Math2041/2042 Statistics for Civil and Environmental Engineering

Sujit K. Sahu
School of Mathematics,
University of Southampton, UK.

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Contents

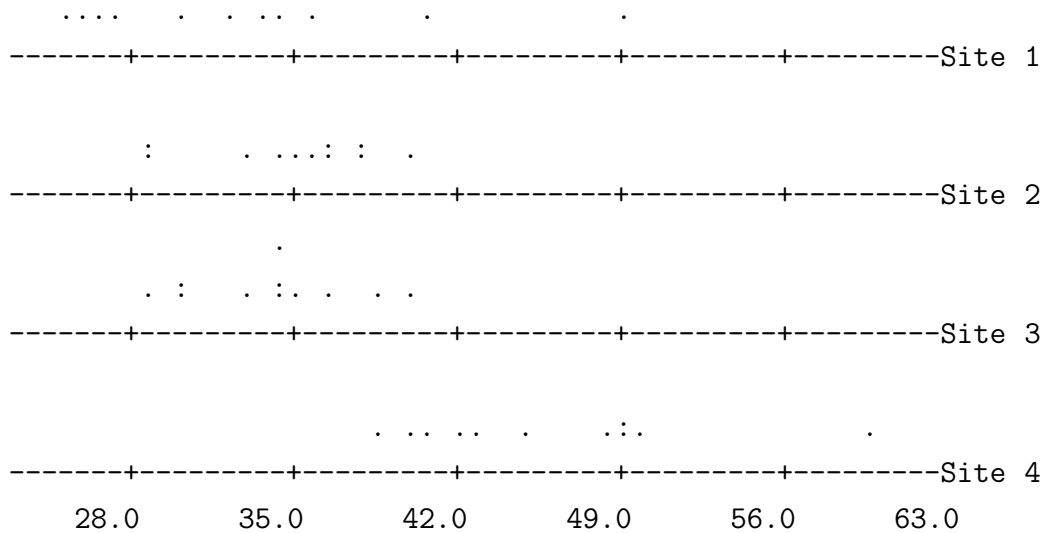
Chapter 1

Summarising Data

In statistical data analysis, the number of experimental or observational units (and the number of variables) is often large. For presentation purposes, it is impractical to present the whole data. Furthermore, the data are often not particularly informative when presented as a complete list of observations. A better way of presenting data is to pick out the important features using **summary measures** or **graphical displays**.

1.1 Summary Measures

The data in the file `silt2.dat` were collected as part of an investigation into soil variability. Soil samples were obtained in each of 4 sites in the province of Murcia, Spain, and the percentage of clay was determined. At each site, 11 observations were made (at random points in a 10m×10m area). The eleven observations for each of the first four sites are presented in the dotplot below.



Clearly there are some differences in the distributions of the observations at each of the sites. These differences can be described in terms of the **location** and **spread** of the data.

1.1.1 The Mean

Any summary measure which indicates the centre of a set of observations is a **measure of location** or a **measure of central tendency**. Perhaps the most often used measure of location is the **mean** of the observations.

Suppose that we have n observations of a variable X, and the values of the observations are denoted by $x_1, x_2, \ldots, x_n$, then we denote the mean by $\overline{x}$, and

$$\overline{x} \;=\; \frac{1}{n}\sum_{i=1}^{n} x_i \;=\; \frac{x_1 + x_2 + x_3 + \cdots + x_n}{n}$$

♡ **Example** 1.1.

For the data in the file `silt2.dat`, the mean percentage clay for the first site is given by

$$\begin{aligned}\overline{x} &= \tfrac{30.3+27.6+40.9+32.2+33.7+26.6+26.1+34.2+25.4+35.4+48.7}{11} \\ &= \tfrac{361.1}{11} \;=\; 32.83\end{aligned}$$

Similarly, the mean percentages of clay for sites 2, 3 and 4 are 34.80, 34.05 and 45.77 respectively. Clearly, presenting the mean conveys the information that the distributions of observations for sites 1,2 and 3 have similar locations while the observations for site 4 are generally larger.

In MINITAB

```
MTB > mean c1
```

Calc→Column Statistics

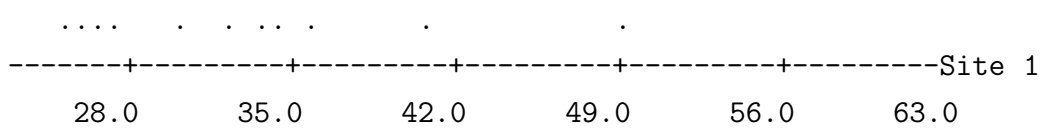
Stat→Basic Statistics→Display Descriptive Statistics

1.1.2 The Median

An alternative to the mean as a measure of location is the **median** of the observations. The median is the 'middle' value.

For example, the eleven observations of the clay percentage for the first site are, when placed in order

25.4 26.1 26.6 27.6 30.3 32.2 33.7 34.2 35.4 40.9 48.7



Similarly, the median percentages of clay for sites 2, 3 and 4 are 35.9, 34.5 and 44.5 respectively. Again, the median conveys the information that the distributions of observations for sites 1,2 and 3 have similar locations while the observations for site 4 are generally larger. If there are an **even** number of observations, then there isn't a single 'middle observation' and the median is defined to be half way between the 'middle two' observations.

In general:

if we have an odd number of observations, then the median is the value of the $\frac{n+1}{2}$th largest.

if we have an even number of observations, then the median is the mean of (half way between) the $\frac{n}{2}$th largest and the $(\frac{n}{2}+1)$th largest.

In MINITAB

```
MTB > median c1
```

Calc→Column Statistics

Stat→Basic Statistics→Display Descriptive Statistics

Why use the median rather than the mean?

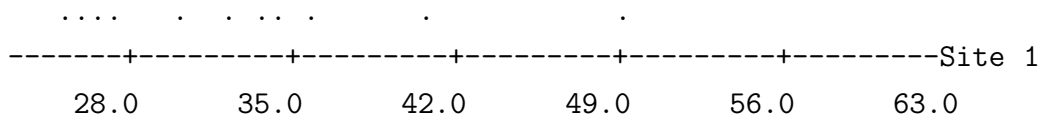
The mean is the summary of location which is most often calculated and quoted. However, there are situations where the median provides a better summary of location.

The median is much less sensitive (more robust) in situations where there are a small number of extreme observations. It is a better measure of a 'typical observation'. (Indeed, it often is the value of an actual observation). However, the mean has many nice 'statistical properties' which we shall discuss later.

1.1.3 Measures of Spread

Any summary measure which indicates the amount of dispersion of a set of observations is a **measure of spread**.

The easiest measure of spread to calculate is the **range** of the data, the difference between the smallest and largest observations. For example, consider the eleven observations of the clay percentage for the first site.



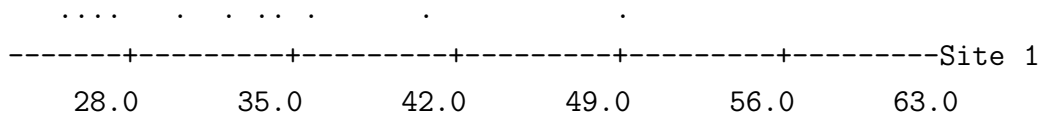
The range for the percentages of clay for sites 2, 3 and 4 are 11.4, 11.3 and 21.4 respectively. This conveys the information that the observations for sites 2 and 3 have a very similar spread, which is somewhat smaller to that for sites 1 or 4.

However, the range is not a very useful measure of spread, as it is extremely sensitive to the values of the two extreme observations. Furthermore, it gives little information about the distribution of the observations between the two extremes.

A more robust measure of spread is the **interquartile range** (or quartile range). This is the difference between the **lower quartile** and **upper quartile**.

The lower and upper quartiles, together with the median, divide the observations up into four sets of equal size.

For example, for the eleven observations of the clay percentage for the first site



In general:

the upper quartile is the value of the $\frac{3}{4}(n+1)$th largest.

the lower quartile is the value of the $\frac{1}{4}(n+1)$th largest

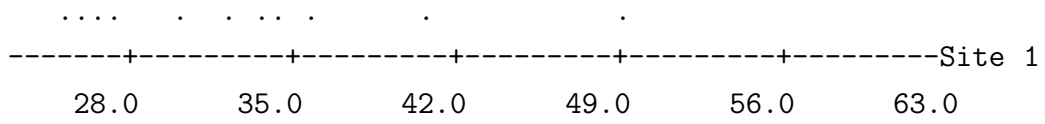
If $n+1$ is not divisible by 4 then some interpolation is required. However, MINITAB does this for us.

The interquartile range may be interpreted as the range in which the 'middle half' of the observations lie.

For the sets of observations of clay percentages for the four sites, the interquartile ranges are 8.8, 4.9, 6.5 and 8.7, which again illustrates the difference in spread between the observations for sites 1 and 4, and those for sites 2 and 3.

Although the range and the interquartile range are easy to calculate and interpret, they do not have nice statistical properties. For future use, we shall define a further measure of spread called the **standard deviation**.

Recall that we denote the n observations by $x_1, x_2, \ldots, x_n$ and the mean of the sample by $\overline{x}$. Then for each observation x_i, $i = 1, 2, \ldots, n$, $x_i - \overline{x}$ is the difference between that observation and the mean.



Some values of $x_i - \overline{x}$ are positive and some are negative.

However, all values of $(x_i - \overline{x})^2$ are positive, and the larger values of $(x_i - \overline{x})^2$ correspond to values which are further away from the mean.

We define the **variance** of the observations to be the sum of the values of $(x_i - \overline{x})^2$ for all observations, divided by $n - 1$. (If we divide by n here, we would have the mean value of $(x_i - \overline{x})^2$, but this does not have such nice statistical properties). Hence the variance, denoted by s^2 is given by

$$s^2 = \frac{1}{n-1} \sum_{i=1}^{n} (x_i - \overline{x})^2$$

The **standard deviation** of the observations, which we denote by s, is the square root of the variance.

If the observations are more highly spread out, then in general they will be a greater distance from the mean (which indicates the 'centre' of the observations) and therefore the standard deviation will be greater.

Therefore, the standard deviation is a measure of spread.

For the sets of observations of clay percentages for the four sites, the standard deviations are 7.07, 3.66, 3.55 and 6.17, which again illustrates the difference in spread between the observations for sites 1 and 4, and those for sites 2 and 3.

Measures of spread in MINITAB

Calc→Column Statistics

Stat→Basic Statistics→Display Descriptive Statistics

1.1.4 Accuracy

Summary statistics such as means and standard deviations may often be produced with a large number of decimal places.

There is no 'golden rule' as to how many decimal places should be reported, but a number of points should be taken into consideration.

1. Consider the accuracy to which the data have been measured.

   If summaries are presented containing many more decimal places, then this provides 'spurious' accuracy which is not justified by the data collection process.

If summaries are presented containing many fewer decimal places, then important information may be lost.

2. For continuous data, consider the variability of the data.

   For example, if all the observations are the same up to and including the first decimal place, with variability occuring in the second decimal place and beyond, then clearly at least two, and probably more decimal places, are required.

3. For discrete data, there is no need for summaries to be reported on the same scale as the data.

   For example, it is perfectly reasonable that the mean of a set of counts may not be a whole number.

4. Do not truncate trailing zeros.

   Once you have decided on a certain number of decimal places to report, then report them all, even if the last one is a zero. Otherwise you are throwing away information.

1.2 Graphical Displays of Data

Often, a simple graphical display provides a more easily interpretable summary of the distribution of the observations than a collection of summary statistics.

One graphical display, which is easy to construct, and incorporates many of the features of the summary measures introduced in §1.1 is the **box-and-whisker plot** (or simply **boxplot**).

1.2.1 The Boxplot

We will illustrate this using data in the file `quake.dat` which represent the time in days between successive serious earthquakes worldwide, between 16th December 1902 and 4th March 1977.

Constructing a boxplot involves the following steps:

1. Draw a vertical (or horizontal) axis representing the interval scale on which the observations are made.

2. Calculate the median, and upper and lower quartiles (Q_1, Q_3) as described in §1.1. Calculate the interquartile range (or 'midspread') $H = Q_3 - Q_1$.

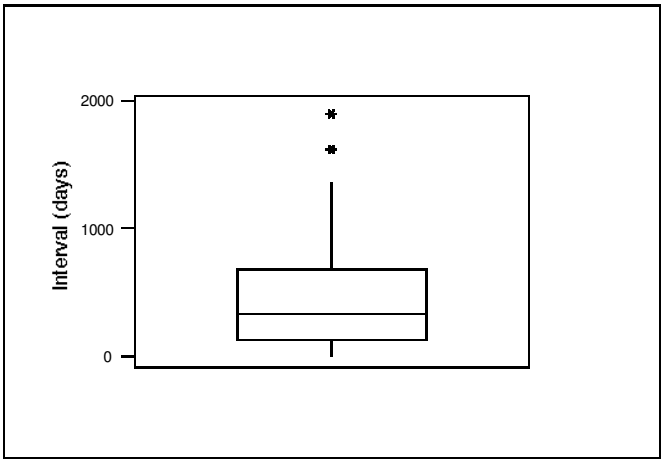
3. Draw a rectangular box alongside the axis, the ends of which are positioned at Q_1 and Q_3. (The box covers the 'middle half' of the observations). Q_1 and Q_3 are referred to as the '**hinges**'.

4. Divide the box into two by drawing a line across it at the median.

5. The **whiskers** are lines which extend from the hinges as far as the most extreme observation which lies within a distance $1.5 \times H$, of the hinges.

6. Any observations beyond the ends of the whiskers (further than $1.5 \times H$ from the hinges) are **outliers** and are each marked on the plot as individual points at the appropriate values. (Sometimes a different style of marking is used for any outliers which are at a distance greater than H from the end of the whiskers).

From a boxplot, you can immediately gain information concerning the centre, spread, and extremes of the distribution of the observations.



In MINITAB

Graph→Boxplot

1.2.2 The Time Series Plot

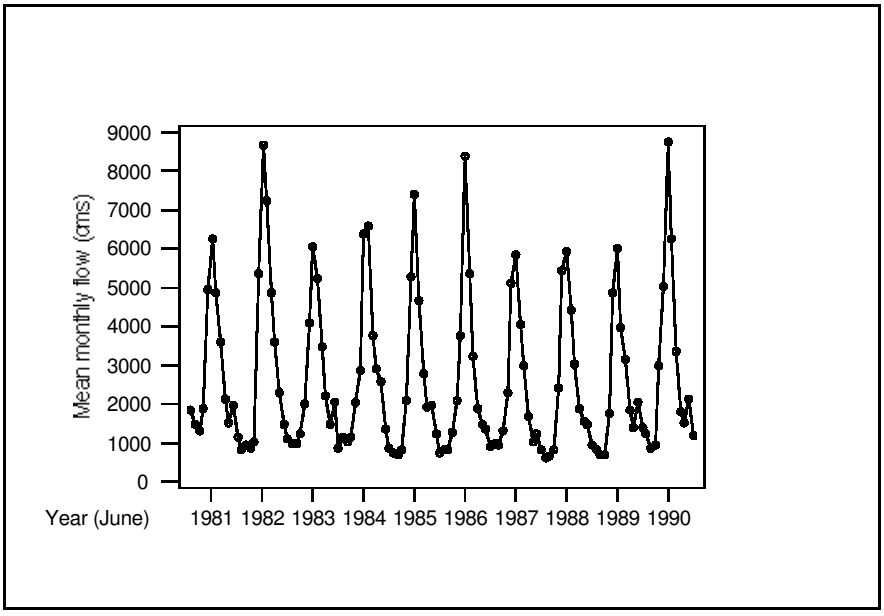
Often, the data collected are observations of the same quantity at different points in time (the units are time points). For example, weekly mean precipitation, monthly maximum sea level ...

Where the time points at which the data have been collected are evenly spaced (or approximately so) then a **time series plot** may be used to illustrate the variation in the observations.

A time series plot is simply a plot of each observation x_i, $i = 1, 2, \ldots, n$ on the y-axis against its **index** i on the x-axis, in other words a plot of the points (i, x_i), $i = 1, 2, \ldots, n$.

Consecutive points are joined together to illustrate the way in which the observations vary over time.

For example, the data in the file `flow.dat` represent the mean monthly flow (in cms) of the Fraser River at Hope, B.C., Canada between January 1981 and December 1990.



In MINITAB

Graph→Time Series Plot

Time series plots may be used to detect **trend** or **seasonal** behaviour (or both).

Note that in many practical examples, there is no natural time ordering of the observations (for example, observations where the units are individuals). In such examples, time series plots are meaningless.

1.2.3 The Histogram

Histograms have the following properties.

1. The horizontal axis represents the scale on which the observations are measured, and the bars of the histogram adjoin each other with the boundaries between bars representing the boundaries between the categories.

2. If bars are not of equal width, then care must be taken when determining the height of each bar (particularly with MINITAB) to ensure that the **area of each bar is proportional to the number of observations in each category**.

3. The best choice of boundaries between bars is the one which best illustrates the distribution of the observations. This usually requires some experimentation (trial and error).

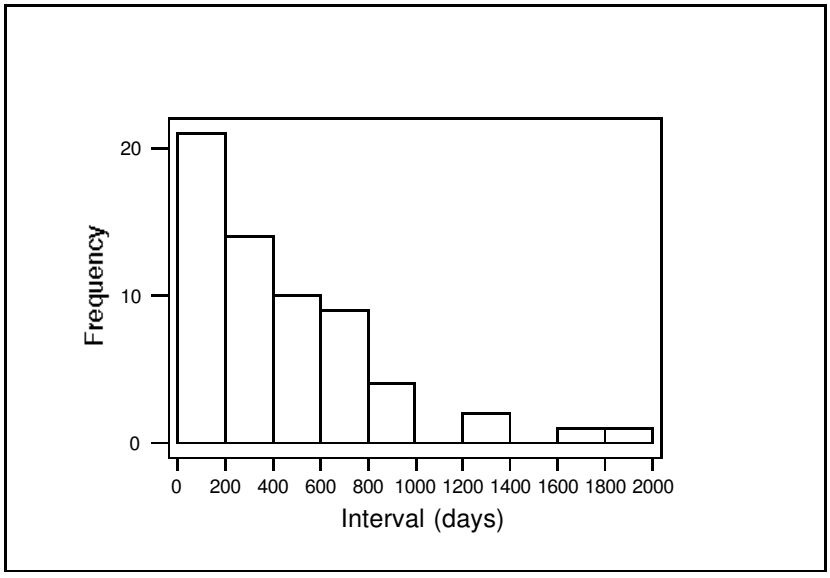


Figure 1.1: A histogram of the earthquake data (`quake.dat`) introduced in §1.2.1.

In MINITAB

Graph→histogram

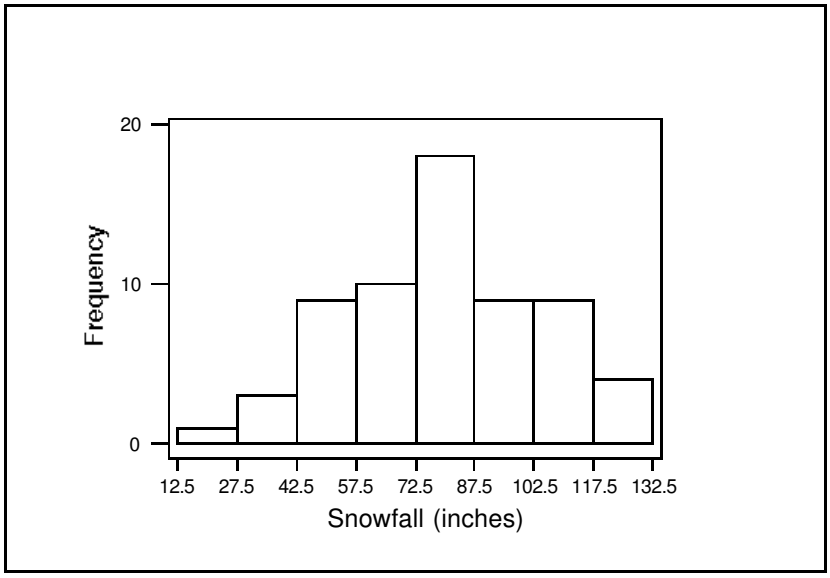
There are a number of features of the distribution of a set of observations which are not summarised by the summary measures described in §1.1. but which are illustrated by a histogram.

For example, we can determine if the distribution of the data is **symmetric** or **skew**.

The data in the file `snow.dat` represent the annual snowfall (in inches) in Buffalo, NY, for the years 1910 to 1972.

A histogram can also be used to determine if the distribution of the observations is **unimodal** (a single 'largest' category with categories generally becoming 'less common', above or below this category) or **multimodal**.

The data in the file `acidity.dat` are the measurements of an acidity index for each of 155 lakes in the Northeastern USA.



1.3 Summarising the Joint Distribution of a Pair of Variables

Many interesting problems in statistical data analysis concern the **relationship** or **association** between a pair of variables. When observations are made of two or more variables, on the same set of units, we can examine such relationships by investigating the **joint distribution** of pairs of observations.

The simplest way of summarising the joint distribution of a pair of variables is by a **scatterplot**. Suppose that we have observed n units and we denote the measurements of one variable by $x_1, x_2, \ldots, x_n$ and the measurements of the other variable by $y_1, y_2, \ldots, y_n$. Then a scatterplot is a plot of the points $(x_1, y_1), (x_2, y_2), \ldots, (x_n, y_n)$.

We consider two examples here, and in each case the question of interest is what, if any, is the relationship between the two variables?.

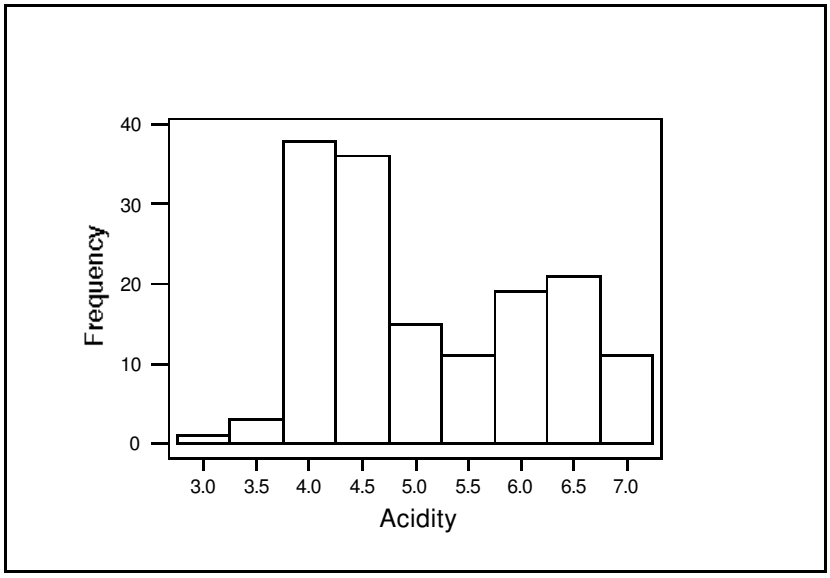
The data in the file `level.dat` record the level of Lake Victoria Nyanza for the years 1902–1921 (relative to a fixed standard) and the number of sunspots in the same years.

The data in the file `paving.dat` are the compression strength (Nmm^{-2}) and percentage dry weight of 24 paving slabs. In each case the question of interest is what, if any, is the relationship between the two variables?

In MINITAB

Graph→Plot

The strength of the association between the variables may be summarised by a single summary measure called the **correlation coefficient**.



To calculate the correlation coefficient, we first need to calculate the mean and standard deviation of the observations $x_1, x_2, \ldots, x_n$ of the first variable (call these $\overline{x}$ and s_x), and the mean and standard deviation of the observations $y_1, y_2, \ldots, y_n$ of the second variable (call these $\overline{y}$ and s_y). The correlation coefficient (denoted by r) is given by

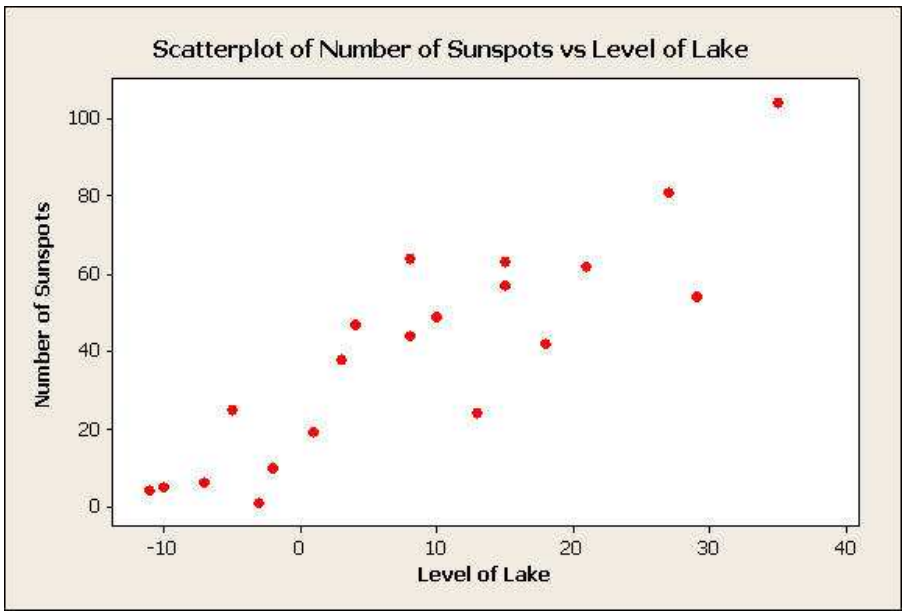
$$r = \frac{1}{n-1}\sum_{i=1}^{n}\frac{(x_i-\overline{x})(y_i-\overline{y})}{s_x s_y}.$$

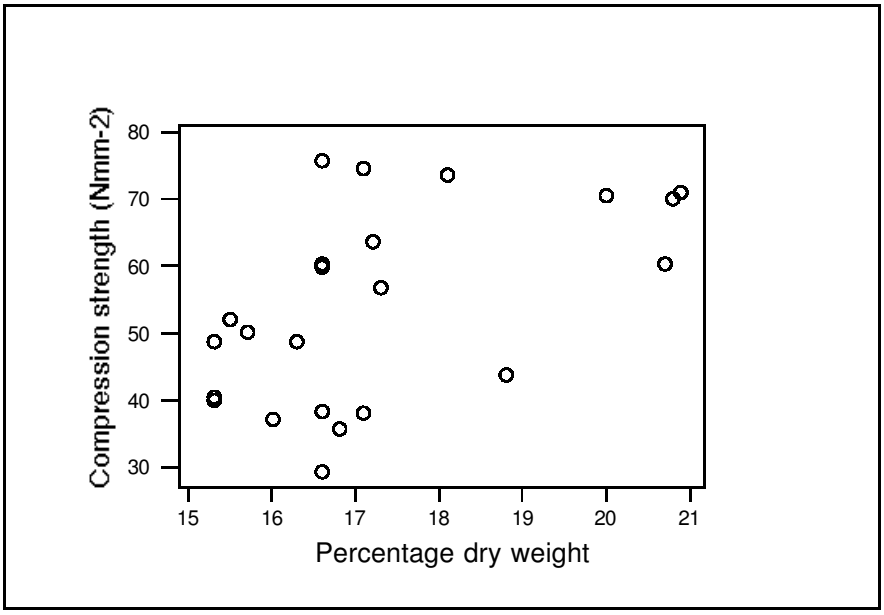
The correlation coefficient, which must lie between -1 and 1, measures the strength of the **linear** (straight line) relationship between the variables. It determines to what extent values of one variable increase as values of the other variable increase, and how close this relationship is to being a perfect straight line.

Hence, the correlation coefficient provides a measure of the extent of linear association. For example, the correlation coefficients for the two examples illustrated by scatterplots on the previous page are 0.526 between 'strength' and 'dry weight' and 0.879 between 'lake level' and 'number of sunspots'. Therefore, both data sets show positive linear association, stronger between lake level and number of sunspots.

In MINITAB

Stat→Basic Statistics→Correlation


Scatterplot of Number of Sunspots vs Level of Lake
Number of Sunspots
Level of Lake
100
80
60
40
20
0
-10
0
10
20
30
40


Compression strength (Nmm-2)
Percentage dry weight
80
70
60
50
40
30
15
16
17
18
19
20
21

Chapter 2

Probability and Probability Distributions

2.1 Introduction

Most of us have an idea about probability from games of chance, from the lottery and from general statements about the likelihood of a particular event occurring. The probability of it raining in Southampton tomorrow might be given or the chance that a particular team will win a given match. It will be necessary to clarify ideas about probability a little in order to tackle the kind of problems that we shall meet later, but you will not be required to delve very deeply into the theory of probability.

Firstly, we shall identify a probability of zero with some event which cannot happen and a probability of unity for something which is certain to occur. All other probabilities will be between zero and one and will reflect the "chance" of an event occurring. For a repeatable event, the probability may be interpreted as the proportion of times the event will occur in the "long run". For other kinds of event, probability may be interpreted as a measure of subjective belief reflecting the likelihood of the event occuring.

In this chapter, we consider tightly controlled situations, where it is possible to calculate probabilities precisely. More generally, we cannot know probabilities precisely, but we can use observed data to learn about probabilities – this is statistical inference and is the subject of later chapters.

For example, suppose that electronic resistors of a similar appearance are either 5 ohms or 10 ohms, and we put 100 of the 5 ohm resistors in a box together with 50 of the 10 ohm resistors. A resistor is then chosen from the box. What is the probability that it is a 5 ohm resistor?

It is not immediately possible to answer this question since we are not told enough about

the conduct of the experiment. If we are told that the 150 resistors are shaken up in the box and that the resistor is chosen "at random" from the box, then we can argue that each of the resistors has an equal probability of being selected. Since there are now 150 resistors in total and they are all equally likely to be chosen, the probability that a 5 ohm resistor is chosen will be given by $100/150 = 2/3$. Thus the probability of choosing a 5 ohm resistor is formally given by

$$P(\text{5 ohm resistor being chosen}) = \frac{\text{Number of 5 ohm resistors in the box}}{\text{Total number of resistors in the box}} = \frac{2}{3}$$

Similarly, P(10 ohm resistor being chosen)$= 50/150 = 1/3$

Suppose now we take out a second resistor at random from those left in the box. What is the probability of getting two 5 ohm resistors?

To answer this, consider the experiment in two stages.

(a) Select the first resistor. The probability of a 5 ohm resistor is 2/3.

(b) Now, assuming that a 5 ohm resistor has been selected, choose the second resistor. There are only 149 resistors left and 99 of them are 5 ohm resistors, so the probability of a 5 ohm resistor being selected is 99/149.

The probability of getting two 5 ohm resistors is now given by

$$\frac{2}{3} \times \frac{99}{149} = \frac{66}{149} = 0.443.$$

Similarly, the probability of two 10 ohm resistors is

$$\frac{1}{3} \times \frac{49}{149} = \frac{49}{447} = 0.110.$$

The other possibility is that we choose one 5 ohm and one 10 ohm resistor. The probability of this is slightly more involved since we could choose the 5 ohm first and then the 10 ohm resistor or the 10 ohm first and then the 5 ohm resistor. The probability is given by

$$\left(\frac{2}{3} \times \frac{50}{149}\right) + \left(\frac{1}{3} \times \frac{100}{149}\right) = \frac{200}{447} = 0.447.$$

Note that $0.443 + 0.110 + 0.447 = 1$, *i.e.* P(two 5 ohm) + P(two 10 ohm) + P(one of each) $= 1$. Since these are the only possible outcomes, the probabilities must sum to 1.

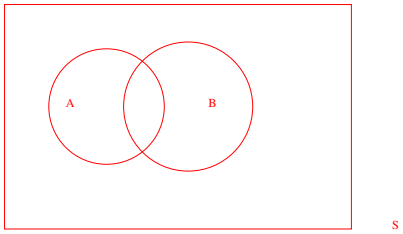
The above example illustrates sampling without replacement, in that the first selected resistor was not replaced in the box before the second was selected.

If we had decided to replace the first resistor, whatever its resistance, before selecting the second, then the probabilities of two 5 ohm, two 10 ohm or one of each would be given by

$$\begin{aligned} P(\text{two 5 ohm}) &= \tfrac{2}{3} \times \tfrac{2}{3} = \tfrac{4}{9} = 0.444 \\ P(\text{two 10 ohm}) &= \tfrac{1}{3} \times \tfrac{1}{3} = \tfrac{1}{9} = 0.111 \\ P(\text{one of each}) &= \left(\tfrac{2}{3} \times \tfrac{1}{3}\right) + \left(\tfrac{1}{3} \times \tfrac{2}{3}\right) = \tfrac{4}{9} = 0.444. \end{aligned}$$

These probabilities for the with replacement scheme are slightly different but, as before, these three situations include all possibilities so the three probabilities must sum to 1.

Notice that we have multiplied probabilities together where considering events occurring together, such as choosing a 5 ohm resistor on the first selection **and** a 5 ohm on the second selection. We have added together probabilities when a situation could arise in two different ways, such as "one of each" could be obtained either as a 5 ohm selected first and a 10 ohm second **or** a 10 ohm selected first and a 5 ohm resistor selected second.



More generally, if we have events A and B, then

$$P(A \text{ or } B) = P(A \cup B) = P(A) + P(B) - P(A \text{ and } B)$$

and

$$P(A \text{ and } B) = P(A \cap B) = P(A) \times P(B \text{ given that } A \text{ has occured}).$$

If the occurence, or otherwise, of A does not affect the probability of B, then we say that A and B are **independent** events, and we can write $P(B \text{ given that } A \text{ has occured}) = P(B)$. In this case

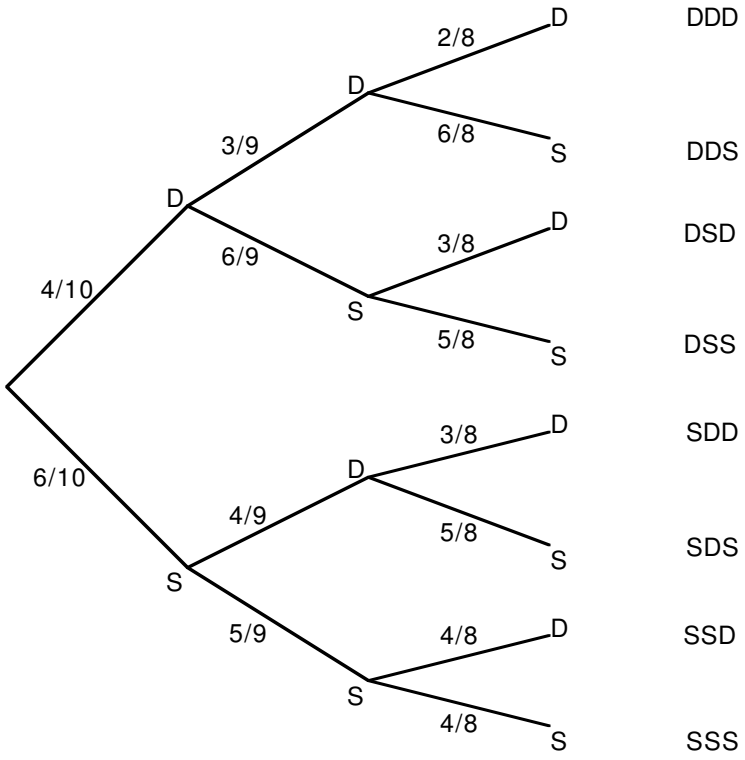
$$P(A \text{ and } B) = P(A \cap B) = P(A) \times P(B).$$

These simple multiplication and addition rules for probabilities are very important for most problems. The rest of this Section is devoted to a series of examples illustrating the calculation of probabilities using these rules. We shall consider conditional probability in more detail in Section 2.2.

♡ **Example** 2.1. Ten items are available and 4 are defective and 6 are satisfactory. A random sample of 3 items is taken from these 10, what is the probability that exactly one is defective?

One way to tackle a problem like this is to construct a probability tree diagram to see what is going on. Consider selecting one item at a time until all three are selected and illustrate the results and the associated probabilities in each case. (D = defective, S = satisfactory).

So the probability for DDD will be: $\frac{4}{10} \times \frac{3}{9} \times \frac{2}{8} = \frac{1}{30}$. All the remaining probabilities can be found similarly.



There are eight possible sequences with the probabilities as given in the table above. Note that the sequences DSS, SDS and SSD all have one defective, so the probability of obtaining one defective is given by

$$\left(\frac{4}{10}\times\frac{6}{9}\times\frac{5}{8}\right)+\left(\frac{6}{10}\times\frac{4}{9}\times\frac{5}{8}\right)+\left(\frac{6}{10}\times\frac{5}{9}\times\frac{4}{8}\right)=3\times\frac{6\times5\times4}{10\times9\times8}=\frac{1}{2}$$

Similarly, the probability of two defectives is

$$\begin{aligned}P(\mathrm{DDS})+P(\mathrm{DSD})+P(\mathrm{SDD}) &= \left(\tfrac{4}{10}\times\tfrac{3}{9}\times\tfrac{6}{8}\right)+\left(\tfrac{4}{10}\times\tfrac{6}{9}\times\tfrac{3}{8}\right)+\left(\tfrac{6}{10}\times\tfrac{4}{9}\times\tfrac{3}{8}\right)\\ &= 3\times\tfrac{6\times4\times3}{10\times9\times8}\\ &= \tfrac{3}{10},\end{aligned}$$

the probability of no defectives is

$$P(\mathrm{SSS})=\frac{6}{10}\times\frac{5}{9}\times\frac{4}{8}=\frac{1}{6}$$

and the probability of three defectives is

$$P(\mathrm{DDD})=\frac{4}{10}\times\frac{3}{9}\times\frac{2}{8}=\frac{1}{30}.$$

Note that these four probabilities must sum to 1, *i.e.*

$$P(0\text{ defectives})+P(1\text{ defective})+P(2\text{ defectives})+P(3\text{ defectives})=\frac{1}{6}+\frac{1}{2}+\frac{3}{10}+\frac{1}{30}=1.$$

In fact, we can calculate these probabilities without constructing a probability tree diagram. To do this, we need to know something about **combinations**.

Suppose that we have n items from which we select r without replacement. The order in which the items are selected does not matter, just which r items comprise the final selection. We denote by $\binom{n}{r}$the number of such distinct combinations of r items which can be selected. It can be shown that

$$\binom{n}{r} = \frac{n!}{r!(n-r)!} = \frac{n \times (n-1) \times \cdots \times (n-r+1)}{1 \times 2 \times \cdots \times r}$$

where $a!$ ("a factorial") is defined to be $a! = a \times (a-1) \times (a-2) \times \cdots \times 3 \times 2 \times 1$. Hence, in particular

$$\begin{aligned} \binom{n}{1} &= n \\ \binom{n}{2} &= \tfrac{n(n-1)}{2} \\ \binom{n}{3} &= \tfrac{n(n-1)(n-2)}{6}. \end{aligned}$$

As we have a total of 10 items, 4 defective and 6 satisfactory. The number of possible ways of selecting 3 items from 10 is

$$\binom{10}{3} = \frac{10 \times 9 \times 8}{6} = 120$$

In order to get one defective and two satisfactory in the sample, the defective must be selected from one of the four defectives and the two satisfactory ones from the six which are satisfactory. Therefore, the number of different selections of one defective and two satisfactory is

$$\binom{4}{1} \times \binom{6}{2} = 4 \times \frac{6 \times 5}{2} = 60$$

Therefore, the probability of choosing one defective in the sample of three is

$$\begin{aligned} P(\text{one defective}) &= \frac{\text{Number of ways of choosing 1 defective and 2 satisfactory}}{\text{Number of ways of choosing 3 items}} \\ &= \frac{\binom{4}{1} \times \binom{6}{2}}{\binom{10}{3}} \\ &= \frac{60}{120} \\ &= \frac{1}{2}. \end{aligned}$$

Similarly

$$\begin{aligned} P(\text{two defectives}) &= \frac{\binom{4}{2} \times \binom{6}{1}}{\binom{10}{3}} \\ &= \frac{6 \times 6}{120} \\ &= \frac{3}{10}. \end{aligned}$$

Either method will produce the answer, but the tree-diagram method can get a bit cumbersome with larger problems.

♡ **Example** 2.2. **The National Lottery** In the National Lottery, the winning ticket has six numbers from 1 to 49 exactly matching those on the balls drawn on a Wednesday or Saturday evening. The 'experiment' consists of drawing the balls. The 'randomness', the equal probability of any set of six numbers being drawn, is ensured by the Lottery machine, which mixes the balls during the selection process.

The probability associated with the winning selection is given by

$$P(\text{Jackpot}) = \frac{\text{Number of winning selections}}{\text{Number of possible selections}}$$

The total number of possible selections is given by

$$\binom{49}{6} = \frac{49 \times 48 \times 47 \times 46 \times 45 \times 44}{1 \times 2 \times 3 \times 4 \times 5 \times 6} = 13\,983\,816$$

(*i.e.* nearly 14 million). Since there is only one winning selection, the probability of matching the jackpot sequence is $1/13\,983\,816 = 0.0000000715$.

Other prizes are given for fewer matches. The corresponding probabilities can be evaluated as follows:

$$\begin{aligned} P(5 \text{ matches}) &= \frac{\text{Number of selections with 5 matches}}{\text{Number of possible selections}} \\ &= \frac{\binom{6}{5} \times \binom{43}{1}}{\binom{49}{6}} \\ &= \frac{\frac{6!}{5!1!} \times \frac{43!}{1!42!}}{13\,983\,816} \\ &= \frac{6 \times 43}{13\,983\,816} \\ &= 0.00001845 \\ &\approx \frac{1}{54\,200} \end{aligned}$$

Similarly,

$$\begin{aligned} P(4 \text{ matches}) &= \frac{\binom{6}{4} \times \binom{43}{2}}{\binom{49}{6}} \\ &= \frac{15 \times 903}{13\,983\,816} \\ &= 0.0009686 \\ &\approx \frac{1}{1\,032} \end{aligned}$$

$$\begin{aligned} P(3 \text{ matches}) &= \frac{\binom{6}{3} \times \binom{43}{3}}{\binom{49}{6}} \\ &= \frac{20 \times 12\,341}{13\,983\,816} \\ &= 0.01765 \\ &\approx \frac{1}{57} \end{aligned}$$

There is one other way of winning, using the bonus ball. Matching five of the selected six balls plus matching the bonus ball gives a share in a prize substantially less than the

jackpot. The probability of this is given by

$$\begin{aligned} P(\text{Matching 5 and the bonus ball}) &= \frac{\text{Number of selections of this type}}{\text{Number of possible selections}} \\ &= \frac{6}{\binom{49}{6}} \\ &= 0.000000429 \\ &\approx \frac{1}{2\,331\,000} \end{aligned}$$

Adding all these probabilities of winning some kind of prize together gives

$$P(\text{Winning}) = 0.0188 \approx \frac{1}{53}$$

so that a player buying one ticket each week would expect to win a prize about once a year. Without further information, it is not possible to work out the expected return on this kind of investment since this involves the amounts of the prizes as well as the probabilities of winning. In the National Lottery, the prize money, (except for the $10 prize), depends on the number of winners and the number of tickets sold.

One of the most common applications of probability calculations in Engineering is in evaluating reliability. The remaining examples focus on this area.

♡ **Example** 2.3. If a communications satellite is to be launched and positioned in space to receive and transmit telephone and data transmissions, various stages of the process are said to succeed or fail with certain probabilities. For example, it may be that the launch will be successful with a probability of 0.9. The reliability, which is the probability that it works, is therefore 0.9 or 90%. Obviously, the probability that the launch will fail is $1 - 0.9 = 0.1$.

Suppose such a satellite has a successful launch with a probability of 0.9 and after launch, the satellite is to be positioned in a suitable orbit with a probability of 0.8. Small retro-rockets on the satellite can then be used to adjust the position, if this is not initially correct, and the probability of success here is 0.5. Once in position, the solar powered batteries are expected to last at least a year with probability 0.7. What is the probability that a satellite due to be launched will still be working in a year's time?

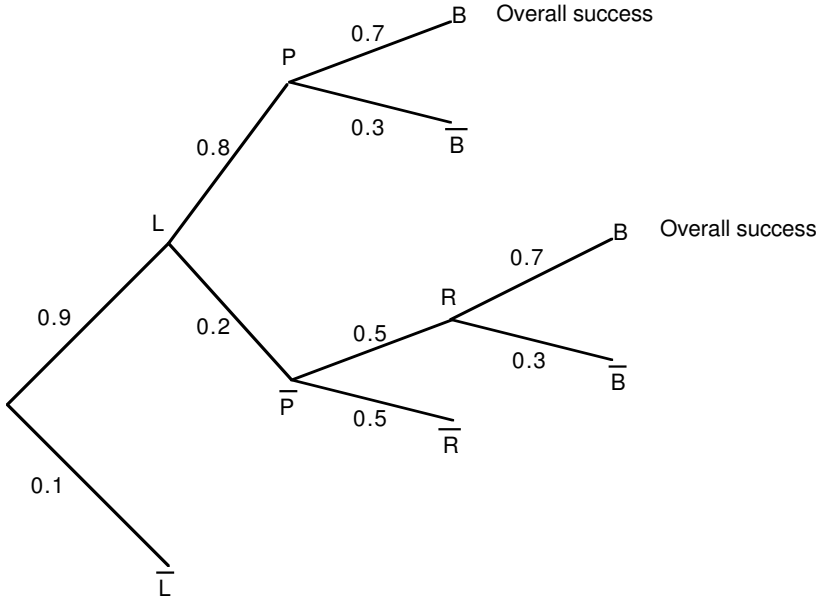
In order to work out this probability, it is necessary to assume that all the different ways of failing are acting independently of each other. This might not be so, of course. if the batteries were used to power the retro-rockets. A simple tree-diagram helps here.

Let L represent a successful launch and $\overline{\text{L}}$ represent a failure, with P, R and B representing successful position, retro-rocket adjustment and battery life, respectively.

The probability of overall success is given by

$$\begin{aligned} (0.9 \times 0.8 \times 0.7) + (0.9 \times 0.2 \times 0.5 \times 0.7) &= 0.504 + 0.063 \\ &= 0.567. \end{aligned}$$

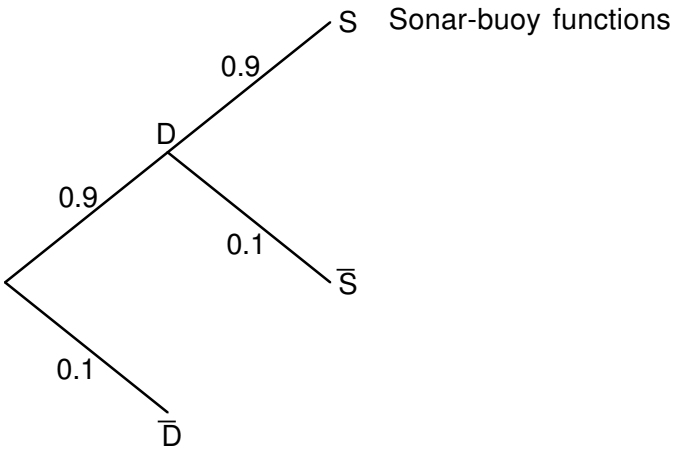
The overall reliability is 56.7%.



Note that whenever a system is affected by a series of different reasons for failure, the overall reliability of the system is reduced. Another example of this follows.

♡ **Example** 2.4. A sonar-buoy dropped from an aircraft to monitor submarines has to deploy its antennae and switch on its transmitter to send signals. If the reliabilities of both the deploying mechanism and the transmitter switch are 90%, what is the reliability of the sonar-buoy?

The following simple diagram will help here.



$$\begin{aligned} P(\text{sonar-buoy functions}) &= P(\text{deploys antennae}) \times P(\text{switch works}) \\ &= 0.9 \times 0.9 \\ &= 0.81 \end{aligned}$$

Therefore the reliability of sonar-buoy is 81%. Although 9 out of 10 of the deploying mechanisms work and 9 out of 10 of the switches work, only 4 out of 5 sonar-buoys work.

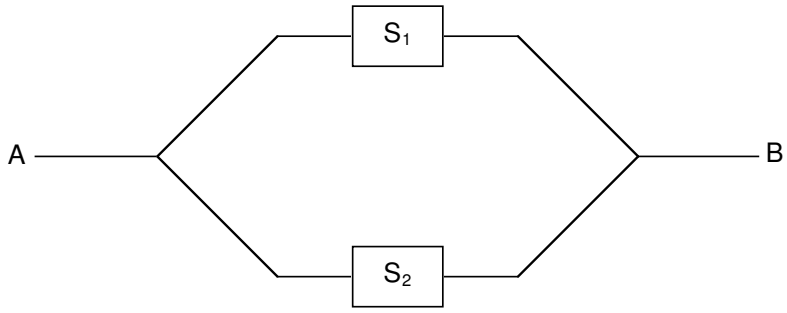
To achieve a 90% reliability for the buoys, we need to have individual reliabilities of $\sqrt{0.9} = 0.9487$ for the switches and deployment mechanisms.

The more components which are required to function to make a system work, the lower the overall reliability. For example, a set of four elements, each with reliability 90%, produces a system with reliability $0.9^4 = 65.6\%$.

Standby redundancy can be used to improve the reliability of a system. It is common practice, when high reliability is required to introduce parallel systems which 'cut-in' if the initial system fails. Some aircraft systems can have as many as three parallel systems, any one of which would be sufficient to fly the plane safely.

♡ **Example** 2.5. Suppose a system consists of two independent switches S_1 and S_2, each with reliability 90% and is arranged so that the system operates if either of the switches, S_1 or S_2, operates. What is the reliability of this system?

This can be represented as below.



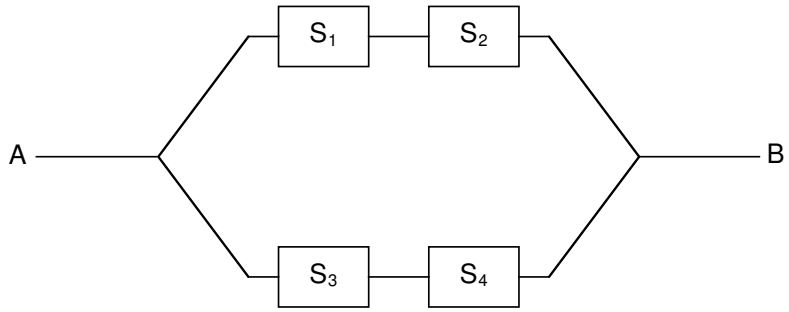
This diagram indicates that the system operates if there is a link from A to B created by the switches operating. The system operates if either or both of the switches are operating. In other words, the system fails only if both switches fail.

$$\begin{aligned} P(\text{system fails}) &= P(\text{switch } S_1 \text{ fails}) \times P(\text{switch } S_2 \text{ fails}) \\ &= 0.1 \times 0.1 \\ &= 0.01 \end{aligned}$$

Therefore, the reliability of the system is 99%.

By introducing a 'spare' switch, the reliability has increased from 90% to 99%, a substantial gain for the potentially small cost of an extra switch.

♡ **Example** 2.6. Systems can be made up of components in 'series' and in 'parallel', including standby redundancy where necessary. Consider the following system.



Here the system consists of four components S_1,S_2,S_3,S_4 and it functions if S_1 and S_2 operate or S_3 and S_4 operate. If the individual reliabilities are 0.9 and the switches all operate independently, what is the reliability of the system?

The system fails if **both** the upper part (S_1, S_2) and the lower part (S_3, S_4) fail. We have already seen, in Example 2.4, that the reliability of the upper part is given by

$$\begin{aligned} P(\text{S}_1 \text{ and } \text{S}_2 \text{ operate}) &= P(\text{S}_1 \text{ operates}) \times P(\text{S}_2 \text{ operates}) \\ &= 0.9 \times 0.9 \\ &= 0.81 \end{aligned}$$

so that the probability that the upper part fails is 0.19. Similarly, the probability that the lower part fails is also 0.19. The probability that the system fails is now given by

$$\begin{aligned} P(\text{system fails}) &= P(\text{upper part fails and lower part fails}) \\ &= P(\text{upper part fails}) \times P(\text{lower part fails}) \\ &= 0.19 \times 0.19 \\ &= 0.0361 \end{aligned}$$

so its reliability is $1 - 0.0361 = 0.9639$ or 96.4%.

In general, if the probabilities of working for S_1,S_2,S_3,S_4 are p_1, p_2, p_3, p_4 respectively, the reliability of such a system is given by

$$1 - (1 - p_1 p_2)(1 - p_3 p_4)$$

and, if $p_1 = p_2 = p_3 = p_4 = p$, the reliability is $1 - (1 - p^2)^2$.

♡ **Example** 2.7. An engineer has designed a storm water sewer system so that the yearly maximum discharge will cause flooding on average once every 10 years. This means that the probability each year that there will be a discharge which causes flooding is 0.1. If it can be assumed that the maximum discharges are independent from year to year, what is the probability that there will be at least one flood in the next five years.

Whenever we require "the probability of **at least** one", it is simpler to determine "the probability of none" and then subtract this from 1. In this case, the probability of no flood in any particular year is $1 - 0.1 = 0.9$, so that the probability of no flood in 5 years is

$$\begin{aligned} P(\text{No flood in 5 years}) &= P(\text{No flood in year 1 } \textbf{and} \text{ no flood in year 2 } \textbf{and} \cdots \\ &\qquad \cdots \textbf{ and} \text{ no flood in year 5}) \\ &= P(\text{No flood in year 1}) \times P(\text{No flood in year 2}) \times \cdots \\ &\qquad \cdots \times P(\text{No flood in year 5}) \\ &= 0.9 \times 0.9 \times 0.9 \times 0.9 \times 0.9 = 0.9^5 = 0.59 \end{aligned}$$

and therefore

$$P(\text{At least one flood in 5 years}) \;=\; 1 - 0.59 \;=\; 0.41$$

Although the sewer system has been designed to withstand a flood which occurs on average once every 10 years, the probability that this will occur within the next 5 years is just over 0.4.

The ideas of **design life**, **reliability** and **return period** will be covered in more detail in a later chapter.

2.2 Conditional Probability and Bayes Theorem

2.2.1 Conditional Probability

The probability of an event B occurring when it is known that some event A has already occurred is called a **conditional probability** and it is denoted by $P(B|A)$. The symbol $P(B|A)$ is usually read as "the probability that B occurs given that A has already occurred', or simply, the probability of B given A.

The formula for finding the conditional probability is:

$$P(B|A) = \frac{P(A \cap B)}{P(A)}, \quad \text{provided } P(A) > 0. \tag{2.1}$$

♡ **Example** 2.8. The probability that a plane departs on time is $P(D) = 0.83$; the probability that it arrives on time is $P(A) = 0.82$; and the probability that it arrives and departs on time is $P(D \cap A) = 0.78$.

The probability that a plane departed on time given that it arrived on time is:

$$P(D|A) = \frac{P(D \cap A)}{P(A)} = \frac{0.78}{0.82} = 0.95.$$

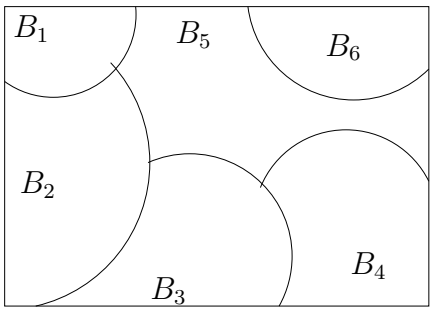
The probability that a plane arrives on time given that it departed on time is:

$$P(A|D) = \frac{P(D \cap A)}{P(D)} = \frac{0.78}{0.83} = 0.94.$$

2.2.2 Theorem of Total Probability

Two events B_1 and B_2 are called **mutually exclusive** if they cannot occur simultaneously. For example, let B_1 denote the event that head turns up and B_2 denote the event that tail turns up when a coin is tossed. Here $P(B_1 \cap B_2) = 0$.

Sometimes we partition (i.e. divide) the sample space by mutually exclusive events. Often a set of such events covering the entire sample space, called **a set of exhaustive** events, are considered. For example, suppose that $B_1, \ldots, B_k$ denote a set of mutually exclusive and exhaustive events. So $B_1 \cup B_2 \cup \cdots \cup B_k = S$ where S is the sample space. In the coin tossing example, B_1 and B_2 provide a set of mutually exclusive and exhaustive events.



To find the probability of another event A (other than the $B_1, \ldots, B_k$), intuition suggests that we can find the intersection probability of A with each of $B_1, \ldots, B_k$ and add them up. The **theorem of total probability** is exactly that and is as follows:

If the events $B_1, \ldots, B_k$ form a partition of the sample space such that $P(B_i) \neq 0, i = 1, \ldots, k$, then for any event A in the sample space S:

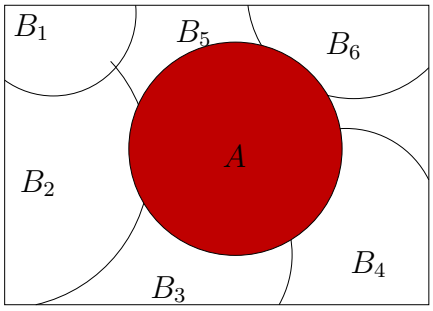
$$P(A) = \sum_{i=1}^{k} P(B_i \cap A).$$

However, using the definition of conditional probability in (2.1) we have:

$$P(B_i \cap A) = P(B_i)P(A|B_i).$$

Hence we have:

$$P(A) = \sum_{i=1}^{k} P(B_i \cap A) = \sum_{i=1}^{k} P(B_i)P(A|B_i).$$



♡ **Example** 2.9. In a certain assembly plant, three machines B_1, B_2, and B_3 make 30%, 45%, and 25%, respectively of the products. It is known from past experience that 2%, 3% and 2% of the products made by each machine, respectively, are defective. Now suppose that a finished product is randomly selected. What is the probability that it is defective?

Consider the following events:

A: the product is defective,

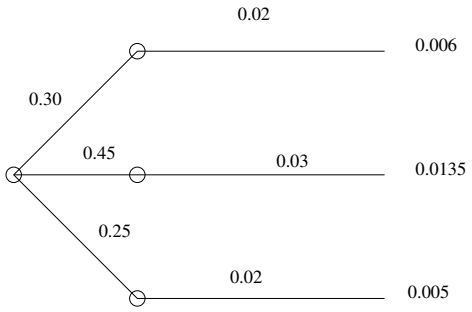
B_1: the product is made by machine B_1,

B_2: the product is made by machine B_2,

B_3: the product is made by machine B_3,

Using the theorem of total probability:

$$P(A) = P(B_1)P(A|B_1) + P(B_2)P(A|B_2) + P(B_3)P(A|B_3).$$



But we have:

$$\begin{aligned} P(B_1) &= 0.30, \quad P(A|B_1) = 0.02 \\ P(B_2) &= 0.45, \quad P(A|B_1) = 0.03 \\ P(B_3) &= 0.25, \quad P(A|B_3) = 0.02 \end{aligned}$$

Hence

$$\begin{aligned} P(B_1)\, P(A|B_1) &= (0.30)(0.02) = 0.006 \\ P(B_2)\, P(A|B_2) &= (0.45)(0.03) = 0.0135 \\ P(B_3)\, P(A|B_3) &= (0.25)(0.02) = 0.005. \end{aligned}$$

and hence:

$$P(A) = 0.006 + 0.00135 + 0.0005 = 0.0245.$$

If instead, we wanted to find the inverse probability that $P(B_1|A)$, i.e. the probability that a randomly selected product was made by machine B_1 given that it is defective? We apply the Bayes theorem to find the inverse probability.

2.2.3 Bayes Theorem

Let $B_1, B_2, \ldots, B_k$ be a set of mutually exclusive and exhaustive events. For any new event A,

$$P(B_r|A) = \frac{P(B_r \cap A)}{P(A)} = \frac{P(A|B_r)P(B_r)}{\sum_{i=1}^{k} P(A|B_i)P(B_i)}, \quad r = 1, \ldots, k. \tag{2.2}$$

♡ **Example** 2.10. For the above example with three machines:

$$P(B_1|A) = \frac{P(B_1)P(A|B_1)}{P(A)} = \frac{(0.30)(0.02)}{0.0245} = 0.2449.$$

So, although there was a 30% chance that a randomly selected product was made by machine B_1, the probability that a randomly selected product was made by machine B_1 given that the product was defective reduces to 24.49%. This is to be expected since machine B_1 produces less defective products than some others.

If, instead, we suppose that machine B_1 produces 5% defective items. Then

$$P(A) = (0.30)(0.05) + 0.00135 + 0.0005 = 0.01685, \text{ and}$$

$$P(B_1|A) = \frac{P(B_1)P(A|B_1)}{P(A)} = \frac{(0.30)(0.05)}{0.01685} = 0.471.$$

Here the probability that a randomly selected product was made by machine B_1 given that the product was defective increases to 47.10%.

$P(B_1)$ and $P(B_1|A)$ are called the **prior** and **posterior** probability, respectively.

♡ **Example** 2.11. Consider a disease that is thought to occur in 1% of the population. Using a particular blood test a physician observes that out of the patients with disease 98% possess a particular symptom. Also assume that 0.1% of the population without the disease have the same symptom. A randomly chosen person from the population is blood tested and is shown to have the symptom. What is the conditional probability that the person has the disease?

Let B_1 be the event that a randomly chosen person has the disease and B_2 is the complement of B_1. Let A be the event that a randomly chosen person has the symptom. The problem is to determine $P(B_1|A)$.

We have $P(B_1) = 0.01$ since 1% of the population has the disease, and $P(A|B_1) = 0.98$. Also $P(B_2) = 0.99$ and $P(A|B_2) = 0.001$. Now

$$\begin{aligned} P(\text{disease} \mid \text{symptom}) = P(B_1|A) &= \frac{P(A|B_1)\,P(B_1)}{P(A|B_1)\,P(B_1)+P(A|B_2)\,P(B_2)} \\ &= \frac{0.98\times 0.01}{0.98\times 0.01+0.001\times 0.99} \\ &= 0.9082. \end{aligned}$$

So the unconditional probability of disease, $P(B_1) = 0.01 = 1\%$, has increased to 90.82% when the symptom is present, $P(B_1|A)$.

Chapter 3

Probability models and statistical inference

3.1 Modelling variability

Just as we use mathematical models for deterministic physical and environmental processes, so we use mathematical models for physical and environmental processes or systems which display variability or randomness. Models allow us to calculate probabilities of the process being in a particular state, or of a particular output of the process being observed. We call these models *probability models* or *stochastic models*.

Chapter 2 contained several examples of probability models for variable physical systems.

We do not expect probability models to be true, in the sense that, many of the processes we model are not truly random – the outputs are the results of many small innovations, mostly unobserved, which combine in an unknown way to produce the output. The probability model is an approximation which replaces our ignorance about the innovations, and the mechanism by which they produce the output, by a random process.

Typically probability models depend on a number of parameters. In Example 2.4 of Chapter 2, the model had two parameters, the probability of successful deployment of the antennae and the probability of correct operation of the transmitter switch. In Chapter 2, we assumed that these parameters were known. However, it is more usual, when we construct a probability model for a process, that the parameters of the process are not known precisely.

When a probability model contains unknown parameters, then we need to try to find out about the parameters. This is achieved by making observations of the outputs of the process, or of parts of the process. For example, we might test a number of transmitter switches and estimate the probability of correct operation of a transmitter switch by the proportion of switches in our test sample which operate correctly. We might also use sample data to

validate our model. In Example 2.4 of Chapter 2 we assumed that successful deployment of the antennae was independent of correct operation of the transmitter switch. We might use sample data to determine whether this is a reasonable assumption, or whether our model needs to be modified.

This process, using sample data to learn about a probability model, is called *statistical inference*. The subject of Statistics concerns how we should use sample data to learn about probability models.

Perhaps the most straightforward probability model, but nevertheless one of the most widely applicable is where our interest is focussed on a single variable. The remainder of this chapter is devoted to models for this situation.

3.2 Populations and density functions

When we talk about a population in Statistics, we mean the totality of the observations obtainable from all units possessing some common characteristics. Therefore, a population is not a set of objects or individuals but a set of possible values of a variable. Populations may be finite, when there are a maximum number of possible observations which can ever be made; or infinite, when no such upper bound exists.

Occasionally, for a finite population, the data collected consist of the entire population. Such a data set is called a **census**. When the data comprise the entire population, then **statistical data analysis merely involves presentation and summary of the data**, using methods such as those discussed in Chapter 1.

Populations consist of observations (or potential observations) of **variables**, and we construct statistical models for the process of making observations from the population. A statistical model for a population takes the form of a **probability distribution**. The probability distribution tells us how likely we are to observe the various possible observations of the variable concerned.

The simplest example is where each observation may take only two possible values. For example, our population of interest may be the correct operation, or otherwise, of all sonar buoy transmitter switches, including those which have not yet been manufactured. Each member of the population takes one of two values ('correct' or 'incorrect'), so a probability model for the population is that any individual switch is taken at random from the population and operates correctly with probability p and incorrectly with probability $1-p$. This model (probability distribution) depends on a single parameter p.

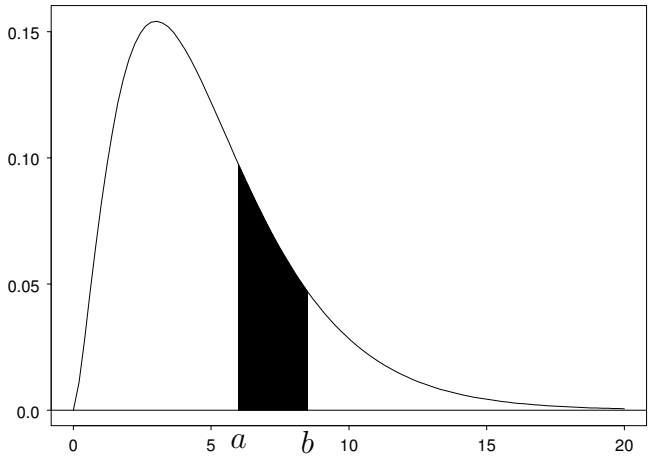
For data which consist of continuous measurements, populations may be summarised by using some of the summary measures described in Chapter 1. Throughout the rest of this course, we will concentrate on three of these: the mean, the median and the standard

deviation.

In statistical data analysis, it is important to distinguish between quantities which have been calculated based on an entire population, and those which have just been calculated using an arbitrary sample of units. We denote the population mean, median and standard deviation, by the Greek letters μ (mu), η (eta) and σ (sigma) respectively.

However, individual measures such as this are only a summary. They are extremely important for many of the statistical methods which we shall consider later, but give only partial information about the population and do not completely describe it.

For populations which are measurements of a continuous variable, we model the population by a continuous probability distribution. A continuous probability distribution is defined by a **probability density function**.



This function **completely describes** the distribution (population). The area under the whole curve is equal to one, and the area under the curve between any two points is the probability of observing a value between those points. In other words if we denote the variable of interest by X, which has probability density function $f(x)$,

$$P(a \leq X \leq b) = \int_a^b f(x)dx.$$

If a and b are the points where the shading starts and ends respectively in the above figure, then the **probability**, $P(a \leq X \leq b)$, is the **area of the shaded region**.

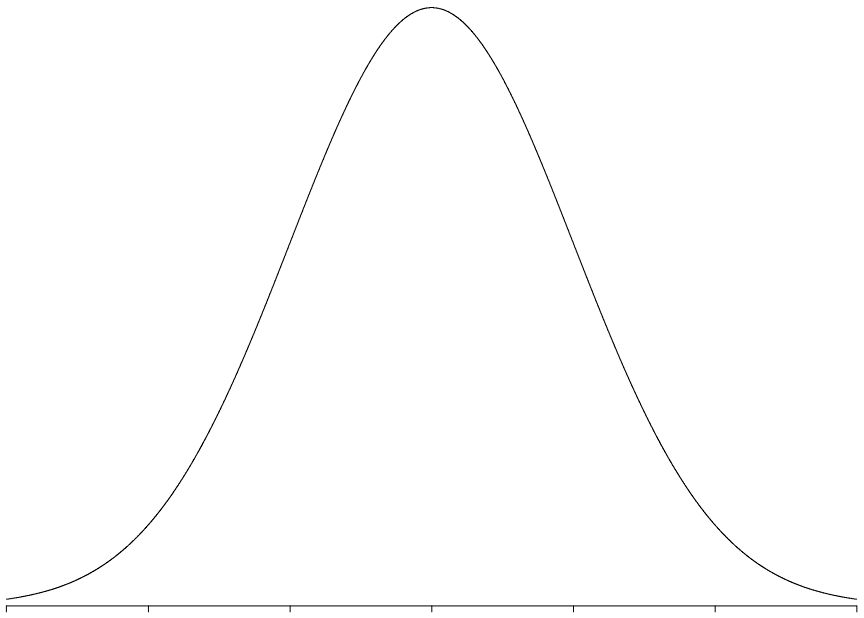
We can also calculate the mean μ and standard deviation σ of the distribution (population) directly from the density function, using

$$\begin{aligned} \mu &= \int_{-\infty}^{\infty} xf(x)dx, \\ \sigma^2 &= \int_{-\infty}^{\infty}(x-\mu)^2 f(x)dx = \int_{-\infty}^{\infty} x^2 f(x)dx - \mu^2. \end{aligned}$$

3.3 The Normal Distribution

One particular form of probability density curve which describes many populations, in practice, is the density curve of the **normal distribution**.

All normal distribution density curves possess a distinctive *bell shape*. The location and spread of the curve are determined by the population mean (μ), and the population standard deviation (σ) and a normal model for a population is completely specified by these two parameters.



$\mu - 3\sigma$ $\mu - 2\sigma$ $\mu - \sigma$ μ $\mu + \sigma$ $\mu + 2\sigma$ $\mu + 3\sigma$

The normal distribution curve is centred at μ, and most of the population (99.8%) lie between $\mu - 3\sigma$ and $\mu + 3\sigma$. In fact, the exact mathematical form for the normal density curve is

$$\begin{aligned} f(x) &= \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left(-\frac{(x-\mu)^2}{2\sigma^2}\right) \\ &= \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{(x-\mu)^2}{2\sigma^2}} \end{aligned}$$

The normal curve seems intuitively reasonable for describing a population. It is symmetric about the population mean μ, where the curve is at its maximum (so μ is the 'most common' observation in the population). The curve decreases rapidly away from μ without ever touching the axis (so no values are totally ruled out although values far away from μ are extremely rare).

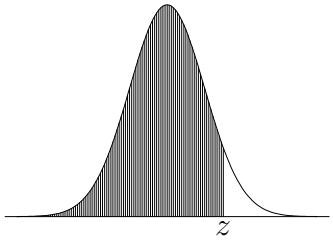
The usual shorthand for the normal distribution with mean μ and standard deviation σ (variance σ^2) is $N(\mu, \sigma^2)$.

3.3.1 The Standard Normal Distribution

The normal distribution with mean 0 and standard deviation 1, $N(0, 1)$, is called the **standard normal distribution**. For the standard normal distribution, tables are available in all published books of statistical tables (For example, table 4 of 'New Cambridge Statistical Tables', 2nd Edition, by D. V. Lindley and W. F. Scott.) giving the probability of the distribution in selected regions.

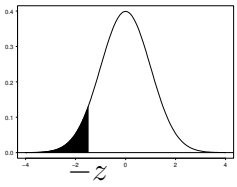
Most tables give areas under the curve to the left of a specified value, *i.e.* the probability of observing a standard normal value less than or equal to a specified value, $P(Z \leq z)$.

Table gives values of $P(Z \leq z)$

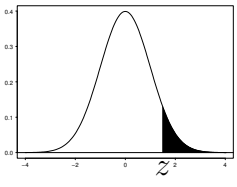


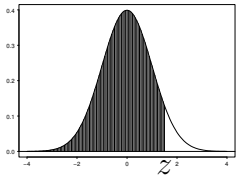
	2nd decimal place of z									
z	0	1	2	3	4	5	6	7	8	9
0.0	0.5000	0.5040	0.5080	0.5120	0.5160	0.5199	0.5239	0.5279	0.5319	0.5359
0.1	0.5398	0.5438	0.5478	0.5517	0.5557	0.5596	0.5636	0.5675	0.5714	0.5753
0.2	0.5793	0.5832	0.5871	0.5910	0.5948	0.5987	0.6026	0.6064	0.6103	0.6141
0.3	0.6179	0.6217	0.6255	0.6293	0.6331	0.6368	0.6406	0.6443	0.6480	0.6517
0.4	0.6554	0.6591	0.6628	0.6664	0.6700	0.6736	0.6772	0.6808	0.6844	0.6879
0.5	0.6915	0.6950	0.6985	0.7019	0.7054	0.7088	0.7123	0.7157	0.7190	0.7224
0.6	0.7257	0.7291	0.7324	0.7357	0.7389	0.7422	0.7454	0.7486	0.7517	0.7549
0.7	0.7580	0.7611	0.7642	0.7673	0.7704	0.7734	0.7764	0.7794	0.7823	0.7852
0.8	0.7881	0.7910	0.7939	0.7967	0.7995	0.8023	0.8051	0.8078	0.8106	0.8133
0.9	0.8159	0.8186	0.8212	0.8238	0.8264	0.8289	0.8315	0.8340	0.8365	0.8389
1.0	0.8413	0.8438	0.8461	0.8485	0.8508	0.8531	0.8554	0.8577	0.8599	0.8621
1.1	0.8643	0.8665	0.8686	0.8708	0.8729	0.8749	0.8770	0.8790	0.8810	0.8830
1.2	0.8849	0.8869	0.8888	0.8907	0.8925	0.8944	0.8962	0.8980	0.8997	0.9015
1.3	0.9032	0.9049	0.9066	0.9082	0.9099	0.9115	0.9131	0.9147	0.9162	0.9177
1.4	0.9192	0.9207	0.9222	0.9236	0.9251	0.9265	0.9279	0.9292	0.9306	0.9319
1.5	0.9332	0.9345	0.9357	0.9370	0.9382	0.9394	0.9406	0.9418	0.9429	0.9441
1.6	0.9452	0.9463	0.9474	0.9484	0.9495	0.9505	0.9515	0.9525	0.9535	0.9545
1.7	0.9554	0.9564	0.9573	0.9582	0.9591	0.9599	0.9608	0.9616	0.9625	0.9633
1.8	0.9641	0.9649	0.9656	0.9664	0.9671	0.9678	0.9686	0.9693	0.9699	0.9706
1.9	0.9713	0.9719	0.9726	0.9732	0.9738	0.9744	0.9750	0.9756	0.9761	0.9767
2.0	0.9772	0.9778	0.9783	0.9788	0.9793	0.9798	0.9803	0.9808	0.9812	0.9817
2.1	0.9821	0.9826	0.9830	0.9834	0.9838	0.9842	0.9846	0.9850	0.9854	0.9857
2.2	0.9861	0.9864	0.9868	0.9871	0.9875	0.9878	0.9881	0.9884	0.9887	0.9890
2.3	0.9893	0.9896	0.9898	0.9901	0.9904	0.9906	0.9909	0.9911	0.9913	0.9916
2.4	0.9918	0.9920	0.9922	0.9925	0.9927	0.9929	0.9931	0.9932	0.9934	0.9936
2.5	0.9938	0.9940	0.9941	0.9943	0.9945	0.9946	0.9948	0.9949	0.9951	0.9952
2.6	0.9953	0.9955	0.9956	0.9957	0.9959	0.9960	0.9961	0.9962	0.9963	0.9964
2.7	0.9965	0.9966	0.9967	0.9968	0.9969	0.9970	0.9971	0.9972	0.9973	0.9974
2.8	0.9974	0.9975	0.9976	0.9977	0.9977	0.9978	0.9979	0.9979	0.9980	0.9981
2.9	0.9981	0.9982	0.9982	0.9983	0.9984	0.9984	0.9985	0.9985	0.9986	0.9986
3.0	0.9987	0.9987	0.9987	0.9988	0.9988	0.9989	0.9989	0.9989	0.9990	0.9990
3.1	0.9990	0.9991	0.9991	0.9991	0.9992	0.9992	0.9992	0.9992	0.9993	0.9993
3.2	0.9993	0.9993	0.9994	0.9994	0.9994	0.9994	0.9994	0.9995	0.9995	0.9995
3.3	0.9995	0.9995	0.9995	0.9996	0.9996	0.9996	0.9996	0.9996	0.9996	0.9997
3.4	0.9997	0.9997	0.9997	0.9997	0.9997	0.9997	0.9997	0.9997	0.9997	0.9998

Usually, tables only give $P(Z \leq z)$ for positive values of z. For negative values, we use the symmetry of the distribution to calculate the required probability.



$=$



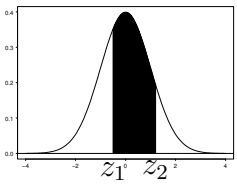


$$= \quad 1 \quad - \quad$$

$$P(Z \leq -z) \quad = \quad 1 \quad - \quad P(Z \leq z)$$

So therefore the probability of an observation of a standard normal population being less than -1.5 is 0.0668.

We can now calculate probabilities for any region.



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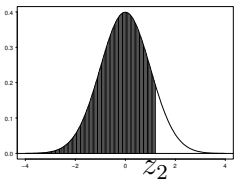

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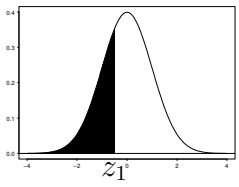


$$P(z_1 \leq Z \leq z_2) \quad = \quad P(Z \leq z_2) \quad - \quad P(Z \leq z_1)$$

So therefore the probability of an observation of a standard normal population being between -0.05 and 1.5 is 0.4531.

3.3.2 Standardising a Normally Distributed Variable

The normal distribution has a particularly convenient property.

Consider a variable whose probability distribution has mean μ and standard deviation σ. Suppose that we subtract μ from this variable and then divide by σ, to obtain a transformed variable. The transformed variable has mean 0 and standard deviation 1. Furthermore, **if the distribution of the original variable is normal**, the transformed variable has a **standard normal distribution**.

The operation of subtracting the mean (μ) of the distribution and dividing by the standard deviation (σ) is called **standardising** the variable, and we write

$$Z = \frac{X - \mu}{\sigma}.$$

By standardising, we can calculate probabilities for **any** normal distribution using tables of the standard normal distribution.

Suppose that the atmospheric SO_2 (sulphur dioxide) concentration at a particular location is, under usual conditions, normally distributed with mean 25.8 micrograms per cubic metre and standard deviation 5.5 micrograms per cubic metre. What is the probability of a SO_2 concentration between 20 and 30 micrograms per cubic metre?

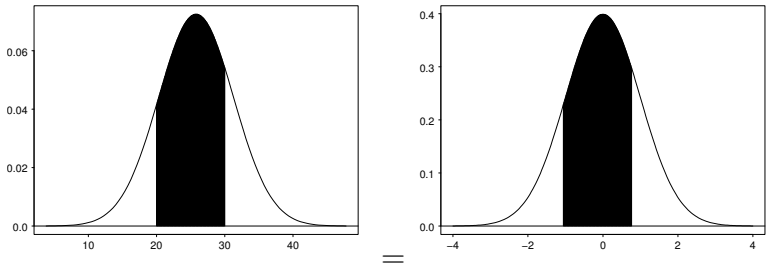
If we denote the SO_2 concentration by X then $Z = (X - 25.8)/5.5$ is a variable with a standard normal distribution.

We require $P(20 \leq X \leq 30)$.

When $x = 20$, $z = -1.05$

When $x = 30$, $z = 0.76$

$P(20 \leq X \leq 30) = P(-1.05 \leq Z \leq 0.76) = 0.7764 - (1 - 0.8531) = 0.6295.$



The fact that a normally distributed population is **completely specified** by its mean and standard deviation means that it is easy to make useful statements and predictions about normal populations.

For example, suppose that on one particular day the SO_2 concentration was measured as 44.3 micrograms per cubic metre. Is this unusually high?

When $x = 44.3$, $\quad z = \frac{44.3 - 25.8}{5.5} = 3.36$

Now $\quad P(X \geq 44.3) = P(Z \geq 3.36) = 1 - P(Z \leq 3.36) = 1 - 0.9996 = 0.0004$

This observation, 44.3, does seem high. Only about 1 in 2500 observations from this population are as high, or higher than this. This might lead us to suspect that conditions for this measurement were unusual, and to seek some explanation as to why the measurement is so high.

Note that **in MINITAB** we can calculate probabilities for any (not just standard) normal distribution using

Calc→Probability Distributions →Normal

but remember to ask for `Cumulative probability`

If we have a normal model for a particular population (and the normal distribution does provide a reasonable model for many populations) and we know the mean and standard deviation of the normal distribution, useful statements and predictions can be made about the variable of interest.

In practice we will rarely know any of these things precisely, but we can use a **sample** of observations from the population to estimate the mean and standard deviation and check to see if the assumption of a normal distribution is sensible.

3.4 Samples

A set of observations which consists of the whole population is a census. In practice, we rarely observe the whole population. Therefore we collect data on a **sample** from the population and use the sample to **make inferences** about the population. A sample is a set of observations which constitutes part of a population.

Most statistical data analysis (§4 onwards) concerns **how** to use a sample to make inferences about a population and **how accurate** conclusions made about populations using sample data are likely to be (as a sample only contains part of the population, using a sample to make conclusions about a population is subject to error).

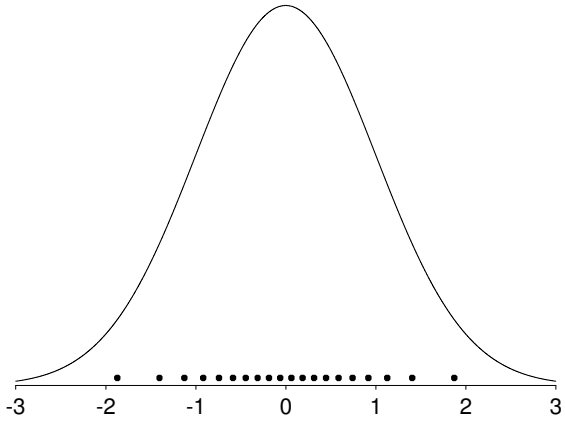
Next, we consider how to use sample data to determine whether or not a normal model may be appropriate for a particular population. This is particularly relevant, as if we can be confident about our model for a population, then useful statements and predictions can be made about the variable of interest.

The further use of sample data to make inferences about populations, for example to estimate model parameters, will be discussed in Chapter 4.

3.5 Testing for Normality

Suppose that we have a **sample** of n observations from a particular population, and a normal model is proposed for the population. One may produce a histogram of the observations, and examine if the distribution is approximately 'bell-shaped'. However, there is a more straightforward procedure to check whether a sample of observations have come from a normal distribution.

For any sample size n, MINITAB can calculate **normal scores**. These are the typical values one would expect to obtain if one had a sample of size n from a standard normal distribution. For example, if $n = 20$



These are the mean values of the **ordered** observations when repeated samples of size 20 are taken from a standard normal distribution.

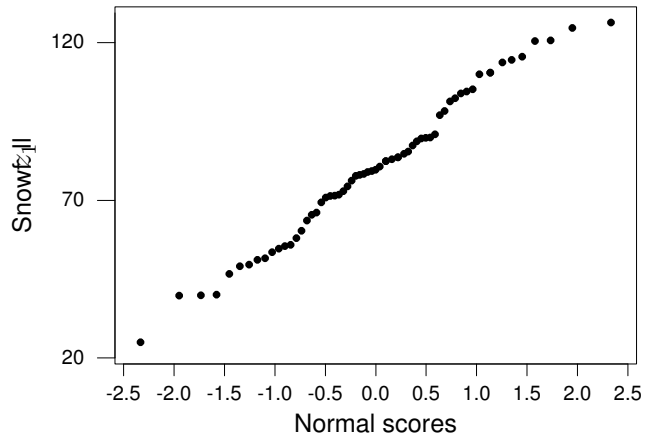
A **normal probability plot** is a plot of the observed data (n values) against the normal scores for a sample of size n. The smallest value in the sample is plotted against the smallest normal score, the second smallest value in the sample is plotted against the against the second smallest normal score, ... , the largest value in the sample is plotted against the largest normal score.

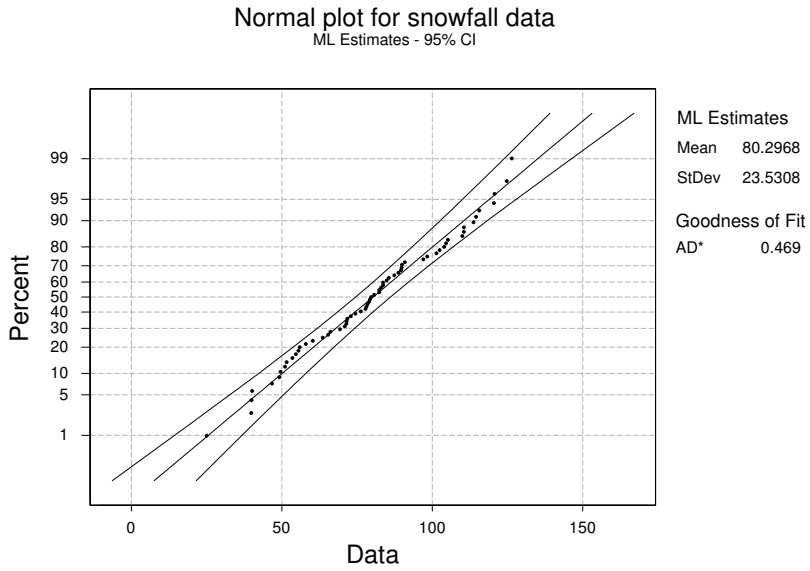
If the sample is from a normally distributed population, then the plot will be **approximately** a straight line. although the variation in the data will ensure that the plot is not a perfect straight line.

There are two ways of producing a normal probability plot in MINITAB.

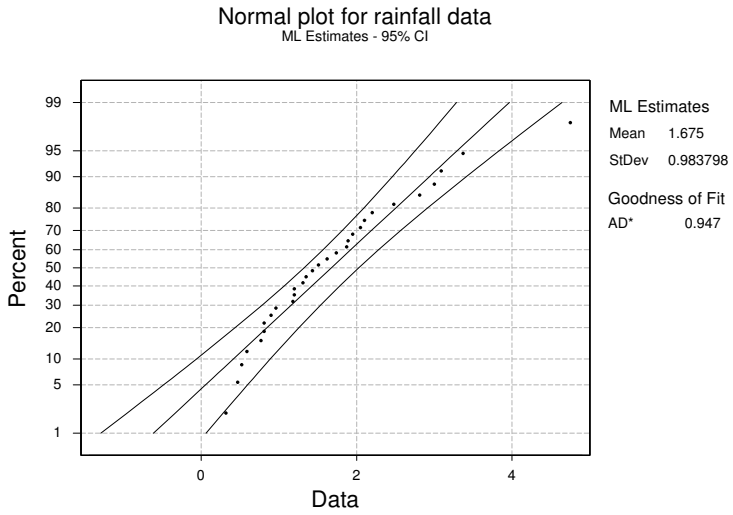
1. **Calc→Calculator** allows you to put normal scores corresponding to the column of data of interest into a new column so that the two columns are the same length and are ordered correctly. Then it is straightforward to produce the plot using
Graph→Scatterplot. If you plot the data of interest along the y-axis, and the normal scores along the x-axis, then, if the data are from a normally distributed population, the resulting straight line will have an intercept (value of y at $x = 0$) approximately equal to the population mean, and a gradient approximately equal to the population standard deviation.
2. **Graph→Probability plot** produces the normal probability plot directly (choose `Normal` in the **distribution** panel of the dialogue box).

For the snowfall data (in file `snow.dat`; see §1.2.3). The top graph is using method 1 and the bottom graph is using method 2.

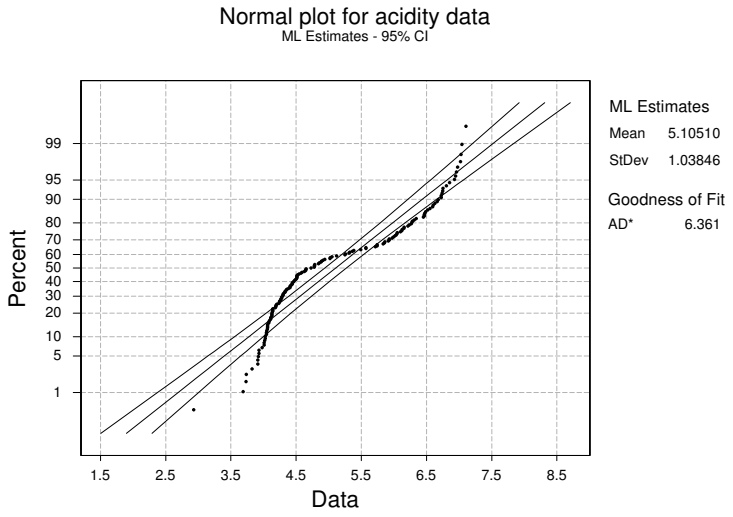




The following normal probability plot is for the data in `rain.dat` which are 30 successive values of March precipitation (in inches) for Minneapolis/St Paul.



The following normal probability plot is for the data in acidity data (in `acidity.dat` which are measurements of an acidity index for each of 155 lakes in the Northeastern USA.

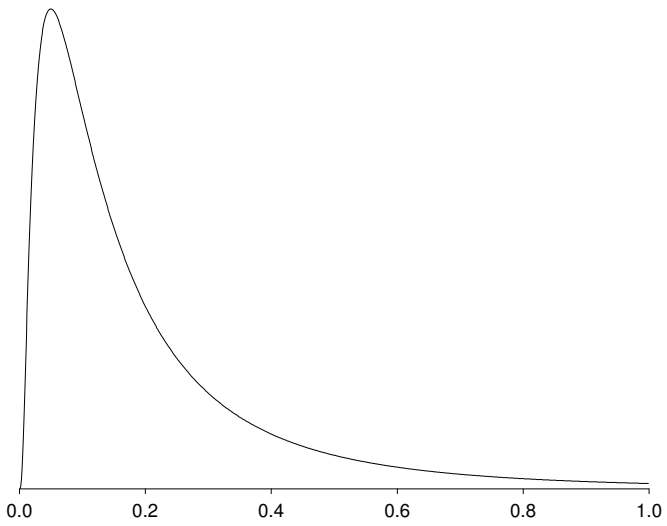


3.6 The Lognormal Distribution

If a normal probability plot produces a result which is clearly not a straight line, then a normal model is inappropriate for the variable of interest, and an alternative model needs to be specified. When the variable of interest can only take positve values, it is quite common for the distribution to be skewed so that more observations lie to the right of (are greater than) the peak (or mode) of the distribution than lie to the left. This kind of behaviour is typical when the variable of interest is a concentration.

The symmetric normal distribution fails as a model for such variables. However, it is often the case that by creating a transformed variable, by taking the logarithm of the original variable, that the transformed variable seems to have a normal distribution. Suppose that X is the original variable and that $Y = \log X$ has a normal distribution. Then we say that X has a **lognormal** distribution. The lognormal distribution has density function

$$f(x) = \frac{1}{x\sqrt{2\pi\sigma^2}} \exp\left(-\frac{(\log x - \mu)^2}{2\sigma^2}\right).$$



The base to which the logarithm is taken is not important, because

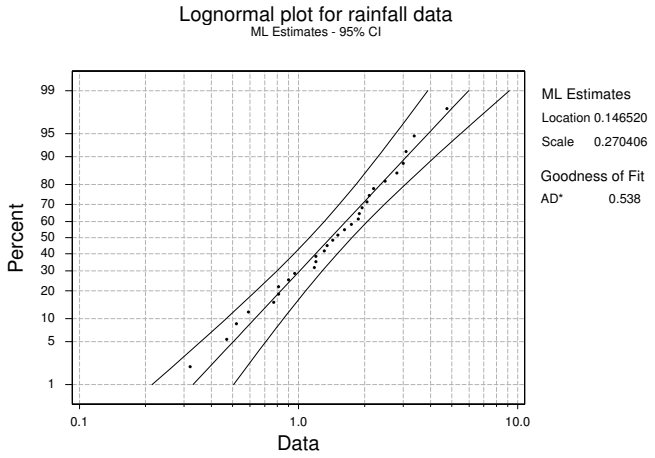
$$\log_a x = \log_a b \log_b x = k \log_b x.$$

In other words, any logarithm can be obtained from any other by multipication by a constant, and if a normally distributed variable is multiplied by a constant, its distribution remains normal. Therefore, if taking logarithms to one particular base transforms a variable to a normal distribution, so will taking logarithms to any other base.

There are two ways in MINITAB of checking to see if a lognormal distribution is appropriate for the variable of interest.

1. **Calc→Calculator** allows you to put the logarithms of the column of data of interest into a new column. Then check to see if the transformed column is normally distributed using a normal probability plot, as in §3.4.

2. **Graph→Probability plot** can produce the lognormal probability plot directly (choose `Lognormal` (either base) in the **distribution** panel of the dialogue box).



3.7 The Exponential and Weibull Distributions

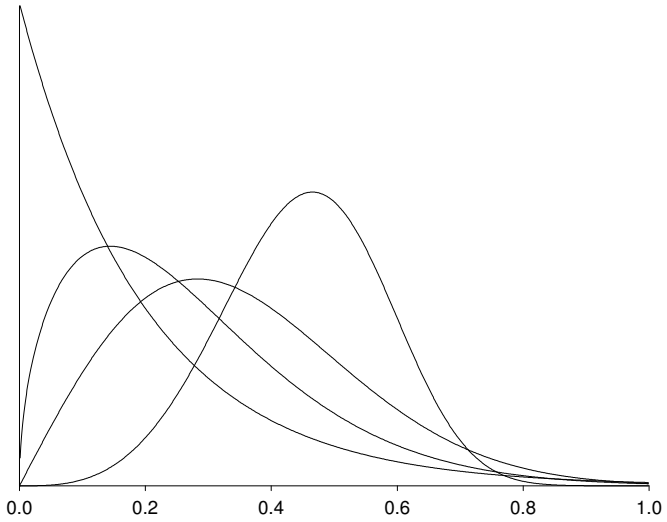
In the previous sections we saw that some data can be described by the normal or lognormal distributions and that sometimes it is possible to transform the data to another variable for which a normal distribution is a reasonable fit. However, there are other practical situations which give rise to variables which cannot be described in this way. In particular, especially in engineering problems, problems arise in which the observations are maximum or minimum values, such as maximum or minimum sea-level. Alternatively, many variables measured in fatigue analyses cannot be transformed to a normal distribution and a wide family of distributions may be called upon to assist with describing the behaviour of data of this kind. We begin by looking at the two-parameter Weibull distribution.

The density function of the Weibull distribution is given by

$$\begin{aligned} f(x) &= \tfrac{\alpha}{\beta^\alpha} x^{\alpha-1} \exp\left\{ -\left(\tfrac{x}{\beta}\right)^\alpha \right\} \\ &= \tfrac{\alpha}{\beta^\alpha} x^{\alpha-1} e^{-\left(\frac{x}{\beta}\right)^\alpha} \end{aligned}$$

for positive x, and zero for negative x so a Weibull distributed variable can only take positive values.

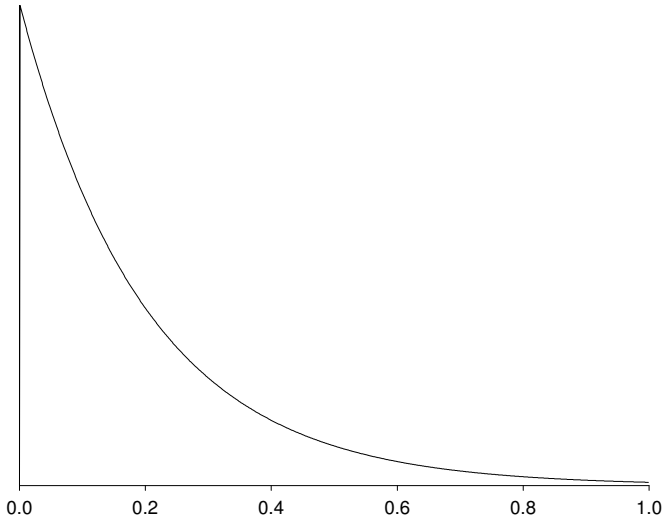
The parameters are α and β, where the value of α determines the shape of the distribution and β its scale. The figure below illustrates this distribution for some different combinations of values of α and β.



When the parameter $\alpha = 1$, the density function takes the form

$$f(x) = \frac{1}{\beta} e^{-\frac{x}{\beta}}$$

which is also known as the exponential or negative exponential distribution. This distribution often occurs in such practical problems as the waiting time between events in some random process of events or as the time between failures in some process where the failures are occurring at random. The figure below illustrates this distribution for $\beta = 0.2$.



The simple form of this particular distribution makes it possible to determine the mean (μ) and standard deviation (σ), by integration as follows

$$\begin{aligned}\mu &= \int_0^\infty x\tfrac{1}{\beta}e^{-\frac{x}{\beta}}dx = \beta \\ \sigma^2 &= \int_0^\infty x^2\tfrac{1}{\beta}e^{-\frac{x}{\beta}}dx - \beta^2 = \beta^2.\end{aligned}$$

Other properties of this distribution, such as the probability of an exponentially distributed variable lying in any region, may also be found using integration. For example, if the variable is X, then

$$P(X \leq t) = \int_0^t \frac{1}{\beta}e^{-\frac{x}{\beta}}dx = 1 - e^{-\frac{t}{\beta}}.$$

This probability may be calculated directly in MINITAB using

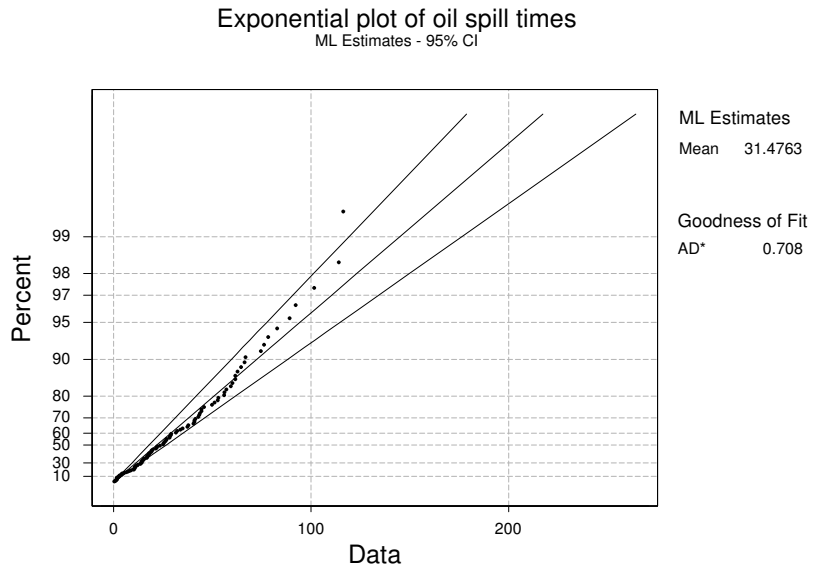
Calc→Probability Distributions→Exponential, asking for `Cumulative probability`. Hence

$$P(s \leq X \leq t) = e^{-\frac{s}{\beta}} - e^{-\frac{t}{\beta}}.$$

As with the normal distribution, if we propose an exponential distribution as a model for a variable of interest, we can use sample data to check whether the model is appropriate. Again, we use a probability plot to perform the check. The ordered sample data are plotted, not against the normal scores, but against the equivalent values for an exponential distribution.

Graph→Probability plot produces the exponential probability plot (if you choose `Exponential` in the **distribution** panel of the dialogue box).

For example, consider the data in the file `oilspill.dat` which are the times between oil spills in or around an oil terminal entrance.



The plot is quite a good straight line and we see that the mean of the distribution is estimated as 31.47. This is the estimate of the value of β for this set of data. Therefore the average time between oil spills is about 31 days.

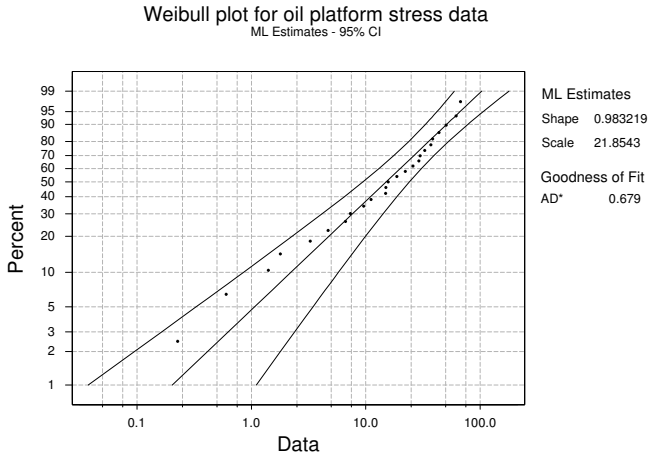
The general Weibull distribution is more difficult to deal with. For example its mean (μ) and standard deviation (σ) are given by

$$\begin{aligned} \mu &= \beta\Gamma\left(1+\tfrac{1}{\alpha}\right) \\ \sigma^2 &= \beta^2\left\{\Gamma\left(1+\tfrac{2}{\alpha}\right)-\Gamma\left(1+\tfrac{1}{\alpha}\right)^2\right\}. \end{aligned}$$

where $\Gamma(t)=\int_0^\infty x^{t-1}e^{-x}dx$. The integrals required to evaluate the probability of a Weibull distributed variable lying in any region can be directly calculated (but are also available in MINITAB by using **Calc→Probability Distributions→Weibull**, and asking for `Cumulative probability`).

This distribution occurs in many engineering problems concerned with stress or fatigue. As an example of a variable having this distribution consider the data in file `stress1.dat` relating to the stresses resulting from wave action on the joints of an off-shore oil-drilling platform. If we propose a Weibull distribution as a model for a variable of interest, We can use these sample data to check whether a Weibull distribution is a reasonable model for these data. Again, we use a probability plot.

Graph→Probability plot produces the Weibull probability plot (if you choose `Weibull` in the **distribution** panel of the dialogue box).



Note that the analysis produces estimates of the parameters in the Weibull model. In this case these are $\alpha = 0.98$ and $\beta = 21.8$. These can be substituted into the expressions above to estimate the population mean and standard deviation if required. Alternatively the probability of the stress taking a value in a particular range can be calculated by using these values of α and β in **Calc→Probability Distributions→Weibull** in MINITAB. Estimation is considered in further detail in Chapter 4.

3.8 Return Periods, Design Life and Reliability

One of the main applications of a probability model for a particular variable is often to extrapolate into the tails of the distribution to determine the value exceeded with a specified probability, say $p = 0.01$.

For example, suppose that the random variable X represents the maximum annual flow rate of a river at a particular location. If we have a probability model for X, and we have estimated the parameters of this model, we can use the density function to find the value x such that $P(X > x) = p$, or alternatively $P(X \leq x) = 1 - p$.

The reciprocal of this probability $T = 1/p$, (for example $T = 100$ if $p = 0.01$) is known as the corresponding **Return Period**. There is often, however, some confusion about the appropriate interpretation of statements of the form "The flow x has a return period of 100 years." This statement does not mean that the flow x will be exceeded once in every 100 years, or that it will take 100 years for x to be exceeded, or that any structure designed to withstand a flow of x will last 100 years.

In order to be able to appreciate the meaning of a return period, particularly the need

sometimes to use large return periods of say 500 years, 1000 years or even 2000 years, we should consider the concepts of **design life** and **reliability** of a structure.

The **design life** of a structure is the time that the designer hopes that it will survive. The **reliability** is the probability that it will survive for that length of time.

The usual position is that the structure under discussion has a design life of a specified number of years and the engineer is prepared to accept a risk, again of specified magnitude, that the structure will fail at some time during its design life. For example, the design life for an irrigation project could be 50 years and an acceptable risk could be 5 per cent. This means that there is a 95% chance that it will survive for 50 years. An alternative acceptable risk not uncommonly used is 10%. We shall observe the effects of modifying risk later.

The problem now is to relate the design life, the specified risk and the return period.

Suppose that the structure is to be built at a point in the river where data has been collected for a period of time. Since we are interested in the extreme flows when designing structures, it is common to consider the annual maximum or the annual minimum flows as the basic data with these values recorded for a number of years. We shall consider the distributions of extremes in the next section, but for the moment suppose that the data consist of annual maximum river flows at that point on the river and that these values are denoted by $x_1, x_2, \ldots, x_n$, where n is the number of years of data.

Suppose that the distribution of these annual maxima has density function $f(x)$, and define $F(x)$ by

$$F(x) = P(X \leq x) = \int_{-\infty}^{x} f(x)dx.$$

We call $F(x)$ the **distribution function** of the random variable. Then

$$P(X > x) = 1 - F(x) = p$$

where p is the probability that the value x is exceeded.

Consider a design life of m years over which the structure is expected to be operational, and that if the flow exceeds x, the structure fails. Each year of the design life the probability that the structure fails is p and therefore the probability that it does not fail is $(1-p) = F(x)$.

Assuming that values of X over succesive years are independent, then the probability that the structure does not fail over its design life of m years is

$$P(X \leq x, \text{every year}) = (1-p)^m$$

and therefore the probability that x is exceeded at some time during the design life, (thus causing a failure of the structure), is $\beta = 1 - (1-p)^m$.

This is the risk of failure and may be set equal to any specified risk such as 5% or 10%. Therefore, specifying a risk β and a design life m acceptable to the engineer, is equivalent to specifying a value of $p = 1 - F(x)$ and this in turn is equivalent to specifying a value of x.

Now, the return period is defined as

$$T = \frac{1}{p} = \frac{1}{1 - F(x)}$$

so that specifying the risk β and the design life m is equivalent to specifying a return period.

For example, determine the flow level to which a structure should be designed if the risk of failure during a 50 year design life is not more than 10%.

Here $\beta = 0.1$ and $m = 50$, so that

$$\begin{aligned}
& 1 - (1-p)^{50} = 0.1 \\
\Rightarrow \quad & (1-p)^{50} = 0.9 \\
\Rightarrow \quad & 1 - p = (0.9)^{1/50} \\
\Rightarrow \quad & p = 1 - (0.9)^{1/50} \\
\Rightarrow \quad & p = 0.0021 \\
\Rightarrow \quad & F(x) = 1 - 0.0021 = 0.9979 \\
\Rightarrow \quad & T = \tfrac{1}{1-F(x)} \approx 475.
\end{aligned}$$

The appropriate flow value is nearly that value with a 500 year return period. Typical combinations of values are shown in the table below.

Risk $\beta = 10\%$			Risk $\beta = 5\%$		
m	p	T	m	p	T
10	0.01048	95	10	0.00511	195
20	0.00525	195	20	0.000256	390
50	0.0021	475	50	0.001025	975
100	0.00105	949	100	0.000512	1950

Values for the appropriate return period may now be calculated using the density function of a probability model for the variable of interest. Recall that use of a return period of 500 years does not mean that the engineer is designing for 500 years; but that the **accumulated** risk, β, is 10% over a period of 50 years.

The return period does have a direct interpretation as follows. It can be shown that T is the average number of years before the flow x is exceeded.

For many probability models, the value of x may be calculated from p in MINITAB using **Calc→Probability Distributions**, and asking for `Inverse Cumulative probability`.

3.9 Extreme value distributions

It is evident that the form of distribution which might be appropriate for maximum and minimum values of samples of data depends primarily on the behaviour of the tails of the

distribution of the original variable. For example, the form of the extreme value distribution which describes annual maximum river flows will depend on the shape of the right tail of the distribution of the daily flows, since the maximum will always be in this tail area each year. Fortunately there are only three different kinds of extreme value distribution that can occur, provided the maxima are obtained over a long enough period of time. When we are dealing with annual maxima taken over 365 days, the asymptotics are very good.

The most common extreme value distribution is the Type I **Extreme Value Distribution for Greatest Values**, EVG1 for short, sometimes also known as Gumbel's distribution. This distribution has the following density function

$$f(x) = \frac{1}{\beta} \exp\left(-\frac{x-\alpha}{\beta} - e^{-\frac{x-\alpha}{\beta}}\right)$$

This has two parameters, α and β. The corresponding cumulative distribution function $F(x)$ is given by

$$F(x) = P(X \leq x) = \exp\left(-e^{-\frac{x-\alpha}{\beta}}\right)$$

This probability cannot be calculated directly in MINITAB.

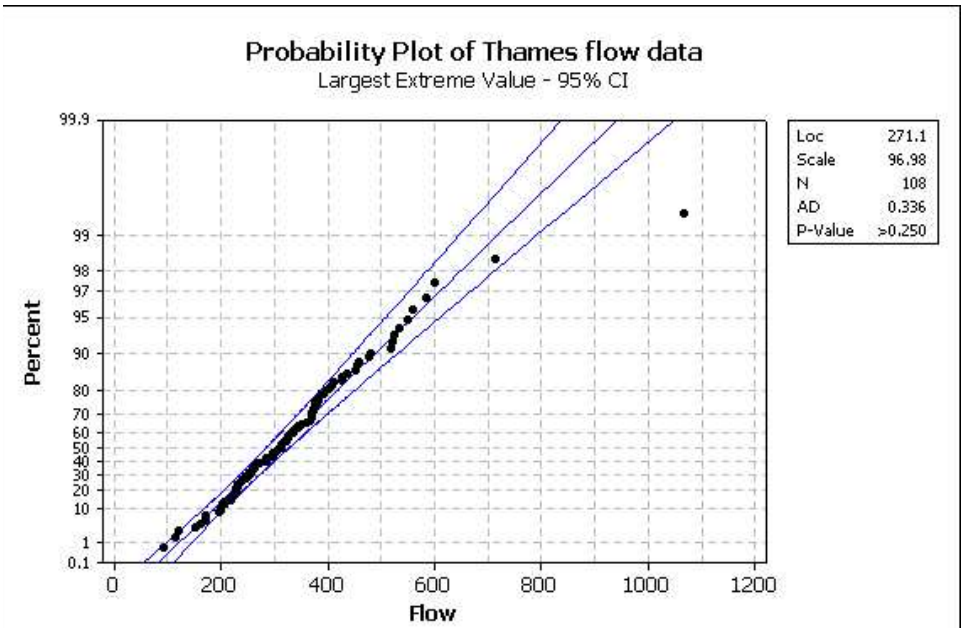
The mean (μ) and standard deviation (σ) of the EVG1 distribution are given by

$$\begin{aligned} \mu &= \alpha + \beta\gamma \\ \sigma &= \frac{\pi\beta}{\sqrt{6}}. \end{aligned}$$

where $\pi \approx 3.1416$ and γ (Euler's constant) ≈ 0.5772.

The file `thames.dat` contains 108 years of annual maximum flows of the River Thames at Kingston. Each value recorded is the maximum of 365 daily values, so we would expect an extreme value distribution to be an appropriate model for this variable. If it is, then we can use it to estimate the flow corresponding to a 100 year return period.

First we use the sample data to check whether a EVG1 distribution is a reasonable model for these data, using a probability plot. **Graph→Probability plot** produces the required probability plot (if you choose `Largest extreme value` in the **distribution** panel of the dialogue box).



The estimated values for the parameters α and β are 271.1 and 96.98.

It would seem that this distribution is reasonable for these data, even though one point is a bit out of line with the others. We can accept this distribution and use it to estimate the flow corresponding to a 100 year return period. This could be obtained from the graph or calculated from the formula developed above. The flow, x, corresponding to a return period of 100 years is such that the probability of exceeding x, $p = 1 - F(x)$, is 0.01, so that $F(x) = P(X < x) = 0.99$. This means that

$$\begin{aligned} \exp\left(-e^{-\frac{x-\alpha}{\beta}}\right) &= 0.99 \\ \Rightarrow \quad e^{-\frac{x-\alpha}{\beta}} &= -\log 0.99 \\ \Rightarrow \quad \frac{x-\alpha}{\beta} &= -\log[-\log 0.99] \\ \Rightarrow \quad x &= \alpha - \beta \log[-\log 0.99] \end{aligned}$$

If we plug in the estimates for α (271.1) and β (96.98), provided by the probability plotting routine, into this expression, we obtain an estimate for x of 717.2 $\mathrm{m^3 s^{-1}}$. This means that we need to design any structure at this point of the Thames to withstand a flow of 717 $\mathrm{m^3 s^{-1}}$, if it is to have a return period of 100 years.

More generally, for EVG1 distributions, we can write the expression

$$x = \alpha - \beta \log[-\log(1-p)]$$

where p is the probability of exceeding thhreshold value x. Therefore, as the return period $T = 1/p$, we can write

$$x = \alpha - \beta \log\left[-\log\left(1 - \frac{1}{T}\right)\right]$$

Now let

$$\begin{aligned} u &= -\log\left[-\log\left(1-\tfrac{1}{T}\right)\right] \\ e^{-u} &= -\log\left(1-\tfrac{1}{T}\right) \\ e^{-u} &= \tfrac{1}{T}+\tfrac{1}{2T^2}+\cdots \\ e^{-u} &= \tfrac{1}{T}\left[1+\tfrac{1}{2T}+\cdots\right] \\ e^{u} &= T\frac{1}{\left[1+\frac{1}{2T}+\cdots\right]} \\ e^{u} &\approx T\left[1-\tfrac{1}{2T}\right] \end{aligned}$$

provided that T is reasonably large. Therefore

$$e^u = T - \frac{1}{2}.$$

If we ignore the 1/2, which is relatively insignificant if T is large, we have that

$$u \approx \log T$$

and therefore

$$x = \alpha + \beta \log T.$$

This is known as the **fundamental formula for flood control**. Once the estimates of the two parameters α and β have been obtained from the available data, they can be substituted into this equation so that the value of x corresponding to any return period T can be found. For example, here the estimates of α and β for the annual flows data for Kingston are $\alpha = 271.1$ and $\beta = 96.98$, so that the estimate of the annual maximum flows corresponding to the 100, 200, 500 and 1000 year return periods are as follows.

Return period T in years	Flow x in $\mathrm{m^3s^{-1}}$
100	717.7
200	784.9
500	873.8
1000	941.0

Chapter 4

Estimation and Hypothesis Testing

4.1 Introduction

A probability model for the distribution of variable of interest will usually depend on one or more unknown *parameters*. For example, if we propose a normal distribution for a particular variable, then we need to know the mean μ and standard deviation σ of that normal distribution, in order to use our model to make predictions about future observations.

Just as we used sample data in §3, to assess whether a particular distributional model is appropriate for a variable of interest, we can also use sample data to estimate the parameters of our model.

4.2 Estimating a mean

The most straightforward situation is where the parameter of interest is the mean of the population distribution, for example the normal parameter μ or the exponential parameter β. There are also cases where it may be sufficient to estimate the mean of a population without necessarily specifying a complete distributional model for the population.

Suppose that we have a sample of size n, $x_1, \ldots x_n$ from a population of interest. It seems obvious that we should use the sample mean ($\overline{x}$) to estimate the population mean μ. This procedure, estimating a population quantity using a sample quantity, is called **point estimation**.

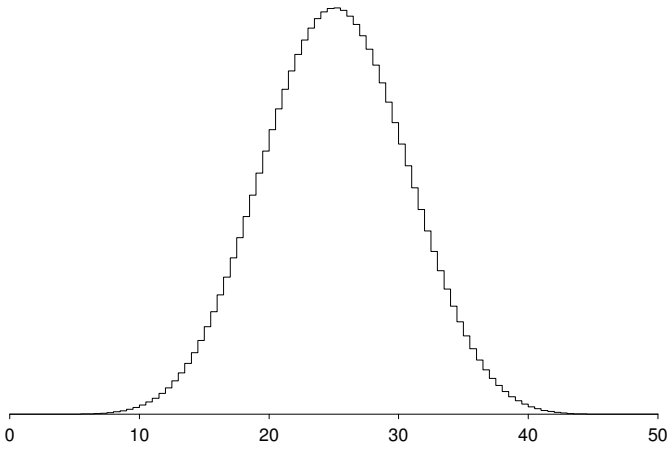
When we calculate a point estimate, it is important that we have some idea how accurate that estimate is likely to be. So how accurate are we, when we use the mean of a sample of size n to estimate the mean of a population distribution?

Samples from a population are variable, and therefore estimates calculated using sample data are also variable, and we can consider their distribution. When a sample of size n is

observed from a distribution, the sample mean $\overline{x}$ is a single observation from the distribution of $\overline{x}$ for all such samples. An important question is 'What does the distribution of $\overline{x}$ look like?' and in particular 'How does it compare with the distribution of the original observations $x_1, x_2, \ldots$?'

The following example is artificial, but serves to illustrate the point

♡ **Example** 4.1. Suppose that the distribution of interest consists of the integers from 1 to 49, each with probability 1/49. Twice a week a 'sample' of six observations is taken from this distribution in the National Lottery. From §2, we know that there are 13 983 816 possible samples of size 6. We can illustrate the distribution of $\overline{x}$ across these possible samples by a histogram.



We can also calculate the mean and standard deviation of this distribution, 25 and 5.7735 respectively.

Note that the mean and standard deviation of the original distribution (the numbers 1 to 49, each with probability 1/49) are 25 and 14.1421 respectively.

We immediately notice three facts about the distribution of $\overline{x}$

1. It has the same mean as the original distribution.
2. It has a smaller standard deviation than the original distribution.
3. The histogram seems 'bell-shaped' suggesting that the distribution may be close to a normal distribution, even though the original distribution is far from normal.

In general Suppose also that $x_1, \ldots, x_n$ is a sample of size n from a distribution with mean μ and standard deviation σ.

Then the distribution of $\overline{x}$, the sample mean has the following three properties.

1. It also has mean μ.
2. It has standard deviation $\dfrac{\sigma}{\sqrt{n}}$.

   For larger sample sizes n, the distribution of sample means has smaller standard deviation, so the sample means for larger samples are less variable and generally closer to μ.

3. It is approximately normally distributed if n is large, **regardless of the shape of the original distribution**.

- This is surprising and remarkable. It is the **Central Limit Theorem**, and one of the reasons why the normal distribution is so important for data analysis.

How large must a sample be before we can assume that the sample mean $\overline{x}$ is from a normal distribution?

There is no ready answer to this question. If the original distribution is 'close to normal', then quite small samples may be adequate. Indeed if the original distribution is exactly normal, then this assumption is appropriate for any size of sample. However, for highly non-normal distributions (very skew or multimodal) larger samples will be required.

What remains true for all distributions is that the larger the sample size, the closer the distribution of sample means is to a normal distribution.

Now, when we use a sample mean $\overline{x}$ to estimate the mean μ of the underlying distribution, we know that $\overline{x}$ can be considered as a single observation from the distribution of sample means for samples of size n.

We know that the mean of this distribution is also μ, but that its standard deviation is $\sigma/\sqrt{n}$. Therefore, 'on average', $\overline{x}$ is equal to μ, the quantity which we want to estimate, so $\overline{x}$ is a sensible estimate. (This property, being 'correct on average', is called **unbiased**).

Furthermore, $\sigma/\sqrt{n}$, the standard deviation, is a measure of the spread of possible sample means around μ, and gives an indication of the error involved when we use a single sample mean $\overline{x}$ to estimate μ.

Unfortunately, $\sigma/\sqrt{n}$, the standard deviation of the distribution of $\overline{x}$, is not known, as it depends on the σ, the standard deviation of the original distribution, which is an unknown quantity. However, if we use the standard deviation, s, of the **sample** to estimate σ, we can use $s/\sqrt{n}$ as a measure of the accuracy of $\overline{x}$ as an estimate of μ.

The quantity $s/\sqrt{n}$ is called the **standard error of the mean** and should be quoted whenever a sample mean $\overline{x}$ is used to estimate a population mean μ, as an indication of the accuracy of the estimate.

In MINITAB

Stat→Basic Statistics→ Display Descriptive Statistics

4.3 Confidence interval for a mean

A better approach to estimating μ than using a single point estimate $\overline{x}$, together with the standard error $s/\sqrt{n}$ as a measure of precision, is to combine the two quantities to give a **range** of plausible values for μ. A **confidence interval** provides this.

Suppose that $\overline{x}$ is the mean of a sample of observations $x_1, \ldots, x_n$ from a distribution with mean μ and standard deviation σ.

Furthermore, suppose that either the sample size n is 'large', or the distribution of interest is close to normal.

Then we know that $\overline{x}$ is a single observation from (approximately) a normal distribution with mean μ and standard deviation $\sigma/\sqrt{n}$. We can standardise the variable $\overline{x}$ by subtracting μ and dividing by $\sigma/\sqrt{n}$. The standardised sample mean will have a standard normal distribution. We can write

$$z = \frac{\overline{x} - \mu}{\sigma/\sqrt{n}}$$

However, as σ is not known, we need to estimate it by the sample standard deviation s. Then,

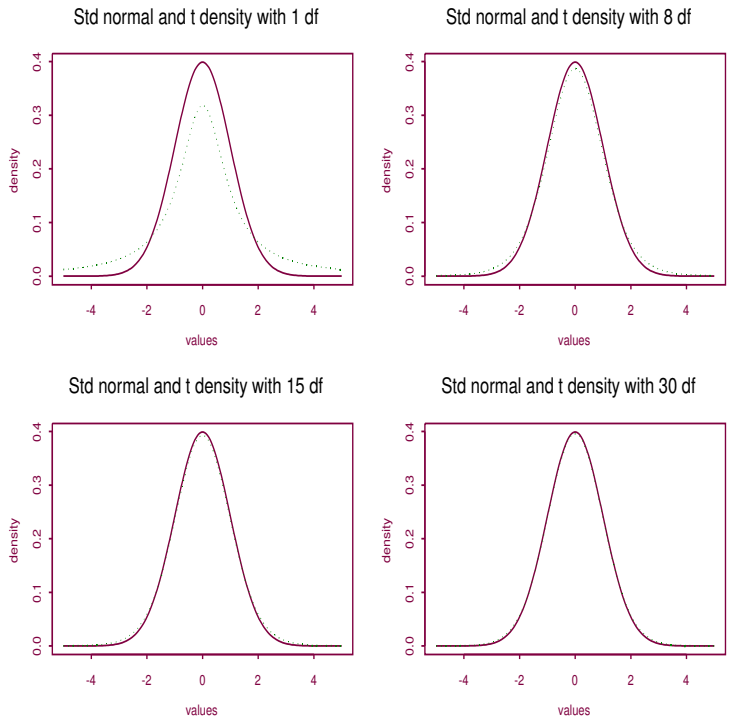
$$t = \frac{\overline{x} - \mu}{s/\sqrt{n}}$$

is an observation from a **t distribution** 'with $n-1$ degrees of freedom'.

The t distribution is a known distribution, with a density curve which looks similar to the standard normal distribution, but has a standard deviation larger than 1. The mean of a t distribution is always zero, but the standard deviation depends on the **degrees of freedom**, and is larger if the degrees of freedom is small.

When the degrees of freedom is large, the t distribution is very similar to the standard normal distribution, and its standard deviation is very close to one.

To distinguish between different t distributions (with different degrees of freedom), we denote the t distribution with k degrees of freedom by t_k.

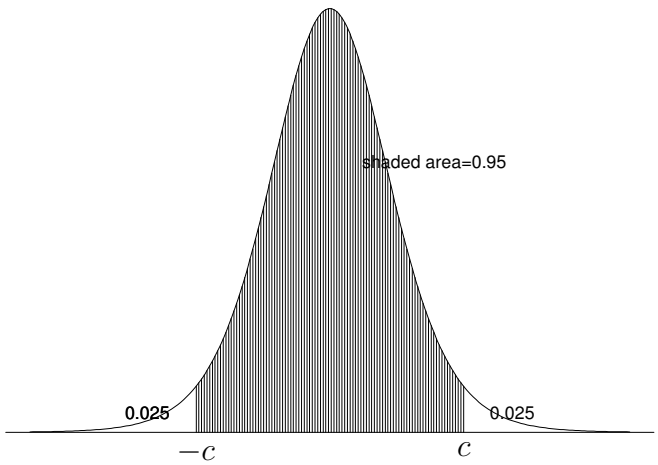


Because the t distribution is well understood, we can make statements about observations from a t distribution. As

$$t \;=\; \frac{\overline{x} \;-\; \mu}{s/\sqrt{n}}$$

is an observation from a t_{n-1} distribution. then we can (in principle), by calculating areas under the density curve of the t_{n-1} distribution, find the value c such that

$$P\left(-c \;\leq\; \frac{\overline{x} \;-\; \mu}{s/\sqrt{n}} \;\leq\; c\right) \;=\; 0.95.$$



Therefore

$$P\left(\overline{x} - c\frac{s}{\sqrt{n}} \;\leq\; \mu \;\leq\; \overline{x} + c\frac{s}{\sqrt{n}}\right) \;=\; 0.95.$$

or, in other words, **for 95% of samples** of size n, drawn from a distribution with mean μ, the interval between

$$\overline{x} - c\frac{s}{\sqrt{n}} \qquad \text{and} \qquad \overline{x} + c\frac{s}{\sqrt{n}}$$

will include μ.

Hence, we can calculate the endpoints of an interval, which will, for 95% of samples, include the population mean μ.
(The endpoints of the interval are often written as $\overline{x} \pm cs/\sqrt{n}$).

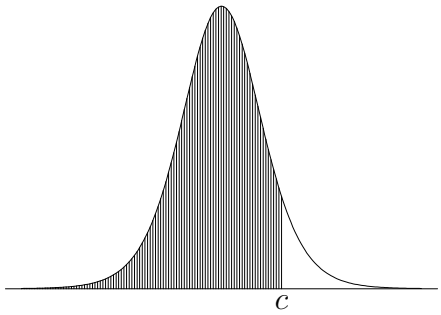
We call this interval a **95% confidence interval** for μ.

It is an interval within which we can be '95% certain' that μ lies. It provides a suumary of the 'most plausible' values for the population mean μ in light of the observed data.

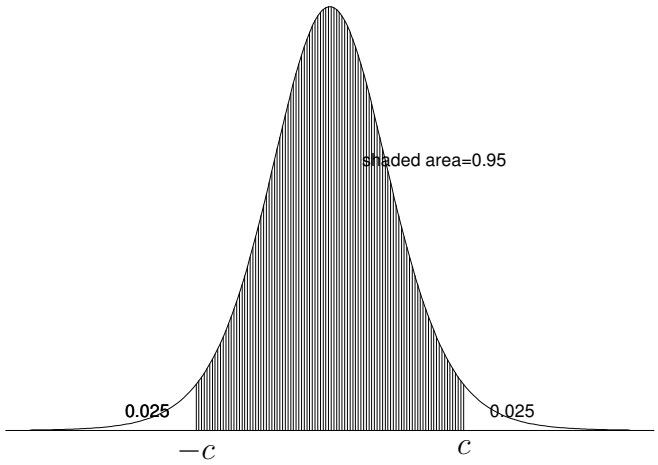
Statistical tables can be used to find c for any sample size n.

Because the t_k distribution is similar to the standard normal distribution for large values of k, then if the sample size n is large, in which case $n - 1$, the degrees of freedom will also be large, then c can be calculated using a standard normal distribution.

Table gives values of c for some $P(t_k \leq c)$



	$P(t_k \leq c)$						$P(t_k \leq c)$				
k	0.9	0.95	0.975	0.99	0.995	k	0.9	0.95	0.975	0.99	0.995
1	3.08	6.31	12.71	31.82	63.66	11	1.36	1.80	2.20	2.72	3.11
2	1.89	2.92	4.30	6.96	9.92	12	1.36	1.78	2.18	2.68	3.05
3	1.64	2.35	3.18	4.54	5.84	15	1.34	1.75	2.13	2.60	2.95
4	1.53	2.13	2.78	3.75	4.60	20	1.33	1.72	2.09	2.53	2.85
5	1.48	2.02	2.57	3.36	4.03	25	1.32	1.71	2.06	2.49	2.79
6	1.44	1.94	2.45	3.14	3.71	30	1.31	1.70	2.04	2.46	2.75
7	1.41	1.89	2.36	3.00	3.50	40	1.30	1.68	2.02	2.42	2.70
8	1.40	1.86	2.31	2.90	3.36	50	1.30	1.68	2.01	2.40	2.68
9	1.38	1.83	2.26	2.82	3.25	60	1.30	1.67	2.00	2.39	2.66
10	1.37	1.81	2.23	2.76	3.17	100	1.29	1.66	1.98	2.36	2.63
						∞	1.28	1.64	1.96	2.33	2.58



The area upto the point c in this graph is 0.975 and we use c to find the 95% CI. Hence

1. For 90% confidence, use the 0.95 values in the table above.

2. For 95% confidence, use the 0.975 values in the table above.

3. For 99% confidence, use the 0.995 values in the table above.

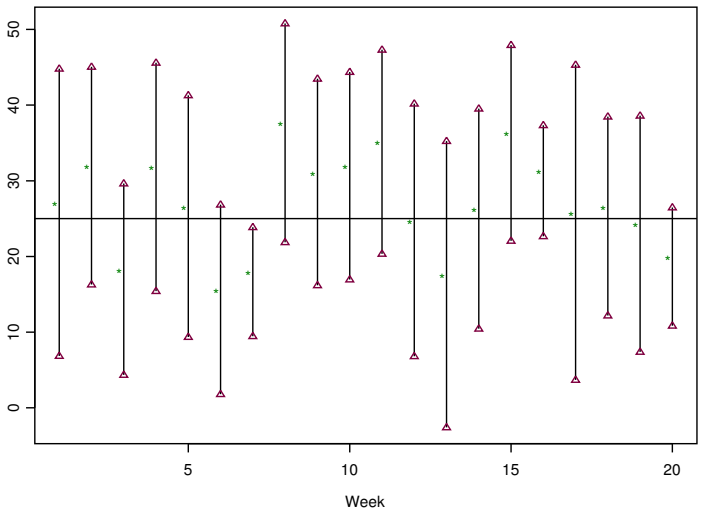
Notes

1. A confidence interval for μ is only a statement about the population mean μ. It does not say anything about other properties of the distribution of interest. In particular, we should not expect 95% of observations from a distribution to lie in the 95% confidence interval. They are likely to be much more variable.

2. If the exact value of k required is not in the table, then use the nearest value that is, or interpolate.

♡ **Example** 4.2. **Lottery example** [This is used purely as an illustration of how confidence intervals behave. The sample size of 6 is not really large enough to be happy with, but we do know in this case that the distribution of sample means is approximately normal. The confidence intervals and the sample means are plotted in the figure below.]

Date			Sample				$\overline{x}$
7/3/98	4	11	14	39	43	44	25.83
4/3/98	6	28	30	34	41	45	30.67
28/2/98	1	7	15	18	30	31	17.00
25/2/98	9	21	27	36	42	48	30.50
21/2/98	2	16	25	27	37	45	25.33
18/2/98	1	5	10	13	25	32	14.33
14/2/98	8	13	14	17	20	28	16.67
11/2/98	11	32	38	42	46	49	36.33
7/2/98	9	25	27	31	42	45	29.83
4/2/98	13	17	32	35	42	45	30.67
31/1/98	17	22	30	40	46	48	33.83
28/1/98	4	12	15	31	32	47	23.50
24/1/98	1	4	6	14	24	49	16.33
21/1/98	5	12	24	35	36	38	25.00
17/1/98	14	31	33	38	46	48	35.00
14/1/98	20	27	28	31	33	41	30.00
10/1/98	3	10	11	27	47	49	24.50
7/1/98	7	14	25	32	36	38	25.33
3/1/98	1	13	26	28	35	45	24.67
31/12/98	8	13	18	21	23	29	18.67



In MINITAB

Stat→Basic Statistics→ 1-sample t

Real examples

♡ **Example** 4.3. The file `concrete.dat` contains the compression strength (Nmm^{-2}) of 180 concrete cubes. Suppose that we are interested in the mean of the distribution of compression strength of all such cubes. The sample size of 180 is large, so there is no problem here.

The sample mean is $\overline{x} = 61.098$, the sample standard deviation is $s = 3.963$, and therefore, as the sample size $n = 180$, the standard error $s/\sqrt{n} = 0.295$. The value of the constant c for a t_{179} distribution is 1.9733 (approximately the same as for a standard normal).

Therefore, a 95% confidence interval for μ, the mean compression strength of all such cubes is $(60.515, 61.681)$.

This interval may also be presented as

$$60.515 \leq \mu \leq 61.681 \qquad \text{or} \qquad 61.098 \pm 0.583$$

A 99% confidence interval for μ is $(60.329, 61.867)$.

A 90% confidence interval for μ is $(60.609, 61.586)$.

♡ **Example** 4.4. Consider the data in the file `latent.dat` (also presented on the introductory handout), which are measurements of the latent heat of water using two methods.

Measurements subject to error are often assumed to be normally distributed with mean μ equal to the 'true' value. Normal probability plots of the sample data produce straight lines for both samples, we can assume that the distribution of measurements is approximately normal, and calculate a confidence interval for the true value μ without any concerns.

Using sample data for method A, the sample mean is $\overline{x} = 80.021$, the sample standard deviation is $s = 0.024$, and therefore, as the sample size $n = 13$, the standard error $s/\sqrt{n} = 0.007$, and $c = 2.18$ using the tables. Therefore, a 95% confidence interval for μ, the true latent heat of water is $(80.006, 80.035)$.

Using sample data for method B, the sample mean is $\overline{x} = 79.979$, the sample standard deviation is $s = 0.031$, and therefore, as the sample size $n = 8$, the standard error $s/\sqrt{n} = 0.011$. Therefore, a 95% confidence interval for μ, the true latent heat of water is $(79.953, 80.005)$.

4.4 Estimating other parameters

When estimating the mean μ of a distribution, a sample mean is an obvious estimator. However, for other parameters, a convenient estimator may not be quite so obvious. For example, how should we estimate the parameters α and β of a Weibull or EVG1 distribution?

The answer is that there exists a flexible estimation procedure, applicaable in simple or complex models, which can be proved theoretically to produce estimators with good properties. The method is called **maximum likelihood estimation**.

To discuss this method in general is betyond the scope of this course. However, we shall attempt to give a flavour of the method, by considering estimating the parameter β of the exponential distribution (See §3 for details).

Suppose we have observations $x_1, x_2, \ldots, x_n$ from an exponential distribution with parameter β. The probability density evaluated at each of these observations is

$$\frac{1}{\beta}e^{-\frac{x_1}{\beta}},\ \frac{1}{\beta}e^{-\frac{x_2}{\beta}},\ \ldots,\ \frac{1}{\beta}e^{-\frac{x_n}{\beta}}.$$

As the observations are assumed to be independent we write their **joint** probability density as

$$\frac{1}{\beta}e^{-\frac{x_1}{\beta}} \times \frac{1}{\beta}e^{-\frac{x_2}{\beta}} \times \ldots \times \frac{1}{\beta}e^{-\frac{x_n}{\beta}} = \frac{1}{\beta^n}e^{-\frac{x_1+\ldots+x_n}{\beta}} = \frac{1}{\beta^n}e^{-\frac{1}{\beta}\sum_{i=1}^n x_i}.$$

This function reflects how likely the observed data are in terms of how great the probability density is at each of the observed data values. The method of maximum likelihood estimates β by the value which makes the observed data more likely than any other value of β would. In other words, we maximise

$$\frac{1}{\beta^n}e^{-\frac{1}{\beta}\sum_{i=1}^n x_i}$$

as a function of β.

Differentiating this expression with respect to β, we get

$$\begin{aligned}\tfrac{d}{d\beta}\left[\beta^{-n}e^{-\beta^{-1}\sum_{i=1}^n x_i}\right] &= -n\beta^{-n-1}e^{-\beta^{-1}\sum_{i=1}^n x_i} + \beta^{-n}\beta^{-2}\textstyle\sum_{i=1}^n x_i e^{-\beta^{-1}\sum_{i=1}^n x_i} \\ &= \left[-n\beta + \textstyle\sum_{i=1}^n x_i\right]\beta^{-n-2}e^{-\beta^{-1}\sum_{i=1}^n x_i} \\ &= 0 \qquad \text{if} \quad \beta = \tfrac{1}{n}\textstyle\sum_{i=1}^n x_i = \overline{x}.\end{aligned}$$

Therefore, setting β equal to the sample mean $\overline{x}$ makes the observed data $x_1, \ldots, x_n$ more likely than any other value of β, so the sample mean is the maximum likelihood estimate for β. [Recall that β is the mean of an exponential distribution, so estimating it by a sample mean seems intuitively sensible. Similarly, the maximum likelihood estimate for the mean μ of a normal distribution os also the sample mean, although the maximum likelihood estimate for the standard deviation σ is not the sample standard deviation s. It is $\sqrt{\frac{n-1}{n}}s$]. In practice, maximum likelihood estimates can be calculated for any parameter.

MINITAB provides maximum likelihood estimates for model parameters using **Graph→Probability plot**, along with the probability plot to check whether the model is appropriate.

Ideally, we would also like to be able to get standard errors or (even better) confidence intervals for these parameters but **MINITAB** does not provide these in general. However, what **MINITAB** does provide are estimates of the distribution function $F(x) = P(X \leq x)$ based on the parameter estimates.

In particular, for a number of values of p (and more can be specified using `Options`), estimates of the value of x for which $P(X \leq x) = p$ are given. Furthermore, the uncertainty in these estimates is represented by confidence intervals.

♡ **Example** 4.5. Consider the data in file `stress1.dat` relating to the stresses resulting from wave action on the joints of an off-shore oil-drilling platform. In §3 we used a Weibull distribution as a model for this variable, and estimated the parameters as $\alpha = 0.98$ and $\beta = 21.8$. Suppose, for design purposes we want to estimate the value of stress which is exceeded with probability 0.01. Then the relevant MINITAB output is as follows.

```
Percentile Estimates

                      95% CI       95% CI
                      Approximate  Approximate
Percent  Percentile   Lower Limit  Upper Limit

 1         0.203       0.0374        1.104
 2         0.413       0.0950        1.796
 ...
98        87.508      52.2537      146.548
99       103.300      59.5150      179.299
```

Hence, although the stress value exceeded with probability 0.01 is estimated to be 103.3, there is considerable uncertainty, as the 95% confidence interval $(59.5, 179.3)$ is very wide.

4.5 Hypothesis Tests for the Mean of a Population

Sometimes, sample data are collected with the purpose of examining a conjecture or **hypothesis** concerning a distribution. For example, data may be collected to ensure that certain standards are being satisfied, or a change may have been made to a process and data is collected on an output of that process to see if its distribution has changed from the (known) previous distribution.

We will focus on hypotheses which concern the (unknown) distribution mean μ, although in principle a hypothesis may concern any property of the distribution which might be of interest (for example, any parameter of the distribution).

Again, we suppose that $\overline{x}$ is the mean of a sample of n observations $x_1, \ldots, x_n$ from a distribution with mean μ and standard deviation σ. Let the hypothesised value of μ be denoted by μ_0.

A confidence interval gives a range of plausible values of μ, based on the observed data, so a sensible procedure would seem to be to reject the hypothesis that $\mu = \mu_0$ if the value of μ_0 does not lie inside our confidence interval.

For example, if we have a 95% confidence interval, and the mean of the distribution is indeed equal to μ_0, then for 95% of samples, the confidence interval will include μ_0. If it does not then, either we have been unlucky, and observed one of the 5% of samples with erroneous confidence intervals, or the mean of the distribution is not, in fact, equal to μ_0.

Therefore, if the hypothesised value, μ_0 does not lie in the 95% confidence interval, we use this fact as evidence against the hypothesis that $\mu = \mu_0$ and reject the hypothesis **at the 5% level of significance**. Another way of saying this is that the evidence against the hypothesis $\mu = \mu_0$ is **statistically significant** at the 5% level.

More generally, the significance level for the test is 1− the confidence level of the associated interval. Smaller significance levels correspond to wider confidence intervals, so require greater evidence in order to reject.

Recall that, for large samples, or distributions which are close to normal, we calculate confidence intervals based on the fact that

$$t \;=\; \frac{\overline{x} \;-\; \mu}{s/\sqrt{n}}$$

is an observation from a t_{n-1} distribution. Hence, if our hypothesis that $\mu = \mu_0$ is true, then

$$T \;=\; \frac{\overline{x} \;-\; \mu_0}{s/\sqrt{n}}$$

is an observation from a t_{n-1} distribution.

The hypothesised mean μ_0 will fall inside the confidence interval if

$$\overline{x} - c\frac{s}{\sqrt{n}} \;\leq\; \mu_0 \;\leq\; \overline{x} + c\frac{s}{\sqrt{n}}$$

$$\Rightarrow \qquad -c \;\leq\; \frac{\overline{x} \;-\; \mu_0}{s/\sqrt{n}} \;\leq\; c$$

$$\Rightarrow \qquad -c \;\leq\; T \;\leq\; c$$

where c is the relevant value calculated using the t_{n-1} distribution

If $|T| > c$, then μ_0 is outside the confidence interval and the hypothesis is rejected.

Therefore, a hypothesis test involves calculating the **test statistic** T and seeing if it falls in the rejection region $|T| > c$ evaluated using the t_{n-1} distribution together with the significance (confidence) level for the test. This is intuitively sensible. The test will reject when the sample mean $\overline{x}$ and the hypothesised distribution mean μ_0 are far apart.

Sometimes we calculate a p-value for a hypothesis test. A p-value is the highest significance level at which the hypothesis would **not** be rejected. Therefore the p-value is the significance value of the test for which T lies right on the edge of the rejection region *i.e.* $|T| = c$. Hence the p-value is the probability that an observation from a t_{n-1} distribution is greater than $|T|$ or less than $-|T|$.

Recall that smaller significance levels require greater evidence, so if the p-value is small, the data are providing strong evidence against the hypothesis, because the hypothesis is rejected, even at small significance levels.

Usually, we reject the hypothesis if the p-value $p < 0.05$. In other words, we tend to use a 5% significance level. Other values of significance which are commonly used are 1% and 0.1%. These imply even stronger evidence against H_0.

If the hypothesis is not rejected, then that is exactly what has happened – we have not rejected it. This does not mean that we have accepted it. Try to avoid using the word 'accept' when talking about statistical hypotheses. The reason that we have not rejected the hypothesis may be simply that we have not observed a sufficiently large sample for the evidence against it to be statistically significant.

Another issue to be aware of is the difference between statistical and practical significance. We reject a hypothesised mean μ_0 because the data provide strong evidence that the true distribution mean μ is not equal to μ_0. However, this does not necessarily mean that there is a large discrepancy between μ and μ_0. Indeed, in practical terms it is possible for the discrepancy between μ and μ_0 to be of a magnitude which is relatively unimportant in the application concerned. What constitutes a practically significant discrepancy depends on the application and is not a statistical issue. A confidence interval is a particularly useful summary, as it enables you to assess both statistical significance (is the hypothesised value in the interval) and practical significance (how far is the interval away from the hypothesised value).

♡ **Example** 4.6. The file `concrete.dat` contains the compression strength (Nmm^{-2}) of 180 concrete cubes. Suppose that the cubes are required to be manufactured with a mean compression strength of 62 Nmm^{-2}. Test the hypothesis that the process is manufacturing cubes to the required standard.

Here we are required to test the hypothesis that $\mu = 62$ (cubes are of the required standard).

Recall that a 95% confidence interval for μ is $(60.515, 61.681)$. As this interval does not

include 62, we reject the hypothesis that $\mu = 62$ at the 5% level of significance. Furthermore, as a 99% confidence interval for μ is $(60.329, 61.867)$, and this we also reject the hypothesis that $\mu = 62$ at the 1% level of significance.

The test statistic for this test is

$$T = \frac{\overline{x} - 62}{s/\sqrt{n}} = \frac{61.098 - 62}{0.295} = -3.05$$

which gives a p-value of 0.003. This is a very small p-value, indicating that these data provide extremely strong evidence against the hypothesis that $\mu = 62$.

On the other hand, if the required standard for the mean of the distribution is 61.5 Nmm^{-2}, this value falls inside the 90% confidence interval so, even at the 10% level of significance, there is no evidence that μ is not equal to 61.5. The test statistic for this test is

$$T = \frac{\overline{x} - 61.5}{s/\sqrt{n}} = \frac{61.098 - 61.5}{0.295} = -1.36$$

which gives a p-value of 0.175. This is quite a moderate p-value, indicating that these data provide no significant evidence against the hypothesis that $\mu = 61.5$.

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4.6 Comparing Two Distributions

Often, the most interesting hypotheses arise when we are comparing two (or more) distributions. Usually, we are interested in whether the observations of one distribution are larger than those of the other.

To investigate this, we again focus on the distribution means, and use samples from each of the distributions concerned to test a hypothesis concerning the distribution means.

Suppose that we observe a sample of n observations $x_1, \ldots, x_n$, from the distribution of variable X and a sample of m observations $y_1, \ldots, y_m$, from the distribution of variable Y.

We assume that the distribution of X has mean μ_x and standard deviation σ_x, and that the sample $x_1, \ldots, x_n$ has sample mean $\overline{x}$ and sample standard deviation s_x. Similarly, the distribution of Y has mean μ_y and standard deviation σ_y, and the sample $y_1, \ldots, y_m$ has sample mean $\overline{y}$ and sample standard deviation s_y.

Two cases arise depending on whether we can assume that $\sigma_x = \sigma_y$.

4.6.1 Case 1: The Two Sample t Test under equal variance assumption

Suppose we can assume that $\sigma_x = \sigma_y$. We can check this assumption by considering a normal-probability plot. We need to see if the slopes of the two probability plots are roughly same or not. (Recall that the slopes are standard deviations in a normal probability plot.)

We calculate the following to test if the two means are equal,

$$T = \frac{\bar{x} - \bar{y}}{\sqrt{\frac{1}{m} + \frac{1}{n}}\sqrt{\frac{(n-1)s_x^2 + (m-1)s_y^2}{m+n-2}}},$$

follows the $t-$ distribution with $m + n - 2$ degrees of freedom.

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and check the box for equal variances. For the **latent.dat** we get $T = 3.47$ on 19 degrees of freedom. The 95% confidence interval for $\mu_x - \mu_y$ is (0.0167, 0.0673). Since this does not include zero we reject the hypothesis that the mean are equal at 5% level of significance.

4.6.2 Case 2: An approximate two Sample t-test when variances are unequal

If we cannot assume that $\sigma_x = \sigma_y$ we do not have an exact general solution. However, **provided that** either

(a) the sample sizes n and m are large, or

(b) the distributions of X and Y are approximately normal, (this may need to be checked using normal probability plots)

it can be shown that

$$T = \frac{\overline{x} - \overline{y} - (\mu_x - \mu_y)}{\sqrt{\frac{s_x^2}{n} + \frac{s_y^2}{m}}}$$

is an observation from a distribution which has (approximately) a t distribution with k degrees of freedom where

$$k = \frac{\left(\frac{s_x^2}{n} + \frac{s_y^2}{m}\right)^2}{\frac{(s_x^2/n)^2}{n-1} + \frac{(s_y^2/m)^2}{m-1}}.$$

Hence, using the t_k distribution, we can find c such that

$$P\left(-c \leq \frac{\overline{x} - \overline{y} - (\mu_x - \mu_y)}{\sqrt{\frac{s_x^2}{n} + \frac{s_y^2}{m}}} \leq c\right) = 0.95.$$

$$\Rightarrow \qquad P\left(\overline{x}-\overline{y}-c\sqrt{\frac{s_x^2}{n}+\frac{s_y^2}{m}} \;\leq\; \mu_x-\mu_y \;\leq\; \overline{x}-\overline{y}+c\sqrt{\frac{s_x^2}{n}+\frac{s_y^2}{m}}\right) \;=\; 0.95.$$

so the endpoints of a 95% confidence interval for the difference between the means, $\mu_x - \mu_y$ are

$$\overline{x}-\overline{y} \pm c\sqrt{\frac{s_x^2}{n}+\frac{s_y^2}{m}}$$

where c is evaluated using the t_k distribution, with k calculated as above.

Most commonly, we are interested in whether the distributions of X and Y are the same, or whether the data provide significant evidence that they differ. Hence a common hypothesis of interest is $\mu_x = \mu_y$, or equivalently $\mu_x - \mu_y = 0$. To test this hypothesis at the 5% level of significance, all that is required is to check whether or not zero falls in the confidence interval for $\mu_x - \mu_y$, or equivalently whether the test statistic T given above falls in the rejection region $|T| > c$. Again, a p-value for the test gives the largest significance level at which the hypothesis is not rejected, and small p-values indicate strong evidence against the hypothesis.

♡ **Example** 4.7. Consider the data in the file `latent.dat`, which are measurements of the latent heat of water using two methods. As measurements subject to error are often assumed to be normally distributed, and normal probability plots of the sample data produce straight lines for both samples, we assume that the population of measurements are approximately normal, for both methods.

A question of interest is whether there is a systematic difference between the measuring methods. We might conclude that there is a systematic difference if μ_x, the mean of all possible measurements made using method A was different from μ_y, the mean of all possible measurements made using method B. To determine this we test the hypothesis $\mu_x = \mu_y$.

Here, $\overline{x} = 80.021$, $s_x = 0.024$, $n = 13$, $\overline{y} = 79.979$, $s_y = 0.031$, $m = 8$, so $T = 3.25$ and $k = 12$ (rounded), and a 95% confidence interval for $\mu_x - \mu_y$ is $(0.0138, 0.0702)$, which does not include zero. Therefore, we reject the hypothesis that the means are equal at the 5% significance level.

The p-value for this test is 0.007 so there is highly significant evidence of a systematic difference between the measurement methods.

Recall that the 95% confidence interval for $\mu_x - \mu_y$ in under the equal variance assumption is (0.0167, 0.0673) and this is wider than the interval (0.0138, 0.0702). This is expected since we get tighter inferences under more assumptions (the equality of variances).

In real life problems the choice between the two tests depends on which assumptions we can justify, i.e. can we assume that the variances are equal? Are the sample sizes large?

4.6.3 The paired t Test

The two sample t test is carried out under the assumption that the samples from the two distributions are **independent of one another**. In some situations this assumption is clearly violated. For example, consider the data in the file `labs.dat`.

♡ **Example** 4.8. In the USA, municipal wastewater treatment plants are required by law to monitor their discharges into rivers and streams on a regular basis. Concern about the reliability of data from one of these self-monitoring programs led to a study in which 11 volumes of effluent were divided and set to two laboratories for testing. One half of each volume was sent to the Wisconsin State Laboratory of Hygiene and one half was sent to a private commercial laboratory routinely used in the monitoring program. The data in the file `labs.dat` are measurements of biochemical oxygen demand (BOD – `c1`; commercial laboratory, `c3`; state laboratory) and suspended solids (SS – `c2`; commercial laboratory, `c4`; state laboratory) for each of the 11 volumes.

To investigate whether there is a systematic difference between the state and commercial laboratories we can test whether μ_x, the mean of the distribution of X, the BOD as measured by the commercial laboratory differs from μ_y, the mean of the distribution of Y, the BOD as measured by the state laboratory.

However, we have **not** observed **independent** samples from these two distributions, as the 11 volumes analysed by each of the two laboratories were not obtained as 22 independent volumes, but by splitting 11 larger volumes.

The observations of one sample are **paired** with the observations of the other sample. Therefore, we ought to expect x_1, the first measurement from the commercial laboratory, to be more closely related to y_1, the first measurement from the state laboratory, than to any other measurement, as these measurements were made on (essentially) the same volume of effluent.

In general, assume that we have n observations from each of the two populations, and that these observations have been collected in such a way that they are clearly paired, so that the samples are not independent. Denote the pairs of observations $(x_1, y_1), \ldots, (x_n, y_n)$.

In this situation, we consider the variable $D = X - Y$, the **difference between a pair of observations**. This distribution has mean μ_d and standard deviation σ_d. We rewrite our hypothesis of interest $\mu_x = \mu_y$, as $\mu_d = 0$, a hypothesis concerning the distribution of D.

A sample of differences $d_1, \ldots d_n$ from the distribution of D is calculated using the paired observations.

$$d_1 = x_1 - y_1 \qquad d_2 = x_2 - y_2 \quad \ldots \quad d_n = x_n - y_n.$$

We can test a hypothesis about the mean μ_d, of the distribution of D using a sample $d_1, \ldots d_n$, from that population, using the methods of §4.5.

♡ **Example** 4.9. Consider the data in `labs.dat`. Is there a systematic difference between the laboratories in the way in which they measure biochemical oxygen demand?

To examine this, we test the hypothesis that μ_d, the mean of the distribution of D, the difference between BOD measurements of a volume of water split and analysed by the two laboratories is zero ($\mu_d = 0$; no difference between laboratories).

We have a sample

$$-19 \quad -22 \quad -18 \quad -27 \quad -4 \quad -10 \quad -14 \quad 17 \quad 9 \quad 4 \quad -19$$

of differences (values of D). Here $\overline{d} = -9.36$, $s/\sqrt{n} = 4.26$, and $T = -2.20$. A 95% confidence interval for μ_d is $(-18.85, 0.12)$. This includes the hypothesised value, $\mu_d = 0$ so we do not reject the hypothesis at the 5% significance level.

The p-value is 5.2% so the evidence of a difference between the laboratories is very close to being significant, but not quite. Is there a systematic difference between the laboratories in the way in which they measure suspended solids?

To examine this, we test the hypothesis that μ_d, the mean of the distribution of D, the difference between SS measurements of a volume of water split and analysed by the two laboratories is zero ($\mu_d = 0$; no difference between laboratories).

We have a sample

$$12 \quad 10 \quad 42 \quad 15 \quad -1 \quad 11 \quad -4 \quad 60 \quad -2 \quad 10 \quad -7$$

from the population of differences. Here $\overline{d} = 13.27$, $s/\sqrt{n} = 6.17$, and $T = 2.15$. A 95% confidence interval for μ_d is $(-0.47, 27.02)$. This includes the hypothesised value, $\mu_d = 0$ so we do not reject the hypothesis at the 5% significance level.

The p-value is 5.7% so, again, the evidence of a difference between the laboratories is close to being significant, but not quite. In this example, it seems clear that collecting more data might lead one to conclude that there was a difference but, with the data available, we have not observed significant evidence of a difference.

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Stat→Basic Statistics→ Paired t

Chapter 5

Regression

5.1 Introduction

In §1.3 we used graphical methods to examine the association between a pair of variables. Regression is the formal statistical analysis of association between variables. A regression analysis uses sample data to determine if two variables are associated, and if so, exactly what form that relationship takes.

The most common form of regression analysis concerns the relationship between two variables, which we will call X and Y, measured on a continuous underlying scale. Suppose that we have observed n units (pairs of X and Y) and we denote the measurements of X by $x_1, x_2, \ldots, x_n$ and the measurements of Y by $y_1, y_2, \ldots, y_n$.

A regression analysis is concerned with using the sample data to answer the questions

Is there a relationship between X and Y?

and if so

What is the form of the relationship?

and

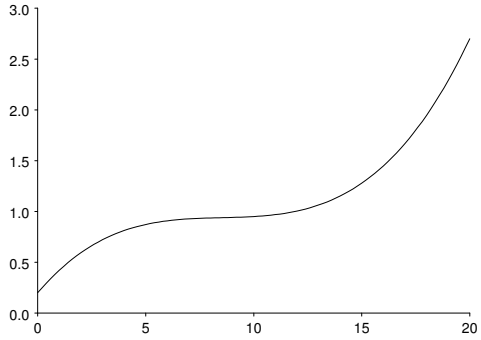
Can we use the relationship to predict one variable using another?

Often, in a scientific study, the investigator specifies the values of one of the variables X (perhaps an experimental setting) and observes the values of the other variable Y which arise. In other situations, neither variable is specified, but the intention of the analysis is to be able to predict the value of one variable Y using the other variable X.

Then, we call Y the **response** (or outcome or dependent) variable and X the **explanatory** (or predictor or independent) variable.

A regression analysis assumes that for every possible value x of the explanatory variable X, the value of the response variable Y can be predicted by the function $\mu(x)$, evaluated at x. We can plot the value of $\mu(x)$ for each possible value of X. This is the **regression line**,

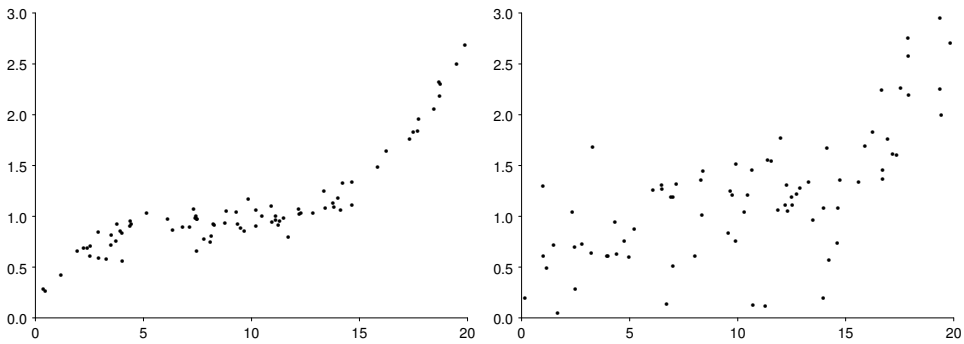
which explains the relationship between Y and X.



However, variability is present, so the prediction is not perfect; for the same value of X, we may observe different values of Y. In other words, when we observe a pair of observations of X and Y we do not expect them to lie exactly on the regression line. The relationship between Y and X, given by the function $\mu(x)$ is disguised by **residual variation**. Therefore, we write the relationship between observed values y and x as

$$y \quad = \quad \mu(x) + \epsilon$$

Here, ϵ is a random variable, representing the residual variability about the regression line. We assume that the distribution of ϵ has mean zero, so that, on average, for a given value of X, the value of Y is perfectly described by the regression equation $y = \mu(x)$. However, the closeness of observed data points to the regression line will depend on the standard deviation, σ of the distribution of ϵ. If σ is small, then observations will generally be close to the regression line, but if σ is large, then this may not be the case.



In practice, we do not know the regression line. A regression analysis uses sample data to **estimate** the form of the regression line.

5.2 Linear Regression

5.2.1 Introduction

It is usually assumed that the regression line has a reasonably simple shape. The most obvious shape is a **straight line**. The mathematical equation of a straight line is

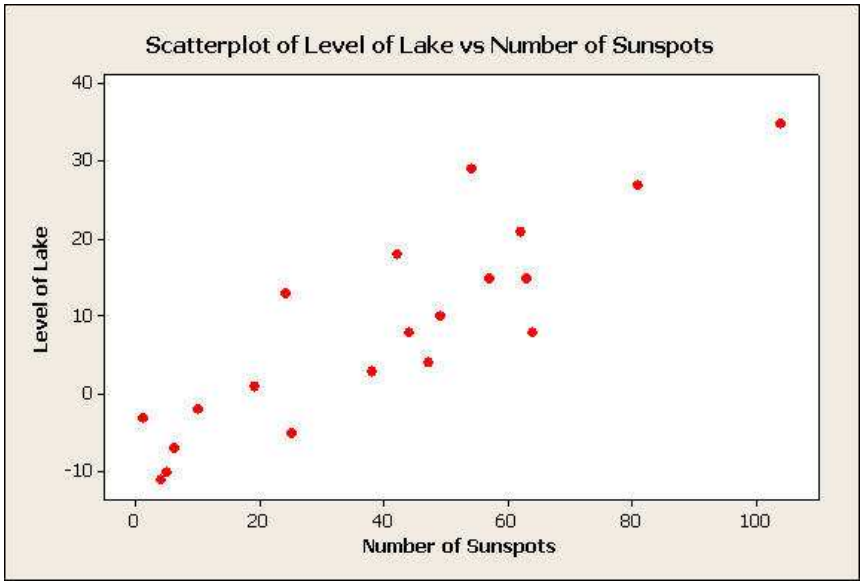
$$\mu(x) \;=\; \alpha \;+\; \beta x.$$

The **coefficients** (or parameters) of the regression line, α and β represent the **intercept** and **slope** (gradient) of the line. Alternatively, we might write a linear regression as

$$y \;=\; \alpha \;+\; \beta x \;+\; \epsilon$$

[Sometimes this expression is written in a shorthand form as $Y = \alpha + \beta X$. This is a little sloppy, as Y and X are not exactly related by the regression equation. The relationship is hidden by the residual variation.]

For the remainder of this section we will consider the data in the file `level.dat` which are the level of Lake Victoria Nyanza for the years 1902–1921 (relative to a fixed standard) and the number of sunspots in the same years. Is there a relationship between these two variables, and can we use the number of sunspots (X) to predict the level of the lake (Y)?



5.2.2 Least squares estimation

As we do not observe the whole population of possible values of X and Y, we do not know the coefficients α and β of the regression line. A linear regression analysis uses sample data

to **estimate** the coefficients, α and β, of the regression line. This is sometimes referred to as **fitting** the line to the data. To do this, we use the **method of least squares**.

The observed sample data is a set of n pairs, $(x_1, y_1), \ldots, (x_n, y_n)$. For any line of the form $y = a + bx$, we define the **sum of squares** of the sample data about the line to be

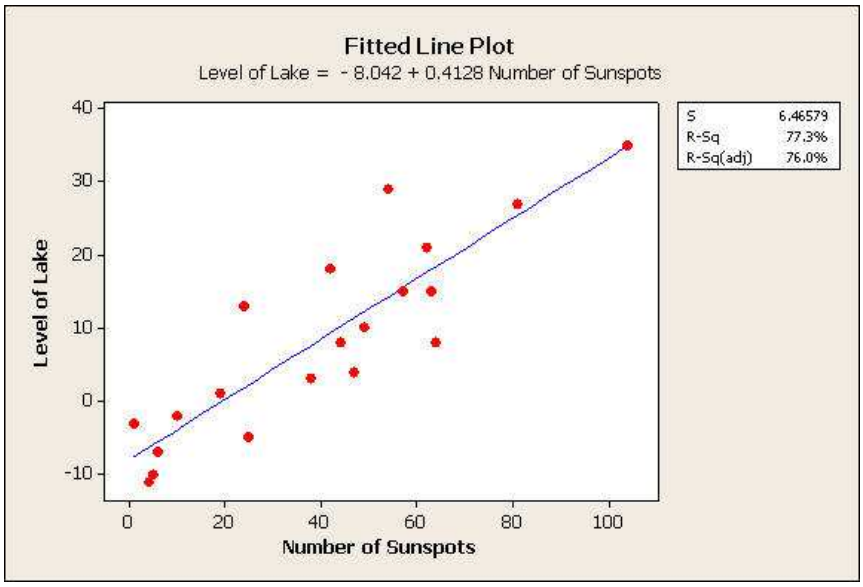
$$D = \sum_{i=1}^{n} (y_i - [a + bx_i])^2$$

The least squares estimates $\hat{\alpha}$ and $\hat{\beta}$ of α and β, the coefficients of the regression line, are the values of a and b which minimise the sum of squares D.

By partially differentiating D with respect to a and b, it can be shown that the values of $\hat{\alpha}$ and $\hat{\beta}$ are given D are given by

$$\hat{\beta} = \frac{\sum_{i=1}^{n} x_i y_i - n\overline{x}\,\overline{y}}{\sum_{i=1}^{n} x_i^2 - n\overline{x}^2} = r\frac{s_y}{s_x} \qquad \text{and} \qquad \hat{\alpha} = \overline{y} - \hat{\beta}\overline{x}.$$

Therefore, we can calculate $\hat{\alpha}$ and $\hat{\beta}$ using the mean and standard deviation $\overline{x}$ and s_x of the sample of values of X, the mean and standard deviation $\overline{y}$ and s_y of the sample of values of Y, and the sample correlation coefficient r (see §1.3).



The **estimated** regression line is

$$\hat{\mu}(x) = \hat{\alpha} + \hat{\beta}x$$

(or, in shorthand form, $Y = \hat{\alpha} + \hat{\beta}X$).

For the data in the file `level.dat`, $\hat{\alpha} = -8.042$, $\hat{\beta} = 0.4128$.

5.2.3 Confidence intervals and Hypothesis tests

The least squares estimates $\hat{\alpha}$ and $\hat{\beta}$ depend on the sample values of X and Y. Different samples lead to different estimates, and therefore we consider the estimates as **variables**. What can we say about the distribution of $\hat{\alpha}$ and $\hat{\beta}$?

We assume (throughout the remainder of this chapter) that

1. The residual variable ϵ has a **normal distribution** (with zero mean).
2. The standard deviation σ of the distribution of ϵ is the same for any value of X.

Then

$\frac{\hat{\alpha}-\alpha}{s_\alpha}$ is an observation from a t_{n-2} distribution.

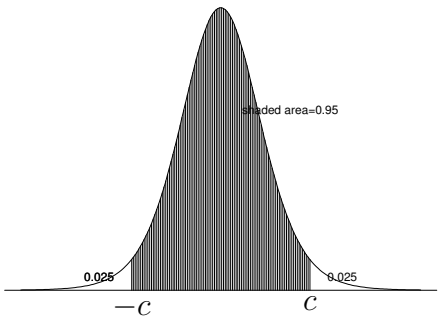
$\frac{\hat{\beta}-\beta}{s_\beta}$ is an observation from a t_{n-2} distribution.

Here s_α and s_β are the **standard errors** of $\hat{\alpha}$, and $\hat{\beta}$, and summarise the variability involved in the process of least squares estimation. Note the similarities with §4.3. There, $\overline{x}$ was used as an estimate of μ, and $(\overline{x}-\mu)/s_{\overline{x}}$ was an observation from a t_{n-1} distribution, where $s_{\overline{x}} = s/\sqrt{n}$, the standard error of $\overline{x}$. Now, just as in §4.3, we can use the results above to calculate confidence intervals for the unknown regression coefficients α and β.

$\hat{\alpha} \pm cs_\alpha$ are the end points of a confidence interval for α

$\hat{\beta} \pm cs_\beta$ are the end points of a confidence interval for β

The appropriate value of c depends on the level of confidence required, and on the sample size n.



For the data in the file `level.dat`, $s_a = 2.556$, $s_b = 0.05275$ and $n = 20$. Therefore a 95% confidence interval for α is $(-13.412, -2.672)$ and a 95% confidence interval for β is $(0.3020, 0.5236)$.

The confidence intervals allow us to test hypotheses concerning the regression coefficients α and β. One such hypothesis which is of particular interest is whether $\beta = 0$. The reason this hypothesis is interesting is that if it is true then $\mu(x) = \alpha$, and does not depend on x. In other words, Y does not depend on X and therefore there is **no relationship** between Y and X. On the other hand, if we reject the hypothesis and conclude that $\beta \neq 0$, we are concluding that the data do provide significant evidence of a relationship between Y and X.

For the data in the file `level.dat`, the hypothesis of $\beta = 0$ is clearly rejected at the 5% level of significance, as zero is not in the confidence interval $(0.3020, 0.5236)$. Indeed, the p-value for this test is given by MINITAB, as being less than 0.001. There is highly significant evidence of a relationship between sunspots and level of the lake.

5.2.4 Prediction

Often, the motivation for performing a regression analysis is to be able to predict Y from X. In other words, given a future value x of X, what would we predict the corresponding value of Y to be, and how confident would we be about that prediction? For example, what would we predict the level of Lake Victoria Nyanza to be in a year in which there were 50 sunspots?

Recall that we can write the regression equation as

$$y \;=\; \mu(x) \;+\; \epsilon \;=\; \alpha \;+\; \beta x \;+\; \epsilon.$$

Therefore, given a particular value x, we can use this equation to predict y. We do not know α, β or ϵ, but we can use the estimates $\hat{\alpha}$ and $\hat{\beta}$ for α and β. In other words, we replace $\mu(x) = \alpha + \beta x$ with $\hat{\mu}(x) = \hat{\alpha} + \hat{\beta}x$. As the distribution of ϵ is assumed to have mean zero, we estimate ϵ for a future observation to be zero.

Therefore, our prediction for future observation y is

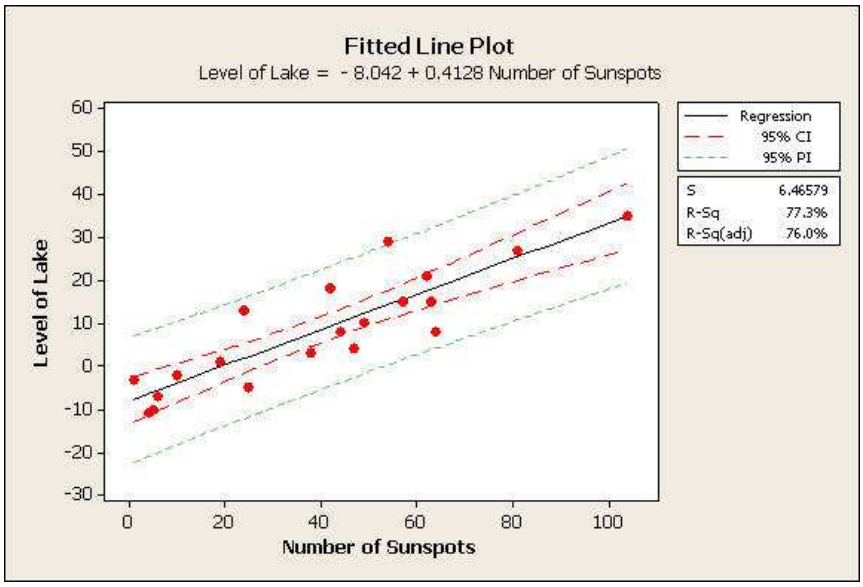
$$\hat{y} \;=\; \hat{\alpha} \;+\; \hat{\beta}x.$$

So we use the estimated regression equation $\hat{\mu}(x)$ to predict y.

In a year in which there were 50 sunspots we would predict the level of Lake Victoria Nyanza to be

$$\hat{y} \;=\; -8.042 \;+\; 0.4128 \times 50 \;=\; 12.6.$$

Uncertainty about the prediction $\hat{y}$ arises from two sources. Firstly, we are using estimates $\hat{\alpha}$ and $\hat{\beta}$ in place of α and β (using $\hat{\mu}(x)$ rather than $\mu(x)$). Secondly, we are estimating the residual variation ϵ to be zero, when it is a normally distributed with mean zero and standard deviation σ.



The error involved in using $\hat{\mu}(x)$ rather than $\mu(x)$ is determined by the variability of $\hat{\mu}(x)$, which is summarised by $s_{\hat{\mu}(x)}$ the **standard error** of $\hat{\mu}(x)$. We can use the prediction, together with its standard error, to obtain a confidence interval for $\mu(x)$ using $\hat{\mu}(x) \pm cs_{\hat{\mu}(x)}$, where c is again determined using a t_{n-2} distribution. This confidence interval summarises our uncertainty, in light of the sample data, about the value of the regression line at a particular value x.

As far as our prediction is concerned, we have still to incorporate the uncertainty associated with the residual variation. A confidence interval for the value y which we are trying to predict incorporates both the uncertainty about $\mu(x)$ as above, together with the uncertainty associated with the residual variation for our predicted observation. We call such a confidence interval a **predictive interval**.

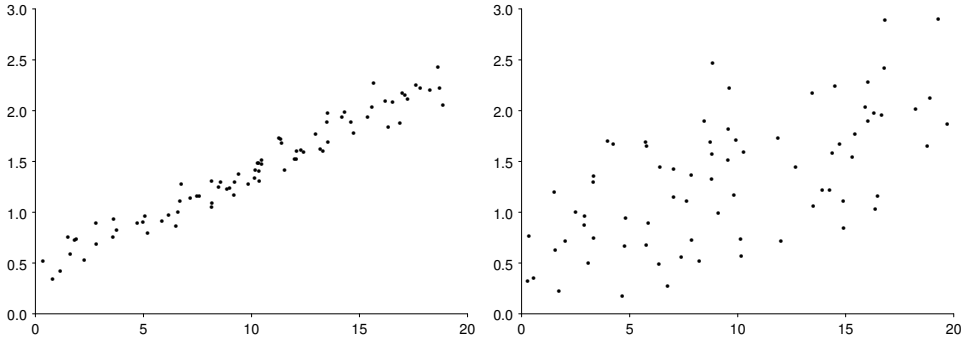
Confidence intervals for $\mu(x)$ and predictive intervals for y at **any value** x of X may be displayed as **bands** on a plot.

5.2.5 Goodness-of-fit

A linear regression is a **statistical model** for the variables X and Y. The statistical modelling process involves (at least) three important stages. Firstly, estimation of the unknown coefficients of the model, and assessment of uncertainty about these estimates. For a linear regression model, we have discussed these in §5.2.2 and §5.2.3. The final stage is using the model for prediction, and we have discussed this in §5.2.4.

The intermediate stage is assessment of the quality of the model. How well does the model describe the observed sample data, and how valid are the assumptions required by the modelling process. Here we focus on how well the model fits the data. Checking assumptions is discussed in §5.2.6.

A regression model which fits the data well is one where we would expect predictions provided by the model to be highly accurate. Good regression models have small residual variation. Poor regression models have large residual variation.



Therefore, any measure of residual variation provides a measure of goodness-of-fit of the model to the data. The most straightforward measure of residual variation is the sum of squares

$$D = \sum_{i=1}^{n} (y_i - [\hat{\alpha} + \hat{\beta} x_i])^2$$

(Recall that $\hat{\alpha}$ and $\hat{\beta}$ were chosen so as to make D as small as possible for the observed data).

However, it is not straightforward to interpret what large and small values of D are. In particular, if the scale of measurement of the Y values is changed (from metres to centimetres, say) then the value of D will change, even though the regression model will still explain the data in the same way.

In order to interpret D, we compare it with $(n-1)s_y^2 = \sum_{i=1}^{n} (y_i - \overline{y})^2$ which is the sum of the squares of the distances of each observation of Y from $\overline{y}$. The value of $(n-1)s_y^2$ represents the **natural variation** in Y, whereas D represents the variation in Y, when we have estimated the regression relationship between Y and X.

Therefore the difference in these quantities represents the amount of the natural variation in Y which has been **explained** by the regression relationship between Y and X. The quantity

$$R^2 = \frac{(n-1)s_y^2 - D}{(n-1)s_y^2}$$

is the proportion of the natural variation in Y which has been explained by the regression relationship between Y and X.

Therefore R^2 provides an easily interpretable measure of how well the regression model fits the data. If R^2 is close to 1 (100%), then the regression explains most of the natural variation, whereas if it is close to 0, then the regression line is a poor fit to the data.

For a linear regression model, it happens that R^2 is just the square of the correlation coefficient r, introduced in §1.3. This seems sensible, as we recall that r measures the strength of linear relationship between Y and X, and is close to ± 1 (so R^2 is close to 1) when the relationship between Y and X is close to a straight line.

For the data in the file `level.dat`, the value of R^2 is 0.773, so 77.3% of the natural variation in level of the lake is explained by the number of sunspots. This figure is quite high, so we might describe this regression as a reasonable fit to the data. In order to make accurate predictions using a regression line, high values of R^2 are required (at least 90%). Many examples in science and engineering exhibit a significant relationship between two variables, but not one which can be described as very close. Values of R^2 of less than 50% are common. While one may conclude that there is an association in these cases, and be reasonably confident about the form of the association (coefficients of the regression line). accurate prediction is prohibited by the large residual variation.

5.2.6 Checking assumptions

We can use the sample data to check whether the assumptions we have made in the modelling process are valid. Recall that the regression model can be written as

$$y \;=\; \mu(x) \;+\; \epsilon \;=\; \alpha \;+\; \beta x \;+\; \epsilon.$$

Our sample data consists of n pairs of observations $(x_1, y_1), \ldots, (x_n, y_n)$. Therefore, for each pair of observations

$$y_i \;=\; \alpha \;+\; \beta x_i \;+\; \epsilon_i.$$

where ϵ_i represents the residual variation for the ith pair of observations. As we do not know α or β, we do not know ϵ, but we can estimate it for each observation using

$$\hat{\epsilon}_i \;=\; y_i \;-\; (\hat{\alpha} \;+\; \hat{\beta} x_i).$$

We call the n values of $\hat{\epsilon}_i$ the **residuals**. We can use the residuals to assess how reasonable our model assumptions are. We have made two key assumptions

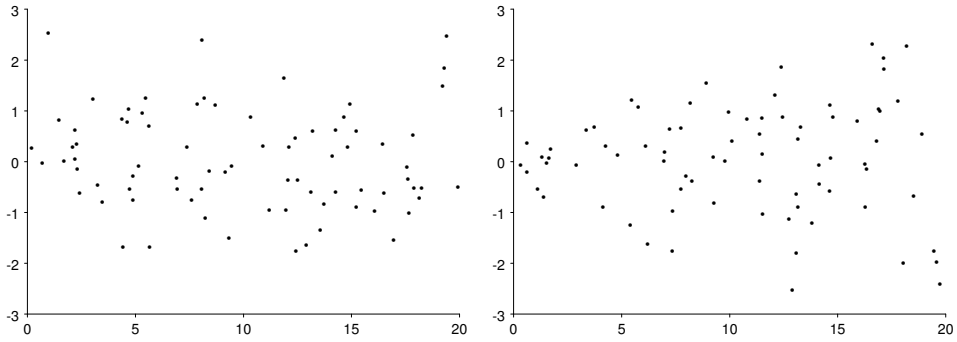
1. The residual variable ϵ has a **normal distribution** (with zero mean).

2. The standard deviation σ of the distribution of ϵ is the same for any value of X.

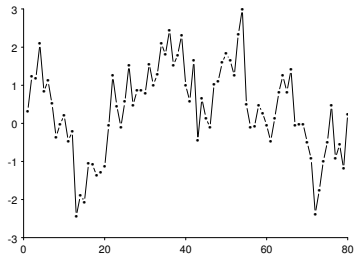
If the first assumption is true, then the residuals are observations from a normal distribution. We can check this assumption by inspecting a normal probability plot of the residuals. If the plot is approximately a straight line, then the assumption is justified.

The second assumption is more difficult to assess. However the most common departure from this assumption occurs when the standard deviation of the distribution of ϵ has a larger

standard deviation when the regression function $\mu(x)$ is larger. We can check this by plotting each residual $\hat{\epsilon}_i$ against the estimated value of the regression line $\hat{\mu}(x_i)$ corresponding to that residual. This plot should be a random scatter. Behaviour to beware of is 'funnelling'.



A third assumption required is that the observations are made independently of one another. Again, this is very difficult to assess, but in situations where the data have been collected in a particular serial (time) order (and **only** in such situations) a time series plot of the residuals may help to detect departures from this assumption. The time series plot should be a random scatter. Beware of examples where each residual is more closely related to the previous one than might be expected.



For the data in the file `level.dat` (where the data have been presented year by year in serial order) there is nothing in the residual plots which casts doubt on any of the assumptions.

5.2.7 Linear Regression in MINITAB

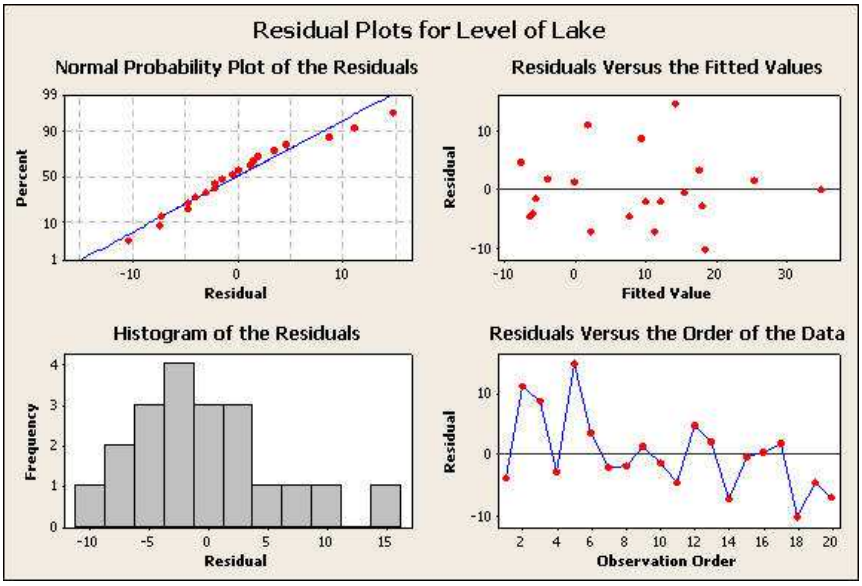
In MINITAB

Stat→Regression→Regression

Stat→Regression→Fitted Line Plot

Regression Analysis: level versus sunspots

```
The regression equation is
level = - 8.04 + 0.413 sunspots

Predictor        Coef     SE Coef          T        P
Constant       -8.042       2.556      -3.15    0.006
sunspots      0.41281     0.05275       7.83    0.000

S = 6.466       R-Sq = 77.3%     R-Sq(adj) = 76.0%

Analysis of Variance

Source            DF          SS          MS         F        P
Regression         1      2560.4      2560.4     61.24    0.000
Residual Error    18       752.5        41.8
Total             19      3313.0

Unusual Observations
Obs   sunspots      level         Fit      SE Fit    Residual    St Resid
  5         54      29.00       14.25        1.62       14.75        2.36R
 16        104      35.00       34.89        3.67        0.11        0.02 X

R denotes an observation with a large standardized residual
X denotes an observation whose X value gives it large influence.
```



5.3 Multiple Regression

In many practical examples, the variability in the response variable Y is influenced by more than one explanatory variable. For example, consider the data in the file `soil.dat` which arise from the study of the phosphorus content of soil. Interest was focussed on how the plant-available phosphorus (Y in ppm; `c3`) was related to two explanatory variables, the inorganic phosphorus (X_1 in ppm; `c1`) and a component of the organic phosphorus (X_2 in ppm; `c2`) of the soil.

It is very straightforward to extend the linear regression model when there is more than one explanatory variable. Recall that for a single explanatory variable the linear regression equation was

$$y \;=\; \alpha \;+\; \beta x \;+\; \epsilon$$

When we have two explanatory variables X_1 and X_2, we use the **multiple regression equation**

$$y \;=\; \alpha \;+\; \beta_1 x_1 \;+\; \beta_2 x_2 \;+\; \epsilon$$

where the residual ϵ is a normally distributed random variable with zero mean and constant standard deviation σ. (We can easily extend this to three or more explanatory variables).

Again, the coefficients α, β_1 and β_2 of the regression equation are unknown, so we estimate them using the method of least squares, that is, we find estimates $\hat{\alpha}$, $\hat{\beta}_1$ and $\hat{\beta}_2$ which give the smallest value of the sum of squares

$$D \;=\; \sum_{i=1}^{n} (y_i - [\hat{\alpha} + \hat{\beta}_1 x_{1i} + \hat{\beta}_2 x_{2i}])^2.$$

Here $y_1, \ldots y_n$ are the n values of the response variable and $(x_{11}, x_{21}), \ldots, (x_{1n}, x_{2n})$ are the corresponding n pairs of values of the explanatory variables.

The estimated regression equation

$$y \;=\; \hat{\alpha} \;+\; \hat{\beta}_1 x_1 \;+\; \hat{\beta}_2 x_2$$

can be used to predict future values of Y, at specified values of X_1 and X_2. In all other aspects, multiple regression proceeds in exactly the same way as linear regression. Confidence intervals for coefficients of the regression equation, or for predictions, can be made. Confidence intervals are based on the t distribution with $n-p-1$ degrees of freedom, where p is the number of explanatory variables.

Goodness-of-fit can still be assessed using the R^2 coefficient, calculated and interpreted in the same way, as the 'proportion of natural variation in the response variable which has been explained by the regression equation'. Residuals, now calculated using

$$\hat{\epsilon}_i \;=\; y_i \;-\; (\hat{\alpha} \;+\; \hat{\beta}_1 x_{1i} \;+\; \hat{\beta}_2 x_{2i})$$

can again be used to check the key assumptions (normality, independence, constant standard deviation).

When there are many potential explanatory variables in a multiple regression analysis, it is particularly important to determine which variables are important predictors of the response variable and which are not. If an explanatory variable is not an important predictor, then we can set the corresponding coefficient of the regression equation to zero, and the variable dissappears from the equation. Determining whether or not a variable is an important predictor is equivalent to testing the hypothesis that the corresponding regression coefficient can be set to zero.

Therefore, testing whether regression coefficients are zero is an important procedure in a multiple regression analysis. Tests can proceed as in §5.2.3, by examining whether zero is within an appropriate confidence interval for the regression coefficient. Alternatively, a p-value for the test that a regression coefficient can be set to zero is provided automatically by MINITAB.

In MINITAB

Stat→Regression→Regression

Regression Analysis: Y versus X1, X2

```
The regression equation is
Y = 56.3 + 1.79 X1 + 0.087 X2

Predictor        Coef     SE Coef          T        P
Constant        56.25       16.31       3.45    0.004
X1             1.7898      0.5567       3.21    0.006
X2             0.0866      0.4149       0.21    0.837

S = 20.68       R-Sq = 48.2%     R-Sq(adj) = 41.3%

Analysis of Variance

Source            DF          SS          MS         F        P
Regression         2      5975.7      2987.8      6.99    0.007
Residual Error    15      6413.9       427.6
Total             17     12389.6

Source       DF      Seq SS
X1            1      5957.0
X2            1        18.6
```

```
Unusual Observations
Obs         X1          Y         Fit      SE Fit    Residual    St Resid
 17       26.8     168.00      109.24        9.24       58.76        3.18R

R denotes an observation with a large standardized residual
```

There are many strategies for determining which explanatory variables are important predictors. One reasonable strategy is to fit the model with all possible predictors, determine if any are not required (high p-value, so corresponding regression coefficient is not significantly different from zero) and if so, ignore the explanatory variable which is least useful (highest p-value). Then refit the model without this explanatory variable. Proceed like this until all explanatory variables are useful predictors (low p-values, so corresponding regression coefficients are significantly different from zero). Use this final model as your 'best' regression model for prediction *etc.*

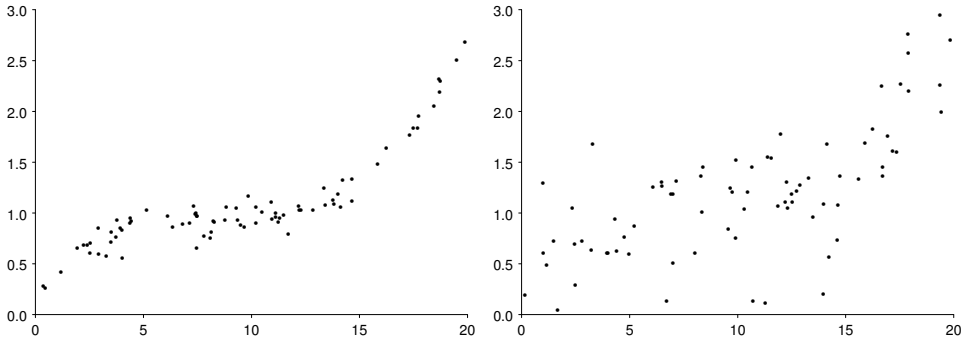
It is important that each time you decide to omit an explanatory variable, you refit the regression before making another decision, as estimates and p-values will change.

```
The regression equation is
Y = 59.3 + 1.84 X1
Predictor        Coef     SE Coef           T        P
Constant       59.259       7.420        7.99    0.000
X1             1.8434      0.4789        3.85    0.001

S = 20.05       R-Sq = 48.1%     R-Sq(adj) = 44.8%

Analysis of Variance

Source            DF          SS          MS         F        P
Regression         1      5957.0      5957.0     14.82    0.001
Residual Error    16      6432.6       402.0
Total             17     12389.6

Unusual Observations
Obs         X1          Y         Fit      SE Fit    Residual    St Resid
 17       26.8     168.00      108.66        8.54       59.34        3.27R

R denotes an observation with a large standardized residual
```

Note that there is not necessarily a single best model. You may find that two different sets of explanatory variables provide similar explanantions of the variability in the response variable. Then other considerations (such as scientific reasoning) may determine which regression equation you prefer.

5.4 Fitting Curves

A regression analysis can also be used when the regression equation describing the way in which the response variable Y depends on an explanatory variable X is not a straight line.



The simplest way to fit a curve is by using a **polynomial** regression equation. For example

$$\begin{aligned} y &= \alpha + \beta x + \gamma x^2 + \epsilon \\ y &= \alpha + \beta x + \gamma x^2 + \delta x^3 + \epsilon. \end{aligned}$$

(More complicated polynomials are possible, but are rarely required in practice).

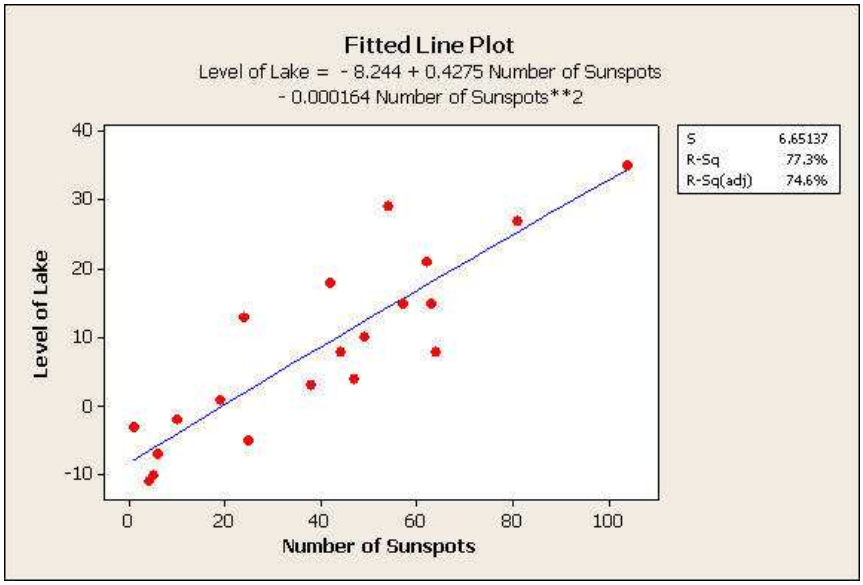
Again, the coefficients α, β, γ (and δ if required) of the regression equation are unknown, so we estimate them using the method of least squares, that is, we find the values of the coefficients which minimise the sum of squares of the distances between the data points and the regression **curve**.

We can fit polynomial regression models in exactly the same way as we fitted multiple regression models in §5.3. For example, for the quadratic model, we create a 'new variable' X^2 containing the values of x^2 for each observation x of explanatory variable X. [In MINITAB, **Calc→Calculator** can be used to achieve this.] Then, a quadratic regression is just a multiple regression with explanatory variables X and X^2.

Polynomial models can be fitted, confidence intervals calculated, predictions made, and the model assessed by using R^2 and residual plots, exactly as described in §5.2 and §5.3.

It is important to determine what kind of polynomial is required to describe the dependence of Y on X. It is usual practice to start with a linear regression model and successively

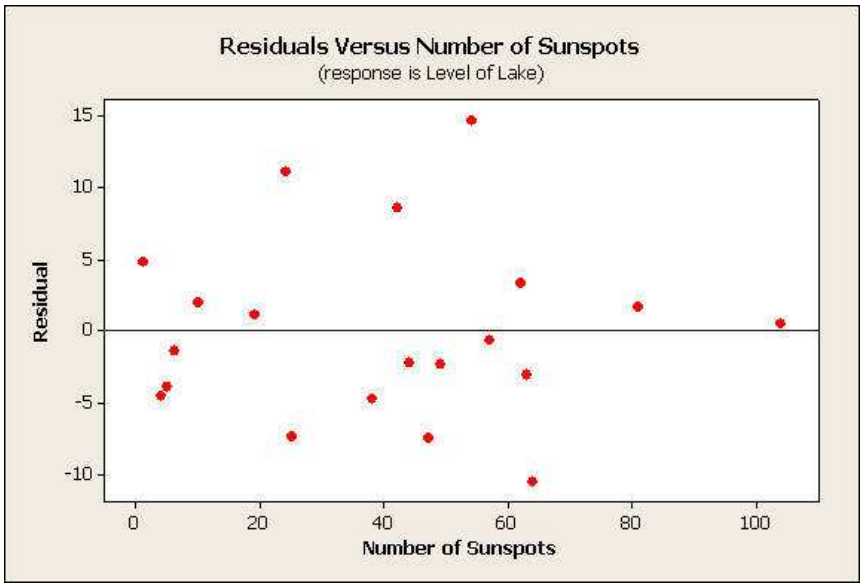
add terms (X^2, X^3 *etc.*) until the coefficient of the term you are trying to add is not significantly different from zero. (Note that is is rarely sensible to fit a polynomial model with 'missing lower order terms' *e.g.* if X^3 is in the model, then X and X^2 should be as well.)




```
The regression equation is
level = - 8.24 + 0.427 sunspots - 0.00016 sunspots^2

Predictor        Coef     SE Coef          T        P
Constant       -8.244       3.343      -2.47    0.025
sunspots       0.4275      0.1594       2.68    0.016
sunspots    -0.000164    0.001671      -0.10    0.923

S = 6.651       R-Sq = 77.3%     R-Sq(adj) = 74.6%

Analysis of Variance

Source            DF          SS          MS         F         P
Regression         2      2560.9      1280.4     28.94     0.000
Residual Error    17       752.1        44.2
Total             19      3313.0

Source       DF      Seq SS
sunspots      1      2560.4
sunspots      1         0.4
```

```
Unusual Observations
Obs    sunspots      level         Fit      SE Fit    Residual    St Resid
  5          54      29.00       14.36        2.03       14.64       2.31R
 16         104      35.00       34.44        5.92        0.56       0.18 X

R denotes an observation with a large standardized residual
X denotes an observation whose X value gives it large influence.
```

The estimated regression line (and associated confidence and predictive intervals) may again be obtained, in MINITAB, using **Stat→Regression→Fitted Line Plot**.



One additional way of determining whether or not you require further polynomial terms in your model is to plot the residuals $\hat{\epsilon}_i$ against the values x_i of the explanatory variable X. If any kind of pattern is evident, then further polynomial terms may help. Otherwise, the plot should appear as a random scatter.

There are many other ways of fitting curves to data, outside the scope of this course. One popular way is to consider transforming the data. For example, if the regression curve takes the form

$$Y \;=\; \alpha X^{\beta}$$

then we can write

$$\log Y \;=\; \log \alpha \;+\; \beta \log X.$$

Hence, if we transform our data points by taking logs, the relationship between the transformed variables $\log Y$ and $\log X$ is described by a straight line, with intercept $\log \alpha$ and slope β.

Similarly if the regression curve takes the form

$$Y = \alpha\beta^X$$

then we can write

$$\log Y = \log\alpha + X\log\beta.$$

Hence, if we transform our data points by taking logs of the response variable Y (only), the relationship between the transformed variable $\log Y$ and X is described by a straight line, with intercept $\log\alpha$ and slope $\log\beta$.

The key to these approaches is transforming an awkward problem, based on complicated curves, to a simple problem based on linear regression. If the relationship between Y and X seems to be described by a curve, and a polynomial model does not fit well, then it may be worth invesigating possible linear relationships between $\log Y$ and X or between $\log Y$ and $\log X$.

In MINITAB, **Calc→Calculator** can be used to create the transformed variables $\log Y$ and $\log X$.