HW4

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October 2, 2016

13.2

Models for adjusting individual ratings: a committee of 10 persons is evaluating 100 job applications. Each person on the committee reads 30 applications (structured so that each application is read by three people) and gives each a numerical rating between 1 and 10.

- (a) It would be natural to rate the applications based on their combined scores; however, there is a worry that different raters use different standards, and we would like to correct for this. Set up a model for the ratings (with parameters for the applicants and the raters).
- (b) It is possible that some persons on the committee show more variation than others in their ratings. Expand your model to allow for this.

 \mathbf{A}

$$rating = \beta_0 + \beta_1 applicant + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3 + \dots + \beta_{10} x_{10}$$

 x_1 , x_2 ... x_1 0 are set to 0/1 depending on if committee_member1, 2 ... 10 are involved. Every individual gets his/her own coefficient, this could be combined into the intercept if each individual is rated only once it could reflect the mean score for that individual.

 \mathbf{B}

$$rating = \beta_0 + \beta_1 applicant + \beta_{i1[i]} x_1 + \beta_{i2[i]} x_2 + \beta_{i3[i]} x_3$$

Here J1, J2 and J3 are the coefficients for the first, second and third committee member. Each committee member has a group consisting of all his scores. The variance of each committee member is reflected in his/her group scores.

13.4

Models with unequal variances: the folder age.guessing contains a dataset from Gelman and Nolan (2002) from a classroom demonstration in which 10 groups of students guess the ages of 10 different persons based on photographs. The dataset also includes the true ages of the people in the photographs. Set up a non-nested model to these data, including a coefficient for each of the persons in the photos (indicating their apparent age), a coefficient for each of the 10 groups (indicating potential systematic patterns of groups guessing high or low), and a separate error variance for each group (so that some groups are more consistent than others).

$$y_i = 1 + true - age + (1|person) + (1|group)$$

```
age <- read.table("age.guessing.transformed.csv", head = T, sep = "\t")
head(age)
##
      y group person true.age
## 1 14
           1
                  1
## 2 -6
            1
                   2
                           30
## 3 5
            1
                   3
                           14
## 4 19
            1
                   4
                           42
## 5 0
            1
                   5
                           37
## 6 -5
                   6
                           57
            1
lmer1 <- lmer(y ~ 1 + (1 | person) + (1 | group), data = age)</pre>
display(lmer1)
## lmer(formula = y ~ 1 + (1 | person) + (1 | group), data = age)
## coef.est coef.se
      -0.65
##
                2.05
##
## Error terms:
## Groups
                         Std.Dev.
           Name
## person
            (Intercept) 6.39
             (Intercept) 0.00
## group
## Residual
                         3.72
## ---
## number of obs: 100, groups: person, 10; group, 10
## AIC = 584.2, DIC = 582.7
## deviance = 579.5
```

Grouping by person explains a std-dev of 6.39 while grouping by the group explains a variance of zero and hence can be removed. There does not appear to be a group specific pattern of guessing.

13.5

Return to the CD4 data introduced from Exercise 11.4.

- (a) Extend the model in Exercise 12.2 to allow for varying slopes for the time predictor.
- (b) Next fit a model that does not allow for varying slopes but does allow for different coefficients for each time point (rather than fitting the linear trend).
- (c) Compare the results of these models both numerically and graphically.

 \mathbf{A}

$$\sqrt{CD4PCT} = \beta_0 + \beta_1 time + \beta_{j1[i]} time + \beta_{j2[i]} treatment + \beta_{j3[i]} baseage$$

```
cd4 <- read.table("../hw3/dat/allvar.csv", head = T, sep = ",")
cd4$time <- cd4$visage - cd4$baseage
lmer2 <- lmer(sqrt(CD4PCT) ~ time + (time + treatmnt + baseage | newpid), data = cd4)</pre>
```

Warning in checkConv(attr(opt, "derivs"), opt\$par, ctrl = control\$checkConv, : Model is nearly unider
- Rescale variables?

```
## lmer(formula = sqrt(CD4PCT) ~ time + (time + treatmnt + baseage |
##
       newpid), data = cd4)
##
              coef.est coef.se
## (Intercept) 4.85
                         0.09
## time
               -0.37
                         0.07
##
## Error terms:
                         Std.Dev. Corr
## Groups Name
## newpid (Intercept) 1.93
##
             time
                         0.58
                                  -0.11
##
             treatmnt 0.47
                                 -0.91 0.48
##
                         0.26
                                  -0.48 -0.16 0.49
             baseage
## Residual
                         0.72
## ---
## number of obs: 1072, groups: newpid, 250
## AIC = 3127.4, DIC = 3088.2
## deviance = 3094.8
a_hat_lmer2 <- fixef(lmer2)[1] + ranef(lmer2)$newpid[1] + ranef(lmer2)$newpid[2]*cd4$time + ranef(lmer
b_hat_lmer2 <- fixef(lmer2)[2]</pre>
\mathbf{B}
                    \sqrt{CD4PCT} = \beta_0 + \beta_1 time + \beta_{i1[i]} treatment + \beta_{i2[i]} baseage
#Make time a factor here:
cd4$newtime <- as.factor(round(cd4$time, 1))</pre>
lmer3 <- lmer(sqrt(CD4PCT) ~ newtime + (treatmnt + baseage | newpid), data=cd4)</pre>
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : unable to evaluate scaled gradient
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : Model failed to converge: degenerate Hessian with 1 negative
## eigenvalues
display(lmer3)
## lmer(formula = sqrt(CD4PCT) ~ newtime + (treatmnt + baseage |
       newpid), data = cd4)
##
               coef.est coef.se
## (Intercept) 4.86
                         0.10
## newtime0.2 -0.14
                         0.09
## newtime0.3 0.02
                         0.16
## newtime0.4 -0.11
                        0.29
## newtime0.5 -0.20
                       0.09
## newtime0.6 -0.15
                      0.27
## newtime0.7 -0.30 0.09
```

display(lmer2)

```
## newtime0.8 -0.35
                         0.18
## newtime0.9 -0.25
                         0.11
## newtime1
               -0.46
                         0.13
## newtime1.1 -0.38
                         0.17
## newtime1.2
              -0.50
                         0.11
## newtime1.3 -0.55
                         0.25
## newtime1.4 -0.56
                         0.12
## newtime1.5
              -0.48
                         0.16
## newtime1.6
               0.20
                         0.43
## newtime1.7 -0.49
                         0.61
## newtime1.8
               0.12
                         0.85
## newtime1.9 -0.84
                         0.50
##
## Error terms:
                         Std.Dev. Corr
##
   Groups
             Name
##
   newpid
             (Intercept) 1.78
##
                         0.28
             treatmnt
                                  -1.00
##
             baseage
                         0.25
                                  -0.40 0.40
                         0.78
##
   Residual
## ---
## number of obs: 1072, groups: newpid, 250
## AIC = 3199.8, DIC = 3087.5
## deviance = 3117.6
```

\mathbf{C}

In terms of the residuals both models are pretty similar 0.72 vs 0.78. The coefficient for time in the model in 13.5 A is -0.37 and is significant. The coefficients for time in model 13.5 B is negative mostly and is positive at two time-points.

In the model 13.5A the coefficients for time are significant in the fixed effects indicating a decrease in CD4PCT with time. At the group level, time treatment and age contribute towards explaining the residual variance.

In the model 13.5B, in the fixed effects the coefficients of time are not significant sometimes and significant sometimes probably reflecting the number of samples at these time points. At the group level, treatment and age contribute towards explaining the residual variance and should be retained at the group level.

Plotting the results of the models for a sample of 8 patients.

```
a_hat_lmer3 <- fixef(lmer3)[1] + ranef(lmer3)$newpid[1] + ranef(lmer3)$newpid[2] * cd4$treatmnt + rane
b_hat_lmer3 <- fixef(lmer3)[2]

subset_index <- sample(cd4$newpid, 8, replace=F)
par(mfrow = c(2, 4))
for (j in subset_index){
   cd4_subset = cd4[cd4$newpid == j, ]
   plot(cd4_subset$time, sqrt(cd4_subset$CD4PCT), xlab = "time", ylab = "sqrt(CD4PCT)")
   curve(a_hat_lmer2[j,] + b_hat_lmer2*x, lty=3, lwd=2, col="forestgreen", add=TRUE)
   curve(a_hat_lmer3[j,] + b_hat_lmer3*x, lty=3, lwd=2, col="red", add=TRUE)
}</pre>
```

