

STA303/1002 - Class 23 R Markdown

April 3, 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 461.6236 -216.8786
```

```
##
## 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
```

MM Example I- Difference error variance by sex

② 10.5

```
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

LRT

```
## 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
```

$$\sigma^2 \begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix} / \text{Sex}$$

$$\hat{\sigma}_{e, \text{Males}} = \hat{\sigma}_e(1) = \hat{\sigma}_e$$

$$\hat{\sigma}_{e, \text{Females}} = \hat{\sigma}_e(0.468)$$

```
## 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
```

10.6: $3+3=6$

10.5: $3+4=7$

H_0 : Reduced, 10.6

H_a : Full model, 10.5

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
```

$\Delta 2 = -2$ Res Log M.

Log $DF \sim \chi^2_1$

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
```

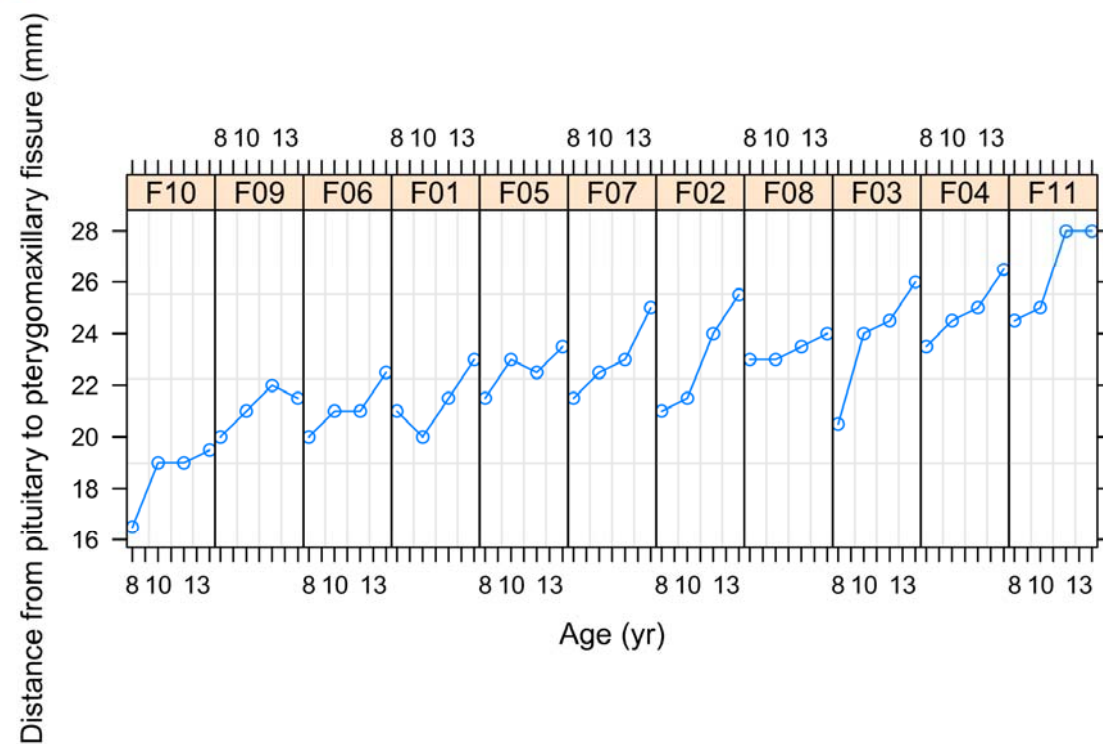
```
## factor(age)10:SexFemale 0.107955 0.6869020 75 0.15716 0.8755
## factor(age)12:SexFemale -0.934659 0.6869020 75 -1.36069 0.1777
## factor(age)14:SexFemale -1.684659 0.6869020 75 -2.45255 0.0165
## Correlation:
## (Intr) fc()10 fc()12 fc()14 SexFml f()10: f()12:
## factor(age)10 -0.476
## factor(age)12 -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
```

Testing this set of β 's correspond to testing interaction b/w Sex & Age.

MM Example I- Females only

④

```
#Figure 10.1 on page 333
FOrthodont <- Orthodont[Orthodont$Sex=="Female",]
plot(FOrthodont)
```



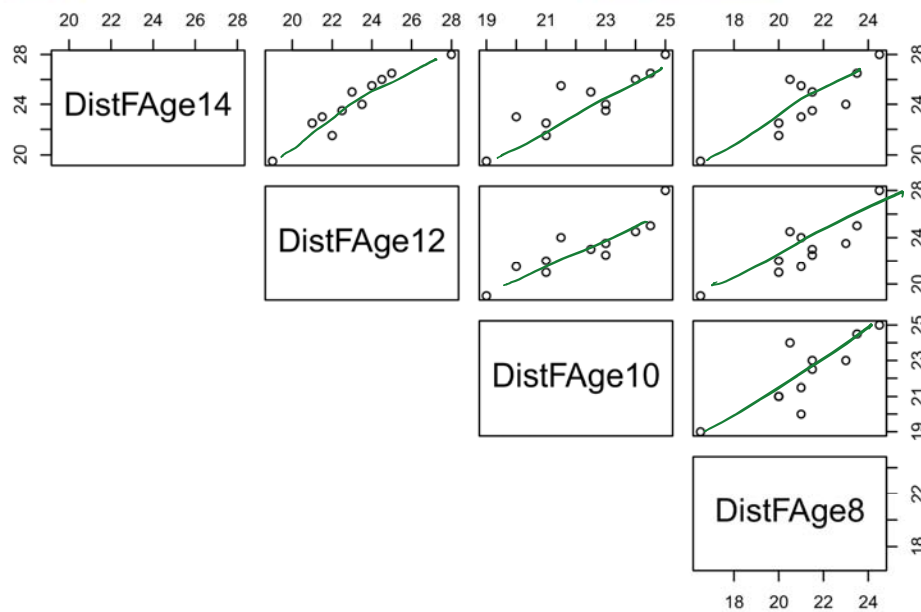
11 Females.

```
#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
```

#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)
```

```
## 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
```

Sub

	8	10	12	14
1				

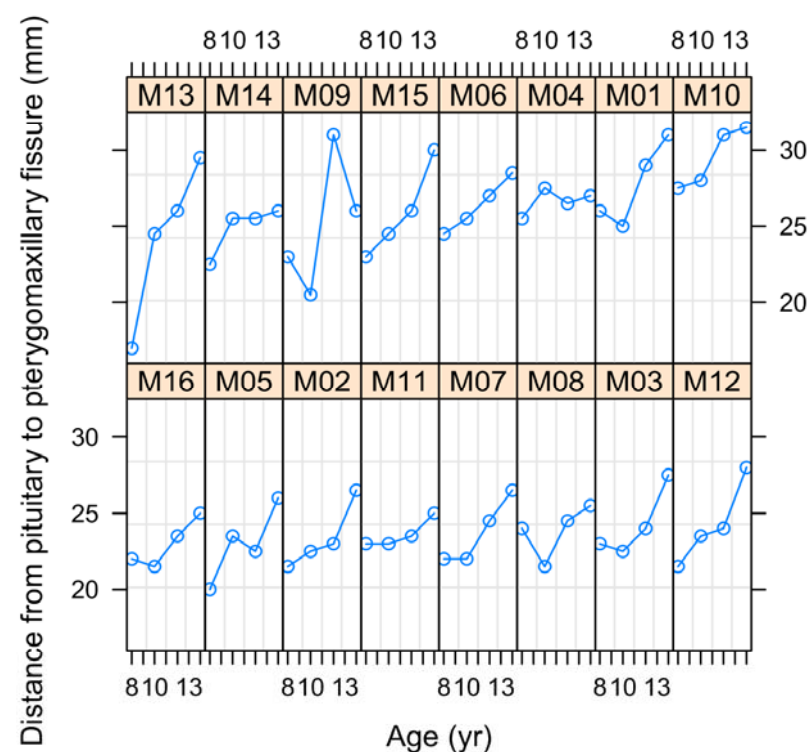
$\begin{matrix} \text{Cor}(y_8, y_{10}) \\ \text{Cor}(y_8, y_{12}) \\ \text{Cor}(y_8, y_{14}) \\ \text{Cor}(y_{10}, y_{12}) \\ \text{Cor}(y_{10}, y_{14}) \\ \text{Cor}(y_{12}, y_{14}) \end{matrix} \left. \vphantom{\begin{matrix} \text{Cor}(y_8, y_{10}) \\ \text{Cor}(y_8, y_{12}) \\ \text{Cor}(y_8, y_{14}) \\ \text{Cor}(y_{10}, y_{12}) \\ \text{Cor}(y_{10}, y_{14}) \\ \text{Cor}(y_{12}, y_{14}) \end{matrix}} \right\} \in (0.83, 0.95)$


```
##
## 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
## Number of Groups: 11
```

MM Example I- Males only

#Figure 10.4 on page 339

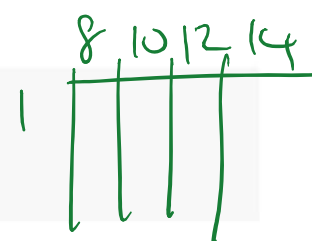
```
MOrthodont <- Orthodont[Orthodont$Sex=="Male",]
plot(MOrthodont)
```



16 Males

#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]
```



16

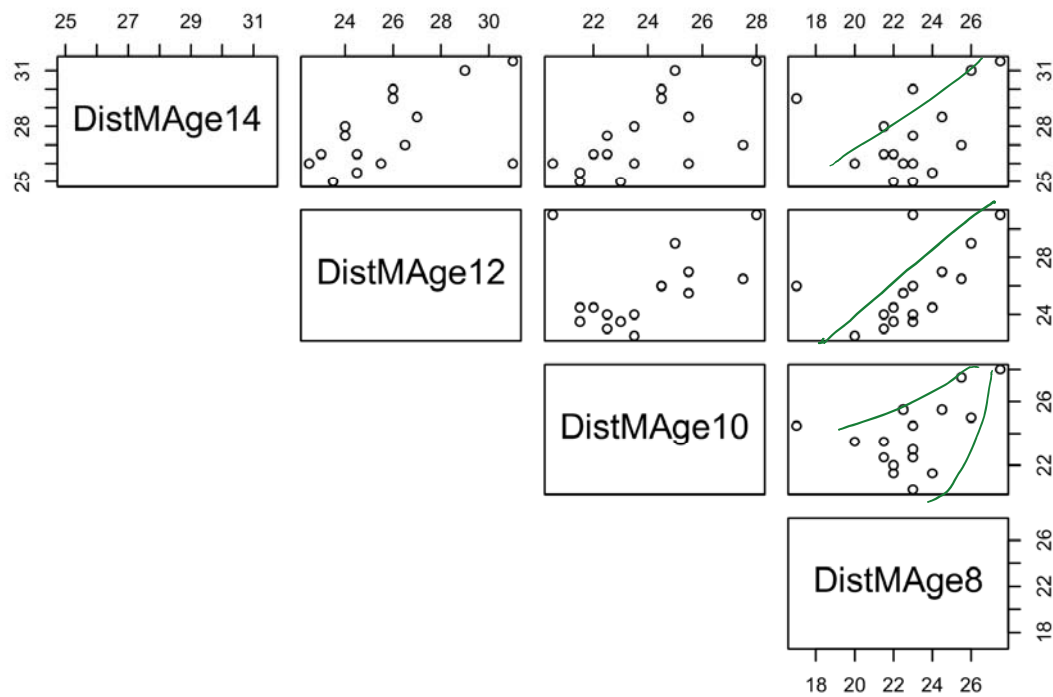
```
T <- cbind(DistMAge8,DistMAge10,DistMAge12,DistMAge14)
c<-cor(T)
round(c,3)
```

```
##           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
```

0.315 — 0.586

#Figure 10.5 on page 340

```
pairs(~DistMAge14+DistMAge12+DistMAge10+DistMAge8,lower.panel=NULL)
```



#Output from R on page 341

```
mMRI <- lme(distance~age,data=MOrthodont,random=~1|Subject,method="REML")
summary(mMRI)
```

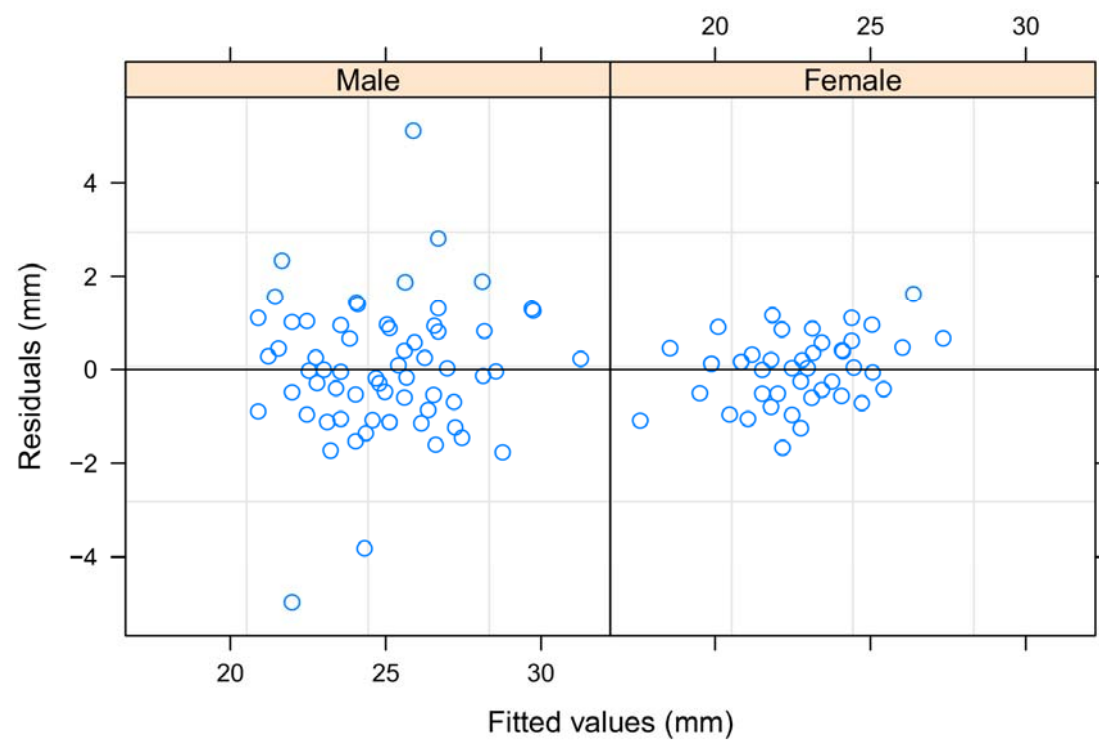
```
## Linear mixed-effects model fit by REML
## Data: MOrthodont
##      AIC      BIC    logLik
## 281.448 289.9566 -136.724
##
## Random effects:
## Formula: ~1 | Subject
##      (Intercept) Residual
## StdDev:    1.625019  1.67822
##
## Fixed effects: distance ~ age
##              Value Std.Error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

```
## 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
## Number of Groups: 16
```

Mixed Models: Diagnostic Plots

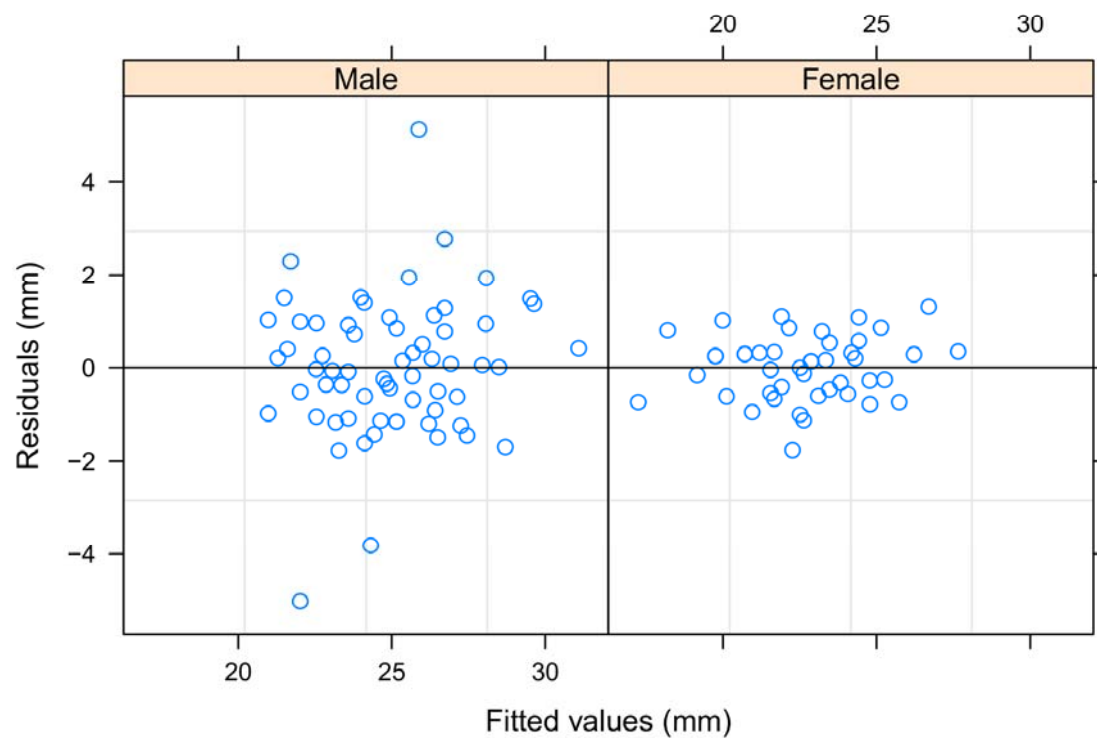
#Figure 10.10 on page 350

```
plot(m10.6,form = resid(., type = "response",level=1) ~ fitted(.,level=1) | Sex,abline=0)
```



#Figure 10.11 on page 351

```
plot(m10.5,form = resid(., type = "response",level=1) ~ fitted(.,level=1) | Sex,abline=0)
```

Mixed Models: Diagnostic Plots

```
#Figure 10.12 on page 352
#Choleski Residuals for m10.5
attach(Orthodont)
m10.5.a <- lm(distance~age*Sex, data=Orthodont)
m10.5.b <- lm(distance~(Subject-1), data=Orthodont)
m10.5.X <- model.matrix(m10.5.a)
m10.5.Z <- model.matrix(m10.5.b)
m10.5.G <- diag(rep(getVarCov(m10.5), ncol(m10.5.Z)))
m10.5.R <- diag(attr(m10.5[[15]], "std")^2)
m10.5.V <- m10.5.Z %*% m10.5.G %*% t(m10.5.Z) + m10.5.R
m10.5.tCHOLinv <- solve(t(chol(m10.5.V)))
# Now to premultiply terms by m10.5.tCHOLinv to get Choleski residuals, etc.
dist.CHOL.m10.5 <- m10.5.tCHOLinv %*% Orthodont$distance
x1.CHOL.m10.5 <- m10.5.tCHOLinv %*% m10.5.X[,1]
x2.CHOL.m10.5 <- m10.5.tCHOLinv %*% m10.5.X[,2]
x3.CHOL.m10.5 <- m10.5.tCHOLinv %*% m10.5.X[,3]
x4.CHOL.m10.5 <- m10.5.tCHOLinv %*% m10.5.X[,4]
m10.5.CHOL <- lm(dist.CHOL.m10.5 ~ x1.CHOL.m10.5 + x2.CHOL.m10.5 +
  x3.CHOL.m10.5 + x4.CHOL.m10.5 -1)
#summary(m10.5.CHOL)

#Choleski Residuals for m10.6
m10.6.a <- lm(distance~age*Sex, data=Orthodont)
m10.6.b <- lm(distance~(Subject-1), data=Orthodont)
m10.6.X <- model.matrix(m10.6.a)
```

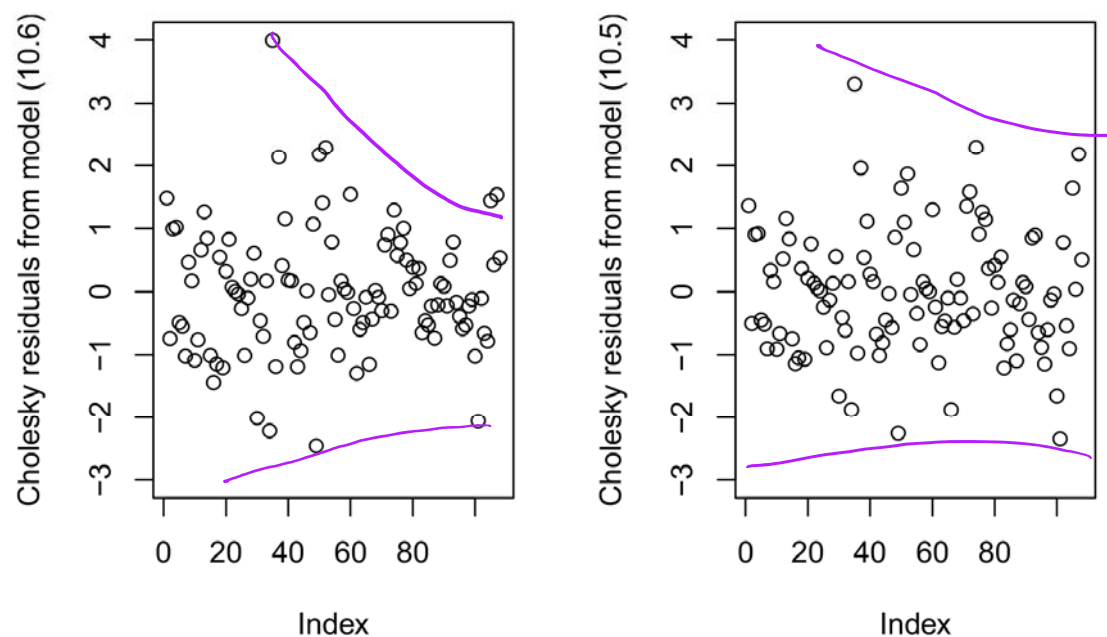
```

m10.6.Z <- model.matrix(m10.6.b)
m10.6.G <- diag(rep(getVarCov(m10.6),ncol(m10.6.Z)))
m10.6.R <- diag(attr(m10.6[[15]],"std")^2)
m10.6.V <- m10.6.Z %*% m10.6.G %*% t(m10.6.Z) + m10.6.R
m10.6.tCHOLinv <- solve(t(chol(m10.6.V)))
# Now to premultiply terms by m10.6.tCHOLinv to get Choleski residuals, etc.
dist.CHOL.m10.6<- m10.6.tCHOLinv %*% Orthodont$distance
x1.CHOL.m10.6 <- m10.6.tCHOLinv %*% m10.6.X[,1]
x2.CHOL.m10.6 <- m10.6.tCHOLinv %*% m10.6.X[,2]
x3.CHOL.m10.6 <- m10.6.tCHOLinv %*% m10.6.X[,3]
x4.CHOL.m10.6 <- m10.6.tCHOLinv %*% m10.6.X[,4]
m10.6.CHOL <- lm(dist.CHOL.m10.6 ~ x1.CHOL.m10.6 + x2.CHOL.m10.6 +
  x3.CHOL.m10.6 + x4.CHOL.m10.6 -1)
#summary(m10.6.CHOL)

CholeskyResid10.5 <- m10.5.CHOL$residuals
CholeskyResid10.6 <- m10.6.CHOL$residuals

par(mfrow=c(1,2))
plot(CholeskyResid10.6, ylab="Cholesky residuals from model (10.6)",ylim=c(-3,4))
plot(CholeskyResid10.5,ylab="Cholesky residuals from model (10.5)",ylim=c(-3,4))

```



Mixed Models: Residuals Plots

```

par(mfrow=c(1,2))
plot(CholeskyResid10.6~Sex,ylab="Cholesky residuals from model (10.6)",ylim=c(-3,4))
plot(CholeskyResid10.5~Sex,ylab="Cholesky residuals from model (10.5)",ylim=c(-3,4))

```

