R Workshop 4

July 12, 2017

Review from Workshop 3

Continuous Random Variables

We squeezed in continous random variables just before running out of time in the last workshop. Let's summarize some of the concepts.

Calculus provides us a convenient two-way relationship between the CDF and the density function for a random variable.

$$f_X(x) = \frac{dF_X}{dx}$$
$$F_X(b) - F_X(a) = \int_a^b f_X(x)dx$$

Expectation is the natural analog to summation for discrete random variables.

$$E[X] = \int_{-\infty}^{\infty} x f_X(x)dx$$

Finally, the moment generating function is also analogous to the discrete case.

$$m_X(t) = E[e^{xt}] = \int_{-\infty}^{\infty} e^{xt} f_X(x)dx$$

Normal Random Variables

The granddaddy of all the distributions is the *normal distribution*. It is also known as the *Gaussian distribution*. It has the symmetric "bell-shape" that most people recognize. It has two parameters.

- μ - the mean of the distribution
- σ^2 - the variance of the distribution

The *probability density function* is

$$f_X(x; \mu, \sigma^2) = \frac{1}{\sqrt{2\pi}\sigma} e^{\frac{1}{2}\left(\frac{x-\mu}{\sigma}\right)^2} \quad x \in (-\infty, \infty)$$

Sometimes a normal random variable with mean μ and variance σ^2 is written $\mathcal{N}(\mu, \sigma^2)$. The "*standard normal*" is $\mathcal{N}(0, 1)$.

The first thing different about this distribution than past ones we've discussed is that it is a *continuous* distribution. Its domain is not a countable discrete set. In the case of the normal distribution, the domain is the entire real number line.

You might think that with parameter names like "mean" and "variance" you would be off the hook to verify what they are. Alas, here are some verifications for you to make during your boring meetings over the next two weeks.

1. Show the area under f_X is 1 with $\mu = 0$ and $\sigma = 1$. The integral is not obvious. The trick is to compute its square: $\int_0^\infty f_X(x)dx \int_0^\infty f_X(y)dy$. Convert the x and y to polar coordinates r and θ and integrate in two dimensions.
2. Show that the moment generating function for $\mathcal{N}(\mu, \sigma^2)$ is $\exp\left[t\mu + \left(\frac{t\sigma}{2}\right)^2\right]$. The trick is completing the square in the exponent.
3. Use the moment generating function for $\mathcal{N}(\mu, \sigma^2)$ to verify the mean and variance.

The moment generating function for $\mathcal{N}(\mu, \sigma^2)$ comes in handy for more than simply calculating moments. We'll refer back to this when determining if a function of random variables is normal through comparing the moment generating functions.

Dates and Times

In this section we'll address several classes and functions that address dates and times.

Date

Dates are represented by the **Date** class. Internally, it's the number of days since January 1, 1970. Create an instance of `Date` with the `as.Date()` function.

```
In [13]: x <- as.Date('2017-03-15')
         x
```

```
2017-03-15
```

The second parameter allows you to specify a different date format.

```
In [14]: as.Date(c('3/15/17', '2/21/17'), '%m/%d/%y')
         as.Date('20170315', '%Y%m%d')
         as.Date('March 15, 2017', '%B %d, %Y')
```

```
    2017-03-15   2017-02-21

2017-03-15

2017-03-15
```

In the examples above, we see that the format string uses a percent sign to indicate a special field.

- `%d` - day of the month
- `%m` - number of the month
- `%y` - two digit year
- `%Y` - four digit year
- `%B` - full name of the month (in English).

A full list of the abbreviations can be found from the R help for the `strptime` function which we'll be covering below.

```
?strptime
```

Note how the first example supplies a vector for the first argument. A column of a dataframe is often the first argument.

To retieve the current date, use `Sys.Date()`.

```
In [15]: Sys.Date()
```

```
2017-07-10
```

Times

Times are represented by two nice classes with ugly names: **POSIXct** and **POSIXlt**.

- `POSIXct` is just a large integer under the hood. It's good for dataframe calculations.
- `POSIXlt` is a list that maintains info about day of the week, day of the year, day of the month, and lots of other things. It's good for presenting date-times in human readable form.

POSIXct

The `as.POSIXct` function creates a `POSIXct` object from another object such as a string or `Date`.

In [16]:
```
as.POSIXct(Sys.Date())
as.POSIXct(Sys.time())
as.POSIXct("2017-02-25 13:30")
as.POSIXct("2017-02-25 13:30 PDT")
```

```
[1] "2017-07-09 17:00:00 PDT"

[1] "2017-07-10 15:50:47 PDT"

[1] "2017-02-25 13:30:00 PST"

[1] "2017-02-25 13:30:00 PST"
```

Be wary of the timezone settings. In my R console, the last two entries returned `PDT` instead of `PST`.

The `print` method converts `POSIXct` instances into a human-friendly string. But at its heart, it's an integer suitable for calculation.

In [17]:
```
ctime <- as.POSIXct("2017-07-12 15:20:30")
ctime
unclass(ctime)
```

```
[1] "2017-07-12 15:20:30 PDT"
```

1499898030

POSIXlt

The `as.POSIXlt` function creates a `POSIXlt` instance. From the way it is constructed and printed, the `POSIXlt` doesn't seem any different than `POSIXct`. Indeed, they can be converted back and forth. But the `POSIXlt` stores various attributes of a time.

In [18]:
```
ltime <- as.POSIXlt("2017-04-05 12:30:00")
ltime
unclass(ltime)
```

```
[1] "2017-04-05 12:30:00 PDT"
```

$sec
0
$min
30
$hour
12
$mday
5
$mon
3
$year
117
$wday
3
$yday
94
$isdst
1
$zone
'PDT'
$gmtoff
<NA>

In [19]:
```
paste("Number of seconds is", ltime$sec, "and hours are", ltime$hour)
```

'Number of seconds is 0 and hours are 12'

The `paste` function "pastes" strings together.

Parsing and Formating

Our dates and time objects are easily constructed from strings are formatted in a reasonable way. But often we need to parse exotic date and time formats. Or we may need to present them in exotic ways. R provides the following functions for this.

- `strptime` - parse a date and/or time string.
- `strftime` - format a string from a date or time object.

The parsing function `strptime` always returns a `POSIXlt`. This may be converted to either a `Date` or `POSIXct` through their respective `as` functions: `as.Date()` and `as.POSIXct`. The **conversion specification** used by the parse and format function is documented in the help for `strptime`.

In [20]:
```
strptime('06/13/2017 14:20', "%m/%d/%Y")
strptime('Oct 20, 2014 at 16:15', "%b %d, %Y at %H:%M")
```

```
[1] "2017-06-13 PDT"
```

```
[1] "2014-10-20 16:15:00 PDT"
```

Exercise Parse the following date/times with `strptime`.

1. `170628 3:36` - Assume military time.
2. `2016136` - This is just a date. The first four characters are the year; the last three are the number of days since January 1. Some mainframe systems still use this.
3. `July 4, 1976 at 15:30` - Remember the difference between long month and short month.
4. `Day 7 of January at 20:00 in the year 2016` - Hopefully you don't run into many of these.

Comparisons

The usual comparison operators apply to the date time classes.

In [21]:
```
ts <- as.POSIXlt(c("2017-03-01", "2017-04-01", "2017-05-01", "2017-06-01"))
ts > as.POSIXlt("2017-04-15")
```

FALSE FALSE TRUE TRUE

Time Differences

The **difftime** class supports arithmetic based on the difference between two times. A **difftime** can be created implicitly by the subtraction operator.

In [22]:
```
td1 <- as.POSIXlt("2017-04-15") - as.POSIXlt("2017-04-07")
td1
```

```
Time difference of 8 days
```

Or it can be created by a direct call to the `difftime` function with two dates.

In [23]:
```
td2 <- difftime("2017-04-15", "2017-04-07")
td2
```

```
Time difference of 8 days
```

Finally, it can be created by specifying the units directly to the **as.difftime** function.

In [24]:
```
td3 <- as.difftime(10, units="days")
td3
```

```
Time difference of 10 days
```

You can compare time differences.

In [25]:
```
td1 > td3
```

FALSE

And you can add a difference back to a date or time.

In [26]:
```
ts + td3
```

```
[1] "2017-03-11 PST" "2017-04-11 PDT" "2017-05-11 PDT" "2017-06-11 PDT"
```

Split (revisited)

In the last workshop we investigated several ways to create factor variables for the purpose of the *split* phase of the **split-apply-combine** paradigm. One important technique that was left out was the **cut** function. Its first three parametes are

1. a numeric vector to cut
2. a specfication for the cuts
3. labels for the cuts (optional)

The result is a factor vector with the same length as the first argument. The value of each entry is the cut to which the original entry is placed. A few examples should clear this up. We'll use the `InsectSprays` dataset on which to demonstrate some cutting techniques.

In [27]:
```
head(InsectSprays)
```

count	spray
10	A
7	A
20	A
14	A
14	A
12	A

We'll split the dataset based on the "quality" of the spray, which we presume to be proportional to the eradication count. We'll create **quality** factor variable with values of either `bad`, `ok`, or `good` depending on the eradication count in two ways.

1. `qualityA` - based on absolute values of the count
2. `qualityC` - based on quantiles (college students refer to this as "the curve".

For the absolute case, we simply divide the range of values into equal intervals. In this case, there are three such intervals: `bad`, `ok`, and `good`.

In [28]:
```
qualityA <- cut(InsectSprays$count, 3 )
table(qualityA)
```

```
qualityA
(-0.026,8.67]   (8.67,17.3]     (17.3,26]
           37            25            10
```

We can see that the intervals are about equal length (no curve). The interval names are informative, but somewhat awkward. We can assign friendlier names with the `labels` parameter.

```
In [29]: qualityA <- cut(InsectSprays$count, 3, labels=c('bad', 'ok', 'good') )
         table(qualityA)
```

```
qualityA
 bad   ok good 
  37   25   10 
```

Instead of specifying the number of breaks (in which case they are all of equal length), we can specify the actual breakpoints themselves. Since we're "grading on a curve", we'll assign

- `bad` - to the lower third
- `ok` - to the middle third
- `good` - to the upper third

We'll use the `quantile` function introduced in Workshop 1 to determine these break points.

```
In [30]: curveLevels <- quantile(InsectSprays$count, c(0, .33, .67, 1) )
         curveLevels
```

0%	0
33%	4.43
67%	13
100%	26

Then provide these break points to the `cut` function.

```
In [31]: qualityC <- cut(InsectSprays$count, curveLevels, labels=c('bad', 'ok', 'good') )
         table(qualityC)
```

```
qualityC
 bad   ok good 
  22   26   22 
```

We expect each level to have the same number of entries. This is only approximate due to the different ways quantiles can be computed. (Check the `quantile` help documentation; there are no fewer than **nine** algorithms from which to choose.) The default is usually fine and only deviates significantly when the sample size is small.

Now we have two factor variables, one absolute and one curved, that split the `InsectSprays` dataframe into "quality buckets." Let's see how the quality values were divided among the spray brands.

In [32]:
```
table(InsectSprays$spray, qualityA)
table(InsectSprays$spray, qualityC)
```

```
   qualityA
    bad ok good
  A   1  8    3
  B   1  8    3
  C  12  0    0
  D  11  1    0
  E  12  0    0
  F   0  8    4

   qualityC
    bad ok good
  A   0  5    7
  B   0  4    8
  C   9  1    0
  D   5  7    0
  E   8  4    0
  F   0  5    7
```

Cutting Dates and Times

Hopefully we haven't completely forgotten dates and times. It turns out we can cut these, too. Remember that we can add a `difftime` duration to a `POSIXlt` time instant to get a new instant.

In [33]:
```
as.POSIXlt("2017-03-31 12:00") + as.difftime(1, units="days")
```

```
[1] "2017-04-01 12:00:00 PDT"
```

Let's create a sequence of 100 consecutive days.

In [34]:
```
dtvec <- as.POSIXlt("2017-03-31 12:00") + as.difftime(seq(0, 99), units="days")
dtvec[1:5]
```

```
[1] "2017-03-31 12:00:00 PDT" "2017-04-01 12:00:00 PDT"
[3] "2017-04-02 12:00:00 PDT" "2017-04-03 12:00:00 PDT"
[5] "2017-04-04 12:00:00 PDT"
```

Like in the numeric case, we can break into equal intervals by specifying the number of breaks.

In [35]:
```
promptness <- cut(dtvec, 3, labels=c('early', 'ontime', 'late'))
table(promptness)
```

```
promptness
 early ontime   late 
    33     33     34 
```

Since the intervals were equal, it's no surprise that they are evenly distributed in this case.

We can generate break points based on the day of the week.

In [36]:
```
mondays <- cut(dtvec, breaks="week")
mondays[1:5]
```

```
2017-03-27   2017-03-27   2017-03-27   2017-04-03   2017-04-03
```

In this example, the times were evenly spaced. The power of the last cut above becomes more apparent when applied to uneven intervals. Some weeks might have many values, some might have few, you just want to sum by week. Your *split-apply-combine* technique would use this operation for the `split` component.

Aggregation

In the last workshop we introduced the *split-apply-combine* paradigm in detail by investigating each step in detail. As a quick review, let's recall the analysis we performed on the `InsectSprays` dataset.

In [37]:
```
head(InsectSprays)
```

count	spray
10	A
7	A
20	A
14	A
14	A
12	A

In [38]:
```
isl       <- split(InsectSprays, InsectSprays$spray)
isMeanLst <- lapply(isl, function(x) { mean(x$count) })
isMeanVec <- unlist(isMeanLst)
isMeanVec
```

A	14.5
B	15.3333333333333
C	2.08333333333333
D	4.91666666666667
E	3.5
F	16.6666666666667

The first line is the **split**, which was done based on the value of the `spray` column. This yielded an insect spray list (`isl`) where each element of the list was a subset of the original dataset with a particular `spray` value.

The next line was the **apply**, which applied to the `mean` function to the `count` column. It returns a new list (`isMeanLst`) that has the same number of elements as `isl`. The value of an element in `isMeanLst` is the average of the `count` column of the corresponding subset in `isl`.

The third line is the **combine**, which converts the list of numbers into a vector of numbers. The last two steps are so common that a function named **sapply** is provided to combine them. The **s** in `sapply` means "simplify". It's equivalent to `lapply` followed by `unlist`.

```
In [39]: isMeanVec <- sapply(isl, function(x) { mean(x$count) })
         isMeanVec
```

A	14.5
B	15.3333333333333
C	2.08333333333333
D	4.91666666666667
E	3.5
F	16.6666666666667

The **aggregate** function combines all three steps into a single call.

```
In [40]: aggregate(count ~ spray, data=InsectSprays, mean)
```

spray	count
A	14.500000
B	15.333333
C	2.083333
D	4.916667
E	3.500000
F	16.666667

Wow! That was easy. Let's break down what we just did.

The first parameter of `aggregate` is a formula. We saw formulas a few workshops ago when we studied the `xtabs` function. In general each function that uses a formula interprets it differently. In the case of `aggregate` we have the following.

- **LHS** - This is the column on which the aggegation function will operate. In the example above it was `count`. If multiple columns are specified, they are acted upon individually. To operate on all numeric columns, specify a dot on the LHS.
- **RHS** - This is a factor variable that this the basis for the aggregation. It's just like the RHS of the `xtabs` formula. If you specify multiple factor variables, the result is an interaction.

The second parameter is the name of the data frame. The final parameter is the name of the function to apply to the LHS of the formula.

Exercise: Apply some of these other functions:

1. `sum`
2. `sd`
3. `max`
4. `min`
5. `function(x) { max(x) - min(x) }`

Pivot Tables

Pivot tables are much easier to see than to describe. So let's just do one and you'll get the idea. We'll practice on the `ChickWeight` dataset.

In [41]:
```
cw <- ChickWeight
head(cw)
```

weight	Time	Chick	Diet
42	0	1	1
51	2	1	1
59	4	1	1
64	6	1	1
76	8	1	1
93	10	1	1

This data frame records a bunch of baby chicks divided into four groups according to their diet. Their weight was recorded at several points in time. To determine the affect of the diet, let's aggregate the weight of chicks within a group using the `mean` function rather than analyzing each chick individually.

In [42]:
```
cwag <- aggregate(weight ~ Time + Diet, data=cw, mean)
head(cwag, n=20)
```

Time	Diet	weight
0	1	41.40000
2	1	47.25000
4	1	56.47368
6	1	66.78947
8	1	79.68421
10	1	93.05263
12	1	108.52632
14	1	123.38889
16	1	144.64706
18	1	158.94118
20	1	170.41176
21	1	177.75000
0	2	40.70000
2	2	49.40000
4	2	59.80000
6	2	75.40000
8	2	91.70000
10	2	108.50000
12	2	131.30000
14	2	141.90000

For each combination of `Time` and `Diet` we average the weight for all chicks. The `cwag` data frame shows the weights over time for diet 1 and the beginning of weights of time for diet 2. This organization is awkward if we wish to compare diets. We have to scroll the table up and down to see comparable values in time for each of the diets. It would be better to have a colum for each diet so they appeared next to each other. We should *pivot the Diet column into a set of columns*.

For this operation we need to another library. There are many libraries out there for this kind of thing and we'll investigate some of them in future workshops. For this workshop we'll use the **reshape2** library. Note that it must be installed since it does not come with a base R installation. The command to install it is

```
install.packages('reshape2')
```

Once its installed, the library is loaded via the `library` command.

In [43]:
```
library(reshape2)
```

The function in `reshape2` that performs a pivot is **dcast**. The `d` in `dcast` indicates the result is a data frame (the alternative is `acast` for an array or vector).

In [44]:
```
pcwag <- dcast(cwag, Time ~ Diet, value.var='weight')
pcwag
```

Time	1	2	3	4
0	41.40000	40.7	40.8	41.0000
2	47.25000	49.4	50.4	51.8000
4	56.47368	59.8	62.2	64.5000
6	66.78947	75.4	77.9	83.9000
8	79.68421	91.7	98.4	105.6000
10	93.05263	108.5	117.1	126.0000
12	108.52632	131.3	144.4	151.4000
14	123.38889	141.9	164.5	161.8000
16	144.64706	164.7	197.4	182.0000
18	158.94118	187.7	233.1	202.9000
20	170.41176	205.6	258.9	233.8889
21	177.75000	214.7	270.3	238.5556

The `dcast` function also employs a formula for one of its parameters.

- **LHS** - the variables that will identify a row. In the example above each row is identified by the value of `Time`.
- **RHS** - the column to be pivoted. In the example above, we pivot on the values of the `Diet` column.

Each value of the column specified on the RHS becomes a column in the resulting data frame. What determines the values in the new columns? The last parameter to `dcast` provides the value variable.

To clarify the meaning of the new columns, let's rename them.

In [45]:
```
colnames(pcwag) <- c("Time", "diet1", "diet2", "diet3", "diet4")
pcwag
```

Time	diet1	diet2	diet3	diet4
0	41.40000	40.7	40.8	41.0000
2	47.25000	49.4	50.4	51.8000
4	56.47368	59.8	62.2	64.5000
6	66.78947	75.4	77.9	83.9000
8	79.68421	91.7	98.4	105.6000
10	93.05263	108.5	117.1	126.0000
12	108.52632	131.3	144.4	151.4000
14	123.38889	141.9	164.5	161.8000
16	144.64706	164.7	197.4	182.0000
18	158.94118	187.7	233.1	202.9000
20	170.41176	205.6	258.9	233.8889
21	177.75000	214.7	270.3	238.5556

Now it is much easier to compare diets for each time at which the chicks were weighed.

The reverse of the pivot (or `dcast`) is the **melt** function. That is, we melt all the columns into a single column like we had before.

```
In [46]: mcwag <- melt(pcwag, id.vars='Time', variable.name='Diet', value.name='weight')
         head(mcwag, n=20)
```

Time	Diet	weight
0	diet1	41.40000
2	diet1	47.25000
4	diet1	56.47368
6	diet1	66.78947
8	diet1	79.68421
10	diet1	93.05263
12	diet1	108.52632
14	diet1	123.38889
16	diet1	144.64706
18	diet1	158.94118
20	diet1	170.41176
21	diet1	177.75000
0	diet2	40.70000
2	diet2	49.40000
4	diet2	59.80000
6	diet2	75.40000
8	diet2	91.70000
10	diet2	108.50000
12	diet2	131.30000
14	diet2	141.90000

Notice it's the same form as before. The only difference is that the `Diet` column has values of `diet1`, `diet2`, `diet3`, and `diet4` instead of `1`, `2`, `3`, and `4` because we changed the column names before we melted the data frame. This is probably better than the original values because it makes clear these values should be considered categorical instead of quantitative.

Let's review some of the `melt` parameters.

- `id.vars` - the columns that are **not** going to be melted.
- `variable.name` - the column that will hold the names of the variables that **will** be melted.
- `value.name` - the name of the column that will hold the value of the variables that will be melted.

Pivoting is a core skill of any data scientist. There are many tools available for it. It's most important to understand the concept.

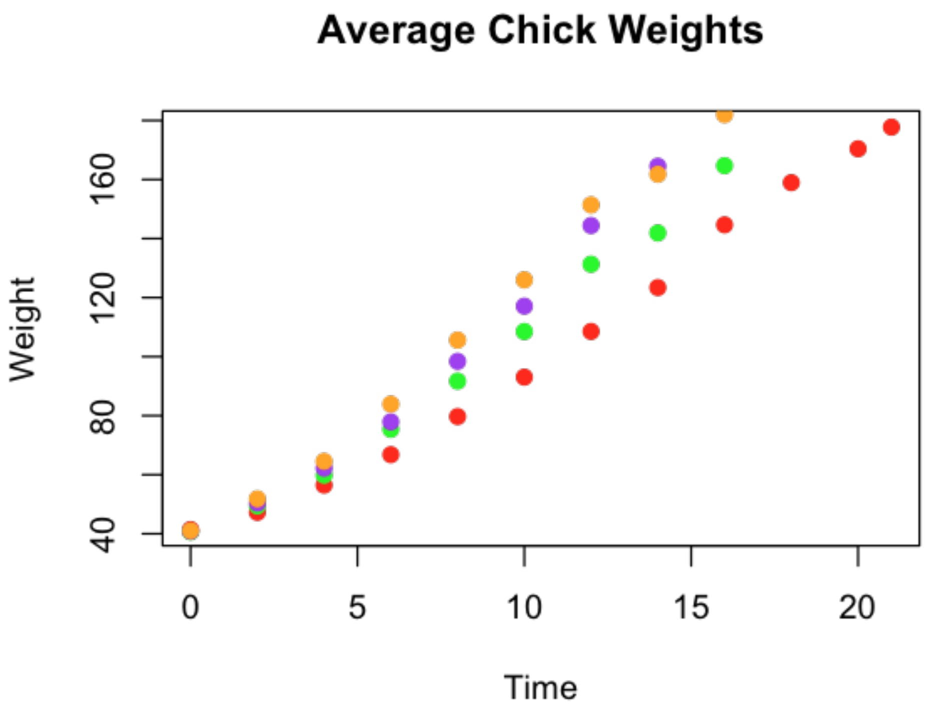
Two Variable Plots

We addressed single variable plotting over the last few workshops. Let's apply this aggregated dataset to plot two variables. The function for plotting two variables is `plot`.

Note: The `options` command is there to format this Jupyter notebook. It isn't necessary at the R console or RStudio.

In [47]:
```
options(repr.plot.width=5, repr.plot.height=4)  # Used for Jupyter notebooks.
```

In [48]:
```
plot(pcwag$Time,   pcwag$diet1, pch=19, col='red', xlab="Time", ylab="Weight")
points(pcwag$Time, pcwag$diet2, pch=19, col='green')
points(pcwag$Time, pcwag$diet3, pch=19, col='purple')
points(pcwag$Time, pcwag$diet4, pch=19, col='orange')
title(main="Average Chick Weights")
```

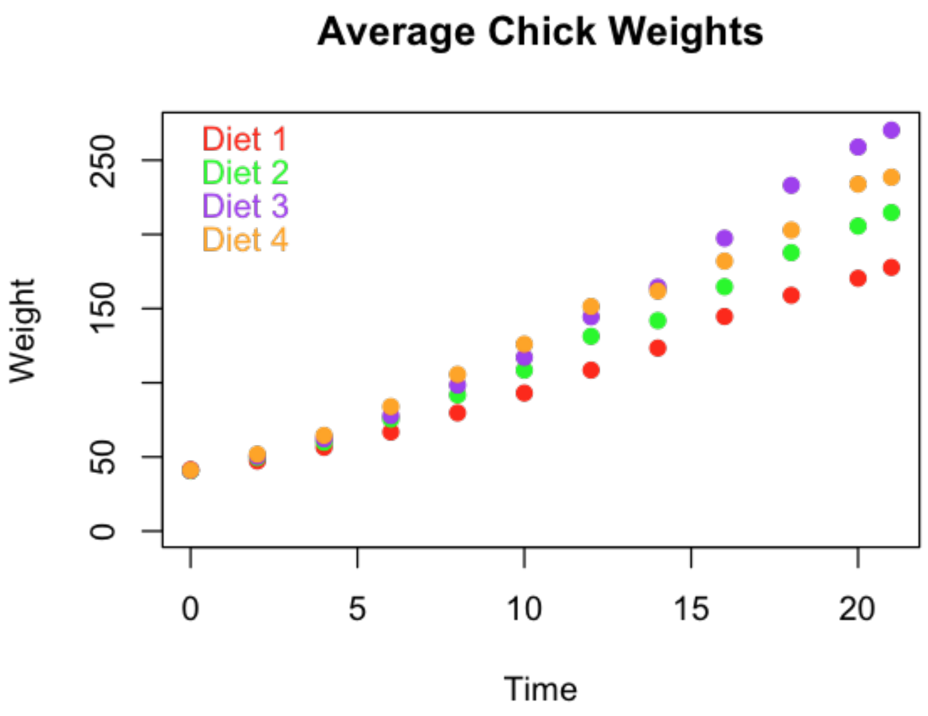


Let's make a few observations.

- The `plot` function creates a new plot window each time it is called. If you want to plot multiple sets, you have to call something else that does't start a new plot window. In this case, since we're making points, we call the `points` function.
- We changed the point character from its default (which is a hollow circle) to a solid circle (`pch=19`).
- Note that the y-axis was optimized for `diet1`. But the other diets have larger weights that run off the top of the graph. We can fix this by determining the range before hand and setting it with the `xlim` parametr in the `plot` command.
- There is no legend indicating which color maps to which diet.

Let's remedy the last two issues.

```
In [49]: max_weight <- max(pcwag)
         plot(pcwag$Time,   pcwag$diet1, pch=19, col='red',
              xlab="Time", ylab="Weight", ylim=c(0, max_weight + 1))
         points(pcwag$Time, pcwag$diet2, pch=19, col='green')
         points(pcwag$Time, pcwag$diet3, pch=19, col='purple')
         points(pcwag$Time, pcwag$diet4, pch=19, col='orange')
         title(main="Average Chick Weights")
         legend('topleft', c('Diet 1', 'Diet 2', 'Diet 3', 'Diet 4'),
                  text.col=c('red', 'green', 'purple', 'orange'),
                  bty='n', cex=1, y.intersp=2)
```



Exercise Now it's your turn. Make the same plot with lines instead of points. Are the the differences.

- The plot command defaults to points. You override this default with the `type` parameter. For a line, you want `type='l'` where the value is the letter `l` for "line". This parameter should replace the `pch=19` parameter. You don't a `pch` parameter for lines.
- Instead of the `points` command, use the `lines` command. The `line` command doesn't need a `pch` parameter.