Chapter 11

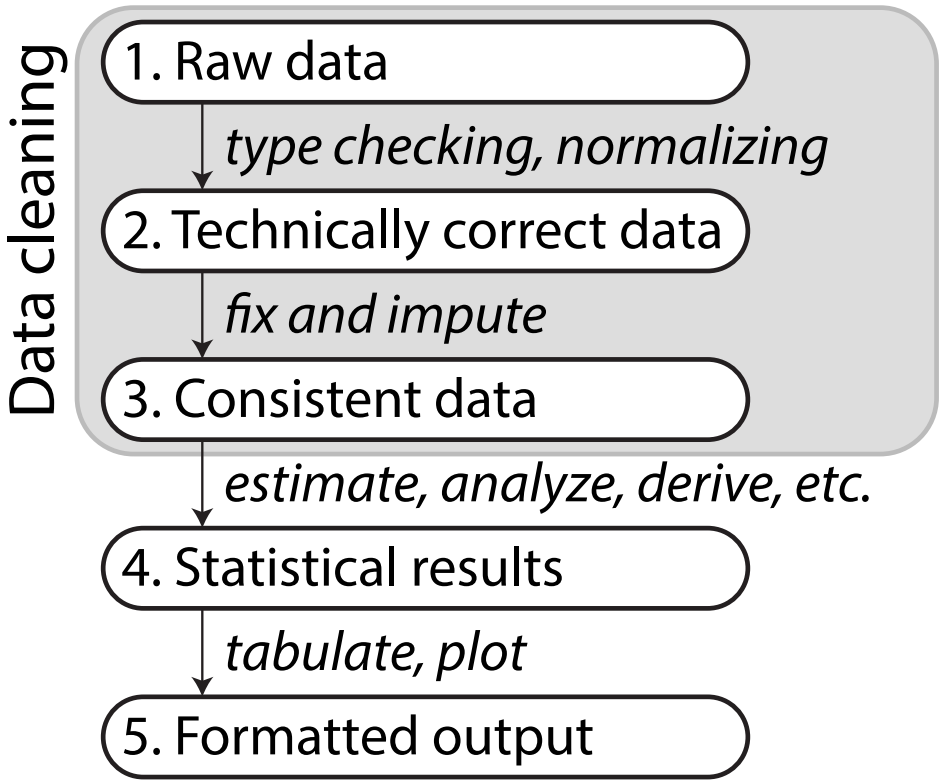
Data Cleaning

Data cleaning[1], or data preparation, is an essential part of statistical analysis. In fact, in practice it is often more time-consuming than the statistical analysis itself. Data cleaning may profoundly influence the statistical statements based on the data. Typical actions like imputation or outlier handling obviously influence the results of a statistical analyses. For this reason, data cleaning should be considered a statistical operation, to be performed in a reproducible manner. The R statistical environment provides a good environment for reproducible data cleaning since all cleaning actions can be scripted and therefore reproduced.

11.1 The five steps of statistical analysis

Statistical analysis can be viewed as the result of a number of value-increasing data processing steps.

[1]Content in this chapter is derived with permission from Statistics Netherlands at `http://cran.r-project.org/doc/contrib/de_Jonge+van_der_Loo-Introduction_to_data_cleaning_with_R.pdf`



Each box represents data in a certain state while each arrow represents the activities needed to get from one state to the other.

1. Raw Data The data "as is" may lack headers, contain wrong data types (e.g., numbers stored as strings), wrong category labels, unknown or unexpected character encoding and so on. Reading such files into an R `data.frame` directly is either difficult or impossible without some sort of preprocessing.

2. Technically correct data The data can be read into an R `data.frame`, with correct names, types and labels, without further trouble. However, that does not mean that the values are error-free or complete.

For example, an age variable may be reported negative, an under-aged person may be registered to possess a driver's license, or data may simply be missing. Such inconsistencies obviously depend on the subject matter that the data pertains to, and they should be ironed out before valid statistical inference from such data can be produced.

3. Consistent data The data is ready for statistical inference. It is the data that most statistical theories use as a starting point. Ideally, such theories can still be applied without taking previous data cleaning steps into

account. In practice however, data cleaning methods like imputation of missing values will influence statistical results and so must be accounted for in the following analyses or interpretation thereof.

4. Statistical results The results of the analysis have been produced and can be stored for reuse.

5. Formatted output The results in tables and figures ready to include in statistical reports or publications.

Best practice Store the input data for each stage (raw, technically correct, consistent, results, and formatted) separately for reuse. Each step between the stages may be performed by a separate R script for reproducibility.

11.2 R background review

11.2.1 Variable types

The most basic variable in R is a vector. An R vector is a sequence of values of the same type. All basic operations in R act on vectors (think of the element-wise arithmetic, for example). The basic types in R are as follows.

numeric Numeric data (approximations of the real numbers)

integer Integer data (whole numbers)

factor Categorical data (simple classifications, like gender)

ordered Ordinal data (ordered classifications, like educational level)

character Character data (strings)

raw Binary data (rarely used)

All basic operations in R work element-wise on vectors where the shortest argument is recycled if necessary. Why does the following code work the way it does?

```
# vectors have variables of _one_ type
c(1, 2, "three")
```

```
## [1] "1"     "2"     "three"
```

```
# shorter arguments are recycled
(1:3) * 2
```

```
## [1] 2 4 6
(1:4) * c(1, 2)
## [1] 1 4 3 8
# warning! (why?)
(1:4) * (1:3)
## Warning in (1:4) * (1:3): longer object length is not a multiple of shorter object length
## [1] 1 4 9 4
```

11.2.2 Special values and value-checking functions

Below are the definitions and some illustrations of the special values `NA`, `NULL`, ±`Inf`, and `NaN`.

- `NA` Stands for "not available". `NA` is a placeholder for a missing value. All basic operations in R handle NA without crashing and mostly return NA as an answer whenever one of the input arguments is NA. If you understand NA, you should be able to predict the result of the following R statements.

```
NA + 1
sum(c(NA, 1, 2))
median(c(NA, 1, 2, 3), na.rm = TRUE)
length(c(NA, 2, 3, 4))
3 == NA
NA == NA
TRUE | NA
# use is.na() to detect NAs
is.na(c(1, NA, 3))
```

- `NULL` Think of `NULL` as the empty set from mathematics; it has no class (its class is `NULL`) and has length 0 so it does not take up any space in a vector.

```
length(c(1, 2, NULL, 4))
sum(c(1, 2, NULL, 4))
x <- NULL
length(x)
c(x, 2)
# use is.null() to detect NULL variables
is.null(x)
```

- `Inf` Stands for "infinity" and only applies to vectors of class numeric (not integer). Technically, `Inf` is a valid numeric that results from calculations like division of a number by zero. Since `Inf` is a numeric, operations be-

tween `Inf` and a finite numeric are well-defined and comparison operators work as expected.

```
pi/0
2 * Inf
Inf - 1e+10
Inf + Inf
3 < -Inf
Inf == Inf
# use is.infinite() to detect Inf variables
is.infinite(-Inf)
```

- `NaN` Stands for "not a number". This is generally the result of a calculation of which the result is unknown, but it is surely not a number. In particular operations like 0/0, `Inf - Inf` and `Inf/Inf` result in `NaN`. Technically, `NaN` is of class numeric, which may seem odd since it is used to indicate that something is not numeric. Computations involving numbers and `NaN` always result in `NaN`.

```
NaN + 1
exp(NaN)
# use is.nan() to detect NULL variables
is.nan(0/0)
```

Note that `is.finite()` checks a numeric vector for the occurrence of any non-numerical or special values.

```
is.finite(c(1, NA, 2, Inf, 3, -Inf, 4, NULL, 5, NaN, 6))
```

```
##  [1]  TRUE FALSE  TRUE FALSE  TRUE FALSE  TRUE  TRUE FALSE  TRUE
```

11.3 From raw to technically correct data

11.3.1 Technically correct data

Limiting ourselves to "rectangular" data sets read from a text-based format, **technically correct** data in R

1. is stored in a `data.frame` with suitable columns names, and
2. each column of the `data.frame` is of the R type that adequately represents the value domain.

The second demand implies that numeric data should be stored as `numeric` or `integer`, textual data should be stored as `character` and categorical data should be stored as a `factor` or `ordered` vector, with the appropriate levels.

Best practice Whenever you need to read data from a foreign file format, like a spreadsheet or proprietary statistical software that uses undisclosed file formats, make that software responsible for exporting the data to an open format that can be read by R.

11.3.2 Reading text data into an R data.frame

In the following, we assume that the text-files we are reading contain data of at most one unit per line. The number of attributes, their format and separation symbols in lines containing data may differ over the lines. This includes files in fixed-width or csv-like format, but excludes XML-like storage formats.

Reading text

`read.table()` and similar functions below will read a text file and return a `data.frame`.

Best practice. A freshly read `data.frame` should always be inspected with functions like `head()`, `str()`, and `summary()`.

The `read.table()` function is the most flexible function to read tabular data that is stored in a textual format. The other read-functions below all eventually use `read.table()` with some fixed parameters and possibly after some preprocessing. Specifically

- `read.csv()` for comma separated values with period as decimal separator.
- `read.csv2()` for semicolon separated values with comma as decimal separator.
- `read.delim()` tab-delimited files with period as decimal separator.
- `read.delim2()` tab-delimited files with comma as decimal separator.
- `read.fwf()` data with a predetermined number of bytes per column.

Additional optional arguments include:

Argument	Description
`header`	Does the first line contain column names?
`col.names`	`character` vector with column names.
`na.string`	Which strings should be considered `NA`?
`colClasses`	`character` vector with the types of columns. Will coerce the columns to the specified types.
`stringsAsFactors`	If `TRUE`, converts all `character` vectors into `factor` vectors.
`sep`	Field separator.

Except for `read.table()` and `read.fwf()`, each of the above functions assumes by default that the first line in the text file contains column headers. The following demonstrates this on the following text file.

```
21,6.0
42,5.9
18,5.7*
21,NA
```

Read the file with defaults, then specifying necessary options.

```
fn.data <- "http://statacumen.com/teach/ADA2/ADA2_notes_Ch18_unnamed.txt"
# first line is erroneously interpreted as column names
person <- read.csv(fn.data)
person
```

```
##   X21 X6.0
## 1  42  5.9
## 2  18 5.7*
## 3  21 <NA>
```

```
# instead, use header = FALSE and specify the column names
person <- read.csv(file = fn.data
                   , header = FALSE
                   , col.names = c("age", "height")
                    )
person
```

```
##   age height
## 1  21    6.0
## 2  42    5.9
## 3  18   5.7*
## 4  21   <NA>
```

If `colClasses` is not specified by the user, `read.table()` will try to determine the column types. Although this may seem convenient, it is noticeably slower for larger files (say, larger than a few MiB) and it may yield unexpected results. For example, in the above script, one of the rows contains a malformed numerical

variable (`5.7*`), causing R to interpret the whole column as a text variable. Moreover, by default text variables are converted to factor, so we are now stuck with a height variable expressed as levels in a categorical variable:

```
str(person)
```

```
## 'data.frame': 4 obs. of  2 variables:
##  $ age   : int  21 42 18 21
##  $ height: Factor w/ 3 levels "5.7*","5.9","6.0": 3 2 1 NA
```

As an alternative, columns can be read in as character by setting `stringsAsFactors`. Next, one of the `as.`-functions can be applied to convert to the desired type, as shown below.

```
person <- read.csv(file = fn.data
                   , header = FALSE
                   , col.names = c("age", "height")
                   , stringsAsFactors = FALSE)
person
```

```
##   age height
## 1  21    6.0
## 2  42    5.9
## 3  18   5.7*
## 4  21   <NA>
```

```
person$height <- as.numeric(person$height)
```

```
## Warning:  NAs introduced by coercion
```

```
person
```

```
##   age height
## 1  21    6.0
## 2  42    5.9
## 3  18     NA
## 4  21     NA
```

Now, everything is read in and the `height` column is translated to `numeric`, with the exception of the row containing `5.7*`. Moreover, since we now get a warning instead of an error, a script containing this statement will continue to run, albeit with less data to analyse than it was supposed to. It is of course up to the programmer to check for these extra `NA`'s and handle them appropriately.

11.4 Type conversion

Converting a variable from one type to another is called coercion. The reader is probably familiar with R's basic coercion functions, but as a reference they are listed here.

```
as.numeric
as.integer
as.character
as.logical
as.factor
as.ordered
```

Each of these functions takes an R object and tries to convert it to the class specified behind the "`as.`". By default, values that cannot be converted to the specified type will be converted to a `NA` value while a warning is issued.

```
as.numeric(c("7", "7*", "7.0", "7,0"))
```

```
## Warning:  NAs introduced by coercion
## [1]  7 NA  7 NA
```

In the remainder of this section we introduce R's typing and storage system and explain the difference between R types and classes. After that we discuss date conversion.

11.4.1 Introduction to R's typing system

Everything in R is an object. An object is a container of data endowed with a label describing the data. Objects can be created, destroyed, or overwritten on-the-fly by the user. The function class returns the class label of an R object.

```
class(c("abc", "def"))
```

```
## [1] "character"
```

```
class(1:10)
```

```
## [1] "integer"
```

```
class(c(pi, exp(1)))
```

```
## [1] "numeric"
```

```
class(factor(c("abc", "def")))
```

```
## [1] "factor"
```

```
# all columns in a data.frame
sapply(dalton.df, class)
```

```
##        name       birth       death
## "character"   "numeric"   "numeric"
```

For the user of R these class labels are usually enough to handle R objects in R scripts. Under the hood, the basic R objects are stored as C structures as C is the language in which R itself has been written. The type of C structure that is used to store a basic type can be found with the typeof function. Compare the results below with those in the previous code snippet.

```
typeof(c("abc", "def"))
## [1] "character"
typeof(1:10)
## [1] "integer"
typeof(c(pi, exp(1)))
## [1] "double"
typeof(factor(c("abc", "def")))
## [1] "integer"
```

Note that the type of an R object of class `numeric` is `double`. The term `double` refers to double precision, which is a standard way for lower-level computer languages such as C to store approximations of real numbers. Also, the type of an object of class `factor` is `integer`. The reason is that R saves memory (and computational time!) by storing factor values as integers, while a translation table between factor and integers are kept in memory. Normally, a user should not have to worry about these subtleties, but there are exceptions (the homework includes an example of the subtleties).

In short, one may regard the class of an object as the object's type from the user's point of view while the type of an object is the way R looks at the object. It is important to realize that R's coercion functions are fundamentally functions that change the underlying type of an object and that class changes are a consequence of the type changes.

11.4.2 Recoding factors

In R, the value of categorical variables is stored in factor variables. A factor is an integer vector endowed with a table specifying what integer value corresponds to what level. The values in this translation table can be requested with the levels function.

```
f <- factor(c("a", "b", "a", "a", "c"))
f
## [1] a b a a c
## Levels: a b c
levels(f)
## [1] "a" "b" "c"
as.numeric(f)
```

```
## [1] 1 2 1 1 3
```

You may need to create a translation table by hand. For example, suppose we read in a vector where `1` stands for `male`, `2` stands for `female` and `0` stands for `unknown`. Conversion to a factor variable can be done as in the example below.

```
# example:
gender <- c(2, 1, 1, 2, 0, 1, 1)
gender
```

```
## [1] 2 1 1 2 0 1 1
```

```
# recoding table, stored in a simple vector
recode <- c(male = 1, female = 2)
recode
```

```
##   male female
##      1      2
```

```
gender <- factor(gender, levels = recode, labels = names(recode))
gender
```

```
## [1] female male   male   female <NA>   male   male
## Levels: male female
```

Note that we do not explicitly need to set NA as a label. Every integer value that is encountered in the first argument, but not in the levels argument will be regarded missing.

Levels in a factor variable have no natural ordering. However in multivariate (regression) analyses it can be beneficial to fix one of the levels as the reference level. R's standard multivariate routines (lm, glm) use the first level as reference level. The relevel function allows you to determine which level comes first.

```
gender <- relevel(gender, ref = "female")
gender
```

```
## [1] female male   male   female <NA>   male   male
## Levels: female male
```

Levels can also be reordered, depending on the mean value of another variable, for example:

```
age <- c(27, 52, 65, 34, 89, 45, 68)
gender <- reorder(gender, age)
gender
```

```
## [1] female male   male   female <NA>   male   male
## attr(,"scores")
## female   male
##   30.5   57.5
## Levels: female male
```

Here, the means are added as a named vector attribute to gender. It can be removed by setting that attribute to NULL.

```
attr(gender, "scores") <- NULL
gender
## [1] female male   male   female <NA>   male   male
## Levels: female male
```

11.4.3 Converting dates

The base R installation has three types of objects to store a time instance: `Date`, `POSIXlt`, and `POSIXct`. The `Date` object can only be used to store dates, the other two store date and/or time. Here, we focus on converting text to `POSIXct` objects since this is the most portable way to store such information.

Under the hood, a `POSIXct` object stores the number of seconds that have passed since January 1, 1970 00:00. Such a storage format facilitates the calculation of durations by subtraction of two `POSIXct` objects.

When a `POSIXct` object is printed, R shows it in a human-readable calender format. For example, the command `Sys.time()` returns the system time provided by the operating system in `POSIXct` format.

```
current_time <- Sys.time()
class(current_time)
## [1] "POSIXct" "POSIXt"
current_time
## [1] "2015-08-29 16:20:25 MDT"
```

Here, `Sys.time()` uses the time zone that is stored in the locale settings of the machine running R.

Converting from a calender time to POSIXct and back is not entirely trivial, since there are many idiosyncrasies to handle in calender systems. These include leap days, leap seconds, daylight saving times, time zones and so on. Converting from text to `POSIXct` is further complicated by the many textual conventions of time/date denotation. For example, both 28 September 1976 and 1976/09/28 indicate the same day of the same year. Moreover, the name of the month (or weekday) is language-dependent, where the language is again defined in the operating system's locale settings.

The `lubridate` package contains a number of functions facilitating the conversion of text to `POSIXct` dates. As an example, consider the following code.

```
library(lubridate)
dates <- c("15/02/2013"
         , "15 Feb 13"
         , "It happened on 15 02 '13")
dmy(dates)
```

```
## [1] "2013-02-15 UTC" "2013-02-15 UTC" "2013-02-15 UTC"
```

Here, the function `dmy` assumes that dates are denoted in the order day-month-year and tries to extract valid dates. Note that the code above will only work properly in locale settings where the name of the second month is abbreviated to Feb. This holds for English or Dutch locales, but fails for example in a French locale (Fevrier).

There are similar functions for all permutations of `d`, `m`, and `y`. Explicitly, all of the following functions exist.

```
dmy()
dym()
mdy()
myd()
ydm()
ymd()
```

So once it is known in what order days, months and years are denoted, extraction is very easy.

Note It is not uncommon to indicate years with two numbers, leaving out the indication of century. Recently in R, 00-69 was interpreted as 2000-2069 and 70-99 as 1970-1999; this behaviour is according to the 2008 POSIX standard, but one should expect that this interpretation changes over time. Currently all are now 2000-2099.

```
dmy("01 01 68")
```

```
## [1] "2068-01-01 UTC"
```

```
dmy("01 01 69")
```

```
## [1] "2069-01-01 UTC"
```

```
dmy("01 01 90")
```

```
## [1] "2090-01-01 UTC"
```

```
dmy("01 01 00")
```

```
## [1] "2000-01-01 UTC"
```

It should be noted that `lubridate` (as well as R's base functionality) is only

capable of converting certain standard notations. For example, the following notation does not convert.

```
dmy("15 Febr. 2013")
```

```
## Warning:  All formats failed to parse.  No formats found.
## [1] NA
```

The standard notations that can be recognized by R, either using `lubridate` or R's built-in functionality are shown below. The complete list can be found by typing `?strptime` in the R console. These are the day, month, and year formats recognized by R.

Code	Description	Example
`%a`	Abbreviated weekday name in the current locale.	`Mon`
`%A`	Full weekday name in the current locale.	`Monday`
`%b`	Abbreviated month name in the current locale.	`Sep`
`%B`	Full month name in the current locale.	`September`
`%m`	Month number (01-12)	`09`
`%d`	Day of the month as decimal number (01-31).	`28`
`%y`	Year without century (00-99)	`13`
`%Y`	Year including century.	`2013`

Here, the names of (abbreviated) week or month names that are sought for in the text depend on the locale settings of the machine that is running R.

If you know the textual format that is used to describe a date in the input, you may want to use R's core functionality to convert from text to `POSIXct`. This can be done with the `as.POSIXct` function. It takes as arguments a character vector with time/date strings and a string describing the format.

```
dates <- c("15-9-2009", "16-07-2008", "17 12-2007", "29-02-2011")
as.POSIXct(dates, format = "%d-%m-%Y")
```

```
## [1] "2009-09-15 MDT" "2008-07-16 MDT" NA
## [4] NA
```

In the format string, date and time fields are indicated by a letter preceded by a percent sign (`%`). Basically, such a `%`-code tells R to look for a range of substrings. For example, the `%d` indicator makes R look for numbers 1-31 where precursor zeros are allowed, so 01, 02, ..., 31 are recognized as well. Strings that are not in the exact format specified by the format argument (like the third

string in the above example) will not be converted by `as.POSIXct`. Impossible dates, such as the leap day in the fourth date above are also not converted.

Finally, to convert dates from `POSIXct` back to `character`, one may use the format function that comes with base R. It accepts a `POSIXct` date/time object and an output format string.

```
mybirth <- dmy("28 Sep 1976")
format(mybirth, format = "I was born on %B %d, %Y")
```

```
## [1] "I was born on September 28, 1976"
```

11.5 From technically correct data to consistent data

Consistent data are technically correct data that are fit for statistical analysis. They are data in which missing values, special values, (obvious) errors and outliers are either removed, corrected, or imputed. The data are consistent with constraints based on real-world knowledge about the subject that the data describe.

Consistency can be understood to include **in-record consistency**, meaning that no contradictory information is stored in a single record, and **cross-record consistency**, meaning that statistical summaries of different variables do not conflict with each other. Finally, one can include cross-dataset consistency, meaning that the dataset that is currently analyzed is consistent with other datasets pertaining to the same subject matter. In this tutorial *we mainly focus on methods dealing with in-record consistency*, with the exception of outlier handling which can be considered a cross-record consistency issue.

The process towards consistent data always involves the following three steps.

- **Detection** *of an inconsistency.* That is, one establishes which constraints are violated. For example, an age variable is constrained to non-negative values.

- **Selection** *of the field or fields causing the inconsistency.* This is trivial in the case of a univariate demand as in the previous step, but may be more cumbersome when cross-variable relations are expected to hold. For example the marital status of a child must be unmarried. In the case of a violation it is not immediately clear whether age, marital status, or both are wrong.

- **Correction** *of the fields that are deemed erroneous by the selection method.* This may be done through deterministic (model-based) or stochastic methods.

For many data correction methods these steps are not necessarily neatly separated.

First, we introduce a number of techniques dedicated to the detection of errors and the selection of erroneous fields. If the field selection procedure is performed separately from the error detection procedure, it is generally referred to as **error localization**. Next, we describe techniques that implement correction methods based on "direct rules" or "deductive correction". In these techniques, erroneous values are replaced by better ones by directly deriving them from other values in the same record. Finally, we give an overview of some commonly used imputation techniques that are available in R.

11.5.1 Detection and localization of errors

This section details a number of techniques to detect univariate and multivariate constraint violations.

Missing values

A missing value, represented by `NA` in R, is a placeholder for a datum of which the type is known but its value isn't. Therefore, it is impossible to perform statistical analysis on data where one or more values in the data are missing. One may choose to either omit elements from a dataset that contain missing

values or to impute a value, but missingness is something to be dealt with prior to any analysis.

In practice, analysts, but also commonly used numerical software may confuse a missing value with a default value or category. For instance, in Excel 2010, the result of adding the contents of a field containing the number 1 with an empty field results in 1. This behaviour is most definitely unwanted since Excel silently imputes "0" where it should have said something along the lines of "unable to compute". It should be up to the analyst to decide how empty values are handled, since a default imputation may yield unexpected or erroneous results for reasons that are hard to trace.

Another commonly encountered mistake is to confuse an `NA` in categorical data with the category *unknown*. If *unknown* is indeed a category, it should be added as a factor level so it can be appropriately analyzed. Consider as an example a categorical variable representing place of birth. Here, the category *unknown* means that we have no knowledge about where a person is born. In contrast, `NA` indicates that we have no information to determine whether the birth place is known or not.

The behaviour of R's core functionality is completely consistent with the idea that the analyst must decide what to do with missing data. A common choice, namely "leave out records with missing data" is supported by many base functions through the `na.rm` option.

```
age <- c(23, 16, NA)
mean(age)
## [1] NA
mean(age, na.rm = TRUE)
## [1] 19.5
```

Functions such as `sum()`, `prod()`, `quantile()`, `sd()`, and so on all have this option. Functions implementing bivariate statistics such as `cor()` and `cov()` offer options to include complete or pairwise complete values.

Besides the `is.na()` function, that was already mentioned previously, R comes with a few other functions facilitating `NA` handling. The `complete.cases()` function detects rows in a `data.frame` that do not contain any missing value.

Recall the person data set example from earlier.

```
print(person)
```

```
##   age height
## 1  21    6.0
## 2  42    5.9
## 3  18     NA
## 4  21     NA
```

```
complete.cases(person)
```

```
## [1]  TRUE  TRUE FALSE FALSE
```

The resulting logical can be used to remove incomplete records from the `data.frame`. Alternatively the `na.omit()` function, does the same.

```
persons_complete <- na.omit(person)
persons_complete
```

```
##   age height
## 1  21    6.0
## 2  42    5.9
```

```
na.action(persons_complete)
```

```
## 3 4
## 3 4
## attr(,"class")
## [1] "omit"
```

The result of the `na.omit()` function is a `data.frame` where incomplete rows have been deleted. The `row.names` of the removed records are stored in an attribute called `na.action`.

Note. It may happen that a missing value in a data set means 0 or Not applicable. If that is the case, it should be explicitly imputed with that value, because it is not unknown, but was coded as empty.

Special values

As explained previously, numeric variables are endowed with several formalized special values including $\pm$`Inf`, `NA`, and `NaN`. Calculations involving special values often result in special values, and since a statistical statement about a real-world phenomenon should never include a special value, it is desirable to handle special values prior to analysis. For numeric variables, special values indicate values

that are not an element of the mathematical set of real numbers. The function `is.finite()` determines which values are "regular" values.

```
is.finite(c(1, Inf, NaN, NA))
```

```
## [1]  TRUE FALSE FALSE FALSE
```

This function accepts vectorial input. With little effort we can write a function that may be used to check every numerical column in a `data.frame`.

```
f.is.special <- function(x) {
  if (is.numeric(x)) {
    return(!is.finite(x))
  } else {
    return(is.na(x))
  }
}
person
```

```
##   age height
## 1  21    6.0
## 2  42    5.9
## 3  18     NA
## 4  21     NA
```

```
sapply(person, f.is.special)
```

```
##        age height
## [1,] FALSE  FALSE
## [2,] FALSE  FALSE
## [3,] FALSE   TRUE
## [4,] FALSE   TRUE
```

Here, the `f.is.special()` function is applied to each column of person using `sapply()`. `f.is.special()` checks its input vector for numerical special values if the type is `numeric`, otherwise it only checks for `NA`.

11.5.2 Edit rules for detecting obvious inconsistencies

An obvious inconsistency occurs when a record contains a value or combination of values that cannot correspond to a real-world situation. For example, a person's age cannot be negative, a man cannot be pregnant and an under-aged person cannot possess a drivers license.

Such knowledge can be expressed as *rules* or constraints. In data editing

literature these rules are referred to as *edit rules* or *edits*, in short. Checking for obvious inconsistencies can be done straightforwardly in R using logical indices and recycling. For example, to check which elements of `x` obey the rule '`x` must be non negative' one simply uses the following.

```
x_nonnegative <- (x >= 0)
```

However, as the number of variables increases, the number of rules may increase rapidly and it may be beneficial to manage the rules separate from the data. Moreover, since multivariate rules may be interconnected by common variables, deciding which variable or variables in a record cause an inconsistency may not be straightforward.

The `editrules` package allows one to define rules on categorical, numerical or mixed-type data sets which each record must obey. Furthermore, `editrules` can check which rules are obeyed or not and allows one to find the minimal set of variables to adapt so that all rules can be obeyed. The package also implements a number of basic rule operations allowing users to test rule sets for contradictions and certain redundancies.

As an example, we will work with a small file containing the following data.

```
age,agegroup,height,status,yearsmarried
21,adult,6.0,single,-1
2,child,3,married, 0
18,adult,5.7,married, 20
221,elderly, 5,widowed, 2
34,child, -7,married, 3
```

We read this data into a variable called people and define some restrictions on age using `editset()`.

```
fn.data <- "http://statacumen.com/teach/ADA2/ADA2_notes_Ch18_people.txt"
people <- read.csv(fn.data)

people
##   age agegroup height  status yearsmarried
## 1  21    adult    6.0  single          -1
## 2   2    child    3.0 married           0
## 3  18    adult    5.7 married          20
## 4 221  elderly    5.0 widowed           2
## 5  34    child   -7.0 married           3
library(editrules)
E <- editset(c("age >=0", "age <= 150"))
```

```
E
```

```
##
## Edit set:
## num1 : 0 <= age
## num2 : age <= 150
```

The `editset()` function parses the textual rules and stores them in an `editset` object. Each rule is assigned a name according to it's type (`numeric`, `categorical`, or `mixed`) and a number. The data can be checked against these rules with the `violatedEdits()` function. Record 4 contains an error according to one of the rules: an `age` of 221 is not allowed.

```
violatedEdits(E, people)
```

```
##       edit
## record  num1  num2
##      1 FALSE FALSE
##      2 FALSE FALSE
##      3 FALSE FALSE
##      4 FALSE  TRUE
##      5 FALSE FALSE
```

`violatedEdits()` returns a `logical` array indicating for each row of the data, which rules are violated. The number and type of rules applying to a data set usually quickly grow with the number of variables. With `editrules`, users may read rules, specified in a limited R-syntax, directly from a text file using the `editfile()` function. As an example consider the contents of the following text file (note, you can't include braces in your `if()` statement).

```
# numerical rules
age >= 0
height > 0
age <= 150
age > yearsmarried

# categorical rules
status %in% c("married", "single", "widowed")
agegroup %in% c("child", "adult", "elderly")
if ( status == "married" )  agegroup %in% c("adult","elderly")

# mixed rules
if ( status %in% c("married","widowed"))  age - yearsmarried >= 17
if ( age < 18 )               agegroup == "child"
if ( age >= 18 && age <65 )   agegroup == "adult"
if ( age >= 65 )              agegroup == "elderly"
```

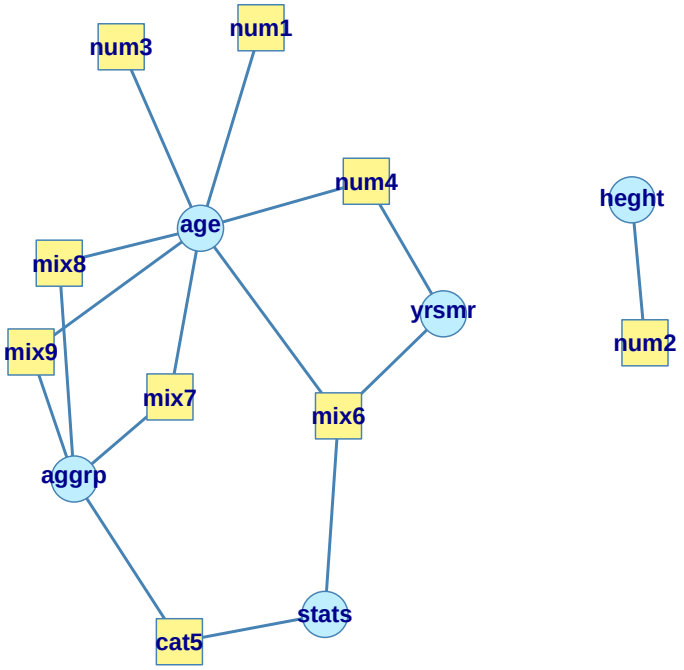
There are rules pertaining to purely numerical, purely categorical and rules pertaining to both data types. Moreover, there are univariate as well as multivariate rules. Comments are written behind the usual # character. The rule set can be read as follows.

```
fn.data <- "http://statacumen.com/teach/ADA2/ADA2_notes_Ch18_edits.txt"
E <- editfile(fn.data)
E
```

```
##
## Data model:
## dat6 : agegroup %in% c('adult', 'child', 'elderly')
## dat7 : status %in% c('married', 'single', 'widowed')
##
## Edit set:
## num1 : 0 <= age
## num2 : 0 < height
## num3 : age <= 150
## num4 : yearsmarried < age
## cat5 : if( agegroup == 'child' ) status != 'married'
## mix6 : if( age < yearsmarried + 17 ) !( status %in% c('married', 'widowed') )
## mix7 : if( age < 18 ) !( agegroup %in% c('adult', 'elderly') )
## mix8 : if( 18 <= age & age < 65 ) !( agegroup %in% c('child', 'elderly') )
## mix9 : if( 65 <= age ) !( agegroup %in% c('adult', 'child') )
```

Since rules may pertain to multiple variables, and variables may occur in several rules (e.g., the `age` variable in the current example), there is a dependency between rules and variables. It can be informative to show these dependencies in a graph using the plot function. Below the graph plot shows the interconnection of restrictions. Blue circles represent variables and yellow boxes represent restrictions. The lines indicate which restrictions pertain to what variables.

```
op <- par(no.readonly = TRUE)          # save plot settings
par(mfrow=c(1,1), mar = c(0,0,0,0))
plot(E)
par(op)                                # restore plot settings
```

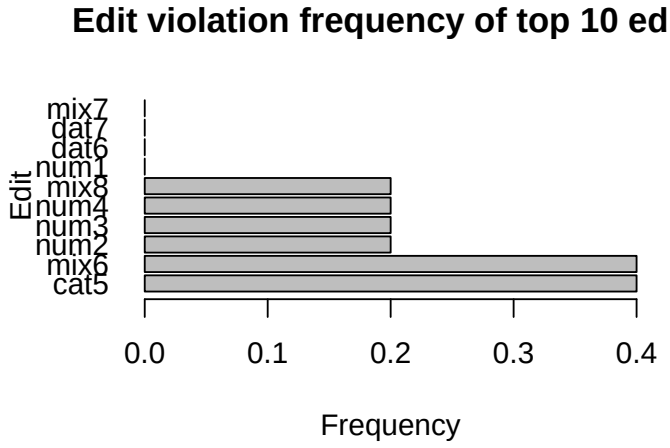


As the number of rules grows, looking at the full array produced by `violatedEdits(` becomes cumbersome. For this reason, `editrules` offers methods to summarize or visualize the result.

```
ve <- violatedEdits(E, people)
summary(ve)
```

```
## Edit violations, 5 observations, 0 completely missing (0%):
##
##  editname freq rel
##      cat5    2 40%
##      mix6    2 40%
##      num2    1 20%
##      num3    1 20%
##      num4    1 20%
##      mix8    1 20%
##
## Edit violations per record:
##
##  errors freq rel
##       0    1 20%
##       1    1 20%
##       2    2 40%
##       3    1 20%
```

```
plot(ve)
```



Here, the edit labeled `cat5` is violated by two records (20% of all records). Violated edits are sorted from most to least often violated. The plot visualizes the same information.

Error localization

The interconnectivity of edits is what makes error localization difficult. For example, the graph above shows that a record violating edit `num4` may contain an error in `age` and/or `yrsmr` (years married). Suppose that we alter `age` so that `num4` is not violated anymore. We then run the risk of violating up to *six* other edits containing `age`.

If we have no other information available but the edit violations, it makes sense to minimize the number of fields being altered. This principle, commonly

referred to as the principle of Fellegi and Holt, is based on the idea that errors occur relatively few times and when they do, they occur randomly across variables. Over the years several algorithms have been developed to solve this minimization problem of which two have been implemented in `editrules`. The `localizeErrors()` function provides access to this functionality.

As an example we take two records from the `people` dataset from the previous subsection.

```
id <- c(2, 5)
people[id, ]
```

```
##   age agegroup height  status yearsmarried
## 2   2    child      3 married            0
## 5  34    child     -7 married            3
```

```
violatedEdits(E, people[id, ])
```

```
##       edit
## record  num1  num2  num3  num4  dat6  dat7 cat5  mix6  mix7  mix8
##      2 FALSE FALSE FALSE FALSE FALSE FALSE TRUE  TRUE FALSE FALSE
##      5 FALSE  TRUE FALSE FALSE FALSE FALSE TRUE FALSE FALSE  TRUE
##       edit
## record  mix9
##      2 FALSE
##      5 FALSE
```

Record 2 violates `mix6` while record 5 violates edits `num2`, `cat5`, and `mix8`. We use `localizeErrors()`, with a mixed-integer programming (MIP) approach to find the minimal set of variables to adapt.

```
le <- localizeErrors(E, people[id, ], method = "mip")
le$adapt
```

```
##     age agegroup height status yearsmarried
## 1 FALSE    FALSE  FALSE   TRUE        FALSE
## 2 FALSE     TRUE   TRUE  FALSE        FALSE
```

Here, the `le` object contains some processing metadata and a logical array labeled `adapt` which indicates the minimal set of variables to be altered in each record. It can be used in correction and imputation procedures for filling in valid values. Such procedures are not part of `editrules`, but for demonstration purposes we will manually fill in new values showing that the solution computed by `localizeErrors()` indeed allows one to repair records to full compliance with all edit rules.

```
people[2, "status"]   <- "single"
people[5, "height"]   <- 7
people[5, "agegroup"] <- "adult"
summary(violatedEdits(E, people[id, ]))
```

```
## No violations detected, 0 checks evaluated to NA
## NULL
```

The behaviour of `localizeErrors()` can be tuned with various options. It is possible to supply a confidence weight for each variable allowing for fine grained control on which values should be adapted. It is also possible to choose a branch-and-bound based solver (instead of the MIP solver used here), which is typically slower but allows for more control.

11.5.3 Correction

Correction methods aim to fix inconsistent observations by altering invalid values in a record based on information from valid values. Depending on the method this is either a single-step procedure or a two-step procedure where first, an error localization method is used to empty certain fields, followed by an imputation step.

In some cases, the cause of errors in data can be determined with enough certainty so that the solution is almost automatically known. In recent years, several such methods have been developed and implemented in the `deducorrect` package.

For the purposes of ADA1, we will manually correct errors, either by replacing values or by excluding observations.