Good Relations with R

David Meyer and Kurt Hornik
2008-08-13

Given \( k \) sets of objects \( X_1, \ldots, X_k \), a \( k \)-ary relation \( R \) on \( D(R) = (X_1, \ldots, X_k) \) is a subset \( G(R) \) of the Cartesian product \( X_1 \times \cdots \times X_k \). I.e., \( D(R) \) is a \( k \)-tuple of sets and \( G(R) \) is a set of \( k \)-tuples. We refer to \( D(R) \) and \( G(R) \) as the domain and the graph of the relation \( R \), respectively (alternative notions are that of ground and figure, respectively).

Relations are a very fundamental mathematical concept: well-known examples include the linear order defined on the set of integers, the equivalence relation, notions of preference relations used in economics and political sciences, etc. Package \texttt{relations} provides data structures along with common basic operations for relations and also relation ensembles (collections of relations with the same domain), as well as various algorithms for finding suitable consensus relations for given relation ensembles.

1 Relations and Relation Ensembles

1.1 Relations

For a \( k \)-ary relation \( R \) with domain \( D(R) = (X_1, \ldots, X_k) \), we refer to \( s = (s_1, \ldots, s_k) \), where each \( s_i \) gives the cardinality of \( X_i \), as the size of the relation. Note that often, relations are identified with their graph: strictly speaking, the relation is the pair \( (D(R), G(R)) \). We say that a \( k \)-tuple \( t \) is contained in the relation \( R \) iff it is an element of \( G(R) \). The incidence (array) \( I(R) \) of \( R \) is a \( k \)-dimensional 0/1 array of size \( s \) whose elements indicate whether the corresponding \( k \)-tuples are contained in \( R \) or not.

Package \texttt{relations} implements finite relations as an S3 class which allows for a variety of representations (even though currently, typically dense array representations of the incidences are employed). Other than by the generator \texttt{relation()} , relations can be obtained by coercion via the generic function \texttt{as.relation()}, which has methods for at least logical and numeric vectors, unordered and ordered factors, arrays including matrices, and data frames. Unordered factors are coerced to equivalence relations; ordered factors and numeric vectors are coerced to order relations. Logical vectors give unary relations (predicates). A (feasible) \( k \)-dimensional array is taken as the incidence of a \( k \)-ary relation. Finally, a data frame is taken as a relation table (object by attribute representation of the relation graph). Note that missing values will be propagated in the coercion.

\begin{verbatim}
> ## A relation created by specifying the graph:
> R <- relation(graph = data.frame(A = c(1, 1:3), B = c(2:4, 4)))
> ## extract domain
> relation_domain(R)

Relation domain:
A pair (A, B) with elements:
{1, 2, 3}
{2, 3, 4}

> ## extract graph
> relation_graph(R)
\end{verbatim}
Relation graph:
A set with pairs ("A", "B"):
(1, 2)
(1, 3)
(2, 4)
(3, 4)

> ## both ("a pair of domain and graph" ...)
> as.tuple(R)

(Domain = (A = {1, 2, 3}, B = {2, 3, 4}), Graph = {(1, 2), (1, 3), (2, 4), (3, 4)})

> ## extract incidence
> relation_incidence(R)

Incidences:
B
A 2 3 4
1 1 1 0
2 0 0 1
3 0 0 1

> ## (Almost) the same using the set specification
> ## (the domain labels are missing).
> R <- relation(graph = set(tuple(1,2), tuple(1,3), tuple(2,4), tuple(3,4)))
> ## equivalent to:
> ## relation(graph = list(1:2, c(1,3), c(2,4), c(3,4)))
> relation_incidence(R)

Incidences:
2 3 4
1 1 1 0
2 0 0 1
3 0 0 1

> ## Domains can be composed of arbitrary R objects:
> R <- relation(domain = set(c, "test"),
+ graph = set(tuple(c, c), tuple(c, "test")))
> relation_incidence(R)

Incidences:
X
X test <<function>>
test 0 0
<<function>> 1 1

> as.relation(1:3)
A binary relation of size 3 x 3.

> relation_graph(as.relation(c(TRUE, FALSE, TRUE)))

Relation graph:
A set with singletons:
("1")
("3")
\[
\text{Relation graph:}
\]
A set with pairs:
- ("1", "1")
- ("1", "3")
- ("2", "2")
- ("3", "1")
- ("3", "3")

The characteristic function \( f_R \) (sometimes also referred to as indicator function) of a relation \( R \) is the predicate (Boolean-valued) function on the Cartesian product \( X_1 \times \cdots \times X_k \) such that \( f_R(t) \) is true iff the \( k \)-tuple \( t \) is in \( G(R) \). Characteristic functions can both be recovered from a relation via \texttt{relation_charfun()}\texttt{,} and be used in the generator for the creation. In the following, \( R \) represents “a divides b”:

```r
> divides <- function(a, b) b %% a == 0
> R <- relation(domain = list(1:10, 1:10), charfun = divides)
> R
A binary relation of size 10 x 10.
> "%|%" <- relation_charfun(R)
> 2L %|% 6L
[1] TRUE
> 2L %|% c(2:3, 6L)
[1] TRUE FALSE TRUE
> "%|%"(2L, 6L)
[1] TRUE
```

Quite a few \texttt{relation_is_\_\_\_()} predicate functions are available. For example, relations with arity 2, 3, and 4 are typically referred to as \textit{binary}, \textit{ternary}, and \textit{quaternary} relations, respectively—the corresponding functions in package \texttt{relations} are \texttt{relation_is_binary()}, \texttt{relation_is_ternary()}, etc. For binary relations \( R \), it is customary to write \( xRy \) iff \((x, y)\) is contained in \( R \). For predicates available on binary relations, see Table 1. An \textit{endorelation} on \( X \) (or binary relation \textit{over} \( X \)) is a binary relation with domain \((X, X)\). Endorelations may or may not have certain basic properties (such as transitivity, reflexivity, etc.) which can be tested in \texttt{relations} using the corresponding predicates (see Table 2 for an overview). Some combinations of these basic properties have special names because of their widespread use (such as linear order or weak order), and can again be tested using the functions provided (see Table 3).

```r
> R <- as.relation(1:5)
> relation_is_binary(R)
[1] TRUE
> relation_is_transitive(R)
[1] TRUE
```
left-total for all $x$ there is at least one $y$ such that $xRy$.
right-total for all $y$ there is at least one $x$ such that $xRy$.
functional for all $x$ there is at most one $y$ such that $xRy$.
surjective the same as right-total.
injective for all $y$ there is at most one $x$ such that $xRy$.
bijective left-total, right-total, functional and injective.

Table 1: Some properties $foo$ of binary relations—the predicates in relations are $relation_is_foo()$ (with hyphens replaced by underscores).

reflexive $xRx$ for all $x$.
irreflexive there is no $x$ such that $xRx$.
coreflexive $xRy$ implies $x = y$.
symmetric $xRy$ implies $yRx$.
asymmetric $xRy$ implies that not $yRx$.
antisymmetric $xRy$ and $yRx$ imply that $x = y$.
transitive $xRy$ and $yRz$ imply that $xRz$.
complete for all distinct $x$ and $y$, $xRy$ or $yRx$.
strongly complete for all $x$ and $y$, $xRy$ or $yRx$.
negatively transitive not $xRy$ and not $yRz$ imply that not $xRz$.
Ferrers $xRy$ and $zRw$ imply $xRw$ or $yRz$.
semitransitive $xRy$ and $yRz$ imply $xRw$ or $wRz$.
quasitransitive $xRy$ and not $yRx$ and $yRz$ and not $zRy$ imply that $xRz$ and not $zRx$ (i.e., the asymmetric part of $R$ is transitive).
trichotomous exactly one of $xRy$, $yRx$, or $x = y$ holds.
Euclidean $xRy$ and $xRz$ imply $yRz$.

Table 2: Some properties $bar$ of endorelations—the predicates in relations are $relation_is_bar()$ (with spaces replaced by underscores).

preorder reflexive and transitive.
quasiorder the same as preorder.
equivalence a symmetric preorder.
weak order complete and transitive.
preference the same as weak order.
partial order an antisymmetric preorder.
strict partial order irreflexive, transitive and antisymmetric.
linear order a complete partial order.
strict linear order strongly complete.
tournament complete and antisymmetric.
turnament complete and Ferrers.
tournament a semitransitive interval order.

Table 3: Some categories $baz$ of endorelations—the predicates in relations are $relation_is_baz()$ (with spaces replaced by underscores).
> relation_is_partial_order(R)

[1] TRUE

While relations with the same domain can naturally be ordered according to their graphs. I.e., 
\( R_1 \leq R_2 \) if \( G(R_1) \) is a subset of \( G(R_2) \), or equivalently, if every \( k \)-tuple \( t \) contained in \( R_1 \) is 
also contained in \( R_2 \). This induces a lattice structure, with meet (greatest lower bound) and 
join (least upper bound) the intersection and union of the graphs, respectively, also known as 
the *intersection* and *union* of the relations. The least element moves metric on this lattice is 
the *symmetric difference metric*, i.e., the cardinality of the symmetric difference of the graphs 
(the number of tuples in exactly one of the relation graphs). This “symdiff” dissimilarity between 
(ensembles of) relations can be computed by `relation_dissimilarity()`.

```r
> x <- matrix(0, 3L, 3L)
> R1 <- as.relation(row(x) >= col(x))
> R2 <- as.relation(row(x) <= col(x))
> R3 <- as.relation(row(x) < col(x))
> relation_incidence(max(R1, R2))

Incidences:
  1 2 3
 1 1 1 1
2 1 1 1
3 1 1 1

> relation_incidence(min(R1, R2))

Incidences:
  1 2 3
 1 1 0 0
2 0 1 0
3 0 0 1

> R3 < R2

[1] TRUE

> relation_dissimilarity(min(R1, R2), max(R1, R2))

[,1]
[1,]  6

The *complement* of a relation \( R \) is the relation with domain \( D(R) \) whose graph is the comple-
ment of \( G(R) \), i.e., which contains exactly the tuples not contained in \( R \). For binary relations \( R \) 
and \( S \) with domains \((X, Y)\) and \((Y, Z)\), the *composition* of \( R \) and \( S \) is defined by taking \( xSz \) iff 
there is a \( y \) such that \( xRy \) and \( ySz \). The *dual* (or *converse*) \( R^* \) of the relation \( R \) with domain 
\((X, Y)\) is the relation with domain \((Y, X)\) such that \( xR^*y \) iff \( yRx \).

```r
> relation_incidence(R1 * R2)

Incidences:
  1 2 3
 1 1 1 1
2 1 1 1
3 1 1 1

> relation_incidence(! R1)
```
Incidences:
1 2 3
1 0 1 1
2 0 0 1
3 0 0 0

> relation_incidence(t(R2))

Incidences:
1 2 3
1 1 0 0
2 1 1 0
3 1 1 1

There is a plot() method for certain endorelations (currently, only complete or antisymmetric transitive relations are supported) provided that package Rgraphviz [Gentry, Long, Gentleman, Falcon, Hahne, and Sarkar 2008] is available, creating a Hasse diagram of the relation. The following code produces the Hasse diagram corresponding to the inclusion relation on the power set of \{1, 2, 3\} which is a partial order (see Figure 1).

> ps <- 2 ^ set("a", "b", "c")
> inc <- set_outer(ps, "<=")
> if (require("Rgraphviz")) plot(relation(incidence = inc))

![Hasse Diagram of the inclusion relation on the power set of \{a, b, c\}](image)

Figure 1: Hasse Diagram of the inclusion relation on the power set of \{a, b, c\}.

### 1.2 Relation Ensembles

"Relation ensembles" are collections of relations \(R_i = (D, G_i)\) with the same domain \(D\) and possibly different graphs \(G_i\). Such ensembles are implemented as suitably classed lists of relation objects (of class relation_ensemble and inheriting from tuple), making it possible to use lapply() for computations on the individual relations in the ensemble. Relation ensembles can be created via relation_ensemble(), or by coercion via the generic function as.relation_ensemble() which has methods for at least data frames (regarding each variable as a separate relation). Available
methods for relation ensembles include those for subscripting, \( c() \), \( t() \), \( \text{rep()} \), \( \text{print()} \), and \( \text{plot()} \). In addition, there are summary methods defined (\( \text{min()} \), \( \text{max()} \), and \( \text{range()} \)). Other operations work element-wise like on tuples due to the inheritance.

The Cetacea data set (Vescia, 1985) is a data frame with 15 variables relating to morphology, osteology, or behavior, with both self-explanatory names and levels, and a common zoological classification (variable CLASS) for 36 types of cetacea. We consider each variable an equivalence relation on the objects, excluding 2 variables with missing values, giving a relation ensemble of length 14 (number of complete variables in the data set).

```r
> data("Cetacea")
> ind <- sapply(Cetacea, function(s) all(!is.na(s)))
> relations <- as.relation_ensemble(Cetacea[, ind])
> print(relations)
An ensemble of 14 relations of size 36 x 36.
```

Available methods for relation ensembles allow to determine duplicated (relation) entries, to replicate and combine, and extract unique elements:

```r
> any(duplicated(relations))
[1] FALSE
> thrice <- c(rep(relations, 2L), relations)
> all.equal(unique(thrice), relations)
[1] "names for current but not for target"
```

Note that \( \text{unique()} \) does not preserve attributes, and hence names. In case one wants otherwise, one can subscript by a logical vector indicating the non-duplicated entries:

```r
> all.equal(thrice[!duplicated(thrice)], relations)
[1] TRUE
```

Relation (cross-)dissimilarities can be computed for relations and ensembles thereof:

```r
> relation_dissimilarity(relations[1 : 2], relations["CLASS"])
```

```r
               CLASS
NECK       584
FORM_OF_THE_HEAD  330
```

To determine which single variable is “closest” to the zoological classification:

```r
> d <- relation_dissimilarity(relations)
> sort(as.matrix(d)[, "CLASS"])[\[-1L\]]
```
There is also an Ops group method for relation ensembles which works elementwise (in essence, as for tuples):

```r
> complement <- !relations
> complement

An ensemble of 14 relations of size 36 x 36.
```

## 2 Relational Algebra

In addition to the basic operations defined on relations, the package provides functionality similar to the corresponding operations defined in relational algebra theory as introduced by [Codd](1970).

Note, however, that domains in database relations, unlike the concept of relations we use here, are unordered. In fact, a database relation (“table”) is defined as a set of elements called “tuples”, where the “tuple” components are named, but unordered. Thus, a “tuple” in this Codd sense is a set of mappings from the attribute names into the union of the attribute domains. The functions defined in `relations`, however, preserve and respect the column ordering.

The `projection` of a relation on a specified margin (i.e., a vector of domain names or indices) is the relation obtained when all tuples are restricted to this margin. As a consequence, duplicate tuples are removed. The corresponding function in package `relations` is `relation_projection()`.

```r
> ## projection
> Person <-
+  data.frame(Name = c("Harry", "Sally", "George", "Helena", "Peter"),
+              Age = c(34, 28, 29, 54, 34),
+              Weight = c(80, 64, 70, 54, 80),
+              stringsAsFactors = FALSE)
> Person <- as.relation(Person)
> relation_table(Person)

<table>
<thead>
<tr>
<th>Name</th>
<th>Age</th>
<th>Weight</th>
</tr>
</thead>
<tbody>
<tr>
<td>Helena</td>
<td>54</td>
<td>54</td>
</tr>
<tr>
<td>Sally</td>
<td>28</td>
<td>64</td>
</tr>
<tr>
<td>George</td>
<td>29</td>
<td>70</td>
</tr>
<tr>
<td>Harry</td>
<td>34</td>
<td>80</td>
</tr>
<tr>
<td>Peter</td>
<td>34</td>
<td>80</td>
</tr>
</tbody>
</table>

> relation_table(relation_projection(Person, c("Age", "Weight")))

<table>
<thead>
<tr>
<th>Age</th>
<th>Weight</th>
</tr>
</thead>
<tbody>
<tr>
<td>54</td>
<td>54</td>
</tr>
<tr>
<td>28</td>
<td>64</td>
</tr>
<tr>
<td>29</td>
<td>70</td>
</tr>
<tr>
<td>34</td>
<td>80</td>
</tr>
</tbody>
</table>

(Note that Harry and Peter have the same age and weight.)

The `selection` of a relation is the relation obtained by taking a subset of the relation graph, defined by some logical expression. The corresponding function in `relations` is `relation_selection()`.

```r
> ## selection
> relation_table(R1 <- relation_selection(Person, Age < 29))

<table>
<thead>
<tr>
<th>Name</th>
<th>Age</th>
<th>Weight</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sally</td>
<td>28</td>
<td>64</td>
</tr>
</tbody>
</table>
```
> relation_table(R2 <- relation_selection(Person, Age >= 34))

<table>
<thead>
<tr>
<th>Name</th>
<th>Age</th>
<th>Weight</th>
</tr>
</thead>
<tbody>
<tr>
<td>Helena</td>
<td>54</td>
<td>54</td>
</tr>
<tr>
<td>Harry</td>
<td>34</td>
<td>80</td>
</tr>
<tr>
<td>Peter</td>
<td>34</td>
<td>80</td>
</tr>
</tbody>
</table>

> relation_table(R3 <- relation_selection(Person, Age == Weight))

<table>
<thead>
<tr>
<th>Name</th>
<th>Age</th>
<th>Weight</th>
</tr>
</thead>
<tbody>
<tr>
<td>Helena</td>
<td>54</td>
<td>54</td>
</tr>
</tbody>
</table>

The union of two relations simply combines the graph elements of both relations; the complement of two relations $X$ and $Y$ removes the tuples of $Y$ from $X$. One can use `~` as a shortcut for `relation_complement()`, and `%U%` or `|` for `relation_union()`. The difference between `%U%` and `|` is that the latter only works for identical domains.

> ## union
> relation_table(R1 %U% R2)

<table>
<thead>
<tr>
<th>Name</th>
<th>Age</th>
<th>Weight</th>
</tr>
</thead>
<tbody>
<tr>
<td>Helena</td>
<td>54</td>
<td>54</td>
</tr>
<tr>
<td>Sally</td>
<td>28</td>
<td>64</td>
</tr>
<tr>
<td>Harry</td>
<td>34</td>
<td>80</td>
</tr>
<tr>
<td>Peter</td>
<td>34</td>
<td>80</td>
</tr>
</tbody>
</table>

> ## works only for the same domains:
> relation_table(R2 | R3)

<table>
<thead>
<tr>
<th>Name</th>
<th>Age</th>
<th>Weight</th>
</tr>
</thead>
<tbody>
<tr>
<td>Helena</td>
<td>54</td>
<td>54</td>
</tr>
<tr>
<td>Harry</td>
<td>34</td>
<td>80</td>
</tr>
<tr>
<td>Peter</td>
<td>34</td>
<td>80</td>
</tr>
</tbody>
</table>

> ## complement
> relation_table(Person ~ R2)

<table>
<thead>
<tr>
<th>Name</th>
<th>Age</th>
<th>Weight</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sally</td>
<td>28</td>
<td>64</td>
</tr>
<tr>
<td>George</td>
<td>29</td>
<td>70</td>
</tr>
</tbody>
</table>

The intersection (symmetric difference) of two relations is the relation with all tuples they have (do not have) in common. One can use `&` instead of `relation_intersection()` in case of identical domains.

> ## intersection
> relation_table(relation_intersection(R2, R3))

<table>
<thead>
<tr>
<th>Name</th>
<th>Age</th>
<th>Weight</th>
</tr>
</thead>
<tbody>
<tr>
<td>Helena</td>
<td>54</td>
<td>54</td>
</tr>
</tbody>
</table>

> ## works only for the same domains:
> relation_table(R2 & R3)

<table>
<thead>
<tr>
<th>Name</th>
<th>Age</th>
<th>Weight</th>
</tr>
</thead>
<tbody>
<tr>
<td>Helena</td>
<td>54</td>
<td>54</td>
</tr>
</tbody>
</table>
The **Cartesian product** of two relations is obtained by basically building the Cartesian product of all graph elements, but combining the resulting pairs into single tuples. A shortcut for `relation_cartesian()` is `%><%`.

```r
Employee <- data.frame(Name = c("Harry", "Sally", "George", "Harriet", "John"),
EmpId = c(3415, 2241, 3401, 2202, 3999),
DeptName = c("Finance", "Sales", "Finance", "Sales", "N.N."),
stringsAsFactors = FALSE)
Employee <- as.relation(Employee)
relation_table(Employee)

Name   EmpId DeptName
George 3401 Finance
Harry 3415 Finance
John 3999 N.N.
Harriet 2202 Sales
Sally 2241 Sales

Dept <- data.frame(DeptName = c("Finance", "Sales", "Production"),
Manager = c("George", "Harriet", "Charles"),
stringsAsFactors = FALSE)
Dept <- as.relation(Dept)
relation_table(Dept)

DeptName  Manager
Production Charles
Finance George
Sales Harriet

relation_table(Employee %><% Dept)

Name   EmpId DeptName DeptName  Manager
George 3401 Finance Production Charles
Harry 3415 Finance Production Charles
John 3999 N.N. Production Charles
Harriet 2202 Sales Production Charles
Sally 2241 Sales Production Charles
George 3401 Finance Finance George
Harry 3415 Finance Finance George
John 3999 N.N. Finance George
Harriet 2202 Sales Finance George
Sally 2241 Sales Finance George
George 3401 Finance Sales Harriet
Harry 3415 Finance Sales Harriet
John 3999 N.N. Sales Harriet
Harriet 2202 Sales Sales Harriet
Sally 2241 Sales Sales Harriet
```
The division of relation $X$ by relation $Y$ is the reversed Cartesian product. The result is a relation with the domain unique to $X$ and containing the maximum number of tuples which, multiplied by $Y$, are contained in $X$. The remainder of this operation is the complement of $X$ and the division of $X$ by $Y$. Note that for both operations, the domain of $Y$ must be contained in the domain of $X$. The shortcuts for relation\_division() and relation\_remainder() are \%/\% and %\%, respectively.

> ## division
> Completed <-
+ data.frame(Student = c("Fred", "Fred", "Fred", "Eugene",
+ "Eugene", "Sara", "Sara"),
+ Task = c("Database1", "Database2", "Compiler1",
+ "Database1", "Compiler1", "Database1",
+ "Database2"),
+ stringsAsFactors = FALSE)
> Completed <- as.relation(Completed)
> relation_table(Completed)

<table>
<thead>
<tr>
<th>Student</th>
<th>Task</th>
</tr>
</thead>
<tbody>
<tr>
<td>Eugene</td>
<td>Compiler1</td>
</tr>
<tr>
<td>Fred</td>
<td>Compiler1</td>
</tr>
<tr>
<td>Eugene</td>
<td>Database1</td>
</tr>
<tr>
<td>Fred</td>
<td>Database1</td>
</tr>
<tr>
<td>Sara</td>
<td>Database1</td>
</tr>
<tr>
<td>Fred</td>
<td>Database2</td>
</tr>
<tr>
<td>Sara</td>
<td>Database2</td>
</tr>
</tbody>
</table>

> DBProject <- data.frame(Task = c("Database1", "Database2"),
+ stringsAsFactors = FALSE)
> DBProject <- as.relation(DBProject)
> relation_table(DBProject)

<table>
<thead>
<tr>
<th>Task</th>
</tr>
</thead>
<tbody>
<tr>
<td>Database1</td>
</tr>
<tr>
<td>Database2</td>
</tr>
</tbody>
</table>

> relation_table(Completed %/% DBProject)

<table>
<thead>
<tr>
<th>Student</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fred</td>
</tr>
<tr>
<td>Sara</td>
</tr>
</tbody>
</table>

> ## division remainder
> relation_table(Completed %%% DBProject)

<table>
<thead>
<tr>
<th>Student</th>
<th>Task</th>
</tr>
</thead>
<tbody>
<tr>
<td>Eugene</td>
<td>Compiler1</td>
</tr>
<tr>
<td>Fred</td>
<td>Compiler1</td>
</tr>
<tr>
<td>Eugene</td>
<td>Database1</td>
</tr>
</tbody>
</table>

The (natural) join of two relations is their Cartesian product, restricted to the subset where the elements of the common attributes do match. The left/right/full outer join of two relations $X$ and $Y$ is the union of $X/Y/(X \text{ and } Y)$, and the inner join of $X$ and $Y$. The implementation of relation\_join() uses merge(), and so the left/right/full outer joins are obtained by setting all.x=all.y=all to TRUE in relation\_join(). The domains to be matched are specified using by. Alternatively, one can use the operators %>||%, %>=<%, %><=%, and %>=<=% for the natural join, left join, right join, and full outer join, respectively.
## Natural join

```
# relation_table(Employee %|><|% Dept)

<table>
<thead>
<tr>
<th>Name</th>
<th>EmpId</th>
<th>DeptName</th>
<th>Manager</th>
</tr>
</thead>
<tbody>
<tr>
<td>George</td>
<td>3401</td>
<td>Finance</td>
<td>George</td>
</tr>
<tr>
<td>Harry</td>
<td>3415</td>
<td>Finance</td>
<td>George</td>
</tr>
<tr>
<td>Harriet</td>
<td>2202</td>
<td>Sales</td>
<td>Harriet</td>
</tr>
<tr>
<td>Sally</td>
<td>2241</td>
<td>Sales</td>
<td>Harriet</td>
</tr>
</tbody>
</table>
```

## left (outer) join

```
# relation_table(Employee %=><% Dept)

<table>
<thead>
<tr>
<th>Name</th>
<th>EmpId</th>
<th>DeptName</th>
<th>Manager</th>
</tr>
</thead>
<tbody>
<tr>
<td>George</td>
<td>3401</td>
<td>Finance</td>
<td>George</td>
</tr>
<tr>
<td>Harry</td>
<td>3415</td>
<td>Finance</td>
<td>George</td>
</tr>
<tr>
<td>Harriet</td>
<td>2202</td>
<td>Sales</td>
<td>Harriet</td>
</tr>
<tr>
<td>Sally</td>
<td>2241</td>
<td>Sales</td>
<td>Harriet</td>
</tr>
<tr>
<td>John</td>
<td>3999</td>
<td>N.N.</td>
<td>NA</td>
</tr>
</tbody>
</table>
```

## right (outer) join

```
# relation_table(Employee %><=% Dept)

<table>
<thead>
<tr>
<th>Name</th>
<th>EmpId</th>
<th>DeptName</th>
<th>Manager</th>
</tr>
</thead>
<tbody>
<tr>
<td>NA</td>
<td>NA</td>
<td>Production</td>
<td>Charles</td>
</tr>
<tr>
<td>George</td>
<td>3401</td>
<td>Finance</td>
<td>George</td>
</tr>
<tr>
<td>Harry</td>
<td>3415</td>
<td>Finance</td>
<td>George</td>
</tr>
<tr>
<td>Harriet</td>
<td>2202</td>
<td>Sales</td>
<td>Harriet</td>
</tr>
<tr>
<td>Sally</td>
<td>2241</td>
<td>Sales</td>
<td>Harriet</td>
</tr>
</tbody>
</table>
```

## full outer join

```
# relation_table(Employee %=><=% Dept)

<table>
<thead>
<tr>
<th>Name</th>
<th>EmpId</th>
<th>DeptName</th>
<th>Manager</th>
</tr>
</thead>
<tbody>
<tr>
<td>NA</td>
<td>NA</td>
<td>Production</td>
<td>Charles</td>
</tr>
<tr>
<td>George</td>
<td>3401</td>
<td>Finance</td>
<td>George</td>
</tr>
<tr>
<td>Harry</td>
<td>3415</td>
<td>Finance</td>
<td>George</td>
</tr>
<tr>
<td>Harriet</td>
<td>2202</td>
<td>Sales</td>
<td>Harriet</td>
</tr>
<tr>
<td>Sally</td>
<td>2241</td>
<td>Sales</td>
<td>Harriet</td>
</tr>
<tr>
<td>John</td>
<td>3999</td>
<td>N.N.</td>
<td>NA</td>
</tr>
</tbody>
</table>
```

The left (right) semijoin of two relations $X$ and $Y$ is the join of these, projected to the attributes of $X$ ($Y$). Thus, it yields all tuples of $X$ ($Y$) participating in the join of $X$ and $Y$. Shortcuts for `relation_semijoin()` are `%|><%` and `%><|%` for left and right semijoin, respectively.

## semijoin

```
# relation_table(Employee %|><% Dept)

<table>
<thead>
<tr>
<th>Name</th>
<th>EmpId</th>
<th>DeptName</th>
</tr>
</thead>
<tbody>
<tr>
<td>George</td>
<td>3401</td>
<td>Finance</td>
</tr>
<tr>
<td>Harry</td>
<td>3415</td>
<td>Finance</td>
</tr>
<tr>
<td>Harriet</td>
<td>2202</td>
<td>Sales</td>
</tr>
<tr>
<td>Sally</td>
<td>2241</td>
<td>Sales</td>
</tr>
</tbody>
</table>
```

```
# relation_table(Employee %><|% Dept)

<table>
<thead>
<tr>
<th>DeptName</th>
<th>Manager</th>
</tr>
</thead>
<tbody>
<tr>
<td>Finance</td>
<td>George</td>
</tr>
<tr>
<td>Sales</td>
<td>Harriet</td>
</tr>
</tbody>
</table>
```
The left (right) antijoin of two relations $X$ and $Y$ is the complement of $X (Y)$ and the join of both, projected to the attributes of $X (Y)$. Thus, it yields all tuples of $X (Y)$ not participating in the join of $X$ and $Y$. Shortcuts for `relation_antijoin()` are `%|>%` and `%<|%` for left and right antijoin, respectively.

> ## antijoin
> relation_table(Employee %|>% Dept)

Name      EmpId DeptName
John     3999  N.N.

> relation_table(Employee %<|% Dept)

DeptName  Manager
Production Charles

3 Consensus Relations

Consensus relations “synthesize” the information in the elements of a relation ensemble into a single relation, often by minimizing a criterion function measuring how dissimilar consensus candidates are from the (elements of) the ensemble (the so-called “optimization approach”), typically of the form $L(R) = \sum w_b d(R_b, R)^p$, where $d$ is a suitable dissimilarity measure, $w_b$ is the case weight given to element $R_b$ of the ensemble, and $p \geq 1$. Such consensus relations are called “central relations” in Kégl [1965]. For $p = 1$, we obtain (generalized) medians; $p = 2$ gives (generalized) means (least squares consensus relations).

Consensus relations can be computed by `relation_consensus()`, which has the following built-in methods. Apart from Condorcet’s and the unrestricted Manhattan and Euclidean consensus methods, these are applicable to ensembles of endorelations only.

"Borda" the consensus method proposed by Borda [1781]. For each relation $R_b$ and object $x$, one determines the Borda/Kendall scores, i.e., the number of objects $y$ such that $yR_bx$ (“wins” in case of orderings). These are then aggregated across relations by weighted averaging. Finally, objects are ordered according to their aggregated scores.

"Copeland" the consensus method proposed by Copeland [1951] is similar to the Borda method, except that the Copeland scores are the number of objects $y$ such that $yR_bx$, minus the number of objects $y$ such that $xR_by$ (“defeats” in case of orderings).

"Condorcet" the consensus method proposed by Condorcet [1785], in fact minimizing the criterion function $L$ with $d$ as symmetric difference distance over all possible relations. In the case of endorelations, consensus is obtained by weighting voting, such that $xRy$ if the weighted number of times that $xR_by$ is no less than the weighted number of times that this is not the case. Even when aggregating linear orders, this can lead to intransitive consensus solutions (“effet Condorcet”).

"CS" the consensus method of Cook and Seiford [1978] which determines a linear order minimizing the criterion function $L$ with $d$ as generalized Cook-Seiford (ranking) distance and $p = 1$ via solving a linear sum assignment problem.

"SD/F" an exact solver for determining the consensus relation by minimizing the criterion function $L$ with $d$ as symmetric difference distance (“SD”) and $p = 1$ over a suitable class (“Family”) of endorelations as indicated by $F$, with values:

G general (crisp) endorelations.
A antisymmetric relations.
C complete relations.
equivalence relations: reflexive, symmetric, and transitive.
linear orders: complete, reflexive, antisymmetric, and transitive.
matches: complete and reflexive.
partial orders: reflexive, antisymmetric and transitive.
partial orders: reflexive, antisymmetric and transitive.
tournaments: complete, irreflexive and antisymmetric (i.e., complete and asymmetric).
weak orders (complete preorders, preferences, “orderings”): complete, reflexive and transitive.

These consensus relations are determined by reformulating the consensus problem as an integer program (for the relation incidences), see Hornik and Meyer (2007) for details. The solver employed can be specified via the control argument `solver`, with currently possible values "glpk", "lpSolve", "symphony", or "cplex" or a unique abbreviation thereof, specifying to use the solvers from packages `Rglpk` (Theussl and Hornik, 2008, default), `lpSolve` (Buttrey, 2005), `Rsymphony` (Harter, Hornik, and Theussl, 2008), or `Rcplex` (Bravo, 2008), respectively. Unless control option `sparse` is false, a sparse formulation of the binary program is used, which is typically more efficient.

For fitting equivalences and weak orders (cases E and W) it is possible to specify the number of classes $k$ using the control parameter `k`. For fitting weak orders, one can also specify the number of elements in the classes via control parameter `l`.

"CKS/F" an exact solver for determining the consensus relation by minimizing the criterion function $L$ with $d$ as Cook-Kress-Seiford distance (“CKS”) and $p = 1$ over a suitable class (“Family)) of endorelations as indicated by $F$, with available families and control parameters as for methods "SD/F".

"manhattan" the (unrestricted) median of the ensemble, minimizing $L$ with $d$ as Manhattan (symmetric difference) distance and $p = 1$ over all (possibly fuzzy) relations.

"euclidean" the (unrestricted) mean of the ensemble, minimizing $L$ with $d$ as Euclidean distance and $p = 2$ over all (possibly fuzzy) relations.

"majority" a generalized majority method for which the consensus relation contains of all tuples occurring with a relative frequency of more than 100$p$ percent (of 100 percent if $p = 1$). The fraction $p$ can be specified via the control parameter `p`. By default, $p = 1/2$ is used.

For the Condorcet, CS and SD methods, one can obtain a relation ensemble with all consensus relations by setting the control parameter `all` to TRUE.

In the following, we first show an example of computing a consensus equivalence (i.e., a consensus partition) of 30 felines repeating the classical analysis of Marcotorchino and Michaud (1982).

The data comprises 10 morphological and 4 behavioral variables, taken here as different classifications of the same 30 animals:

```r
> data("Felines")
> relations <- as.relation_ensemble(Felines)
```

Now fit an equivalence relation to this, and look at the classes:

```r
> E <- relation_consensus(relations, "SD/E")
> ids <- relation_class_ids(E)
> split(rownames(Felines), ids)
```
Next, we demonstrate the computation of consensus preferences, using an example from [Cook and Kress (1992), pp. 48ff]. The input data is a “preference matrix” of paired comparisons where entry \((i, j)\) is one iff object \(i\) is preferred to object \(j\) \((i \succ j)\). We set up the corresponding ‘\(<\)’ relation.

\[
\begin{pmatrix}
0 & 1 & 0 & 1 & 1 \\
1 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 1 & 1 \\
0 & 0 & 0 & 1 & 0 \\
0 & 0 & 0 & 0 & 0
\end{pmatrix}
\]

Next, we seek a linear consensus order:

\[
\begin{pmatrix}
1 & 0 & 0 & 0 & 0 \\
1 & 1 & 0 & 0 & 0 \\
1 & 1 & 0 & 1 & 1 \\
1 & 1 & 1 & 1 & 1 \\
1 & 1 & 0 & 0 & 1
\end{pmatrix}
\]

or perhaps more conveniently, the class ids sorted according to increasing preference:
Note, however, that this linear order is not unique; we can compute all consensus linear orders, and also produce a comparing plot (see Figure 2):

```r
> L <- relation_consensus(R, "SD/L", control = list(all = TRUE))
> print(L)

An ensemble of 2 relations of size 5 x 5.

> if(require("Rgraphviz")) plot(L)

Quite annoyingly, object c comes out first and last, respectively:

```r
> lapply(L, relation_class_ids)

[[1]]
a b c d e
5 4 1 2 3

[[2]]
a b c d e
4 3 5 1 2
```

Finally, we compute the closest weak order with at most 3 indifference classes:

```r
> W3 <- relation_consensus(R, "SD/W", control = list(k = 3))
> relation_incidence(W3)

Incidences:
a b c d e
a 1 1 1 0 0
b 1 1 1 0 0
c 0 0 1 0 0
d 1 1 1 1 1
e 1 1 1 1 1

> relation_class_ids(W3)

a b c d e
2 2 3 1 1
```

(Note again that this is not unique; there are 6 consensus weak orders with \(k = 3\) classes, which can be computed as above by adding \(all = TRUE\) to the \(control\) list.)

References


Figure 2: Hasse Diagram of all consensus relations (linear orders) for an example provided by Cook and Kress.


Index

-, [9]
%/%, [11]
%=><=%, [11]
%=><%, [11]
%<==%, [11]
%><%, [10]
%U%, [9]
%%, [11]
&., [9]

as.relation_ensemble, [9]
as.relation, [1]
relation_antijoin, [13]
relation_cartesian, [10]
relation_charfun, [9]
relation_complement, [9]
relation_consensus, [15]
relation_dissimilarity, [5]
relation_ensemble, [9]
relation_intersection, [9]
relation_is_binary, [3]
relation_is_ternary, [3]
relation_projection, [8]
relation_remainder, [14]
relation_selection, [8]
relation_semijoin, [12]
relation_union, [9]
relation, [1]