Advanced Data Analysis
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1. Do the analyses assuming compound symmetry, unstructured and AR(1) covariance structures and compare the results.

a). Compound Symmetry:

```
> anova(fit.cs)
Denom. DF: 220
            numDF   F-value p-value
(Intercept)     1 1125.1238  <.0001
Diet            3    7.3713   1e-04
Time            4  255.4254  <.0001
Diet:Time      12    4.0659  <.0001
```

b). Unconstructed

```
> anova(fit.un)
Denom. DF: 220
            numDF   F-value p-value
(Intercept)     1 18685.611  <.0001
Diet            3     9.377  <.0001
Time            4   137.297  <.0001
Diet:Time      12     5.218  <.0001
```

c). AR(1) Covariance Structure

```
> anova(fit.ar1)
Denom. DF: 220
            numDF  F-value p-value
(Intercept)     1 706.9114  <.0001
Diet            3   5.4191  0.0013
Time            4 213.6314  <.0001
Diet:Time      12   4.5165  <.0001
```

The p-values in the three covariance structures assumptions are < 0.05, thus there is a significant difference in the mean weights of the four groups using the measurements on Days 4, 8,12, 16 and 20.

d). Model Comparison:

```
> anova(fit.cs,fit.un)
       Model df      AIC      BIC     logLik   Test L.Ratio p-value
fit.cs     1 22 2215.694 2290.354 -1085.8471
fit.un     2 35 1727.939 1846.716  -828.9696 1 vs 2 513.755  <.0001
> anova(fit.cs,fit.ar1)
        Model df      AIC      BIC    logLik
fit.cs      1 22 2215.694 2290.354 -1085.847
fit.ar1     2 22 2067.107 2141.766 -1011.553
```

Based on the result, the unconstructed covariance structure may be more suitable for this data as its AIC are lowest and Log-likelihood are highest.

2. In each case determine whether it might be appropriate to adjust for Birth Weight

a). Compound Symmetry:

```
> anova(fit.cs1)
Denom. DF: 219
            numDF   F-value p-value
(Intercept)     1 1136.2864  <.0001
Diet            3    7.4424  0.0001
Time            4  255.4010  <.0001
BirthWeight     1    1.5354  0.2166
Diet:Time      12    4.0547  <.0001
```

b). Unconstructed

```
> anova(fit.un1)
Denom. DF: 219
            numDF   F-value p-value
(Intercept)     1 19377.395  <.0001
Diet            3     9.852  <.0001
Time            4   137.174  <.0001
BirthWeight     1     3.164  0.0767
Diet:Time      12     5.218  <.0001
```

c). AR(1) Covariance Structure

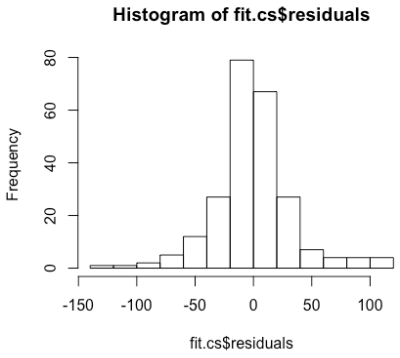
```
> anova(fit.ar11)
Denom. DF: 219
            numDF  F-value p-value
(Intercept)     1 707.5728  <.0001
Diet            3   5.4240  0.0013
Time            4 213.7039  <.0001
BirthWeight     1   1.1872  0.2771
Diet:Time      12   4.5091  <.0001
```

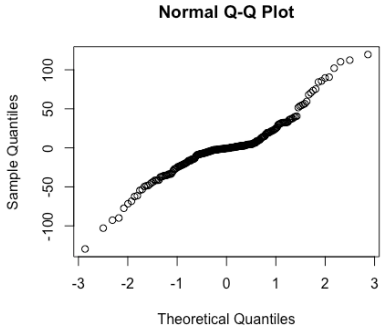
The p-values for the birthweight are greater than 0.05, which means that it is not significant to adjust for birth weight.

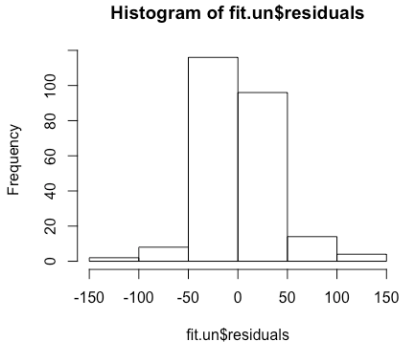
3.Check the validity of your assumptions

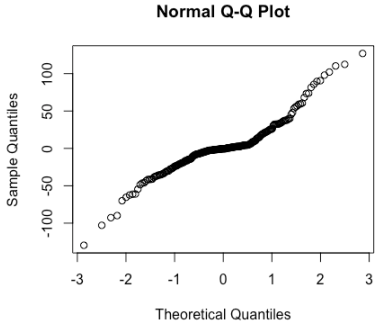
1). Normality

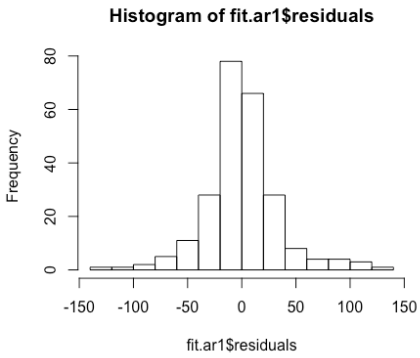
The normality assumption is not well satisfied for all three models

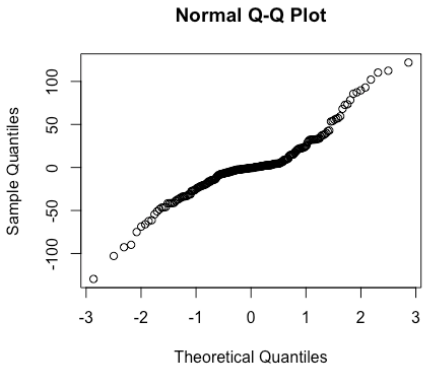












2). Homogeneity of Variance

Homogeneity of variance assumption is not satisfied

```
        Bartlett test of homogeneity of variances

data:  ChickWeight.filter$weight and ChickWeight.filter$Diet
Bartlett's K-squared = 10.472, df = 3, p-value = 0.01496
```

3). Parallelism

```
> summary(aov(ChickWeight.filter$weight ~ ChickWeight.filter$Diet*ChickWeight.filter$Time))
                                             Df Sum Sq Mean Sq
ChickWeight.filter$Diet                       3  73462   24487
ChickWeight.filter$Time                       4 667841  166960
ChickWeight.filter$Diet:ChickWeight.filter$Time  12  30033    2503
Residuals                                   220 272910    1240
                                            F value   Pr(>F)
ChickWeight.filter$Diet                      19.740 2.28e-11 ***
ChickWeight.filter$Time                     134.591  < 2e-16 ***
ChickWeight.filter$Diet:ChickWeight.filter$Time   2.018   0.0239 *
Residuals
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Parallelism is not satisfied

R Code:

```
library(dplyr)
library(MASS)

data("ChickWeight")
ChickWeight$Diet <- factor(ChickWeight$Diet)
ChickWeight$Time <- factor(ChickWeight$Time)
ChickWeight$Chick <- factor(ChickWeight$Chick)
ChickWeight.filter <- filter(ChickWeight,Time==4 | Time==8 |Time==12 | Time==16 | Time==20)

# 1
library(nlme)
ChickWeight.repeat <- groupedData(weight~as.numeric(Diet)*as.numeric(Time)|Chick,data=ChickWeight.filter)
fit.cs <- gls(weight ~ Diet * Time, data=ChickWeight.repeat, corr=corCompSymm(,form=~1|Chick))
anova(fit.cs)


fit.un <- gls(weight~Diet*Time,data=ChickWeight.repeat,corr=corSymm(form = ~1|Chick),weights = varIdent(form = ~1|Time))
anova(fit.un)

fit.ar1 <- gls(weight~Diet*Time,data=ChickWeight.repeat,corr=corAR1(,form=~1|Chick))
anova(fit.ar1)

anova(fit.cs,fit.un)
anova(fit.cs,fit.ar1)

# 2
BirthWeight <- ChickWeight$weight
ChickWeight.birth <- cbind(ChickWeight,BirthWeight)
for (i in 1 : nrow(ChickWeight.birth)){
   chick.index <- ChickWeight.birth$Chick[i]
   ChickWeight.birth$BirthWeight[i] <-
      ChickWeight.birth$weight[which(ChickWeight.birth$Chick == chick.index
                        & ChickWeight.birth$Time == 0)]
}
ChickWeight.birth_filter <- filter(ChickWeight.birth,Time==4 | Time==8 |Time==12 | Time==16 | Time==20)
ChickWeight.birth_repeated <- groupedData(weight~as.numeric(Diet)*as.numeric(Time)|Chick,data=ChickWeight.birth_filter)

fit.cs1 <- gls(weight~Diet*Time+BirthWeight,data=ChickWeight.birth_repeated,corr=corCompSymm(,form=~1|Chick))
anova(fit.cs1)

fit.un1 <- gls(weight~Diet*Time+BirthWeight,data=ChickWeight.birth_repeated,corr=corSymm(form = ~1|Chick),weights = varIdent(form =
~1|Time))
anova(fit.un1)

fit.ar11 <- gls(weight~Diet*Time+BirthWeight,data=ChickWeight.birth_repeated,corr=corAR1(,form=~1|Chick))
anova(fit.ar11)

# 3
qqnorm(fit.cs$residuals)
hist(fit.cs$residuals)
qqnorm(fit.un$residuals)
hist(fit.un$residuals)
qqnorm(fit.ar1$residuals)
hist(fit.ar1$residuals)

bartlett.test(x=ChickWeight.filter$weight,g=ChickWeight.filter$Diet)

summary(aov(ChickWeight.filter$weight ~ ChickWeight.filter$Diet*ChickWeight.filter$Time))
```