

# Module 2 solutions

## Module 2: Solutions to Learning Activities

### Activity 2.1

In a Randomised Controlled Trial, the preference of a new drug was tested against an established drug by giving both drugs to each of 90 people. Assume that the two drugs are equally preferred, that is, the probability that a patient prefers either of the drugs is equal (50%). Use one of the binomial functions in Stata or R to compute the probability that 60 or more patients would prefer the new drug. In completing this question, determine:

- a) The number of trials (`n` for Stata, `size` for R)
- b) The number of successes we are interested in (`k` for Stata, `x` or `q` for R)
- c) The probability of success for each trial (`p` for Stata, `prob` for R)
- d) The form of the binomial function
  - for Stata: `binomialp`, `binomial` or `binomialtail`;
  - for R: `dbinom`, `pbinom` or `pbinom(lower.tail=FALSE)`
- e) The final probability.

### Answers

- a) Here, each participant represents a 'trial', so `size` is 90.
- b) We are interested in determining the probability that 60 or more participants prefer the new drug. This corresponds to *more than 59*, so we need to define `q` as 59.
- c) We are told to assume that the two drugs are equally preferred, so `prob` is 0.5.
- d) We need to calculate the probability that 60 or more participants prefer the new drug. The two R functions can be interpreted as follows:
  - the `dbinom` function gives the probability of observing 60 successes;
  - the `pbinom` function gives the probability of observing 60 or fewer successes;
  - the `pbinom` function with `lower.tail=FALSE` gives the probability of observing more than 59 successes. We therefore want to use `pbinom` function with `lower.tail=FALSE` here.

- e) The result computed by R is 0.00103013. Therefore, the probability that 60 or more patients would prefer the new drug is 0.001 or 0.1%.

### Process

We used the pbinom function, completed as follows:

```
pbinom(q=59, size=90, prob=0.5, lower.tail = FALSE)
```

```
[1] 0.001030133
```

## Activity 2.2

A case of Schistosomiasis is identified by the detection of schistosome ova in a faecal sample. In patients with a low level of infection, a field technique of faecal examination has a probability of 0.35 of detecting ova in any one faecal sample. If five samples are routinely examined for each patient, use Stata or R to compute the probability that a patient with a low level of infection:

- a) Will not be identified?
- b) Will be identified in two of the samples?
- c) Will be identified in all the samples?
- d) Will be identified in at most 3 of the samples?

## Answers

- a) The probability  $P(X=0) = 0.116$  or 11.6%.
- b) The probability  $P(X=2) = 0.336$  or 33.6%.
- c) The probability  $P(X=5) = .005$  or 0.5%.
- d) The probability  $P(X \leq 3) = .946$  or 94.6%.

## Process

In all of these questions, size is 5 and prob is 0.35. For (a) to (c), we need to calculate the probability of finding a certain number of infected samples, and we can use the `dbinom` function:

```
# Part (a)
dbinom(x=0, size=5, prob=0.35)
```

```
[1] 0.1160291
```

```
# Part (b)
dbinom(x=2, size=5, prob=0.35)
```

```
[1] 0.3364156
```

```
# Part (c)
dbinom(x=5, size=5, prob=0.35)
```

```
[1] 0.005252187
```

For part (d), “at most 3 samples” is the same as 3 or fewer samples, so we can use the `pbinom` function.

```
pbinom(q=3, size=5, prob=0.35)
```

```
[1] 0.9459775
```

### Activity 2.3

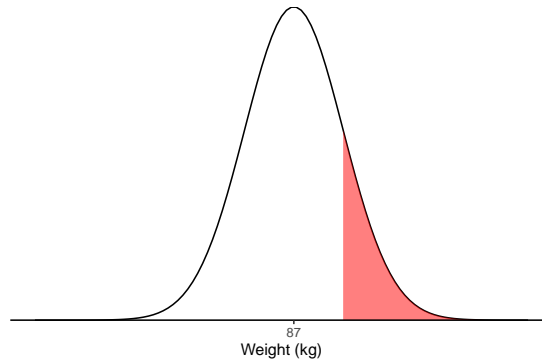
If weights of men are Normally distributed with a population mean  $\mu = 87$ , and a population standard deviation,  $\sigma = 8$  kg:

- What is the probability that a man will weigh 95 kg or more? Draw a Normal curve of the area represented by this probability in the population (i.e. with  $\mu = 87$  kg and  $\sigma = 8$  kg).
- What is the probability that a man will weigh more than 75 kg but less than 95 kg? Draw the area represented by this probability on a Normal curve.

### Answers

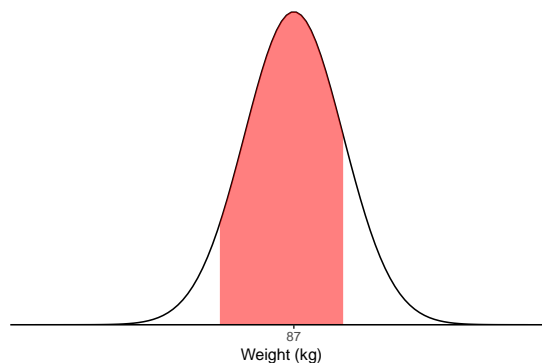
- The probability that a man from this population weighs 95 kg or more is 0.16 or 16% (Figure 1).

Figure 1: Probability that a man will weigh 95kg or more



- The probability that a man will weigh more than 75 kg but less than 95 kg is 0.77, or 77% (Figure 2).

Figure 2: Probability that a man will weigh more than 75kg by less than 95kg



## Process

- a) The curve representing the desired probability is shown in Figure 1, with the region above 95kg shaded to represent the probability of interest. Note that this curve was generated by a computer: a hand-drawn figure is completely acceptable. A hand-drawn figure will probably look much less tidy, but the main thing to notice is that the shaded area looks like it would represent less than 50% of the total curve. Therefore, our final probability should be less than 0.5.

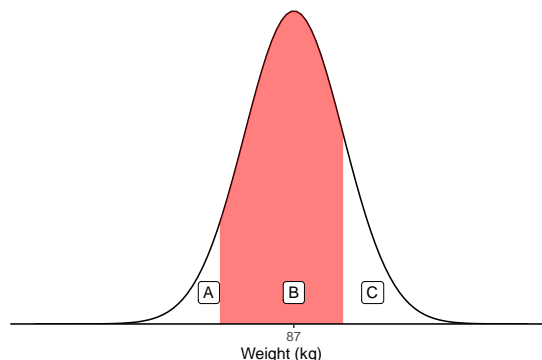
We can calculate the probability directly from R using the `pnorm` function. As we are calculating the probability above a certain value, we use `lower.tail=FALSE`

```
pnorm(95, mean=87, sd=8, lower.tail=FALSE)
```

```
[1] 0.1586553
```

- b) The curve to represent this probability is shown below. To obtain the probability represented by the shaded region, we again use the fact that the total area under a Normal curve must add to 1. Let's break the curve into three parts, which we will call A, B and C.

Figure 3: Probability that a man will weigh more than 75kg by less than 95kg



We use that fact that  $A + B + C = 1$  to derive that  $B = 1 - A - C$ .

We have already calculated C in Part (a) of this question. To calculate A:

```
pnorm(75, mean=87, sd=8, lower.tail=TRUE)
```

```
[1] 0.0668072
```

The region B is calculated as:  $1 - 0.1587 - 0.0668 = 0.7745$ .

Alternatively, we could calculate:

```
pnorm(95, mean=87, sd=8, lower.tail=TRUE) -  
  pnorm(75, mean=87, sd=8, lower.tail=TRUE)
```

```
[1] 0.7745375
```

## Activity 2.4

Using the health survey data (`Activity_S2.4.xlsx`) described in the computing notes of this module, create a new variable, BMI, which is equal to a person's weight (in kg) divided by their height (in metres) squared (i.e.  $BMI = \frac{\text{weight (kg)}}{[\text{height (m)}]^2}$ ). Categorise BMI using the WHO categories:

- Underweight:  $BMI < 18.5$
- Normal weight:  $18.5 \leq BMI < 25$
- Pre-obesity:  $25 \leq BMI < 30$
- Obesity Class I:  $30 \leq BMI < 35$
- Obesity Class II:  $35 \leq BMI < 40$
- Obesity Class III:  $BMI \geq 40$

Create a two-way table to display the distribution of BMI categories by sex (sex: 1 = respondent identifies as male; 2 = respondent identifies as female). Does there appear to be a difference in categorised BMI between males and females?

## Answers

Attaching package: 'huxtable'

The following object is masked from 'package:ggplot2':

`theme_grey`

Table 1: Frequencies of BMI category by sex for 1140 participants in a health survey

BMI category	Male	Female	Total
Underweight	6 (1.2%)	12 (1.9%)	18 (1.6%)
Normal weight	134 (26.1%)	228 (36.4%)	362 (31.8%)
Pre-obesity	216 (42.1%)	195 (31.1%)	411 (36.1%)
Obesity Class I	95 (18.5%)	106 (16.9%)	201 (17.6%)
Obesity Class II	46 (9.0%)	55 (8.8%)	101 (8.9%)
Obesity Class III	16 (3.1%)	31 (4.9%)	47 (4.1%)
<b>Total</b>	<b>513 (100.0%)</b>	<b>627 (100.0%)</b>	<b>1,140 (100.0%)</b>



From this health survey, it appears that men are more likely to have BMIs indicating Pre-Obesity (men 42% vs women 31%) and Obesity Class I (men 19% vs women 17%), compared to women who are more likely to have BMIs indicating Normal weight (women 36% vs men 26%).

## Process

We first read the Excel data into R, using the `readxl` package. It is useful to examine the dataset - here using the `summary()` function:

```
library(readxl)
library(jmv)

survey <- read_excel("data/activities/Activity_S2.4-health-survey.xlsx")
summary(survey)
```

	sex	height	weight
Min.	:1.00	Min. :1.220	Min. : 22.70
1st Qu.:	1.00	1st Qu.:1.630	1st Qu.: 68.00
Median :	2.00	Median :1.700	Median : 79.40
Mean :	1.55	Mean :1.698	Mean : 81.19
3rd Qu.:	2.00	3rd Qu.:1.780	3rd Qu.: 90.70
Max.	:2.00	Max. :2.010	Max. :213.20

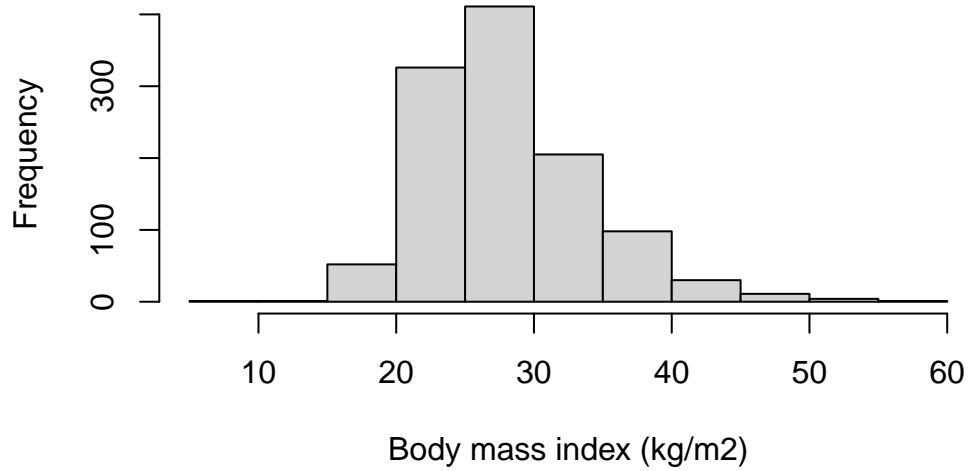
Note that `sex` has been entered as a numeric variable. We should define `sex` as a factor, and then create BMI. After creating BMI, we should examine its distribution using a histogram and/or a boxplot:

```
# Define sex as a factor
survey$sex <- factor(survey$sex, level=c(1,2), labels=c("Male", "Female"))

# Create BMI
survey$bmi = survey$weight / (survey$height^2)

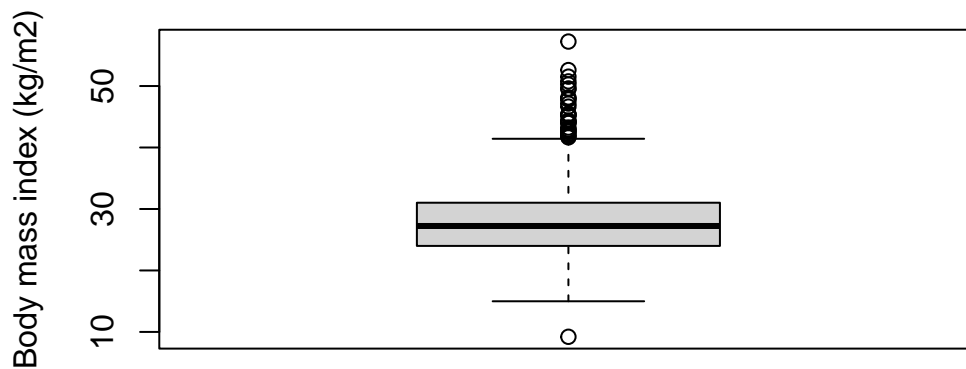
# Examine the distribution of BMI
hist(survey$bmi, main="Histogram of BMI", xlab="Body mass index (kg/m2)")
```

## Histogram of BMI



```
boxplot(survey$bmi, main="Boxplot of BMI", ylab="Body mass index (kg/m2)")
```

## Boxplot of BMI



The boxplot in particular shows that there are some extreme values of BMI. We can examine some records using the `subset()` function:

```
subset(survey, bmi<15)
```

sex	height	weight	bmi
Female	1.57	22.7	9.21
Female	1.65	40.8	15

```
subset(survey, bmi>45)
```

sex	height	weight	bmi
Female	1.52	105	45.4
Male	1.85	174	50.8
Female	1.22	74.8	50.3
Male	1.93	213	57.2
Female	1.63	127	47.8
Female	1.55	115	48
Female	1.65	131	48.2
Female	1.55	109	45.3
Male	1.78	143	45.1
Female	1.65	127	46.6
Female	1.63	132	49.5
Female	1.7	152	52.6
Female	1.6	127	49.6
Female	1.5	106	47.2
Female	1.73	154	51.5
Female	1.6	116	45.4

The smallest BMI of 9.2 kg/m<sup>2</sup> is very low, with a weight of 22.7 kg. We should check the recorded height and weight values against the original data (paper records, survey responses) if they were available. However, as a weight of 22.7kg is not impossible, this record will not be deleted. An alternative approach would be to analyse the data including the very low BMI and again excluding the very low BMI as a sensitivity analysis.

The largest BMI values are based on participants with large weights, and none of these seem biologically implausible. Therefore, no changes will be made to participants with small or large values of BMI.

We can use the `cut()` function to create the BMI categories. The WHO cutpoints are inclusive of the lower-bound, so we use `right=FALSE`. After creating the categories, it is good practice to check the resulting categories using `summary()`:

```
survey$bmi_cat <- cut(survey$bmi,
                      c(0, 18.5, 25, 30, 35, 40, 100),
                      right=FALSE)

summary(survey$bmi_cat)
```

```
[0,18.5) [18.5,25) [25,30) [30,35) [35,40) [40,100)
      18      362      411      201      101      47
```

Finally, we can create a two-way table using the `contTables()` function within the `jmv` package. We can define the rows by BMI category, and the columns by sex:

```
contTables(data=survey,
           rows = bmi_cat,
           cols = sex)
```

## CONTINGENCY TABLES

### Contingency Tables

bmi_cat	Male	Female	Total
[0,18.5)	6	12	18
[18.5,25)	134	228	362
[25,30)	216	195	411
[30,35)	95	106	201
[35,40)	46	55	101
[40,100)	16	31	47
Total	513	627	1140

### <sup>2</sup> Tests

Value	df	p
-------	----	---

<sup>2</sup> 22.49802 5 0.0004209  
 N 1140

To assess whether there is a difference in BMI between males and females, we should look at the within-sex relative frequencies. In other words, column percents (for this table), by specifying `pcCol = TRUE`:

```
contTables(data=survey,
            rows = bmi_cat,
            cols = sex,
            pcCol = TRUE)
```

## CONTINGENCY TABLES

### Contingency Tables

bmi_cat		Male	Female	Total
[0,18.5)	Observed	6	12	18
	% within column	1.16959	1.91388	1.57895
[18.5,25)	Observed	134	228	362
	% within column	26.12086	36.36364	31.75439
[25,30)	Observed	216	195	411
	% within column	42.10526	31.10048	36.05263
[30,35)	Observed	95	106	201
	% within column	18.51852	16.90590	17.63158
[35,40)	Observed	46	55	101
	% within column	8.96686	8.77193	8.85965
[40,100)	Observed	16	31	47
	% within column	3.11891	4.94418	4.12281
Total	Observed	513	627	1140
	% within column	100.00000	100.00000	100.00000

## <sup>2</sup> Tests

	Value	df	p
<sup>2</sup>	22.49802	5	0.0004209
N	1140		

## Activity 2.5

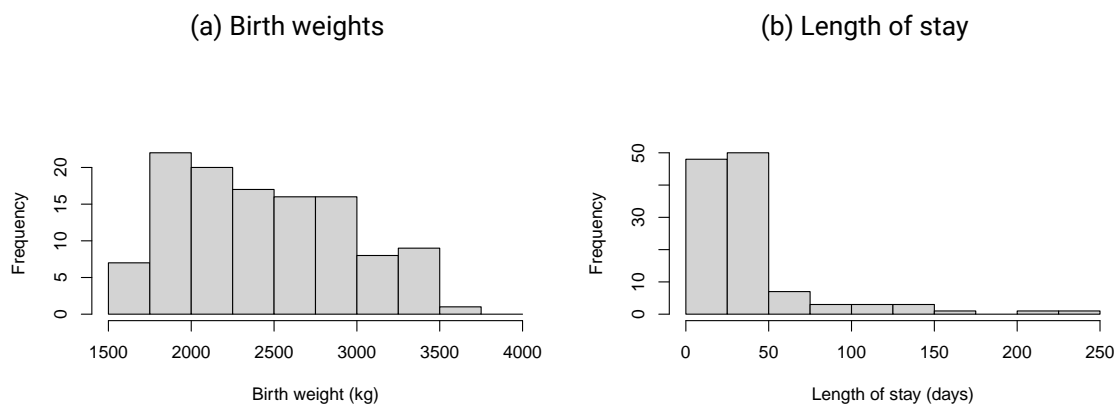
The data in the files `Activity_S2.5.dta` and `Activity_S2.5.rds` (available on Moodle) has information about birth weight and length of stay collected from 117 babies admitted consecutively to a hospital for surgery. For each variable: a) Create a histogram to inspect the distribution of the variable; b) Complete the following summary statistics for each variable: - mean and median; - standard deviation and interquartile range; - skewness and kurtosis.

Make a decision about whether each variable is symmetric or not, and which measure of central tendency and variability should be reported.

## Answers

a) See Figure 4.

Figure 4: Summary of data from 117 babies admitted to a hospital



b) See Table 2.

Table 2: Summary of data from 117 babies admitted to a hospital

	Birthweight (grams)	Length of stay (days)
Mean (Standard deviation)	2451 (504.8)	41 (36.9)
Median [Interquartile range]	2438 [2004 to 2830]	30 [21 to 43]
Skewness	0.35	3.1
Kurtosis	2.2	14.0

As the histogram for birthweight shows a roughly symmetric distribution, we should present the mean and standard deviation as the appropriate measures of central tendency and spread. Notice that the mean and median are similar, which is to be expected for a symmetric distribution.

The histogram for length of stay shows a highly skewed distribution (skewed to the right). In this case, the median and interquartile range are the appropriate measures to present. Notice that the mean is higher than the median, which is typical for distributions that are skewed to the right.



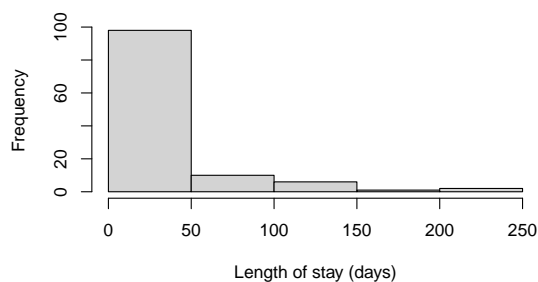
## Activity 2.6

The data set of hospital stay data for 1323 hypothetical patients is available on Moodle in csv format (**Activity2.6.csv**). Import this dataset into Stata or R. There are two variables in this dataset: - female: female=1; male=0 - los: length of stay in days

- Use Stata or R to examine the distribution of length of stay: overall; and separately for females and males. Comment on the distributions.
  - Use Stata or R to calculate measures of central tendency for hospital stay to obtain information about the average duration of hospital stay. Which summary statistics should you report and why? Report the appropriate statistics of the spread and measure of central tendency chosen.
  - Calculate the measures of central tendency for hospital duration separately for males and females. What can you conclude from comparing these measures for males and females?
- a) The histograms for overall length of stay (Figure 4) and length of stay by gender (Figure 5) all show that length of stay is heavily skewed (skewed to the right).

Figure 5: Summary of length of hospital stay

(a) Histogram



(b) Boxplot

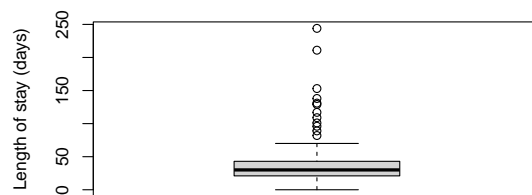
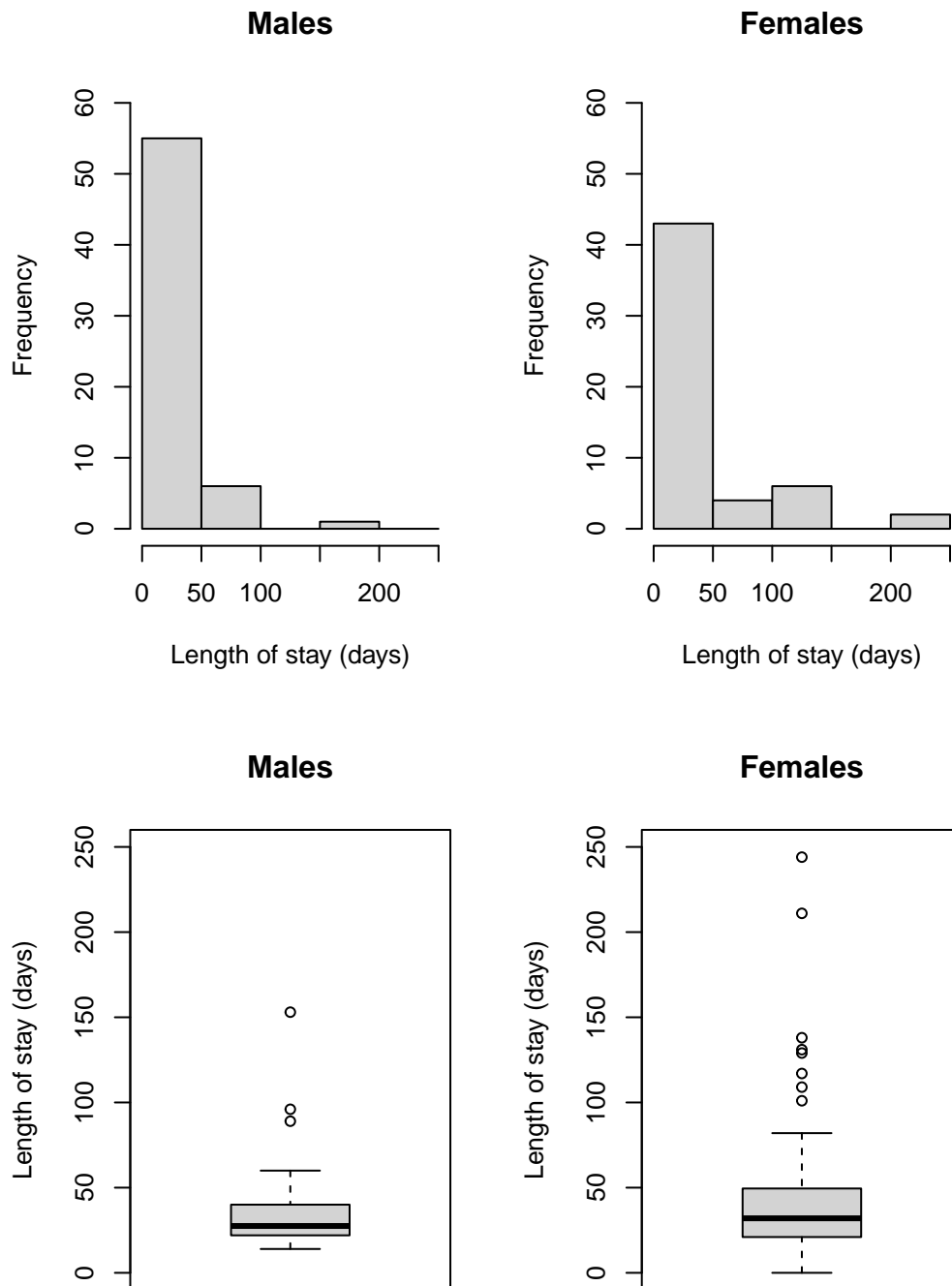


Figure 6: Summary of length of hospital stay



## Process

The process of plotting histograms and boxplots by another variable (here, sex) is discussed in Section 2.30 in the course notes. Essentially, we can split the graphics window into 2 rows and 2 columns using the `par` function. It is important to keep both the x- and y-axes consistent for both plots, which we can do by specifying the limits and the breaks:

```
# Set the graphics parameters to plot 2 rows and 2 columns:
par(mfrow=c(2,2))

# Specify each plot separately
# First, the histograms
# Notice we specify the x-limits (from 0 to 250) and the breaks to keep
# the x-axes consistent

# We also specify the y-limits to keep the y-axes consistent

hist(hospstay_males$LengthStay,
     xlab="Length of stay (days)", main="Males",
     xlim=c(0, 250), breaks=c(0, 50, 100, 150, 200, 250),
     ylim=c(0, 60))

hist(hospstay_females$LengthStay,
     xlab="Length of stay (days)", main="Females",
     xlim=c(0, 250), breaks=c(0, 50, 100, 150, 200, 250),
     ylim=c(0, 60))

# Next, the boxplots
# Notice we specify the y limits and the breaks

boxplot(hospstay_males$LengthStay,
        ylab="Length of stay (days)", main="Males",
        ylim=c(0, 250), breaks=c(0, 50, 100, 150, 200, 250))

boxplot(hospstay_females$LengthStay,
        ylab="Length of stay (days)", main="Females",
        ylim=c(0, 250), breaks=c(0, 50, 100, 150, 200, 250))

# Reset graphics parameters
par(mfrow=c(1,1))
```