

BIOS6643. L9 Specifying LMM through G_i and R_i structures

Dental study

Description

- The orthodontic study data of Potthoff and Roy (1964).
- World famous data set that is used to introduce features of longitudinal data modeling and analysis
- A study was conducted involving 27 children, 16 boys and 11 girls
- For each child, the distance (mm) from the center of the pituitary to the pterygomaxillary fissure was measured at ages 8, 10, 12, and 14 years of age
- The pterygomaxillary fissure is a vertical opening in the human skull.
- **Objectives** of the study included:
 - Determine if distances over time are larger on average for boys than for girls
 - Determine if the rate of change of distance over time is different for boys and girls.

```
# Read in the data
dat.den <- read.table("/Users/juarezce/Documents/OneDrive - The University of Colorado Denver/BIOS6643/1")
dat.den <- dat.den[,2:5]      # remove the first column
colnames(dat.den) <- c("id", "age", "distance", "gender")

# Total number of individuals
m <- max(dat.den$id)

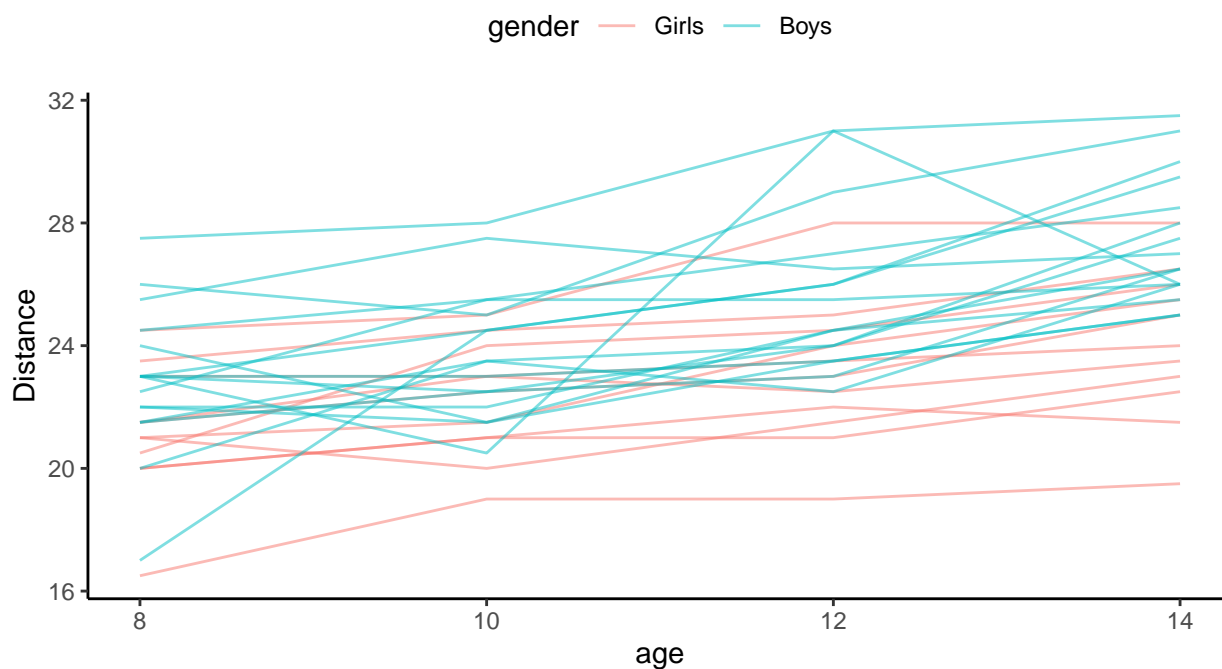
head(dat.den, 2)

##   id age distance gender
## 1  1  8         21      0
## 2  1 10         20      0

table(dat.den$gender)

##
##  0  1
## 44 64
```

Some descriptives:



a. Common G matrix for both genders with random intercept and slopes

```
# (a) Common G matrix for both genders, default diagonal within-child
#      covariance matrix R_i with same variance sigma^2 for each
#      gender.
```

```
dental.lme.a <- lme(distance ~ -1 + gender + age:gender, data=dat.den,
                    random = ~ age | id, method="ML")
summary(dental.lme.a)
```

```
## Linear mixed-effects model fit by maximum likelihood
##   Data: dat.den
##       AIC      BIC    logLik
##   443.806 465.263 -213.903
##
## Random effects:
## Formula: ~age | id
## Structure: General positive-definite, Log-Cholesky parametrization
##           StdDev   Corr
## (Intercept) 2.134688 (Intr)
## age          0.154139 -0.603
## Residual    1.310040
##
## Fixed effects: distance ~ -1 + gender + age:gender
##           Value Std.Error DF   t-value p-value
## genderGirls  17.372727 1.2045404 25 14.422702     0
## genderBoys   16.340625 0.9987521 25 16.361042     0
## genderGirls:age 0.479545 0.1017051 80  4.715058     0
## genderBoys:age  0.784375 0.0843294 80  9.301321     0
```

```

## Correlation:
##               gndrGr gndrBy gndrG:
## genderBoys      0.00
## genderGirls:age -0.88  0.00
## genderBoys:age   0.00 -0.88  0.00
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.33603363 -0.41539842  0.01039175  0.49169519  3.85819292
##
## Number of Observations: 108
## Number of Groups: 27

beta.a <- fixed.effects(dental.lme.a) # beta, also fixef(dental.lme.a)
b.a <- random.effects(dental.lme.a)   # posterior modes bi, also ranef(dental.lme.a)
sebeta.a <- summary(dental.lme.a)$tTable[, "Std.Error"]
## Recall we can get the var-cov of fixed coefficients using 'varFix'
## dental.lme.a$varFix

G.a <- getVarCov(dental.lme.a, type="random.effects") # G matrix
sigma2.a <- dental.lme.a$sigma^2 # sigma^2
V.a <- getVarCov(dental.lme.a, type="marginal", individual=1) # V_i
R.a <- getVarCov(dental.lme.a, type="conditional", individual=1) # R_i
G.a

## Random effects variance covariance matrix
##      (Intercept)      age
## (Intercept)    4.55690 -0.198250
## age           -0.19825  0.023759
## Standard Deviations: 2.1347 0.15414

V.a

## id 1
## Marginal variance covariance matrix
##      1      2      3      4
## 1 4.6216 2.8891 2.8727 2.8563
## 2 2.8891 4.6839 3.0464 3.1251
## 3 2.8727 3.0464 4.9363 3.3938
## 4 2.8563 3.1251 3.3938 5.3788
## Standard Deviations: 2.1498 2.1642 2.2218 2.3192

R.a

## id 1
## Conditional variance covariance matrix
##      1      2      3      4
## 1 1.7162 0.0000 0.0000 0.0000
## 2 0.0000 1.7162 0.0000 0.0000
## 3 0.0000 0.0000 1.7162 0.0000
## 4 0.0000 0.0000 0.0000 1.7162
## Standard Deviations: 1.31 1.31 1.31 1.31

```

b. Common G matrix with random intercepts and slopes, diagonal within-child covariance matrix R_i with different variance for each gender

```
dental.lme.b <- lme(distance ~ -1 + gender + age:gender, data=dat.den,
                    random = ~ age | id, weights = varIdent(form = ~ 1 | gender),
                    method="ML")
beta.b <- fixed.effects(dental.lme.b) # beta
sebeta.model.b <- sqrt(diag(dental.lme.b$varFix))
b.b <- random.effects(dental.lme.b) # posterior modes bi
G.b <- getVarCov(dental.lme.b, type="random.effects") # G matrix
R.b.1 <- getVarCov(dental.lme.b, type="conditional", individual=1) # R_1; first girl
R.b.12 <- getVarCov(dental.lme.b, type="conditional", individual=12) # R_12; first boy
G.b
```

```
## Random effects variance covariance matrix
##           (Intercept)      age
## (Intercept)  3.19860 -0.110360
## age          -0.11036  0.019766
## Standard Deviations: 1.7885 0.14059
```

R.b.1

```
## id 1
## Conditional variance covariance matrix
##           1      2      3      4
## 1 0.44491 0.00000 0.00000 0.00000
## 2 0.00000 0.44491 0.00000 0.00000
## 3 0.00000 0.00000 0.44491 0.00000
## 4 0.00000 0.00000 0.00000 0.44491
## Standard Deviations: 0.66702 0.66702 0.66702 0.66702
```

R.b.12

```
## id 12
## Conditional variance covariance matrix
##           1      2      3      4
## 1 2.6294 0.0000 0.0000 0.0000
## 2 0.0000 2.6294 0.0000 0.0000
## 3 0.0000 0.0000 2.6294 0.0000
## 4 0.0000 0.0000 0.0000 2.6294
## Standard Deviations: 1.6215 1.6215 1.6215 1.6215
```

```
V.b.1 <- getVarCov(dental.lme.b, type="marginal", individual=1) # V_1 (girl)
V.b.12 <- getVarCov(dental.lme.b, type="marginal", individual=12) # V_12 (boy)
V.b.1
```

```
## id 1
## Marginal variance covariance matrix
##           1      2      3      4
## 1 3.1428 2.7934 2.8889 2.9845
## 2 2.7934 3.4129 3.1426 3.3172
## 3 2.8889 3.1426 3.8412 3.6499
## 4 2.9845 3.3172 3.6499 4.4275
## Standard Deviations: 1.7728 1.8474 1.9599 2.1042
```

V.b.12

```
## id 12
```

```
## Marginal variance covariance matrix
##      1      2      3      4
## 1 5.3272 2.7934 2.8889 2.9845
## 2 2.7934 5.5973 3.1426 3.3172
## 3 2.8889 3.1426 6.0256 3.6499
## 4 2.9845 3.3172 3.6499 6.6120
## Standard Deviations: 2.3081 2.3659 2.4547 2.5714
```

c. Fit a common G matrix for both genders, and common within-child AR(1)

d. Fit a common G matrix for both genders, common within-child AR(1) exponential correlation

Compare models

Refit final model using REML. Obtain population (PA) and subject-specific (SS) fitted values and residuals.

Note: You may use *fitted(fit,level=0:1)* and *residuals(fit,level=0:1)*, where level=0 gives PA, level = 1 gives SS (default), and level = 0:1 gives both.

Fit a LMM with random intercept and slopes using lme4:lmer