Chapter 3
Descriptive statistics

Any 21st century linguist will be required to read about and understand mathematical models as well as understand statistical methods of analysis. Whether you are interested in Shakespearean meter, the sociolinguistic perception of identity, Hindi verb agreement violations, or the perception of vowel duration, the use of math as a tool of analysis is already here and its prevalence will only grow over the next few decades. If you're not prepared to read articles involving the term *Bayesian*, or *(p<.01)*, k-*means clustering*, *confidence interval*, *latent semantic analysis*, *bimodal and unimodal distributions*, N-*grams*, etc, then you will be but a shy guest at the feast of linguistics.
(<http://thelousylinguist.blogspot.com/2010/01/why-linguists-should-study-math.html>)

In this chapter, I will explain how you obtain descriptive results. In section 3.1, I will discuss univariate statistics, i.e. statistics that summarize the distribution of one variable, of one vector, of one factor. Section 3.2 then is concerned with bivariate statistics, statistics that characterize the relation of two variables, two vectors, two factors to each other. Both sections also introduce ways of representing the data graphically; many additional graphs will be illustrated in Chapters 4 and 5.

1. Univariate statistics

1.1. Frequency data

The probably simplest way to describe the distribution of data points are frequency tables, i.e. lists that state how often each individual outcome was observed. In R, generating a frequency table is extremely easy. Let us look at a psycholinguistic example. Imagine you extracted all occurrences of the disfluencies *uh*, *uhm*, and 'silence' and noted for each disfluency whether it was produced by a male or a female speaker, whether it was produced in a monolog or in a dialog, and how long in milliseconds the disfluency lasted. First, we load these data from the file <_inputfiles/03-1_uh(m).csv>.

```
> UHM<-read.delim(file.choose())¶
> str(UHM)¶
'data.frame':   1000 obs. of  5 variables:
 $ CASE  : int  1 2 3 4 5 6 7 8 9 10 ...
 $ SEX   : Factor w/ 2 levels "female","male": 2 1 1 1 2  ...
 $ FILLER: Factor w/ 3 levels "silence","uh",..: 3 1 1 3  ...
 $ GENRE : Factor w/ 2 levels "dialog","monolog": 2 2 1 1 ...
 $ LENGTH: int  1014 1188 889 265 465 1278 671 1079 643 ...
> attach(UHM)¶
```

To see which disfluency or filler occurs how often, you use the function `table`, which creates a frequency list of the elements of a vector or factor:

```
> table(FILLER)¶
FILLER
silence      uh     uhm
    332     394     274
```

If you also want to know the percentages of each disfluency, then you can either do this rather manually or you use the function `prop.table`, whose argument is a table generated with `table` and which returns the percentages of the frequencies in that table (cf. also below).

```
> table(FILLER)/length(FILLER)¶
FILLER
silence      uh     uhm
  0.332   0.394   0.274
> prop.table(table(FILLER))¶
FILLER
silence      uh     uhm
  0.332   0.394   0.274
```

Often, it is also useful to generate a cumulative frequency table of the observed values or of the percentages. R has a function `cumsum`, which successively adds the values of a vector and returns all sums, which is exemplified in the following two lines:

```
> 1:5¶
[1] 1 2 3 4 5
> cumsum(1:5)¶
[1]  1  3  6 10 15
```

And of course you can apply `cumsum` to our tables:

```
> cumsum(table(FILLER))¶
silence      uh     uhm
    332     726    1000
```

```
> cumsum(prop.table(table(FILLER)))¶
silence      uh     uhm
  0.332   0.726   1.000
```

Usually, it is instructive to represent the observed distribution graphically and the sections below introduce a few graphical formats. For reasons of space, I only discuss some ways to tweak graphs, but you can turn to the help pages of these functions (using `?…`) and Murrell (2011) for more info.

1.1.1. Scatterplots and line plots

Before we begin to summarize vectors and factors graphically in groups of elements, we discuss how the data points of a vector are plotted individually. The simplest approach just requires the function `plot`. This is a very versatile function, which, depending on the arguments you use with it, creates many different graphs. (This may be a little confusing at first, but allows for an economical style of working, as you will see later.) If you provide just one numerical vector as an argument, then R plots a scatterplot, i.e., a two-dimensional coordinate system in which the values of the vector are interpreted as coordinates of the *y*-axis, and the order in which they appear in the vector are the coordinates of the *x*-axis. Here's an example:

```
> a<-c(1, 3, 5, 2, 4); b<-1:5¶
> plot(a) # left panel of Figure 15¶
```

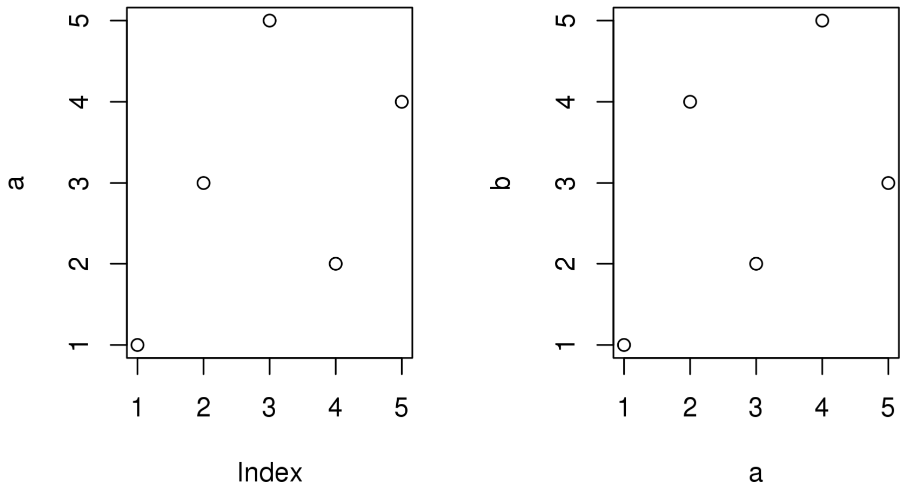


Figure 15. Simple scatterplots

But if you give two vectors as arguments, then the values of the first and the second are interpreted as coordinates on the *x*-axis and the *y*-axis respectively (and the names of the vectors will be used as axis labels):

```
> plot(a, b) # right panel of Figure 15¶
```

With the argument `type=…`, you can specify the kind of graph you want. The default, which was used because you did not specify anything else, is `type="p"` (for *points*). If you use `type="b"` (for *both*), you get points and lines connecting the points; if you use `type="l"` (for *lines*), you get a line plot; cf. Figure 16. (With `type="n"`, nothing gets plotted into the main plotting area, but the coordinate system is set up.)

```
> plot(b, a, type="b") # left panel of Figure 16¶
> plot(b, a, type="l") # right panel of Figure 16¶
```

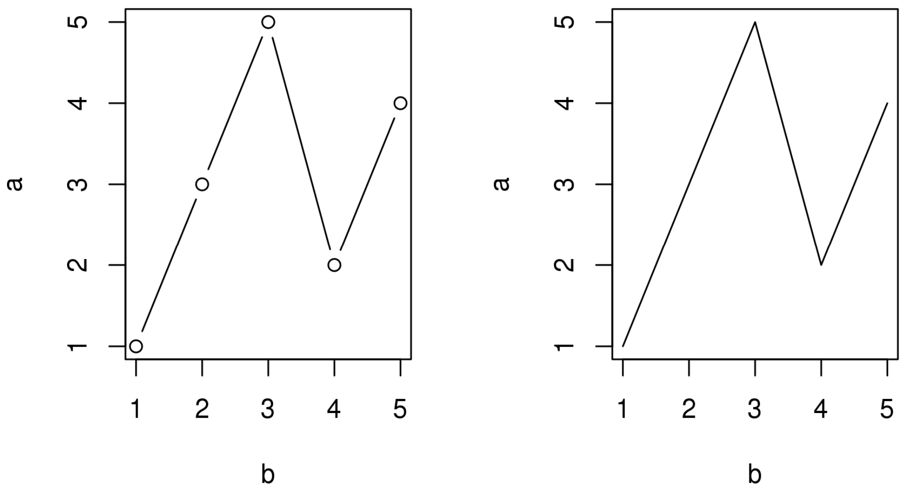


Figure 16. Simple line plots

Other simple but useful ways to tweak graphs involve defining labels for the axes (`xlab="…"` and `ylab="…"`), a bold heading for the whole graph (`main="…"`), the ranges of values of the axes (`xlim=…` and `ylim=…`), and the addition of a grid (`grid()¶`). With `col="…"`, you can also set the color of the plotted element, as you will see more often below.

```
> plot(b, a, xlab="A vector b", ylab="A vector a", xlim=c(0,
   8), ylim=c(0, 8), type="b"); grid() # Figure 17¶
```

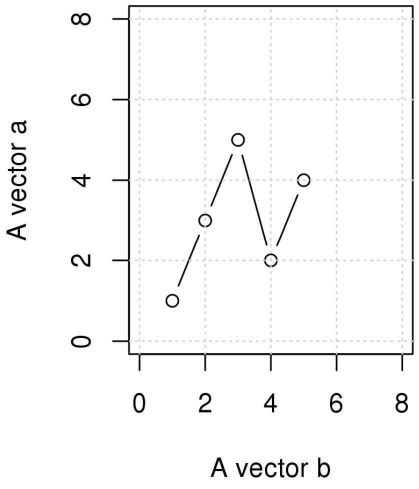


Figure 17. A scatterplot exemplifying a few simple plot settings

An important rule of thumb is that the ranges of the axes must be chosen such that the distribution of the data is represented most meaningfully. It is often useful to include the point (0, 0) within the ranges of the axes and to make sure that graphs to be compared have the same and sufficient axis ranges. For example, if you want to compare the ranges of values of two vectors `x` and `y` in two graphs, then you usually may not want to let R decide on the ranges of axes. Consider the upper panel of Figure 18.

The clouds of points look very similar and you only notice the distributional difference between `x` and `y` when you specifically look at the range of values on the *y*-axis. The values in the upper left panel range from 0 to 2 but those in the upper right panel range from 0 to 6. This difference between the two vectors is immediately obvious, however, when you use `ylim=`... to manually set the ranges of the *y*-axes to the same range of values, as I did for the lower panel of Figure 18.

Note: whenever you use `plot`, by default a new graph is created and the old graph is lost (In RStudio, you can go back to previous plots, however, with the arrow button or the menu *Plots: ...*) If you want to plot two lines into a graph, you first generate the first with `plot` (and `type="l"` or `type="b"`) and then add the second one with `points` (or `lines`; sometimes you can also use the argument `add=TRUE`). That also means that you must define the ranges of the axes in the first plot in such a way that the values of the second graph can also be plotted into it.

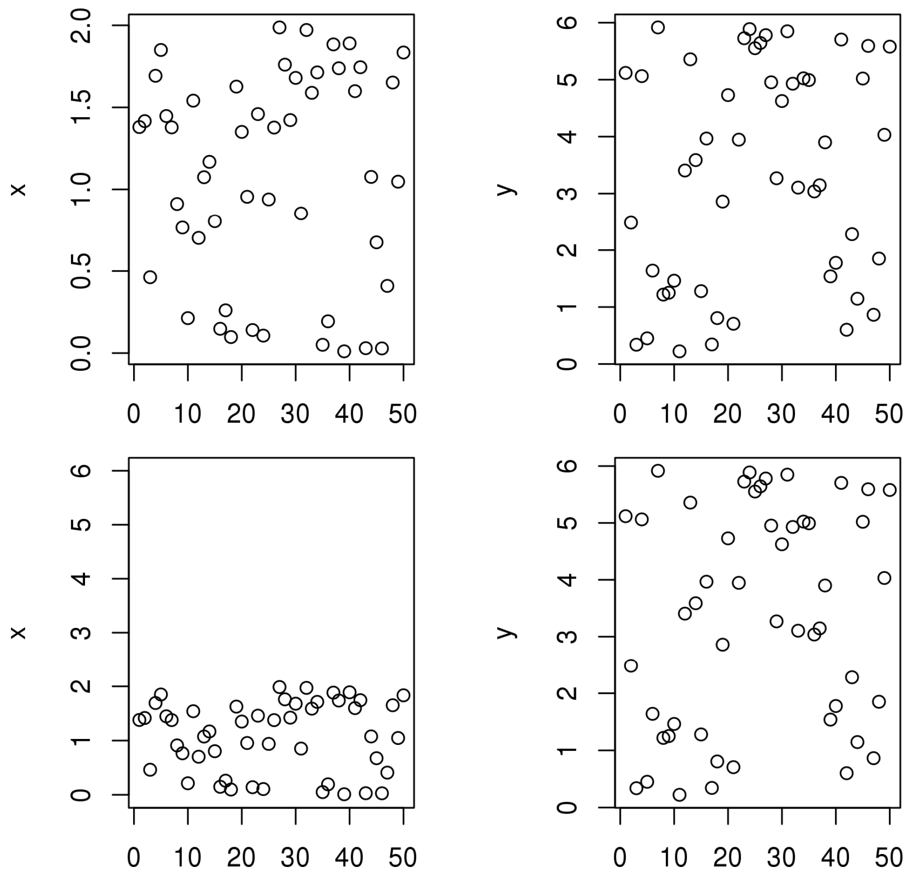


Figure 18. Scatterplots and the importance of properly-defined ranges of axes

An example will clarify that point. If you want to plot the points of the vectors m and n, and then want to add into the same plot the points of the vectors x and y, then this does *not* work, as you can see in the left panel of Figure 19.

```
> m<-1:5; n<-5:1¶
> x<-6:10; y<-6:10¶
> plot(m, n, type="b"); points(x, y, type="b"); grid()¶
```

The left panel of Figure 19 shows the points defined by m and n, but not those of x and y because the ranges of the axes that R used to plot m and n are too small for x and y, which is why you must define those manually while creating the first coordinate system. One way to do this is to use the function `max`, which returns the maximum value of a vector (and `min` returns the minimum). The right panel of Figure 19 shows that this does the trick. (In this line, the minimum is set to 0 manually – of course, you could also use `min(m, x)` and `min(n, y)` for that, but I wanted to include (0, 0) in the graph.)

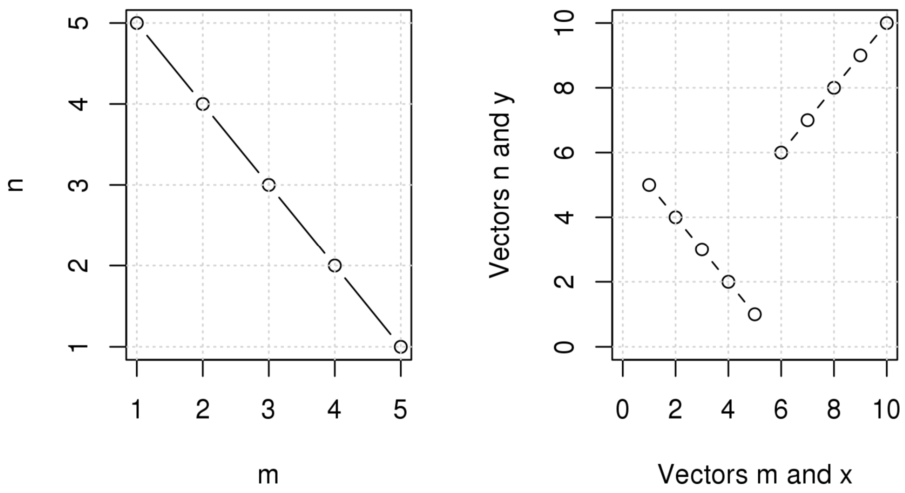


Figure 19. Scatterplots and the importance of properly-defined ranges of axes

```
> plot(m, n, type="b", xlim=c(0, max(m, x)), ylim=
   c(0, max(n, y)), xlab="Vectors m and x",
   ylab="Vectors n and y"); grid()¶
> points(x, y, type="b")¶
```

Recommendation(s) for further study
the functions `pmin` and `pmax` to determine the minima and maxima at each position of different vectors (try `pmin(c(1, 5, 3), c(2, 4, 6))¶`)

1.1.2. Pie charts

The function to generate a pie chart is `pie`. Its most important argument is a table generated with `table`. You can either just leave it at that or, for example, change category names with `labels=…` or use different colors with `col=…` etc.:

```
> pie(table(FILLER), col=c("grey20", "grey50", "grey80"))¶
```

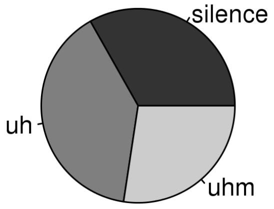


Figure 20. A pie chart with the frequencies of disfluencies

One thing that's a bit annoying about this is that, to use different colors with `col=…` as above, you have to know how many colors there are and assign names to them, which becomes cumbersome with many different colors and/or graphs. For situations like these, the function `rainbow` can be very useful. In its simplest use, it requires only one argument, namely the number of different colors you want. Thus, how would you re-write the above line for the pie chart in such a way that you let R find out how many colors are needed rather than saying `col=rainbow(3)`?

THINK BREAK

Let R use as many colors as the table you are plotting has elements:

```
> pie(table(FILLER), col=rainbow(length(table(FILLER))))¶
```

Note that pie charts are usually not a good way to summarize data because humans are not very good at inferring quantities from angles. Thus, `pie` is not a function you should use too often – the function `rainbow`, on the other hand, is one you should definitely bear in mind.

1.1.3. Bar plots

To create a bar plot, you can use the function `barplot`. Again, its most important argument is a table generated with `table` and again you can create either a standard version or more customized ones. If you want to define your own category names, you unfortunately must use `names.arg=…`, not `labels=…` (cf. Figure 21 below).

```
> barplot(table(FILLER)) # left panel of Figure 21¶
> barplot(table(FILLER), col=c("grey20", "grey40",
   "grey60")) # right panel of Figure 21¶
```

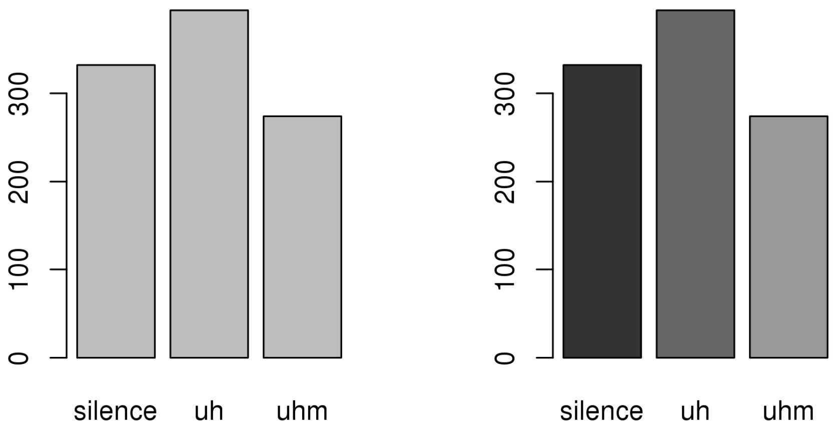


Figure 21. Bar plots with the frequencies of disfluencies

An interesting way to configure bar plots is to use `space=0` to have the bars be immediately next to each other. That is of course not exactly mind-blowing in itself, but it is one of two ways to make it easier to add further data/annotation to the plot. For example, you can then easily plot the observed frequencies into the middle of each bar using the function `text`. The first argument of `text` is a vector with the *x*-axis coordinates of the text to be printed (with `space=0`, 0.5 for the middle of the first bar, 1.5 for the middle of the second bar, and 2.5 for the middle of the third bar), the second argument is a vector with the *y*-axis coordinates of that text (half of each observed frequency so that the text ends up in the middle of the bars), and `labels=`... provides the text to be printed; cf. the left panel of Figure 22.

```
> barplot(table(FILLER), col=c("grey40", "grey60", "grey80"),
   names.arg=c("Silence", "Uh", "Uhm"), space=0)¶
> text(c(0.5, 1.5, 2.5), table(FILLER)/2, labels=
   table(FILLER))¶
```

The second way to create a similar graph – cf. the right panel of Figure 22 – involves some useful changes:

```
> mids<-barplot(table(FILLER), col=c("grey40", "grey60",
   "grey80"))¶
> text(mids, table(FILLER), labels=table(FILLER), pos=1)¶
```

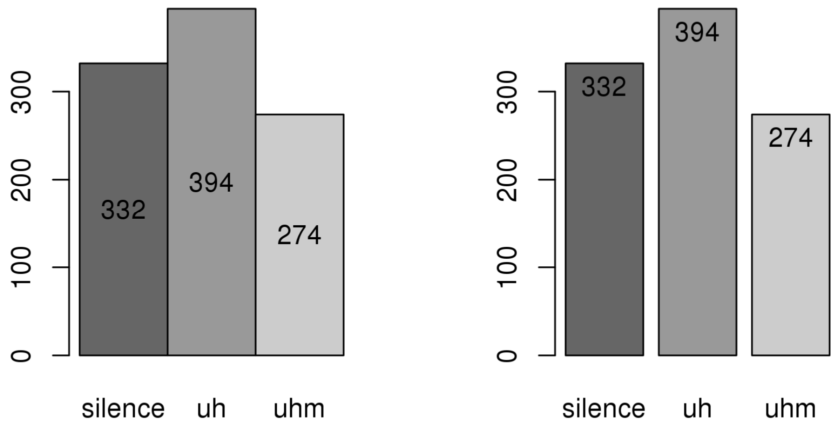


Figure 22. Bar plots with the frequencies of disfluencies

The first line now does not just plot the barplot, it also assigns what R returns to a data structure called `mids`, which contains the *x*-coordinates of the middles of the bars, which we can then use for `text`ing. (Look at `mids`.) Second, the second line now uses `mids` for the *x*-coordinates of the text to be printed and it uses `pos=1` to make R print the text a bit below the specified coordinates; `pos=2`, `pos=3`, and `pos=4` would print the text a bit to the left, above, and to the right of the specified coordinates respectively.

The functions `plot` and `text` allow for another powerful graph: first, you generate a plot that contains nothing but the axes and their labels (with `type="n"`, cf. above), and then with `text` you plot words or numbers. Try this for an illustration of a kind of plot you will more often see below:

```
> tab<-table(FILLER)¶
> plot(tab, type="n", xlab="Disfluencies", ylab="Observed
   frequencies", xlim=c(0, 4), ylim=c(0, 500)); grid()¶
> text(seq(tab), tab, labels=tab)¶
```

Recommendation(s) for further study
the function `dotchart` for dot plot and the parameter settings `cex`, `srt`, `col`, `pch`, and `font` to tweak plots: `?par¶`.

1.1.4. Pareto-charts

A related way to represent the frequencies of the disfluencies is a pareto-chart. In pareto-charts, the frequencies of the observed categories are represented as in a bar plot, but they are first sorted in descending order of frequency and then overlaid by a line plot of cumulative percentages that indicates what percent of all data one category *and* all other categories to the left of that category account for. The function `pareto.chart` comes with the library `qcc` that you must (install and/or) load first; cf. Figure 23.

```
> library(qcc)¶
> pareto.chart(table(FILLER), main="")¶
Pareto chart analysis for table(FILLER)
         Frequency Cum.Freq. Percentage Cum.Percent.
  uh         394.0     394.0       39.4         39.4
  silence    332.0     726.0       33.2         72.6
  uhm        274.0    1000.0       27.4        100.0
```

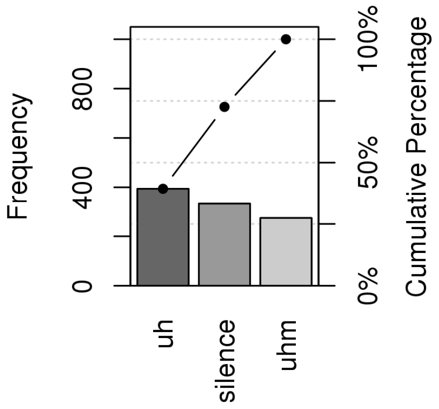


Figure 23. Pareto-chart with the frequencies of disfluencies

1.1.5. Histograms

While bar plots are probably the most frequent forms of representing the frequencies of nominal/categorical variables, histograms are most widespread for the frequencies of interval/ratio variables. In R, you can use `hist`, which just requires the relevant vector as its argument.

```
> hist(LENGTH)¶
```

For some ways to make the graph nicer, cf. Figure 24, whose left panel contains a histogram of the variable `LENGTH` with axis labels and grey bars.

```
> hist(LENGTH, main="", xlab="Length in ms", ylab=
   "Frequency", xlim=c(0, 2000), ylim=c(0, 100),
   col="grey80")¶
```

The right panel of Figure 24 contains a histogram of the probability densities (generated by `freq=FALSE`) with a curve (generated by `lines`).

```
> hist(LENGTH, main="", xlab="Length in ms", ylab="Density",
   freq=FALSE, xlim=c(0, 2000), col="grey50")¶
> lines(density(LENGTH))¶
```

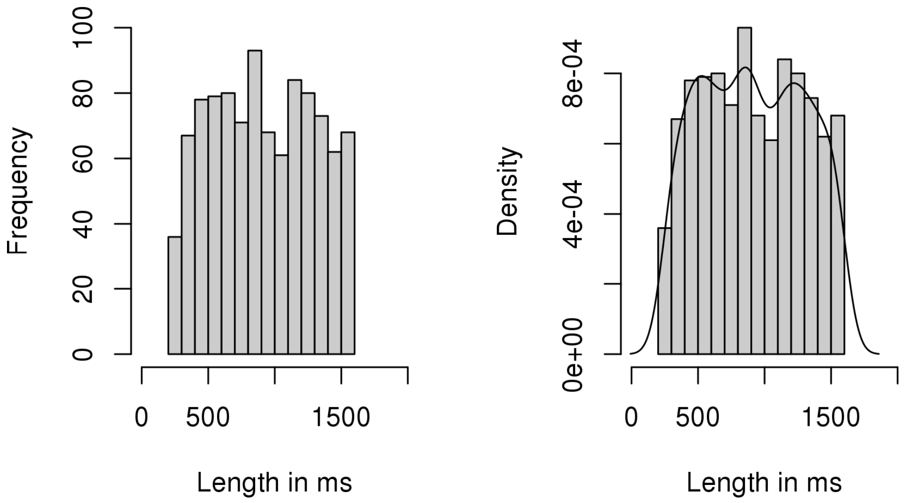


Figure 24. Histograms for the frequencies of lengths of disfluencies

With the argument `breaks=…` to `hist`, you can instruct R to try to use a particular number of bins (or bars). You either provide one integer – then R tries to create a histogram with as many bins – or you provide a vector with the boundaries of the bins. The latter raises the question of how many bins should or may be chosen? In general, you should not have more than 20 bins, and as one rule of thumb for the number of bins to choose you can use the formula in (14) (cf. Keen 2010:143–160 for discussion). The most important aspect is that the bins you choose do not misrepresent the data.

(14) Number of bins for a histogram of n data points = $1+3.32\cdot\log_{10} n$

1.1.6. Empirical cumulatuive distributions

A very useful visualization of numerical data is the empirical cumulative distribution (function, abbreviated ecdf) plot, an example of which you have already seen as part of the pareto chart in Section 3.1.1.4. On the *x*-axis of an ecdf plot, you find the range of the variable that is visualized, on the *y*-axis you find a percentage scale from 0 to 1 (=100%), and the points in the coordinate system show how much in percent of all data one variable value and all other smaller values to the left of that value account for. Figure 25 shows such a plot for LENGTH and you can see that approximately 18% of all lengths are smaller than 500 ms.

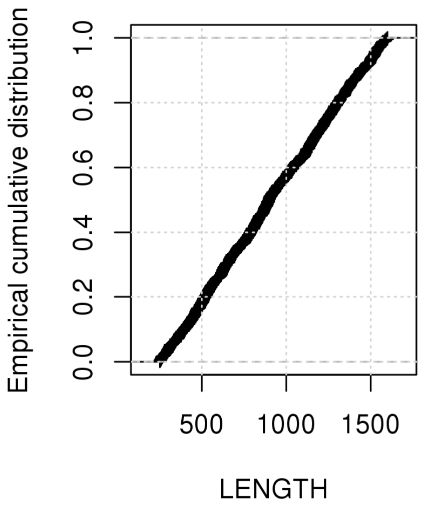


Figure 25. Ecdf plot of lengths of disfluencies

This plot is very useful because it does not lose information by binning data points: every data point is represented in the plot, which is why ecdf plots can be very revealing even for data that most other graphs cannot illustrate well. Let's see whether you've understood this plot: what do ecdf plots of normally-distributed and uniformly-distributed data look like?

THINK BREAK

You will find the answer in the code file (with graphs); make sure you understand why so you can use this very useful type of graph.

Recommendation(s) for further study

- the functions `dotchart` and `stripchart` (with `method="jitter"`) to represent the distribution of individual data points in very efficient ways
- the function `scatterplot` (from the library `car`) for more sophisticated scatterplots
- the functions `plot3d` and `scatterplot3d` (from the library `rgl` and the library `scatterplot3d`) for different three-dimensional scatterplots

1.2. Measures of central tendency

Measures of central tendency are probably the most frequently used statistics. They provide a value that attempts to summarize the behavior of a variable. Put differently, they answer the question, if I wanted to summarize this variable and were allowed to use only one number to do that, which number would that be? Crucially, the choice of a particular measure of central tendency depends on the variable's level of measurement. For nominal/categorical variables, you should use the mode (if you do not simply list frequencies of all values/bins anyway, which is often better), for ordinal variables you should use the median, for interval/ratio variables you can often use the arithmetic mean.

1.2.1. The mode

The mode of a variable or distribution is the value that is most often observed. As far as I know, there is no function for the mode in R, but you can find it very easily. For example, the mode of `FILLER` is *uh*:

```
> which.max(table(FILLER))¶
uh
 2
> max(table(FILLER))¶
[1] 394
```

Careful when there is more than one level that exhibits the maximum number of observations – tabulating is usually safer.

1.2.2. The median

The measure of central tendency for ordinal data is the median, the value you obtain when you sort all values of a distribution according to their size and then pick the middle one (e.g., the median of the numbers from 1 to 5 is 3). If you have an even number of values, the median is the average of the two middle values.

```
> median(LENGTH)¶
[1] 897
```

1.2.3. The arithmetic mean

The best-known measure of central tendency is the arithmetic mean for interval/ratio variables. You compute it by adding up all values of a distribution or a vector and dividing that sum by the number of values, but of course there is also a function for this:

```
> sum(LENGTH)/length(LENGTH)¶
[1] 915.043
> mean(LENGTH)¶
[1] 915.043
```

One weakness of the arithmetic mean is its sensitivity to outliers:

```
> a<-1:10; a¶
[1]  1  2  3  4  5  6  7  8  9 10
> b<-c(1:9, 1000); b¶
[1]    1    2    3    4    5    6    7    8    9 1000
> mean(a)¶
[1] 5.5
> mean(b)¶
[1] 104.5
```

Although the vectors `a` and `b` differ with regard to only a single value, the mean of `b` is much larger than that of `a` because of that one outlier, in fact so much larger that `b`'s mean of 104.5 neither summarizes the values from 1 to 9 nor the value 1000 very well. There are two ways of handling such problems. First, you can add the argument `trim=…`, the percentage of elements from the top and the bottom of the distribution that are discarded before the mean is computed. The following lines compute the means of `a` and `b` after the highest and the lowest value have been discarded:

```
> mean(a, trim=0.1)¶
[1] 5.5
> mean(b, trim=0.1)¶
[1] 5.5
```

Second, you can just use the median, which is also a good idea if the data whose central tendency you want to report are not normally distributed.

```
> median(a); median(b)¶
[1] 5.5
[1] 5.5
```

Warning/advice
Just because R or your spreadsheet software can return many decimals does not mean you have to report them all. Use a number of decimals that makes sense given the statistic that you report.

1.2.4. The geometric mean

The geometric mean is used to compute averages of factors or ratios (whereas the arithmetic mean is computed to get the average of sums). Let's assume you have six recordings of a child at the ages 2;1 (two years and one month), 2;2, 2;3, 2;4, 2;5, and 2;6. Let us also assume you had a vector `lexicon` that contains the cumulative numbers of different words (types!) that the child produced at each age:

```
> lexicon<-c(132, 158, 169, 188, 221, 240)¶
> names(lexicon)<-c("2;1", "2;2", "2;3", "2;4", "2;5",
   "2;6")¶
```

You now want to know the average rate at which the lexicon increased. First, you compute the successive increases:

```
> increases<-lexicon[2:6]/lexicon[1:5]; increases¶
     2;2      2;3      2;4      2;5      2;6
1.196970 1.069620 1.112426 1.175532 1.085973
```

That is, by age 2;2, the child produced 19.697% more types than by age 2;1, by age 2;3, the child produced 6.962% more types than by age 2;2, etc. Now, you must *not* think that the average rate of increase of the lexicon is the arithmetic mean of these increases:

```
> mean(increases) # wrong!¶
[1] 1.128104
```

You can easily test that this is not the correct result. If this number was the true average rate of increase, then the product of 132 (the first lexicon size) and this rate of 1.128104 to the power of 5 (the number of times the supposed 'average rate' applies) should be the final value of 240. This is not the case:

```
> 132*mean(increases)^5¶
[1] 241.1681
```

Instead, you must compute the geometric mean. The geometric mean of a vector `x` with *n* elements is computed according to formula (15), and if you use this as the average rate of increase, you get the right result:

(15) $$mean_{\text{geom}} = (x_1 \cdot x_2 \cdot \ldots \cdot x_{n-1} \cdot x_n)^{1/n}$$

```
> rate.increase<-prod(increases)^(1/length(increases));
   rate.increase¶
[1] 1.127009
> 132*rate.increase^5¶
[1] 240
```

True, the difference between 240 – the correct value – and 241.1681 – the incorrect value – may seem negligible, but 241.1681 is still wrong and the difference is not always that small, as an example from Wikipedia (s.v. *geometric mean*) illustrates: If you do an experiment and get an increase rate of 10.000 and then you do a second experiment and get an increase rate of 0.0001 (i.e., a decrease), then the average rate of increase is not approximately 5.000 – the arithmetic mean of the two rates – but 1 – their geometric mean.[13]

Finally, let me again point out how useful it can be to plot words or numbers instead of points, triangles, … Try to generate Figure 26, in which the position of each word on the *y*-axis corresponds to the average length of the disfluency (e.g., 928.4 for women, 901.6 for men, etc.). (The horizontal line is the overall average length – you may not know yet how to plot that one.) Many tendencies are immediately obvious: men are below the average, women are above, silent disfluencies are of about average length, etc.

13. Alternatively, you can compute the geometric mean of `increases` as follows: `exp(mean(log(increases)))¶`.

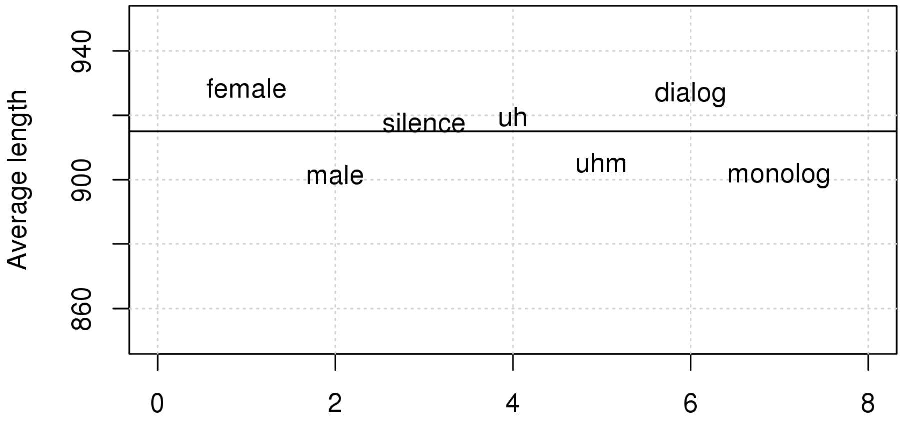


Figure 26. Mean lengths of disfluencies

1.3. Measures of dispersion

Most people know what measures of central tendencies are. What many people do not know is that they should never – NEVER! – report a measure of central tendency without some corresponding measure of dispersion. The reason for this rule is that without such a measure of dispersion you never know how good the measure of central tendency actually is at summarizing the data. Let us look at a non-linguistic example, the monthly temperatures of two towns and their averages:

```
> town1<-c(-5, -12, 5, 12, 15, 18, 22, 23, 20, 16, 8, 1)¶
> town2<-c(6, 7, 8, 9, 10, 12, 16, 15, 11, 9, 8, 7)¶
> mean(town1); mean(town2)¶
[1] 10.25
[1] 9.833333
```

On the basis of the means alone, the towns seem to have a very similar climate, but even a quick glance at Figure 27 shows that that is not true – in spite of the similar means, I know where I would want to be in February. Obviously, the mean of Town 2 summarizes the central tendency of Town 2 much better than the mean of Town 1 does for Town 1: the values of Town 1 vary much more widely around their mean. Thus, always provide a measure of dispersion for your measure of central tendency: relative entropy for the mode, the interquartile range or quantiles for the median and interval/ratio-scaled data that are non-normal or exhibit outliers, and the standard deviation or the variance for normal interval/ratio-scaled data.

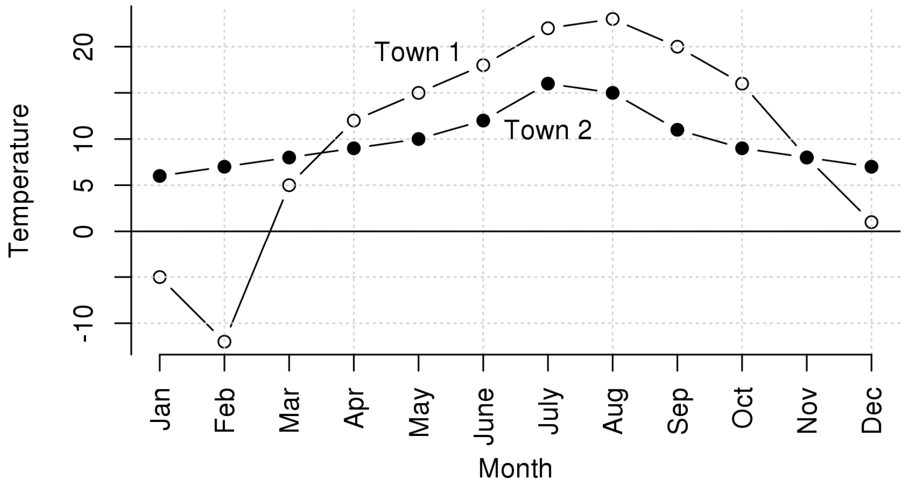


Figure 27. Temperature curves of two towns

1.3.1. Relative entropy

A simple dispersion measure for categorical data is relative entropy H_{rel}. H_{rel} is 1 when the levels of the relevant categorical variable are all equally frequent, and it is 0 when all data points have only one and the same variable level. For categorical variables with *n* levels, H_{rel} is computed as shown in formula (16), in which p_i corresponds to the frequency in percent of the *i*-th level of the variable:

$$(16) \qquad H_{\text{rel}} = -\frac{\sum_{i=1}^{n}\left(p_i \cdot \ln p_i\right)}{\ln n}$$

Thus, if you count the articles of 300 noun phrases and find 164 cases with no determiner, 33 indefinite articles, and 103 definite articles, this is how you compute H_{rel}:

```
> article<-c(164, 33, 103)¶
> perc<-article/sum(article)¶
> hrel<--sum(perc*log(perc))/log(length(perc)); hrel¶
[1] 0.8556091
```

It is worth pointing out that the above formula does not produce the desired result of 0 when only no-determiner cases are observed because `log(0)` is not defined:

```
> article<-c(300, 0, 0)¶
> perc<-article/sum(article)¶
> hrel<--sum(perc*log(perc))/log(length(perc)); hrel¶
[1] NaN
```

Usually, this is taken care of by simply setting the result of `log(0)` to zero (or sometimes also by incrementing all values by 1 before logging). This is a case where writing a function to compute logarithms that *can* handle 0s can be useful. For example, this is how you could define your own logarithm function `logw0` and then use that function instead of `log` to get the desired result:

```
> logw0<-function(x) {¶
+    ifelse (x==0, 0, log(x))¶
+ }¶
> hrel<--sum(perc*logw0(perc))/logw0(length(perc)); hrel¶
[1] 0
```

Distributions of categorical variables will be dealt with in much more detail below in Section 4.1.1.2.

1.3.2. The range

The simplest measure of dispersion for interval/ratio data is the range, the difference of the largest and the smallest value. You can either just use the function `range`, which requires the vector in question as its only argument, and then compute the difference from the two values with `diff`, or you just compute the range from the minimum and maximum yourself:

```
> range(LENGTH)¶
[1]  251 1600
> diff(range(LENGTH))¶
[1] 1349
> max(LENGTH)-min(LENGTH)¶
[1] 1349
```

This measure is extremely simple to compute but obviously also very sensitive: one outlier is enough to yield results that are not particularly meaningful anymore. For this reason, the range is not used very often.

1.3.3. Quantiles and quartiles

Another simple but useful and flexible measure of dispersion involves the quantiles of a distribution. We have met quantiles before in the context of probability distributions in Section 1.3.4. Theoretically, you compute quantiles by sorting the values in ascending order and then counting which values delimit the lowest *x*%, *y*%, etc. of the data; when these percentages are 25%, 50%, and 75%, then they are called quartiles. In R you can use the function `quantile`, (see below on `type=1`):

```
> a<-1:100¶
> quantile(a, type=1)¶
  0%  25%  50%  75% 100%
   1   25   50   75  100
```

If you write the integers from 1 to 100 next to each other, then 25 is the value that cuts off the lower 25%, etc. The value for 50% corresponds to the median, and the values for 0% and 100% are the minimum and the maximum. Let me briefly mention two arguments of this function. First, the argument `probs` allows you to specify other percentages. Second, the argument `type=…` allows you to choose other ways in which quantiles are computed. For discrete distributions, `type=1` is probably best, for continuous variables the default setting `type=7` is best.

```
> quantile(a, probs=c(0.05, 0.1, 0.5, 0.9, 0.95), type=1)¶
 5% 10% 50% 90% 95%
  5  10  50  90  95
```

The bottom line of using quantiles as a measure of dispersion of course is that the more the 25% quartile and the 75% quartile differ from each other, the more heterogeneous the data are, which is confirmed by looking at the data for the two towns: the so-called interquartile range – the difference between the 75% quartile and the 25% quartile – is much larger for Town 1 than for Town 2.

```
> quantile(town1)¶
   0%    25%    50%    75%   100%
-12.0    4.0   13.5   18.5   23.0
> IQR(town1)¶
[1] 14.5
> quantile(town2)¶
   0%    25%    50%    75%   100%
 6.00   7.75   9.00  11.25  16.00
> IQR(town2)¶
```

```
[1] 3.5
```

You can now apply this function to the lengths of the disfluencies:

```
> quantile(LENGTH, probs=c(0.2, 0.4, 0.5, 0.6, 0.8, 1),
   type=1)¶
 20%  40%  50%  60%  80% 100%
 519  788  897 1039 1307 1600
```

That is, the central 20% of all the lengths of disfluencies are greater than 788 and range up to 1039 (as you can verify with `sort(LENGTH)[401:600]¶`), 20% of the lengths are smaller than or equal to 519, 20% of the values are 1307 or larger, etc.

An interesting application of `quantile` is to use it to split vectors of continuous variables up into groups. For example, if you wanted to split the vector `LENGTH` into five groups of nearly equal ranges of values, you can use the function `cut` from Section 2.4.1 again, which splits up vectors into groups, and the function `quantile`, which tells `cut` what the groups should look like. That is, there are 200 values of `LENGTH` between and including 251 and 521 etc.

```
> LENGTH.GRP<-cut(LENGTH, breaks=quantile(LENGTH, probs=
   c(0, 0.2, 0.4, 0.6, 0.8, 1)), include.lowest=TRUE)¶
> table(LENGTH.GRP)¶
LENGTH.GRP
          [251,521]           (521,789]      (789,1.04e+03]
                200                 200                 200
(1.04e+03,1.31e+03]  (1.31e+03,1.6e+03]
                203                 197
```

1.3.4. The average deviation

Another way to characterize the dispersion of a distribution is the average deviation. You compute the absolute difference of every data point from the mean of the distribution (cf. `abs`), and then you compute the mean of these absolute differences. For Town 1, the average deviation is 9.04:

```
> town1¶
 [1]  -5 -12   5  12  15  18  22  23  20  16   8   1
> town1-mean(town1)¶
 [1] -15.25 -22.25  -5.25   1.75   4.75   7.75  11.75
   12.75  9.75   5.75  -2.25  -9.25
> abs(town1-mean(town1))¶
 [1] 15.25 22.25  5.25  1.75  4.75  7.75 11.75 12.75
```

```
   9.75  5.75  2.25  9.25
> mean(abs(town1-mean(town1)))¶
[1] 9.041667
> mean(abs(town2-mean(town2)))¶
[1] 2.472222
```

For the lengths of the disfluencies, we obtain:

```
> mean(abs(LENGTH-mean(LENGTH)))¶
[1] 329.2946
```

Although this is a quite intuitive measure, it is unfortunately hardly used anymore. For better or for worse (cf. Gorard 2004), you will more often find the dispersion measure discussed next, the standard deviation.

1.3.5. The standard deviation/variance

The standard deviation *sd* of a distribution *x* with *n* elements is defined in (17). This may look difficult at first, but the standard deviation is conceptually similar to the average deviation. For the average deviation, you compute the difference of each data point to the mean and take its absolute value – for the standard deviation you compute the difference of each data point to the mean, square these differences, sum them up, and after dividing the sum by *n*-1, you take the square root (to 'undo' the previous squaring).

(17) $$sd = \left(\frac{\sum_{i=1}^{n} \left(x_i - \bar{x}\right)^2}{n-1} \right)^{\frac{1}{2}}$$

Once we 'translate' this into R, it probably becomes clearer:

```
> town1¶
 [1]  -5 -12   5  12  15  18  22  23  20  16   8   1
> town1-mean(town1)¶
 [1] -15.25 -22.25  -5.25   1.75   4.75   7.75  11.75
   12.75   9.75   5.75  -2.25  -9.25
> (town1-mean(town1))^2¶
 [1] 232.5625 495.0625  27.5625   3.0625  22.5625  60.0625
   138.0625 162.5625  95.0625  33.0625   5.0625  85.5625
> sum((town1-mean(town1))^2)¶
[1] 1360.25
> sum((town1-mean(town1))^2)/(length(town1)-1)¶
```

```
[1] 123.6591
> sqrt(sum((town1-mean(town1))^2)/(length(town1)-1))¶
[1] 11.12021
```

There is of course an easier way …

```
> sd(town1); sd(town2)¶
[1] 11.12021
[1] 3.157483
```

Note in passing: the standard deviation is the square root of another measure, the *variance*, which you can also compute with the function `var`.

Recommendation(s) for further study
the function `mad` to compute another very robust measure of dispersion, the median absolute deviation

1.3.6. The variation coefficient

Even though the standard deviation is probably the most widespread measure of dispersion, it has a potential weakness: its size is dependent on the mean of the distribution, as you can see in the following example:

```
> sd(town1)¶
[1] 11.12021
> sd(town1*10)¶
[1] 111.2021
```

When the values, and hence the mean, is increased by one order of magnitude, then so is the standard deviation. You can therefore not compare standard deviations from distributions with different means if you do not first normalize them. If you divide the standard deviation of a distribution by its mean, you get the variation coefficient. You see that the variation coefficient is not affected by the multiplication with 10, and Town 1 still has a larger degree of dispersion.

```
> sd(town1)/mean(town1)¶
[1] 1.084899
> sd(town1*10)/mean(town1*10)¶
[1] 1.084899
> sd(town2)/mean(town2)¶
[1] 0.3210999
```

1.3.7. Summary functions

If you want to obtain several summarizing statistics for a vector (or a factor), you can use `summary`, whose output is self-explanatory.

```
> summary(town1)¶
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 -12.00    4.00   13.50   10.25   18.50   23.00
```

An immensely useful graph is the so-called boxplot. In its simplest form, the function `boxplot` just requires one vector as an argument, but we also add `notch=TRUE`, which I will explain shortly, as well as a line that adds little plus signs for the arithmetic means. Note that I am assigning the output of `boxplot` to a data structure called `boxsum` for later inspection.

```
> boxsum<-boxplot(town1, town2, notch=TRUE,
  names=c("Town 1", "Town 2"))¶
> text(1:2, c(mean(town1), mean(town2)), c("+", "+"))¶
```

This plot, see Figure 28, contains a lot of valuable information:

- the bold-typed horizontal lines represent the medians of the two vectors;
- the regular horizontal lines that make up the upper and lower boundary of the boxes represent the hinges (approximately the 75%- and the 25% quartiles);

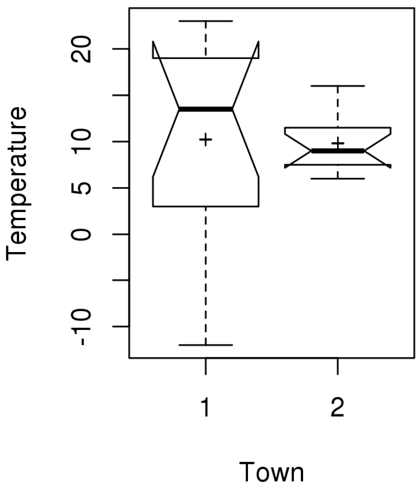


Figure 28. Boxplot of the temperatures of the two towns

– the whiskers – the dashed vertical lines extending from the box until the upper and lower limit – represent the largest and smallest values that are not more than 1.5 interquartile ranges away from the box;
– each data point that would be outside of the range of the whiskers would be represented as an outlier with an individual small circle;
– the notches on the left and right sides of the boxes extend across the range `±1.58*IQR/sqrt(n)`: if the notches of two boxplots do not overlap, then their medians will most likely be significantly different.

Figure 28 shows that the average temperatures of the two towns are very similar and probably not significantly different from each other. Also, the dispersion of Town 1 is much larger than that of Town 2. Sometimes, a good boxplot nearly obviates the need for further analysis; boxplots are extremely useful and will often be used in the chapters to follow. However, there are situations where the ecdf plot introduced above is better and the following example is modeled after what happened in a real dataset of a student I supervised. Run the code in the code file and consider Figure 29.

As you could see in the code file, I created a vector `x1` that actually contains data from two very different distributions whereas the vector `x2` contains data from only one but wider distribution.

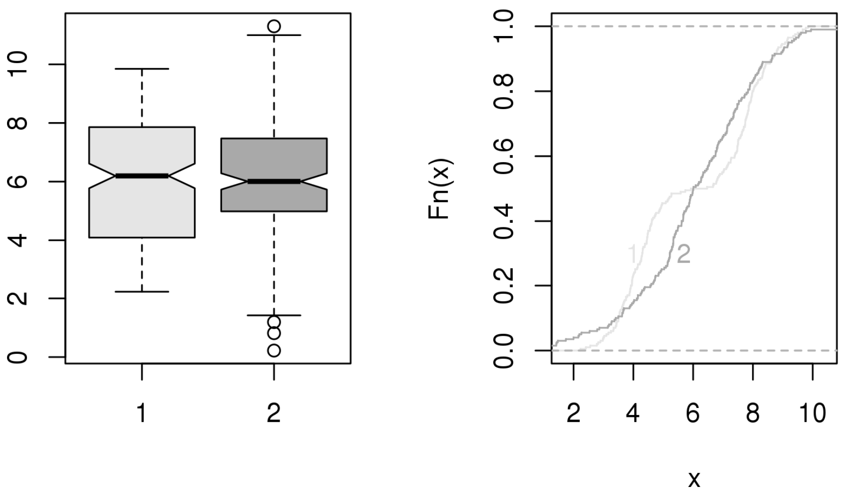


Figure 29. Boxplots (left panel) and ecdf plots (right panel) of two vectors

Crucially, the boxplots do not reveal that at all. Yes, the second darker boxplot is wider and has some outliers but the fact that the first lighter boxplot represents a vector containing data from two different distributions is completely absent from the graph. The ecdf plots in the right panel show that very clearly, however: the darker line for the second vector increases steadily in a way that suggests one normal distribution whereas the lighter line for the first vector shows that it contains two normal distributions, given the two *s*-shaped curve segments. Thus, while the ecdf plot is not as intuitively understandable as a boxplot, it can be much more informative.

Recommendation(s) for further study
the functions `hdr.boxplot` (from the library `hdrcde`), `vioplot` (from the library `vioplot`), and `bpplot` (from the library `Hmisc`) for interesting alternatives to, or extensions of, boxplots

1.3.8. The standard error

The standard error of an arithmetic mean is defined as the standard deviation of the means of equally large samples drawn randomly from a population with replacement. Imagine you took a sample from a population and computed the arithmetic mean of some variable. Unless your sample is *perfectly* representative of the population, this mean will not correspond exactly to the arithmetic mean of that variable in the population, and it will also not correspond exactly to the arithmetic mean you would get from another equally large sample from the same population. If you take many (e.g., 10,000) random and equally large samples from the population with replacement and computed the arithmetic mean of each of them, then the standard deviation of all these means is the standard error.

```
> means<-vector(length=10000)¶
> for (i in 1:10000) {¶
+    means[i]<-mean(sample(LENGTH, size=1000, replace=TRUE))¶
+ }¶
> sd(means)¶
[1] 12.10577
```

The standard error of an arithmetic mean is computed according to the formula in (18), and from (18) you can already see that the larger the standard error of a mean, the smaller the likelihood that that mean is a good estimate of the population mean, and that the larger sample size *n*, the smaller the standard error becomes:

(18) $$se_{\text{mean}} = \sqrt{\frac{var}{n}} = \frac{sd}{\sqrt{n}}$$

Thus, the standard error of the mean length of disfluencies here is this, which is very close to our resampled result from above.

```
> mean(LENGTH)¶
[1] 915.043
> sqrt(var(LENGTH)/length(LENGTH))¶
[1] 12.08127
```

You can also compute standard errors for statistics other than arithmetic means but the only other example we look at here is the standard error of a relative frequency *p*, which is computed according to the formula in (19):

(19) $$se_{\text{percentage}} = \sqrt{\frac{p \cdot (1-p)}{n}}$$

Thus, the standard error of the percentage of all silent disfluencies out of all disfluencies (33.2% of 1000 disfluencies) is:

```
> prop.table(table(FILLER))¶
FILLER
silence      uh     uhm
  0.332   0.394   0.274
> sqrt(0.332*(1-0.332)/1000)¶
[1] 0.01489215
```

Standard errors will be much more important in Section 3.1.5 because they are used to compute so-called confidence intervals. Note that when you compare means of two roughly equally large samples and their intervals means±standard errors overlap, then you know the sample means are not significantly different. However, if these intervals do not overlap, this does not show that the means are significantly different (cf. Crawley 2005: 169f.). In Chapter 5, you will also get to see standard errors of differences of means, which are computed according to the formula in (20).

(20) $$se_{\text{difference between means}} = \sqrt{SE_{mean\_group1}{}^{2} + SE_{mean\_group2}{}^{2}}$$

Warning/advice
Standard errors are only really useful if the data to which they are applied are distributed pretty normally or when the sample size $n \geq 30$.

1.4. Centering and standardization (*z*-scores)

Very often it is useful or even necessary to compare values coming from different scales. An example (from Bortz 2005): if a student X scored 80% in a course and a student Y scored 60% in another course, can you then say that student X was better than student Y? On the one hand, sure you can: 80% is better than 60%. On the other hand, the test in which student Y participated could have been much more difficult than the one in which student X participated. It can therefore be useful to relativize/normalize the individual grades of the two students on the basis of the overall performance of students in their courses. (You encountered a similar situation above in Section 3.1.3.6 when you learned that it is not always appropriate to compare different standard deviations directly.) Let us assume the grades obtained in the two courses look as follows:

```
> grades.course.X<-rep((seq(0, 100, 20)), 1:6);
   grades.course.X¶
[1]   0  20  20  40  40  40  60  60  60  60  80  80  80  80
   80 100 100 100 100 100 100
> grades.course.Y<-rep((seq(0, 100, 20)), 6:1);
   grades.course.Y¶
[1]   0   0   0   0   0   0  20  20  20  20  20  40  40  40
   40  60  60  60  80  80 100
```

One way to normalize the grades is called *centering* and simply involves subtracting from each individual value within one course the average of that course.

```
> a<-1:5¶
> centered.scores<-a-mean(a); centered.scores¶
[1] -2 -1  0  1  2
```

You can see how these scores relate to the original values in a: since the mean of a is obviously 3, the first two centered scores are negative (i.e., smaller than a's mean), the third is 0 (it does not deviate from a's mean), and the last two centered scores are positive (i.e., larger than a's mean).

Another more sophisticated way involves *standardizing*, i.e. transforming the values to be compared into so-called *z*-scores, which indicate how many standard deviations each value of the vector deviates from the mean of the vector. The *z*-score of a value from a vector is the difference of that value from the mean of the vector, divided by the vector's standard deviation. You can compute that manually as in this simple example:

```
> z.scores<-(a-mean(a))/sd(a); z.scores¶
[1] -1.2649111 -0.6324555  0.0000000  0.6324555  1.2649111
```

The relationship between the *z*-scores and a's original values is very similar to that between the centered scores and a's values: since the mean of a is obviously 3, the first two *z*-scores are negative (i.e., smaller than a's mean), the third *z*-score is 0 (it does not deviate from a's mean), and the last two *z*-scores are positive (i.e., larger than a's mean). Note that such *z*-scores have a mean of 0 and a standard deviation of 1:

```
> mean(z.scores)¶
[1] 0
> sd(z.scores)¶
[1] 1
```

Both normalizations can be performed with the function `scale`, which takes three arguments: the vector to be normalized, `center=…` (the default is `TRUE`) and `scale=…` (the default is `TRUE`). If you do not provide any arguments other than the vector to be standardized, then `scale`'s default setting returns a matrix that contains the *z*-scores and whose attributes correspond to the mean and the standard deviation of the vector:

```
> scale(a)¶
           [,1]
[1,] -1.2649111
[2,] -0.6324555
[3,]  0.0000000
[4,]  0.6324555
[5,]  1.2649111
attr(,"scaled:center")
[1] 3
attr(,"scaled:scale")
[1] 1.581139
```

If you set `scale` to `FALSE`, then you get centered scores:

```
> scale(a, scale=FALSE)¶
     [,1]
[1,]   -2
```

```
[2,]   -1
[3,]    0
[4,]    1
[5,]    2
attr(,"scaled:center")
[1] 3
```

If we apply both versions to our example with the two courses, then you see that the 80% scored by student X is only 0.436 standard deviations (and 13.33 percent points) better than the mean of his course whereas the 60% scored by student Y is actually 0.873 standard deviations (and 26.67 percent points) above the mean of his course. Thus, X's score is higher than Y's, but if we take the overall results in the two courses into consideration, then Y's performance is better; standardizing data is often useful.

1.5. Confidence intervals

In most cases, you are not able to investigate the whole population you are actually interested in because that population is not accessible and/or too large so investigating it is impossible, too time-consuming, or too expensive. However, even though you know that different samples will yield different statistics, you of course hope that your sample would yield a reliable estimate that tells you much about the population you are interested in:

– if you find in your sample of 1000 disfluencies that their average length is approximately 915 ms, then you hope that you can generalize from that to the population and future investigations;
– if you find in your sample of 1000 disfluencies that 33.2% of these are silences, then you hope that you can generalize from that to the population and future investigations.

So far, we have only discussed how you can compute percentages and means for samples – the question of how valid these are for populations is the topic of this section. In Section 3.1.5.1, I explain how you can compute confidence intervals for arithmetic means, and Section 3.1.5.2 explains how to compute confidence intervals for percentages. The relevance of such confidence intervals must not be underestimated: without a confidence interval it is unclear how well you can generalize from a sample to a population; apart from the statistics we discuss here, one can also compute confidence intervals for many others.

1.5.1. Confidence intervals of arithmetic means

If you compute a mean on the basis of a sample, you of course hope that it represents that of the population well. As you know, the average length of disfluencies in our example data is 915.043 ms (standard deviation: 382.04). But as we said above, other samples' means will be different so you would ideally want to quantify your confidence in this estimate. The so-called confidence interval, which is useful to provide with your mean, is the interval of values around the sample mean around which we will assume there is no significant difference with the sample mean. From the expression "significant difference", it follows that a confidence interval is typically defined as 1-significance level, i.e., typically as 1-0.05 = 0.95.

In a first step, you again compute the standard error of the arithmetic mean according to the formula in (18).

```
> se<-sqrt(var(LENGTH)/length(LENGTH)); se¶
[1] 12.08127
```

This standard error is used in (21) to compute the confidence interval. The parameter *t* in formula (21) refers to the distribution mentioned in Section 1.3.4.3, and its computation requires the number of degrees of freedom. In this case, the number of degrees of freedom *df* is the length of the vector-1, i.e. 999. Since you want to compute a *t*-value on the basis of a *p*-value, you need the function `qt`, and since you want a two-tailed interval – 95% of the values around the observed mean, i.e. values larger and smaller than the mean – you must compute the *t*-value for 2.5% (because 2.5% on both sides result in the desired 5%):

(21) $CI = \bar{x} \pm t \cdot SE$

```
> t.value<-qt(0.025, df=999, lower.tail=FALSE); t.value¶
[1] 1.962341
```

Now you can compute the confidence interval:

```
> mean(LENGTH)-(se*t.value); mean(LENGTH)+(se*t.value)¶
[1] 891.3354
[1] 938.7506
```

To do this more simply, you can use the function `t.test` with the relevant vector and use `conf.level=…` to define the relevant percentage. R then computes a significance test the details of which are not relevant yet, which is why we only look at the confidence interval (with `$conf.int`):

```
> t.test(LENGTH, conf.level=0.95)$conf.int¶
[1] 891.3354 938.7506
attr(,"conf.level")
[1] 0.95
```

This confidence interval

> identifies a range of values a researcher can be 95% confident contains the true value of a population parameter (e.g., a population mean). Stated in probabilistic terms, the researcher can state there is a probability/likelihood of .95 that the confidence interval contains the true value of the population parameter. (Sheskin 2011:75; see also Field, Miles, and Field 2012:45)[14]

Note that when you compare means of two roughly equally large samples and their 95%-confidence intervals do not overlap, then you know the sample means are significantly different and, therefore, you would assume that there is a real difference between the population means, too. However, if these intervals do overlap, this does not show that the means are not significantly different from each other (cf. Crawley 2005: 169f.).

1.5.2. Confidence intervals of percentages

The above logic with regard to means also applies to percentages. Given a particular percentage from a sample, you want to know what the corresponding percentage in the population is. As you already know, the percentage of silent disfluencies in our sample is 33.2%. Again, you would like to quantify your confidence in that sample percentage. As above, you compute the standard error for percentages according to the formula in (19), and then this standard error is inserted into the formula in (22).

14 A different way of explaining confidence intervals is this: "A common error is to misinterpret the confidence interval as a statement about the unknown parameter [here, the percentage in the population, STG]. It is not true that the probability that a parameter is included in a 95% confidence interval is 95%. What is true is that if we derive a large number of 95% confidence intervals, we can expect the true value of the parameter to be included in the computed intervals 95% of the time" (Good and Hardin 2012:156)

```
> se<-sqrt(0.332*(1-0.332)/1000); se¶
[1] 0.01489215
```

(22) $CI = a \pm z \cdot SE$

The parameter *z* in (22) corresponds to the *z*-score mentioned above in Section 1.3.4.3, which defines 5% of the area under a standard normal distribution – 2.5% from the upper part and 2.5% from the lower part:

```
> z.score<-qnorm(0.025, lower.tail=FALSE); z.score¶
[1] 1.959964
```

For a 95% confidence interval for the percentage of silences, you enter:

```
> z.score<-qnorm(0.025, lower.tail=FALSE)¶
> 0.332-z.score*se; 0.332+z.score*se¶
[1] 0.3028119
[1] 0.3611881
```

The simpler way requires the function `prop.test`, which tests whether a percentage obtained in a sample is significantly different from an expected percentage. Again, the functionality of that significance test is not relevant yet, but this function also returns the confidence interval for the observed percentage. R needs the observed frequency (332), the sample size (1000), and the probability for the confidence interval. R uses a formula different from ours but returns nearly the same result.

```
> prop.test(332, 1000, conf.level=0.95)$conf.int¶
[1] 0.3030166 0.3622912
attr(,"conf.level")
[1] 0.95
```

Recommendation(s) for further study
Dalgaard (2002: Ch. 7.1 and 4.1), Crawley (2005: 167ff.)

Warning/advice
Since confidence intervals are based on standard errors, the warning from above applies here, too: if data are not normally distributed or the samples too small, then you should probably use other methods to estimate confidence intervals (e.g., bootstrapping).

2. Bivariate statistics

We have so far dealt with statistics and graphs that describe one variable or vector/factor. In this section, we now turn to methods to characterize two variables and their relation. We will again begin with frequencies, then we will discuss means, and finally talk about correlations. You will see that we can use many functions from the previous sections.

2.1. Frequencies and crosstabulation

We begin with the case of two nominal/categorical variables. Usually, one wants to know which combinations of variable levels occur how often. The simplest way to do this is cross-tabulation. Let's return to the disfluencies:

```
> UHM<-read.delim(file.choose())¶
> attach(UHM)¶
```

Let's assume you wanted to see whether men and women differ with regard to the kind of disfluencies they produce. First two questions: are there dependent and independent variables in this design and, if so, which?

THINK BREAK

In this case, SEX is the independent variable and FILLER is the dependent variable. Computing the frequencies of variable level combinations in R is easy because you can use the same function that you use to compute frequencies of an individual variable's levels: `table`. You just give `table` a second vector or factor as an argument and R lists the levels of the first vector in the rows and the levels of the second in the columns:

```
> freqs<-table(FILLER, SEX); freqs¶
        SEX
FILLER    female male
  silence    171  161
  uh         161  233
  uhm        170  104
```

In fact you can provide even more vectors to `table`, just try it out, and we will return to this below. Again, you can create tables of percentages with `prop.table`, but with two-dimensional tables there are different ways to compute percentages and you can specify one with `margin=`…. The default is `margin=NULL`, which computes the percentages on the basis of all elements in the table. In other words, all percentages in the table add up to 1. Another possibility is to compute row percentages: set `margin=1` and you get percentages that add up to 1 in every row. Finally, you can choose column percentages by setting `margin=2`: the percentages in each column add up to 1. This is probably the best way here since then the percentages adding up to 1 are those of the dependent variable.

```
> percents<-prop.table(table(FILLER, SEX), margin=2)¶
> percents¶
         SEX
FILLER       female      male
  silence 0.3406375 0.3232932
  uh      0.3207171 0.4678715
  uhm     0.3386454 0.2088353
```

You can immediately see that men appear to prefer *uh* and disprefer *uhm* while women appear to have no real preference for any disfluency. However, we of course do not know yet whether this is a significant result.

The function `addmargins` outputs row and column totals (or other user-defined margins, such as means):

```
> addmargins(freqs) # cf. also colSums and rowSums¶
         SEX
FILLER    female male  Sum
  silence    171  161  332
  uh         161  233  394
  uhm        170  104  274
  Sum        502  498 1000
```

Recommendation(s) for further study
the functions `xtabs` and especially `ftable` to generate more complex tables

2.1.1. Bar plots and mosaic plots

Of course you can also represent such tables graphically. The simplest way involves providing a formula as the main argument to `plot`. Such formulae consist of a dependent variable (here: FILLER: `FILLER`), a tilde ("~" meaning 'as a function of'), and an independent variable (here: GENRE: `GENRE`).

```
> plot(FILLER~GENRE)¶
```

The widths and heights of rows, columns, and the six boxes represent the observed frequencies. For example, the column for dialogs is a little wider than that for monologs because there are more dialogs in the data; the row for *uh* is widest because *uh* is the most frequent disfluency, etc.

Other similar graphs can be generated with the following lines:

```
> plot(GENRE, FILLER)¶
> plot(table(GENRE, FILLER))¶
> mosaicplot(table(GENRE, FILLER))¶
```

These graphs are called stacked bar plots or mosaic plots and are – together with association plots to be introduced below – often effective ways of representing crosstabulated data. In the code file for this chapter you will find R code for another kind of useful graph.

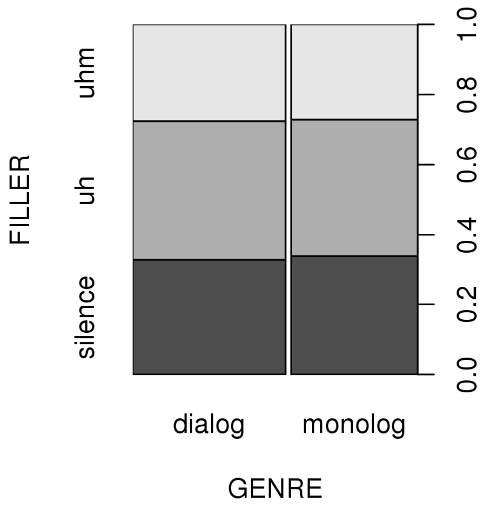


Figure 30. Stacked bar plot / mosaic plot for FILLER~GENRE

2.1.2. Spineplots

Sometimes, the dependent variable is nominal/categorical and the independent variable is interval/ratio-scaled. Let us assume that FILLER is the dependent variable, which is influenced by the independent variable LENGTH. (This does not make much sense here, we just do this for expository purposes.) You can use the function `spineplot` with a formula:

```
> spineplot(FILLER~LENGTH)¶
```

The *y*-axis represents the dependent variable and its three levels. The *x*-axis represents the independent ratio-scaled variable, which is split up into the value ranges that would also result from `hist` (which also means you can change the ranges with `breaks=`…; cf. Section 3.1.1.5 above).

2.1.3. Line plots

Apart from these plots, you can also generate line plots that summarize frequencies. If you generate a table of relative frequencies, then you can create a primitive line plot by entering the code shown below.

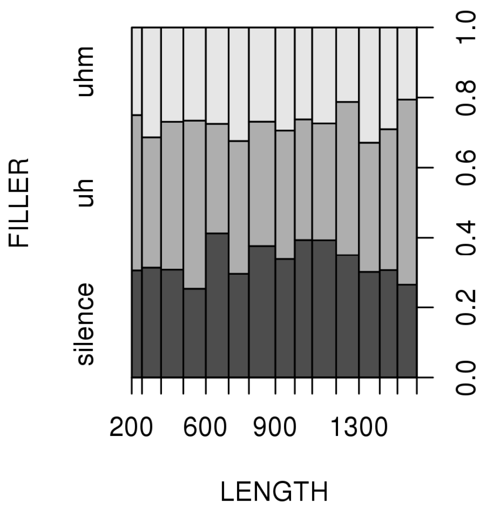


Figure 31. Spineplot for FILLER~LENGTH

```
> fill.table<-prop.table(table(FILLER, SEX), 2); fill.table¶
         SEX
FILLER       female      male
  silence 0.3406375 0.3232932
  uh      0.3207171 0.4678715
  uhm     0.3386454 0.2088353
> plot(fil.table[,1], ylim=c(0, 0.5), xlab="Disfluency",
   ylab="Relative frequency", type="b")¶
> points(fil.table[,2], type="b")¶
```

However, somewhat more advanced code in the companion file shows you how you can generate the graph in Figure 32. (Again, you may not understand the code immediately, but it will not take you long.)

Warning/advice
Sometimes, it is recommended to not represent such frequency data with a line plot like this because the lines ‘suggest’ that there are frequency values between the levels of the categorical variable, which is of course not the case. Again, you should definitely explore the function `dotchart` for this.

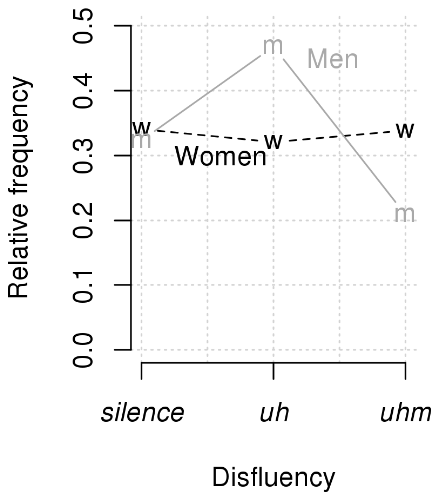


Figure 32. Line plot with the percentages of the interaction of SEX and FILLER

Recommendation(s) for further study
the function `plotmeans` (from the library `gplots`) to plot line plots with means and confidence intervals

2.2. Means

If the dependent variable is interval/ratio-scaled or ordinal and the independent variable is nominal/categorical, then one is often not interested in the frequencies of particular values of the dependent variable, but its central tendencies at each level of the independent variable. For example, you might want to determine whether men and women differ with regard to the average disfluency lengths. One way to get these means is the following:

```
> mean(LENGTH[SEX=="female"])¶
[1] 928.3984
> mean(LENGTH[SEX=="male"])¶
[1] 901.5803
```

This approach is too primitive for three reasons:

– you must define the values of LENGTH that you want to include manually, which requires a lot of typing (especially when the independent variable has more than two levels or, even worse, when you have more than one independent variable);
– you must know all relevant levels of the independent variables – otherwise you couldn't use them for subsetting in the first place;
– you only get the means of the variable levels you have explicitly asked for. However, if, for example, you made a coding mistake in one row – such as entering "malle" instead of "male" – this approach will not show you that.

Thus, we use an extremely useful function called `tapply`, which mostly takes three arguments. The first is a vector or factor to which you want to apply a function – here, this is LENGTH, to which we want to apply `mean`. The second argument is a vector or factor that has as many elements as the first one and that specifies the groups of values from the first vector/factor to which the function is to be applied. The last argument is the relevant function, here `mean`. We get:

```
> tapply(LENGTH, SEX, mean)¶
  female     male
928.3984 901.5803
```

Of course the result is the same as above, but you obtained it in a better way. You can of course use functions other than `mean`: `median`, `IQR`, `sd`, `var`, …, even functions you wrote yourself. For example, what do you get when you use `length`? The numbers of lengths observed for each sex.

2.2.1. Boxplots

In Section 3.1.3.7 above, we looked at boxplots, but restricted our attention to cases where we have one or more dependent variables (such as `town1` and `town2`). However, you can also use boxplots for cases where you have one or more independent variables and a dependent variable. Again, the easiest way is to use a formula with the tilde meaning 'as a function of':

```
> boxplot(LENGTH~GENRE, notch=TRUE, ylim=c(0, 1600))¶
```

(If you only want to plot a boxplot and not provide any further arguments, it is actually enough to just enter `plot(LENGTH~GENRE)¶`: R 'infers' you want a boxplot because `LENGTH` is a numerical vector and `GENRE` is a factor.) Again, you can infer a lot from that plot: both medians are close to 900 ms and do most likely not differ significantly from each other (since the notches overlap). Both genres appear to have about the same amount of dispersion since the notches, the boxes, and the whiskers are nearly equally large, and both genres have no outliers.

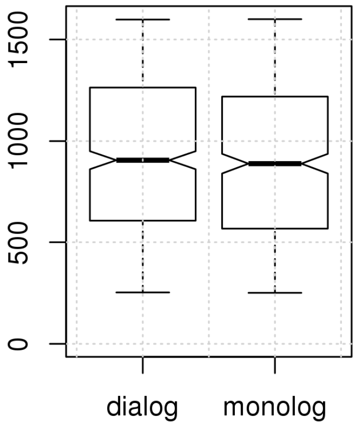


Figure 33. Boxplot for LENGTH~GENRE

Quick question: can you infer what this line does?

```
> text(seq(levels(GENRE)), tapply(LENGTH, GENRE, mean), "+")¶
```

THINK BREAK

It adds plusses into the boxplot representing the means of `LENGTH` for each `GENRE`: `seq(levels(GENRE))` returns 1:2, which is used as the *x*-

coordinates; the `tapply` code returns the means of `LENGTH` for each `GENRE`, and the `"+"` is what is plotted.

2.2.2. Interaction plots

So far we have looked at graphs representing one variable or one variable depending on another variable. However, there are also cases where you want to characterize the distribution of one interval/ratio-scaled variable depending on two, say, nominal/categorical variables. You can again obtain the means of the variable level combinations of the independent variables with `tapply`. You must specify the two independent variables in the form of a list, and the following two examples show you how you get the same means in two different ways (so that you see which variable goes into the rows and which into the columns):

```
> tapply(LENGTH, list(SEX, FILLER), mean)¶
        silence       uh      uhm
female 942.3333 940.5652 902.8588
male   891.6894 904.9785 909.2788
> tapply(LENGTH, list(FILLER, SEX), mean)¶
          female     male
silence 942.3333 891.6894
uh      940.5652 904.9785
uhm     902.8588 909.2788
```

Such results are best shown in tabular form such that you don't just provide the above means of the interactions as they were represented in Figure 32 above, but also the means of the individual variables. Consider Table 17 and the formula in its caption exemplifying the relevant R syntax.

Table 17. Means for LENGTH ~ FILLER * SEX

	SEX: *FEMALE*	SEX: *MALE*	Total
FILLER: *SILENCE*	942.33	891.69	917.77
FILLER: *UH*	940.57	904.98	919.52
FILLER: *UHM*	902.86	909.28	905.3
TOTAL	928.4	901.58	915.04

A plus sign between variables refers to just adding *main effects* of variables (i.e., effects of variables *in isolation*, e.g. when you only inspect the two means for SEX in the bottom row of totals or the three means for FILLER in the rightmost column of totals). A colon between variables refers to only the interaction of the variables (i.e., effects of combinations of variables as when you inspect the six means in the main body of the table where SEX and FILLER are *combined*). Finally, an asterisk between variables denotes both the main effects *and* the interaction (here, all 12 means). With two variables `A` and `B`, `A*B` is the same as `A + B + A:B`.

Now to the results. These are often easier to understand when they are represented graphically. You can create and configure an interaction plot manually, but for a quick and dirty glance at the data, you can also use the function `interaction.plot`. As you might expect, this function takes at least three arguments:

– `x.factor`: a vector/factor whose values/levels are represented on the *x*-axis;
– `trace.factor`: the second argument is a vector/factor whose values/levels are represented with different lines;
– `response`: the third argument is a vector whose means for all variable level combinations will be represented on the *y*-axis by the lines.

That means, you can choose one of two formats, depending on which independent variable is shown on the *x*-axis and which is shown with different lines. While the represented means will of course be identical, I advise you to *always* generate and inspect both graphs anyway because one of the two graphs is usually easier to interpret. In Figure 34, you find both graphs for the above values and I prefer the lower panel.

```
> interaction.plot(FILLER, SEX, LENGTH); grid()¶
> interaction.plot(SEX, FILLER, LENGTH); grid()¶
```

Obviously, *uhm* behaves differently from *uh* and silences: the average lengths of women's *uh* and silence are larger than those of men, but the average length of women's *uhm* is smaller than that of men. But now an important question: why should you now not just report the means you computed with `tapply` and the graphs in Figure 34 in your study?

THINK BREAK

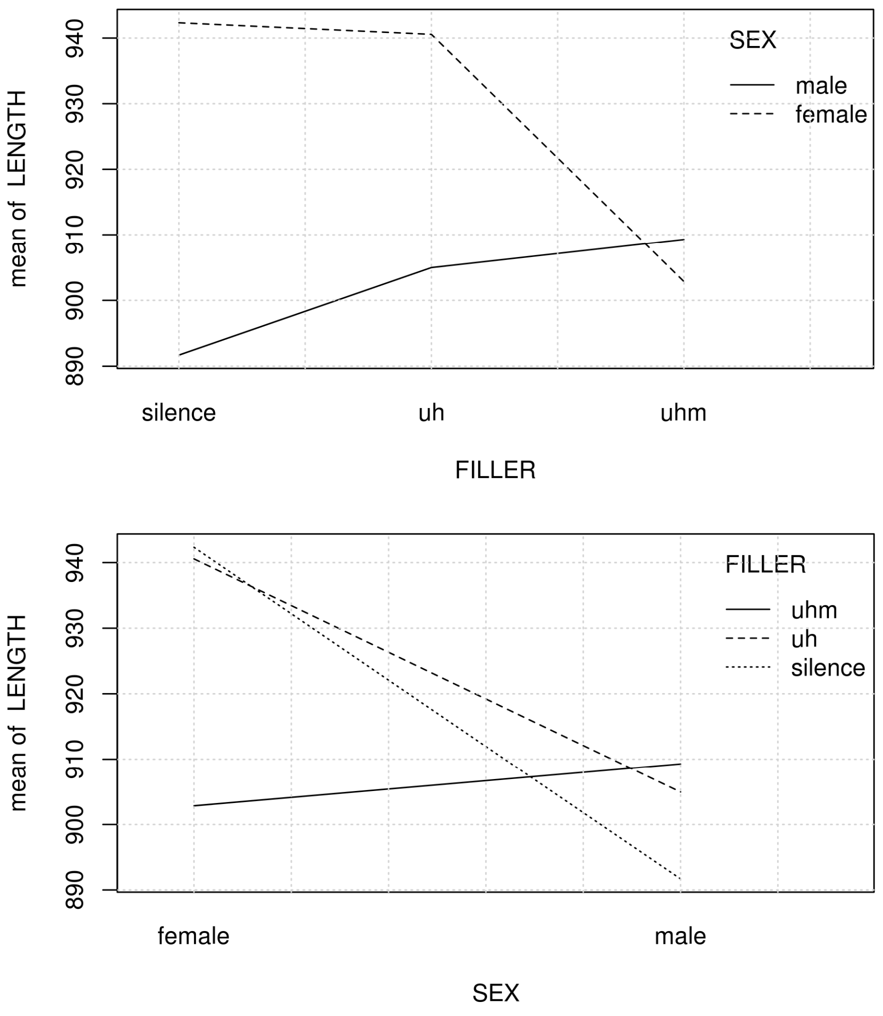
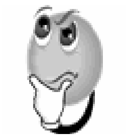


Figure 34. Interaction plot for LENGTH ~ FILLER : SEX

First, you should not just report the means like this because I told you to never ever report means without a measure of dispersion. Thus, when you want to provide the means, you must also add, say, standard deviations, standard errors, confidence intervals:

```
> tapply(LENGTH, list(SEX, FILLER), sd)¶
        silence       uh      uhm
female 361.9081 397.4948 378.8790
male   370.6995 397.1380 382.3137
```

How do you get the standard errors and the confidence intervals?



THINK BREAK

```
> se<-tapply(LENGTH, list(SEX, FILLER), sd)/
   sqrt(tapply(LENGTH, list(SEX, FILLER), length)); se¶
        silence       uh      uhm
female 27.67581 31.32698 29.05869
male   29.21522 26.01738 37.48895

> t.value<-qt(0.025, df=999, lower.tail=FALSE); t.value¶
[1] 1.962341
> tapply(LENGTH, list(SEX, FILLER), mean)-(t.value*se)¶
        silence       uh      uhm
female 888.0240 879.0910 845.8357
male   834.3592 853.9236 835.7127
> tapply(LENGTH, list(SEX, FILLER), mean)+(t.value*se)¶
        silence       uh      uhm
female 996.6427 1002.0394 959.882
male   949.0197  956.0335 982.845
```

And this output immediately shows again why measures of dispersion are important: the standard deviations are large and the means plus/minus one standard error overlap (as do the confidence intervals), which shows that the differences are not significant. You can see this with `boxplot`, which allows formulae with more than one independent variable (`boxplot( LENGTH~SEX*FILLER, notch=TRUE)¶`, with an asterisk for the interaction).

Second, the graphs should not be used as they are (at least not uncritically) because R has chosen the range of the *y*-axis such that it is as small as possible but still covers all necessary data points. However, this small range on the *y*-axis has visually inflated the differences in Figure 34 – a more realistic representation would have either included the value $y = 0$ (as in the first pair of the following four lines) or chosen the range of the *y*-axis such that the complete range of LENGTH is included (as in the second pair of the following four lines):

```
> interaction.plot(SEX, FILLER, LENGTH, ylim=c(0, 1000))¶
> interaction.plot(FILLER, SEX, LENGTH, ylim=c(0, 1000))¶
> interaction.plot(SEX, FILLER, LENGTH, ylim=range(LENGTH))¶
> interaction.plot(FILLER, SEX, LENGTH, ylim=range(LENGTH))¶
```

2.3. Coefficients of correlation and linear regression

The last section in this chapter is devoted to cases where both the dependent and the independent variable are ratio-scaled. For this scenario we turn to a new data set. First, we clear our memory of all data structures we have used so far:

```
> rm(list=ls(all=TRUE))¶
```

We look at data to determine whether there is a correlation between the reaction times in ms of second language learners in a lexical decision task and the length of the stimulus words. We have

– a dependent ratio-scaled variable: the reaction time in ms MS_LEARNER, whose correlation with the following independent variable we are interested in;
– an independent ratio-scaled variable: the length of the stimulus words LENGTH (in letters).

Such correlations are typically quantified using a so-called coefficient of correlation *r*. This coefficient, and many others, are defined to fall in the range between -1 and +1. Table 18 explains what the values mean: the sign of a correlation coefficient reflects the *direction* of the correlation, and the absolute size reflects the *strength* of the correlation. When the correlation coefficient is 0, then there is no correlation between the two variables in question, which is why H_0 says $r = 0$ – the two-tailed H_1 says $r \neq 0$.

Table 18. Correlation coefficients and their interpretation

Correlation coefficient	Labeling the correlation	Kind of correlation
$0.7 < r \leq 1$	very high	positive correlation:
$0.5 < r \leq 0.7$	high	the more/higher …, the more/higher …
$0.2 < r \leq 0.5$	intermediate	the less/lower …, the less/lower …
$0 < r \leq 0.2$	low	
$r \approx 0$	no statistical correlation (H_0)	
$0 > r \geq -0.2$	low	negative correlation:
$-0.2 > r \geq -0.5$	intermediate	the more/higher …, the less/lower …
$-0.5 > r \geq -0.7$	high	the less/lower …, the more/higher …
$-0.7 > r \geq -1$	very high	

Let us load and plot the data, using by now familiar lines of code:

```
> ReactTime<-read.delim(file.choose())¶
> str(ReactTime); attach(ReactTime)¶
'data.frame':   20 obs. of  3 variables:
 $ CASE      : int  1 2 3 4 5 6 7 8 9 10 ...
 $ LENGTH    : int  14 12 11 12 5 9 8 11 9 11 ...
 $ MS_LEARNER: int  233 213 221 206 123 176 195 207 172 ...
> plot(MS_LEARNER~LENGTH, xlim=c(0, 15), ylim=c(0, 300),
   xlab="Word length in letters", ylab="Reaction time of
   learners in ms"); grid()¶
```

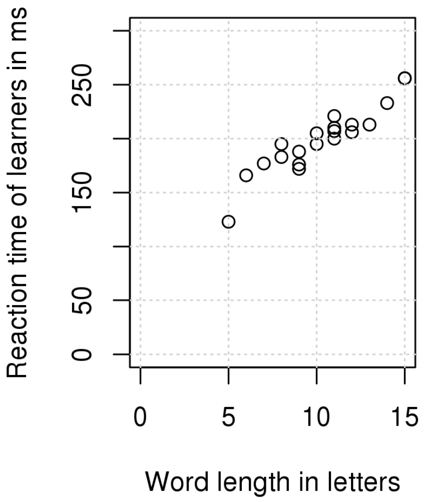


Figure 35. Scatterplot[15] for MS_LEARNER~LENGTH

What kind of correlation is that, a positive or a negative one?

THINK BREAK

This is a positive correlation, because we can describe it with a "the more …, the more …" statement: the longer the word, the longer the reaction time: when you move from the left (short words) to the right (long words), the reaction times get higher. But we also want to quantify the correlation and compute the Pearson product-moment correlation *r*.

15 Check the code file for how to handle overlapping points.

First, we do this manually: We begin by computing the *covariance* of the two variables according to the formula in (23).

(23) $$Covariance_{x,\,y} = \frac{\sum_{i=1}^{n} \left(x_i - \bar{x}\right) \cdot \left(y_i - \bar{y}\right)}{n-1}$$

As you can see, the covariance involves computing the differences of each variable's value from the variable's mean. For example, when the *i*-th value of both the vector *x* and the vector *y* are above the averages of *x* and *y*, then this pair of *i*-th values will contribute a positive value to the covariance. In R, we can compute the covariance manually or with the function `cov`, which requires the two relevant vectors:

```
> covariance<-sum((LENGTH-mean(LENGTH))*(MS_LEARNER-
  mean(MS_LEARNER)))/(length(MS_LEARNER)-1)¶
> covariance<-cov(LENGTH, MS_LEARNER); covariance¶
[1] 79.28947
```

The sign of the covariance already indicates whether two variables are positively or negatively correlated; here it is positive. However, we cannot use the covariance to quantify the correlation between two vectors because its size depends on the scale of the two vectors: if you multiply both vectors with 10, the covariance becomes 100 times as large as before although the correlation as such has of course not changed:

```
> cov(MS_LEARNER*10, LENGTH*10)¶
[1] 7928.947
```

Therefore, we divide the covariance by the product of the standard deviations of the two vectors and obtain *r*. This is a very high positive correlation, *r* is close to the theoretical maximum of 1. In R, we can do all this more efficiently with the function `cor`. Its first two arguments are the two vectors in question, and the third specifies the desired kind of correlation:

```
> covariance/(sd(LENGTH)*sd(MS_LEARNER))¶
[1] 0.9337171
> cor(MS_LEARNER, LENGTH, method="pearson")¶
[1] 0.9337171
```

The correlation can be investigated more closely, though. We can try to predict values of the dependent variable on the basis of the independent one. This method is called *linear regression*. In its simplest form, it involves trying to draw a straight line in such a way that it represents the scattercloud best. Here, *best* is defined as 'minimizing the sums of the squared vertical distances of the observed *y*-values (here: reaction times) and the predicted *y*-values reflected by the regression line.' That is, the regression line is drawn fairly directly through the scattercloud because then these deviations are smallest. It is defined by a regression equation with two parameters, an intercept *a* and a slope *b*. Without discussing the relevant formulae here, I immediately explain how to get these values with R. Using the formula notation you already know, you define and inspect a so-called linear model using the function `lm`:

```
> model<-lm(MS_LEARNER~LENGTH); model¶
Call:
lm(formula = MS_LEARNER ~ LENGTH)
Coefficients:
(Intercept)       LENGTH
      93.61        10.30
```

That is, the intercept – the *y*-value of the regression line at $x = 0$ – is 93.61, and the slope of the regression line is 10.3, which means that for every letter of a word the estimated reaction time increases by 10.3 ms. For example, our data do not contain a word with 16 letters, but since the correlation between the variables is so strong, we can come up with a good prediction for the reaction time such words might result in:

$$\begin{array}{ccccc} \text{predicted reaction time} & = & \text{intercept} & + & b \cdot \textsc{Length} \\ 258.41 & \approx & 93.61 & + & 10.3 \cdot 16 \end{array}$$

```
> 93.61+10.3*16¶
[1] 258.41
```

(This prediction of the reaction time is of course overly simplistic as it neglects the large number of other factors that influence reaction times but within the current linear model this is how it would be computed.) Alternatively, you can use the function `predict`, whose first argument is the (linear) model and whose second argument can be a data frame called `newdata` that contains a column with values for each independent variable for which you want to make a prediction. With the exception of differences resulting from me only using two decimals, you get the same result:

```
> predict(model, newdata=expand.grid(LENGTH=16))¶
[1] 258.4850
```

The use of `expand.grid` is overkill here for a data frame with a single length but I am using it here because it anticipates our uses of `predict` and `expand.grid` below where we can actually get predictions for a large number of values in one go (as in the following; the output is not shown here):

```
> predict(model, newdata=expand.grid(LENGTH=1:16))¶
```

If you only use the model as an argument to `predict`, you get the values the model predicts for every observed word length in your data in the order of the data points (same with `fitted`).

```
> round(predict(model), 2)¶
     1      2      3      4      5      6      7      8
237.88 217.27 206.96 217.27 145.14 186.35 176.05 206.96
     9     10     11     12     13     14     15     16
186.35 206.96 196.66 165.75 248.18 227.57 248.18 186.35
    17     18     19     20
196.66 155.44 176.05 206.96
```

The first value of LENGTH is 14, so the first of the above values is the reaction time we expect for a word with 14 letters, etc. Since you now have the needed parameters, you can also draw the regression line. You do this with the function `abline`, which either takes a linear model object as an argument or the intercept and the slope; cf. Figure 36:

```
> plot(MS_LEARNER~LENGTH, xlim=c(0, 15), ylim=c(0, 300),
   xlab="Word length in letters", ylab="Reaction time of
   learners in ms"); grid()¶
> abline(model) # abline(93.61, 10.3)¶
```

It is obvious why the correlation coefficient is so high: the regression line is an excellent summary of the data points since all points are fairly close to it. (Below, we will see two ways of making this graph more informative.) We can even easily check how far away every predicted value is from its observed value.

This difference – the vertical distance between an observed y-value / reaction time and the y-value on the regression line for the corresponding x-value – is called a *residual*, and the function `residuals` requires just the linear model object as its argument.

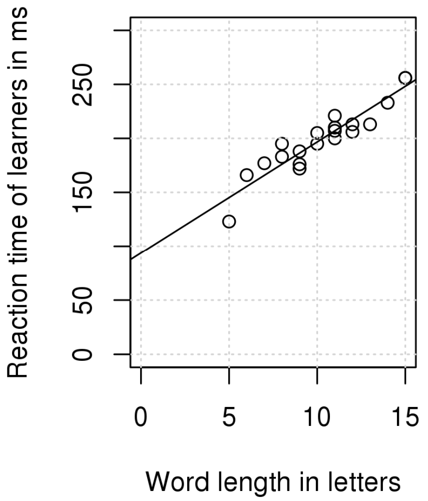


Figure 36. Scatterplot with regressions line for MS_LEARNER~LENGTH

```
> round(residuals(model), 2)¶
     1      2      3      4      5      6      7      8
 -4.88  -4.27  14.04 -11.27 -22.14 -10.35  18.95   0.04
     9     10     11     12     13     14     15     16
-14.35  -6.96   8.34  11.25   7.82 -14.57   7.82   1.65
    17     18     19     20
  -1.66 10.56   6.95   3.04
```

You can easily test manually that these are in fact the residuals:

```
> round(MS_LEARNER-(predict(model)+residuals(model)), 2)¶
 1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20
 0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0
```

Note two important points though: First, regression equations and lines are most useful for the range of values covered by the observed values. Here, the regression equation was computed on the basis of lengths between 5 and 15 letters, which means that it will probably be much less reliable for lengths of 50+ letters. Second, in this case the regression equation also makes some rather non-sensical predictions because theoretically/mathematically it predicts reactions times of around 0 ms for word lengths of -9. Such considerations will become important later on.

The correlation coefficient *r* also allows you to specify how much of the variance of one variable can be accounted for by the other variable. What does that mean? In our example, the values of both variables –

MS_LEARNER and LENGTH – are not all identical: they vary around their means and this variation was called dispersion and quantified with the standard deviation or the variance. If you square *r* and multiply the result by 100, then you obtain the amount of variance of one variable that the other variable accounts for. In our example, $r = 0.933$, which means that 87.18% of the variance of the reaction times can be accounted for – in a statistical sense, not necessarily a cause-effect sense – on the basis of the word lengths. This value, r^2, is referred to as *coefficient of determination*.

Incidentally, I sometimes heard students or colleages compare two *r*-values such that they say something like, "Oh, here $r = 0.6$, nice, that's twice as much as in this other data set, where $r = 0.3$." Even numerically speaking, this is at least misleading, if nothing worse. Yes, 0.6 is twice as high as 0.3, but one should not compare *r*-values directly like this – one has to apply the so-called Fisher's *Z*-transformation first, which is exemplified in the following two lines:

```
> r<-0.3; 0.5*log((1+r)/(1-r))¶
[1] 0.3095196
> r<-0.6; 0.5*log((1+r)/(1-r))¶
[1] 0.6931472
> 0.6931472/0.3095196
[1] 2.239429
```

Thus, an *r*-value of 0.6 is twice as high as one of 0.3, but it reflects a correlation that is in fact nearly $2^1/_4$ times as strong. How about writing a function `fisher.z` that would compute *Z* from *r* for you …

The product-moment correlation *r* is probably the most frequently used correlation. However, there are a few occasions on which it should not be used. First, when the relevant variables are not interval/ratio-scaled but ordinal or when they are not both normally distributed (cf. below Section 4.4), then it is better to use another correlation coefficient, for example Kendall's tau τ. This correlation coefficient is based only on the ranks of the variable values and thus more suited for ordinal data. Second, when there are marked outliers in the variables, then you should also use Kendall's τ, because as a measure that is based on ordinal information only it is, just like the median, less sensitive to outliers. Cf. Figure 37, which shows a scatterplot with one noteworthy outlier in the top right corner. If you cannot justify excluding this data point, then it can influence *r* very strongly, but not τ. Pearson's *r* and Kendall's τ for all data points but the outlier are 0.11 and 0.1 respectively, and the regression line with the small slope shows that there is clearly no correlation between the two variables. However, if we include the outlier, then Pearson's *r* suddenly becomes 0.75 (and the regression line's slope is changed markedly) while Kendall's *τ* remains appropriately small: 0.14.

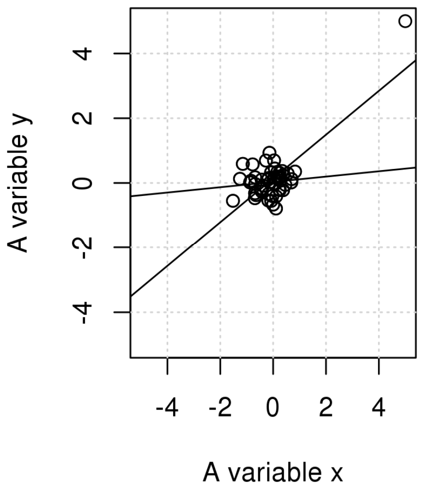


Figure 37. The effect of outliers on *r*

But how do you compute Kendall's *τ*? The computation of Kendall's *τ* is rather complex (especially with larger samples and ties), which is why I only explain how to compute it with R. The function is actually the same as for Pearson's *r* – `cor` – but the argument `method=…` is changed. For our experimental data we again get a high correlation, which turns out to be a little bit smaller than *r*. (Note that correlations are bidirectional – the order of the vectors does not matter – but linear regressions are not because you have a dependent and an independent variable and it matters what goes before the tilde – that which is predicted – and what goes after it.)

```
> cor(LENGTH, MS_LEARNER, method="kendall")¶
[1] 0.8189904
```

The previous explanations were all based on the assumption that there is in fact a linear correlation between the two variables or one that is best characterized with a straight line. This need not be the case, though, and a third scenario in which neither *r* nor *τ* are particularly useful involves cases where these assumptions do not hold. Often, this can be seen by just looking at the data. Figure 38 represents a well-known example from Anscombe (1973) (from <_inputfiles/03-2-3_anscombe.csv>), which has the intriguing characteristics that

– the means and variances of the *x*-variable;
– the means and variances of the *y*-variable;
– the correlations and the linear regression lines of *x* and *y*;

are all identical although the distributions are obviously very different.

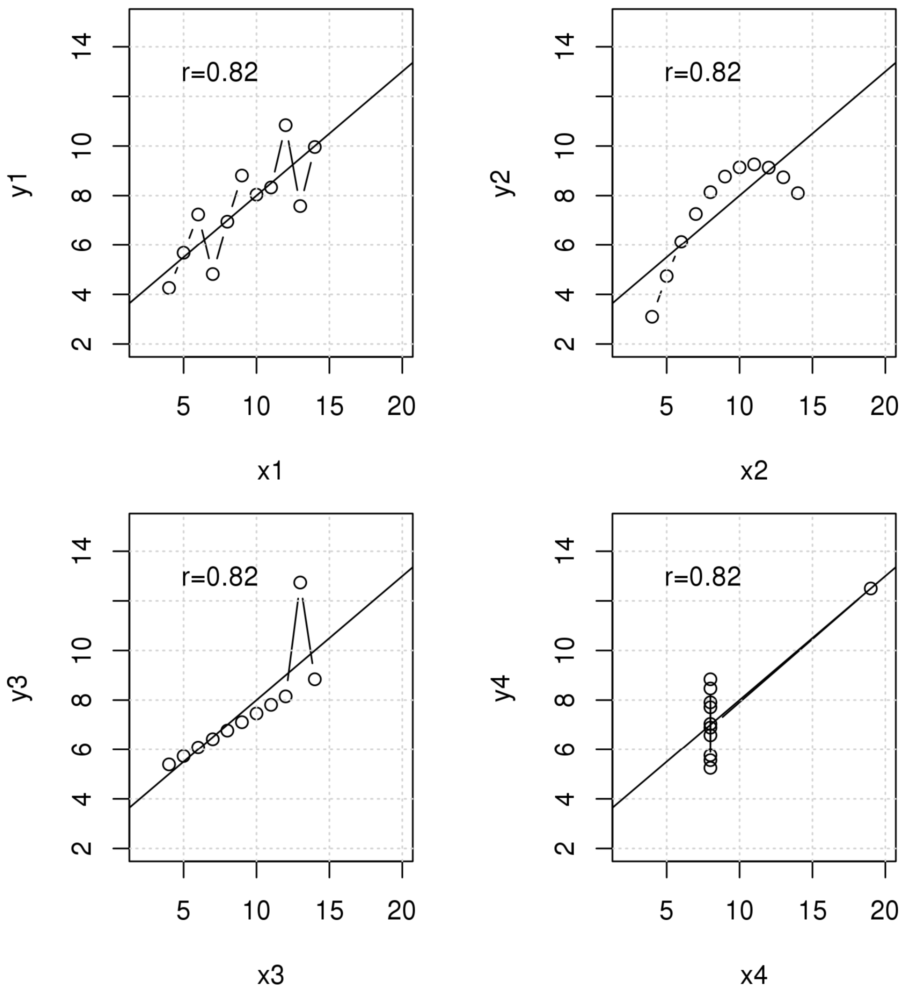


Figure 38. The sensitivity of linear correlations: the Anscombe data

In the top left of Figure 38, there is a case where r and τ are unproblematic. In the top right we have a situation where x and y are related in a curvilinear fashion – using a linear correlation here does not make much sense.[16] In the two lower panels, you see distributions in which individual outliers have a huge influence on r and the regression line. Since all the summary statistics are identical, this example illustrates most beautifully how important, in fact *indispensable*, a visual inspection of your data is, which is why in the following chapters visual exploration nearly always precedes statistical computation.

Now you should do the exercise(s) for Chapter 3 …

Warning/advice

Do not let the multitude of graphical functions and settings of R and/or your spreadsheet software tempt you to produce visual overkill. Just because you *can* use 6 different fonts, 10 colors, and cute little smiley symbols does not mean you *should*: Visualization should help you and/or the reader understand something otherwise difficult to grasp, which also means you should make sure your graphs are fairly self-sufficient, i.e. contain all the information required to understand them (e.g., meaningful graph and axis labels, legends, etc.) – a graph may need an explanation, but if the explanation is three quarters of a page, chances are your graph is not helpful (cf. Keen 2010: Chapter 1).

Recommendation(s) for further study

- the function `s.hist` (from the library `ade4`) and `scatterplot` (from the library `car`) to produce more refined scatterplots with histograms or boxplots
- Good and Hardin (2012: Ch. 8), Crawley (2007: Ch. 5, 27), Braun and Murdoch (2008: Section 3.2), and Keen (2010) for much advice to create good graphs; cf. also <http://cran.r-project.org/src/contrib/Views/Graphics.html>

16. I do not discuss nonlinear regressions; cf. Crawley (2007: Ch. 18, 20) for overviews.