

R_Activity_Assignment_8

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In this study, two animal species (goats or sheep) were fed one of three diets (control, alfalfa hay, and cottonseed meal) and received a drug injection (slaframine in saline or just saline). The 12 treatments were assigned in a randomized complete block design with twelve blocks (replications). So, each combination of animal × diet × drug combination appears twelve times. For this activity we are ONLY going to look at the effects of drug (and reps) on glucose blood levels.

1. Load in the glucose_df.txt dataset.

```
glucose_txt <- read.table(file="C:/Users/chemk/Desktop/Classes/ENT6707_DataAnalysis/week10/glucose_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)
```

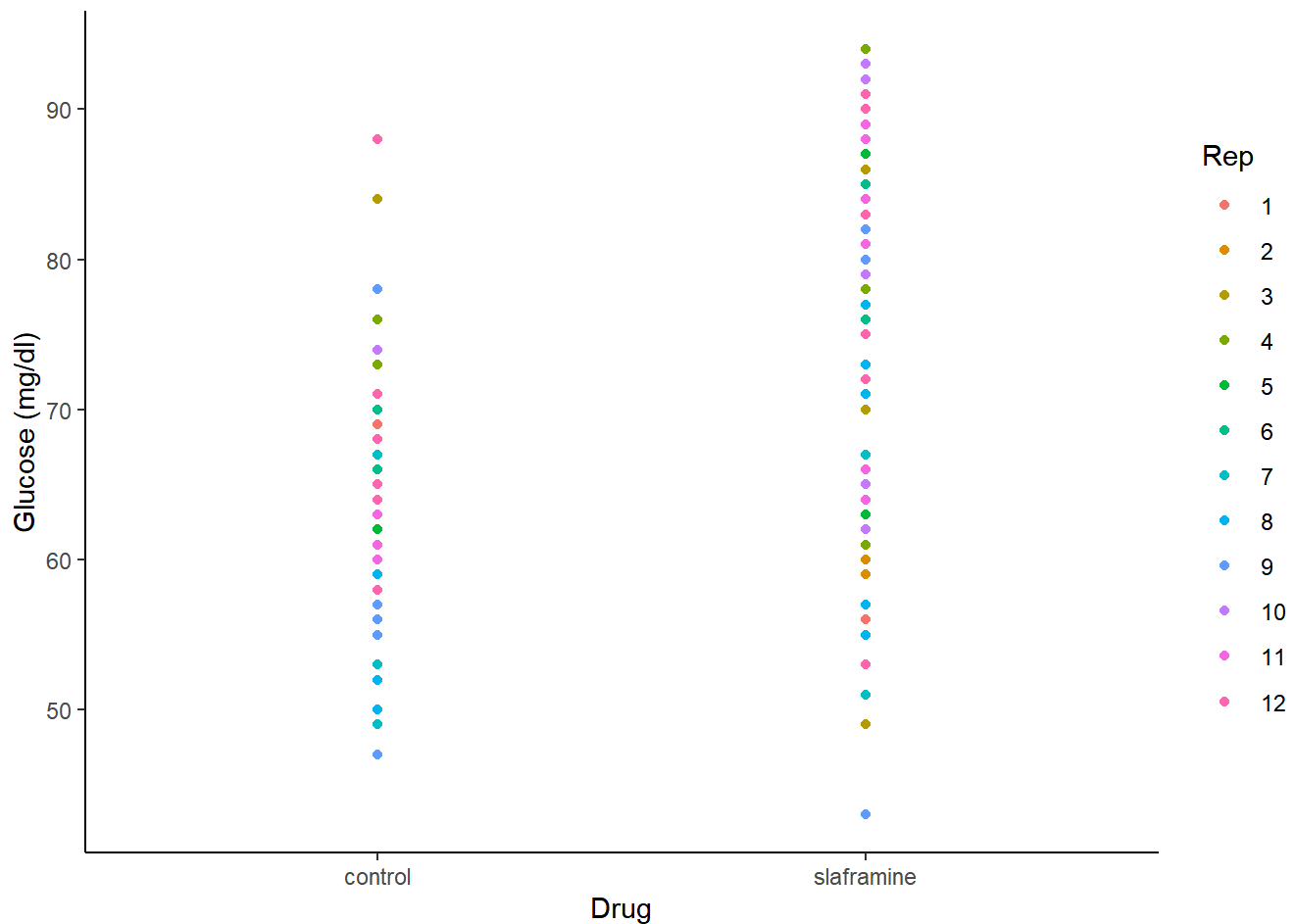
```
##      rep animal      diet      drug glucose
## 139  12  sheep  alfalfa_hay  control      64
## 140  12  sheep  alfalfa_hay slaframine      83
## 141  12  sheep      control  control      58
## 142  12  sheep      control slaframine      91
## 143  12  sheep cottonseed_meal  control      88
## 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. Graph glucose as a function of drug. Color each point by the variable rep and change the axis labels to “Glucose (mg/dl)” and “Drug”.

```
library(ggplot2)
ggplot(data=glucose_txt, aes(x=drug, y=glucose, color=as.factor(rep)))+geom_point()+theme_classic()+labs(x="Drug", y="Glucose (mg/dl)", color="Rep")
```



3. Fit a fixed-effects only model of glucose as a function of rep and drug. Provide a summary() of the model.

```
library(lme4)
```

```
## Loading required package: Matrix
```

```
f_model <- lm(glucose~rep+drug, data=glucose_txt)  
summary(f_model)
```

```
##
## Call:
## lm(formula = glucose ~ rep + drug, data = glucose_txt)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -32.309  -7.094   0.042   7.577  25.634
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    61.2576     2.1342  28.703  < 2e-16 ***
## rep             0.1847     0.2625   0.704   0.483
## drugslafamine  12.3889     1.8126   6.835 2.28e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.88 on 141 degrees of freedom
## Multiple R-squared:  0.2508, Adjusted R-squared:  0.2402
## F-statistic: 23.61 on 2 and 141 DF,  p-value: 1.436e-09
```

4. Fit a linear mixed-effects model of glucose as a function of drug. Include a term for rep as a random intercept. Provide a summary() of the model and check the assumptions (please provide proof you conducted diagnostics and ensure the summary output has p-values). Are you satisfied the assumptions are met? Why or why not?

In the residual plot, the residuals appear to be normally distributed around both the X-axis and Y-axis. However, there are some clustered points and an empty central area that might suggest a violation of the assumption. In the Q-Q plot, the points are closely aligned along the diagonal line, indicating that they follow a normal distribution. Additionally, in the random effects Q-Q plot, the points also align closely along the diagonal line and do not deviate significantly. Overall, I believe the assumptions are well met.

```
library(lme4)
library(lmerTest)
```

```
##
## Attaching package: 'lmerTest'
```

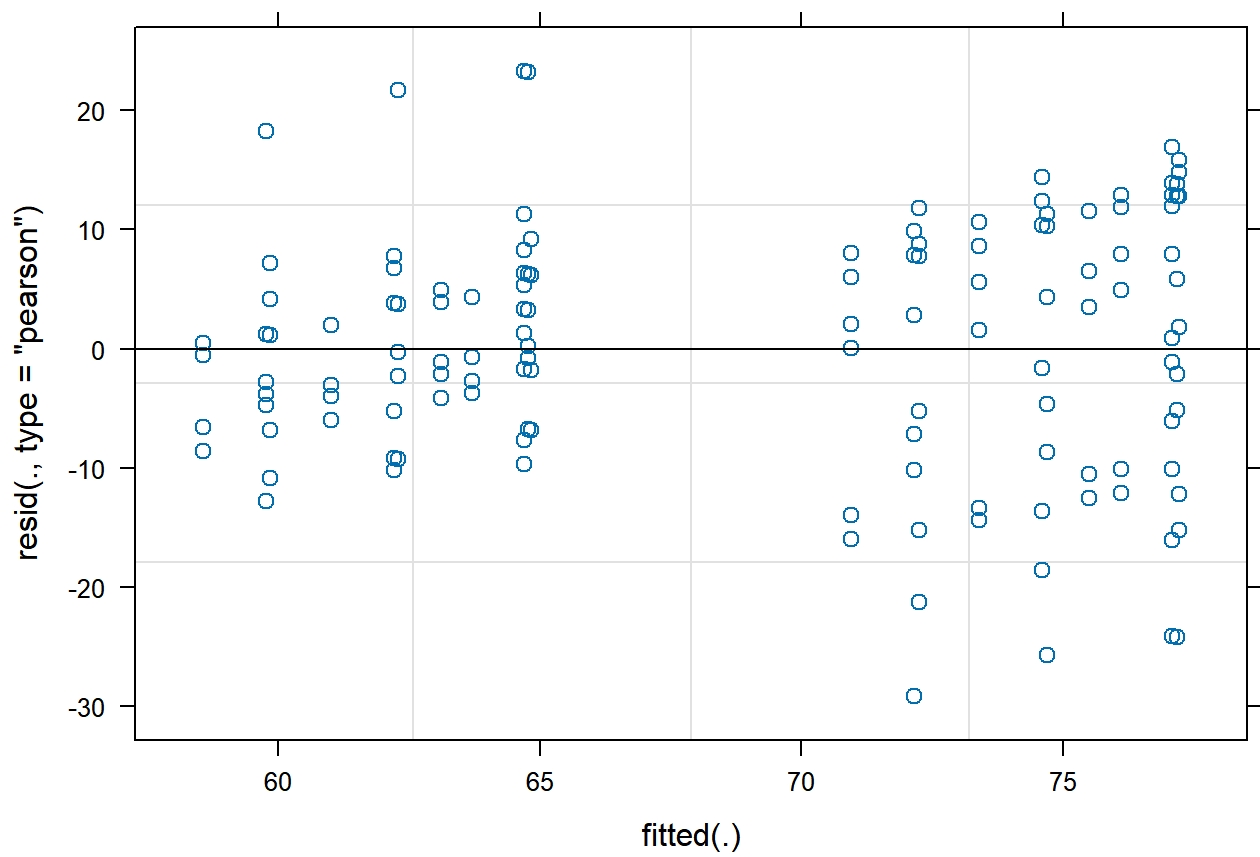
```
## The following object is masked from 'package:lme4':  
##  
## lmer
```

```
## The following object is masked from 'package:stats':  
##  
## step
```

```
m_model <- lmer(glucose~drug+(1|rep), data=glucose_txt)  
summary(m_model)
```

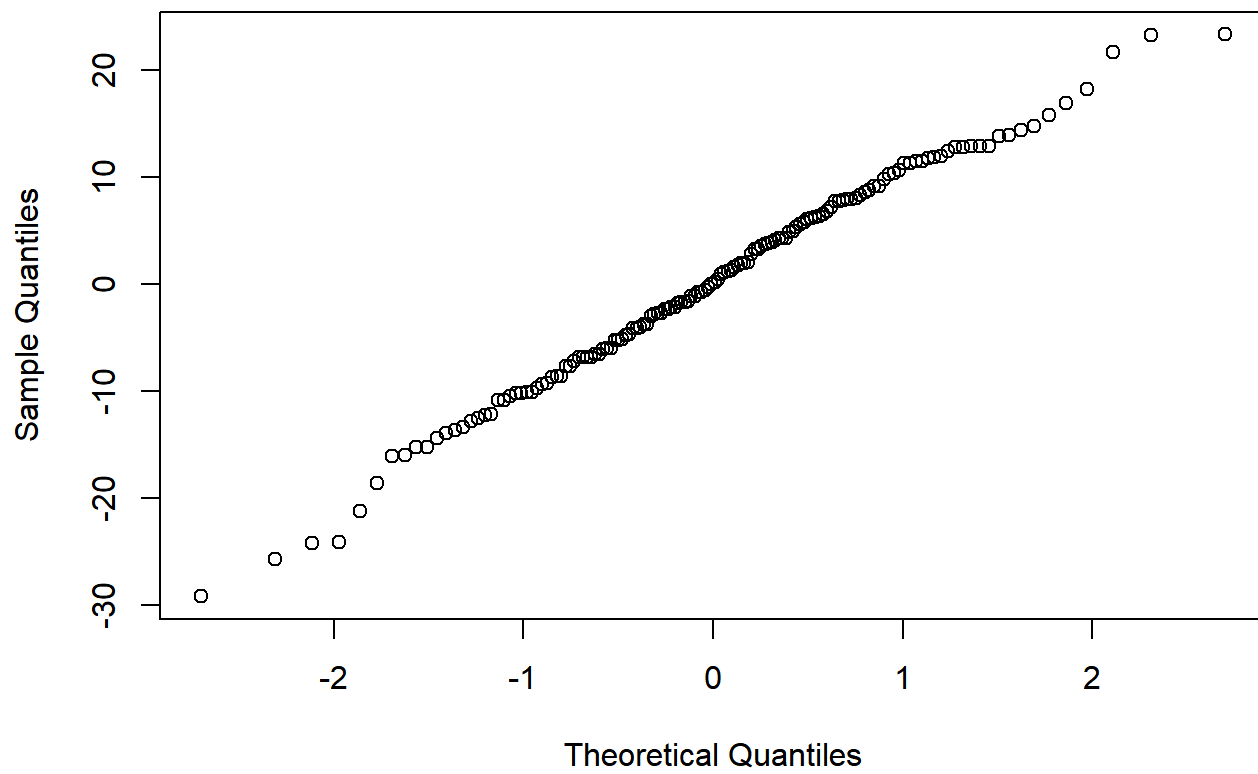
```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [  
## lmerModLmerTest]  
## Formula: glucose ~ drug + (1 | rep)  
## Data: glucose_txt  
##  
## REML criterion at convergence: 1085.5  
##  
## Scaled residuals:  
##      Min       1Q   Median       3Q      Max   
## -2.79352 -0.65366  0.01272  0.74784  2.23314   
##  
## Random effects:  
## Groups   Name      Variance Std.Dev.  
## rep      (Intercept)  9.606    3.099  
## Residual                108.924  10.437  
## Number of obs: 144, groups: rep, 12  
##  
## Fixed effects:  
##              Estimate Std. Error    df t value Pr(>|t|)      
## (Intercept)    62.458     1.521 23.813  41.065 < 2e-16 ***  
## drugslaframine  12.389     1.739 131.000   7.122 6.32e-11 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Correlation of Fixed Effects:  
##              (Intr)  
## drugslafrmn -0.572
```

```
plot(m_model) # To check the assumptions
```



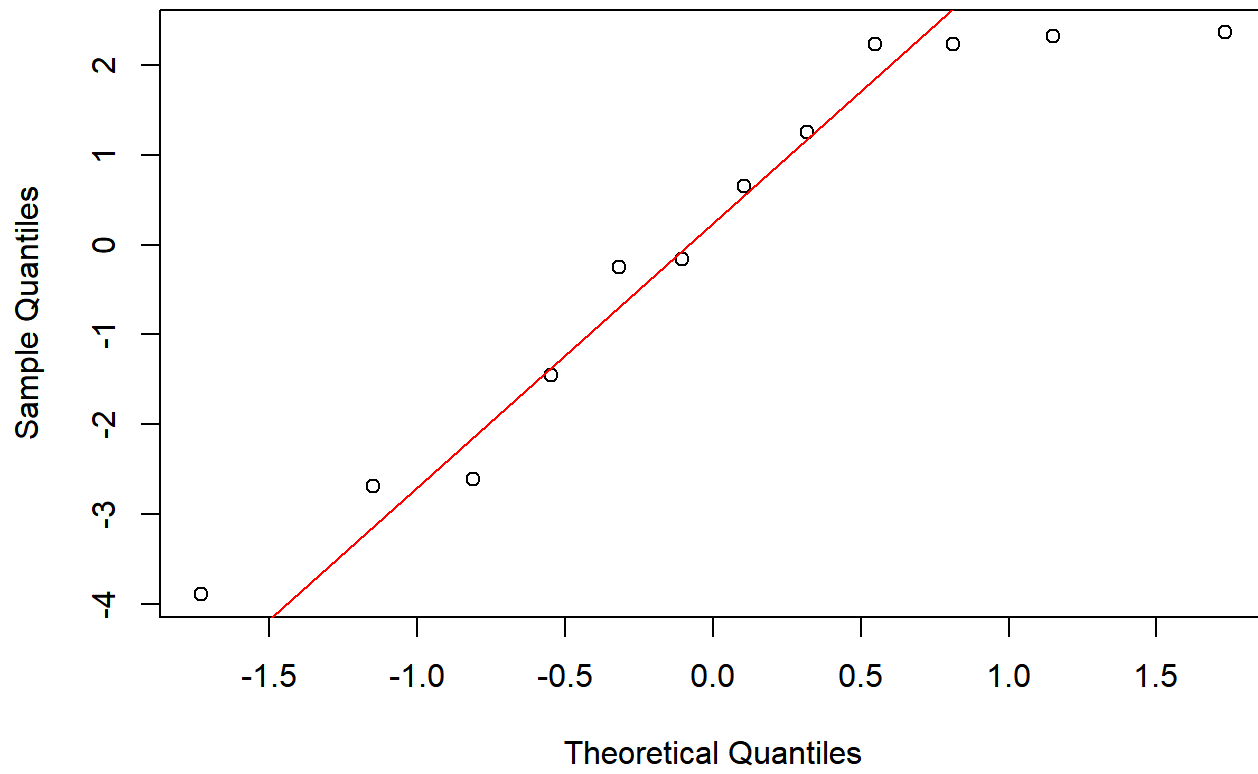
```
qqnorm(residuals(m_model))
```

Normal Q-Q Plot



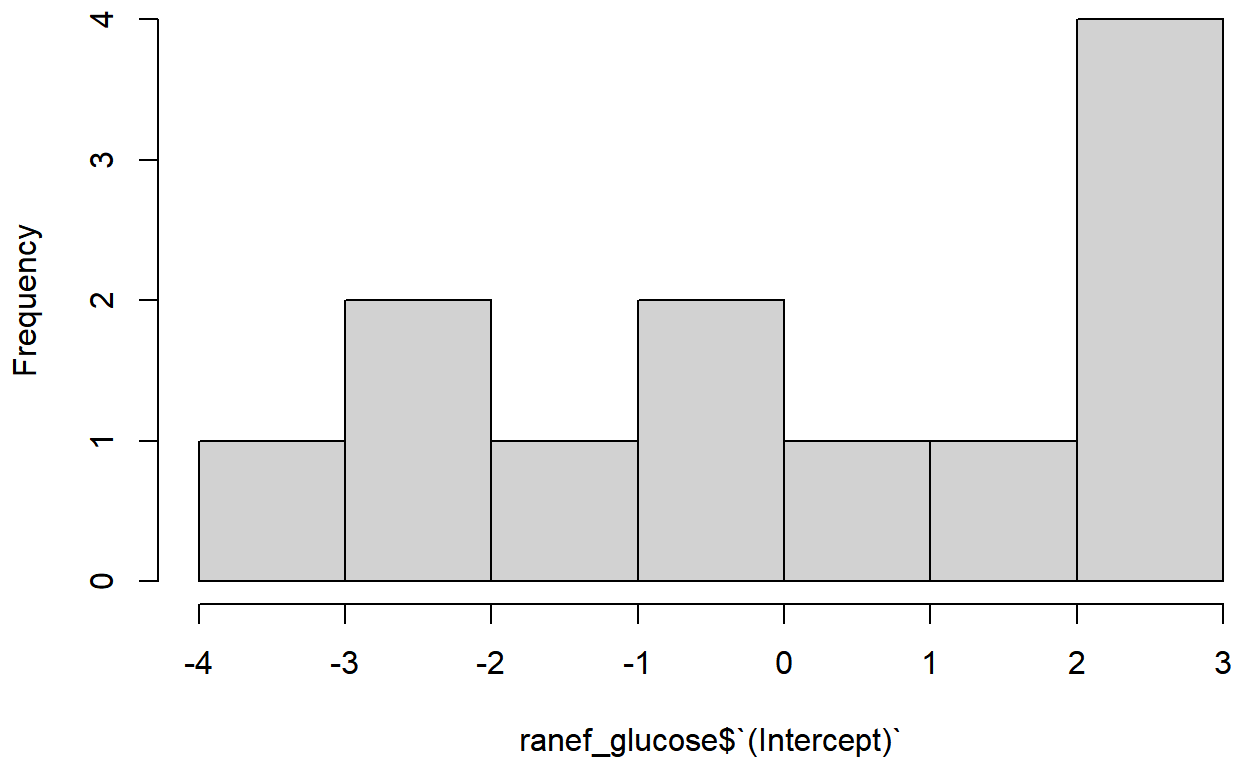
```
ranef_glucose <- ranef(m_model)$rep # To check normality of rep random effect  
qqnorm(ranef_glucose$('Intercept'))  
qqline(ranef_glucose$('Intercept'), col="red")
```

Normal Q-Q Plot



```
hist(ranef_glucose$(Intercept))
```


Histogram of ranef_glucose\$(Intercept)`



5. Write one sentence comparing the conclusions one would draw from each model and one sentence interpreting the mixed-effects model.

A1) In comparing the conclusions from each model, both indicate that the drug slaframine has a significant effect on glucose levels; however, the mixed effects model provides more reliable results by accounting for variability among replicates.

A2) The mixed effects model suggests that slaframine treatment increases glucose levels by approximately 12.39 mg/dl.