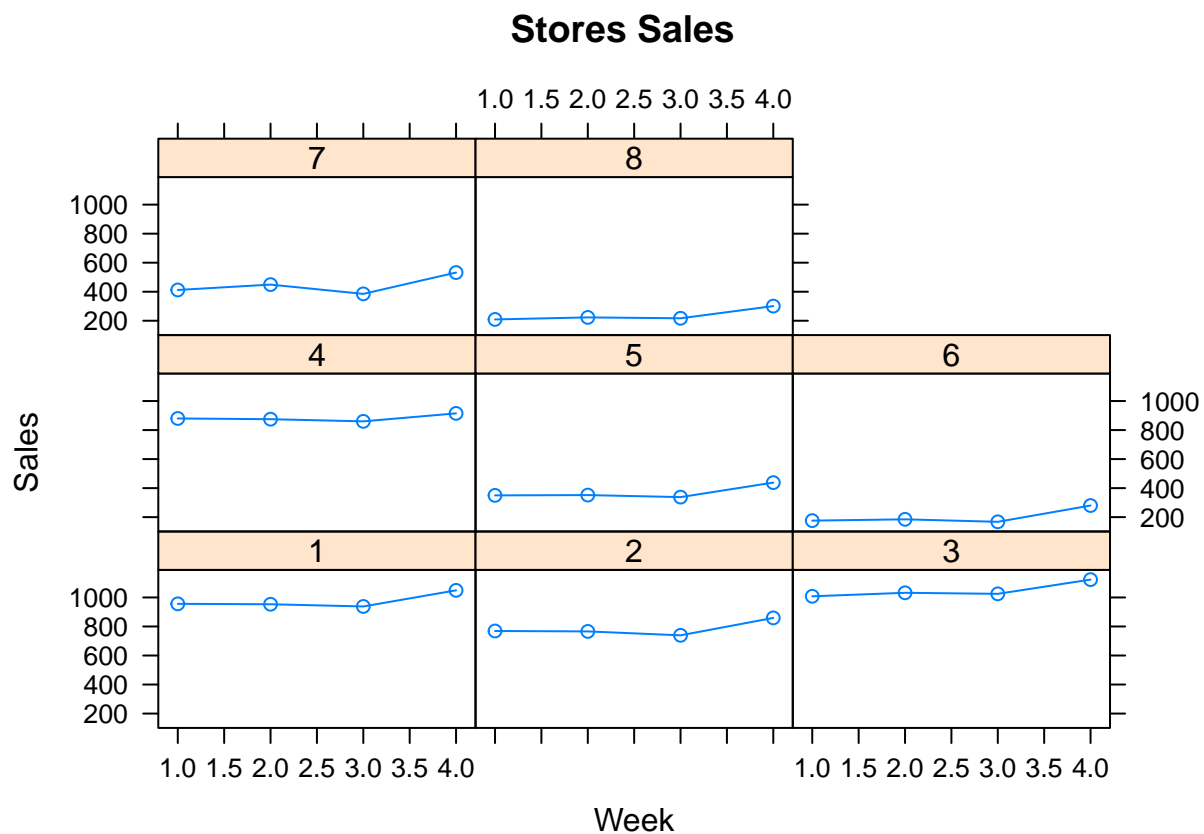# STAT4051Hw7

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12/4/2019

Store Sales Problem

```r
StoreSales<-read.csv("storesales.csv")
```

a.

```r
library(lattice)
xyplot(sales~week|as.factor(store),data = StoreSales,layout=c(3,3),type="o", main="Stores Sales",
ylab="Sales",xlab="Week")
```


From these plots, store 3 sold the most.

Basically,each store had an increase in sales form week3 to week4 but store 1 looks like increased the most.

b.

```r
##Random intercept:
library(lme4)
```

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

```r
model1.1<-lmer(sales~type.display+week+(1|store),data =StoreSales)
summary(model1.1)
```

```
## Linear mixed model fit by REML ['lmerMod']
```

```
## Formula: sales ~ type.display + week + (1 | store)
##    Data: StoreSales
##
## REML criterion at convergence: 336.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.96752 -0.37932  0.07314  0.65918  1.30452
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  store    (Intercept) 124824   353.30
##  Residual              1377     37.11
## Number of obs: 32, groups:  store, 8
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)   827.187    395.822   2.090
## type.display -182.375    250.168  -0.729
## week           25.575      5.868   4.359
##
## Correlation of Fixed Effects:
##             (Intr) typ.ds
## type.disply -0.948
## week        -0.037  0.000
```

```r
model1.2<-lmer(sales~type.display*week+(1|store),data =StoreSales)
summary(model1.2)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: sales ~ type.display * week + (1 | store)
##    Data: StoreSales
##
## REML criterion at convergence: 329.5
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.9783 -0.3539  0.1205  0.6581  1.1588
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  store    (Intercept) 124812   353.29
##  Residual              1422     37.71
## Number of obs: 32, groups:  store, 8
##
## Fixed effects:
##                   Estimate Std. Error t value
## (Intercept)         803.75     398.35   2.018
## type.display       -166.75     251.94  -0.662
## week                 34.95      18.86   1.854
## type.display:week    -6.25      11.93  -0.524
##
## Correlation of Fixed Effects:
##             (Intr) typ.ds week
## type.disply -0.949
```

```
## week         -0.118   0.112
## typ.dsply:w   0.112  -0.118  -0.949
```

```
anova(model1.1,model1.2)
```

```
## refitting model(s) with ML (instead of REML)
```

```
## Data: StoreSales
## Models:
## model1.1: sales ~ type.display + week + (1 | store)
## model1.2: sales ~ type.display * week + (1 | store)
##          Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## model1.1  5 375.95 383.27 -182.97   365.95
## model1.2  6 377.65 386.44 -182.82   365.65 0.2978      1     0.5853
```

```
##model.1 has a samller AIC  and BIC
##Random intercept and Randon Slopes:
model1.3<-lmer(sales~type.display+week+(week|store),data =StoreSales)
```

```
## boundary (singular) fit: see ?isSingular
```

```
summary(model1.3)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: sales ~ type.display + week + (week | store)
##    Data: StoreSales
##
## REML criterion at convergence: 336.4
##
## Scaled residuals:
##      Min      1Q   Median       3Q      Max
## -1.99957 -0.39048  0.05004  0.58510  1.23235
##
## Random effects:
##  Groups   Name        Variance  Std.Dev. Corr
##  store    (Intercept) 1.288e+05 358.935
##           week        5.914e+00   2.432  -1.00
##  Residual             1.368e+03  36.988
## Number of obs: 32, groups:  store, 8
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  855.966    392.241   2.182
## type.display -201.561    247.199  -0.815
## week          25.575      5.911   4.327
##
## Correlation of Fixed Effects:
##            (Intr) typ.ds
## type.disply -0.945
## week        -0.084  0.000
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

```
model1.4<-lmer(sales~type.display*week+(week|store),data =StoreSales)
```

```
## boundary (singular) fit: see ?isSingular
```

```
summary(model1.4)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: sales ~ type.display * week + (week | store)
##    Data: StoreSales
##
## REML criterion at convergence: 329.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.01143 -0.34711  0.09401  0.62559  1.21742
##
## Random effects:
##  Groups   Name        Variance  Std.Dev. Corr
##  store    (Intercept) 1.292e+05 359.440
##           week        7.218e+00   2.687  -1.00
##  Residual             1.413e+03  37.591
## Number of obs: 32, groups:  store, 8
##
## Fixed effects:
##                   Estimate Std. Error t value
## (Intercept)         803.75     405.15   1.984
## type.display       -166.75     256.24  -0.651
## week                 34.95      19.03   1.836
## type.display:week    -6.25      12.04  -0.519
##
## Correlation of Fixed Effects:
##             (Intr) typ.ds week
## type.disply -0.949
## week        -0.271  0.257
## typ.dsply:w  0.257 -0.271 -0.949
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

```
anova(model1.3,model1.4)
```

```
## refitting model(s) with ML (instead of REML)
```

```
## Data: StoreSales
## Models:
## model1.3: sales ~ type.display + week + (week | store)
## model1.4: sales ~ type.display * week + (week | store)
##          Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## model1.3  7 379.77 390.03 -182.88   365.77
## model1.4  8 381.48 393.20 -182.74   365.48 0.2935      1      0.588
```

```
##model.3 has a samller AIC  and BIC
##Random intercept and Randon Slopes Uncorrelated:
model1.5<-lmer(sales~type.display+week+(1|store)+(0+week|store),data =StoreSales)
```

```
## boundary (singular) fit: see ?isSingular
```

```
summary(model1.5)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: sales ~ type.display + week + (1 | store) + (0 + week | store)
```

```
##      Data: StoreSales
##
## REML criterion at convergence: 336.5
##
## Scaled residuals:
##      Min        1Q    Median        3Q       Max
## -1.96752 -0.37932   0.07314   0.65918   1.30452
##
## Random effects:
##  Groups    Name        Variance Std.Dev.
##  store     (Intercept) 124823   353.30
##  store.1   week             0     0.00
##  Residual              1377     37.11
## Number of obs: 32, groups:  store, 8
##
## Fixed effects:
##               Estimate Std. Error t value
## (Intercept)    827.188    395.821   2.090
## type.display  -182.375    250.167  -0.729
## week            25.575      5.868   4.359
##
## Correlation of Fixed Effects:
##             (Intr) typ.ds
## type.disply -0.948
## week        -0.037  0.000
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

```r
model1.6<-lmer(sales~type.display*week+(1|store)+(0+week|store),data =StoreSales)
```

```
## boundary (singular) fit: see ?isSingular
```

```r
summary(model1.6)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: sales ~ type.display * week + (1 | store) + (0 + week | store)
##      Data: StoreSales
##
## REML criterion at convergence: 329.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.9783 -0.3539   0.1205   0.6581   1.1588
##
## Random effects:
##  Groups    Name        Variance Std.Dev.
##  store     (Intercept) 124795   353.26
##  store.1   week             0     0.00
##  Residual              1422     37.71
## Number of obs: 32, groups:  store, 8
##
## Fixed effects:
##                  Estimate Std. Error t value
## (Intercept)        803.75     398.32   2.018
## type.display      -166.75     251.92  -0.662
```

```
## week                        34.95       18.86    1.854
## type.display:week   -6.25       11.93   -0.524
##
## Correlation of Fixed Effects:
##              (Intr) typ.ds week
## type.disply -0.949
## week         -0.118  0.112
## typ.dsply:w  0.112 -0.118 -0.949
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

```r
anova(model1.5,model1.6)
```

```
## refitting model(s) with ML (instead of REML)
```

```
## Data: StoreSales
## Models:
## model1.5: sales ~ type.display + week + (1 | store) + (0 + week | store)
## model1.6: sales ~ type.display * week + (1 | store) + (0 + week | store)
##          Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## model1.5  6 377.95 386.74 -182.97   365.95
## model1.6  7 379.65 389.91 -182.82   365.65 0.2978      1     0.5853
```

```r
##model.5 has a samller AIC  and BIC
anova(model1.1,model1.3,model1.5)
```

```
## refitting model(s) with ML (instead of REML)
```

```
## Data: StoreSales
## Models:
## model1.1: sales ~ type.display + week + (1 | store)
## model1.5: sales ~ type.display + week + (1 | store) + (0 + week | store)
## model1.3: sales ~ type.display + week + (week | store)
##          Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## model1.1  5 375.95 383.27 -182.97   365.95
## model1.5  6 377.95 386.74 -182.97   365.95 0.0000      1     1.0000
## model1.3  7 379.77 390.03 -182.88   365.77 0.1751      1     0.6756
```

```r
####model.1 has a samller AIC  and BIC
##Final model:
##sales~type.display+week+(1|store)
```

c.

```r
##Final model: Random intercept model
model1.1<-lmer(sales~type.display+week+(1|store),data =StoreSales)
summary(model1.1)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: sales ~ type.display + week + (1 | store)
##    Data: StoreSales
##
## REML criterion at convergence: 336.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.96752 -0.37932  0.07314  0.65918  1.30452
##
```

```
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  store   (Intercept) 124824   353.30
##  Residual              1377    37.11
## Number of obs: 32, groups:  store, 8
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)   827.187    395.822   2.090
## type.display -182.375    250.168  -0.729
## week           25.575      5.868   4.359
##
## Correlation of Fixed Effects:
##            (Intr) typ.ds
## type.disply -0.948
## week        -0.037  0.000
```

```
##Check assumptions:
##Random intercept:
Random<-ranef(model1.1)$store[["(Intercept)"]]
qqnorm(Random,main = "Random Intercept")
```
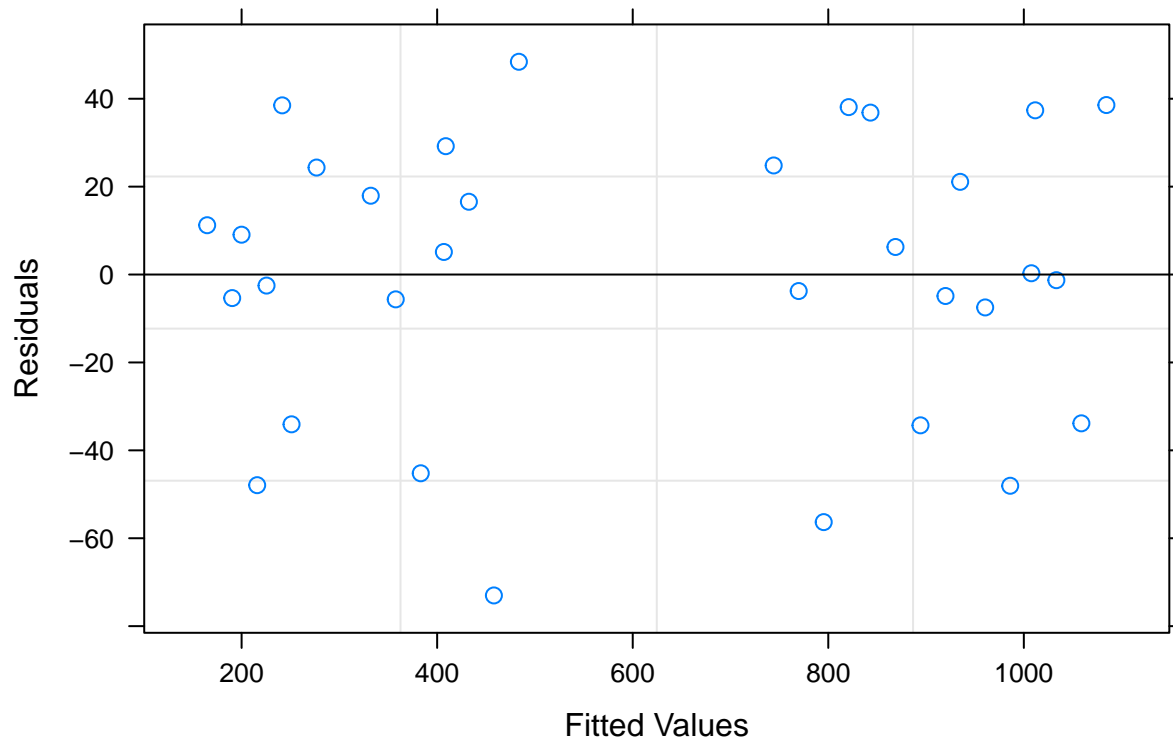
Random Intercept
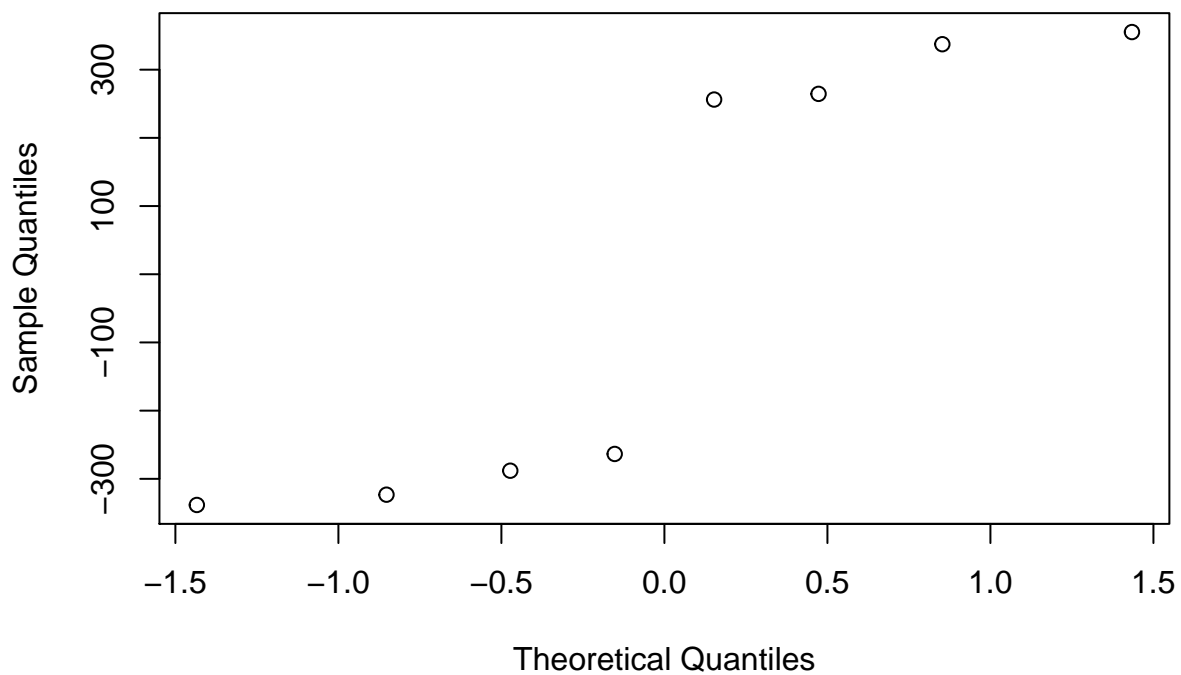

```
##qqline(Random)
##Residuals:
Residuals<-residuals(model1.1)
qqnorm(Residuals,main="Residuals")
```

Residuals
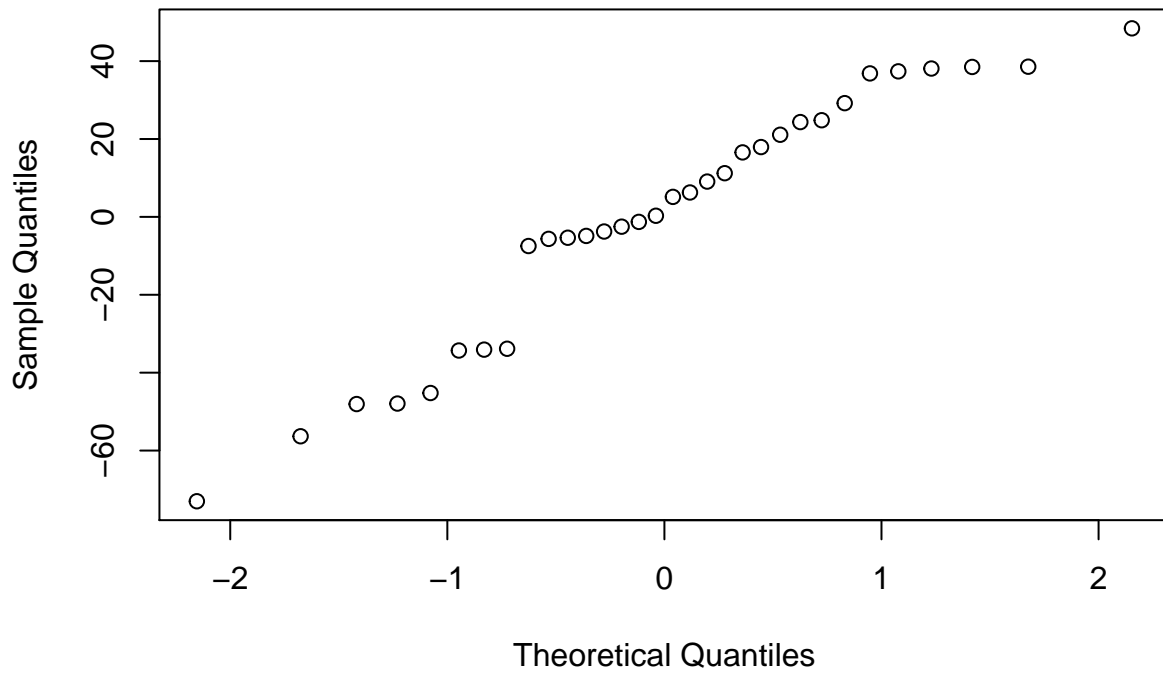

```
##qqline(Residuals)
##Constant Variance:
plot(model1.1,xlab = "Fitted Values",ylab="Residuals",main = "Constant Variance Asumption-Random Interc
```

Constant Variance Asumption–Random Intercept Model

```
##The assumptions look good
```

d.

```
est.intraclass=124824/(124824+1377)
est.intraclass
```

```
## [1] 0.9890888
```

It represents that the proportion of the total residual variability that is due to variability between stores is 98.90888%.

e.

```
ranef(model1.1)
```

```
## $store
##   (Intercept)
## 1    264.5204
## 2    256.1684
## 3    337.3196
## 4    355.1454
## 5   -338.3169
## 6   -323.2335
## 7   -263.5232
## 8   -288.0804
##
## with conditional variances for "store"
```

```
(827.187-288.0804)+25.575*4-182.375*2
```
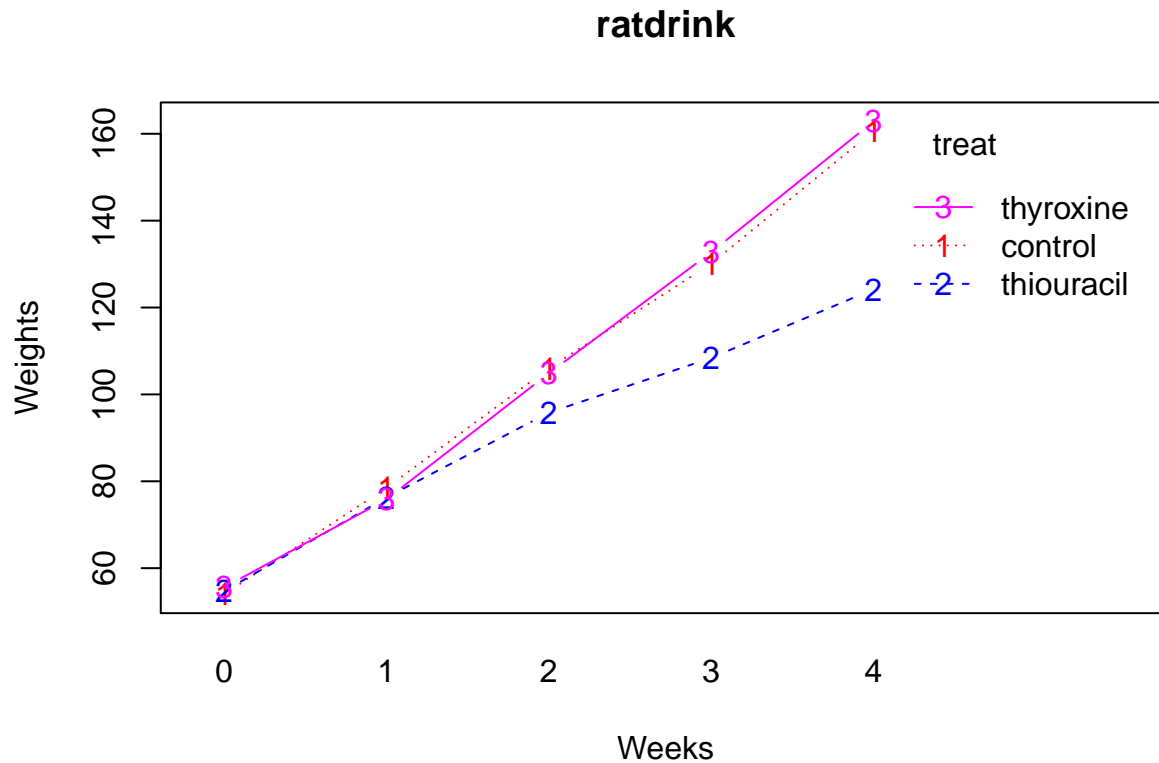
```
## [1] 276.6566
```

Ratdrink Problem

```
data(ratdrink,package = "faraway")
attach(ratdrink)
```

a.

```
interaction.plot(ratdrink$weeks,ratdrink$treat,ratdrink$wt, type="b",
                 xlab="Weeks",ylab="Weights",main="ratdrink",col=c(2,4,6),trace.label="treat")
```

ratdrink

In the three treatment groups, the weight keeps going up in these four weeks.

From this plot, we are difficult to see there is a diffrence between thyroxine and control but it is obvious that thiouracil is diffrent to thyroxine and control.

b.

```r
ratdrink.wide<-reshape(ratdrink,direction = "wide",idvar = c("subject","treat"),timevar = "weeks")
renw.rat.new<-ratdrink.wide[,-(1:2)]
round(cor(renw.rat.new),4)
```

```
##        wt.0   wt.1   wt.2   wt.3   wt.4
## wt.0 1.0000 0.8214 0.6065 0.3491 0.2023
## wt.1 0.8214 1.0000 0.7893 0.4478 0.2982
## wt.2 0.6065 0.7893 1.0000 0.8732 0.7741
## wt.3 0.3491 0.4478 0.8732 1.0000 0.9582
## wt.4 0.2023 0.2982 0.7741 0.9582 1.0000
```

```r
##control:
renw.rat<-ratdrink.wide[(1:10),-(1:2)]
round(cor(renw.rat),4)
```

```
##        wt.0   wt.1   wt.2   wt.3   wt.4
## wt.0 1.0000 0.9455 0.7333 0.4083 0.3174
## wt.1 0.9455 1.0000 0.8828 0.5939 0.4695
## wt.2 0.7333 0.8828 1.0000 0.8895 0.7959
## wt.3 0.4083 0.5939 0.8895 1.0000 0.9429
## wt.4 0.3174 0.4695 0.7959 0.9429 1.0000
```

```r
##thyromine:
renw.rat.th<-ratdrink.wide[(11:17),-(1:2)]
round(cor(renw.rat.th),4)
```

```
##         wt.0   wt.1   wt.2   wt.3   wt.4
## wt.0 1.0000 0.8266 0.6755 0.5385 0.4833
## wt.1 0.8266 1.0000 0.8649 0.6428 0.5823
## wt.2 0.6755 0.8649 1.0000 0.8950 0.8596
## wt.3 0.5385 0.6428 0.8950 1.0000 0.9882
## wt.4 0.4833 0.5823 0.8596 0.9882 1.0000
```

```r
##thiouracil
renw.rat.t<-ratdrink.wide[(18:27),-(1:2)]
round(cor(renw.rat.t),4)
```

```
##         wt.0   wt.1   wt.2   wt.3   wt.4
## wt.0 1.0000 0.7506 0.7454 0.6271 0.2905
## wt.1 0.7506 1.0000 0.8699 0.5298 0.1853
## wt.2 0.7454 0.8699 1.0000 0.8134 0.5340
## wt.3 0.6271 0.5298 0.8134 1.0000 0.8079
## wt.4 0.2905 0.1853 0.5340 0.8079 1.0000
```

The correlations are positive but they are not closely. And, correaltions decrease with increasing time separations.

c.

```r
##control:
renw.rat<-ratdrink.wide[(1:10),-(1:2)]
cov(renw.rat)
```

```
##          wt.0     wt.1     wt.2      wt.3      wt.4
## wt.0 29.55556 49.55556  39.55556  27.88889  26.22222
## wt.1 49.55556 92.94444  84.44444  71.94444  68.77778
## wt.2 39.55556 84.44444  98.44444 110.88889 120.00000
## wt.3 27.88889 71.94444 110.88889 157.87778 180.04444
## wt.4 26.22222 68.77778 120.00000 180.04444 230.93333
```

```r
##Variance:
(157.87778+230.93333-2*180.04444)/10
```

```
## [1] 2.872223
```

d.

```r
#Variance without covariance:
(157.87778+230.93333)/10
```

```
## [1] 38.88111
```

The result in part d is larger than part e.Because we ignored that the there is correaltions among the repeated measures.

e.

```r
##Random intercept:
library(lme4)
model2.1<-lmer(wt~treat+weeks+(1|subject),data=ratdrink)
summary(model2.1)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: wt ~ treat + weeks + (1 | subject)
##    Data: ratdrink
##
## REML criterion at convergence: 1031.1
```

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```
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.66861 -0.59657 -0.07263  0.59456  2.85455
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  subject  (Intercept)  60.42    7.773
##  Residual             105.15   10.254
## Number of obs: 135, groups:  subject, 27
##
## Fixed effects:
##                Estimate Std. Error t value
## (Intercept)     59.4770     3.1150  19.094
## treatthiouracil -13.9600     4.0361  -3.459
## treatthyroxine   0.5314     4.4476   0.119
## weeks           23.1815     0.6241  37.146
##
## Correlation of Fixed Effects:
##            (Intr) trtthr trtthy
## treatthircl -0.648
## treatthyrxn -0.588  0.454
## weeks       -0.401  0.000  0.000
```

```r
model2.2<-lmer(wt~treat*weeks+(1|subject),data =ratdrink)
summary(model2.2)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: wt ~ treat * weeks + (1 | subject)
##    Data: ratdrink
##
## REML criterion at convergence: 948.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.05506 -0.65511 -0.04848  0.57702  2.80847
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  subject  (Intercept) 71.21     8.438
##  Residual             51.22     7.157
## Number of obs: 135, groups:  subject, 27
##
## Fixed effects:
##                      Estimate Std. Error t value
## (Intercept)           52.8800     3.1928  16.562
## treatthiouracil        4.7800     4.5153   1.059
## treatthyroxine        -0.7943     4.9756  -0.160
## weeks                 26.4800     0.7157  36.999
## treatthiouracil:weeks -9.3700     1.0121  -9.258
## treatthyroxine:weeks   0.6629     1.1153   0.594
##
## Correlation of Fixed Effects:
##            (Intr) trtthr trtthy weeks  trtthr:
## treatthircl -0.707
```

```
## treatthyrxn -0.642  0.454
## weeks        -0.448  0.317  0.288
## trtthrcl:wk  0.317 -0.448 -0.203 -0.707
## trtthyrxn:w  0.288 -0.203 -0.448 -0.642  0.454
```

```
anova(model2.1,model2.2)
```

```
## refitting model(s) with ML (instead of REML)
```

```
## Data: ratdrink
## Models:
## model2.1: wt ~ treat + weeks + (1 | subject)
## model2.2: wt ~ treat * weeks + (1 | subject)
##          Df     AIC     BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## model2.1  6 1055.97 1073.4 -521.98  1043.97
## model2.2  8  980.25 1003.5 -482.13   964.25 79.714      2  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##selected model : wt ~ treat * weeks + (1 | subject) because it has samller AIC and BIC.
```

f.

```
model2.2<-lmer(wt~treat*weeks+(1|subject),data =ratdrink)
summary(model2.2)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: wt ~ treat * weeks + (1 | subject)
##    Data: ratdrink
##
## REML criterion at convergence: 948.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.05506 -0.65511 -0.04848  0.57702  2.80847
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  subject  (Intercept) 71.21    8.438
##  Residual             51.22    7.157
## Number of obs: 135, groups:  subject, 27
##
## Fixed effects:
##                       Estimate Std. Error t value
## (Intercept)            52.8800     3.1928  16.562
## treatthiouracil         4.7800     4.5153   1.059
## treatthyroxine         -0.7943     4.9756  -0.160
## weeks                  26.4800     0.7157  36.999
## treatthiouracil:weeks  -9.3700     1.0121  -9.258
## treatthyroxine:weeks    0.6629     1.1153   0.594
##
## Correlation of Fixed Effects:
##             (Intr) trtthr trtthy weeks  trtthr:
## treatthircl -0.707
## treatthyrxn -0.642  0.454
## weeks       -0.448  0.317  0.288
## trtthrcl:wk  0.317 -0.448 -0.203 -0.707
```

```
## trtthyrxn:w  0.288 -0.203 -0.448 -0.642  0.454
```

```
##intra-class correlation :
71.21/(71.21+51.22)
```

```
## [1] 0.5816385
```

```
in_cla=71.21/(71.21+51.22)
##matrix
c0=c(1,in_cla,in_cla,in_cla,in_cla)
c1=c(in_cla,1,in_cla,in_cla,in_cla)
c2=c(in_cla,in_cla,1,in_cla,in_cla)
c3=c(in_cla,in_cla,in_cla,1,in_cla)
c4=c(in_cla,in_cla,in_cla,in_cla,1)
rbind(c0,c1,c2,c3,c4)
```

```
##          [,1]      [,2]      [,3]      [,4]      [,5]
## c0 1.0000000 0.5816385 0.5816385 0.5816385 0.5816385
## c1 0.5816385 1.0000000 0.5816385 0.5816385 0.5816385
## c2 0.5816385 0.5816385 1.0000000 0.5816385 0.5816385
## c3 0.5816385 0.5816385 0.5816385 1.0000000 0.5816385
## c4 0.5816385 0.5816385 0.5816385 0.5816385 1.0000000
```

The values are not close to the observed correlations in the correaltion matrix in part b.

g.

```
##part e:model2.2<-lmer(wt~treat*weeks+(1|subject),data =ratdrink)
library(nlme)
```

```
##
## Attaching package: 'nlme'
```

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

```
#Compound Symmetry
model.cs<-lme(wt~treat*weeks,random=~1|subject,
              correlation=corCompSymm(),data=ratdrink)
summary(model.cs)
```

```
## Linear mixed-effects model fit by REML
##  Data: ratdrink
##      AIC      BIC    logLik
##   966.449 992.1873 -474.2245
##
## Random effects:
##  Formula: ~1 | subject
##         (Intercept) Residual
## StdDev:    8.438424 7.156962
##
## Correlation Structure: Compound symmetry
##  Formula: ~1 | subject
##  Parameter estimate(s):
## Rho
##   0
## Fixed effects: wt ~ treat * weeks
##                        Value Std.Error  DF  t-value p-value
```

```
## (Intercept)                 52.88000  3.192809 105 16.56222  0.0000
## treatthiouracil              4.78000  4.515313  24  1.05862  0.3003
## treatthyroxine              -0.79429  4.975633  24 -0.15964  0.8745
## weeks                        26.48000  0.715696 105 36.99894  0.0000
## treatthiouracil:weeks -9.37000  1.012147 105 -9.25755  0.0000
## treatthyroxine:weeks   0.66286  1.115332 105  0.59431  0.5536
##   Correlation:
##                        (Intr) trtthr trtthy weeks  trtthr:
## treatthiouracil        -0.707
## treatthyroxine         -0.642  0.454
## weeks                  -0.448  0.317  0.288
## treatthiouracil:weeks   0.317 -0.448 -0.203 -0.707
## treatthyroxine:weeks    0.288 -0.203 -0.448 -0.642  0.454
##
## Standardized Within-Group Residuals:
##        Min          Q1         Med          Q3         Max
## -2.05506194 -0.65511142 -0.04848034  0.57701921  2.80847492
##
## Number of Observations: 135
## Number of Groups: 27
```

```
##AIC:966.449 BIC:992.1873  Residual:7.156962
#AR1:
model.ar<-lme(wt~treat*weeks,random=~1|subject,
              correlation=corAR1(),data=ratdrink)
summary(model.ar)
```

```
## Linear mixed-effects model fit by REML
##  Data: ratdrink
##        AIC      BIC    logLik
##   900.2353 925.9736 -441.1176
##
## Random effects:
##  Formula: ~1 | subject
##         (Intercept) Residual
## StdDev: 0.001679146 11.49777
##
## Correlation Structure: AR(1)
##  Formula: ~1 | subject
##  Parameter estimate(s):
##       Phi
## 0.8467006
## Fixed effects: wt ~ treat * weeks
##                        Value Std.Error  DF    t-value p-value
## (Intercept)           53.56221  3.624471 105 14.777940  0.0000
## treatthiouracil        1.92169  5.125776  24  0.374908  0.7110
## treatthyroxine         1.09097  5.648330  24  0.193149  0.8485
## weeks                 26.64143  0.896149 105 29.728803  0.0000
## treatthiouracil:weeks -9.27979  1.267346 105 -7.322226  0.0000
## treatthyroxine:weeks   0.19621  1.396547 105  0.140497  0.8885
##   Correlation:
##                        (Intr) trtthr trtthy weeks  trtthr:
## treatthiouracil        -0.707
## treatthyroxine         -0.642  0.454
## weeks                  -0.494  0.350  0.317
```

```
## treatthiouracil:weeks  0.350 -0.494 -0.224 -0.707
## treatthyroxine:weeks   0.317 -0.224 -0.494 -0.642  0.454
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -2.18877989 -0.60763893  0.06926202  0.59108141  2.34795570
##
## Number of Observations: 135
## Number of Groups: 27
```

```
##AIC:900.2353   BIC:925.9736  Residual:11.49777
#Unstructured:
model.un<-lme(wt~treat*weeks,random=~1|subject,
              correlation=corSymm(),data=ratdrink)
summary(model.un)
```

```
## Linear mixed-effects model fit by REML
##  Data: ratdrink
##       AIC       BIC    logLik
##   890.1378 941.6144 -427.0689
##
## Random effects:
##  Formula: ~1 | subject
##         (Intercept) Residual
## StdDev:    8.349935 9.062099
##
## Correlation Structure: General
##  Formula: ~1 | subject
##  Parameter estimate(s):
##  Correlation:
##   1      2      3      4
## 2  0.774
## 3  0.668  0.879
## 4  0.081  0.308  0.639
## 5 -0.496 -0.344  0.111  0.704
## Fixed effects: wt ~ treat * weeks
##                        Value Std.Error  DF   t-value p-value
## (Intercept)          53.28689  3.141953 105 16.959801  0.0000
## treatthiouracil      -5.74146  4.443392  24 -1.292134  0.2086
## treatthyroxine        1.71779  4.896380  24  0.350829  0.7288
## weeks                27.07603  1.049693 105 25.794231  0.0000
## treatthiouracil:weeks -7.32052  1.484491 105 -4.931333  0.0000
## treatthyroxine:weeks  -0.84091  1.635829 105 -0.514058  0.6083
##   Correlation:
##                        (Intr) trtthr trtthy weeks  trtthr:
## treatthiouracil        -0.707
## treatthyroxine         -0.642  0.454
## weeks                  -0.539  0.381  0.346
## treatthiouracil:weeks   0.381 -0.539 -0.245 -0.707
## treatthyroxine:weeks    0.346 -0.245 -0.539 -0.642  0.454
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -2.30470027 -0.57975984  0.07056203  0.71075996  2.52047056
##
```

```
## Number of Observations: 135
## Number of Groups: 27
```

```
##AIC:890.1378 BIC:941.6144   Residual: 9.062099
##Compund Symmetry has the samllest StdDev residual
##AR(1) has the samllesst BIC
##Unstructures has the samllest AIC
##A diffrent matrix fits the data better
```

h.

```
#Random Intercept and Random Slope:
model2.3<-lmer(wt~treat+weeks+(weeks|subject),data=ratdrink)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl =
## control$checkConv, : Model failed to converge with max|grad| = 0.00400474
## (tol = 0.002, component 1)
```

```
summary(model2.3)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: wt ~ treat + weeks + (weeks | subject)
##    Data: ratdrink
##
## REML criterion at convergence: 908.7
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.8313 -0.5423 -0.0109  0.5490  2.0364
##
## Random effects:
##  Groups   Name        Variance Std.Dev. Corr
##  subject  (Intercept) 36.15    6.013
##           weeks       35.46    5.955    -0.33
##  Residual             18.91    4.348
## Number of obs: 135, groups:  subject, 27
##
## Fixed effects:
##                 Estimate Std. Error t value
## (Intercept)      54.2428     2.0852  26.013
## treatthiouracil   0.9086     2.8677   0.317
## treatthyroxine   -0.5204     3.1600  -0.165
## weeks            23.1815     1.1762  19.709
##
## Correlation of Fixed Effects:
##             (Intr) trtthr trtthy
## treatthircl -0.688
## treatthyrxn -0.624  0.454
## weeks       -0.233  0.000  0.000
## convergence code: 0
## Model failed to converge with max|grad| = 0.00400474 (tol = 0.002, component 1)
```

```
model2.4<-lmer(wt~treat*weeks+(weeks|subject),data =ratdrink)
summary(model2.4)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: wt ~ treat * weeks + (weeks | subject)
```

```
##     Data: ratdrink
##
## REML criterion at convergence: 878.7
##
## Scaled residuals:
##       Min       1Q   Median       3Q      Max
## -1.83137 -0.54991  0.04003  0.58233  2.03661
##
## Random effects:
##  Groups    Name        Variance Std.Dev. Corr
##  subject  (Intercept) 32.50    5.700
##            weeks       14.14    3.760   -0.13
##  Residual              18.90    4.348
## Number of obs: 135, groups:  subject, 27
##
## Fixed effects:
##                        Estimate Std. Error t value
## (Intercept)             52.8800     2.0938  25.256
## treatthiouracil          4.7800     2.9610   1.614
## treatthyroxine          -0.7943     3.2629  -0.243
## weeks                   26.4800     1.2661  20.915
## treatthiouracil:weeks   -9.3700     1.7905  -5.233
## treatthyroxine:weeks     0.6629     1.9731   0.336
##
## Correlation of Fixed Effects:
##             (Intr) trtthr trtthy weeks  trtthr:
## treatthircl -0.707
## treatthyrxn -0.642  0.454
## weeks       -0.250  0.177  0.160
## trtthrcl:wk  0.177 -0.250 -0.113 -0.707
## trtthyrxn:w  0.160 -0.113 -0.250 -0.642  0.454
```

```r
anova(model2.3,model2.4)
```

```
## refitting model(s) with ML (instead of REML)
```

```
## Data: ratdrink
## Models:
## model2.3: wt ~ treat + weeks + (weeks | subject)
## model2.4: wt ~ treat * weeks + (weeks | subject)
##          Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## model2.3  8 936.74 959.98 -460.37   920.74
## model2.4 10 915.71 944.76 -447.86   895.71 25.025      2   3.68e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#Random Intercept and Random Slope Uncorrealted:
model2.5<-lmer(wt~treat+weeks+(1|subject)+(0+weeks|subject),data=ratdrink)
summary(model2.5)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: wt ~ treat + weeks + (1 | subject) + (0 + weeks | subject)
##     Data: ratdrink
##
## REML criterion at convergence: 909.5
##
```

```
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.86835 -0.54256  0.06058  0.56014  2.02428
##
## Random effects:
##  Groups    Name        Variance Std.Dev.
##  subject   (Intercept) 31.60    5.622
##  subject.1 weeks       34.66    5.887
##  Residual              19.04    4.364
## Number of obs: 135, groups:  subject, 27
##
## Fixed effects:
##                 Estimate Std. Error t value
## (Intercept)      53.2236     2.0683  25.734
## treatthiouracil   3.8041     2.9199   1.303
## treatthyroxine   -0.7252     3.2176  -0.225
## weeks            23.1815     1.1637  19.920
##
## Correlation of Fixed Effects:
##            (Intr) trtthr trtthy
## treatthircl -0.706
## treatthyrxn -0.641  0.454
## weeks       -0.059  0.000  0.000
```

```
model2.6<-lmer(wt~treat*weeks+(1|subject)+(0+weeks|subject),data =ratdrink)
summary(model2.6)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: wt ~ treat * weeks + (1 | subject) + (0 + weeks | subject)
##    Data: ratdrink
##
## REML criterion at convergence: 879
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.8475 -0.5634  0.0523  0.5627  2.0271
##
## Random effects:
##  Groups    Name        Variance Std.Dev.
##  subject   (Intercept) 31.04    5.571
##  subject.1 weeks       13.63    3.691
##  Residual              19.08    4.369
## Number of obs: 135, groups:  subject, 27
##
## Fixed effects:
##                       Estimate Std. Error t value
## (Intercept)            52.8800     2.0612  25.655
## treatthiouracil         4.7800     2.9150   1.640
## treatthyroxine         -0.7943     3.2122  -0.247
## weeks                  26.4800     1.2464  21.245
## treatthiouracil:weeks  -9.3700     1.7627  -5.316
## treatthyroxine:weeks    0.6629     1.9424   0.341
##
## Correlation of Fixed Effects:
##             (Intr) trtthr trtthy weeks  trtthr:
```

```
## treatthircl -0.707
## treatthyrxn -0.642  0.454
## weeks        -0.149  0.105  0.095
## trtthrcl:wk  0.105 -0.149 -0.067 -0.707
## trtthyrxn:w  0.095 -0.067 -0.149 -0.642  0.454
```

`anova(model2.5,model2.6)`

```
## refitting model(s) with ML (instead of REML)

## Data: ratdrink
## Models:
## model2.5: wt ~ treat + weeks + (1 | subject) + (0 + weeks | subject)
## model2.6: wt ~ treat * weeks + (1 | subject) + (0 + weeks | subject)
##          Df   AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## model2.5  7 935.71 956.05 -460.85   921.71
## model2.6  9 913.93 940.07 -447.96   895.93 25.784      2  2.518e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

`anova(model2.4,model2.6)`

```
## refitting model(s) with ML (instead of REML)

## Data: ratdrink
## Models:
## model2.6: wt ~ treat * weeks + (1 | subject) + (0 + weeks | subject)
## model2.4: wt ~ treat * weeks + (weeks | subject)
##          Df   AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## model2.6  9 913.93 940.07 -447.96   895.93
## model2.4 10 915.71 944.76 -447.86   895.71 0.2137      1     0.6439
```

##There is no statistical diffrence between this two models because of large p-value..I will select mode

   i.

##The correlation of   between the random intercept   and random slope is -0.13.
##This value shows that the random intercept has a negative relationship with the random slop.

   j.

##The best model of random intercept is model2.2 wt ~ treat * weeks + (1 | subject)
##The best model of random intercept and random slope is model2.6 wt ~ treat * weeks + (1 | subject) +

`anova(model2.6,model2.2)`

```
## refitting model(s) with ML (instead of REML)

## Data: ratdrink
## Models:
## model2.2: wt ~ treat * weeks + (1 | subject)
## model2.6: wt ~ treat * weeks + (1 | subject) + (0 + weeks | subject)
##          Df   AIC     BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## model2.2  8 980.25 1003.49 -482.13   964.25
## model2.6  9 913.93  940.07 -447.96   895.93 68.327      1  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

##Because model2.6 has a smaller AIC and BIC,we choose model2.6

```
##model2.6: try alternate variance-covariance matrices:
library(nlme)
#Compound Symmetry
model.css<-lme(wt~treat*weeks,random=~1|subject+weeks|subject,
               correlation=corCompSymm(),data=ratdrink)
```

```
## Warning in Ops.factor(subject, weeks): '+' not meaningful for factors
```

```
summary(model.css)
```

```
## Linear mixed-effects model fit by REML
##  Data: ratdrink
##       AIC      BIC    logLik
##   970.449 1001.907 -474.2245
##
## Random effects:
##  Formula: ~1 | subject + weeks | subject
##  Structure: General positive-definite, Log-Cholesky parametrization
##                          StdDev   Corr
## (Intercept)            7.363855 (Intr)
## 1 | subject + weeksTRUE 7.363855 -0.343
## Residual               7.156962
##
## Correlation Structure: Compound symmetry
##  Formula: ~1 | subject
##  Parameter estimate(s):
## Rho
##   0
## Fixed effects: wt ~ treat * weeks
##                            Value Std.Error  DF  t-value p-value
## (Intercept)             52.88000  3.192809 105 16.56222  0.0000
## treatthiouracil          4.78000  4.515313  24  1.05862  0.3003
## treatthyroxine          -0.79429  4.975633  24 -0.15964  0.8745
## weeks                   26.48000  0.715696 105 36.99894  0.0000
## treatthiouracil:weeks   -9.37000  1.012147 105 -9.25755  0.0000
## treatthyroxine:weeks     0.66286  1.115332 105  0.59431  0.5536
##  Correlation:
##                       (Intr) trtthr trtthy weeks  trtthr:
## treatthiouracil       -0.707
## treatthyroxine        -0.642  0.454
## weeks                 -0.448  0.317  0.288
## treatthiouracil:weeks  0.317 -0.448 -0.203 -0.707
## treatthyroxine:weeks   0.288 -0.203 -0.448 -0.642  0.454
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -2.05506194 -0.65511142 -0.04848034  0.57701921  2.80847492
##
## Number of Observations: 135
## Number of Groups: 27
```

```
#AR 1:
model.arr<-lme(wt~treat*weeks,random=~1|subject+weeks|subject,
               correlation=corAR1(),data=ratdrink)
```

```
## Warning in Ops.factor(subject, weeks): '+' not meaningful for factors
```

```
summary(model.arr)
```

```
## Linear mixed-effects model fit by REML
##   Data: ratdrink
##         AIC       BIC     logLik
##    904.2353 935.6932 -441.1176
##
## Random effects:
##   Formula: ~1 | subject + weeks | subject
##   Structure: General positive-definite, Log-Cholesky parametrization
##                          StdDev       Corr
## (Intercept)             5.657452e-04 (Intr)
## 1 | subject + weeksTRUE 1.198724e-03 0
## Residual                1.149779e+01
##
## Correlation Structure: AR(1)
##   Formula: ~1 | subject
##   Parameter estimate(s):
##        Phi
## 0.8467011
## Fixed effects: wt ~ treat * weeks
##                           Value Std.Error  DF   t-value p-value
## (Intercept)            53.56222  3.624476 105 14.777920  0.0000
## treatthiouracil         1.92169  5.125783  24  0.374907  0.7110
## treatthyroxine          1.09097  5.648338  24  0.193149  0.8485
## weeks                  26.64143  0.896149 105 29.728804  0.0000
## treatthiouracil:weeks  -9.27979  1.267346 105 -7.322226  0.0000
## treatthyroxine:weeks    0.19621  1.396547 105  0.140497  0.8885
##   Correlation:
##                       (Intr) trtthr trtthy weeks  trtthr:
## treatthiouracil       -0.707
## treatthyroxine        -0.642  0.454
## weeks                 -0.494  0.350  0.317
## treatthiouracil:weeks  0.350 -0.494 -0.224 -0.707
## treatthyroxine:weeks   0.317 -0.224 -0.494 -0.642  0.454
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -2.18877714 -0.60763823  0.06926181  0.59108065  2.34795230
##
## Number of Observations: 135
## Number of Groups: 27
```

```
#Unstructured:
model.unn<-lme(wt~treat*weeks,random=~1|subject+weeks|subject,
               correlation=corSymm(),data=ratdrink)
```

```
## Warning in Ops.factor(subject, weeks): '+' not meaningful for factors
```

```
summary(model.unn)
```

```
## Linear mixed-effects model fit by REML
##   Data: ratdrink
##         AIC       BIC     logLik
```

```
##    894.1378 951.334 -427.0689
##
## Random effects:
##  Formula: ~1 | subject + weeks | subject
##  Structure: General positive-definite, Log-Cholesky parametrization
##                          StdDev   Corr
## (Intercept)             7.478228 (Intr)
## 1 | subject + weeksTRUE 7.720133 -0.396
## Residual                9.058342
##
## Correlation Structure: General
##  Formula: ~1 | subject
##  Parameter estimate(s):
##  Correlation:
##    1      2     3     4
## 2  0.774
## 3  0.668  0.879
## 4  0.080  0.308  0.639
## 5 -0.497 -0.346  0.110  0.703
## Fixed effects: wt ~ treat * weeks
##                          Value Std.Error  DF   t-value p-value
## (Intercept)           53.28691  3.141965 105 16.959741  0.0000
## treatthiouracil       -5.74142  4.443409  24 -1.292121  0.2086
## treatthyroxine         1.71774  4.896399  24  0.350817  0.7288
## weeks                 27.07601  1.049694 105 25.794205  0.0000
## treatthiouracil:weeks -7.32052  1.484491 105 -4.931335  0.0000
## treatthyroxine:weeks  -0.84090  1.635829 105 -0.514052  0.6083
##  Correlation:
##                       (Intr) trtthr trtthy weeks  trtthr:
## treatthiouracil       -0.707
## treatthyroxine        -0.642  0.454
## weeks                 -0.539  0.381  0.346
## treatthiouracil:weeks  0.381 -0.539 -0.245 -0.707
## treatthyroxine:weeks   0.346 -0.245 -0.539 -0.642  0.454
##
## Standardized Within-Group Residuals:
##         Min         Q1        Med         Q3        Max
## -2.30722133 -0.57928670  0.06996929  0.71110541  2.52161052
##
## Number of Observations: 135
## Number of Groups: 27
```

```
##CS:AIC:970.449       BIC:1001.907      Residual:7.156962
##AR(1):AIC:904.2353         BIC:935.6932      Residual:1.149779e+01
##Uns:AIC:894.1378  BIC:894.1378 Residual:9.058342
##I will choose AR(1) because it has smaller AIC nd smaller BIC and the smallest residual
```

   j.

```
##final model:
#AR 1:
model.arr<-lme(wt~treat*weeks,random=~1|subject+weeks|subject,
              correlation=corAR1(),data=ratdrink)
```

```
## Warning in Ops.factor(subject, weeks): '+' not meaningful for factors
```

```
summary(model.arr)
```

```
## Linear mixed-effects model fit by REML
##  Data: ratdrink
##        AIC      BIC    logLik
##   904.2353 935.6932 -441.1176
##
## Random effects:
##  Formula: ~1 | subject + weeks | subject
##  Structure: General positive-definite, Log-Cholesky parametrization
##                        StdDev       Corr
## (Intercept)           5.657452e-04 (Intr)
## 1 | subject + weeksTRUE 1.198724e-03 0
## Residual              1.149779e+01
##
## Correlation Structure: AR(1)
##  Formula: ~1 | subject
##  Parameter estimate(s):
##      Phi
## 0.8467011
## Fixed effects: wt ~ treat * weeks
##                          Value Std.Error  DF   t-value p-value
## (Intercept)           53.56222  3.624476 105 14.777920  0.0000
## treatthiouracil        1.92169  5.125783  24  0.374907  0.7110
## treatthyroxine         1.09097  5.648338  24  0.193149  0.8485
## weeks                 26.64143  0.896149 105 29.728804  0.0000
## treatthiouracil:weeks -9.27979  1.267346 105 -7.322226  0.0000
## treatthyroxine:weeks   0.19621  1.396547 105  0.140497  0.8885
##  Correlation:
##                       (Intr) trtthr trtthy weeks  trtthr:
## treatthiouracil       -0.707
## treatthyroxine        -0.642  0.454
## weeks                 -0.494  0.350  0.317
## treatthiouracil:weeks  0.350 -0.494 -0.224 -0.707
## treatthyroxine:weeks   0.317 -0.224 -0.494 -0.642  0.454
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -2.18877714 -0.60763823  0.06926181  0.59108065  2.34795230
##
## Number of Observations: 135
## Number of Groups: 27
```

control:53.5622+26.6414weeks thyroxine:53.5622+26.6414weeks+1.0910+0.1962weeks=54.6532+26.8376weeks thiouracil:53.5622+26.6414weeks+1.9217-9.2798weeks=55.4839+17.3616weeks
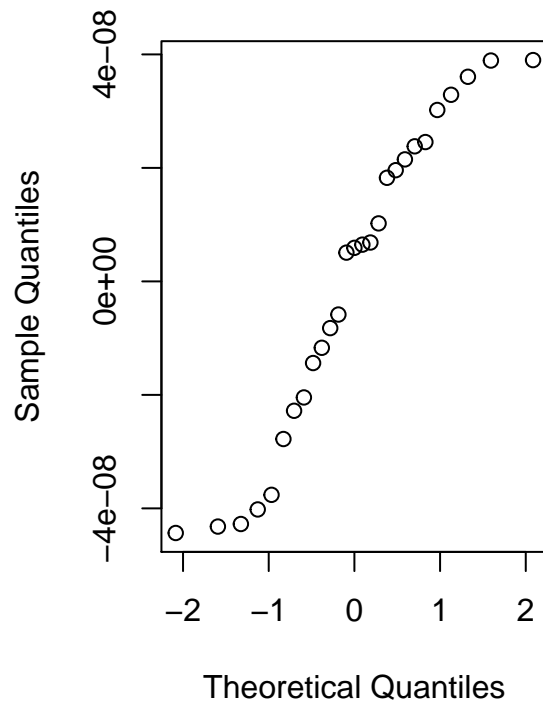
k.

```
#Examine Normality from AR(1) model
#Random Intercept
par(mfrow=c(1,2))
RandomComponents<-ranef(model.arr)
RandomIntercept<-RandomComponents[1:27,1]
qqnorm(RandomIntercept,main="Random Intercept-AR(1) Model")
##qqline(RandomIntercept)
```
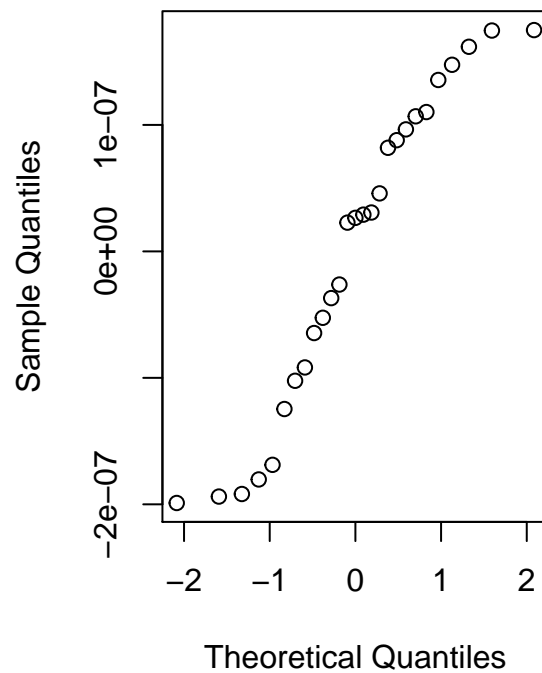
```
#Random Slope
RandomSlope<-RandomComponents[1:27,2]
qqnorm(RandomSlope,main="Random Slope-AR(1) Model")
```
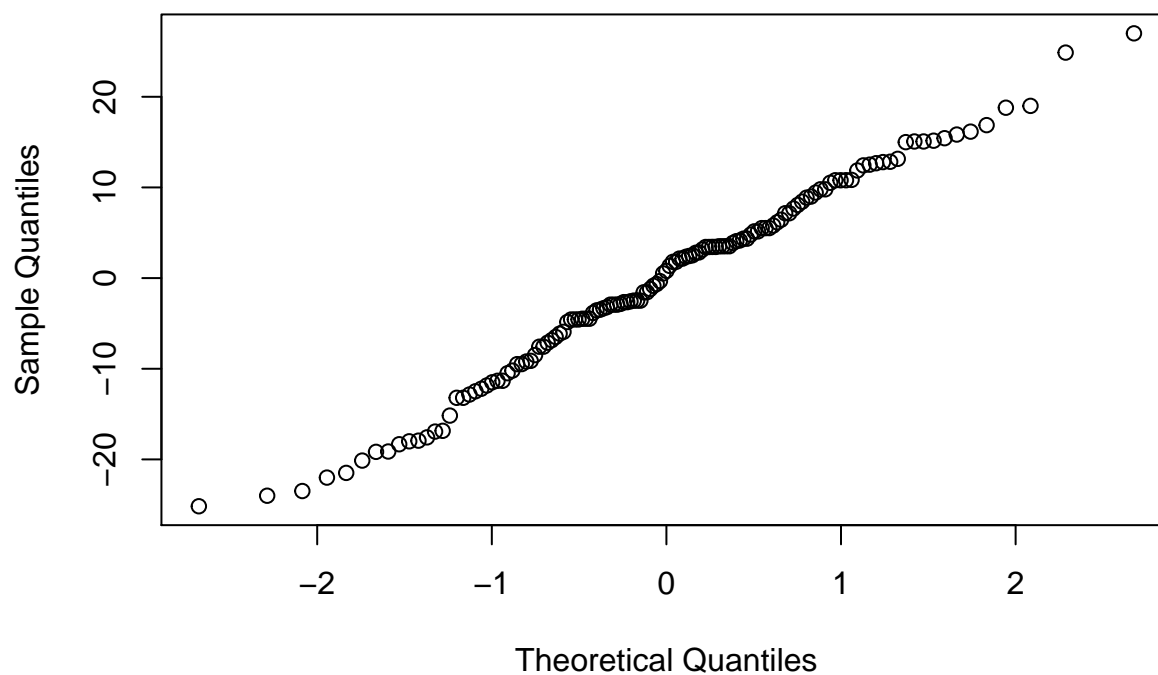
Random Intercept–AR(1) Model   ### Random Slope–AR(1) Model


```
##qqline(RandomSlope)

par(mfrow=c(1,1))
#Residuals
Residuals<-residuals(model.arr)
qqnorm(Residuals,main="Residuals-AR(1) Model")
```

Residuals–AR(1) Model


```
##qqline(Residuals)
```

l.

```
anova(model.arr)
```

```
##             numDF denDF   F-value p-value
## (Intercept)     1   105 2778.9329  <.0001
## treat           2    24    9.4832   9e-04
## weeks           1   105 1818.2305  <.0001
## treat:weeks     2   105   34.3578  <.0001
```

From my final model and graph from part a. I could say that there are differences in weight over time and these
differences in weight vary by treatment over time.