STA303/1002 - Class 22 R Markdown

March 29, 2018

MM Example I: Orthodontic Growth Data

```
library(nlme)
head(Orthodont)
```

```
## Grouped Data: distance ~ age | Subject
##   distance age Subject  Sex
## 1    26.0   8     M01 Male
## 2    25.0  10     M01 Male
## 3    29.0  12     M01 Male
## 4    31.0  14     M01 Male
## 5    21.5   8     M02 Male
## 6    22.5  10     M02 Male
```

MM Example I: Orthodontic Growth Data

```
str(Orthodont)
```

```
## Classes 'nfnGroupedData', 'nfGroupedData', 'groupedData' and 'data.frame':  108 obs. of  4 variable:
##  $ distance: num  26 25 29 31 21.5 22.5 23 26.5 23 22.5 ...
##  $ age     : num  8 10 12 14 8 10 12 14 8 10 ...
##  $ Subject : Ord.factor w/ 27 levels "M16"<"M05"<"M02"<..: 15 15 15 15 3 3 3 3 7 7 ...
##  $ Sex     : Factor w/ 2 levels "Male","Female": 1 1 1 1 1 1 1 1 1 1 ...
##  - attr(*, "outer")=Class 'formula'  language ~Sex
##   .. ..- attr(*, ".Environment")=<environment: R_GlobalEnv>
##  - attr(*, "formula")=Class 'formula'  language distance ~ age | Subject
##   .. ..- attr(*, ".Environment")=<environment: R_GlobalEnv>
##  - attr(*, "labels")=List of 2
##   ..$ x: chr "Age"
##   ..$ y: chr "Distance from pituitary to pterygomaxillary fissure"
##  - attr(*, "units")=List of 2
##   ..$ x: chr "(yr)"
##   ..$ y: chr "(mm)"
##  - attr(*, "FUN")=function (x)
##   ..- attr(*, "source")= chr "function (x) max(x, na.rm = TRUE)"
##  - attr(*, "order.groups")= logi TRUE
```

MM Example I- Same error variance by sex

```
m10.6 <- lme(distance~age*Sex,data=Orthodont,random=~1|Subject,method="REML")
summary(m10.6)
```

```
## Linear mixed-effects model fit by REML
##  Data: Orthodont
##       AIC      BIC    logLik
##  445.7572 461.1236 -216.8786
```

$logLik \longrightarrow L$

$$AIC = -2L + 2p$$
$$BIC = -2L + p \ln(n)$$

$$Deviance = -2 \log L$$
$$= -2(216.8786)$$

Same for all sexes.

$$D = \begin{bmatrix} \sigma_u^2 + \sigma_e^2 & \sigma_u^2 & \sigma_u^2 & \sigma_u^2 \\ & \sigma_u^2+\sigma_e^2 & \sigma_u^2 & \sigma_u^2 \\ & & \sigma_u^2+\sigma_e^2 & \sigma_u^2 \\ & & & \sigma_u^2+\sigma_e^2 \end{bmatrix}$$

D is 4×4

```
## 
## Random effects:
##  Formula: -1 | Subject
##          (Intercept) Residual
## StdDev:    1.816214 1.386382
## 
## Fixed effects: distance ~ age * Sex
##                 Value Std.Error DF  t-value p-value
## (Intercept)  16.340625 0.9813122 79 16.651810  0.0000
## age           0.784375 0.0775011 79 10.120823  0.0000
## SexFemale     1.032102 1.5374208 25  0.671321  0.5082
## age:SexFemale -0.304830 0.1214209 79 -2.510520  0.0141
##  Correlation:
##              (Intr) age   SexFml
## age          -0.869
## SexFemale    -0.638  0.555
## age:SexFemale 0.555 -0.638 -0.869
## 
## Standardized Within-Group Residuals:
##       Min         Q1        Med        Q3       Max
## -3.59804400 -0.45461690 0.01578365 0.50244658 3.68620792
## 
## Number of Observations: 108
## Number of Groups: 27
```

(handwritten annotations) $\hat{\sigma}_u = 1.816$ $\hat{\sigma}_e = 1.386$

$$\rho_{IC} = \frac{1.816^2}{1.816^2 + 1.386^2} =$$

MM Example I – Difference in error variance by sex

(handwritten: Change σ_e^2 by Sex)

```
m10.5 <- lme(distance~age*Sex,data=Orthodont,random=~1|Subject,method="REML",
weights=varIdent(form=~1|Sex))
summary(m10.5)

## Linear mixed-effects model fit by REML
##  Data: Orthodont
##       AIC      BIC    logLik
##   429.2205 447.7312 -207.6102
## 
## Random effects:
##  Formula: -1 | Subject
##          (Intercept) Residual
## StdDev:    1.84757  1.669823
## 
## Variance function:
##  Structure: Different standard deviations per stratum
##  Formula: -1 | Sex
##  Parameter estimates:
##      Male    Female
## 1.0000000 0.4678944
## Fixed effects: distance ~ age * Sex
##                 Value Std.Error DF  t-value p-value
## (Intercept)  16.340625 1.1450945 79 14.270111  0.0000
## age           0.784375 0.0933459 79  8.402883  0.0000
## SexFemale     1.032102 1.4039842 25  0.735124  0.4691
## age:SexFemale -0.304830 0.1071828 79 -2.844016  0.0057
```

(handwritten annotations: $\sigma_{e,Females}^2$, $\sigma_{e,Males}^2$, σ_u^2)

(handwritten: $\hat{\sigma}_u$, $\hat{\sigma}_{e,Males}$)

(handwritten: $\hat{\sigma}_{e,Female} = 1.669823 \times 0.468$)

2

```
##   Correlation:
##                (Intr) age    SexFml
## age            -0.897
## SexFemale      -0.816  0.731
## age:SexFemale  0.781 -0.871 -0.840
##
## Standardized Within-Group Residuals:
##        Min         Q1        Med         Q3        Max
## -3.00556474 -0.63419474  0.01890475  0.55016878  3.06446971
##
## Number of Observations: 108
## Number of Groups: 27
```

MM Example I- LR test to compare models

```
anova(m10.6,m10.5)

##        Model df      AIC      BIC    logLik   Test L.Ratio p-value
## m10.6      1  6 445.7572 461.6236 -216.8786
## m10.5      2  7 429.2205 447.7312 -207.6102 1 vs 2 18.53677  <.0001
```

(handwritten annotations)

$(2+4)$ $(3+4)$.

① $H_0: 10.6$ $H_a: 10.5$

② $G^2 = -2(-216.8786 - (-207.402))$
$= -2 \log \frac{L_R}{L_F} = D_R - D_F$

$\sim \chi^2_{7-6}$

③ p-value $= P(\chi^2_1 > 18.54)$
< 0.0001

③ 10.5c

MM Example I- Difference error variance by sex, with Age as a factor

```
m10.5c <- lme(distance~factor(age)*Sex,data=Orthodont,random=~1|Subject,method="REML",
    weights=varIdent(form=~1|Sex))
summary(m10.5c)

## Linear mixed-effects model fit by REML
##  Data: Orthodont
##        AIC      BIC    logLik
##   428.9083 457.5652 -203.4541
##
## Random effects:
##  Formula: ~1 | Subject
##         (Intercept) Residual
## StdDev:    1.844873 1.682306
##
## Variance function:
##  Structure: Different standard deviations per stratum
##  Formula: ~1 | Sex
##  Parameter estimates:
##       Male    Female
## 1.0000000 0.4790022
## Fixed effects: distance ~ factor(age) * Sex
##                      Value Std.Error DF t-value p-value
## (Intercept)      22.875000 0.6241849 75 36.64780  0.0000
## factor(age)10     0.937500 0.5947849 75  1.57620  0.1192
## factor(age)12     2.843750 0.5947849 75  4.78114  0.0000
## factor(age)14     4.593750 0.5947849 75  7.72338  0.0000
## SexFemale        -1.693182 0.8706627 25 -1.94470  0.0631
```

(handwritten annotations)

$\hat{\sigma}_u$

$\hat{\sigma}_{\varepsilon, M}$

$\hat{\sigma}_{\varepsilon, F} = 0.479 \times 1.682$

```
## factor(age)10:SexFemale  0.107955 0.6869020 75  0.15716  0.8755
## factor(age)12:SexFemale -0.934659 0.6869020 75 -1.36069  0.1777
## factor(age)14:SexFemale -1.684659 0.6869020 75 -2.45255  0.0165
##  Correlation:
##                            (Intr) fc()10 fc()12 fc()14 SexFml f()10: f()12:
## factor(age)10              -0.476
## factor(age)12              -0.476  0.500
## factor(age)14              -0.476  0.500  0.500
## SexFemale                  -0.717  0.342  0.342  0.342
## factor(age)10:SexFemale     0.413 -0.866 -0.433 -0.433 -0.394
## factor(age)12:SexFemale     0.413 -0.433 -0.866 -0.433 -0.394  0.500
## factor(age)14:SexFemale     0.413 -0.433 -0.433 -0.866 -0.394  0.500  0.500
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -3.13851983 -0.55555492  0.01403007  0.45959680  3.06239880
##
## Number of Observations: 108
## Number of Groups: 27
```

MM Example I- Females only

```
#Figure 10.1 on page 333
FOrthodont <- Orthodont[Orthodont$Sex=="Female",]
plot(FOrthodont)
```
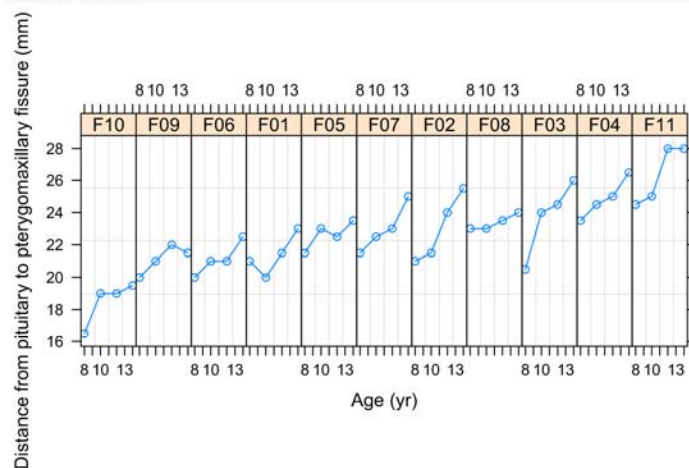
```
#Output from R on page 334
DistFAge8 <- FOrthodont$distance[FOrthodont$age==8]
DistFAge10 <- FOrthodont$distance[FOrthodont$age==10]
DistFAge12 <- FOrthodont$distance[FOrthodont$age==12]
DistFAge14 <- FOrthodont$distance[FOrthodont$age==14]
T <- cbind(DistFAge8,DistFAge10,DistFAge12,DistFAge14)
c<-cor(T)
round(c,3)
```
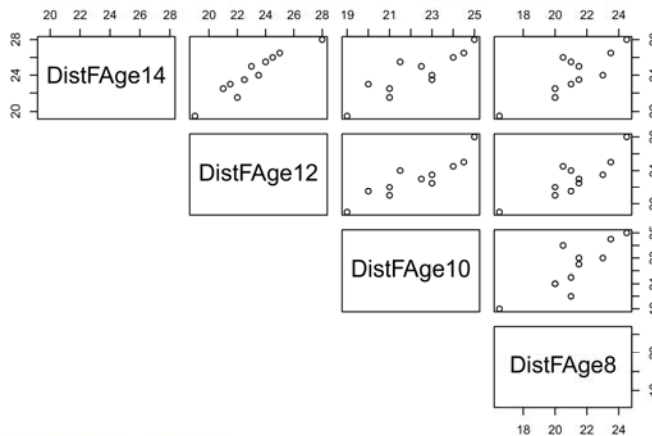
```
##         DistFAge8 DistFAge10 DistFAge12 DistFAge14
## DistFAge8    1.000      0.830      0.862      0.841
## DistFAge10   0.830      1.000      0.895      0.879
## DistFAge12   0.862      0.895      1.000      0.948
## DistFAge14   0.841      0.879      0.948      1.000
```

0.83 — 0.895

0.88 (Females only)

0.85 (10.5)

```
#Figure 10.2 on page 335
pairs(~DistFAge14+DistFAge12+DistFAge10+DistFAge8,lower.panel=NULL)
```



```
#Output from R on page 337
mFRI <- lme(distance~age,data=FOrthodont,random=~-1|Subject,method="REML")
summary(mFRI)
```

④Females only

```
## Linear mixed-effects model fit by REML
##  Data: FOrthodont
##       AIC      BIC    logLik
##   149.2183 156.169 -70.60916
##
## Random effects:
##  Formula: ~-1 | Subject
##         (Intercept)  Residual
## StdDev:    2.06847  0.7800331
```

$\hat{\sigma}_u$ $\hat{\sigma}_{\varepsilon_5}$

(10.5)
*→ 0.85*
$\rho_{IC} = 0.88$

```
## 
## Fixed effects: distance - age
##                 Value Std.Error DF  t-value p-value
## (Intercept) 17.372727 0.8587419 32 20.230440       0
## age          0.479545 0.0525898 32  9.118598       0
##  Correlation:
##     (Intr)
## age -0.674
## 
## Standardized Within-Group Residuals:
##        Min         Q1        Med        Q3        Max
## -2.2736479 -0.7090164  0.1728237  0.4122128  1.6325181
## 
## Number of Observations: 44    =11x4
## Number of Groups: 11
```

MM Example I- Males only

```
#Figure 10.4 on page 339
MOrthodont <- Orthodont[Orthodont$Sex=="Male",]
plot(MOrthodont)
```
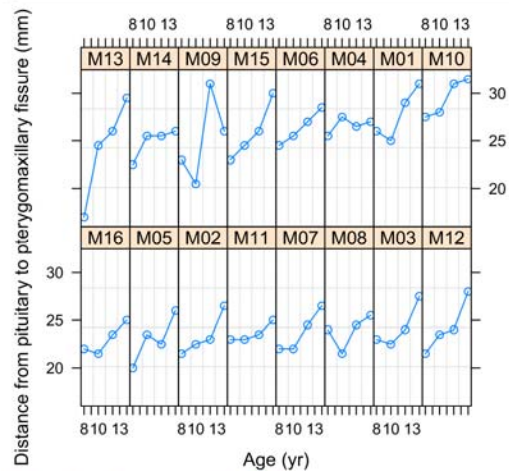


```
#Output from R on pages 340 and 341
DistMAge8 <- MOrthodont$distance[MOrthodont$age==8]
DistMAge10 <- MOrthodont$distance[MOrthodont$age==10]
DistMAge12 <- MOrthodont$distance[MOrthodont$age==12]
DistMAge14 <- MOrthodont$distance[MOrthodont$age==14]
```

```
T <- cbind(DistMAge8,DistMAge10,DistMAge12,DistMAge14)
c<-cor(T)
round(c,3)
```

```
##            DistMAge8 DistMAge10 DistMAge12 DistMAge14
## DistMAge8      1.000      0.437      0.558      0.315
## DistMAge10     0.437      1.000      0.387      0.631
## DistMAge12     0.558      0.387      1.000      0.586
## DistMAge14     0.315      0.631      0.586      1.000
```

#Figure 10.5 on page 340
```
pairs(~DistMAge14+DistMAge12+DistMAge10+DistMAge8,lower.panel=NULL)
```
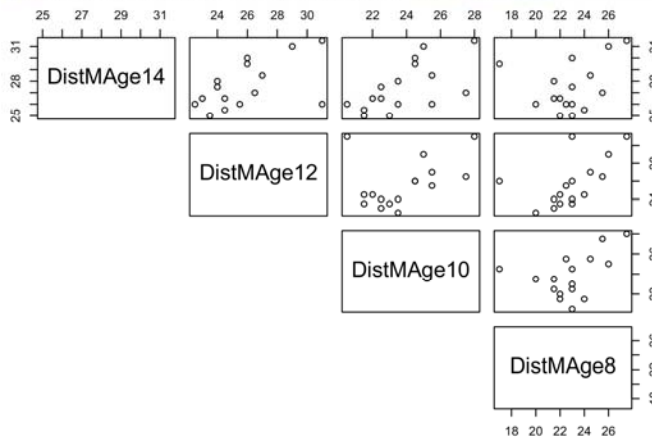
0.315 — 0.631

0.55 (10.5)

0.48 (Males only)

#Output from R on page 341
```
mMRI <- lme(distance~age,data=MOrthodont,random=-1|Subject,method="REML")
summary(mMRI)
```

③ Males only

```
## Linear mixed-effects model fit by REML
##  Data: MOrthodont
##      AIC      BIC    logLik
##  281.448 289.9566 -136.724
##
## Random effects:
##  Formula: ~1 | Subject
##         (Intercept) Residual
## StdDev:    1.625019  1.67822
##
## Fixed effects: distance ~ age
##               Value Std.Error DF  t-value p-value
## (Intercept) 16.340625 1.1287202 47 14.477126       0
## age          0.784375 0.0938154 47  8.360838       0
```

$\hat{\sigma}_u$

$\hat{\sigma}_e$

(from 10.5) 0.55

$\rho_{IC} = 0.48$

7

```
##   Correlation:
##      (Intr)
## age -0.914
##
## Standardized Within-Group Residuals:
##          Min          Q1         Med          Q3         Max
## -3.008054554 -0.640688586  0.007833248  0.534480581  3.052946887
##
## Number of Observations: 64    = 16×4
## Number of Groups: 16
```