

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 variables:
## $ 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

```
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
```

```
## 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
```

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)
```

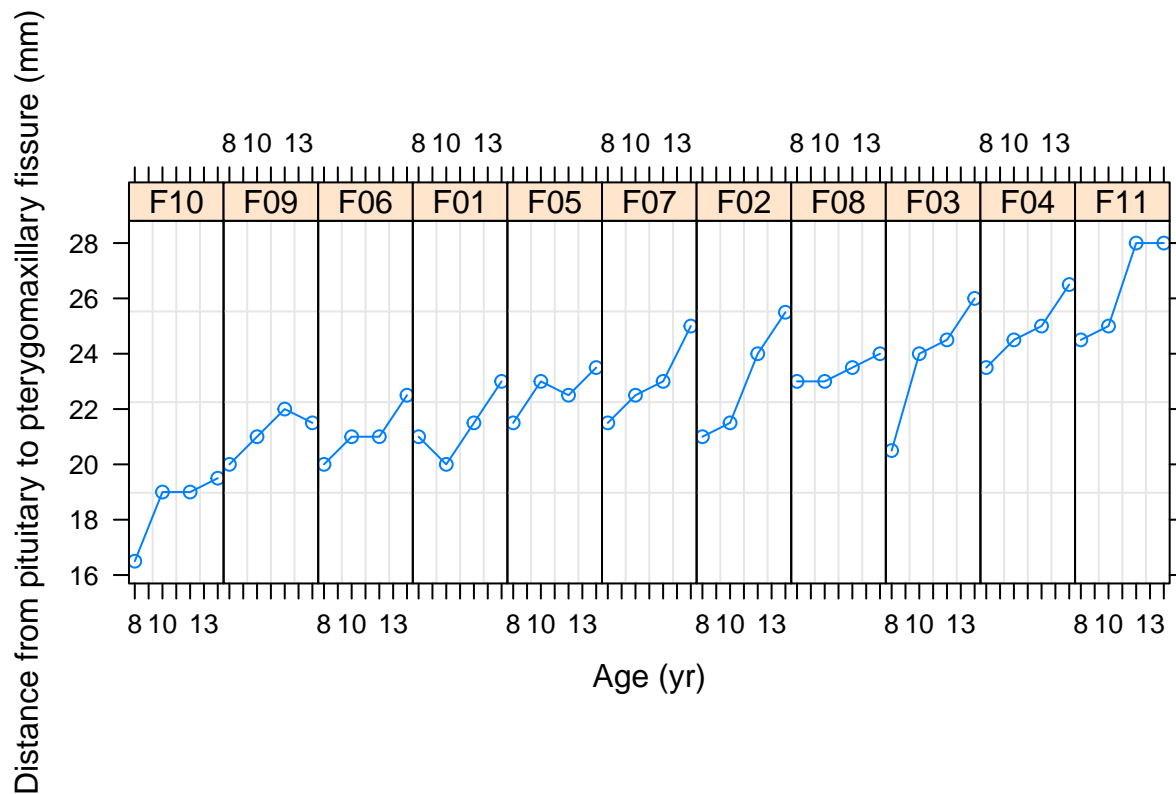
```
## Linear mixed-effects model fit by REML
## Data: Orthodont
##      AIC      BIC   logLik
##  428.9083 457.5652 -203.4541
##
## Random effects:
## Formula: ~1 | Subject
##      (Intercept) Residual
## StdDev:      1.844873 1.682306
##
## Variance function:
## Structure: Different standard deviations 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
```

MM Example I- Females only

#Figure 10.1 on page 333

```
FOrthodont <- Orthodont[Orthodont$Sex=="Female",]
plot(FOrthodont)
```



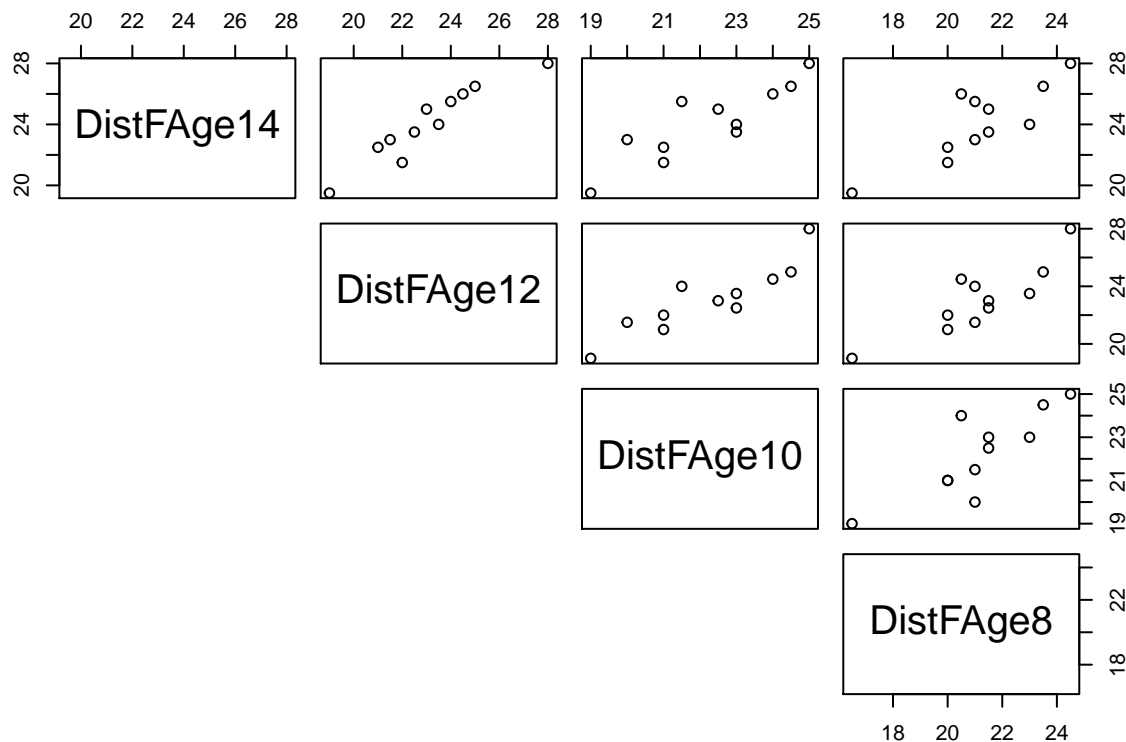
#Output from R on page 334

```
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
```

#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)
```

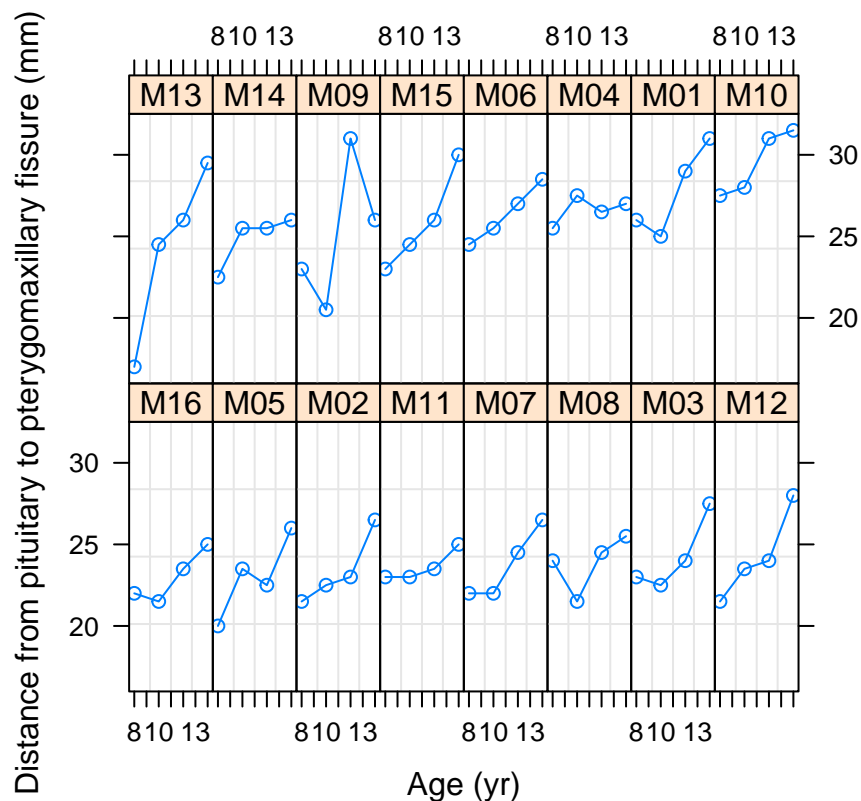
```
## Linear mixed-effects model fit by REML
## Data: FOrthodont
##      AIC      BIC    logLik
## 149.2183 156.169 -70.60916
##
## Random effects:
## Formula: ~1 | Subject
##      (Intercept) Residual
## StdDev:      2.06847 0.7800331
```

```
##
## 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)
```



#Output from R on pages 340 and 341

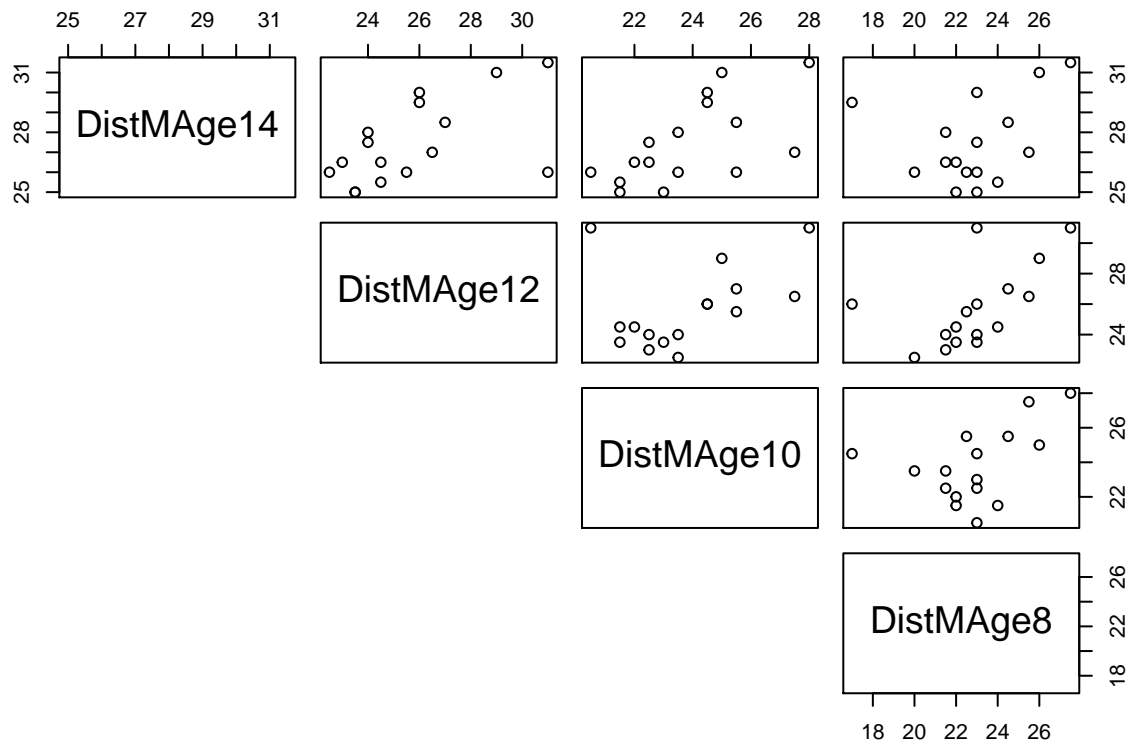
```
DistMAge8 <- MOrthodont$distance[MOrthodont$age==8]
DistMAge10 <- MOrthodont$distance[MOrthodont$age==10]
DistMAge12 <- MOrthodont$distance[MOrthodont$age==12]
DistMAge14 <- MOrthodont$distance[MOrthodont$age==14]
```

```
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)
```



#Output from R on page 341

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

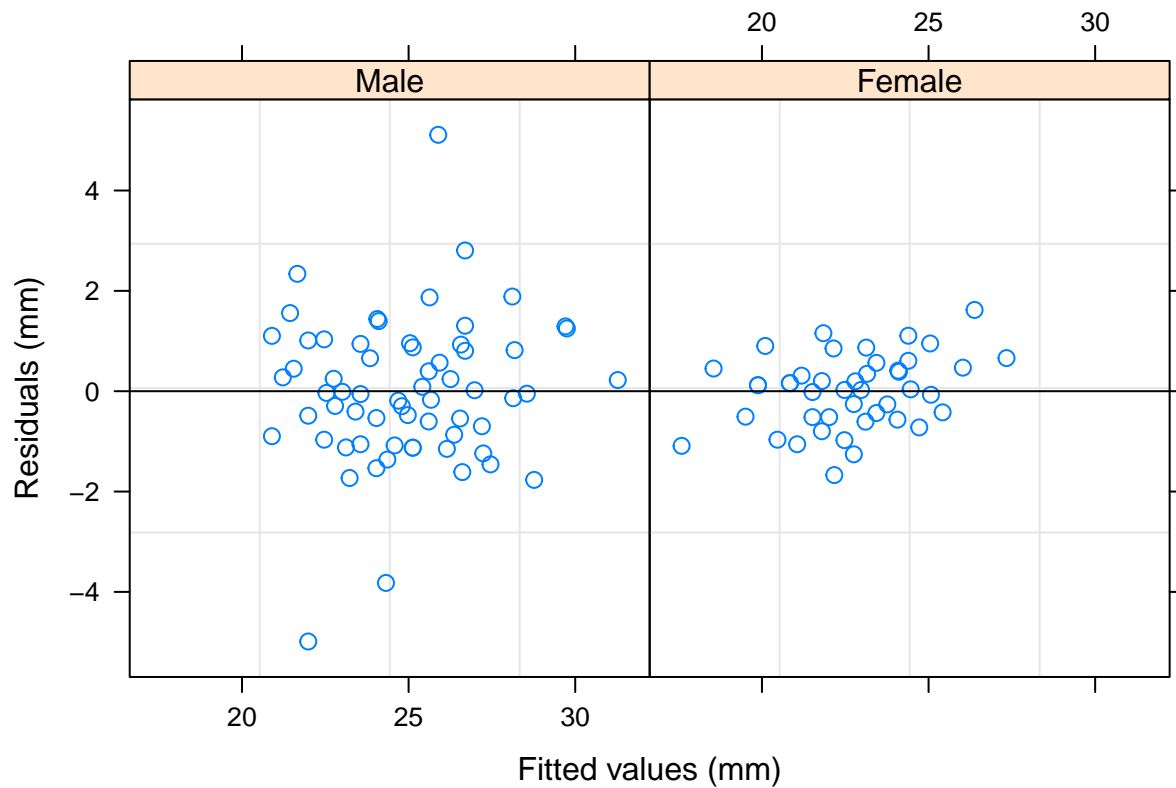
```
## Linear mixed-effects model fit by REML
## Data: MOrthodont
##      AIC      BIC    logLik
## 281.448 289.9566 -136.724
##
## Random effects:
## Formula: ~1 | Subject
##      (Intercept) Residual
## StdDev:    1.625019  1.67822
##
## Fixed effects: distance ~ age
##      Value Std.Error DF   t-value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

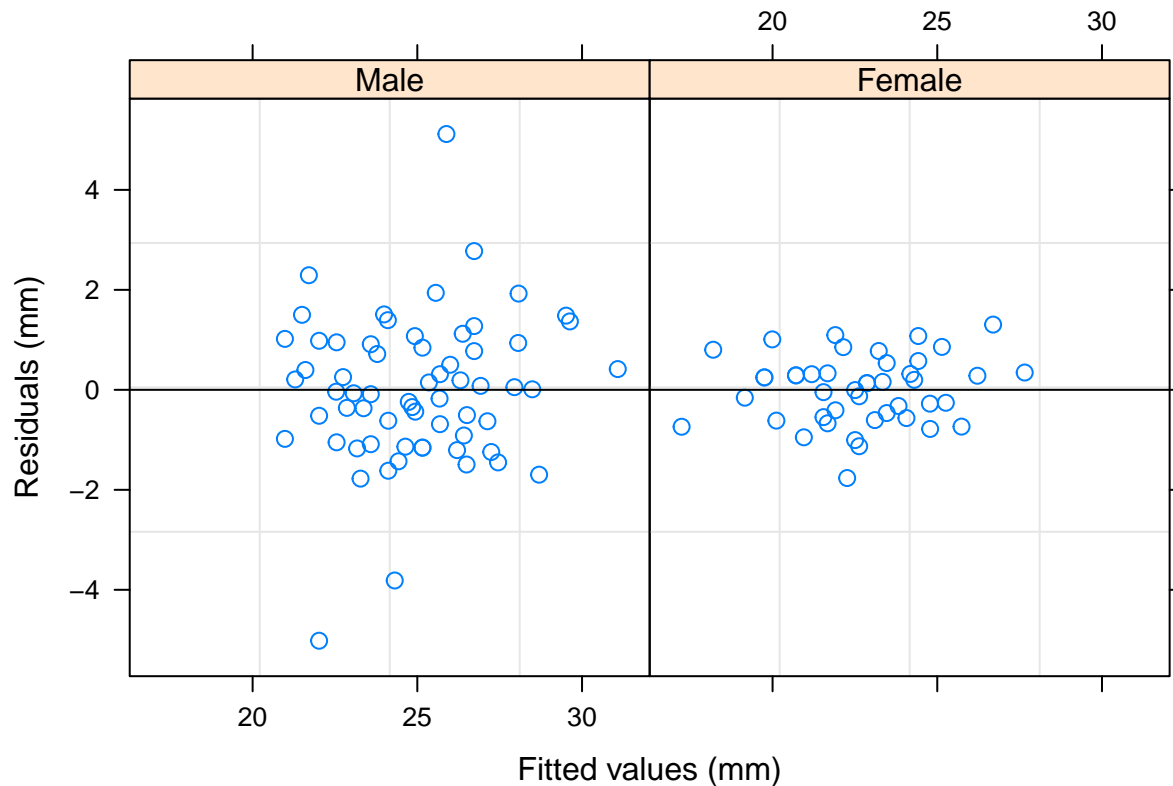
#Figure 10.10 on page 350

```
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)
```

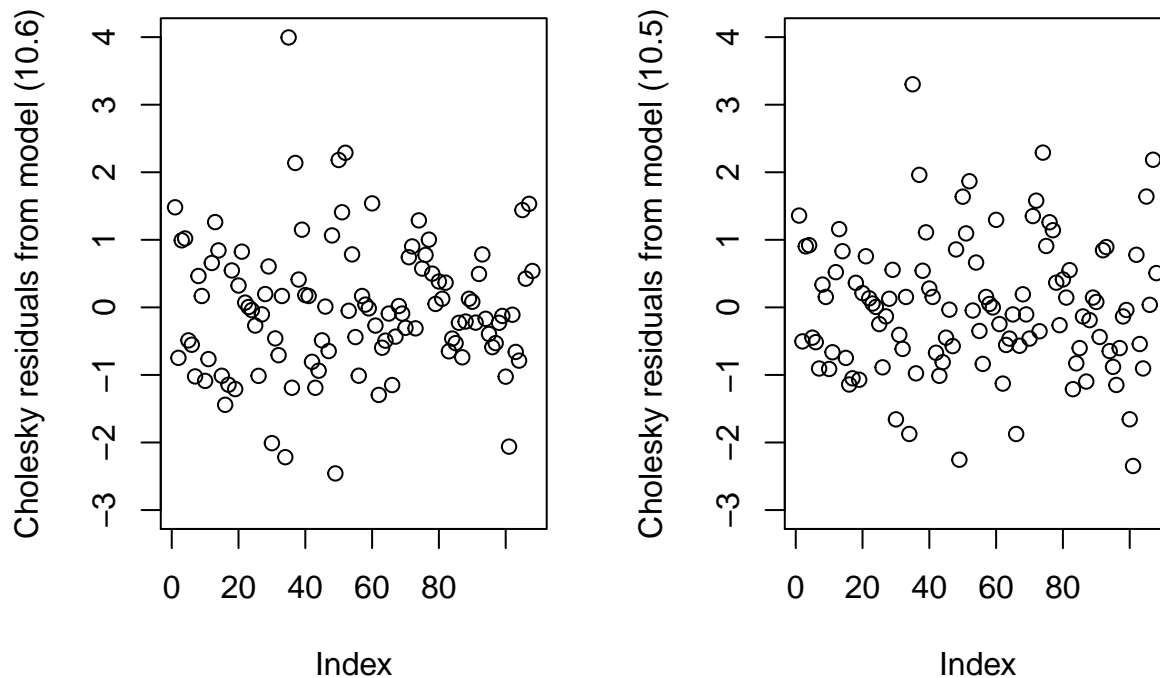
```

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))

```

