

Reading and Annotating Activity

Quantitative Analysis of Vertebrate Populations

1. Find a paper in the journal *Ecology*, *Ecological Applications*, or *Journal of Wildlife Management* that uses one of the methods we have learned in class this semester and has R code included as an online supplement.
2. Describe what was done in the methods (experimental design and analysis). Explain why you think this is an appropriate analysis based on what you've learned in this course.
3. Print out the online supplementary R code and annotate it by hand next to the code. Describe what each line of code is doing and why. Indicated where you do not know or are confused (do not put this for the whole thing).

```
# t-tests in R
# Created by: Sarah Bray
# Date: Oct 2014
# Updated: February 15 2016
```

(2 males fighting)

Lizards → horn length vs. wins

1-sided - 2 sample t-test

```
cm(list=ls())
```

```
# Is there a difference in horn length between winners and losers?
```

```
fight <- read.csv("lizardfight.csv", header = TRUE)
```

```
str(fight) → explains variable setup
```

```
winner <- subset(fight, fight$win == 1)
```

```
loser <- subset(fight, fight$win == 0)
```

```
shapiro.test(winner$horn_length)
```

```
shapiro.test(loser$horn_length)
```

```
lizard <- wilcox.test(winner$horn_length, loser$horn_length, alternative = "greater")
```

```
t.test(fight$horn_length ~ fight$win)
```

```
wilcox.test(horn_length ~ win, data = fight)
```

```
t.test(winner$horn_length, loser$horn_length, alternative = "greater")
```

→ p-value < .05 → means are different

Comparing whitefly abundance on targets: 1/2 of target yellow; other 1/2 white

```
Pair <- read.table("Paired Data.txt", sep = '\t', comment = '#', header = T)
```

```
str(Pair)
```

```
shapiro.test(Pair$Yellow) → normal? → yes
```

```
shapiro.test(Pair$White) → yes
```

```
var.test(Pair$White, Pair$Yellow) p = 0.1416 → variances are equal
```

```
t.test(Pair$White, Pair$Yellow, paired = T, equal.var = T)
```

→ p-value = .1416 → means aren't different (no preference for color)

```
# Do CO emissions exceed limit of 5.4?
```

```
pollute <- read.csv("pollutants.csv", header = T)
```

```
shapiro.test(pollute$co) → not normal
```

```
hist(pollute$co) → transform data → log
```

```
logCO <- log(pollute$co)
```

```
shapiro.test(logCO) (p = .2379)
```

```
t.test(logCO, alternative = "greater", mu = log(5.4))
```

```
cotest <- wilcox.test(pollute$co, alternative = "greater", mu = 5.4)
```

→ use if you didn't transform

```
# graphing for comparison of means, boxplot
```

```
boxplot(horn_length ~ win, data = fight,
```

```
notch = TRUE,
```

```
col = "red",
```

```
xlab = "Outcome", ylab = "Horn length (cm)",
```

```
names = c("Losers", "Winners"))
```

paired t-test

1-sample t-test

have to transform as well

→ p = .01346
→ different means
→ CO > 6.4

notch → places notch in bar graph in box plot



→ shows that means really are different b/c notches don't overlap.

Figure 1: Annotating Example