#### Introduction to R and RStudio

Part 3: Introduction to Descriptive and Inferential Statistics with R

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#### **Example Data Set**

- A researcher is interested in evaluating two therapies for perfectionism; specifically, investigating whether they will be effective in reducing levels of perfectionism
  - Levels of perfectionism are recorded at baseline (perf1), after 1 month of therapy (perf2) and after 2 months of therapy (perf3) for each experimental group (General Stress, CBT) and a control group
- At baseline the researcher also records levels of depression and the sex of each subject

#### Dataset

#### > head(dat)

sex group dep1 perf1 perf2 perf3

cbt m cbt m cbt m cbt m cbt m cbt m

#### Frequencies

- The 'table' function is helpful for obtaining frequencies for single or multiple variables
- > table(dat\$sex) > table(dat\$sex,dat\$group)
  f m cbt control stress
  f 13 15 12
  40 50 m 17 15 18

#### Frequencies

- We can also obtain simple graphical descriptions of frequencies
- > fgroup<-table(dat\$group)</pre>
- > barplot(fgroup)



#### Frequencies

- Or, slightly more sophisticated graphical descriptions of frequencies
- > freq<-table(dat\$sex, dat\$group)</pre>
- > barplot(freq, legend=rownames(freq))



#### **Basic Descriptive Statistics**

- There are numerous ways to obtain basic descriptive statistics, for example:
  - summary(x)
  - max(x)
  - min(x)
  - range(x)
  - mean(x)
  - median(x)
  - var(x)
  - sd(x)
  - o quantile(x,probs=)
- These can also be used with all the subsetting/indexing we previously discussed

#### **Basic Descriptive Statistics**

 However, there are also packages with functions for obtaining a lot of descriptive info quickly
 E.g., 'describe' function in the 'psych' package

> library(psych)												
<pre>&gt; describe(dat)</pre>												
	vars	n	mean	sd	median	trimmed	mad	min	max	range		
sex*	1	90	1.56	0.50	2.00	1.57	0.00	1.00	2.00	1.00		
group*	2	90	2.00	0.82	2.00	2.00	1.48	1.00	3.00	2.00		
dep1	3	90	81.51	16.79	80.08	80.83	17.61	49.25	129.48	80.24		
perf1	4	90	80.53	9.79	80.24	80.09	8.73	59.67	111.19	51.52		
perf2	5	90	72.55	13.39	71.96	72.06	11.65	43.80	109.34	65.54		
perf3	6	90	69.50	14.83	68.09	68.54	15.17	40.81	119.09	78.28		
skew kurtosis se												
sex*	-0.22	2	-1.97	0.05								
group*	0.00	)	-1.53	3 0.09								
dep1	0.43	3	-0.30	) 1.77								
perf1	0.50	)	0.40	1.03								
perf2	0.37	7	0.26	5 1.41								
perf3	0.63	3	0.37	7 1.56								

#### **Basic Descriptive Statistics**

A similar function in the 'psych' package also allows us to obtain descriptive statistics separated by a grouping variable

This is just the first few lines,

> desci	ribeBy	/(da	at, se>	several statistics and the info for males is left out			
group:	f						
	vars	n	mean	sd	median	trimmed	mad
sex*	1	40	1.00	0.00	1.00	1.00	0.00
group*	2	40	1.98	0.80	2.00	1.97	1.48
dep1	3	40	81.36	18.32	80.62	80.61	20.18
perf1	4	40	79.47	10.28	79.33	79.24	8.28
perf2	5	40	72.30	13.70	72.96	71.76	13.72
perf3	6	40	69.66	14.76	68.21	68.78	15.22

#### **Pearson Correlation**

- Hypothesis #1: Are baseline depression and perfectionism scores correlated?
  - > cor.test(dat\$perf1,dat\$dep1)

```
Pearson's product-moment correlation
```

```
data: dat$perf1 and dat$dep1
t = 6.047, df = 88, p-value =
3.493e-08
alternative hypothesis: true correlation
is not equal to 0
95 percent confidence interval:
    0.3770138 0.6733433
sample estimates:
        cor
0.541803
```

#### **Rank-based Correlation**

 Hypothesis #1: Are baseline depression and perfectionism scores correlated

Spearman's rank-based correlation coefficient

```
> cor.test(dat$perf1,dat$dep1,method="sp
earman")
```

Spearman's rank correlation rho

#### Simple Regression

- Hypothesis #2: Can we predict posttest perfectionism scores from pretest depression scores?
- Scatterplot
  - >plot(dat\$dep1,dat\$perf3)



#### Simple Regression, cont'd

 Create a linear model object and print a summary of the results

```
> mod1 < -1m(perf3 ~ dep1, data=dat)
> summary(mod1)
Call:
lm(formula = perf3 \sim dep1, data = dat)
Residuals:
   Min 10 Median 30
                                 Max
-26.540 -10.605 -0.683 9.031 47.663
Coefficients:
           Estimate Std. Error t value Pr(>|t|)
(Intercept) 45.47798 7.38149 6.161 2.12e-08
                                              ***
dep1 0.29476 0.08871 3.323 0.0013 **
Signif. codes:
0^{'}***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Residual standard error: 14.06 on 88 degrees of freedom Multiple R-squared: 0.1115, Adjusted R-squared: 0.1014 F-statistic: 11.04 on 1 and 88 DF, p-value: 0.001301

#### Simple Regression, cont'd

- Diagnostics are available for identifying normality issues
  - hist(resid(mod1))

Normal probability (qq) plots are also available



#### **Regression Diagnostics**

- It is also easy to produce several diagnostic plots simply by typing:
  - plot(mod)
    - Where you replace 'mod' with the name of your model
- These plots include:
  - Residuals vs Fitted
  - Normal Probability Plot of the Residuals
  - Scale vs Location Plot
  - Residuals vs Leverage

#### Simple Regression, cont'd

- Regression Diagnostics
  - We can compute Studentized Deleted Residuals to identify outlying cases in the solution
    - There are also tools for identifying cases with extreme leverage
  - Below case 31 seems discrepant
  - > library(car)
  - > outlierTest(mod1)
     rstudent unadjusted p-value Bonferonni p
    31 3.643018 0.00045739 0.041165

#### Simple Regression, cont'd

- It is also important to identify influential observations (e.g., Cook's Distance)
- This plot indicates which cases exceed a cutoff for Cook's distance of 4/(N - p) where p is the number of predictors
  - >cutoff <- 4/(length(perf1)-1)</li>
  - >plot(mod1, which=4, cook.levels=cutoff)

Based on fourth plot created when you plot a model object



#### **Multiple Regression**

 Hypothesis #3: Can posttest perfectionism scores be predicted from depression scores, controlling for pretest perfectionism?

```
> mod2 < -1m(perf3 ~ dep1 + perf1, data=dat)
> summary(mod2)
call:
lm(formula = perf3 \sim dep1 + perf1, data = dat)
Residuals:
              10 Median 30
    Min
                                      Max
-27.4451 -9.1199 -0.8234 10.2411 25.3162
Coefficients:
           Estimate Std. Error t value Pr(>|t|)
(Intercept) -4.75514 10.47354 -0.454 0.651
dep1
          0.00531 0.08938 0.059 0.953
perf1 0.91674 0.15337 5.977 4.87e-08 ***
                '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Signif. codes:
              0
```

Residual standard error: 11.9 on 87 degrees of freedom Multiple R-squared: 0.3701, Adjusted R-squared: 0.3557 F-statistic: 25.56 on 2 and 87 DF, p-value: 1.851e-09

#### **Multiple Regression Diagnostics**

- All of the same diagnostics used in a simple regression can also be applied in a multiple regression
- For example: plot(mod2,which=4,cook.levels=cutoff)



#### **Multiple Regression Diagnostics**

- There are also diagnostics that are unique to multiple regression, such as collinearity diagnostics
  - Time 1 Depression and Perfectionism do not seem to be too highly related

# > vif(mod2) dep1 perf1 1.415529 1.415529

#### Interactions in Multiple Regression



#### **Interaction Plot**

- > library(effects)
- > plot(effect(term="dep1c:perf1c",mod=mod3,default.levels=3))

There are infinite numbers of

cool stats, plots, etc. that you

can find just by playing around

with R



#### dep1c\*perf1c effect plot

dep1c

#### Logistic Regression

- Imagine that we wanted to determine if a perfectionism diagnosis (normal, clinical) at time 1 is related to depression at time 1
- In this case we might want to use a logistic regression, a type of generalized linear model (glm)
- First, we will split our time 1 perfectionism scores into normal/clinical > 90 is the
  - > library(Hmisc)
  - > dat\$perfdich<-cut2(dat\$perf1,cuts=90)</li>
  - > levels(dat\$perfdich)<-c("normal","clinical")</li>

cut2 performs a split at the specified cutoff

clinical cutoff

#### Logistic Regression

> mod4<- glm(perfdich~dep1, family=binomial(link="logit"), data=dat)
> summary(mod4)

Call: glm(formula = perfdich ~ dep1, family = binomial(link = "logit"), data = dat) Deviance Residuals: **Generalized Linear** Min 1Q Median 3Q Max Model (glm) -1.4817 -0.5411 -0.3710 -0.2329 2.2472Coefficients: Estimate Std. Error z value Pr(>|z|)(Intercept) -7.70958 1.95033 -3.953 7.72e-05 \*\*\* dep1 0.02088 3.295 0.000983 \*\*\* 0.06880

#### Independent Samples t-tests

- Hypothesis #4: Is there a difference between males and females on pretest perfectionism?
- In this case we would likely want to use a t-test

```
> t.test(perf1~sex, data=dat, var.equal=TRUE)
 Two Sample t-test
data: perf1 by sex
t = -0.9167, df = 88, p-value = 0.3618
alternative hypothesis: true difference in means
is not equal to 0
                                       This statement is
95 percent confidence interval:
                                       required since the
 -6.034613 2.224762
                                     default test is the Welch
sample estimates:
                                       test that does not
mean in group f mean in group m
                                     assume equal variances
       79.47360
                         81.37852
```

#### Independent Samples t-tests

We can also run a *t*-test by specifying the groups to be compared

```
> t.test(perf1[sex == "m"],perf1[sex == "f"], var
.equal=TRUE, data=dat)
Two Sample t-test
data: perf1[sex == "m"] and perf1[sex == "f"]
t = 0.9167, df = 88, p-value =
0.3618
alternative hypothesis: true difference in means
is not equal to 0
95 percent confidence interval:
 -2.224762 6.034613
sample estimates:
mean of x mean of y
81.37852 79.47360
```

## Independent Samples *t*-tests Under Variance Heterogeneity

- Welch's two independent samples *t*-test
  - This is the default since this a better overall test than the traditional t-test
  - > t.test(perf1~sex, data=dat)

welch Two Sample t-test

```
data: perf1 by sex
t = -0.9075, df = 80.079,
p-value = 0.3669
alternative hypothesis: true difference
in means is not equal to 0
95 percent confidence interval:
-6.082220 2.272369
sample estimates:
mean in group f mean in group m
79.47360 81.37852
```

## Independent Samples *t*-tests Under Nonnormality

- Wilcoxon-Mann-Whitney nonparametric two independent samples test
  - > wilcox.test(dat\$perf1~dat\$sex)

Wilcoxon rank sum test with continuity correction

data: dat\$perf1 by dat\$sex
W = 905, p-value = 0.4429
alternative hypothesis: true location
shift is not equal to 0

This time we skipped the 'data' statement and specified the dataset for each variable

## What about a t-test for Nonnormality and Variance Inequality?

- Several procedures have been proposed, although the Welch *t*-test on trimmed means has garnered the most attention
- Rand Wilcox has written functions that accompany his texts on robust statistics that includes a function for computing the trimmed Welch t (which was developed by Yuen and often referred to as the Yuen test)
  - We will use a package called 'WRS2' that makes available many of Wilcox's most popular functions

### Working with Trimmed Means

- Since we will be testing the null hypothesis that the population trimmed means are equal, it is informative to look at the trimmed means
- 79.04677 80.44451

#### Yuen Test

Note that like many of Wilcox's functions, the output is not very fancy

Population trimmed means do not differ significantly

```
> yuen(dat$perf1~dat$sex)
Call:
yuen(formula = dat$perf1 ~ dat$sex)
Test statistic: 0.7588, p-value = 0.45194
95 percent confidence interval:
-5.108 2.3125
```

#### Paired Samples t-tests

- Hypothesis #5: Is there a difference between pre and post perfectionism scores?
- > t.test(dat\$perf1, dat\$perf3, paired=TRUE)

```
Paired t-test
```

```
data: dat$perf1 and dat$perf3
t = 8.8712, df = 89, p-value =
6.942e-14
alternative hypothesis: true difference in
means is not equal to 0
95 percent confidence interval:
  8.557716 13.497733
sample estimates:
mean of the differences
               11.02772
```

#### Paired Samples under Nonnormality

 If the distribution of difference scores is not normally distributed, the Wilcoxon signed ranks test can be much more powerful than the paired samples t-test

> wilcox.test(dat\$perf1, dat\$perf3, paired=TRUE)

Wilcoxon signed rank test with continuity correction

```
data: dat$perf1 and dat$perf3
V = 3676, p-value = 5.732e-11
alternative hypothesis: true location shift is not
equal to 0
```