

Module 8: Programming

BIOSTAT 213: Introduction to Computing in the R Software Environment

Monday, November 18, 2019

Dropping and renaming variables

Dropping variables

Module 8:
Programming

BIOSTAT 213:
Introduction to
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Dropping and
renaming variables

Writing functions

`if()`

The apply
functions

`tapply()`

`apply()`

`sapply()`

Beyond this course

Exercise

- ▶ frequently asked question: how do you **drop a variable** in R?

Dropping variables

- ▶ one way to drop variables in R is to use **indexing** and **object assignment**:

```
> ii<-read.csv('nhanes.csv')
> dim(ii)
[1] 4209 691
> ii<-ii[,names(ii)!='highlidl']
> dim(ii)
[1] 4209 690
```

Dropping and
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Dropping variables

► or, using `is.element()`:

```
> ii<-read.csv('nhanes.csv')
> dim(ii)
[1] 4209  691
> ii<-ii[,!is.element(names(ii),c('hdlcat','highhdl','asthma'))]
> dim(ii)
[1] 4209  688
```

Renaming variables

- ▶ how do you rename a variable in R?

Renaming variables

- ▶ one way to rename variables in R is to use [indexing](#) and [object assignment](#):

```
> table(ii$va)
```

No Vigorous activity	
2314	1893

```
> names(ii)[names(ii)=='va']<-'vigorous.activity'
```

```
> table(ii$vigorous.activity)
```

No Vigorous activity	
2314	1893

Writing functions

Functions

- ▶ we've seen many examples over the last few weeks of **built-in R functions**:

```
> mean(ii$bpxdi1, na.rm=TRUE)
[1] 70.47576
> round(pi, 4)
[1] 3.1416
```

- ▶ note that often times, **functions output some value**

Writing functions

- ▶ it is possible to write your own functions

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Writing functions

```
nothing<-function(){  
  # this function does nothing  
}
```

- ▶ **function**: a function, indicating you are defining a function
- ▶ **()**: a space for including **arguments** to your functions
- ▶ **{ }**: a space for including the function's **R code**
- ▶ **<-**: object assignment, to save your function
- ▶ **nothing**: an arbitrary name for the new function

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Writing functions

- ▶ the **last line of the function** should be the value you want the function to return:

```
something<-function(x,y){  
  x*y  
  x/y  
  x-y  
  x+y  
}
```

```
> something(3,4)  
[1] 7
```

Example: absolute values

```
absolute.value<-function(x){  
  ifelse(x<0,x*-1,x)  
}
```

```
> absolute.value(-4:6)  
[1] 4 3 2 1 0 1 2 3 4 5 6  
> abs(-4:6)  
[1] 4 3 2 1 0 1 2 3 4 5 6
```

When to write a function

- ▶ it may be tempting to *always* write functions
- ▶ but, functions may not always be necessary!
- ▶ in general, it is helpful to write a function if you plan on using it over and over again, using different inputs

Example: $y = ax^2 + bx + c$

```
quadratic<-function(x,a,b,c){  
  a*x^2+b*x+c  
}
```

```
> quadratic(3,2,-3,5)  
[1] 14  
> quadratic(0,5,5,100)  
[1] 100
```

Example: fancy univariate tables

```
ut<-function(xx){  
  tt<-table(xx)  
  data.frame(  
    Group=names(tt),  
    Count=as.numeric(tt),  
    Percent=as.numeric(prop.table(tt))*100  
  )  
}
```

Example: fancy univariate tables

```
> ut(ii$hs)
```

	Group	Count	Percent
1	History of smoking	1687	40.11891
2	No	2518	59.88109

```
> ut(ii$military)
```

	Group	Count	Percent
1	History of military service	275	6.533618
2	No	3934	93.466382

Default argument values

- ▶ to include **default argument values**, use the equal sign (=) when defining the function:

```
> exponent<-function(x,power=2){x^power}  
> exponent(3,2)  
[1] 9  
> exponent(3,3)  
[1] 27  
> exponent(3)  
[1] 9
```

Example: dichotomous factors

```
cc<-function(xx,level1,level2='No',codings=1:2){  
  xx<-factor(xx,levels=codings)  
  levels(xx)<-c(level1,level2)  
  xx  
}
```

Example: dichotomous factors

```
> table(ii$smq020,useNA='always')

    1     2     7     9 <NA>
1687 2518     1     3     0

> ii$hs.new<-cc(ii$smq020,'Smoking')
> table(ii$hs.new,useNA='always')

Smoking      No      <NA>
  1687    2518        4
```

Isolation of functions

- ▶ object assignment within functions will not affect the rest of the R workspace:

```
> x<-3
> change.x<-function(newx){x<-newx}
> change.x(1000)
> x
[1] 3
```

- ▶ R isolates the function, to prevent inadvertent modification of objects in the workspace

Isolation of functions

- ▶ if you must modify something outside of the function, use `<<-`:

```
> x<-3
> change.x<-function(newx){x<<-newx}
> change.x(1000)
> x
[1] 1000
```

Isolation of functions

- ▶ I suggest using `<-` sparingly, as you probably need it less often than you may think
- ▶ note, for example, that you can store the output of R functions:

```
> x<-3
> change.x<-function(y){y}
> change.x(1000)
[1] 1000
> x
[1] 3
> x<-change.x(1000)
> x
[1] 1000
```

if()

if()

- ▶ the `if()` function provides a way to conditionally evaluate code

if()

```
> x<--3  
> if(x<0){x*-1}  
[1] 3
```

- ▶ the argument to `if()` must be a **single logical value**
- ▶ the code after `if()` is evaluated **if and only if** the value inside `if()` is TRUE
- ▶ the **curly brackets** are not strictly necessary but are helpful if you have several lines of code
- ▶ the feature is broadly known as **control flow**
- ▶ to access the built-in help file, type `help(Control)` or `?Control`

if()

```
> x<--3
> if(x<0){x*-1}
[1] 3
> x
[1] -3
```

- ▶ here, x did not change because we did not include **object assignment**

if()

```
> x<--3
> if(x<0){x<-x*-1}
> x
[1] 3
```

- ▶ here, x changed because we included **object assignment**

Example: the season

```
> Sys.Date()
[1] "2019-11-18"
> today<-Sys.Date()
> if((today>='2019-06-21')&(today<='2019-09-22')){'Summer'}
> if((today>='2019-09-23')&(today<='2019-12-20')){'Autumn'}
[1] "Autumn"
> if((today>='2019-12-20')&(today<='2020-03-19')){'Winter'}
```

else

```
> x<-100  
> if(x<0){sign<-'positive'} else {sign<-'negative'}  
> sign  
[1] "negative"
```

- ▶ the else code will be evaluated **if and only if** the value inside `if()` is FALSE
- ▶ else must appear on **the same line** as the TRUE expression's closing bracket

else

```
x<-100
if(x<0){
  sign<-'positive'
} else {
  sign<-'negative'
}
```

```
> sign
[1] "negative"
```

if() versus Stata's if

- ▶ if() is not at all analogous to Stata's if
- ▶ Stata's if is more analogous to indexing
- ▶ for example, from Stata's help file on if:

```
> list make mpg if mpg>25
```

- ▶ this is analogous to the following in R:

```
> mydata[mydata$mpg>25, c('make', 'mpg')]
```

if() versus Stata's if

- ▶ Stata's if allows for data manipulation
- ▶ in comparison, my recommendation is that you view R's if() as a way to implement decision trees
- ▶ there are other features in R that are more useful than if() for data manipulation, which we've discussed

Example: hypothesis testing

```
two.sample.test<-function(y,x,non.parametric=FALSE){  
  if(!non.parametric){  
    t.test(y~x)  
  } else {  
    wilcox.test(y~x)  
  }  
}
```

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Example: hypothesis testing

```
> two.sample.test(y=ii$bpxdi1,x=ii$gender)
```

Welch Two Sample t-test

data: y by x

t = -7.6465, df = 3958.9, p-value = 2.576e-14

alternative hypothesis: true difference in means is not equal to 0

95 percent confidence interval:

-3.698357 -2.188874

sample estimates:

mean in group Female	mean in group Male
69.03505	71.97867

Example: hypothesis testing

```
> two.sample.test(y=ii$bpxdi1,x=ii$gender,non.parametric=TRUE)
```

Wilcoxon rank sum test with continuity correction

data: y by x

W = 1719260, p-value < 2.2e-16

alternative hypothesis: true location shift is not equal to 0

The apply functions

`tapply()`

The apply functions

- ▶ the apply functions provide a way to repeatedly use (*apply*) functions
- ▶ these include:
 - ▶ `tapply()` to apply functions to groups (useful for stratified analysis)
 - ▶ `apply()` to apply functions to rows or columns of data frames
 - ▶ `sapply()` and `lapply()` to apply functions to elements in vectors

tapply()

- ▶ `tapply()` applies functions to groups
- ▶ it is very useful for **stratified analysis**

Example: stratified means

- ▶ suppose we want to find the mean body mass index for each gender
- ▶ we can repeatedly apply the `mean()` function:

```
> mean(ii$bmx bmi[ii$gender=='Female'])  
[1] 30.24384  
> mean(ii$bmx bmi[ii$gender=='Male'])  
[1] 29.01464
```

Example: stratified means

- ▶ a more efficient solution is to use `tapply()`:

```
> tapply(X=ii$bmxbmi, INDEX=ii$gender, FUN=mean)
  Female      Male 
30.24384 29.01464
```

- ▶ `X`: the data of interest
- ▶ `INDEX`: the stratifying variable
- ▶ `FUN`: the function to apply

Example: stratified means

► without argument names:

```
> tapply(ii$bmxbmi, ii$gender, mean)
  Female      Male 
30.24384 29.01464
```

Example: stratified means

- ▶ mean systolic blood pressure, by gender:

```
> mean(ii$bpxsy1[ii$gender=='Female'])  
[1] NA  
> mean(ii$bpxsy1[ii$gender=='Male'])  
[1] NA
```

- ▶ here, we get NA because there are missing values in bpxsy1

Example: stratified means

- ▶ to remove the missing values, we can add the `na.rm` argument:

```
> mean(ii$bpxsy1[ii$gender=='Female'],na.rm=TRUE)
[1] 120.4031
> mean(ii$bpxsy1[ii$gender=='Male'],na.rm=TRUE)
[1] 124.9325
```

Example: stratified means

- ▶ we can add pass the `na.rm` argument on to `tapply()`:

```
> tapply(ii$bpxsy1, ii$gender, mean, na.rm=TRUE)
  Female      Male 
120.4031 124.9325
```

- ▶ to emphasize: `na.rm` is not an argument to `tapply()`
- ▶ rather, it is an argument to `mean()`

Example: stratified means

- ▶ mean systolic blood pressure, by BMI category:

```
> tapply(ii$bpxsy1, ii$bmicat, mean, na.rm=TRUE)
```

	Overweight	Underweight or normal weight
	122.9266	117.7426
Class I obesity		Class II obesity
	124.2016	126.1900
Class III obesity		
	129.1705	

Example: stratified means

► equivalently, the long way:

```
> mean(ii$bpxsy1[ii$bmecat=='Underweight or normal weight'],  
+       na.rm=TRUE)  
[1] 117.7426  
> mean(ii$bpxsy1[ii$bmecat=='Overweight'],na.rm=TRUE)  
[1] 122.9266  
> mean(ii$bpxsy1[ii$bmecat=='Class I obesity'],na.rm=TRUE)  
[1] 124.2016  
> mean(ii$bpxsy1[ii$bmecat=='Class II obesity'],na.rm=TRUE)  
[1] 126.19  
> mean(ii$bpxsy1[ii$bmecat=='Class III obesity'],na.rm=TRUE)  
[1] 129.1705
```

Example: stratified percentiles

- ▶ 80th percentile of systolic blood pressure, *by gender*:

```
> tapply(ii$bpxsy1, ii$gender, quantile, na.rm=TRUE, probs=0.8)
Female      Male
    132      136
```

- ▶ as with previous examples, note that `na.rm` and `probs` are not actually arguments to `tapply()`
- ▶ rather, they are arguments to `quantile()`, which we've passed on to `tapply()`!

`apply()`

apply()

- ▶ `apply()` applies functions to rows or columns of data frames

Example: row means

- diastolic blood pressure in NHANES:

```
> head(ii[,c('bpxdi1','bpxdi2','bpxdi3','bpxdi4')])
  bpxdi1 bpxdi2 bpxdi3 bpxdi4
1      70     64     62     NA
2      88     88     82     NA
3      72     68     70     NA
4      70     54     56     NA
5      70     74     74     NA
6      70     70     72     NA
```

Example: row means

- ▶ how could we find **each individual's mean measurement**?
- ▶ we might try something like this:

```
> ii$diastolic.mean<-with(ii,(bpxdi1+bpxdi2+bpxdi3+bpxdi4)/4)
```

- ▶ but **this is not quite right!**
- ▶ most individuals are missing at least 1 measurement, and we should be adjusting the denominator as needed

Example: row means

- ▶ the following is better, conceptually:

```
> row1<-ii[1,c('bpxdi1','bpxdi2','bpxdi3','bpxdi4')]
> row1<-as.numeric(row1)
> mean(row1,na.rm=TRUE)
[1] 65.33333
```

- ▶ here, the denominator is appropriate, because we've made use of built-in function `mean()` and its `na.rm` argument
- ▶ but, we've only found the mean for the first individual!
- ▶ we need to apply the `mean()` function to each row

Example: row means

- ▶ to `apply` the `mean()` function to each row, we can use `apply()`:

```
ii$diastolic.mean<-apply(  
  X=ii[,c('bpxdi1','bpxdi2','bpxdi3','bpxdi4')],  
  MARGIN=1,  
  FUN=mean,na.rm=TRUE  
)
```

- ▶ `X`: the data frame
- ▶ `MARGIN`: indicates whether to apply the function to the rows or the columns
- ▶ `FUN`: the function to apply

Example: row means

► without argument names:

```
ii$diastolic.mean<-apply(  
  ii[,c('bpxdi1','bpxdi2','bpxdi3','bpxdi4')],1,  
  mean,na.rm=TRUE  
)
```

Example: row means

► equivalently, using `rowMeans()`:

```
ii$diastolic.mean.2<-rowMeans(  
  ii[,c('bpxdi1','bpxdi2','bpxdi3','bpxdi4')],  
  na.rm=TRUE  
)
```

apply()-like functions

- ▶ functions that can be thought of as special cases of `apply()`:
 - ▶ `rowMeans()` for row means, conceptually equivalent to using `apply()` with `MARGIN=1` and `FUN=mean`
 - ▶ `colMeans()` for column means, conceptually equivalent to using `apply()` with `MARGIN=2` and `FUN=mean`
 - ▶ `rowSums()` for row sums, conceptually equivalent to using `apply()` with `MARGIN=1` and `FUN=sum`
 - ▶ `colSums()` for column sums, conceptually equivalent to using `apply()` with `MARGIN=2` and `FUN=sum`
- ▶ `apply()` is very useful nevertheless!

Example: Biostat 213 grades

- consider the following [hypothetical homework scores](#) for this course:

```
> grades
  hw1 hw2 hw3 hw4
1  92  94  89  91
2  90  94  88  90
3  87  96  89  91
4  92  94  86  92
5  93  95  86  91
```

Example: Biostat 213 grades

- ▶ how can I implement the course's homework policy?
- ▶ I can define a function for each student's grade, and apply that function to each student:

```
> drop.lowest<-function(grades){mean(sort(grades)[-1])}  
> apply(grades,1,drop.lowest)  
[1] 92.33333 91.33333 92.00000 92.66667 93.00000
```

Example: grades

► equivalently, defining the function within `apply()`:

```
> apply(grades, 1, function(grades){mean(sort(grades)[-1])})  
[1] 92.33333 91.33333 92.00000 92.66667 93.00000
```

`sapply()`

sapply()

- ▶ `sapply()` applies functions to elements in vectors

Example: square roots

```
> sapply(X=1:4,FUN=sqrt)
[1] 1.000000 1.414214 1.732051 2.000000
> sqrt(1:4)
[1] 1.000000 1.414214 1.732051 2.000000
```

- ▶ **X**: the vector
- ▶ **FUN**: the function to apply
- ▶ `sapply()` was not necessary in this example, as shown in the last line

Example: object types

- ▶ the **object type** of each of the first 10 columns of the NHANES data:

```
> sapply(X=1:10,FUN=function(ee){class(ii[,ee])})  
[1] "integer" "integer" "integer" "integer" "integer" "logical"  
[7] "integer" "integer" "integer" "integer"
```

- ▶ you could, in theory, do this with `apply()`, but it turns out that this does not work

Example: moving averages

- ▶ the Kevin Love data:

```
> ll[1:4,1:11]
  season age  tm  lg pos  g  gs  mp  fg  fga  fgp
1 2008-09  20 MIN NBA   C 81 37 25.3 3.9  8.5 0.459
2 2009-10  21 MIN NBA  PF 60 22 28.6 4.9 10.8 0.450
3 2010-11  22 MIN NBA  PF 73 73 35.8 6.6 14.1 0.470
4 2011-12  23 MIN NBA  PF 55 55 39.0 8.6 19.3 0.448
```

- ▶ suppose we want to examine a 3-year moving average of Kevin Love's field goal percent (fgp)

Example: moving averages

- ▶ first, we define a function for the moving average:

```
> ma3<-function(year,y){mean(c(y[year],y[year-1],y[year-2]))}
```

- ▶ then, we repeatedly apply the function, beginning with the 3rd year:

```
> sapply(3:nrow(ll),ma3,y=ll$fgp)
[1] 0.4596667 0.4560000 0.4233333 0.4190000 0.4143333 0.4366667
[7] 0.4266667 0.4346667 0.3996667
```

Example: moving averages

- ▶ 3-year moving averages of Love's free-throw percent:

```
> sapply(3:nrow(l1),ma3,y=l1$ftp)
[1] 0.8180000 0.8296667 0.7926667 0.7830000 0.7763333 0.8156667
[7] 0.8323333 0.8576667 0.8600000
```

Beyond this course

Other object types

- ▶ lists
- ▶ matrices and arrays

Regular expressions

- ▶ regular expressions for advanced character manipulation: `grep()` and `gsub()`
- ▶ you may consider *Handling Strings with R*

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for() loops

- ▶ `for()` loops for iteratively running code

dplyr and tidyr

- ▶ the **dplyr** package for data manipulation
- ▶ the **tidyr** package for reshaping data

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Statistical/epidemiological analysis

- ▶ the `epitools` package for measures of association
- ▶ `glm()` for `generalized linear models` (including logistic regression)
- ▶ the `survival` package for survival analysis (including Kaplan-Meier estimation and Cox proportional hazards models)
- ▶ the `lmer` package for mixed models
- ▶ the `geepack` package for generalized estimating equations
- ▶ the `survey` package for analysis of surveys
- ▶ the `rmeta` package for meta-analysis

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Probability distributions

- ▶ various built-in functions exist for **probability distributions**
- ▶ for a list, see `help(Distributions)`
- ▶ for example, for normal distributions:
 - ▶ `rnorm()` for generating random numbers from normal distributions (useful for simulations or generating fake data)
 - ▶ `qnorm()` for finding z-scores corresponding to areas under the curve
 - ▶ `pnorm()` for finding areas under the curve

Probability distributions

- ▶ for example, for the z-score corresponding to a lower-tail area under the curve of 0.975:

```
> qnorm(0.975)
[1] 1.959964
```

Simulations

- ▶ for simulations, be sure to use `set.seed()`
- ▶ you may also consider using packages that take advantage of parallel computing, such as `doParallel` and `doRNG`

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Exercise

You may work in groups of 2–3. Use `nhanes.csv` for all of the following problems.

1. Use `tapply()` to find the median systolic blood pressure (`bpxsy1`) in each `bmicat` group. Preferably, first re-order the levels of `bmicat` so they are in scientific order.
2. Use one of the `apply` functions to find the maximum systolic blood pressure among the 4 possible measurements (`bpxsy1`, `bpxsy2`, `bpxsy3`, and `bpxsy4`) for the first 10 individuals in the data. You should obtain 10 values (each represents the maximum measurement for a unique individual). Hint: you may want to include indexing.

More on the next slide...

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Exercise

3. Write a function that implements the quadratic formula:

$$x = \frac{-b \pm \sqrt{b^2 - 4ac}}{2a}$$

The symbol $\pm$ means plus or minus. For example, 2 ± 3 means $2 - 3$ and $2 + 3$.

The function should accept 3 arguments and output 1 value.

Check your function with a few values of a , b , and c .

More on the next slide...

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4. Use `tapply()` to find the median systolic blood pressure (`bpxsy1`) in each `bpcat` group. Preferably, first re-order the levels of `bpcat` so they are in scientific order. Note that `bpcat` depends on `bpxsy1` (as well as `bpxdi1`) so you should notice a pattern.
5. Use one of the apply functions to output the number of missing values in each variable.

More on the next slide...

Exercise

6. The `format()` function can be used to format dates. For example:

```
> format(Sys.Date(), '%Y-%m-%d')  
[1] "2019-11-18"
```

Write a function that will output a formatted version of `Sys.Date()` (a function that outputs the current date). The function should accept an argument that indicates whether the date should be outputted in a month-day-year format (as in the United States) or a day-month-year format (the convention in most other places). You might consider the [list of codes](#) shared in Module 7. Here's an example function:

```
> today()  
[1] "11/18/2019"  
> today(us=FALSE)  
[1] "18 November 2019"
```