R_Activity_Assignment_7

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```
rm(list=ls())
```

1. Load in the glucose_df.txt dataset.

```
glucose_txt <- read.table("C:/Users/chemk/OneDrive/Desktop/Classes/ENT6707_DataAnalysis/week9/gl
ucose_df.txt", header = TRUE, sep = "\t")
nrow(glucose_txt)
```

```
## [1] 144
```

```
str(glucose_txt)
```

```
## 'data.frame':    144 obs. of  5 variables:
##  $ rep    : int  1 1 1 1 1 1 1 1 1 1 ...
##  $ animal : chr  "goat" "goat" "goat" "goat" ...
##  $ diet   : chr  "alfalfa_hay" "alfalfa_hay" "control" "control" ...
##  $ drug   : chr  "control" "slaframine" "control" "slaframine" ...
##  $ glucose: int  66 56 70 89 69 61 57 85 52 87 ...
```

```
head(glucose_txt)
```

```
##   rep animal           diet       drug glucose
## 1   1   goat     alfalfa_hay    control      66
## 2   1   goat     alfalfa_hay slaframine      56
## 3   1   goat         control    control      70
## 4   1   goat         control slaframine      89
## 5   1   goat cottonseed_meal    control      69
## 6   1   goat cottonseed_meal slaframine      61
```

```
tail(glucose_txt)
```

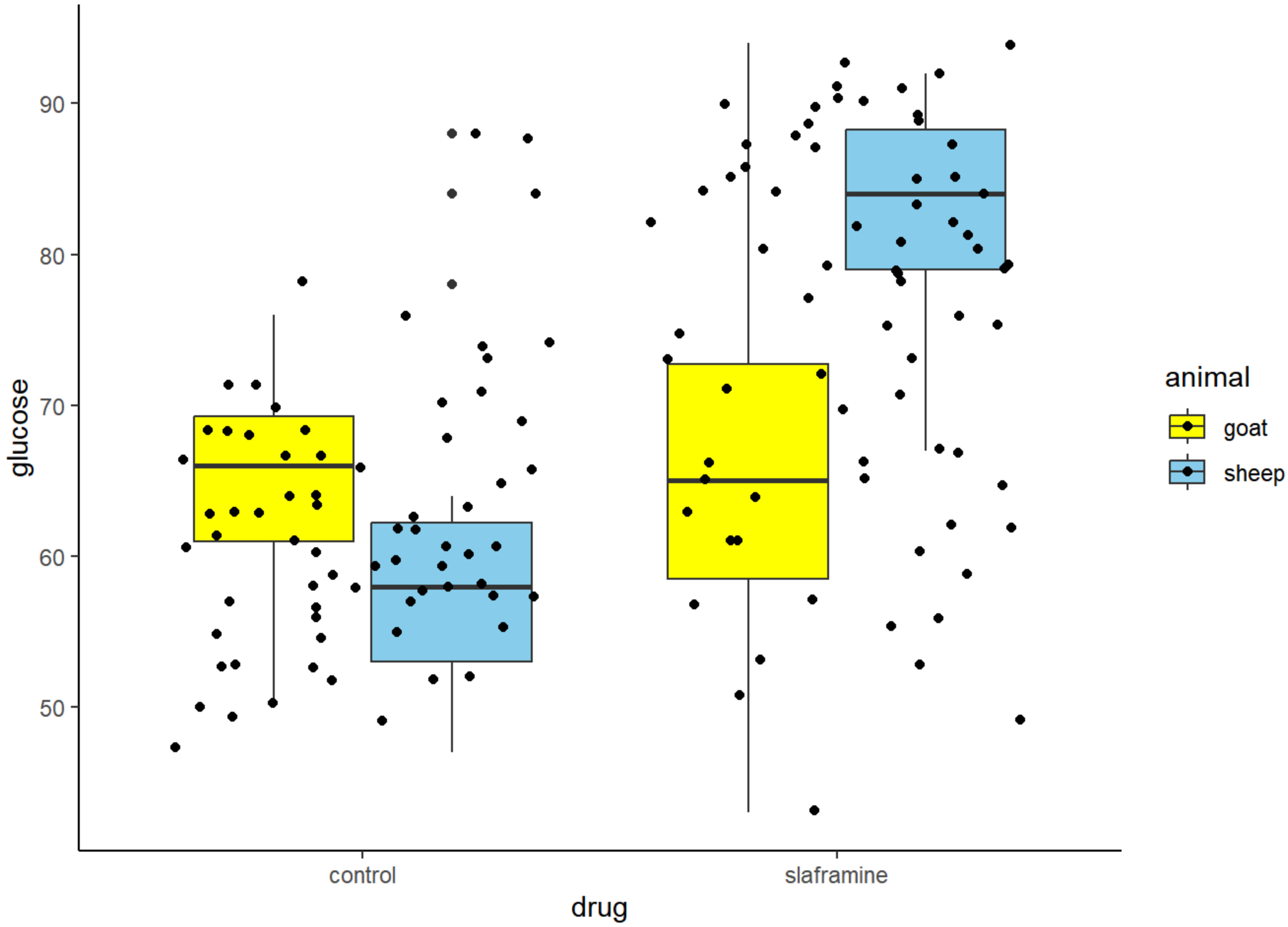
```
##     rep animal            diet       drug glucose
## 139  12  sheep     alfalfa_hay    control      64
## 140  12  sheep     alfalfa_hay slaframine      83
## 141  12  sheep         control    control      58
## 142  12  sheep         control slaframine      91
## 143  12  sheep cottonseed_meal    control      88
## 144  12  sheep cottonseed_meal slaframine      90
```

```
summary(glucose_txt)
```

```
##       rep           animal              diet               drug          
##  Min.   : 1.00   Length:144         Length:144         Length:144        
##  1st Qu.: 3.75   Class :character   Class :character   Class :character  
##  Median : 6.50   Mode  :character   Mode  :character   Mode  :character  
##  Mean   : 6.50                                                           
##  3rd Qu.: 9.25                                                           
##  Max.   :12.00                                                           
##     glucose     
##  Min.   :43.00  
##  1st Qu.:59.00  
##  Median :66.00  
##  Mean   :68.65  
##  3rd Qu.:79.00  
##  Max.   :94.00  
```

2. Create a grouped boxplot of glucose as a function of drug and animal. Use any colors you want, but make sure to overlay the raw data points on top of your boxes. Based on eyeballing the plot, provide a 1-2 sentence description of any pattern(s).

```
library(ggplot2)
ggplot(glucose_txt, aes(x= drug, y = glucose, fill = animal)) + geom_boxplot()+ geom_jitter()+ t
heme_classic()+scale_fill_manual(values=c("yellow", "skyblue"))
```



Overall, the animals that received a drug injection of slaframine in saline had higher blood glucose levels. Additionally, the effect of the drug appeared significant in sheep when compared control and treatment, while it did not show a substantial difference in goats.

3. We are interested in quantifying variation in glucose (our response variable). Note that we could analyze these data in the “historical” way by fitting rep (the column for blocks) as a so-called “fixed effect” (i.edic., as a regular old pretor). Next week, you will get practice fitting mixed-effects models, in which rep would be fit as a so-called “random intercept” or “random effect”. Do not worry, as I will also further explain the terms fixed, random, and mixed-

effect next week. However, for this week, we are going to simplify things: ignore rep and just fit animal, drug, and their interaction (animal × drug) as the predictors (again, we are ignoring the diet column).

```
fit_glucose_interaction <- lm(glucose~drug*animal, data=glucose_txt)
summary(fit_glucose_interaction)
```

```
##
## Call:
## lm(formula = glucose ~ drug * animal, data = glucose_txt)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -23.3889  -5.1597  -0.9583   3.9653  28.1944
##
## Coefficients:
##                             Estimate Std. Error t value Pr(>|t|)
## (Intercept)                   65.111      1.483  43.919  < 2e-16 ***
## drugslaframine                 1.278      2.097   0.609   0.5432
## animalsheep                   -5.306      2.097  -2.531   0.0125 *
## drugslaframine:animalsheep   22.222      2.965   7.495 6.87e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 8.895 on 140 degrees of freedom
## Multiple R-squared:  0.5024, Adjusted R-squared:  0.4917
## F-statistic: 47.11 on 3 and 140 DF,  p-value: < 2.2e-16
```

4. Run an Anova() on the model and ensure you are using marginal fits (Type III sums of squares).

```
library(car)
```

```
## Loading required package: carData
```

```
fit_ex1 <- lm(glucose~drug+animal+animal*drug, data=glucose_txt)
Anova(fit_ex1, type="III")
```

```
## Anova Table (Type III tests)
##
## Response: glucose
##             Sum Sq  Df   F value    Pr(>F)
## (Intercept) 152620   1 1928.8717 < 2.2e-16 ***
## drug            29   1    0.3714    0.5432
## animal         507   1    6.4036    0.0125 *
## drug:animal   4444   1   56.1705  6.87e-12 ***
## Residuals    11077 140
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Different method

```
fit_ex_SS <- lm(glucose~animal+drug+drug*animal, data=glucose_txt)
Anova(fit_ex_SS, type="III")
```

```
## Anova Table (Type III tests)
##
## Response: glucose
##             Sum Sq  Df   F value    Pr(>F)
## (Intercept) 152620   1 1928.8717 < 2.2e-16 ***
## animal         507   1    6.4036    0.0125 *
## drug            29   1    0.3714    0.5432
## animal:drug   4444   1   56.1705  6.87e-12 ***
## Residuals    11077 140
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

5. Conduct a pairwise comparisons of the interaction term.

```
library(emmeans)
```

```
## Welcome to emmeans.
## Caution: You lose important information if you filter this package's results.
## See '? untidy'
```

```
fit_manova <- lm(glucose~animal+drug+drug*animal, data=glucose_txt)
anova(fit_manova)
```

```
## Analysis of Variance Table
##
## Response: glucose
##              Df  Sum Sq Mean Sq F value    Pr(>F)
## animal        1  1213.4  1213.4  15.335 0.0001401 ***
## drug          1  5525.4  5525.4  69.832  5.74e-14 ***
## animal:drug   1  4444.4  4444.4  56.170  6.87e-12 ***
## Residuals   140 11077.4    79.1
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(fit_manova)
```

```
##
## Call:
## lm(formula = glucose ~ animal + drug + drug * animal, data = glucose_txt)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -23.3889  -5.1597  -0.9583   3.9653  28.1944
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                  65.111      1.483  43.919  < 2e-16 ***
## animalsheep                  -5.306      2.097  -2.531   0.0125 *
## drugslaframine                1.278      2.097   0.609   0.5432
## animalsheep:drugslaframine   22.222      2.965   7.495 6.87e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 8.895 on 140 degrees of freedom
## Multiple R-squared:  0.5024, Adjusted R-squared:  0.4917
## F-statistic: 47.11 on 3 and 140 DF,  p-value: < 2.2e-16
```

```
manova_emm <- emmeans(fit_manova, ~drug*animal)
pairs(manova_emm)
```

```
##  contrast                           estimate  SE  df t.ratio p.value
##  control goat - slaframine goat        -1.28 2.1 140  -0.609  0.9289
##  control goat - control sheep           5.31 2.1 140   2.531  0.0596
##  control goat - slaframine sheep      -18.19 2.1 140  -8.678  <.0001
##  slaframine goat - control sheep        6.58 2.1 140   3.140  0.0110
##  slaframine goat - slaframine sheep   -16.92 2.1 140  -8.069  <.0001
##  control sheep - slaframine sheep     -23.50 2.1 140 -11.209  <.0001
##
## P value adjustment: tukey method for comparing a family of 4 estimates
```

6. Write 3-4 sentences interpreting the results of your analyses. Please try to write in biological terms, not statistical, but make sure to include the relevant summary statistics for any claims you make.

1. There was no significant difference between the goats that received slaframine in saline and those that received only saline, while the sheep in the control group had a 23.50 mg/dl higher blood glucose level than those that received slaframine ($p < 0.0001$).
2. Goats in the control group had a 18.19 mg/dl ($p < 0.0001$) higher blood glucose level than sheep injected with slaframine, while goats in the treatment group had a 6.58 mg/dl ($p = 0.01$) higher blood glucose level than sheep in the control group.
3. Goats in the treatment group had a 16.92 mg/dl ($p < 0.0001$) lower blood glucose level than sheep in the treatment group. However, goats in the control group had a higher blood glucose level than sheep in the control group, although this difference was not significant ($p = 0.06$).