Homework 11

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b)

```
heartrate <- read.table(file="HeartRate.txt",header=T)
heartrate$woman <- factor(heartrate$woman); heartrate$drug <-
factor(heartrate$drug);heartrate$time <- factor(heartrate$time)
glmc <- lme(y~drug*time, data=heartrate, random = ~1|woman)
bvec <- glmc$coefficients$fixed
#The final line in the anova table should give us the correct test for
interactions
anova(glmc)[4,]
```

```
##           numDF denDF  F-value p-value
## drug:time     6    36 7.115244  <.0001
```

From the last line in the ANOVA table, we have the correct test. For the null hypothesis of no interactions, we get a test statistic (F-value) of 7.115244, with 6 and 36 degrees of freedom. The p-value is <.0001, indicating that we have strong evidence to reject the null hypothesis and conclude that there are statistically significant evidence for interactions between drug type and time for at least 1 combination.

c)

The null hypothesis is that $\mu_{14} = \mu_{24} = \mu_{34}$, the cell means are equal after accounting for random effect of woman. We can test this using a CB test as follows, which will get us two test statistics. One compares group 1 mean to group 2, the other group 1 to group 3 based on the R-parameterization.

```
C1 <- c(0,1,rep(0,times=8),1,0)
C2 <- c(0,0,1,rep(0,times=7),0,1)
C<-rbind(C1,C2)
est<-C%*%bvec
se <- sqrt(C%*%glmc$varFix%*%t(C))
#test statistic 1 and its p-value
est[1]/se[1,1]
```

```
## [1] 1.446074
```

```
pt(est[1]/se[1,1], df=48, lower.tail=F)
```

```
## [1] 0.07732736

#test statistic 2 and its p-value
est[2]/se[2,2]

## [1] 0.4131641

pt(est[2]/se[2,2], df=48, lower.tail=F)

## [1] 0.3406632
```

Both test statistics are t-distributed with 48 = 60-(5-1)*(4-1) degrees of freedom. Both p-values are greater than .05, indicating that we do not have enough statistically significant evidence to reject the null hypothesis. I conclude that the mean heart rate for all three drugs 15 minutes after treatment are not different from each other.

d)

```
estd <- C1%*%bvec
sed <- sqrt(t(C1)%*%vcov(glmc)%*%C1)
upd <- estd + qt(.975,48)*sed
lowd <- estd - qt(.975,48)*sed
#Below is the confidence interval
c(lowd, upd)

## [1] -2.18629 13.38629
```

3)

a)

```
alm <- gls(y~drug*time, data=heartrate,
correlation=corCompSymm(form=~1|woman))
rho <- 0.7769134
alm$sigma^2

## [1] 37.49167
```

From the above model, we get the REML estimate of W to be a 4x4 matrix with 1 on the diagonals and $\rho = 0.7769134$ on the off-diagonals, multiplied by $\sigma^2 = 37.49167$.

b)

```
b.aic <- -2*logLik(alm) + 2*(12+2)
b.bic <- -2*logLik(alm) + (12+2)*log(60-12)
b.aic

## 'log Lik.' 317.9204 (df=14)

b.bic

## 'log Lik.' 344.1172 (df=14)
```

c)

```
clm <- gls(y~drug*time, data=heartrate, correlation=corAR1(form=~1|woman))
rho <- 0.8277814
clm$sigma^2

## [1] 36.01068
```

From the above model, we get the REML estimate of W to be a 4x4 matrix with 1 on the diagonals and $\rho = 0.8277814$ on the 1st off-diagonal,$\rho^2 = 0.685222$ on the 2nd off-diagonal,$\rho^3 = 0.5672141$ on the 3rd off-diagonal, and multiplied by constant $\sigma^2 = 36.01068$.

d)

```
d.aic <- -2*logLik(clm) + 2*(12+2)
d.bic <- -2*logLik(clm) + (12+2)*log(60-12)
d.aic

## 'log Lik.' 313.9425 (df=14)

d.bic

## 'log Lik.' 340.1394 (df=14)
```

e)

```
elm <- gls(y~drug*time, data=heartrate, correlation=corSymm(form=~1|woman))
elm

## Generalized least squares fit by REML
##   Model: y ~ drug * time
##   Data: heartrate
##   Log-restricted-likelihood: -139.7176
##
## Coefficients:
##  (Intercept)        drugB        drugC        time5       time10
##         71.8          9.6          2.4         10.8         10.2
##       time15  drugB:time5  drugC:time5 drugB:time10 drugC:time10
##          1.8         -7.6         -9.4        -14.0         -9.8
## drugB:time15 drugC:time15
##         -4.0         -0.8
##
## Correlation Structure: General
##  Formula: ~1 | woman
##  Parameter estimate(s):
##  Correlation:
##   1     2     3
## 2 0.836
## 3 0.884 0.855
## 4 0.631 0.626 0.808
## Degrees of freedom: 60 total; 48 residual
## Residual standard error: 6.083528
```

```
elm$sigma^2

## [1] 37.00932
```

From the above model, we get the REML estimate of W to be a symmetric 4x4 matrix with 1 on the diagonals and the lower off-diagonals to be the highlighted portion above, and multiplied by constant $\sigma^2 = 37.00932$.

f)

```
f.aic <- -2*logLik(elm) + 2*(12+7)
f.bic <- -2*logLik(elm) + (12+7)*log(60-12)
f.aic

## 'log Lik.' 317.4352 (df=19)

f.bic

## 'log Lik.' 352.9881 (df=19)
```

g)

```
anova(alm,clm,elm)

##     Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## alm     1 14 317.9204 344.1172 -144.9602
## clm     2 14 313.9425 340.1394 -142.9713
## elm     3 19 317.4352 352.9881 -139.7176 2 vs 3 6.507307  0.2599
```

From the above, we see that AIC and BIC are minimized for the model in c), which is the AR(1) model, so that correlation structure is preferred for this data set.

h)

```
esth <- C1%*%coef(clm)
seh <- sqrt(t(C1)%*%vcov(clm)%*%C1)
uph <- esth + qt(.975,48)*seh
lowh <- esth - qt(.975,48)*seh
#The 95% confidence interval is:
c(lowh, uph)

## [1] -2.030954 13.230954
```

4)

a)

```
d <- read.table(file="ExamScores.txt",header=T)
d$exam <- factor(d$exam)
d$student <- factor(d$student)
scoremod <- lme(score ~ 0 + exam, random = ~ 1 | student, weights =
varIdent(form = ~ 1 | exam), data = d)
scoremod
```

```
## Linear mixed-effects model fit by REML
##   Data: d
##   Log-restricted-likelihood: -552.6604
##   Fixed: score ~ 0 + exam
##    exam1    exam2    exam3
## 46.84000 58.16000 67.25471
##
## Random effects:
##  Formula: ~1 | student
##         (Intercept) Residual
## StdDev:    13.43525 7.933829
##
## Variance function:
##  Structure: Different standard deviations per stratum
##  Formula: ~1 | exam
##  Parameter estimates:
##         1         2         3
## 1.0000000 0.9787570 0.5222791
## Number of Observations: 149
## Number of Groups: 50
```

```
sigs <- 13.43525^2
sig1 <- 7.933829^2 ; sig2 <- .9787570*sig1 ; sig3 <- .5222791*sig1
sigs
```

```
## [1] 180.5059
```

```
sig1
```

```
## [1] 62.94564
```

```
sig2
```

```
## [1] 61.60849
```

```
sig3
```

```
## [1] 32.87519
```

From the model, we can quickly get $\sigma_s^2 = 13.43525^2 = 180.5059$. From the documentation for varIdent, "For identifiability reasons, the coefficients of the variance function represent the ratios between the variances and a reference variance (corresponding to a reference group level)." So if we set $\sigma_1^2 = \sigma_e^2 = 7.933829^2 = 62.94564$. To get the other two components, take the estimated ratio from the model and multiply times σ_1^2: $\sigma_2^2 = 61.60849$ and $\sigma_3^2 = 32.87519$

b)

```
eblup <- fixed.effects(scoremod)[3] + random.effects(scoremod)[1,1]
eblup
```

```
##    exam3
## 83.73545
```