

Premedical course

Solution to MINITAB practical 1

Question 1. The first illustration shows the MINITAB system after the data have been entered – the haemoglobins for males in column 1 and those for females in column 2 – and the **H**elp menu has been invoked to find out how to produce stem-and-leaf plots. The windows have been arranged for maximum legibility; you should make a habit of this. (By using the 'print screen' key the screen may be copied to the notepad and pasted in to a word-processing document. Practicals should be written up in this way, though not necessarily as extensively as is done here.)

The screenshot shows the MINITAB software interface. On the left, the 'Data' window displays a table with two columns, C1 and C2, containing 12 rows of numerical data. On the right, the 'MINITAB' help window is open, displaying the 'Stem-and-Leaf Character Graph' help page. The help page includes a navigation path, a description of the plot, and detailed instructions for the 'Dialog Box Items' such as 'Variables', 'By variable', 'Trim outliers', and 'Increment'.

	C1	C2
1	15.7	14.2
2	15.1	14.0
3	16.7	13.7
4	16.3	16.0
5	16.0	14.5
6	16.5	13.7
7	16.0	13.6
8	16.4	13.6
9	16.0	13.9
10	18.1	14.2
11	16.5	14.8
12	15.8	14.2

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Stem-and-Leaf Character Graph

Graph > Character Graphs > Stem-and-Leaf
Stat > EDA > Stem-and-Leaf

Produces a character-based **stem-and-leaf** plot in the Session window.

Dialog Box Items

Variables: Enter column(s) you want to display. Each column generates a separate stem-and-leaf diagram.

By variable: Click and enter a column to produce stem-and-leaf displays for the subsets defined by distinct values in the By variable, which must contain integers from -10000 to +10000 or the **missing value symbol** (*). This option cannot be used with the Trim outliers option.

Trim outliers: Click to trim all **outliers** and show them on special lines labeled LO and HI. This option cannot be used with By variable.

Increment: Enter a number to control vertical scaling by setting the increment between display lines (the difference between the smallest possible values on adjacent lines).

Although the exact form of the stem-leaf plot may be controlled by the user, we have only used the defaults (which are satisfactory in this instance) and the output to the **Session** window is shown in the next illustration. The column of figures to the left of the graph contains a cumulative count of the observations from either end of the distribution. The number in parentheses is the frequency count for the interval containing the median. We may easily read the male median as 16.4 and the female median as 13.9 mg/100ml. Notice that names have been given to the variables in the **Data** window to make the output more understandable. Make sure that you can do this.

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Session

MTB > Stem-and-Leaf 'males' 'females'

Stem-and-leaf of males N = 36
Leaf Unit = 0.10

```

2  14 59
3  15 1
9  15 778889
(10) 16 0002334444
17  16 555667779
8  17 1134
4  17 59
2  18 12

```

Stem-and-leaf of females N = 35
Leaf Unit = 0.10

```

1  11 3
1  11
1  12
3  12 79
7  13 0444
(11) 13 5667777999
17  14 00022224
9  14 55678
4  15 03
2  15 9

```

Data

	C1	C2	C3
→	males	females	
1	15.7	14.2	
2	15.1	14.0	
3	16.7	13.7	
4	16.3	16.0	
5	16.0	14.5	
6	16.5	13.7	
7	16.0	13.6	
8	16.4	13.6	
9	16.0	13.9	
10	18.1	14.2	
11	16.5	14.8	
12	15.8	14.2	
13	16.7	14.5	
14	16.3	12.9	
15	17.1	12.7	
16	16.6	14.6	
17	17.3	15.3	
18	16.6	13.4	

The next illustration shows how the **Help** system is invoked to enquire about basic statistics.

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Type a word, or select one from the list. Then choose Show Topics.

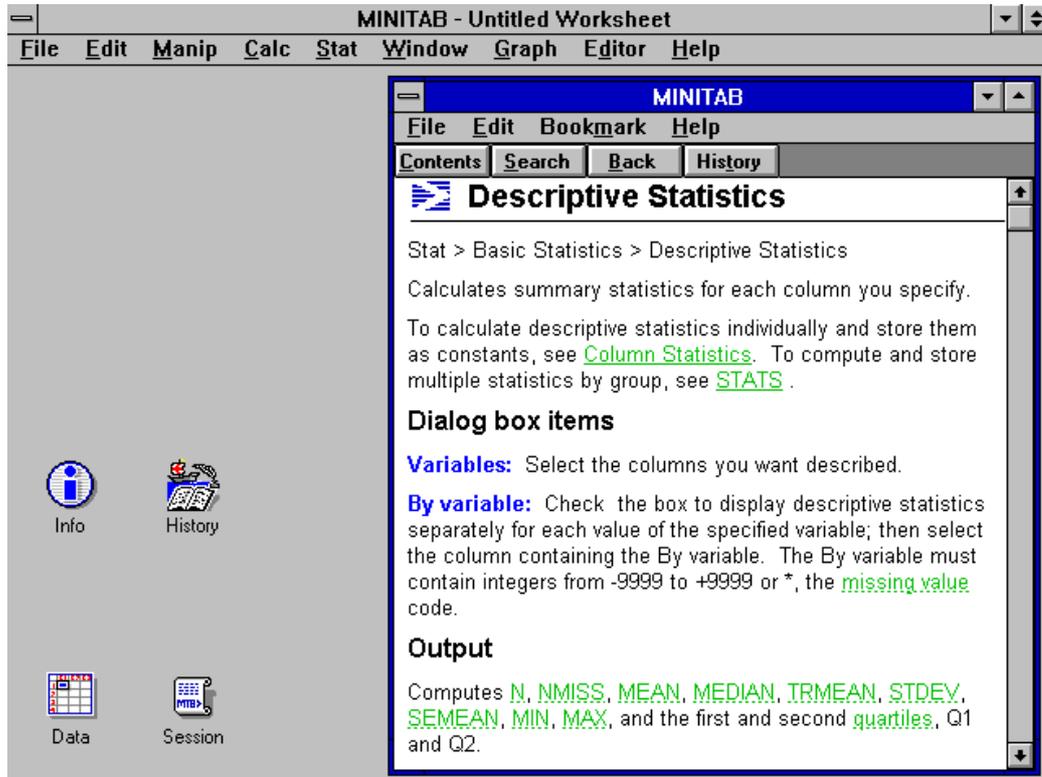
Basic Statistics

Basic Statistics
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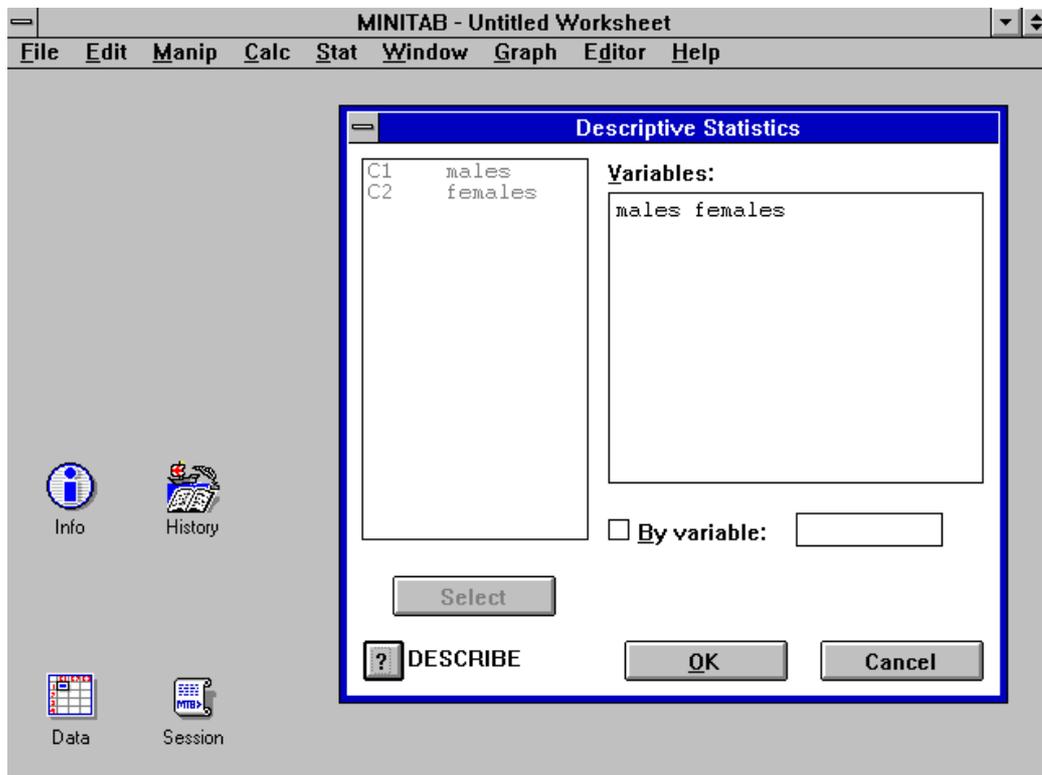
Select a topic, then choose Go To.

1-Sample t
1-Sample Z
2-Sample t
Basic Statistics
Correlation
Covariance
Descriptive Statistics

And this one shows the result. The other windows have been minimised ( symbol at the top right) for convenience.



The following window is typical of one way of using MINITAB; sometimes it is easier to type the commands directly into the **Session** window.



Here we see the command which has been produced, the route through the menus to produce it, and the output. When you write down the relevant numbers for the five-point summaries only use the appropriate number of decimals; here one is enough.

The screenshot shows the Minitab interface with the 'Stat' menu open. The path taken is: Stat > Basic Statistics > Descriptive Statistics... The Session window displays the following output:

```

MTB > Describe 'males' 'females'.

      N      MEAN    MEDIAN   TRMEAN   STDEV   SEMEAN
males  36  16.442  16.400  16.444   0.817   0.136
females 35  13.986  13.900  13.987   0.873   0.148

      MIN      MAX      Q1      Q3
males  14.500  18.200  15.925  16.850
females 11.300  16.000  13.600  14.500

MTB > |
  
```

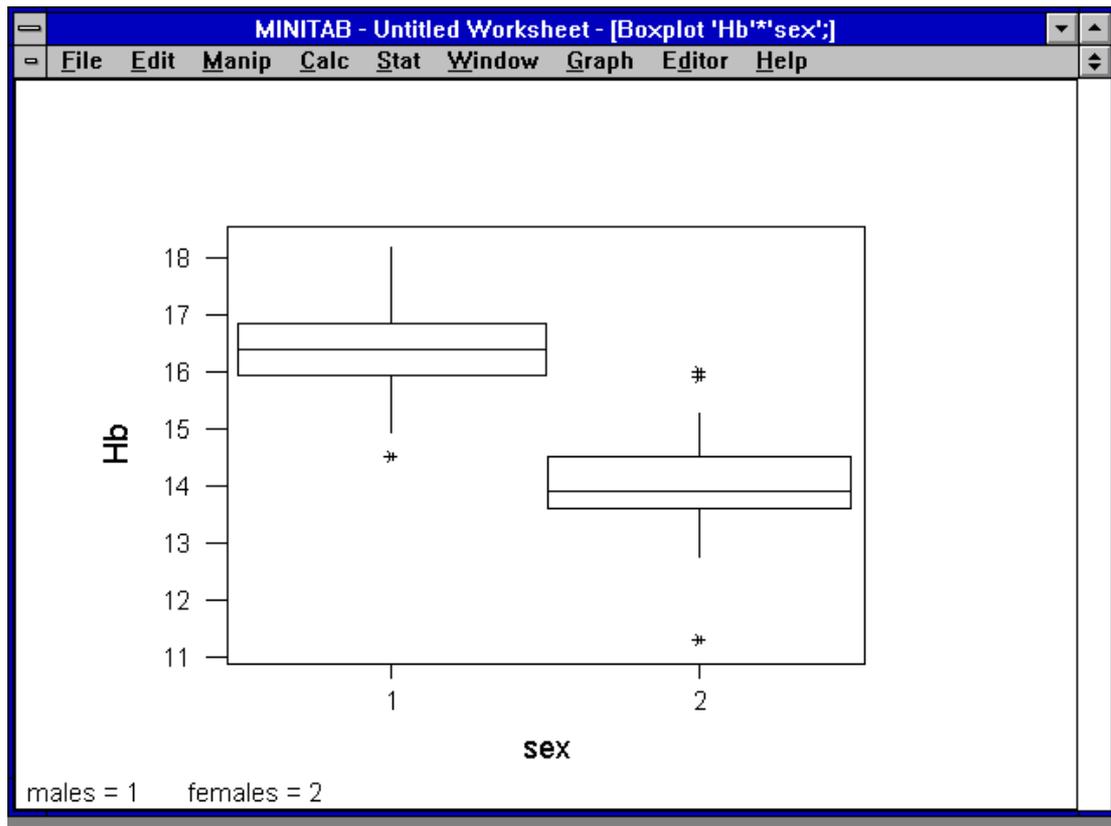
The screenshot shows two side-by-side boxplots for 'males' and 'females'. The 'males' boxplot has a median around 16.4, with whiskers extending from approximately 14.5 to 18.2. The 'females' boxplot has a median around 13.9, with whiskers extending from approximately 11.3 to 16.0. Both plots show outliers as small '+' symbols. Below the plots, the Session window shows the command history:

```

MTB > Boxplot 'males' 'females';
SUBC>   Box;
SUBC>   Symbol;
SUBC>   Outlier.
MTB >
  
```

By arranging the windows you can compare male and female boxplots, but it is preferable if they both use the same scale. To achieve this you must put all of the haemoglobins in one column and indicate in another to which group (male or female) they belong. In general this will be a better way to store data. You should make sure that you can use the **Manip** and **Calc** menus to do this. Sometimes it may also be convenient to select data items using the mouse and copy them to other parts of the spreadsheet.

It is essential to be able to label the graphs so that anyone may subsequently know what they represent; here the identification of the sexes has been added as a footnote.



You should look at the **?** button on the boxplot menu so that you are sure what the "whiskers" represent. The values are $Q1-1.5(Q3-Q1)$ and $Q3+1.5(Q3-Q1)$. For a Normal distribution these are equivalent to the mean ± 2.7 standard deviations.