Class 4 Lab*

Introduction to Data in R

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i Instructions

Save this document to your computer and open it in a PDF viewer such as Preview (available on every mac) or Adobe Acrobat Reader (free for PC and Linux). Be sure to add your name and UC San Diego personal identification number (PID) and email below before answering all questions in the space provided.

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Overview

This short lab supplement introduces basic tools for working with data.frames in R, as well as several commands for producing numerical and graphical summaries. We will build on these fundamentals next day when we delve into the powerful **ggplot2** package for making beautiful data visualizations.

Section 1: BRFSS as an example data.frame

The Behavioral Risk Factor Surveillance System (BRFSS) is an annual telephone survey of 350,000 people in the United States. The survey is designed to identify risk factors in the adult population and report emerging health trends.

For example, respondents are asked about their diet, weekly exercise, possible tobacco use, and healthcare coverage.

^{*}http://thegrantlab.org/teaching/

Use the following command to download the dataset cdc from a URL. This dataset is a sample of 20,000 people from the survey conducted in 2000, and contains responses from a subset of the questions asked on the survey.

```
source("http://thegrantlab.org/misc/cdc.R")
```

Take a look at the Environment tab, where cdc should now be visible. Click the blue button next to the dataset name to view a summary of the 9 variables contained in the data matrix (see Figure 1).

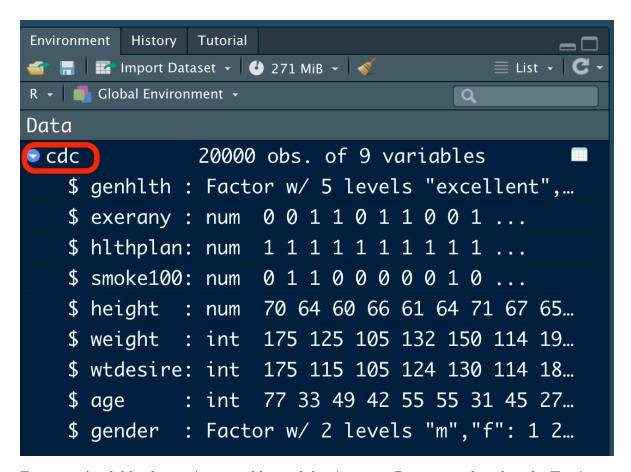


Figure 1: Available objects (e.g. variables and data) in your R session is listed in the **Environment** panel of RStudio. Click on these to see more details.

To view the dataset itself, click on the name of the dataset in the **Environment** panel; alternatively, enter the command:

View(cdc)

Each row of the **data.frame** represents a **case** and each column represents a **variable**. Each case is a person and each variable corresponds to a question that was asked in the survey.

- For genhlth, respondents were asked to evaluate their general health as either "excellent", "very good", "good", "fair", or "poor".
- The variables exerany, hlthplan, and smoke100 are binary variables, with responses recorded as either 0 for "no" and 1 for "yes": whether the respondent exercised in the past month, has health coverage, or has smoked at least 100 cigarettes in their lifetime.
- The other variables record the respondents' height in inches, weight in pounds, their desired weight (wtdesire), age in years, and gender (m for male and f for female).

Key-point: The \$ operator in R is used to access variables (i.e. **columns**) within a data.frame; for example, **cdc\$height** tells R to look in the **cdc** data.frame for the **height** variable:

head(cdc\$height)

[1] 70 64 60 66 61 64

Note that the **head()** function prints out just the first 6 entries (rather than all 20,000). Guess what the **tail()** function does!

Q1 How would you "argue" with the tail() function to print out the last 20 weight values? Provide your code below: tail(cdc\$height, 20)

Q2 Make a scatterplot of height vs weight using the plot() function. Add the code you used to generate this plot here:



If you already know how to use ggplot feel free to use it here (and elsewhere in this lab) in place of the "base R" plot() function.

plot(cdc\$height, cdc\$weight) in an R.script file

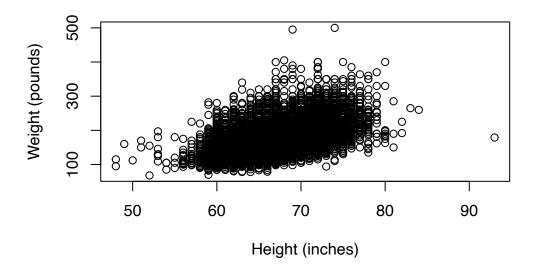


Figure 2: Scatterplot of height vs weight generated with the plot() function. Note custom axis labels generated with the xlab and ylab arguments. It is still rather basic and ugly - we will use ggplot to make beautiful versions next day;-)

Q3 Do height and weight appear to be associated? If so are they positively associated or negatively associated?

Positively associated. There is an upwards trend.

Side-Note: We can use the 'cor() function to calculate the Pearson correlation of height and weight. A correlation coefficient of 0.1 is thought to represent a weak or small association; a correlation coefficient of 0.3 is considered a moderate correlation; and a correlation coefficient of 0.5 or larger is thought to represent a strong or large correlation.

Q4 What is the Pearson correlation value for height and weight?



Your code should look something like this: cor(___\$height, cdc\$___) with the ___ blanks filled in obviously.

correlation coefficient: 0.556. Strong/ large correlation

Key-Point: When we use the \$ notation we extract a vector from the data.frame

Many "base R" graphics functions work with vectors as input just like the plot() function. For example to make a histogram we can use:

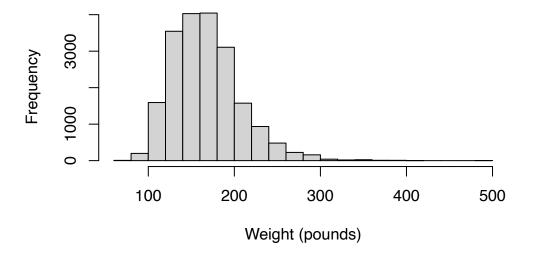


Figure 3: Distribution of weight values in the dataset

Now do the same for height.

```
hist(cdc$height)
```

Side-Note: Do you notice a difference between the distributions for weight and height? Is one more scewed than the other? Why do you think this is?

Creating new vectors

The conversion from inches to meters is 1 in = .0254 m. The code below creates a new object height_m that records height in meters. Similarly, the conversion from pounds to kilograms is 1 lb = .454 kg.

```
# Create height.m
height_m <- cdc$height * 0.0254</pre>
```

Q5 Create a new object weight_kg that records weight in kilograms. Provide your code

weight_kg <- cdc\$weight * 0.454

Section 2: BMI

BMI is calculated as weight in kilograms divided by height in meters squared.

Q6 Create a new object bmi and make a plot of height vs BMI. Provide your code below and comment on whether height and BMI seem to be associated?



? Tip

Your code should look something like this: (weight_kg)/(height_m^2) and then ${\tt plot(cdc\$height, __)}$ again with the blanks filled in.

There doesn't seem to be that much of a correlation since most points are condensed in a relatively large area with no visible trend line/ pattern.

Q7 Are height and BMI strongly associated? What are their correlation value?



Tip

Since height and BMI have a much weaker association, it is more useful to use BMI as a measure of obesity. Using BMI is one way to account for the fact that taller people tend to have more tissue and thus, weigh more than shorter people.

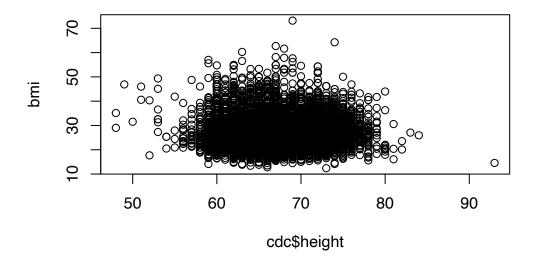


Figure 4: Height vs Body Mass Index (BMI)

correlation of 0.03251694. Relatively weak correlation

Using logical vectors to count and subset

A BMI of 30 or above is considered obese. In R we can use code like the following to return a logical vector (i.e. TRUE and FALSE values) that can in turn help us find how many obese individuals are in our dataset.

```
# Note that I only have patience to print out the first 100 entries here
head(bmi >= 30, 100)
```

[1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE

```
[13] FALSE FALSE
[25] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE TRUE FALSE
[37] FALSE FALSE FALSE FALSE FALSE FALSE FALSE TRUE FALSE FALSE FALSE
[49] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE TRUE FALSE FALSE
[61] FALSE FALSE TRUE
                    TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[73] FALSE TRUE TRUE
                     TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[85] FALSE FALSE FALSE
                          TRUE FALSE TRUE FALSE FALSE FALSE FALSE
[97] TRUE FALSE FALSE FALSE
```

A very useful trick that we will turn to over and over again is to treat logical vectors as equivalent to zero and one values. For example:

```
eg <- c(TRUE, TRUE, FALSE, FALSE)
sum(eg)
```

[1] 2

Q8 Can you use this summing of a logical vector approach to find out how many obese

```
individuals there are in the dataset? Provide your code and answer below:
  Tip
  Try sum(bmi \geq 30)
3897
x <- bmi >= 30
sum(x)
```

To find the proportion of obese individuals we can use the following code:

```
sum(bmi >= 30)/length(bmi)
```

[1] 0.19485

Or to get percent value:

```
(sum(bmi >= 30)/length(bmi)) * 100
```

[1] 19.485

And to round this percent value to one significant figure:

```
round( (sum(bmi >= 30)/length(bmi)) * 100, 1)
```

[1] 19.5

Section 3: Accessing subsets of data using row and column indices

Row-and-column notation in combination with square brackets can be used to access a subset of the data. For example, to access the sixth variable (weight) of the 567th respondent, use the command:

```
cdc[567, 6]
```

[1] 160

To see the weight for the first ten respondents, use:

```
cdc[1:10, 6]
[1] 175 125 105 132 150 114 194 170 150 180
```

If the column number is omitted, then all the columns will be returned for rows 1 through 10:

```
cdc[1:10, ]
```

genhlth exerany hlthplan smoke100 height weight wtdesire age gender good m f good f good f good very good f

6	very	good	1	1	0	64	114	114	55	f
7	very	good	1	1	0	71	194	185	31	m
8	very	good	0	1	0	67	170	160	45	m
9		good	0	1	1	65	150	130	27	f
10		good	1	1	0	70	180	170	44	m

Q9 Use bracket notation to make a scatterplot of height and weight for the first 100 respondents. Provide your code below.



Tip

There are multiple ways to do this—find one that works! For example cdc[1:100,] \$height or cdc[1:100, "height"] or cdc[1:100, 5] all return the first 100 height values. Which one do you prefer and why?

plot(cdc[1:100, 5], cdc[1:100, 6])

Section 4: Optional (for now)

Q10 How many obese individuals are male in the full dataset? Give your code and answer below:



Tip

Again there are multiple ways to do this. A very useful function in R is the table() function that will count up the number of different entries in a vector. For example table(c("f", "f", "m")).

To answer a question like this, first break it down into sub-steps like:

- How do I first get at the data I need (i.e. the gender column)?
- Then how do I subset this vector to have only bmi >= 30 folks?
- Then finally, how do I pass this to the table() function to count up the m and f values.

Discussion

With these codding skills there are lot's of other advanced questions we could ask and answer, for example:

- what portion of obese individuals judge their health to be "good"?
- Is this higher for male or female individuals?
- Is this difference significant?
- Do obese people smoke more, etc. etc.

Next class we will cover **ggplot** and in a couple of classes time we will cover the excellent **dplyr** package and the so-called **tidyverse** that together will make answering these types of questions much more tractable.

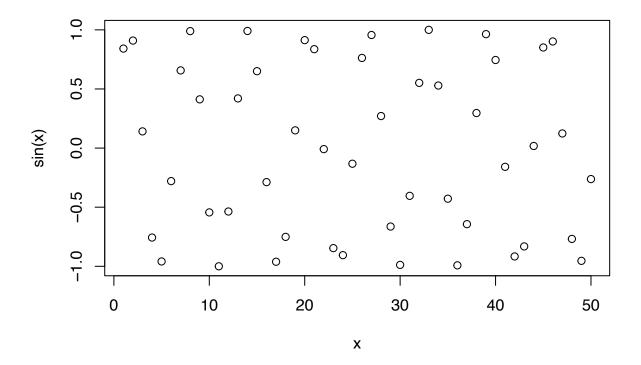
N.B. Note that it is exactly this sort of approach we will need to answer important bioinformatics questions like: "What proportion of my genes are up-regulated?"; "Of these, what proportion are from a certain key pathway?" etc.

class04.R

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```
x <- 1:50
plot(x, sin(x))
```



plot(x, sin(x), typ="1", col="blue", lwd=2, xlab="Hello")

