

# BIOS 621/821 Session 1

Levi Waldron

# Welcome and outline - session 1

- ▶ syllabus review
- ▶ software usage
- ▶ in-person / online course format
- ▶ multiple regression
  - ▶ continuous & categorical predictors
  - ▶ interactions
  - ▶ ANOVA tables
  - ▶ Model formulae
- ▶ introduction to R

## A bit about me - research interests

- ▶ High-dimensional statistics (more variables than observations)
- ▶ Predictive modeling
- ▶ Cancer genomics
- ▶ Metagenomic profiling of the human microbiome
- ▶ HIV treatment effectiveness
- ▶ <http://www.waldronlab.org> —  
<http://waldronlab.github.io>

## Some of my activities that may interest you

- ▶ “Statistical Learning” book club and data competitions:
  - ▶ [https://groups.google.com/forum/#!forum/stat\\_learning](https://groups.google.com/forum/#!forum/stat_learning)
- ▶ Research opportunities available

# Multiple Linear Regression Model (sec. 4.2)

Systematic part of model:

$$E[y|x] = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \dots + \beta_p x_p$$

- ▶  $E[y|x]$  is the expected value of  $y$  given  $x$
- ▶  $y$  is the outcome, response, or dependent variable
- ▶  $x$  is the vector of predictors / independent variables
- ▶  $x_p$  are the individual predictors or independent variables
- ▶  $\beta_p$  are the regression coefficients

# Multiple Linear Regression Model (cont'd)

Random part of model:

$$y_i = E[y_i|x_i] + \epsilon_i$$

$$y_i = \beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + \dots + \beta_p x_{pi} + \epsilon_i$$

- ▶  $x_{ji}$  is the value of predictor  $x_j$  for observation  $i$

Assumption:  $\epsilon_i \stackrel{iid}{\sim} N(0, \sigma_\epsilon^2)$

- ▶ Normal distribution
- ▶ Mean zero at every value of predictors
- ▶ Constant variance at every value of predictors
- ▶ Values that are statistically independent

# Continuous predictors

- ▶ **Coding:** as-is, or may be scaled to unit variance (which results in *adjusted* regression coefficients)
- ▶ **Interpretation for linear regression:** An increase of one unit of the predictor results in this much difference in the continuous outcome variable
  - ▶ *additive model*

## Binary predictors (2 levels)

- ▶ **Coding:** indicator or dummy variable (0-1 coding)
- ▶ **Interpretation for linear regression:** the increase or decrease in average outcome levels in the group coded “1”, compared to the reference category (“0”)
- ▶ e.g.  $E(y|x) = \beta_0 + \beta_1 x$
- ▶ where  $x = \{ 1 \text{ if male, } 0 \text{ if female } \}$



# Multilevel Categorical Predictors (Ordinal or Nominal)

- ▶ **Coding:**  $K - 1$  dummy variables for  $K$ -level categorical variables \*
- ▶ **Interpretation for linear regression:** as above, the comparisons are done with respect to the reference category
- ▶ Testing significance of multilevel categorical predictor: partial F-test, a.k.a. nested ANOVA

\* STATA and R code dummy variables automatically, behind-the-scenes

# Inference from multiple linear regression

- ▶ Coefficients are t-distributed when assumptions are correct
- ▶ Variance in the estimates of each coefficient can be calculated
- ▶ The t-test of the null hypothesis  $H_0 : \beta_1 = 0$  and from confidence intervals tests whether  $x_1$  predicts  $y$ , *holding other predictors constant*
  - ▶ often used in causal inference to control for confounding: see section 4.4

# Interaction (effect modification)

Interaction is modeled as the product of two covariates:

$$E[y|x] = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_{12} x_1 * x_2$$

# Interaction (effect modification)

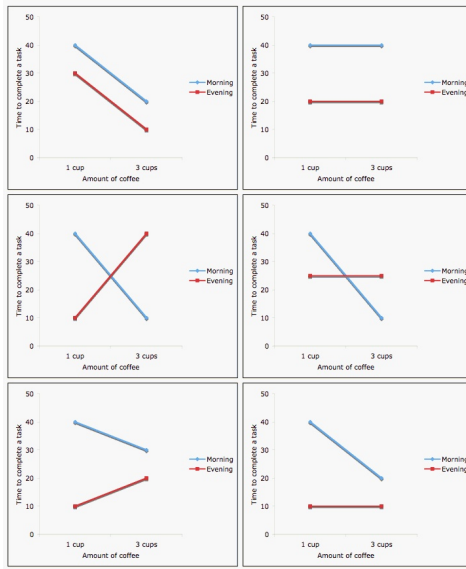


Figure 1: Interaction between coffee and time of day on performance

## ANOVA table

Source of Variation	Sum Sq	Deg Fr	Mean Sq	F
Model	MSS	$k$	$MSS/k$	$(MSS/k)/MSE$
Residual	RSS	$n-(k-1)$	$RSS/(n-k-1)$	
Total	TSS	$n-1$		

- ▶  $k$  = Model degrees of freedom = coefficients - 1
- ▶  $n$  = Number of observations
- ▶ **F** is F-distributed with  $k$  numerator and  $n - (k - 1)$  denominator degrees of freedom

# Regression in R: model formulae

## Model formulae tutorial

- ▶ regression functions in R such as `aov()`, `lm()`, `glm()`, and `coxph()` use a “model formula” interface.
- ▶ The formula determines the model that will be built (and tested) by the R procedure. The basic format is:

*response variable ~ explanatory variables*

- ▶ The tilde means “is modeled by” or “is modeled as a function of.”

## Model formulae (cont'd)

Model formula for simple linear regression:

$$y \sim x$$

- ▶ where “x” is the explanatory (independent) variable
- ▶ “y” is the response (dependent) variable.

## Model formulae (cont'd)

Additional explanatory variables would be added as follows:

$$y \sim x + z$$

Note that “+” does not have its usual meaning, which would be achieved by:

$$y \sim l(x + z)$$



# Types of standard linear models

`lm( y ~ u + v )`

u and v factors: **ANOVA**

u and v numeric: **multiple regression**

one factor, one numeric: **ANCOVA**

## Model formulae (cont'd)

symbol	example	meaning
+	+ x	include this variable
-	- x	delete this variable
:	x : z	include the interaction
	x * z	include these variables and their interactions
/	x / z	nesting: include z nested within x
	x   z	conditioning: include x given z
^	(u + v + w)^3	include these variables and all interactions up to three way
1	-1	intercept: delete the intercept

## Model formulae (cont'd)

How to interpret the following model formulae?

$$y \sim u + v + w + u:v + u:w + v:w$$

$$y \sim u * v * w - u:v:w$$

$$y \sim (u + v + w)^2$$

# Model formulae (cont'd)

How to interpret the following model formulae?

$$y \sim u + v + w + u:v + u:w + v:w + u:v:w$$

$$y \sim u * v * w$$

$$y \sim (u + v + w)^3$$

# Introduction to the R language

- ▶ `5 + 2` #addition
- ▶ `5 - 2` #subtraction
- ▶ `5 * 2` #multiplication
- ▶ `5 / 2` #division
- ▶ `5 ^ 2` #exponentiation
- ▶ `5 ** 2` #exponentiation
- ▶ `5 %% 2` #modulus (a.k.a. remainder)

# Logic

- ▶ `5 < x` #less than
- ▶ `5 <= x` #less than or equal to
- ▶ `5 > x` #greater than
- ▶ `5 >= x` #greater than or equal to
- ▶ `5 == x` #equal to
- ▶ `5 != x` #not equal to
- ▶ `!x` #logical NOT
- ▶ `True || False` #stepwise logical OR
- ▶ `True && False` #stepwise logical AND

# Storing Data: The Rules

- ▶ Letters, numbers, dots, underscores
- ▶ Must start with a letter or a dot not followed by a number
- ▶ No reserve words, No spaces

```
x <- 5  
x * 2
```

```
## [1] 10
```

```
x <- x + 1  
y <- 4  
x * y
```

```
## [1] 24
```

# Basic Data Types

- ▶ numeric (set seed to sync random number generator):

```
set.seed(1)  
rnorm(5)
```

```
## [1] -0.6264538  0.1836433 -0.8356286  1.5952808  0.3295058
```

- ▶ integer:

```
1:5
```

```
## [1] 1 2 3 4 5
```

```
sample( 1:5 )
```

```
## [1] 2 1 3 4 5
```



# Basic Data Types

- ▶ character:

```
c("yes", "no")
```

```
## [1] "yes" "no"
```

- ▶ factor (play with this to show character/integer properties):

```
factor(c("yes", "no"))
```

```
## [1] yes no
```

```
## Levels: no yes
```

# Basic Data Types

- ▶ ordered factor:

```
factor(c("good", "very good", "poor"),  
       levels=c("poor", "good", "very good"),  
       ordered=TRUE)
```

```
## [1] good      very good poor  
## Levels: poor < good < very good
```

- ▶ logical:

```
1:5 %in% 4:5
```

```
## [1] FALSE FALSE FALSE  TRUE  TRUE
```

- ▶ Missing Values and others - **IMPORTANT**

```
c(NA, NaN, -Inf, Inf)
```

```
## [1]  NA  NaN -Inf  Inf
```

# Vectors Must Be of One Data Mode

```
c( 1, "2", FALSE)
```

```
## [1] "1"      "2"      "FALSE"
```

```
c( 1, FALSE )
```

```
## [1] 1 0
```

# Selecting Vector Elements

- ▶ One element

```
x <- 1:4  
x[ 2 ]
```

```
## [1] 2
```

- ▶ A slice of a vector

```
x <- 1:10  
x[ 4:7 ]
```

```
## [1] 4 5 6 7
```

# Selecting Vector Elements

- ▶ Multiple elements ( not contiguous )

```
x <- c( "a", "b", "c", "d", "e", "f" )  
x[ c(5,3,1) ]
```

```
## [1] "e" "c" "a"
```

- ▶ Removing elements

```
x[ -1 ]
```

```
## [1] "b" "c" "d" "e" "f"
```

```
x[-1:-2]
```

```
## [1] "c" "d" "e" "f"
```

# Selecting Vector Elements

- Using logical vector

```
x <- 1:10  
y <- x%%2 == 0  
x[y]
```

```
## [1] 2 4 6 8 10
```

## 2-Dimensional Vectors are Matrices

```
matrix( 1:20, nrow = 5, ncol = 4 )
```

```
##      [,1] [,2] [,3] [,4]  
## [1,]    1    6   11   16  
## [2,]    2    7   12   17  
## [3,]    3    8   13   18  
## [4,]    4    9   14   19  
## [5,]    5   10   15   20
```

# Indexing Matrices

► `matrix[ r, c ]`

```
boring.matrix <- matrix( 1:20, nrow = 5, ncol = 4 )  
dim( boring.matrix )
```

```
## [1] 5 4
```

```
boring.matrix[ ,1 ]
```

```
## [1] 1 2 3 4 5
```

```
boring.matrix[ 2, 1 ]
```

```
## [1] 2
```

```
boring.matrix[ 2, ]
```

```
## [1] 2 7 12 17
```



# Indexing Matrices

```
boring.matrix
```

```
##           [,1] [,2] [,3] [,4]
## [1,]         1     6    11    16
## [2,]         2     7    12    17
## [3,]         3     8    13    18
## [4,]         4     9    14    19
## [5,]         5    10    15    20
```

```
boring.matrix[ boring.matrix[ ,1 ] ==3,]
```

```
## [1]  3  8 13 18
```

# Matrix Operations

## ► Transpose

```
boring.matrix <- matrix(1:9, nrow = 3)
boring.matrix
```

```
##      [,1] [,2] [,3]
## [1,]    1    4    7
## [2,]    2    5    8
## [3,]    3    6    9
```

```
t(boring.matrix)
```

```
##      [,1] [,2] [,3]
## [1,]    1    2    3
## [2,]    4    5    6
## [3,]    7    8    9
```

# Matrix Operations (cont'd)

## ► Adding

```
boring.matrix + 1
```

```
##           [,1] [,2] [,3]  
## [1,]        2    5    8  
## [2,]        3    6    9  
## [3,]        4    7   10
```

```
boring.matrix + 1:3
```

```
##           [,1] [,2] [,3]  
## [1,]        2    5    8  
## [2,]        4    7   10  
## [3,]        6    9   12
```

# Matrix Operations (cont'd)

## ► Adding

```
boring.matrix
```

```
##           [,1] [,2] [,3]  
## [1,]         1   4   7  
## [2,]         2   5   8  
## [3,]         3   6   9
```

```
boring.matrix + boring.matrix
```

```
##           [,1] [,2] [,3]  
## [1,]         2   8  14  
## [2,]         4  10  16  
## [3,]         6  12  18
```

# Matrix Operations (cont'd)

## ► Multiplying

```
boring.matrix * boring.matrix
```

```
##           [,1] [,2] [,3]  
## [1,]         1  16  49  
## [2,]         4  25  64  
## [3,]         9  36  81
```

```
boring.matrix %*% boring.matrix
```

```
##           [,1] [,2] [,3]  
## [1,]        30   66  102  
## [2,]        36   81  126  
## [3,]        42   96  150
```

## Naming rows and columns

```
colnames(boring.matrix) <- c("col.1", "col.2", "col.3")
rownames(boring.matrix) <- c("row.1", "row.2", "row.3")
boring.matrix
```

```
##           col.1 col.2 col.3
## row.1         1     4     7
## row.2         2     5     8
## row.3         3     6     9
```

```
boring.matrix["row.1", ]
```

```
## col.1 col.2 col.3
##      1     4     7
```

## Lists are Filing Cabinets

- ▶ e.g. if we have 5 medical measurements, 10 self-reported measurements, a sex, two parent names:

```
my.person <- list( measurements, self.reporting,  
                  sex, parents)
```

```
my.person
```

```
## [[1]]
```

```
## [1] 1.3 1.6 3.2 9.8 10.2
```

```
##
```

```
## [[2]]
```

```
## [1] 13 6 4 7 6 5 8 9 7 4
```

```
##
```

```
## [[3]]
```

```
## [1] FALSE
```

```
##
```

```
## [[4]]
```

```
## [1] "Parent1.name" "Parent2.name"
```

# Lists are Filing Cabinets

- ▶ Single bracket accessing

```
my.person[1:2]
```

```
## [[1]]
```

```
## [1]  1.3  1.6  3.2  9.8 10.2
```

```
##
```

```
## [[2]]
```

```
## [1] 13  6  4  7  6  5  8  9  7  4
```

- ▶ Double bracket accessing

```
my.person[[1]]
```

```
## [1]  1.3  1.6  3.2  9.8 10.2
```



# Lists are Filing Cabinets

```
my.person <- list( measure = measurements,
                  self.measure = self.reporting,
                  s = sex,
                  parents = parents )

my.person
```

```
## $measure
## [1]  1.3  1.6  3.2  9.8 10.2
##
## $self.measure
## [1] 13  6  4  7  6  5  8  9  7  4
##
## $s
## [1] FALSE
##
## $parents
## [1] "Parent1.name" "Parent2.name"
```

# The data.frame object

- ▶ a data.frame is:
- ▶ a matrix with columns of potentially different data types, and
- ▶ a list with vector elements of equal length

```
x <- 11:16  
y <- seq(0,1,.2)  
z <- c( "one", "two", "three", "four", "five", "six" )  
a <- factor( z )
```

```
test.dataframe <- data.frame(x,y,z,a)
```

## Accessing data.frame elements

```
test.dataframe[[4]]
```

```
## [1] one    two    three four  five  six  
## Levels: five four one six three two
```

```
test.dataframe$parents
```

```
## NULL
```

## Columns of a data.frame May Contain Different Data Modes

```
class( test.dataframe[[1]] )
```

```
## [1] "integer"
```

```
class( test.dataframe[[2]] )
```

```
## [1] "numeric"
```

```
class( test.dataframe[[3]] )
```

```
## [1] "factor"
```

```
class( test.dataframe[[4]] )
```

```
## [1] "factor"
```

# Combining Data Frames

- ▶ binding columns with common row names

```
mini.frame.one <- data.frame( "one" = 1:5 )  
mini.frame.two <- data.frame( "two" = 6:10 )
```

```
cbind( mini.frame.one, mini.frame.two )
```

```
##    one two  
## 1     1   6  
## 2     2   7  
## 3     3   8  
## 4     4   9  
## 5     5  10
```

Alternatively: `c( mini.frame.one, mini.frame.two )`

- ▶ `rbind` for binding rows ( with common column names )

# Updating Data Frames

```
test.dataframe
```

```
##      x    y      z      a
## 1 11 0.0   one   one
## 2 12 0.2   two   two
## 3 13 0.4 three three
## 4 14 0.6 four  four
## 5 15 0.8 five  five
## 6 16 1.0 six   six
```

```
test.dataframe[[1]] = 21:26
test.dataframe
```

```
##      x    y      z      a
## 1 21 0.0   one   one
## 2 22 0.2   two   two
## 3 23 0.4 three three
## 4 24 0.6 four  four
## 5 25 0.8 five  five
## 6 26 1.0 six   six
```

# Navigating Directories

- ▶ Paths start at where you opened R in the terminal
- ▶ Home directory for RStudio
- ▶ “/” inside a folder
- ▶ “parent\_folder/inside\_folder”
- ▶ “..” move up one
- ▶ “../..” move up two
- ▶ `getwd()`
- ▶ `setwd()`

# Reading Tables

- ▶ `read.table`
- ▶ `read.csv`
- ▶ `read.delim`



## Example: Cholesterol vs. Age

```
chol <- read.delim("http://www.statlab.uni-heidelberg.de/da  
summary(chol)
```

##	cholesterol	age	state
##	Min. :112.0	Min. :18.00	Iowa :11
##	1st Qu.:181.2	1st Qu.:39.50	Nebraska:19
##	Median :199.0	Median :48.00	
##	Mean :213.7	Mean :48.57	
##	3rd Qu.:247.0	3rd Qu.:58.00	
##	Max. :356.0	Max. :78.00	

## Example: Cholesterol vs. Age linear model

```
fit <- lm(cholesterol ~ age * state, data=chol)
summary(fit)
```

```
##
## Call:
## lm(formula = cholesterol ~ age * state, data = chol)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -73.480 -31.907  -4.303  22.829  85.833
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    35.8112     55.1166   0.650  0.52156
## age              3.2381      1.0088   3.210  0.00352 **
## stateNebraska   65.4866     61.9834   1.057  0.30045
## age:stateNebraska -0.7177      1.1628  -0.617  0.54247
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 43.14 on 26 degrees of freedom
## Multiple R-squared:  0.5326, Adjusted R-squared:  0.4786
## F-statistic: 9.875 on 3 and 26 DF, p-value: 0.00016
```

## Example: Cholesterol vs. Age ANOVA table

```
anova(fit)
```

```
## Analysis of Variance Table
```

```
##
```

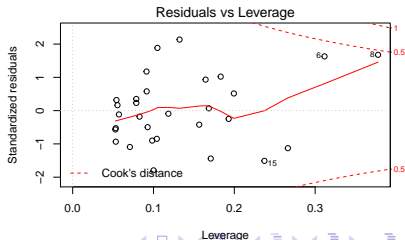
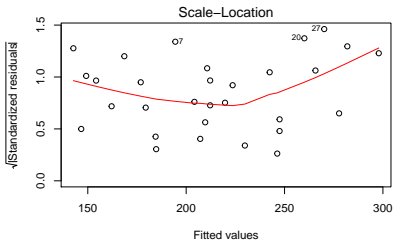
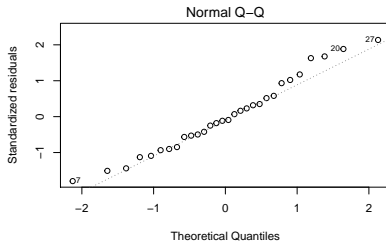
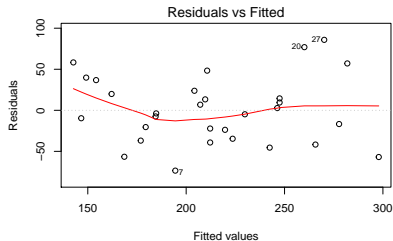
```
## Response: cholesterol
```

##		Df	Sum Sq	Mean Sq	F value	Pr(>F)	
##	age	1	48976	48976	26.3124	2.388e-05	***
##	state	1	5456	5456	2.9315	0.09877	.
##	age:state	1	709	709	0.3809	0.54247	
##	Residuals	26	48395	1861			
##	---						

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
```

# Example: Cholesterol vs. Age diagnostic plots

```
par(mfrow=c(2, 2))  
plot(fit)
```



## Example: Cholesterol vs. Age partial F-test

```
fit1 <- lm(cholesterol ~ state, data=chol)
fit2 <- lm(cholesterol ~ state + age, data=chol)
anova(fit1, fit2)
```

```
## Analysis of Variance Table
```

```
##
```

```
## Model 1: cholesterol ~ state
```

```
## Model 2: cholesterol ~ state + age
```

```
##   Res.Df    RSS Df Sum of Sq    F    Pr(>F)
```

```
## 1      28 102924
```

```
## 2      27  49104  1      53820 29.593 9.361e-06 ***
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
```

## Example: Cholesterol vs. Age backwards selection

```
library(MASS)
fit <- lm(cholesterol ~ age * state, data=chol)
step <- stepAIC(fit, direction="backward")
```

```
## Start:  AIC=229.58
## cholesterol ~ age * state
##
##           Df Sum of Sq  RSS    AIC
## - age:state  1    709.05 49104 228.01
## <none>                                48395 229.58
##
## Step:  AIC=228.01
## cholesterol ~ age + state
##
##           Df Sum of Sq  RSS    AIC
## <none>                                49104 228.01
## - state  1      5456  54560 229.18
## - age    1     53820 102924 248.22
```

AIC = Akaike's Information Criterion