

Statistics 305: Introduction to Biostatistical Methods for Health Sciences

R Demo for Chapters 2 & 3: Data presentations and summaries

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Demo Slides

- ▶ This document shows and explains the R commands used to create the data summaries of the Chapters 2 & 3 lecture slides.
- ▶ This document should be read **after** reading the lecture slides for Chapters 2 & 3.
- ▶ You may find the R commands in this demo useful for your homework assignments.

Data Presentation (Chapter 2)

Tables

- ▶ Tables can be used to display the frequency distribution of a categorical variable
- ▶ Example: Frequency distribution of gender among 21,737 bladder cancer patients. Data from Mungan et al. (2000)

```
uu <- url("http://people.stat.sfu.ca/~jgraham/Teaching/S305_17/Data/mung.csv")
Mungan <- read.csv(uu)
head(Mungan)
```

```
##   Gender Cancer.Stage
## 1   Male             I
## 2   Male             I
## 3   Male             I
## 4   Male             I
## 5   Male             I
## 6   Male             I
```

```
with(Mungan, table(Gender))
```

```
## Gender
## Female   Male
##   5536  16201
```

Software Notes: Reading Data Into R

- ▶ `read.csv()` reads comma-separated-value (CSV) files into R.
 - ▶ By default this function reads files from the “working” directory in which R is running (e.g., the project directory of your RStudio project or the folder of your Jupyter notebook), but it can read files from URLs too.
 - ▶ The `url()` function takes a quoted URL as input and returns an object that `read.csv()` can use to fetch the file from the internet.

- ▶ `read.table()` is a more flexible function than `'read.csv()'` for reading data into R.
- ▶ It can easily read in comma-separated-value (CSV) files as well as files with values separated by other characters such as blank spaces or tabs.
- ▶ For example, the CSV file `mung.csv` can be read into R with `read.table()` as follows:

```
uu <- url("http://people.stat.sfu.ca/~jgraham/Teaching/S305_17/Data/mung.csv")
Mungan <- read.table(uu,header=TRUE,sep=",")
```

- ▶ `read.table()` options include the following:
 - ▶ `header` (default `FALSE`): Does the first line of the file contain the variable names?
 - ▶ `sep` (default `" "`, for blank spaces)
- ▶ To get a full list of options for `'read.table()'`, type `help("read.table")` into R.

Software Notes: `head()`, `with()` and `table()`

- ▶ The `head()` function looks at the first few rows (default is six) of a dataset.
 - ▶ In the example, the dataset is called `Mungan`, and has variables `Gender` and `Cancer.Stage`.
 - ▶ Datasets have as many rows as there are sampled units (e.g., people) and as many columns as there are variables measured on the sampled units.
- ▶ The `with()` function takes a dataset as its first argument and the summary to compute as its second argument.
 - ▶ In the above example, the summary is a table of the values of the `Gender` variable in the `Mungan` dataset.
- ▶ The `table()` function tabulates the unique values of a variable, or, if given two variables, cross-tabulates the two variables (more on cross-tabulation in Chapter 15).

Tables, cont.

- Joint frequency distribution of two categorical variables:

```
with(Mungan, table(Gender, Cancer.Stage))
```

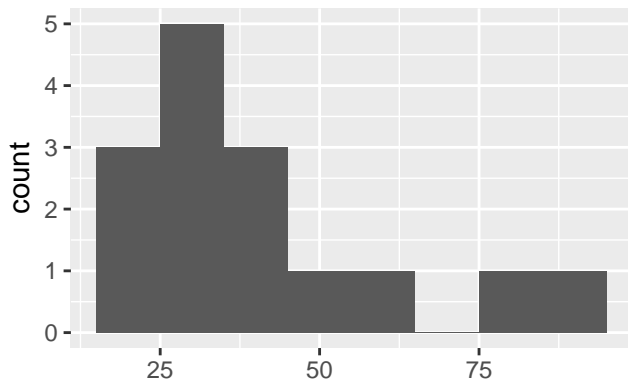
##		Cancer.Stage			
##	Gender	I	II	III	IV
##	Female	3926	402	356	852
##	Male	12418	995	883	1905

Example Histogram

- Data on the numbers of hysterectomies performed by 15 male Swiss doctors:

20 25 25 27 28 31 33 34 36 37 44 50 59 85 86

```
hyst <- data.frame(numHyster = c(20,25,25,27,28,31,33,34,  
                                36,37,44,50,59,85,86))  
library(ggplot2)  
ggplot(hyst,aes(x=numHyster)) + geom_histogram(binwidth=10)
```



Software Notes: Data Frames

- ▶ We used the `data.frame()` function to create a data frame with a single variable `numHyster`.
 - ▶ Data frames are objects used to store datasets in R.
 - ▶ Typically a data frame consists of multiple variables, such as the Mungan data frame with variables `Gender` and `Cancer.Stage`.
 - ▶ Use `names()` to find the names of variables in a data frame:

```
names(Mungan)
```

```
## [1] "Gender"      "Cancer.Stage"
```

Software Notes: Add-on Packages

- ▶ The code chunk that draws the histogram of the hysterectomy data loads an add-on package for R called `ggplot2`.
- ▶ R consists of a “base” distribution plus many add-on packages that contain useful functions.
 - ▶ For example, `ggplot2` is a package that contains the graphics function `ggplot()`.
- ▶ To use the functions in a package you must **first** load the package with `library()`.
 - ▶ For example, `library(ggplot2)` loads `ggplot2` and gives us access to `ggplot()`.
- ▶ If you don't load a package, R can't find its functions.
 - ▶ For example, if you haven't yet loaded `ggplot2` and you try to use `ggplot()` you will get an error message:

Error: could not find function "ggplot"

Software Notes: Installing Add-on Packages

- ▶ See the video <https://www.youtube.com/watch?v=CtOSryChcGg> for more on R packages.
- ▶ RStudio users (RStudio Desktop or RStudio Cloud) will need to install the packages they need before they can load them.
 - ▶ RStudio Desktop users should consult the **R Packages** section of the getting started document at <https://github.com/SFUStatgen/RforStat2/blob/master/Tutorials/GettingStarted/startR-RStudio.Rmd>
 - ▶ RStudio Cloud users should consult step 5 of the getting started document at <https://github.com/SFUStatgen/RforStat2/blob/master/Tutorials/GettingStarted/startRStudioCloud.Rmd>
- ▶ Jupyter should have all the packages we will need for this course installed.
 - ▶ Thus, Jupyter users don't need to install packages (but **do** need to load them before using).

Software Notes: `ggplot()`

- ▶ `ggplot2` is an add-on package for R that implements the graphics function `ggplot()`.
 - ▶ We will use `ggplot()` throughout the course.
- ▶ To draw the histogram of the hysterectomy data, the call to `ggplot()` was

```
ggplot(hyst, aes(x=numHyster)) + geom_histogram(binwidth=10)
```

- ▶ This specifies the dataset (`hyst`) and the “aesthetic”, which is a list of variables to plot as different features of the graph.
 - ▶ This example is a histogram of `numHyster`. We specify that `numHyster` is the x-axis variable with `x=numHyster`.
 - ▶ The function `geom_histogram()` adds the histogram; it takes the bin width as an optional argument.

Summary Statistics (Chapter 3)

Centre: The mean

- ▶ The population mean, μ , is the ordinary arithmetic average of a variable in the population.
- ▶ The corresponding statistic is the sample mean, \bar{x} .
- ▶ The sample mean is the ordinary arithmetic average of the observations in a random sample from the population.
- ▶ For example, the hysterectomy example data:

20 25 25 27 28 31 33 34 36 37 44 50 59 85 86

has sample mean

$$\bar{x} = \frac{20 + 25 + \dots + 86}{n} = 41.3$$

```
library(dplyr)
summarize(hyst, mean(numHyster))
```

```
## mean(numHyster)
## 1 41.33333
```

Software Note

- ▶ `dplyr` is an add-on package for R that includes useful tools for manipulating datasets in R.
 - ▶ The `summarize()` function takes the dataset as its first argument, and the summaries to compute as additional arguments.
 - ▶ In this example we could have instead used `with(hyst, mean(numHyster))`, but we will eventually want to use `summarize()` together with other tools from `dplyr` to produce data summaries.

Centre: The Median

- ▶ The population median is the “middle value” of the variable in the population.
- ▶ The corresponding statistic is the sample median, M .
- ▶ The sample median is the middle value of the variable in a random sample from the population.
- ▶ The sample median of the hysterectomy data is:

20, 25, 25, 27, 28, 31, 33, **34**, 36, 37, 44, 50, 59, 85, 86

- ▶ The centre observation is $M = 34$.

```
summarize(hyst, median(numHyster))
```

```
## median(numHyster)
## 1                 34
```

Spread: The Standard Deviation (SD) and Variance

- ▶ The variance, σ^2 , is the average of squared deviations from the mean in the population
- ▶ The SD, σ , is the square-root of the variance and measures spread about the mean.
- ▶ As for the corresponding statistics:
 - ▶ The sample variance, s^2 , is (almost) an average of squared deviations from the sample mean in a random sample from the population.
 - ▶ The sample SD, s , is the square root of the sample mean.
- ▶ Hysterectomy example: $s = 20.6$

```
summarize(hyst, sd(numHyster))
```

```
## sd(numHyster)
## 1 20.60744
```

Spread: The Inter-Quartile Range (IQR)

- ▶ The first and third quartiles mark the first and third quarters of the observations, whether in a population or in a random sample from the population.
 - ▶ These are also called the 25th and 75th percentiles, respectively.

```
summarize(hyst,  
          Q1=quantile(numHyster,probs=.25),  
          Q3=quantile(numHyster,probs=.75))
```

```
##      Q1 Q3  
## 1 27.5 47
```

- ▶ The middle half of the data lies between.
- ▶ The range of the middle half, or IQR, is $47 - 27.5 = 19.5$.

```
summarize(hyst,IQR(numHyster))
```

```
##      IQR(numHyster)  
## 1              19.5
```

Boxplots

- ▶ The five number summary is the minimum, maximum, median, 1st and 3rd quartiles.
- ▶ Graphed with a boxplot in the hysterectomy data:

```
with(hyst,boxplot(numHyster))
```

