STAT3401: Advanced data analysis
Week 8: Longitudinal Data

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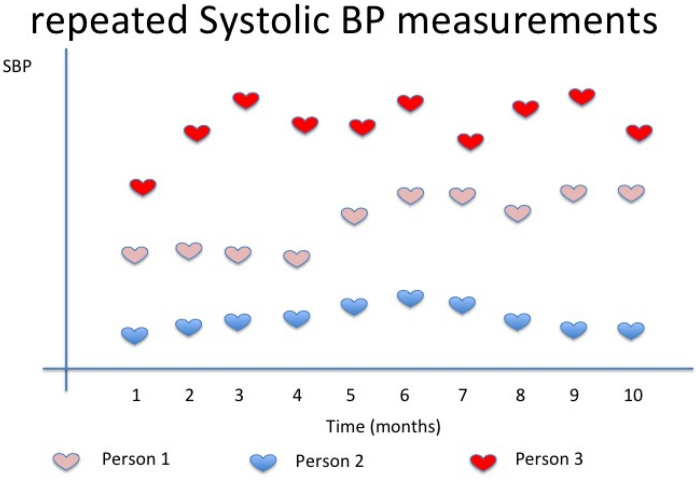
Longitudinal Data

Recap:

- Datasets where the dependent variable is measured once at several points in time for each unit of analysis
- Usually at least two repeated measurements made over a relatively long period
- In contrast to repeated measures data drop out of a subject is a concern
- Some times difficult to differentiate between repeated measures and longitudinal data—do not worry it is not critical if LMMs are used to analyse the data!

Examples of Longitudinal Data



Orthodontic Data (Pinheiro and Bates)

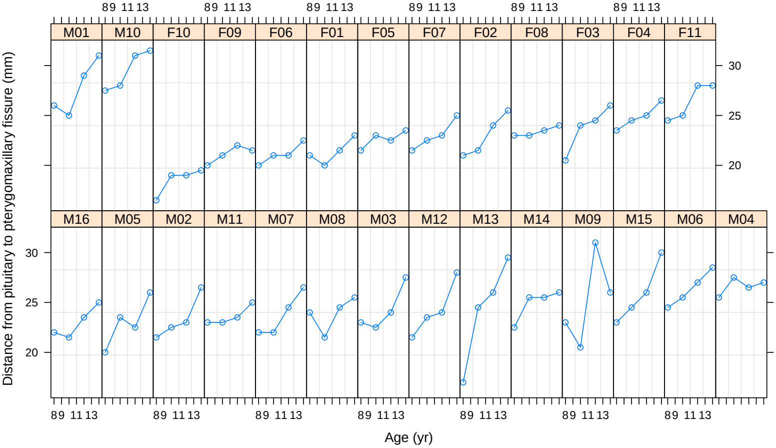
- Subject were 27 children, 16 males and 11 females
- Measurements of the distance from the pituitary gland to the pterygomaxillary fissure were taken every two years from 8 years of age until 14 years of age.
- The data were collected by orthodontists from x-rays of the children's skulls
- The pituitary gland and the pterygomaxillary fissure are easily located points on x-rays.

Orthodontic Data (ctd)

```
library(nlme)
library(lattice)
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

names(Orthodont)

## [1] "distance" "age"      "Subject"  "Sex"

levels(Orthodont$Sex)

## [1] "Male"   "Female"
```

Orthodontic Data (ctd)

```r
plot(Orthodont)
```



Orthodontic Data (ctd)

Concentrating on females for the moment:

```
OrthoFem <- Orthodont[Orthodont$Sex == "Female", ]
fm1OrthF.lis <- lmList(distance ~ age, data = OrthoFem)
coef(fm1OrthF.lis)
```

```
##     (Intercept)   age
## F10       13.55 0.450
## F09       18.10 0.275
## F06       17.00 0.375
## F01       17.25 0.375
## F05       19.60 0.275
## F07       16.95 0.550
## F02       14.20 0.800
## F08       21.45 0.175
## F03       14.40 0.850
## F04       19.65 0.475
## F11       18.95 0.675
```

Orthodontic Data (ctd)

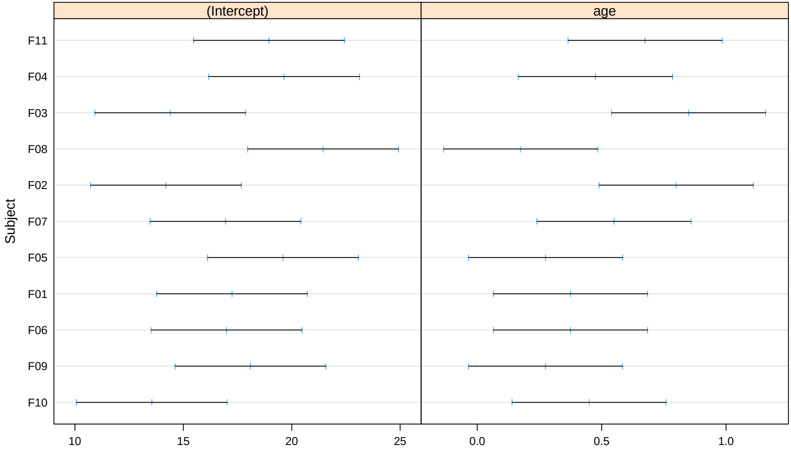
```
summary(fm1OrthF.lis)

## Call:
##   Model: distance ~ age | Subject
##    Data: OrthoFem
##
## Coefficients:
##    (Intercept)
##     Estimate Std. Error t value  Pr(>|t|)
## F10    13.55      1.677   8.078 5.021e-08
## F09    18.10      1.677  10.791 2.970e-10
## F06    17.00      1.677  10.135 9.453e-10
## F01    17.25      1.677  10.284 7.234e-10
## F05    19.60      1.677  11.685 6.614e-11
## F07    16.95      1.677  10.105 9.975e-10
## F02    14.20      1.677   8.466 2.279e-08
## F08    21.45      1.677  12.788 1.161e-11
## F03    14.40      1.677   8.585 1.794e-08
## F04    19.65      1.677  11.715 6.300e-11
## F11    18.95      1.677  11.298 1.255e-10
##    age
##     Estimate Std. Error t value  Pr(>|t|)
## F10    0.450     0.1494   3.011 6.422e-03
## F09    0.275     0.1494   1.840 7.925e-02
## F06    0.375     0.1494   2.510 1.995e-02
## F01    0.375     0.1494   2.510 1.995e-02
## F05    0.275     0.1494   1.840 7.925e-02
## F07    0.550     0.1494   3.681 1.310e-03
## F02    0.800     0.1494   5.354 2.247e-05
## F08    0.175     0.1494   1.171 2.541e-01
## F03    0.850     0.1494   5.688 1.013e-05
## F04    0.475     0.1494   3.179 4.344e-03
```

Orthodontic Data (ctd)

```
intervals(fm1OrthF.lis)

## , , (Intercept)
##
##     lower  est. upper
## F10 10.07 13.55 17.03
## F09 14.62 18.10 21.58
## F06 13.52 17.00 20.48
## F01 13.77 17.25 20.73
## F05 16.12 19.60 23.08
## F07 13.47 16.95 20.43
## F02 10.72 14.20 17.68
## F08 17.97 21.45 24.93
## F03 10.92 14.40 17.88
## F04 16.17 19.65 23.13
## F11 15.47 18.95 22.43
##
## , , age
##
##       lower  est.  upper
## F10  0.1401 0.450 0.7599
## F09 -0.0349 0.275 0.5849
## F06  0.0651 0.375 0.6849
## F01  0.0651 0.375 0.6849
## F05 -0.0349 0.275 0.5849
## F07  0.2401 0.550 0.8599
## F02  0.4901 0.800 1.1099
## F08 -0.1349 0.175 0.4849
## F03  0.5401 0.850 1.1599
## F04  0.1651 0.475 0.7849
## F11  0.3651 0.675 0.9849
```

Orthodontic Data (ctd)

```
plot(intervals(fm1OrthF.lis))
```



Aside: Centring Covariates (Part I)

Advantages of centering covariates:

- The intercept becomes interpretable (estimated mean response when covariates take their average value), and
- Can reduce correlation between estimated fixed effects.

Simple linear regression:
Instead of

$$\mathbf{X} = \begin{pmatrix} 1 & x_1 \\ 1 & x_2 \\ \vdots & \vdots \\ 1 & x_n \end{pmatrix} \quad \text{use} \quad \mathbf{X}_c = \begin{pmatrix} 1 & x_1 - \bar{x} \\ 1 & x_2 - \bar{x} \\ \vdots & \vdots \\ 1 & x_n - \bar{x} \end{pmatrix}$$

where $\bar{x} = \frac{1}{n}\sum_{i=1}^{n} x_i$.

Aside: Centring Covariates (Part I, ctd)

Then

$$\mathbf{X}_c^\mathsf{T}\mathbf{X}_c = \begin{pmatrix} n & 0 \\ 0 & \sum_{i=1}^n (x_i - \bar{x})^2 \end{pmatrix} \quad \text{and} \quad \mathbf{X}_c^\mathsf{T}\mathbf{y} = \begin{pmatrix} \sum_{i=1}^n y_i \\ \sum_{i=1}^n (x_i - \bar{x}) y_i \end{pmatrix}$$

Whence

$$\hat{\boldsymbol{\beta}} = \left(\mathbf{X}_c^\mathsf{T}\mathbf{X}_c\right)^{-1} \mathbf{X}_c^\mathsf{T}\mathbf{y} = \begin{pmatrix} \frac{1}{n}\sum_{i=1}^n y_i \\ \frac{\sum_{i=1}^n (x_i - \bar{x}) y_i}{\sum_{i=1}^n (x_i - \bar{x})^2} \end{pmatrix}$$

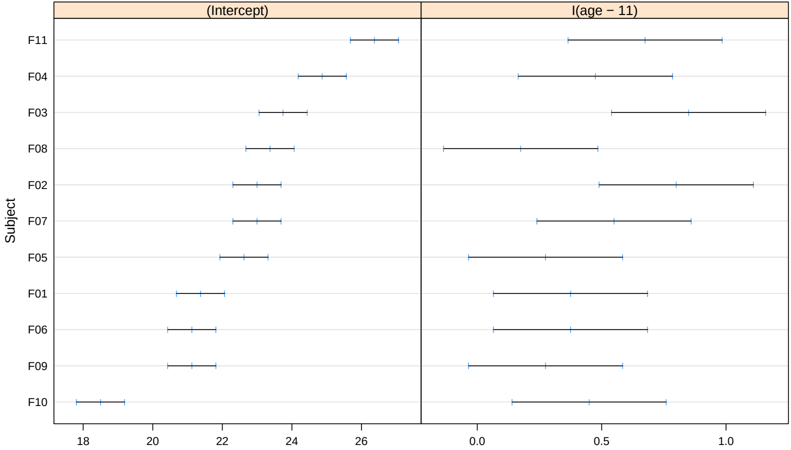
Furthermore, under a normal error model,

$$\hat{\boldsymbol{\beta}} \sim \mathcal{N}_2\left(\boldsymbol{\beta}, \sigma^2 \left(\mathbf{X}_c^\mathsf{T}\mathbf{X}_c\right)^{-1}\right)$$

That is, the estimators $\hat{\beta}_0$ and $\hat{\beta}_1$ for the intercept and slope, respectively, are independent of each other

Orthodontic Data (ctd)

```
fm2OrthF.lis <- update(fm1OrthF.lis, distance ~ I(age - 11))
plot(intervals(fm2OrthF.lis))
```



Model specification

The general specification is given by:

$$
\begin{aligned}
distance_{ti} &= \beta_0 + \beta_1 \times age_{ti} \\
&\qquad + u_{0i} + u_{1i} \times age_{ti} + \varepsilon_{ti} \\
&= (\beta_0 + u_{0i}) + (\beta_1 + u_{1i}) \times age_{ti} + \varepsilon_{ti}
\end{aligned}
$$

with $distance_{ti}$ being the outcome at age $6 + 2\,t$ $(t = 1, \ldots, 4)$ on the ith female $(i = 1, \ldots, 11)$.

Using this model specification we note:

- The u_{0i} term represents the random intercept
- The u_{1i} term represents the random slope (random effect associated with the slope for female i)

Model specification (ctd)

We assume that the distribution of the random effects associated with female i, u_{0i} and u_{1i} is bivariate normal:

$$\mathbf{u}_i = \begin{pmatrix} u_{0i} \\ u_{1i} \end{pmatrix} \sim \mathcal{N}_2\left(\mathbf{0}, \mathbf{D}\right), \qquad \mathbf{D} = \begin{pmatrix} \sigma^2_{int} & \sigma_{int,slope} \\ \sigma_{int,slope} & \sigma^2_{slope} \end{pmatrix}$$

Finally

$$\boldsymbol{\varepsilon}_i = \begin{pmatrix} \varepsilon_{1i} \\ \varepsilon_{2i} \\ \varepsilon_{3i} \\ \varepsilon_{4i} \end{pmatrix} \sim \mathcal{N}_4(\mathbf{0}, \mathbf{R}_i)$$

where we consider $\mathbf{R}_i = \sigma^2 \mathbf{I}_4$.

Model specification: Multilevel notation

Level 1 Model (Time):

$$distance_{ti} = \pi_{0i} + \pi_{1i} \times age_{ti} + \varepsilon_{ti}$$

where $\varepsilon_{ti} \sim N(0, \sigma^2)$

Level 2 Model (Female):

$$\pi_{0i} = \beta_{00} + r_{0i}$$
$$\pi_{1i} = \beta_{10} + r_{1i}$$

where $\mathbf{r}_i = \binom{r_{0i}}{r_{1i}} \sim N(\mathbf{0}, \mathbf{D})$, independent of the ε_{ti}

Model specification: Matrix notation

Model for observation on female i:

$$\mathbf{Y}_i = \mathbf{X}_i\boldsymbol{\beta} + \mathbf{Z}_i\mathbf{u}_i + \boldsymbol{\varepsilon}_i, \quad i = 1, \ldots, 11$$

where

$$\mathbf{Y}_i = \begin{pmatrix} Y_{1i} \\ Y_{2i} \\ Y_{3i} \\ Y_{4i} \end{pmatrix}, \quad \mathbf{X}_i = \begin{pmatrix} 1 & 8 \\ 1 & 10 \\ 1 & 12 \\ 1 & 14 \end{pmatrix} \quad \text{and} \quad \boldsymbol{\beta} = \begin{pmatrix} \beta_0 \\ \beta_1 \end{pmatrix}$$

And for the random terms:

$$\mathbf{Z}_i = \begin{pmatrix} 1 & 8 \\ 1 & 10 \\ 1 & 12 \\ 1 & 14 \end{pmatrix}, \quad \mathbf{u}_i = \begin{pmatrix} u_{0i} \\ u_{1i} \end{pmatrix} \quad \text{and} \quad \boldsymbol{\varepsilon}_i = \begin{pmatrix} \varepsilon_{1i} \\ \varepsilon_{2i} \\ \varepsilon_{3i} \\ \varepsilon_{4i} \end{pmatrix}$$

where $\mathbf{u}_i \sim \mathcal{N}_2(\mathbf{0}, \mathbf{D})$ and $\boldsymbol{\varepsilon}_i \sim \mathcal{N}_4(\mathbf{0}, \mathbf{R}_i)$, $\mathbf{u}_i$ and $\boldsymbol{\varepsilon}_i$ independent of each other.

Model specification: Matrix notation (ctd)

Thus

$$\mathbf{Y} = \mathbf{X}\beta + \mathbf{Z}\mathbf{u} + \varepsilon$$

where (with $n = 11 \times 4 = 44$)

$$\mathbf{Y} = \begin{pmatrix} \mathbf{Y}_1 \\ \mathbf{Y}_2 \\ \vdots \\ \mathbf{Y}_{11} \end{pmatrix}, \quad \mathbf{X} = \begin{pmatrix} \mathbf{X}_1 \\ \mathbf{X}_2 \\ \vdots \\ \mathbf{X}_{11} \end{pmatrix}, \quad \mathbf{Z} = \begin{pmatrix} \mathbf{Z}_1 & & & \\ & \mathbf{Z}_2 & & \\ & & \ddots & \\ & & & \mathbf{Z}_{11} \end{pmatrix}$$

$$\mathbf{u} = \begin{pmatrix} \mathbf{u}_1 \\ \mathbf{u}_2 \\ \vdots \\ \mathbf{u}_{11} \end{pmatrix}, \quad \text{and} \quad \varepsilon = \begin{pmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \vdots \\ \varepsilon_{11} \end{pmatrix}$$

$\mathbf{Y}$ is a 44×1 vector, $\mathbf{X}$ a 44×2 matrix, $\mathbf{Z}$ an 44×22 matrix, $\mathbf{u}$ a 22×1 vector and ε a 44×1 vector.

Model specification: Matrix notation (ctd)

Thus

$$\mathbf{u} \sim \mathcal{N}(\mathbf{0}, \mathbf{G}) \qquad \text{and} \qquad \boldsymbol{\varepsilon} \sim \mathcal{N}(\mathbf{0}, \mathbf{R})$$

where

$$\mathbf{G} = \begin{pmatrix} \mathbf{D} & & & \\ & \mathbf{D} & & \\ & & \ddots & \\ & & & \mathbf{D} \end{pmatrix} \quad \text{and} \quad \mathbf{R} = \begin{pmatrix} \mathbf{R}_1 & & & \\ & \mathbf{R}_2 & & \\ & & \ddots & \\ & & & \mathbf{R}_{11} \end{pmatrix}$$

I.e. $\mathbf{G}$ (22×22) and $\mathbf{R}$ (44×44) are block-diagonal matrices representing the *variance-covariance matrix* for all random effects and for all residuals, respectively.

Orthodontic Data (ctd)

```
fm1OrthF <- lme(distance ~ age, data = OrthoFem, random = ~1 | Subject)
summary(fm1OrthF)
```

```
## Linear mixed-effects model fit by REML
##  Data: OrthoFem
##      AIC   BIC logLik
##    149.2 156.2 -70.61
##
## Random effects:
##  Formula: ~1 | Subject
##         (Intercept) Residual
## StdDev:       2.068     0.78
##
## Fixed effects: distance ~ age
##              Value Std.Error DF t-value p-value
## (Intercept) 17.37    0.8587 32  20.230       0
## age          0.48    0.0526 32   9.119       0
##  Correlation:
##     (Intr)
## age -0.674
##
## Standardized Within-Group Residuals:
##     Min      Q1     Med      Q3     Max
## -2.2736 -0.7090  0.1728  0.4122  1.6325
##
## Number of Observations: 44
## Number of Groups: 11
```

Orthodontic Data (ctd)

```
fm2OrthF <- update(fm1OrthF, random = ~age | Subject)
anova(fm1OrthF, fm2OrthF)

##          Model df   AIC   BIC logLik   Test L.Ratio p-value
## fm1OrthF     1  4 149.2 156.2 -70.61
## fm2OrthF     2  6 149.4 159.8 -68.71 1 vs 2    3.79  0.1503

0.5 * (1 - pchisq(3.79, 1)) + 0.5 * (1 - pchisq(3.79, 2))

## [1] 0.1009
```

Testing

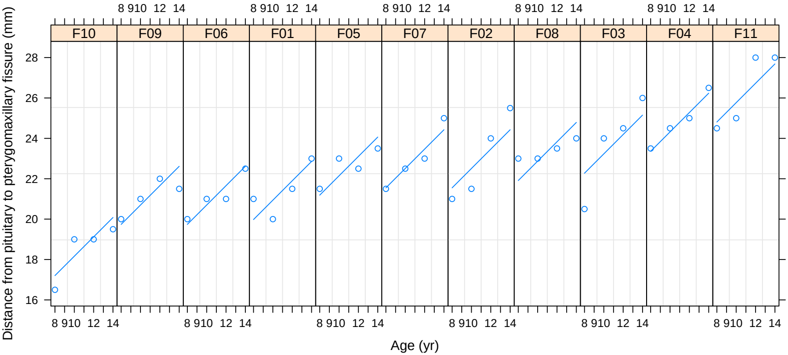
$$H_0 : \mathbf{D} = \begin{pmatrix} \sigma^2_{int} & 0 \\ 0 & 0 \end{pmatrix} \quad \text{against} \quad H_1 : \mathbf{D} = \begin{pmatrix} \sigma^2_{int} & \sigma_{int,slope} \\ \sigma_{int,slope} & \sigma^2_{slope} \end{pmatrix}$$

Orthodontic Data (ctd)

```
coef(fm1OrthF)

##     (Intercept)    age
## F10       13.37 0.4795
## F09       15.90 0.4795
## F06       15.90 0.4795
## F01       16.14 0.4795
## F05       17.35 0.4795
## F07       17.71 0.4795
## F02       17.71 0.4795
## F08       18.08 0.4795
## F03       18.44 0.4795
## F04       19.52 0.4795
## F11       20.97 0.4795
```

Orthodontic Data (ctd)

```
plot(augPred(fm1OrthF), aspect = "xy", grid = T)
```

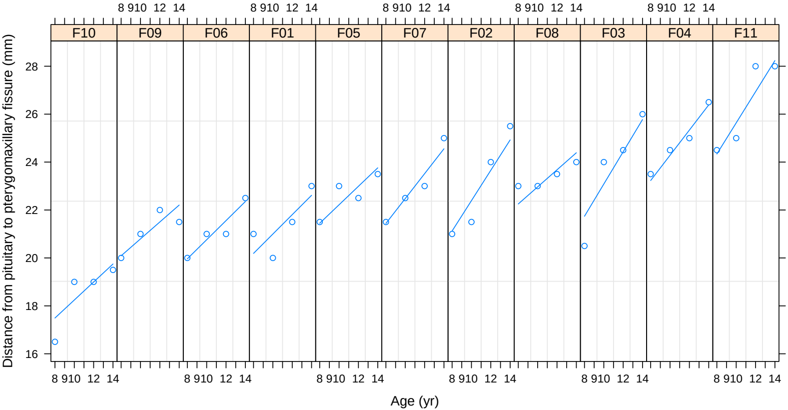


Orthodontic Data (ctd)

```
coef(fm2OrthF)

##     (Intercept)    age
## F10       14.48 0.3759
## F09       17.27 0.3530
## F06       16.77 0.3987
## F01       16.96 0.4041
## F05       18.36 0.3856
## F07       17.28 0.5194
## F02       16.05 0.6337
## F08       19.40 0.3562
## F03       16.36 0.6728
## F04       19.02 0.5259
## F11       19.14 0.6499
```

Orthodontic Data (ctd)

```r
plot(augPred(fm2OrthF), aspect = "xy", grid = T)
```

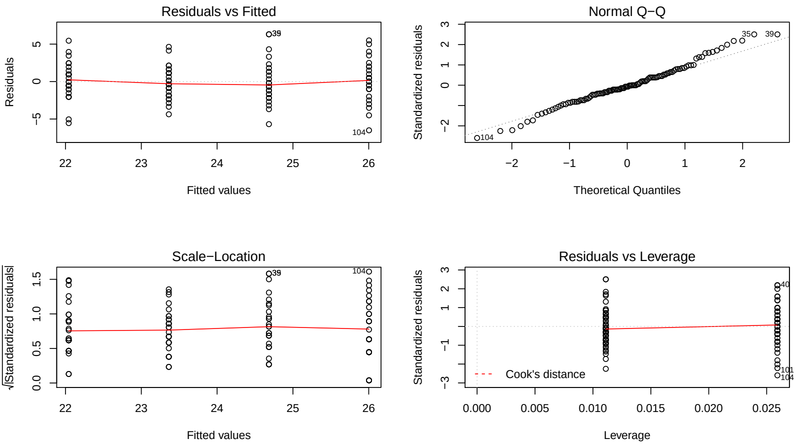


Orthodontic Data (full data, `lm()`)

```
fm1Orth.lm <- lm(distance ~ age, Orthodont)
fm1Orth.lm

##
## Call:
## lm(formula = distance ~ age, data = Orthodont)
##
## Coefficients:
## (Intercept)          age
##       16.76         0.66
```

Orthodontic Data (full data, `lm()`, ctd)

```r
par(mfrow = c(2, 2))
plot(fm1Orth.lm)
```



Orthodontic Data (full data, `lm()`, ctd)

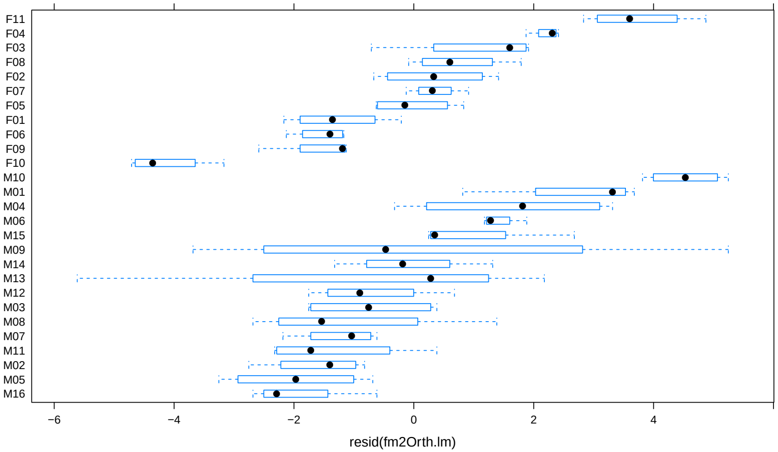
```
fm2Orth.lm <- update(fm1Orth.lm, formula = distance ~ Sex * age)
```

```
summary(fm2Orth.lm)

....
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)       16.341      1.416   11.54  < 2e-16 ***
## SexFemale          1.032      2.219    0.47     0.64
## age                0.784      0.126    6.22  1.1e-08 ***
## SexFemale:age     -0.305      0.198   -1.54     0.13
## ---
....
```

```
anova(fm1Orth.lm, fm2Orth.lm)

## Analysis of Variance Table
##
## Model 1: distance ~ age
## Model 2: distance ~ Sex + age + Sex:age
##   Res.Df RSS Df Sum of Sq  F  Pr(>F)
## 1    106 682
## 2    104 530  2       153 15 1.9e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Orthodontic Data (full data, `lm()`, ctd)

```
bwplot(getGroups(Orthodont) ~ resid(fm2Orth.lm))
```



Orthodontic Data (full data, lmList())

As

```
getGroupsFormula(Orthodont)
```

```
## ~Subject
## <environment: 0x41ac8a8>
```

these two commands are equivalent

```
fm1Orth.lis <- lmList(distance ~ age | Subject, Orthodont)
fm1Orth.lis <- lmList(distance ~ age, Orthodont)
```

And since

```
formula(Orthodont)
```

```
## distance ~ age | Subject
```

we could have just issued the command:

```
fm1Orth.lis <- lmList(Orthodont)
```

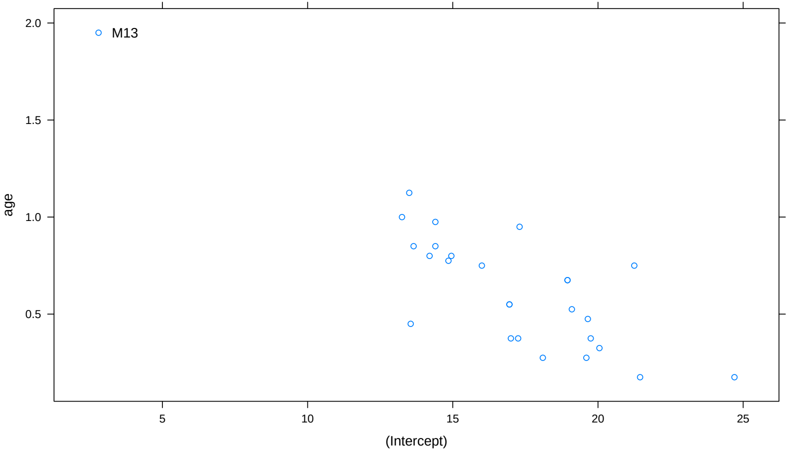
Orthodontic Data (full data, `lmList()`, ctd)

```
summary(fm1Orth.lis)

## Call:
##   Model: distance ~ age | Subject
##    Data: Orthodont
##
## Coefficients:
##    (Intercept)
##     Estimate Std. Error t value   Pr(>|t|)
## M16    16.95      3.288  5.1548 3.695e-06
## M05    13.65      3.288  4.1512 1.182e-04
## M02    14.85      3.288  4.5162 3.459e-05
## M11    20.05      3.288  6.0976 1.189e-07
## M07    14.95      3.288  4.5466 3.117e-05
## M08    19.75      3.288  6.0064 1.666e-07
## M03    16.00      3.288  4.8659 1.028e-05
## M12    13.25      3.288  4.0296 1.763e-04
## M13     2.80      3.288  0.8515 3.982e-01
## M14    19.10      3.288  5.8087 3.450e-07
## M09    14.40      3.288  4.3793 5.510e-05
## M15    13.50      3.288  4.1056 1.374e-04
## M06    18.95      3.288  5.7631 4.078e-07
## M04    24.70      3.288  7.5118 6.082e-10
## M01    17.30      3.288  5.2613 2.524e-06
## M10    21.25      3.288  6.4626 3.066e-08
## F10    13.55      3.288  4.1208 1.307e-04
## F09    18.10      3.288  5.5046 1.048e-06
## F06    17.00      3.288  5.1700 3.500e-06
....
```

```
summary(fm1Orth.lis)

....
## F03    14.40      3.288  4.3793 5.510e-05
## F04    19.65      3.288  5.9760 1.864e-07
## F11    18.95      3.288  5.7631 4.078e-07
##     age
##      Estimate Std. Error t value   Pr(>|t|)
## M16    0.550     0.2929  1.8776 6.585e-02
## M05    0.850     0.2929  2.9017 5.362e-03
## M02    0.775     0.2929  2.6456 1.066e-02
## M11    0.325     0.2929  1.1095 2.721e-01
## M07    0.800     0.2929  2.7310 8.511e-03
## M08    0.375     0.2929  1.2802 2.060e-01
## M03    0.750     0.2929  2.5603 1.329e-02
## M12    1.000     0.2929  3.4137 1.222e-03
## M13    1.950     0.2929  6.6568 1.486e-08
## M14    0.525     0.2929  1.7922 7.870e-02
## M09    0.975     0.2929  3.3284 1.578e-03
## M15    1.125     0.2929  3.8405 3.247e-04
## M06    0.675     0.2929  2.3043 2.508e-02
## M04    0.175     0.2929  0.5974 5.527e-01
## M01    0.950     0.2929  3.2431 2.030e-03
## M10    0.750     0.2929  2.5603 1.329e-02
## F10    0.450     0.2929  1.5362 1.303e-01
## F09    0.275     0.2929  0.9388 3.520e-01
## F06    0.375     0.2929  1.2802 2.060e-01
## F01    0.375     0.2929  1.2802 2.060e-01
....
```

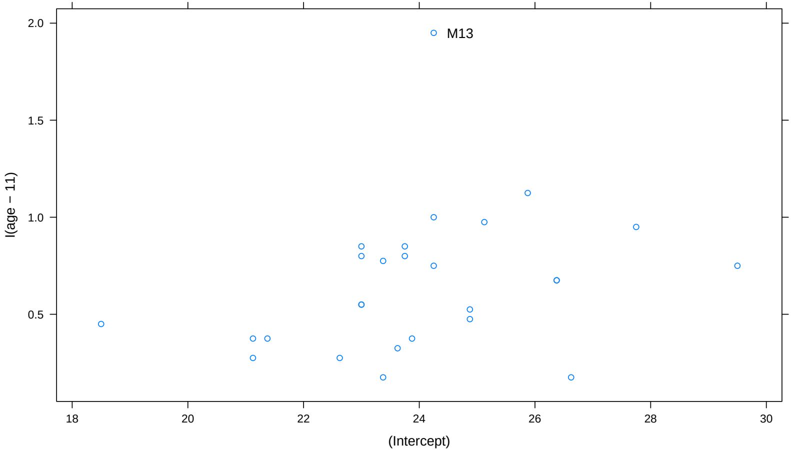
Orthodontic Data (full data, `lmList()`, ctd)

```
pairs(fm1Orth.lis, id = 0.01, adj = -0.5)
```



Orthodontic Data (full data, `lmList()`, ctd)

```
fm2Orth.lis <- update(fm1Orth.lis, distance ~ I(age - 11))
pairs(fm2Orth.lis, id = 0.01, adj = -0.5)
```



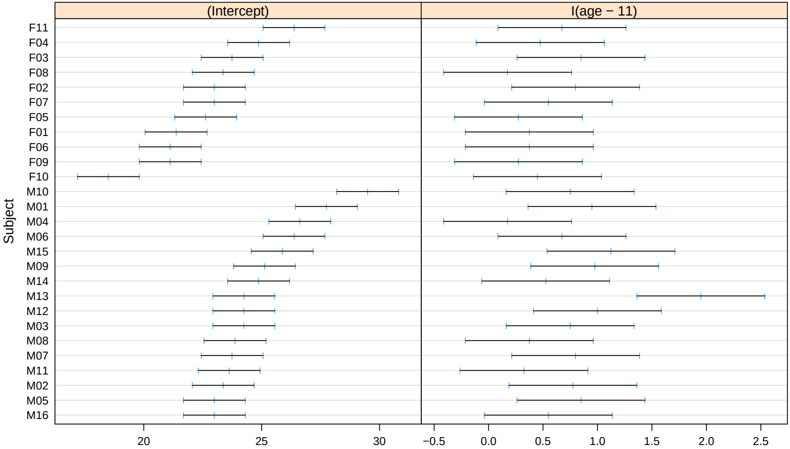
Orthodontic Data (full data, `lmList()`, ctd)

```
intervals(fm2Orth.lis)

## , , (Intercept)
##
##     lower  est. upper
## M16 21.69 23.00 24.31
## M05 21.69 23.00 24.31
## M02 22.06 23.38 24.69
## M11 22.31 23.62 24.94
## M07 22.44 23.75 25.06
## M08 22.56 23.88 25.19
## M03 22.94 24.25 25.56
## M12 22.94 24.25 25.56
## M13 22.94 24.25 25.56
## M14 23.56 24.88 26.19
## M09 23.81 25.12 26.44
## M15 24.56 25.88 27.19
## M06 25.06 26.38 27.69
## M04 25.31 26.62 27.94
## M01 26.44 27.75 29.06
## M10 28.19 29.50 30.81
## F10 17.19 18.50 19.81
## F09 19.81 21.12 22.44
## F06 19.81 21.12 22.44
## F01 20.06 21.38 22.69
## F05 21.31 22.62 23.94
## F07 21.69 23.00 24.31
## F02 21.69 23.00 24.31
....
```

```
intervals(fm2Orth.lis)

....
## , , I(age - 11)
##
##       lower  est.  upper
## M16 -0.0373 0.550 1.1373
## M05  0.2627 0.850 1.4373
## M02  0.1877 0.775 1.3623
## M11 -0.2623 0.325 0.9123
## M07  0.2127 0.800 1.3873
## M08 -0.2123 0.375 0.9623
## M03  0.1627 0.750 1.3373
## M12  0.4127 1.000 1.5873
## M13  1.3627 1.950 2.5373
## M14 -0.0623 0.525 1.1123
## M09  0.3877 0.975 1.5623
## M15  0.5377 1.125 1.7123
## M06  0.0877 0.675 1.2623
## M04 -0.4123 0.175 0.7623
## M01  0.3627 0.950 1.5373
## M10  0.1627 0.750 1.3373
## F10 -0.1373 0.450 1.0373
## F09 -0.3123 0.275 0.8623
## F06 -0.2123 0.375 0.9623
## F01 -0.2123 0.375 0.9623
## F05 -0.3123 0.275 0.8623
## F07 -0.0373 0.550 1.1373
....
```

Orthodontic Data (full data, `lmList()`, ctd)

```
plot(intervals(fm2Orth.lis))
```



Model specification

The general specification is given by:

$$\begin{aligned} distance_{ti} = \beta_0 + \beta_1 \times (age_{ti} - 11) + \beta_2 \times sex_i \\ + \beta_3 \times (age_{ti} - 11) \times sex_i \\ + u_{0i} + u_{1i} \times (age_{ti} - 11) + \varepsilon_{ti} \end{aligned}$$

with $distance_{ti}$ being the outcome at age $6 + 2\,t$ $(t = 1, \ldots, 4)$ on the ith child $(i = 1, \ldots, 27)$ and sex_i is the sex of that child.

Using this model specification we note:

- The u_{0i} term represents the random intercept
- The u_{1i} term represents the random slope (random effect associated with the slope for child i)

Model specification (ctd)

We assume that the distribution of the random effects associated with child i, u_{0i} and u_{1i} is bivariate normal:

$$\mathbf{u}_i = \begin{pmatrix} u_{0i} \\ u_{1i} \end{pmatrix} \sim \mathcal{N}_2\left(\mathbf{0}, \mathbf{D}\right), \qquad \mathbf{D} = \begin{pmatrix} \sigma^2_{int} & \sigma_{int,slope} \\ \sigma_{int,slope} & \sigma^2_{slope} \end{pmatrix}$$

Finally

$$\boldsymbol{\varepsilon}_i = \begin{pmatrix} \varepsilon_{1i} \\ \varepsilon_{2i} \\ \varepsilon_{3i} \\ \varepsilon_{4i} \end{pmatrix} \sim \mathcal{N}_4(\mathbf{0}, \mathbf{R}_i)$$

where we consider $\mathbf{R}_i = \sigma^2 \mathbf{I}_4$.
We will also consider $\mathbf{R}_i = \sigma^2_{male} \mathbf{I}_4$ and $\mathbf{R}_i = \sigma^2_{female} \mathbf{I}_4$ depending on whether the sex of child i is male or female

Model specification: Multilevel notation (homogeneous residual error structure)

Level 1 Model (Time):

$$distance_{ti} = \pi_{0i} + \pi_{1i} \times (age_{ti} - 11) + \varepsilon_{ti}$$

where $\varepsilon_{ti} \sim N(0, \sigma^2)$

Level 2 Model (Child):

$$\pi_{0i} = \beta_{00} + \beta_{01} \times sex_i + r_{0i}$$
$$\pi_{1i} = \beta_{10} + \beta_{11} \times sex_i + r_{1i}$$

where $\mathbf{r}_i = \binom{r_{0i}}{r_{1i}} \sim N(\mathbf{0}, \mathbf{D})$, independent of the ε_{ti}

Model specification: Matrix notation

Model for observation on child i:

$$\mathbf{Y}_i = \mathbf{X}_i\boldsymbol{\beta} + \mathbf{Z}_i\mathbf{u}_i + \boldsymbol{\varepsilon}_i, \quad i = 1, \ldots, 27$$

where

$$\mathbf{Y}_i = \begin{pmatrix} Y_{1i} \\ Y_{2i} \\ Y_{3i} \\ Y_{4i} \end{pmatrix}, \quad \boldsymbol{\beta} = \begin{pmatrix} \beta_0 \\ \beta_1 \\ \beta_2 \\ \beta_3 \end{pmatrix}$$

and

$$\mathbf{X}_i = \begin{pmatrix} 1 & -3 & 0 & 0 \\ 1 & -1 & 0 & 0 \\ 1 & 1 & 0 & 0 \\ 1 & 3 & 0 & 0 \end{pmatrix} \quad \text{or} \quad \mathbf{X}_i = \begin{pmatrix} 1 & -3 & 1 & -3 \\ 1 & -1 & 1 & -1 \\ 1 & 1 & 1 & 1 \\ 1 & 3 & 1 & 3 \end{pmatrix}$$

depending on whether child i is male or female, respectively

Model specification: Matrix notation (ctd)

And for the random terms:

$$\mathbf{Z}_i = \begin{pmatrix} 1 & -3 \\ 1 & -1 \\ 1 & 1 \\ 1 & 3 \end{pmatrix}, \quad \mathbf{u}_i = \begin{pmatrix} u_{0i} \\ u_{1i} \end{pmatrix} \quad \text{and} \quad \boldsymbol{\varepsilon}_i = \begin{pmatrix} \varepsilon_{1i} \\ \varepsilon_{2i} \\ \varepsilon_{3i} \\ \varepsilon_{4i} \end{pmatrix}$$

where $\mathbf{u}_i \sim \mathcal{N}_2(\mathbf{0}, \mathbf{D})$ and $\boldsymbol{\varepsilon}_i \sim \mathcal{N}_4(\mathbf{0}, \mathbf{R}_i)$, $\mathbf{u}_i$ and $\boldsymbol{\varepsilon}_i$ independent of each other.

Model specification: Matrix notation (ctd)

Thus

$$\mathbf{Y} = \mathbf{X}\beta + \mathbf{Z}\mathbf{u} + \varepsilon$$

where (with $n = 27 \times 4 = 108$)

$$\mathbf{Y} = \begin{pmatrix} \mathbf{Y}_1 \\ \mathbf{Y}_2 \\ \vdots \\ \mathbf{Y}_{27} \end{pmatrix}, \quad \mathbf{X} = \begin{pmatrix} \mathbf{X}_1 \\ \mathbf{X}_2 \\ \vdots \\ \mathbf{X}_{27} \end{pmatrix}, \quad \mathbf{Z} = \begin{pmatrix} \mathbf{Z}_1 & & & \\ & \mathbf{Z}_2 & & \\ & & \ddots & \\ & & & \mathbf{Z}_{27} \end{pmatrix}$$

$$\mathbf{u} = \begin{pmatrix} \mathbf{u}_1 \\ \mathbf{u}_2 \\ \vdots \\ \mathbf{u}_{27} \end{pmatrix}, \quad \text{and} \quad \varepsilon = \begin{pmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \vdots \\ \varepsilon_{27} \end{pmatrix}$$

$\mathbf{Y}$ is a 108×1 vector, $\mathbf{X}$ a 108×4 matrix, $\mathbf{Z}$ an 108×54 matrix, $\mathbf{u}$ a 54×1 vector and ε a 108×1 vector.

Model specification: Matrix notation (ctd)

Thus

$$\mathbf{u} \sim \mathcal{N}(\mathbf{0}, \mathbf{G}) \qquad \text{and} \qquad \varepsilon \sim \mathcal{N}(\mathbf{0}, \mathbf{R})$$

where

$$\mathbf{G} = \begin{pmatrix} \mathbf{D} & & & \\ & \mathbf{D} & & \\ & & \ddots & \\ & & & \mathbf{D} \end{pmatrix} \quad \text{and} \quad \mathbf{R} = \begin{pmatrix} \mathbf{R}_1 & & & \\ & \mathbf{R}_2 & & \\ & & \ddots & \\ & & & \mathbf{R}_{27} \end{pmatrix}$$

I.e. $\mathbf{G}$ (54×54) and $\mathbf{R}$ (108×108) are block-diagonal matrices representing the *variance-covariance matrix* for all random effects and for all residuals, respectively.

Aside: Centring Covariates (Part II)

- Remember from week 6:

$$\mathrm{var}[\hat{\beta}] = \left(\sum_{i=1}^{m} \mathbf{X}_i^{\mathsf{T}} \hat{\mathbf{V}}_i^{-1} \mathbf{X}_i \right)^{-1}$$

  where $\hat{\mathbf{V}}_i = \mathbf{Z}_i \hat{\mathbf{D}} \mathbf{Z}_i^{\mathsf{T}} + \hat{\mathbf{R}}_i$. Thus, benefit of centring not immediately obvious.
- Should we centre around the grand-mean $(x_{ti} - \bar{x}_{\bullet\bullet})$ or the group-mean $(x_{ti} - \bar{x}_{\bullet i})$?
- If a multilevel/mixed model has random slopes, then centring a level-1 predictor variable can change some elements of the model (and not just the interpretation of the transformed variable).

Aside: Centring Covariates (Part II, ctd)

- Always base centring decisions on theoretical grounds. Although centring can have statistical consequences, these should be of secondary concern compared to the scientific goals of the analysis
- If any of the predictor variables do not have meaningful zero-points, they should be centred so that the intercepts in the multilevel model will be interpretable.

  For example, a Likert-type variable scored from 1 to 7 should not be used in its raw form. If it were, the intercept would be interpreted as the expected value when the scale is 0, which is an impossible value.
- Binary or indicator variables can also be centred. By adjusting for the grand-mean of a binary variable, you are, in effect, removing the effects of that variable when interpreting the intercept...
- Grand-mean centring of a level-1 predictor affects only the parts of the model associated with the intercept.
- Group-mean centring can be useful in certain situations, but it should be employed only when necessary.

Luke, D.A. (2004). *Multilevel Modeling*, Quantitative Applications in the Social Sciences **143**, Sage Publications, Thousand Oaks

Orthodontic Data (full data, `lme()`)

```
fm1Orth.lme <- lme(distance ~ I(age - 11), data = Orthodont, random = ~I(age - 11) | Subject)
```

Or just:

```
fm1Orth.lme <- lme(distance ~ I(age - 11), data = Orthodont)
fm1Orth.lme

## Linear mixed-effects model fit by REML
##   Data: Orthodont
##   Log-restricted-likelihood: -221.3
##   Fixed: distance ~ I(age - 11)
## (Intercept) I(age - 11)
##     24.0231      0.6602
##
## Random effects:
##  Formula: ~I(age - 11) | Subject
##  Structure: General positive-definite
##             StdDev Corr
## (Intercept) 2.1343 (Intr)
## I(age - 11) 0.2264 0.503
## Residual    1.3100
##
## Number of Observations: 108
## Number of Groups: 27
```

Orthodontic Data (full data, `lme()`, ctd)

```
fm2Orth.lme <- update(fm1Orth.lme, fixed = distance ~ Sex * I(age - 11), random = ~I(age - 11))
summary(fm2Orth.lme)
```

```
## Linear mixed-effects model fit by REML
##  Data: Orthodont
##       AIC   BIC logLik
##   448.6 469.7 -216.3
##
## Random effects:
##  Formula: ~I(age - 11) | Subject
##  Structure: General positive-definite, Log-Cholesky parametrization
##              StdDev Corr
## (Intercept) 1.8303 (Intr)
## I(age - 11) 0.1803 0.206
## Residual    1.3100
##
## Fixed effects: distance ~ Sex + I(age - 11) + Sex:I(age - 11)
##                          Value Std.Error DF t-value p-value
## (Intercept)             24.969    0.4860 79   51.38  0.0000
## SexFemale               -2.321    0.7614 25   -3.05  0.0054
## I(age - 11)              0.784    0.0860 79    9.12  0.0000
## SexFemale:I(age - 11) -0.305    0.1347 79   -2.26  0.0264
##  Correlation:
##                         (Intr) SexFml I(-11)
## SexFemale               -0.638
## I(age - 11)              0.102 -0.065
## SexFemale:I(age - 11) -0.065  0.102 -0.638
##
## Standardized Within-Group Residuals:
##       Min        Q1       Med        Q3       Max
## -3.168078 -0.385939  0.007104  0.445155  3.849463
##
```

Orthodontic Data (full data, `lme()`, ctd)

Recall, `fitted()` and `resid()` have a `level` argument, so has `predict()`:

```
newOrth <- data.frame(Subject = rep(c("M11","F03"), c(3, 3)),
                      Sex = rep(c("Male", "Female"), c(3, 3)),
                      age = rep(16:18, 2))
predict( fm2Orth.lme, newdata = newOrth, level = 0:1 )

##   Subject predict.fixed predict.Subject
## 1     M11         28.89           26.97
## 2     M11         29.68           27.61
## 3     M11         30.46           28.26
## 4     F03         25.05           26.61
## 5     F03         25.53           27.21
## 6     F03         26.00           27.80
```

Orthodontic Data (full data, lme()⟷lmList())

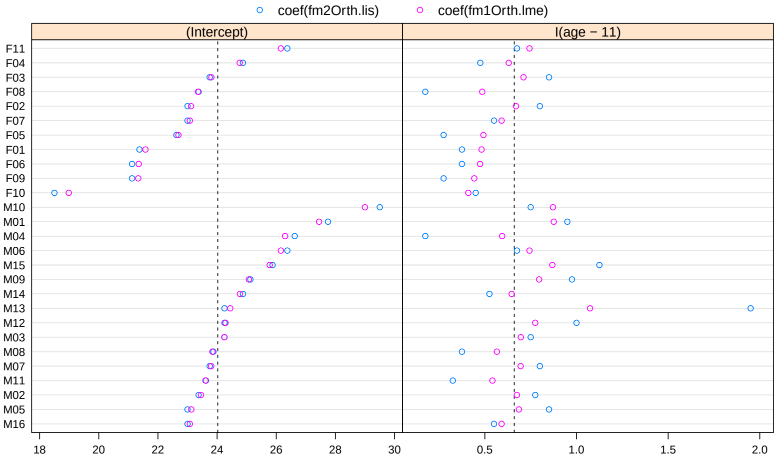
```
compOrth <- compareFits(coef(fm2Orth.lis), coef(fm1Orth.lme))
```

```
compOrth
## , , (Intercept)
##
##     coef(fm2Orth.lis) coef(fm1Orth.lme)
## M16             23.00             23.08
## M05             23.00             23.13
## M02             23.38             23.46
## M11             23.62             23.61
## M07             23.75             23.80
## M08             23.88             23.84
## M03             24.25             24.24
## M12             24.25             24.29
## M13             24.25             24.44
## M14             24.88             24.77
## M09             25.12             25.07
## M15             25.88             25.78
## M06             26.38             26.16
## M04             26.62             26.30
## M01             27.75             27.45
## M10             29.50             29.00
## F10             18.50             18.99
## F09             21.12             21.33
## F06             21.12             21.35
## F01             21.38             21.58
## F05             22.62             22.69
....
```

```
compOrth
....
## F11             26.38             26.16
##
## , , I(age - 11)
##
##     coef(fm2Orth.lis) coef(fm1Orth.lme)
## M16             0.550            0.5913
## M05             0.850            0.6858
## M02             0.775            0.6747
## M11             0.325            0.5414
## M07             0.800            0.6951
## M08             0.375            0.5654
## M03             0.750            0.6960
## M12             1.000            0.7747
## M13             1.950            1.0739
## M14             0.525            0.6461
## M09             0.975            0.7961
## M15             1.125            0.8684
## M06             0.675            0.7434
## M04             0.175            0.5943
## M01             0.950            0.8759
## M10             0.750            0.8713
## F10             0.450            0.4096
## F09             0.275            0.4421
....
```

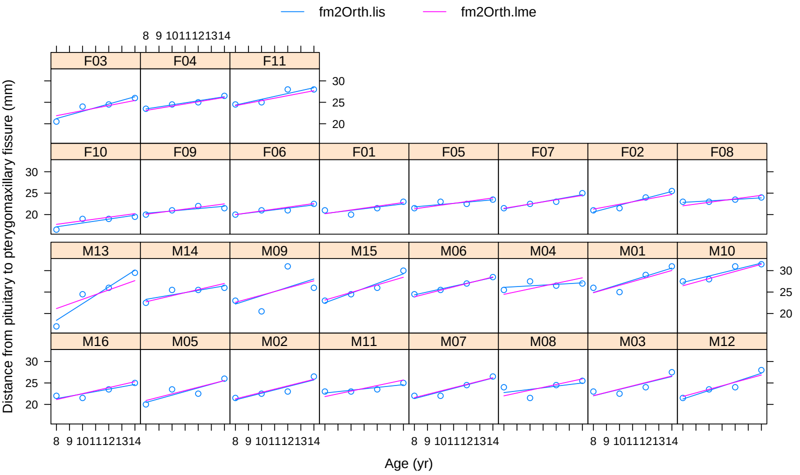
Orthodontic Data (full data, `lme()`⟷`lmList()`, ctd)

```
plot(compOrth, mark = fixef(fm1Orth.lme))
```



Orthodontic Data (full data, `lme()`⟷`lmList()`, ctd)

```r
plot(comparePred(fm2Orth.lis, fm2Orth.lme, length.out = 2), layout = c(8,4),
     between = list(y = c(0, 0.5)))
```



Orthodontic Data (full data, random effects structure)

```
fm4Orth.lm <- lm(distance ~ Sex * I(age - 11), Orthodont)
summary(fm4Orth.lm)
```

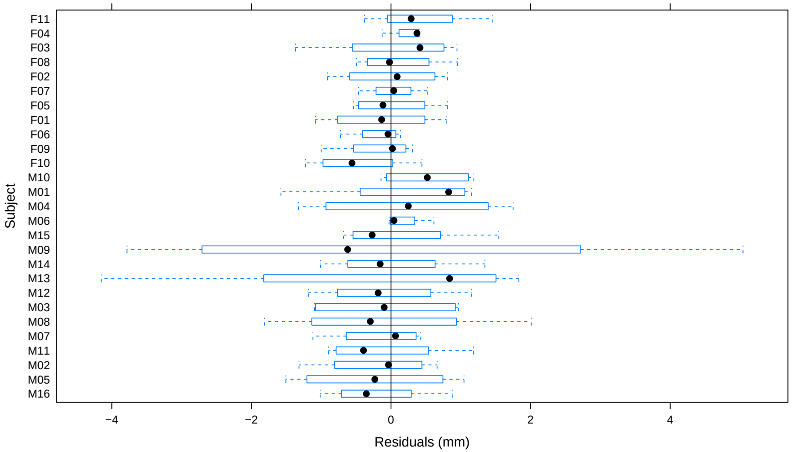
```
##
## Call:
## lm(formula = distance ~ Sex * I(age - 11), data = Orthodont)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -5.616 -1.322 -0.168  1.330  5.247
##
## Coefficients:
##                      Estimate Std. Error t value Pr(>|t|)
## (Intercept)            24.969      0.282   88.50  < 2e-16 ***
## SexFemale              -2.321      0.442   -5.25  8.1e-07 ***
## I(age - 11)             0.784      0.126    6.22  1.1e-08 ***
## SexFemale:I(age - 11)  -0.305      0.198   -1.54     0.13
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.26 on 104 degrees of freedom
## Multiple R-squared:  0.423, Adjusted R-squared:  0.406
## F-statistic: 25.4 on 3 and 104 DF,  p-value: 2.11e-12
```

```
anova(fm2Orth.lme, fm4Orth.lm)
```

```
##             Model df   AIC   BIC logLik   Test L.Ratio p-value
## fm2Orth.lme     1  8 448.6 469.7 -216.3
## fm4Orth.lm      2  5 493.6 506.8 -241.8 1 vs 2   50.98  <.0001
```

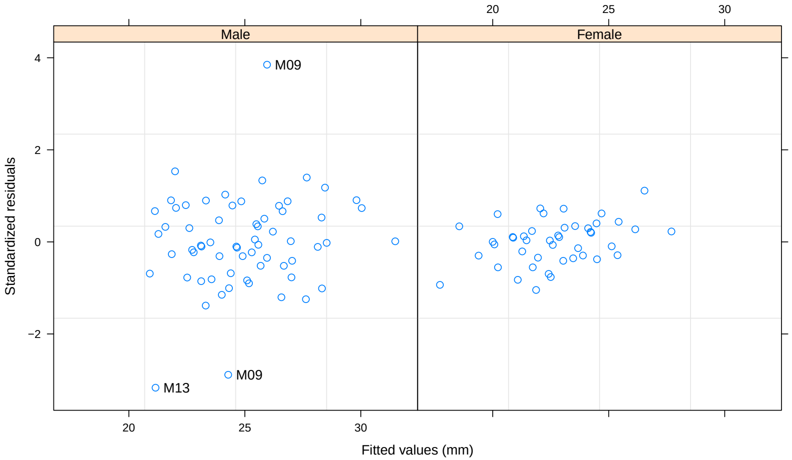
Orthodontic Data (full data, error structure)

```
plot(fm2Orth.lme, Subject ~ resid(.), abline = 0)
```



Orthodontic Data (full data, error structure, ctd)

```r
plot(fm2Orth.lme, resid(., type = "p") ~ fitted(.) | Sex, id = 0.05, adj = -0.3)
```

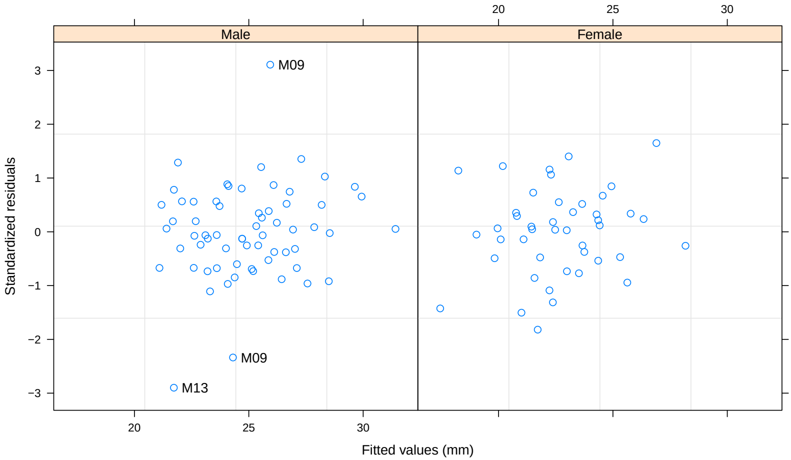


Orthodontic Data (full data, error structure, ctd)

```
fm3Orth.lme <- update(fm2Orth.lme, weights = varIdent(form = ~1 | Sex))
anova(fm2Orth.lme, fm3Orth.lme)

##             Model df   AIC   BIC logLik   Test L.Ratio p-value
## fm2Orth.lme     1  8 448.6 469.7 -216.3
## fm3Orth.lme     2  9 429.5 453.3 -205.8 1 vs 2   21.06  <.0001

anova(fm3Orth.lme)

##                 numDF denDF F-value p-value
## (Intercept)         1    79    3903  <.0001
## Sex                 1    25      16  0.0006
## I(age - 11)         1    79     110  <.0001
## Sex:I(age - 11)     1    79       7  0.0121
```

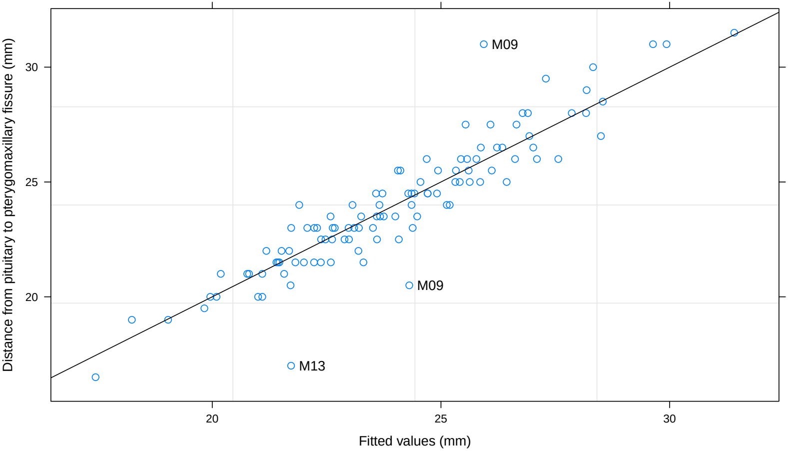
Orthodontic Data (full data, error structure, ctd)

```
plot(fm3Orth.lme, resid(., type = "p") ~ fitted(.) | Sex, id = 0.05, adj = -0.3)
```



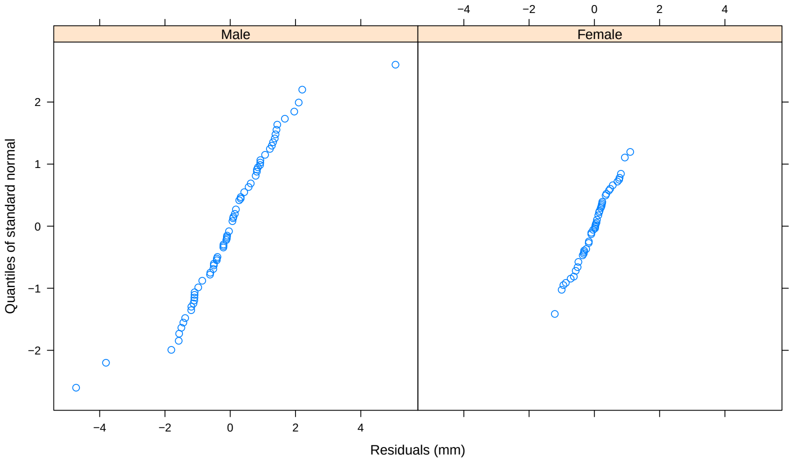
Orthodontic Data (diagnostic plots)

```
plot(fm3Orth.lme, distance ~ fitted(.), id = 0.05, adj = -0.3, abline = c(0, 1))
```



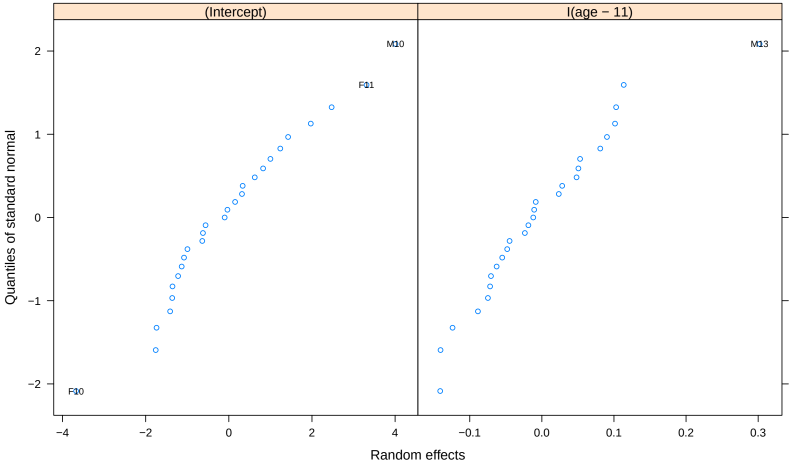
Orthodontic Data (diagnostic plots, ctd)

```
qqnorm(fm3Orth.lme, ~resid(.) | Sex)
```



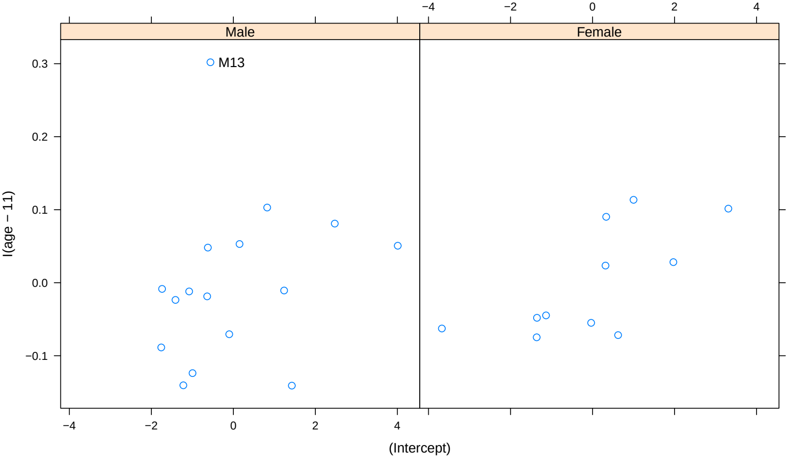
Orthodontic Data (diagnostic plots, ctd)

```
qqnorm(fm2Orth.lme, ~ranef(.), id = 0.1, cex = 0.7)
```



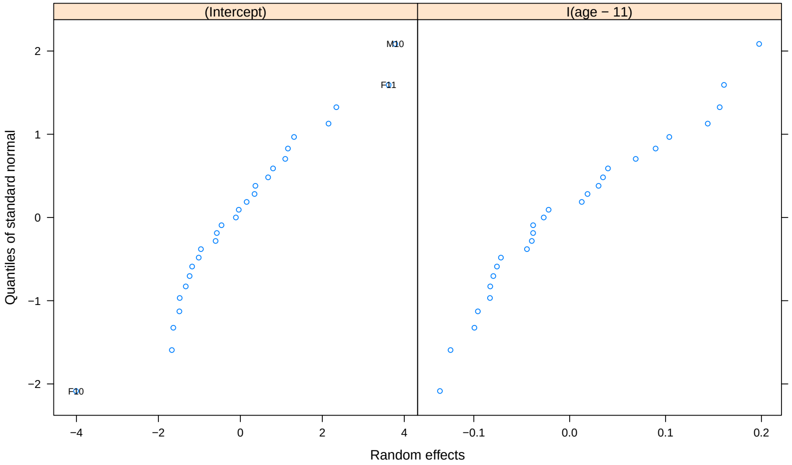
Orthodontic Data (diagnostic plots, ctd)

```
pairs(fm2Orth.lme, ~ranef(.) | Sex, id = ~Subject == "M13", adj = -0.3)
```



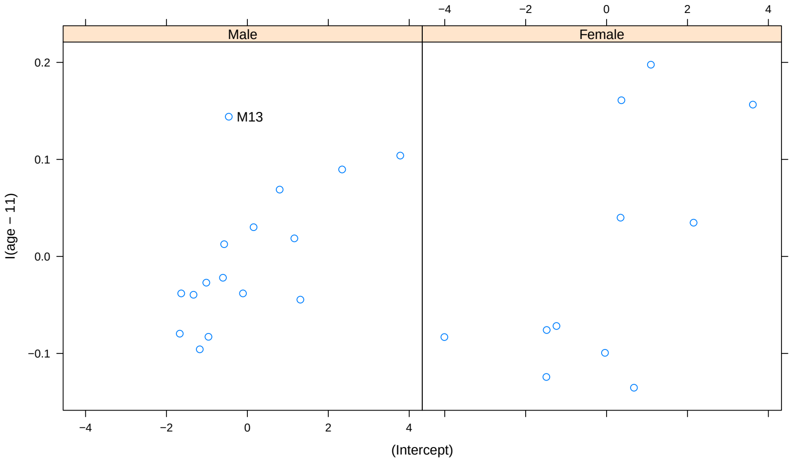
Orthodontic Data (diagnostic plots, ctd)

```
qqnorm(fm3Orth.lme, ~ranef(.), id = 0.1, cex = 0.7)
```



Orthodontic Data (diagnostic plots, ctd)

```
pairs(fm3Orth.lme, ~ranef(.) | Sex, id = ~Subject == "M13", adj = -0.3)
```



Orthodontic Data (diagnostic plots, ctd)

In mixed-effects estimation, there is a trade-off between the within-group variability and the between-group variability, when accounting for the overall variability in the data. The use of a common within-group variance in `fm2Orth.lme` *leads to an increase in the estimated between-group variability, which in turn allows the random-effects estimates to be pulled away by outliers. The heteroscedastic model in* `fm3Orth.lme` *accommodates the impact of the boys outlying observations in the within-group variances estimation and reduces the estimated between-group variability, thus increasing the degree of shrinkage in the random-effects estimates. In this case, the use of different within-group variances by gender adds a certain degree of robustness to the lme fit.*

Pinheiro, J.C. and Bates, D. M. (2000). *Mixed-Effects Models in S and S-PLUS*, Statistics and Computing, Springer-Verlag, New York.

Patterned Variance-Covariance Matrices for Random Effects

We may wish to restrict **D** to special forms of variance-covariance matrices that are parametrised by fewer parameters

The `nlme` package provides the following classes of positive definite matrices by default

`pdBlocked`	block–diagonal
`pdCompSymm`	compound–symmetry structure
`pdDiag`	diagonal
`pdIdent`	multiple of an identity
`pdSymm`	general positive–definite matrix

Patterned Variance-Covariance Matrices for Random Effects (ctd)

```
fm4Orth.lme <- lme(distance ~ Sex*I(age-11), data=Orthodont,
                   random = pdDiag(~I(age-11)))
fm4Orth.lme

## Linear mixed-effects model fit by REML
##   Data: Orthodont
##   Log-restricted-likelihood: -216.4
##   Fixed: distance ~ Sex * I(age - 11)
##           (Intercept)              SexFemale             I(age - 11) SexFemale:I(age - 11)
##               24.9688                -2.3210                  0.7844               -0.3048
##
## Random effects:
##  Formula: ~I(age - 11) | Subject
##  Structure: Diagonal
##         (Intercept) I(age - 11) Residual
## StdDev:        1.83      0.1803     1.31
##
## Number of Observations: 108
## Number of Groups: 27
```

```
getVarCov(fm4Orth.lme)

## Random effects variance covariance matrix
##             (Intercept) I(age - 11)
## (Intercept)        3.35     0.00000
## I(age - 11)        0.00     0.03252
##   Standard Deviations: 1.83 0.1804
```

```
getVarCov(fm2Orth.lme)

## Random effects variance covariance matrix
##             (Intercept) I(age - 11)
## (Intercept)     3.35010     0.06814
## I(age - 11)     0.06814     0.03252
##   Standard Deviations: 1.83 0.1804
```

Patterned Variance-Covariance Matrices for Random Effects (ctd)

```
fm4Orth.lme <- lme(distance ~ Sex*I(age-11), data=Orthodont,
                   random = pdIdent(~I(age-11)))
fm4Orth.lme
```

```
## Linear mixed-effects model fit by REML
##   Data: Orthodont
##   Log-restricted-likelihood: -240.6
##   Fixed: distance ~ Sex * I(age - 11)
##           (Intercept)              SexFemale            I(age - 11) SexFemale:I(age - 11)
##               24.9688                -2.3210                 0.7844               -0.3048
##
## Random effects:
##  Formula: ~I(age - 11) | Subject
##  Structure: Multiple of an Identity
##         (Intercept) I(age - 11) Residual
## StdDev:       1.116       1.116    1.399
##
## Number of Observations: 108
## Number of Groups: 27
```

```
getVarCov(fm4Orth.lme)
```

```
## Random effects variance covariance matrix
##             (Intercept) I(age - 11)
## (Intercept)       1.246       0.000
## I(age - 11)       0.000       1.246
##   Standard Deviations: 1.116 1.116
```

Class room data revisited

We have $k = 1, \dots, 107$ schools, $j = 1, \dots, m_k$ classrooms in school k, $i = 1, \dots, n_{jk}$ students in classroom j in school k
Write the model for school k in matrix form:

$$\mathbf{Y}_k = \mathbf{X}_k\boldsymbol{\beta} + \mathbf{Z}_k\mathbf{u}_k + \boldsymbol{\varepsilon}_k, \qquad k = 1, \dots, 107$$

where with $n_{\bullet k} = \sum_{j=1}^{m_k} n_{jk}$, the number of students in the sample from school k:

- $\mathbf{Y}_k$ are the $n_{\bullet k}$ observations in school k
- $\mathbf{X}_k$ is a $n_{\bullet k} \times p$ design matrix, which represents the known values of the covariates
- $\boldsymbol{\beta}$ is a vector of p unknown regression coefficients (or fixed-effect parameters)
- $\mathbf{Z}_k$ is a $n_{\bullet k} \times 313$ known matrix (the *random effects design matrix*), namely a column of ones in the first column and the remaining columns the indicator variables for the 312 classes.
- $\mathbf{u}_i \sim \mathcal{N}_{313}(\mathbf{0}, \mathbf{D})$ a vector of 313 *random effects*, and
- $\boldsymbol{\varepsilon}_k \sim \mathcal{N}_{n_{\bullet k}}(\mathbf{0}, \mathbf{R}_k)$ is a vector of $n_{\bullet k}$ *residuals*

Class room data revisited (ctd)

Specifically,

$$\mathbf{Y}_k = \begin{pmatrix} Y_{11k} \\ Y_{21k} \\ \vdots \\ Y_{n_{1k}1k} \\ Y_{12k} \\ \vdots \\ Y_{n_{2k}2k} \\ \vdots \\ Y_{n_{m_k k} m_k k} \end{pmatrix}, \quad \varepsilon_k = \begin{pmatrix} \varepsilon_{11k} \\ \varepsilon_{21k} \\ \vdots \\ \varepsilon_{n_{1k}1k} \\ \varepsilon_{12k} \\ \vdots \\ \varepsilon_{n_{2k}2k} \\ \vdots \\ \varepsilon_{n_{m_k k} m_k k} \end{pmatrix}$$

and

$$\mathbf{D} = \begin{pmatrix} \sigma^2_{int:school} & 0 & \dots & 0 \\ 0 & \sigma^2_{int:classroom} & \ddots & \vdots \\ \vdots & \ddots & \ddots & 0 \\ 0 & \dots & 0 & \sigma^2_{int:classroom} \end{pmatrix} = \begin{pmatrix} \sigma^2_{int:school} & \mathbf{0} \\ \mathbf{0} & \sigma^2_{int:classroom}\mathbf{I}_{312} \end{pmatrix}$$

Class room data revisited (ctd)

Thus

$$\mathbf{Y} = \mathbf{X}\beta + \mathbf{Z}\mathbf{u} + \varepsilon$$

where (with $n = \sum_{k=1}^{107} n_{\bullet k}$)

$$\mathbf{Y} = \begin{pmatrix} \mathbf{Y}_1 \\ \mathbf{Y}_2 \\ \vdots \\ \mathbf{Y}_{107} \end{pmatrix}, \quad \mathbf{X} = \begin{pmatrix} \mathbf{X}_1 \\ \mathbf{X}_2 \\ \vdots \\ \mathbf{X}_{107} \end{pmatrix}, \quad \mathbf{Z} = \begin{pmatrix} \mathbf{Z}_1 & & & \\ & \mathbf{Z}_2 & & \\ & & \ddots & \\ & & & \mathbf{Z}_{107} \end{pmatrix}$$

$$\mathbf{u} = \begin{pmatrix} \mathbf{u}_1 \\ \mathbf{u}_2 \\ \vdots \\ \mathbf{u}_{107} \end{pmatrix}, \quad \text{and} \quad \varepsilon = \begin{pmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \vdots \\ \varepsilon_{107} \end{pmatrix}$$

$\mathbf{Y}$ is a $n \times 1$ vector, $\mathbf{X}$ a $n \times p$ matrix, $\mathbf{Z}$ an $n \times 33491$ matrix, $\mathbf{u}$ a 33491×1 vector and ε a $n \times 1$ vector.

Class room data revisited (ctd)

Thus

$$\mathbf{u} \sim \mathcal{N}(\mathbf{0}, \mathbf{G}) \qquad \text{and} \qquad \boldsymbol{\varepsilon} \sim \mathcal{N}(\mathbf{0}, \mathbf{R})$$

where

$$\mathbf{G} = \begin{pmatrix} \mathbf{D} & & & \\ & \mathbf{D} & & \\ & & \ddots & \\ & & & \mathbf{D} \end{pmatrix} \quad \text{and} \quad \mathbf{R} = \begin{pmatrix} \mathbf{R}_1 & & & \\ & \mathbf{R}_2 & & \\ & & \ddots & \\ & & & \mathbf{R}_{107} \end{pmatrix}$$

I.e. **G** and **R** are block-diagonal matrices representing the *variance-covariance matrix* for all random effects and for all residuals, respectively.

Class room data revisited (ctd)

```
classroom <- read.csv("PATH_TO_DATA/classroom.csv")
classroom$classid <- factor(classroom$classid)
```

```
system.time(fm1 <- lme(mathgain ~ 1, data=classroom,
                       random = ~ 1 | schoolid/classid))

##    user  system elapsed
##   0.220   0.000   0.221
```

```
system.time(fm2 <- lme(mathgain ~ 1, data=classroom,
                       random = list(schoolid =
                         pdBlocked(list(pdIdent(~1), pdIdent(~classid-1))))))

## Warning:  fewer observations than random effects in all level 1 groups

##    user  system elapsed
## 372.455   1.084 374.070
```

Class room data revisited (ctd)

We can check the size of the estimate $\hat{\mathbf{D}}$ for $\mathbf{D}$:

```
dim(getVarCov(fm2))
```

```
## [1] 313 313
```

```
nlevels(classroom$classid)
```

```
## [1] 312
```

If we want to have $\hat{\mathbf{V}}_i = \mathbf{Z}_i \hat{\mathbf{D}} \mathbf{Z}_i^\top + \hat{\mathbf{R}}_i$ for school i:

```
getVarCov(fm2, type = "marginal")
```

```
## schoolid 1
## Marginal variance covariance matrix
##          1       2       3       4       5       6       7       8       9      10      11
## 1  1205.00  176.72  176.72   77.49   77.49   77.49   77.49   77.49   77.49   77.49   77.49
## 2   176.72 1205.00  176.72   77.49   77.49   77.49   77.49   77.49   77.49   77.49   77.49
## 3   176.72  176.72 1205.00   77.49   77.49   77.49   77.49   77.49   77.49   77.49   77.49
## 4    77.49   77.49   77.49 1205.00  176.72  176.72  176.72  176.72  176.72  176.72  176.72
## 5    77.49   77.49   77.49  176.72 1205.00  176.72  176.72  176.72  176.72  176.72  176.72
## 6    77.49   77.49   77.49  176.72  176.72 1205.00  176.72  176.72  176.72  176.72  176.72
## 7    77.49   77.49   77.49  176.72  176.72  176.72 1205.00  176.72  176.72  176.72  176.72
## 8    77.49   77.49   77.49  176.72  176.72  176.72  176.72 1205.00  176.72  176.72  176.72
## 9    77.49   77.49   77.49  176.72  176.72  176.72  176.72  176.72 1205.00  176.72  176.72
## 10   77.49   77.49   77.49  176.72  176.72  176.72  176.72  176.72  176.72 1205.00  176.72
## 11   77.49   77.49   77.49  176.72  176.72  176.72  176.72  176.72  176.72  176.72 1205.00
##   Standard Deviations: 34.71 34.71 34.71 34.71 34.71 34.71 34.71 34.71 34.71 34.71 34.71
```

Class room data revisited (ctd)

The estimate $\hat{\mathbf{R}}_i$ for $\mathbf{R}_i$ for school i is:

```
getVarCov(fm2, type = "conditional")

## schoolid 1
## Conditional variance covariance matrix
##       1    2    3    4    5    6    7    8    9   10   11
## 1  1028    0    0    0    0    0    0    0    0    0    0
## 2     0 1028    0    0    0    0    0    0    0    0    0
## 3     0    0 1028    0    0    0    0    0    0    0    0
## 4     0    0    0 1028    0    0    0    0    0    0    0
## 5     0    0    0    0 1028    0    0    0    0    0    0
## 6     0    0    0    0    0 1028    0    0    0    0    0
## 7     0    0    0    0    0    0 1028    0    0    0    0
## 8     0    0    0    0    0    0    0 1028    0    0    0
## 9     0    0    0    0    0    0    0    0 1028    0    0
## 10    0    0    0    0    0    0    0    0    0 1028    0
## 11    0    0    0    0    0    0    0    0    0    0 1028
##   Standard Deviations: 32.07 32.07 32.07 32.07 32.07 32.07 32.07 32.07 32.07 32.07 32.07
```

Class room data revisited (ctd)

If we want to have $\hat{\mathbf{V}}_i = \mathbf{Z}_i \hat{\mathbf{D}} \mathbf{Z}_i^T + \hat{\mathbf{R}}_i$ for school i:

```
getVarCov(fm2, individual = 2, type = "marginal")

## schoolid 2
## Marginal variance covariance matrix
##          1       2       3       4       5       6       7       8       9      10
## 1  1205.00  176.72   77.49   77.49   77.49   77.49   77.49   77.49   77.49   77.49
## 2   176.72 1205.00   77.49   77.49   77.49   77.49   77.49   77.49   77.49   77.49
## 3    77.49   77.49 1205.00  176.72  176.72  176.72   77.49   77.49   77.49   77.49
## 4    77.49   77.49  176.72 1205.00  176.72  176.72   77.49   77.49   77.49   77.49
## 5    77.49   77.49  176.72  176.72 1205.00  176.72   77.49   77.49   77.49   77.49
## 6    77.49   77.49  176.72  176.72  176.72 1205.00   77.49   77.49   77.49   77.49
## 7    77.49   77.49   77.49   77.49   77.49   77.49 1205.00  176.72  176.72  176.72
## 8    77.49   77.49   77.49   77.49   77.49   77.49  176.72 1205.00  176.72  176.72
## 9    77.49   77.49   77.49   77.49   77.49   77.49  176.72  176.72 1205.00  176.72
## 10   77.49   77.49   77.49   77.49   77.49   77.49  176.72  176.72  176.72 1205.00
##   Standard Deviations: 34.71 34.71 34.71 34.71 34.71 34.71 34.71 34.71 34.71 34.71
```

Class room data revisited (ctd)

The estimate $\hat{\mathbf{R}}_i$ for $\mathbf{R}_i$ for school i is:

```
getVarCov(fm2, individual = 2, type = "conditional")
```

```
## schoolid 2
## Conditional variance covariance matrix
##       1    2    3    4    5    6    7    8    9   10
## 1  1028    0    0    0    0    0    0    0    0    0
## 2     0 1028    0    0    0    0    0    0    0    0
## 3     0    0 1028    0    0    0    0    0    0    0
## 4     0    0    0 1028    0    0    0    0    0    0
## 5     0    0    0    0 1028    0    0    0    0    0
## 6     0    0    0    0    0 1028    0    0    0    0
## 7     0    0    0    0    0    0 1028    0    0    0
## 8     0    0    0    0    0    0    0 1028    0    0
## 9     0    0    0    0    0    0    0    0 1028    0
## 10    0    0    0    0    0    0    0    0    0 1028
##   Standard Deviations: 32.07 32.07 32.07 32.07 32.07 32.07 32.07 32.07 32.07 32.07
```