need to decompose TT into its constituent sets.

Applied to our example, the following code displays the list of deviant cases coverage (notice argument cases is set to 4), the membership they have in the entire solution formula, their values on the Formula 3, the truth table row they belong to (columns starting with TT indicating the specific combination of conditions the case presents), the membership they have in that specific truth table row, and membership in the outcome. The cases are sorted by truth table row and ranked according to their appropriateness using formula values Sd . For example, we can notice that truth table row

*emp * bargain * UNI * occup * STOCK * MA* (rows 9, 10, 4, and 5 of the output) is populated by 4 deviant coverage cases, out of which UK_90 is the best available for within case analysis, having the smallest formula value (Sd=0.51).

```
# Get deviant cases coverage for the parsimonious solution:
```

```
mmr (results = sol_yp, outcome = "EXPORT", neg.out = FALSE,
     sol = 1, match = FALSE, cases = 4)
```

```
## Deviant Coverage Cases :
```

```
## -----
```

##	case	solution_membership	Sd	TT_EMP	TT_BARGAIN	TT_UNI
## 8	UK_03	0.12 0.22	0	0	1	
## 3	Germany_99	0.17 0.33	1	1	0	
## 11	UK_99	0.18 0.34	0	0	1	
## 12	USA_99	0.20 0.39	0	0	1	
## 7	Sweden_95	0.36 0.47	1	1	0	
## 1	France_95	0.41 0.50	1	1	0	
## 9	UK_90	0.36 0.51	0	0	1	
## 10	UK_95	0.36 0.59	0	0	1	
## 4	Ireland_03	0.32 0.64	0	0	1	
## 5	Ireland_99	0.32 0.64	0	0	1	
## 2	Germany_03	0.40 0.67	1	1	0	
## 6	Netherlands_95	0.45 0.68	1	1	0	

##	TT_OCCUP	TT_STOCK	TT_MA	TT_row_membership	EXPORT
## 8	0	1	1	0.88	0.98
## 3	1	1	1	0.71	0.67
## 11	0	1	1	0.82	0.98
## 12	0	1	1	0.80	0.99
## 7	1	1	1	0.62	0.71
## 1	1	0	0	0.56	0.62
## 9	0	1	1	0.64	0.79
## 10	0	1	1	0.64	0.87
## 4	0	1	1	0.68	1.00
## 5	0	1	1	0.68	1.00
## 2	1	0	0	0.51	0.69
## 6	1	1	1	0.51	0.70

Individually irrelevant cases

Individually irrelevant (IIR) cases owe their name to the fact that single within-case analyses in this type of cases is not useful. IIR cases do play a crucial role in two forms of comparative within-case analysis (see Section 2.3.2). Even if not useful for single case studies, identifying IIR cases is informative as their list - together with the deviant cases coverage - indicate the diversity among cases without the outcome. The more different truth table rows are populated by IIR cases (and deviant cases coverage), the more heterogeneous this group of cases is.

Function `mmr()` lists all individually irrelevant cases with respect to the entire solution formula (also called globally uncovered IIR cases) and sorts each of them into the truth table to which they belong best. Since these cases are not informative for single case studies and are being used just to indicate diversity among the cases without the outcome, the function does not involve a formula ranking of IIR cases.

```
# Get individually irrelevant cases for the parsimonious solution:
```

```
mmr (results = sol_yp, outcome = "EXPORT", neg.out = FALSE,
     sol = 1, match = FALSE, cases = 5)
```

```
## Individually Irrelevant Cases :
```

```
## -----
```

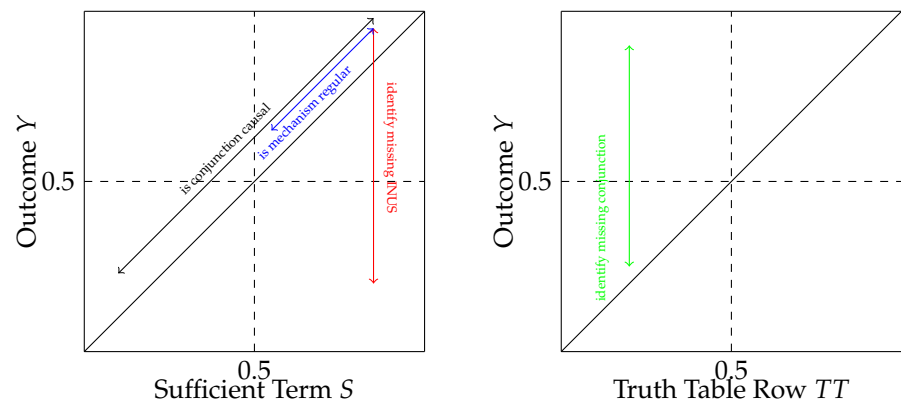
##	case	solution_membership	TT_EMP	TT_BARGAIN	TT_UNI	TT_OCCUP
## 19	New Zealand_90	0.17	0	0	0	0

## 18	New Zealand_03	0.25	0	0	1	0
## 21	New Zealand_99	0.25	0	0	1	0
## 6	Canada_03	0.38	0	0	1	0
## 7	Canada_99	0.20	0	0	1	0
## 20	New Zealand_95	0.20	0	0	1	0
## 4	Belgium_90	0.26	1	1	0	0
## 10	France_90	0.23	1	1	0	0
## 14	Italy_90	0.01	1	1	0	0
## 25	Spain_90	0.03	1	1	0	0
## 1	Austria_90	0.30	1	1	0	1
## 2	Austria_95	0.30	1	1	0	1
## 3	Austria_99	0.30	1	1	0	1
## 9	Finland_90	0.30	1	1	0	1
## 11	Germany_90	0.05	1	1	0	1
## 12	Germany_95	0.17	1	1	0	1
## 13	Italy_03	0.25	1	1	0	1
## 15	Italy_95	0.03	1	1	0	1
## 17	Netherlands_90	0.14	1	1	0	1
## 8	Denmark_90	0.45	1	1	0	1
## 16	Italy_99	0.38	1	1	0	1
## 5	Belgium_95	0.21	1	1	0	1
## 27	Sweden_90	0.07	1	1	0	1
## 26	Spain_95	0.06	1	1	1	0
## 22	Norway_90	0.12	1	1	1	1
## 23	Norway_95	0.49	1	1	1	1
## 24	Norway_99	0.45	1	1	1	1
##	TT_STOCK TT_MA TT_row_membership EXPORT					
## 19	0 1	0.58	0.06			
## 18	0 1	0.75	0.13			
## 21	0 1	0.75	0.08			
## 6	1 1	0.62	0.36			
## 7	1 1	0.80	0.40			
## 20	1 1	0.76	0.09			
## 4	0 0	0.63	0.14			
## 10	0 0	0.54	0.42			
## 14	0 0	0.70	0.20			
## 25	0 0	0.69	0.17			
## 1	0 0	0.70	0.25			
## 2	0 0	0.70	0.25			
## 3	0 0	0.70	0.47			
## 9	0 0	0.70	0.17			
## 11	0 0	0.92	0.27			
## 12	0 0	0.74	0.32			
## 13	0 0	0.67	0.31			
## 15	0 0	0.71	0.18			
## 17	0 0	0.57	0.39			
## 8	1 0	0.53	0.34			
## 16	1 0	0.62	0.29			
## 5	1 1	0.53	0.20			
## 27	1 1	0.74	0.36			
## 26	0 0	0.84	0.19			
## 22	0 0	0.65	0.14			
## 23	0 0	0.51	0.14			
## 24	0 1	0.55	0.32			

Identifying best-matching pairs of cases for comparative process tracing

The literature identifies four feasible within-case comparisons after a QCA between two types of cases each (Schneider and Rohlfing, manuscript). With each comparison a different analytic goal is pursued. Figure 5 summarizes these goals. The two comparisons 'along the main diagonal' pursue a causal inference goal, whereas the two 'vertical' comparisons aim at improving the QCA model specification by identifying either an INUS condition missing from a known sufficient term or an entire new sufficient term missing from the solution formula.

Figure 5: Forms of feasible comparisons



Matching typical and individually irrelevant (IIR) cases

The purpose of the within-case comparison between a typical case and and IIR case is to empirically investigate whether a sufficient term is a difference-maker, i.e. causal, not only for the outcome (Y) at the cross-case level, but also for the mechanism M at the within-case level. Similarly, the within-case comparison of two typical cases empirically probes whether the same mechanism M links the sufficient term S to outcome Y in typical cases that are as different from each other as possible. For both forms of comparison, it holds that if S is a conjunction, each of its conjuncts C must be a difference-maker. Hence, the comparisons between a typical case and an IIR case (or another typical case) must be performed for each single conjunct C at a time. The following sections provide more details for each form of comparison and spells out the sorting mechanisms and mathematical formulas that underly the respective functions in **SetMethods**.

Table 2: Possible membership constellations between focal (FC) and complementary conjuncts (CC) in comparison of typical and IIR case

Rank	Typical	IIR	Difference FC	Deter- minate	Attribution typical	Attribution IIR
1	$FC \leq CC$	$FC < 0.5 < CC$	Yes	Yes	Yes	Yes
2	$FC > CC$	$FC < 0.5 < CC$	Yes	Yes	No	Yes
3	$FC \leq CC$	$FC \leq CC < 0.5$	Yes	No	Yes	Yes
4	$FC \leq CC$	$CC < FC < 0.5$	Yes	No	Yes	No
4	$FC > CC$	$FC \leq CC < 0.5$	Yes	No	No	Yes
6	$FC > CC$	$CC < FC < 0.5$	Yes	No	No	No
7	$FC \leq CC$	$CC < 0.5 < FC$	No	No	Yes	No
8	$FC > CC$	$CC < 0.5 < FC$	No	No	No	No

taken from Schneider and Rohlfing (manuscript)

Function `mmr()` first sorts each pair of typical and IIR cases into ranks 1-8 as defined in Table 2. Cases in smaller rank numbers are more adequate for the analytic goal of the comparative within-case analysis of these two case types. For case pairs in rank 1, for example, it holds that the difference-making quality can be attributed to the focal conjunct *FC* both on the typical and the IIR case, and that it is determinate.

Within each rank, Formula 4 maximizes the following criteria: between both cases, the difference in *FC* and in *Y*, respectively, should be small; both should have high membership in *CC*; and both should be close to the diagonal. Within each rank, case pairs with smaller formula values are more appropriate. Additionally, typical cases should be uniquely covered by the sufficient term under investigation, while IIR cases should be globally uncovered (not covered by any of the sufficient

terms).

$$\begin{aligned}
 TYP - IIR = & [1 - (FC_{TYP} - FC_{IIR})] && \text{large difference in focal condition} \\
 & + [1 - (Y_{TYP} - Y_{IIR})] && \text{large difference in outcome} \\
 & + |\min(CC_{TYP}) - \min(CC_{IIR})| && \text{small difference in complementary conditions} \\
 & + 2 * |(Y_{TYP} - \min(FC_{TYP}, CC_{TYP}))| && \text{typical case close to diagonal} \\
 & + 2 * |(Y_{IIR} - \min(FC_{IIR}, CC_{IIR}))| && \text{IIR case close to diagonal}
 \end{aligned}
 \tag{4}$$

where Y = outcome, FC = focal condition, and CC = complementary condition

For switching to comparative MMR and identifying pairs of cases, argument match must be set to TRUE. Additionally, for getting the best available pairs of typical and IIR cases we set cases to 2. In the output for the first sufficient term (notice argument term set to 1) we will get the best available pairs for each focal conjunct in turn as separate tables. The output lists the names of the typical and IIR case, their value on the above formula (*Distance*), which rank does the pair come from, whether the typical case is uniquely covered, and whether the IIR case is globally uncovered. Researchers should strive to pick cases that are uniquely covered and globally uncovered, have the smallest rank possible, and have the smallest *Distance* value. For example, for focal conjunct *OCCUP*, typical case Denmark_99 and IIR case New Zealand_90 are the best pair available as they are in Rank 1, they have the smallest formula value (*Distance*=1.24), and the typical case is uniquely covered by the term, while the IIR case is globally uncovered by the solution.

```
# Get matching pairs of typical and IIR cases for the first term
# of the parsimonious solution:
```

```
mmr (results = sol_yp, outcome = "EXPORT", neg.out = FALSE,
     sol = 1, match = TRUE, cases = 2, term = 1)
```

```
## Focal Conjunct emp :
```

```
## -----
```

##	Typical	IIR	Distance	PairRank	UniqCovTyp	GlobUncovIIR
## 44	Switzerland_03	Norway_90	1.30	1	TRUE	TRUE
## 43	Denmark_03	Norway_90	1.38	1	TRUE	TRUE
## 88	Switzerland_03	Norway_95	1.38	1	TRUE	TRUE
## 80	Switzerland_03	Italy_95	1.40	1	TRUE	TRUE
## 60	Switzerland_03	Belgium_95	1.55	1	TRUE	TRUE

```
##
```

```
## Focal Conjunct OCCUP :
```

```
## -----
```

##	Typical	IIR	Distance	PairRank	UniqCovTyp
## 37	Denmark_99	New Zealand_90	1.24	1	TRUE
## 81	Denmark_99	New Zealand_95	1.30	1	TRUE
## 133	Denmark_99	New Zealand_03	1.31	1	TRUE
## 38	Switzerland_99	New Zealand_90	1.39	1	TRUE
## 82	Switzerland_99	New Zealand_95	1.45	1	TRUE

##	GlobUncovIIR
## 37	TRUE
## 81	TRUE
## 133	TRUE
## 38	TRUE
## 82	TRUE

Matching two typical cases

The matching of two typical cases follows a logic similar to the one between a typical and an IIR case. The goal is to probe the difference-making properties of each conjunct (FC) in sufficient term S to mechanism M . Table 3 defines the four ranks that can occur based on two typical cases' membership in FC and the complementary conditions CC . After sorting each possible pair of typical cases into one of these ranks, Formula 5 further ranks those pairs such that their difference in FC and the outcome, respectively, is minimized; that their membership in CC is maximized; and that both are close to the

diagonal (test severity principle). Additionally, the two typical cases should be uniquely covered by the sufficient term.

Table 3: Possible membership constellations between focal (*FC*) and complementary conjuncts (*CC*) in comparison of two typical cases

Rank	Typical 1	Typical 2	Attribution typical 1	Attribution typical 2
1	$FC \leq CC$	$FC \leq CC$	Yes	Yes
2	$FC \leq CC$	$FC > CC$	Yes	No
2	$FC > CC$	$FC \leq CC$	No	Yes
4	$FC > CC$	$CC > FC$	No	No

taken from Schneider and Rohlfing (manuscript)

$$\begin{aligned}
 TYP_1 - TYP_2 = & [0.5 - (FC_{TYP_1} - FC_{TYP_2})] && \text{large difference in focal condition} \\
 & + [0.5 - (Y_{TYP_1} - Y_{TYP_2})] && \text{large difference in outcome} \\
 & + |\min(CC_{TYP_1}) - \min(CC_{TYP_2})| && \text{small difference in complementary conditions} \\
 & + 2 * |(Y_{TYP_1} - \min(FC_{TYP_1}, CC_{TYP_1}))| && \text{typical case close to diagonal} \\
 & + 2 * |(Y_{TYP_2} - \min(FC_{TYP_2}, CC_{TYP_2}))| && \text{typical case close to diagonal} \\
 & && (5)
 \end{aligned}$$

For getting the best available pairs of two typical cases argument cases in function `mmr()` must be set to 1. The output is similar to the one for typical-IIR pairs of cases, the best available pair of typical cases for each focal conjunct being situated in as low a rank as possible, having the smaller formula value (*Distance*), and being both uniquely covered. Looking at the first term of the parsimonious solution, we can see that pair Switzerland_03-Denmark_03 is the best available for focal conjunct *emp*, while pair Switzerland_99-Denmark_99 is the best available for focal conjunct *OCCUP*, both pairs containing uniquely covered typical cases, being in Rank 1, and having the smallest *Distance* value for their respective focal conjunct.

```
# Get matching pairs of typical and typical cases for the first term
# of the parsimonious solution:
```

```
mmr (results = sol_yp, outcome = "EXPORT", neg.out = FALSE,
      sol = 1, match = TRUE, cases = 1, term = 1)
```

```
## Focal Conjunct emp :
```

```
## -----
```

```
##           Typical1      Typical2 Distance PairRank UniqCov1 UniqCov2
## 12 Switzerland_03    Denmark_03    1.72         1      TRUE     TRUE
## 4  Switzerland_03    Denmark_99    1.44         2      TRUE     TRUE
## 3    Denmark_03     Denmark_99    1.62         2      TRUE     TRUE
## 8  Switzerland_03    Switzerland_99 2.13         2      TRUE     TRUE
## 7    Denmark_03    Switzerland_99 2.31         2      TRUE     TRUE
##
```

```
## Focal Conjunct OCCUP :
```

```
## -----
```

```
##           Typical1      Typical2 Distance PairRank UniqCov1 UniqCov2
## 2  Switzerland_99    Denmark_99    1.27         1      TRUE     TRUE
## 4  Switzerland_03    Denmark_99    1.44         3      TRUE     TRUE
## 3    Denmark_03     Denmark_99    1.62         3      TRUE     TRUE
## 8  Switzerland_03    Switzerland_99 2.13         3      TRUE     TRUE
## 7    Denmark_03    Switzerland_99 2.31         3      TRUE     TRUE
```

Matching typical and deviant cases consistency

The comparative within-case analysis of a typical and a deviant case consistency aims at identifying the INUS condition missing from the sufficient term *S* in question. The best available pair of cases

maximizes the following criteria: their membership in S should be as high and similar as possible and their membership in Y is different as possible. Formula 6 translates these matching criteria into practice.

$$\begin{aligned}
 TYP - DCON = & [(1 - S_{TYP}) + (1 - S_{DCON})] && \text{large membership in term} \\
 & + [1 - (Y_{TYP} - Y_{DCON})] && \text{large difference in outcome} \\
 & + |S_{TYP} - S_{DCON}| && \text{similar membership in term}
 \end{aligned} \quad (6)$$

Setting cases to 3 we get best available pair of typical and deviant consistency cases for each sufficient term in the parsimonious solution `sol_yp`. For identifying a missing INUS in sufficient term `emp*OCCUP`, the best available pair of cases that we could choose for process-tracing would be the one between typical case `Switzerland_03` and deviant consistency case `Australia_90`, as they have the smallest formula value (Distance=0.84).

```
# Get matching pairs of typical and deviant consistency cases for the
# parsimonious solution:
```

```
mmr (results = sol_yp, outcome = "EXPORT", neg.out = FALSE,
     sol = 1, match = TRUE, cases = 3)
```

```
## Term emp*OCCUP :
```

```
## -----
```

	typical	deviant_consistency	distance	term	best_matching_pair
## 1	Switzerland_03	Australia_90	0.84	emp*OCCUP	TRUE
## 2	Switzerland_99	Australia_90	0.85	emp*OCCUP	FALSE
## 3	Switzerland_99	Switzerland_90	0.85	emp*OCCUP	FALSE
## 4	Switzerland_03	Switzerland_90	0.92	emp*OCCUP	FALSE
## 5	Switzerland_03	Australia_95	0.96	emp*OCCUP	FALSE

```
##
```

```
## Term BARGAIN*UNI*STOCK :
```

```
## -----
```

	typical	deviant_consistency	distance	term
## 1	Netherlands_03	Australia_95	0.55	BARGAIN*UNI*STOCK
## 2	Netherlands_03	Australia_03	0.59	BARGAIN*UNI*STOCK
## 3	Netherlands_99	Australia_95	0.65	BARGAIN*UNI*STOCK
## 4	Netherlands_99	Australia_03	0.69	BARGAIN*UNI*STOCK
## 5	Netherlands_99	Spain_99	0.73	BARGAIN*UNI*STOCK

```
## best_matching_pair
```

## 1	TRUE
## 2	FALSE
## 3	FALSE
## 4	FALSE
## 5	FALSE

```
##
```

```
## Term occup*STOCK*ma :
```

```
## -----
```

	typical	deviant_consistency	distance	term	best_matching_pair
## 1	USA_03	Spain_03	0.84	occup*STOCK*ma	TRUE
## 2	Japan_99	Spain_03	0.86	occup*STOCK*ma	FALSE
## 3	Japan_03	Spain_03	0.88	occup*STOCK*ma	FALSE
## 4	USA_90	Spain_03	0.89	occup*STOCK*ma	FALSE
## 5	USA_95	Spain_03	0.91	occup*STOCK*ma	FALSE

Matching deviant cases coverage and IIR cases

The comparative within-case analysis of a deviant case coverage and an IIR case aims at identifying the sufficient conjunction S_+ missing from the sufficient solution formula generated with QCA. The point of reference for matching cases is their membership in the truth table row TT to which they belong. Analogous to the within-case comparison of a typical and a deviant case consistency case, the goal is to maximize both cases' membership and their similarity in TT and their difference in Y .

Formula 7 achieves this.

$$\begin{aligned}
 DCOV - IIR = & [(1 - TT_{DCOV}) + (1 - TT_{IIR})] && \text{large membership in TT row} \\
 & + [1 - (Y_{DCOV} - Y_{IIR})] && \text{large difference in outcome} \\
 & + |TT_{DCOV} - TT_{IIR}| && \text{similar membership in TT row}
 \end{aligned} \quad (7)$$

Cases for this forth type of comparison can be identified by setting cases to 4. Since for deviant coverage and IIR cases we are interested in identifying an entire missing sufficient term, the output for these pairs is focused on matching pairs in truth table rows, rather than in sufficient terms. Therefore, the output is sorted by truth table rows (the columns starting with *TT* showing the combination of conditions) and for each truth table row we can identify a best matching pair of cases according to formula values in column *distance*. For example, if we focus on truth table row *EMP * BARGAIN * uni * OCCUP * stock * ma* (rows 6, 7, 8, 9, 10 in the output), the deviant case coverage France_95 and the IIR case Finland_90 constitute the best matching pair, having the smallest formula value for this specific truth table row (distance=1.43).

```
# Get matching pairs of deviant coverage and IIR cases for the
# parsimonious solution:
```

```
mmr (results = sol_yp, outcome = "EXPORT", neg.out = FALSE,
     sol = 1, match = TRUE, cases = 4)
```

```
## Matching Deviant Coverage-IIR Cases :
```

```
## -----
```

##	deviant_coverage	individually_irrelevant	distance	best_matching_pair
## 1	USA_99	New Zealand_95	0.58	TRUE
## 2	UK_03	New Zealand_95	0.59	FALSE
## 3	UK_99	New Zealand_95	0.59	FALSE
## 4	Ireland_03	New Zealand_95	0.73	FALSE
## 5	Ireland_99	New Zealand_95	0.73	FALSE
## 6	France_95	Finland_90	1.43	TRUE
## 7	France_95	Italy_95	1.44	FALSE
## 8	Germany_03	Finland_90	1.46	FALSE
## 9	Germany_03	Italy_95	1.47	FALSE
## 10	France_95	Austria_90	1.51	FALSE
## 11	Sweden_95	Sweden_90	1.41	TRUE
## 12	Sweden_95	Belgium_95	1.43	FALSE
## 13	Netherlands_95	Belgium_95	1.48	FALSE
## 14	Netherlands_95	Sweden_90	1.64	FALSE

##	TT_EMP	TT_BARGAIN	TT_UNI	TT_OCCUP	TT_STOCK	TT_MA
## 1	0	0	1	0	1	1
## 2	0	0	1	0	1	1
## 3	0	0	1	0	1	1
## 4	0	0	1	0	1	1
## 5	0	0	1	0	1	1
## 6	1	1	0	1	0	0
## 7	1	1	0	1	0	0
## 8	1	1	0	1	0	0
## 9	1	1	0	1	0	0
## 10	1	1	0	1	0	0
## 11	1	1	0	1	1	1
## 12	1	1	0	1	1	1
## 13	1	1	0	1	1	1
## 14	1	1	0	1	1	1

Enhanced standard analysis (ESA)

Limited empirical diversity is an omnipresent feature in social science data. The treatment of logical remainders rows has been a major theme since the Ragin's path-breaking book (Ragin, 1987, esp. chapter 7). In Ragin (2008, chapters 8 and 9), three approaches towards remainders are proposed under the label of the Standard Analysis (SA). Researchers can decide not to include them into the

logical minimization (yielding the conservative or complex solution CS), to include all remainders that are simplifying (yielding the most parsimonious solution PS), or to include only those simplifying assumption that are easy based on so-called directional expectations (yielding the intermediate solution (IS)).

Schneider and Wagemann (2012, chapter 8) propose the Enhanced Standard Analysis (ESA), which argues that simplifying assumptions on specific remainders can be untenable. There are three sources of untenability. *Incoherent counterfactuals*, which are either logical remainders contradicting claims of necessity⁶ or assumptions made for the negated outcome⁷, and *implausible counterfactuals*, which consist of claims about impossible remainders⁸. ESA simply stipulates that no QCA solution formula can be based on untenable assumptions.

Figure 6 provides a graphical representation of the different types of assumptions as defined by SA and ESA. Both approaches only allow for simplifying assumptions⁹ (i.e. those in the inner circle) and both distinguish between difficult and easy counterfactuals (i.e. the vertical line inside the circle)¹⁰. ESA but not SA does block any untenable assumption (i.e. the gray area on the lower part). A risk of making untenable assumption is given whenever a researcher is claiming the presence of a necessary condition, when statements of sufficiency for both the outcome and its negation are made, and/or when two or more conditions with mutually exclusive categories are used in a truth table. ESA requires that researchers identify those logical remainder rows whose inclusion into the logical minimization would amount to an untenable claim. As a result, one obtains the enhanced PS and the enhanced IS.¹¹

Function `esa()` provides a straightforward tool for avoiding untenable assumptions and thus putting ESA into practice. First, function `esa()` can exclude remainders that contradict single necessary conditions, unions of necessary conditions, or more complicated expressions of necessity. For example, assuming that the disjunction *STOCK + MA* is necessary for the outcome *EXPORT*, we ban all remainder rows implied by this necessity claim in the `nec_cond` argument. All the logical remainder rows that are subsets of $\neg \text{STOCK} \neg \text{MA}$ are subsequently set of `OUT = 0` in the truth table object `tnew` and thus excluded from further logical minimization.

```
# Ban logical reminders contradicting necessity:
# Let's assume that "STOCK + MA" is necessary for "EXPORT":
```

```
newtt <- esa(oldtt = TT_y, nec_cond = "STOCK + MA")
```

##	EMP	BARGAIN	UNI	OCCUP	STOCK	MA	OUT	n	incl	PRI	cases
## 1	0	0	0	0	0	0	0	0	-	-	
## 3	0	0	0	0	1	0	?	0	-	-	
## 4	0	0	0	0	1	1	?	0	-	-	
## 5	0	0	0	1	0	0	0	0	-	-	
## 6	0	0	0	1	0	1	?	0	-	-	
## 7	0	0	0	1	1	0	?	0	-	-	
## 9	0	0	1	0	0	0	0	0	-	-	
## 13	0	0	1	1	0	0	0	0	-	-	
## 14	0	0	1	1	0	1	?	0	-	-	
## 15	0	0	1	1	1	0	?	0	-	-	
## 17	0	1	0	0	0	0	0	0	-	-	
## 18	0	1	0	0	0	1	?	0	-	-	
## 20	0	1	0	0	1	1	?	0	-	-	
## 21	0	1	0	1	0	0	0	0	-	-	
## 22	0	1	0	1	0	1	?	0	-	-	
## 23	0	1	0	1	1	0	?	0	-	-	
## 24	0	1	0	1	1	1	?	0	-	-	
## 25	0	1	1	0	0	0	0	0	-	-	
## 26	0	1	1	0	0	1	?	0	-	-	
## 30	0	1	1	1	0	1	?	0	-	-	

⁶ $X \leftarrow Y$ (implies $\neg X \rightarrow \neg Y$) & $\neg X \rightarrow Y$

⁷ $X \rightarrow Y$ & $X \rightarrow \neg Y$

⁸For instance, X = 'rich-poor country' etc & $X \rightarrow Y$

⁹Schneider and Wagemann (2012) propose Theory-Guided ESA (TESA) as an approach in which parsimony is not the primary decision rule for choosing remainders.

¹⁰It can be noted that all assumptions that contribute to parsimony are either easy or difficult, they cannot be neither. This is because all assumptions not constrained by directional expectations (if there are any or just some) are by default easy.

¹¹For an application of ESA, see, for instance Thomann (2015).

```
## 31  0      1  1      1      1  0  ? 0  -  -
## 33  1      0  0      0      0  0  0 0  -  -
## 34  1      0  0      0      0  1  ? 0  -  -
## 35  1      0  0      0      1  0  ? 0  -  -
## 36  1      0  0      0      1  1  ? 0  -  -
## 37  1      0  0      1      0  0  0 0  -  -
## 38  1      0  0      1      0  1  ? 0  -  -
## 39  1      0  0      1      1  0  ? 0  -  -
## 40  1      0  0      1      1  1  ? 0  -  -
## 41  1      0  1      0      0  0  0 0  -  -
## 42  1      0  1      0      0  1  ? 0  -  -
## 44  1      0  1      0      1  1  ? 0  -  -
## 45  1      0  1      1      0  0  0 0  -  -
## 46  1      0  1      1      0  1  ? 0  -  -
## 47  1      0  1      1      1  0  ? 0  -  -
## 48  1      0  1      1      1  1  ? 0  -  -
## 50  1      1  0      0      0  1  ? 0  -  -
## 51  1      1  0      0      1  0  ? 0  -  -
## 52  1      1  0      0      1  1  ? 0  -  -
## 54  1      1  0      1      0  1  ? 0  -  -
## 58  1      1  1      0      0  1  ? 0  -  -
## 59  1      1  1      0      1  0  ? 0  -  -
```

Secondly, the `esa()` function can also ban implausible counterfactuals to produce truth tables in which specific logical remainders identified through conjunctions are excluded. For example, we can ban all remainder rows that have $BARGAIN+ \sim OCCUP$ by using the Boolean expression in argument `untenable_LR`. Finally, the function can exclude contradictory simplifying assumptions (which are another form of untenable assumptions) and empirically observed rows that are part of simultaneous subset relations¹² by just using the unique truth table row identifier in the argument `contrad_rows`. While argument `untenable_LR` accepts Boolean expression for excluding only logical remainders, argument `contrad_rows` can exclude both empirically observed rows and remainder rows through their unique identifier (row number).¹³

```
# Ban impossible logical remainders:
newtt <- esa(oldtt = TT_y, untenable_LR = "BARGAIN*~OCCUP")

# Ban contradictory rows:
newtt <- esa(oldtt = TT_y, contrad_rows = c("19", "14", "46", "51"))
```

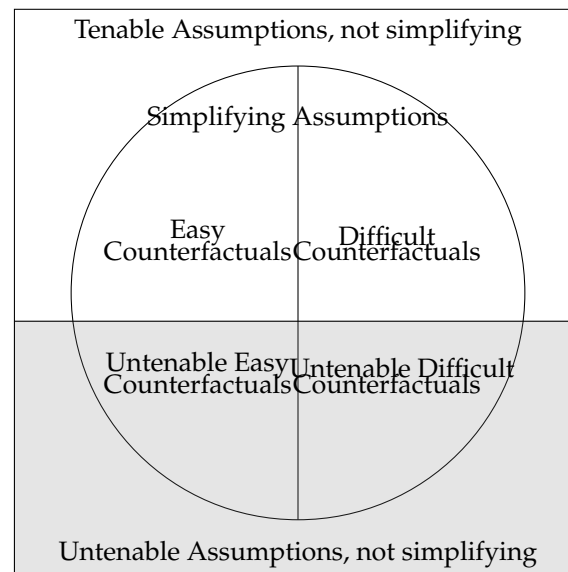
Set-analytic theory evaluation

Ragin (1987, chapter 7) spells out the notion of theory evaluation. In essence, it consists of identifying the overlap between a researcher's theory (T) as formulated prior to the empirical analysis and the empirical results (S) obtained via QCA. With both T and S being represented in the form of Boolean expressions, all four logically possible combinations between T and S can be expressed in Boolean terms as well and each case's membership in each of these four expressions be calculated. Theory evaluation reveals which aspects of T are empirically corroborated by S and which ones are not. It also reveals how strong this empirical support is. Last but not least, theory evaluation can serve as a case selection device by identifying cases that display membership scores in the empirical solution and the outcome that are expected or utterly unexpected based on T .

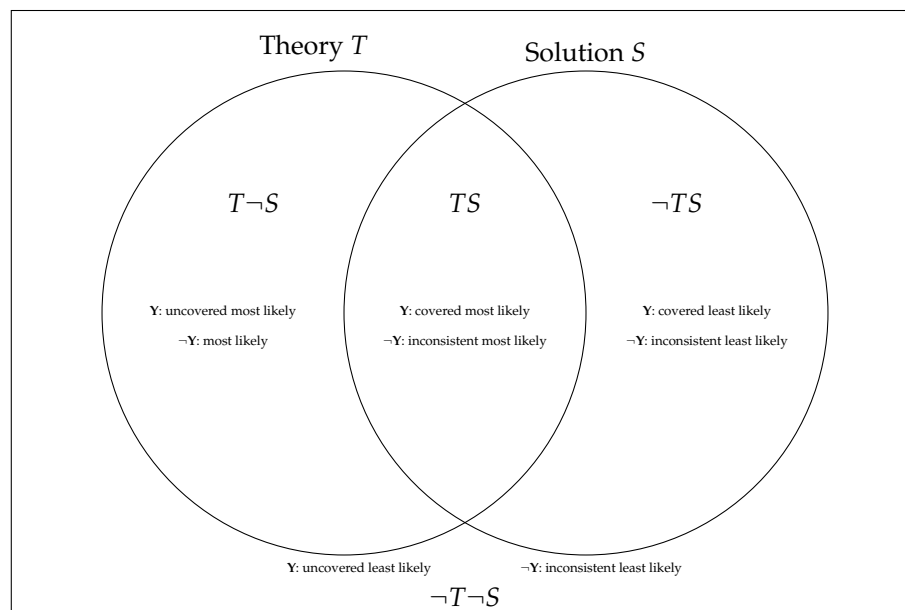
Schneider and Wagemann (2012, chapter 11) refine Theory Evaluation by taking into account each case's membership score not only in T and S , but also outcome Y . This is necessary due to the development of parameters of fit based on which by now it has become widespread practice to allow for solution formulas with less than perfect consistency and coverage scores. This means that in applied QCA, there are cases of $S \& \neg Y$ and of $\neg S \& Y$. This gives rise to eight different areas. Each area can be defined as a Boolean expression, provides different analytic information, and defines

¹²Simultaneous subset relations happen when an empirically observed truth table row is a consistent enough subset of both the outcome and its negation.

¹³Due to space restrictions, output for these functions is not shown here.

Figure 6: Graphical Representation of Different Types of Assumptions on Remainders

different types of cases. Each case has partial membership in all areas but only in one of higher than 0.5. Figure 7 provides a visualization of the areas and the kinds of cases in each area.¹⁴

Figure 7: Graphical Representation of Theory Evaluation

Function `theory.evaluation()` performs the theory evaluation procedure between a theory specified in Boolean terms and results obtained using the **QCA** package. Assuming that the theory can be summarized as $EMP * \sim MA + STOCK$, the example below shows how theory evaluation works using the second intermediate solution for outcome *EXPORT*. The first part of the output shows the names and proportion of cases in each of the intersections between theory and the empirical solution. The second part of the output shows parameters of fit for the solution, the theory, and their intersections, which indicate how much each of these areas are in line with a statement of sufficiency for *EXPORT*. Additionally, the function also stores the membership of each case in each intersection between theory and empirics, which can be accessed by setting argument `print.data` to `TRUE`.

¹⁴For applied examples of theory evaluation, see, for instance, [Sager and Thomann \(2017\)](#); [Schneider and Maerz \(2017\)](#).

```

# Assuming the theory can be summarized as "EMP*~MA + STOCK",
# perform theory evaluation using the second intermediate solution:

theory.evaluation(theory = "EMP*~MA + STOCK", empirics = sol_yi,
                  outcome = "EXPORT", sol = 2, print.data=FALSE)

##
## Cases:
## -----
##
## Covered Most Likely (T*E and Y > 0.5) :
## *****
##
## Cases in the intersection/Total number of cases: 23 / 76 = 30.26 %
##
## Case Names:
## [1] "Ireland_90"      "Japan_90"      "USA_90"      "Ireland_95"
## [5] "Japan_95"        "Switzerland_95" "USA_95"      "Denmark_99"
## [9] "Finland_99"      "France_99"     "Japan_99"    "Netherlands_99"
## [13] "Sweden_99"       "Switzerland_99" "Belgium_03"  "Denmark_03"
## [17] "Finland_03"      "France_03"     "Japan_03"    "Netherlands_03"
## [21] "Sweden_03"       "Switzerland_03" "USA_03"
##
## Covered Least Likely (t*E and Y > 0.5) :
## *****
##
## Cases in the intersection/Total number of cases: 0 / 76 = 0 %
##
## Case Names:
## [1] "No cases in this intersection"
##
## Uncovered Most Likely (T*e and Y > 0.5) :
## *****
##
## Cases in the intersection/Total number of cases: 12 / 76 = 15.79 %
##
## Case Names:
## [1] "UK_90"           "France_95"     "Netherlands_95" "Sweden_95"
## [5] "UK_95"           "Germany_99"    "Ireland_99"     "UK_99"
## [9] "USA_99"          "Germany_03"    "Ireland_03"     "UK_03"
##
## Uncovered Least Likely (t*e and Y > 0.5) :
## *****
##
## Cases in the intersection/Total number of cases: 0 / 76 = 0 %
##
## Case Names:
## [1] "No cases in this intersection"
##
## Inconsistent Most Likely (T*E and Y < 0.5) :
## *****
##
## Cases in the intersection/Total number of cases: 12 / 76 = 15.79 %
##
## Case Names:
## [1] "Canada_90"       "Switzerland_90" "Australia_95"   "Canada_95"
## [5] "Denmark_95"      "Finland_95"     "Australia_99"   "Belgium_99"
## [9] "Spain_99"        "Australia_03"   "Norway_03"      "Spain_03"
##
## Inconsistent Least Likely (t*E and Y < 0.5) :
## *****
##
## Cases in the intersection/Total number of cases: 1 / 76 = 1.32 %
##

```

```

## Case Names:
## [1] "Australia_90"
##
## Consistent Most Likely (T*e and Y < 0.5) :
## *****
##
## Cases in the intersection/Total number of cases:  23 / 76 = 30.26 %
##
## Case Names:
## [1] "Austria_90"      "Belgium_90"      "Denmark_90"      "Finland_90"
## [5] "France_90"       "Germany_90"      "Italy_90"        "Netherlands_90"
## [9] "Norway_90"       "Spain_90"        "Sweden_90"       "Austria_95"
## [13] "Belgium_95"      "Germany_95"      "Italy_95"        "New Zealand_95"
## [17] "Norway_95"       "Spain_95"        "Austria_99"      "Canada_99"
## [21] "Italy_99"        "Canada_03"       "Italy_03"
##
## Consistent Least Likely (t*e and Y < 0.5) :
## *****
##
## Cases in the intersection/Total number of cases:  4 / 76 = 5.26 %
##
## Case Names:
## [1] "New Zealand_90" "New Zealand_99" "Norway_99"      "New Zealand_03"
##
##
## Fit:
## -----
##
##           Cons.Suf  Cov.Suf   PRI  Cons.Suf(H)
## emp*bargain*OCCUP    0.909   0.194 0.721      0.865
## BARGAIN*UNI*STOCK    0.796   0.497 0.665      0.704
## emp*UNI*OCCUP*ma     0.919   0.171 0.611      0.894
## emp*occup*STOCK*ma   0.904   0.298 0.802      0.859
## UNI*occup*STOCK*ma   0.894   0.341 0.795      0.853
## Sol.Formula          0.799   0.705 0.691      0.716
## Theory               0.639   0.973 0.515      0.550
## T*e                 0.811   0.705 0.707      0.726
## t*e                 0.825   0.165 0.423      0.764
## T*e                 0.651   0.547 0.419      0.592
## t*e                 0.697   0.203 0.232      0.640

```

Diagnostic tools for clustered data structures

Most of the data analyzed in the social sciences and neighboring disciplines contains structures, or layers, that might be analytically relevant but are not captured by the models used to analyze that data. [García-Castro and Arino \(2016\)](#) discuss clustering along a *temporal* dimension. This can be days, years, decades, or substantively important periods (before - after a crisis). Clusters can also be of different origin. For instance, cases can be clustered along *geographic* units, such as world regions or subnational units. There can also be clusterings along *substantive* lines, such as e.g. economic sectors, parties, political regime types.

Whenever a researcher is not capturing these differences via a condition in her QCA model, she de facto assumes that the analytic difference does not matter. There are often good reasons to not include additional conditions into an analysis, with keeping limited diversity at bay being one of them. It should, however, been put to an empirical test whether it is ok to pool cases across different time periods, geographic units, and/or substantive areas.

Function `cluster()` provides the tools for performing such a test. It analyzes whether the QCA solution formula obtained from the pooled data also can be found in each of the sub-populations in the data. If it can, then pooling the data is fine. If it cannot, then pooling the data is not fine because it produces a solution that does not hold for all sub-populations. Rather, it is an artifact of having pooled cases that follow different causal logics. In this case, researchers might decide to drop from their analysis those sub-populations that do not follow the general pattern or to include a condition

into their model that captures the difference.

For using the `cluster()` function, researchers need data in the long format, with a column identifying the unit of analysis and a column identifying the clustering element. In our example, using the [Schneider et al. \(2010\)](#) data, the column identifying the units is the `COUNTRY` column, while the cluster element is stored in the `YEAR` column. After having the data in the long format, we can get the diagnostic of how our solution holds throughout the different units and clusters by just imputing the solution (in this case `sol_yi`) in the `cluster()` function, while also specifying the data, the outcome, the unit identifier, and the cluster identifier. The first part of the output shows the consistency sufficiency for the overall, pooled sample for each sufficient term and the entire solution to be diagnosed. This first row of the output should be equivalent to the consistency measures obtained when producing the solution. The rows below show consistency values of the same terms and solution, but for each cluster and each unit in part. These are the values we would obtain if the analysis were to be run for each cluster subsample and each unit subsample separately. For example, the pooled consistency of sufficient term `emp * UNI * OCCUP * ma` is 0.919 but only 0.733 for the year 1990. This might be an indication for the researcher that her sufficiency statement is not as consistent and might not work in the same way for the cluster of cases from 1990. In general, if consistency values between clusters differ greatly from pooled consistency for a term, we might want to reexamine the setup of the analysis to account for this. The Distances: section of the output reports on how much the parameters of fit differ from the clusters to the pooled data. Finally, the last part of the output displays a similar table for coverage, with pooled, between clusters, and within units measures.

```
# Perform cluster diagnostic:
# First we need to load the Schneider et. al. (2010) data in the long format:

data(SCHLF)

# This data has a column identifying the unit (country)
# and the clustering element (year):

head(SCHLF)

##           EMP BARGAIN  UNI OCCUP STOCK  MA EXPORT  COUNTRY YEAR
## Australia_90 0.07    0.90 1.00  0.68  0.45 0.33  0.19 Australia 1990
## Austria_90   0.70    0.98 0.01  0.91  0.01 0.05  0.25  Austria 1990
## Belgium_90   0.94    0.95 0.14  0.37  0.26 0.14  0.14  Belgium 1990
## Canada_90    0.04    0.21 0.99  0.11  0.62 0.31  0.28  Canada 1990
## Denmark_90   0.59    0.78 0.10  0.55  0.53 0.10  0.34  Denmark 1990
## Finland_90   0.70    0.97 0.20  0.95  0.02 0.13  0.17  Finland 1990

# Get the intermediate solution:

sol_yi <- minimize(SCHLF, outcome = "EXPORT",
                  conditions = c("EMP", "BARGAIN", "UNI",
                                "OCCUP", "STOCK", "MA"),
                  incl.cut1 = .9,
                  include = "?",
                  details = TRUE, show.cases = TRUE,
                  dir.exp = c(0,0,0,0,0,0))

# Get pooled, within, and between consistencies for the intermediate solution:

cluster(data = SCHLF, results = sol_yi, outcome = "EXPORT", unit_id = "COUNTRY",
        cluster_id = "YEAR")

## Consistencies:
## -----
##           emp*bargain*OCCUP  BARGAIN*UNI*STOCK  emp*UNI*OCCUP*ma
## Pooled                    0.909              0.796              0.919
## Between 1990              0.839              0.873              0.733
## Between 1995              0.903              0.727              0.953
## Between 1999              0.928              0.802              1.000
## Between 2003              0.951              0.818              1.000
## Within Australia          1.000              0.405              0.634
```

```

## Within Austria      1.000      1.000      1.000
## Within Belgium      1.000      0.803      1.000
## Within Canada        1.000      1.000      1.000
## Within Denmark       1.000      0.757      1.000
## Within Finland       1.000      0.835      0.957
## Within France        1.000      0.916      1.000
## Within Germany       1.000      1.000      1.000
## Within Ireland       1.000      1.000      1.000
## Within Italy          1.000      0.800      1.000
## Within Japan         1.000      1.000      1.000
## Within Netherlands   1.000      1.000      1.000
## Within NewZealand    0.414      0.875      0.727
## Within Norway        0.965      0.486      0.930
## Within Spain         1.000      0.524      1.000
## Within Sweden        1.000      0.926      1.000
## Within Switzerland   0.880      1.000      1.000
## Within UK            1.000      1.000      1.000
## Within USA           1.000      1.000      1.000
##
## emp*occup*STOCK*ma  bargain*occup*STOCK*ma
## Pooled              0.904      0.913
## Between 1990        0.858      0.903
## Between 1995        0.847      0.884
## Between 1999        1.000      1.000
## Between 2003        0.995      0.916
## Within Australia    0.865      1.000
## Within Austria      1.000      1.000
## Within Belgium      1.000      1.000
## Within Canada       0.587      0.587
## Within Denmark      0.732      1.000
## Within Finland      1.000      1.000
## Within France       1.000      1.000
## Within Germany      1.000      1.000
## Within Ireland      1.000      1.000
## Within Italy         1.000      1.000
## Within Japan        1.000      0.997
## Within Netherlands  1.000      1.000
## Within NewZealand   0.710      0.710
## Within Norway       0.930      0.961
## Within Spain        1.000      0.628
## Within Sweden       1.000      1.000
## Within Switzerland  1.000      1.000
## Within UK           1.000      1.000
## Within USA          1.000      1.000
##
##
## Distances:
## -----
##
## emp*bargain*OCCUP  BARGAIN*UNI*STOCK
## From Between to Pooled      0.023      0.032
## From Within to Pooled       0.031      0.050
##
## emp*UNI*OCCUP*ma  emp*occup*STOCK*ma
## From Between to Pooled      0.060      0.039
## From Within to Pooled       0.024      0.030
##
## bargain*occup*STOCK*ma
## From Between to Pooled      0.024
## From Within to Pooled       0.032
##
##
## Coverages:
## -----
##
## emp*bargain*OCCUP  BARGAIN*UNI*STOCK  emp*UNI*OCCUP*ma
## Pooled              0.194      0.497      0.171
## Between 1990        0.231      0.246      0.193
## Between 1995        0.206      0.466      0.271

```

## Between 1999	0.174	0.589	0.042
## Between 2003	0.184	0.570	0.214
## Within Australia	0.415	1.000	0.675
## Within Austria	0.075	0.041	0.279
## Within Belgium	0.138	0.959	0.283
## Within Canada	0.328	0.545	0.246
## Within Denmark	0.273	0.894	0.317
## Within Finland	0.059	0.937	0.282
## Within France	0.070	0.805	0.118
## Within Germany	0.236	0.374	0.205
## Within Ireland	0.113	0.352	0.098
## Within Italy	0.173	0.367	0.112
## Within Japan	0.161	0.064	0.161
## Within Netherlands	0.150	0.748	0.183
## Within NewZealand	1.000	0.778	0.667
## Within Norway	0.598	0.978	0.435
## Within Spain	0.204	0.710	0.204
## Within Sweden	0.061	0.761	0.054
## Within Switzerland	0.738	0.244	0.032
## Within UK	0.075	0.282	0.052
## Within USA	0.037	0.045	0.037
##	emp*occup*STOCK*ma	bargain*occup*STOCK*ma	
## Pooled	0.298	0.278	
## Between 1990	0.452	0.450	
## Between 1995	0.459	0.345	
## Between 1999	0.069	0.117	
## Between 2003	0.321	0.290	
## Within Australia	0.675	0.317	
## Within Austria	0.041	0.034	
## Within Belgium	0.228	0.103	
## Within Canada	0.701	0.701	
## Within Denmark	0.480	0.238	
## Within Finland	0.218	0.042	
## Within France	0.132	0.048	
## Within Germany	0.205	0.169	
## Within Ireland	0.291	0.118	
## Within Italy	0.265	0.184	
## Within Japan	0.456	0.947	
## Within Netherlands	0.196	0.070	
## Within NewZealand	0.611	0.611	
## Within Norway	0.435	0.533	
## Within Spain	0.204	0.581	
## Within Sweden	0.054	0.057	
## Within Switzerland	0.093	0.093	
## Within UK	0.072	0.072	
## Within USA	0.717	0.717	

Function `cluster()` can be applied in a similar fashion for necessary relationships by just setting argument `necessity` to `TRUE` and inputting the necessary condition to be diagnosed in the field `results`. Additionally, we can also diagnose Boolean expressions by just entering this into the `results` argument.

```
# Get pooled, within, and between consistencies for ~EMP
# as necessary for EXPORT:
```

```
cluster(data = SCHLF, results = "~EMP", outcome = "EXPORT",
        unit_id = "COUNTRY", cluster_id = "YEAR", necessity=TRUE)
```

```
# Get pooled, within, and between consistencies for EMP*~MA*STOCK
# as sufficient for EXPORT:
```

```
cluster(data = SCHLF, results = "EMP*~MA*STOCK", outcome = "EXPORT",
        unit_id = "COUNTRY", cluster_id = "YEAR")
```


Additional functions

Plotting sufficient terms and solutions, truth table rows, and necessity relations

Package **SetMethods** also includes a function `pimplot()` for plotting each sufficient term and the solution formula (obtained by using the `minimize()` function in package **QCA**). The function can also plot truth table rows against the outcome by using arguments `incl.tt` or `ttrows` as in the examples below. Additionally, the function can plot results obtained from necessity analyses using an object of class "sS" (obtained by using the `superSubset()` function in package **QCA**) by setting argument `necessity` to `TRUE`.¹⁵

```
# Plot the prime implicants of the parsimonious solution:

pimplot(data = SCHF, results = sol_yp, outcome = "EXPORT")

# Plot all truth table rows with a consistency higher than 0.9:

pimplot(data=SCHF, results = sol_yi, incl.tt=0.9, outcome = "EXPORT", sol = 1)

# Plot truth table rows "60" and "61":

pimplot(data=SCHF, results = sol_yi, ttrows =c("60","61"),
        outcome = "EXPORT", sol = 1)

# For plotting results of necessity analyses using superSubset,
# the first step is to obtain an "sS" object:

SUPSUB <- superSubset(SCHF, outcome="EXPORT",
                     conditions = c("EMP","BARGAIN","UNI","OCCUP","STOCK", "MA"),
                     relation = "necessity", incl.cut = 0.8)

SUPSUB

# This can be imputed as result and necessity should be set to TRUE:

pimplot(data = SCHF, results = SUPSUB, outcome = "EXPORT",
        necessity = TRUE)
```

QCAradar

Another function included in the package is the `QCAradar()` function which allows visualization of QCA results or simple Boolean expressions in the form of a radar chart¹⁶. The function accepts in the argument `results` sufficient solutions obtained through the function `minimize()` in package **QCA**, or Boolean expressions involving more than three conditions, as in the second example below.

```
# Display radar chart for the second intermediate solution:

QCAradar(results = sol_yi, outcome = "EXPORT", fit=TRUE, sol = 2)
```

Figure 8a shows a radar chart for the second intermediate solution formula. The different sufficient terms are overlapping on the radar in different shades. For example, we can see the first term `emp*bargain*OCCUP`, as condition *EMP* is missing it is set to 0 for that respective corner, condition *BARGAIN* is missing and set to 0, and condition *OCCUP* is present and set to 1. Since the rest of the conditions are not specified in this term, they are all left at -.

¹⁵The plots resulting from these functions are not included in the paper due to length reasons.

¹⁶See Maerz (2017) for an applied example of radar charts.

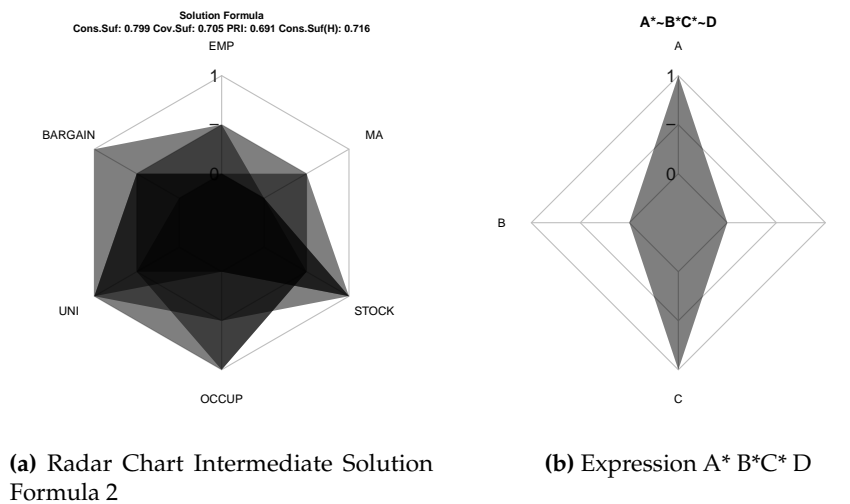


Figure 8: Radar Charts

```
# Show a radar chart for the following boolean expression "A*~B*C*~D"
```

```
QCAradar(results = "A*~B*C*~D")
```

Figure 8b shows a radar chart for the Boolean expression " $A * \sim B * C * \sim D$ ". Conditions A and C that are present are set to 1 for their respective corners, while conditions B and D that are missing and set to 0. There are not conditions left at - in this figure, as all conditions are specified.

Indirect calibration

SetMethods also includes a function for performing the indirect calibration procedure described by Ragin (2008)¹⁷. This procedure assumes that the cases included in the analysis have interval-scale raw scores which can be initially sorted broadly into different levels of fuzzy set membership. Subsequently, the raw scores are transformed into calibrated scores using a binomial or a beta regression. Assuming that vector x contains the initial raw scores, while vector x_cal contains the rough grouping of those values into set membership scores, function `indirectCalibration()` can produce a vector of fuzzy-set scores a by fitting the x to x_cal using a binomial regression if `binom` is set to TRUE.

```
# Generate fake data
```

```
set.seed(4)
x <- runif(20, 0, 1)
```

```
# Find quantiles
```

```
quant <- quantile(x, c(.2, .4, .5, .6, .8))
```

```
# Theoretical calibration
```

```
x_cal <- NA
x_cal[x <= quant[1]] <- 0
x_cal[x > quant[1] & x <= quant[2]] <- .2
x_cal[x > quant[2] & x <= quant[3]] <- .4
x_cal[x > quant[3] & x <= quant[4]] <- .6
x_cal[x > quant[4] & x <= quant[5]] <- .8
x_cal[x > quant[5]] <- 1
x_cal
```

```
# Indirect calibration (binomial)
```

¹⁷The **QCA** package can also perform indirect calibration through its `calibrate` function

```
a <- indirectCalibration(x, x_cal, binom = TRUE)
a
```

Conclusions

In this article, we have presented the main functionalities of the R package **Setmethods**. It is true that starting to perform QCA in R is more onerous than starting with a point-and-click software. Yet, the flexibility offered by R is also its strength, especially for a young method like QCA. As set methods continue to develop, software implementations need to be updated and improved at a fast rate. Package **SetMethods** is designed to do precisely this: providing a tool for implementing new ideas that enhance set-theoretic analyses for applied researchers.

Acknowledgements

We thank Juraj Medzihorsky and Mario Quaranta for their input into previous versions of the **SetMethods** package. We also thank the participants of various ECPR Summer and Winter Schools in Methods and Techniques whose questions and testing are continuously improving the package.

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