

# Chapter 3

## The Linear Mixed Effects Model

## 3.1 The Linear Mixed Model

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- In the previous chapter we focused on the *multivariate regression model*

$$y_i = X_i\beta + \varepsilon_i, \quad \varepsilon_i \sim \mathcal{N}(0, V_i),$$

where

- ▷  $y_i$  the vector of responses for the  $i$ th subject
- ▷  $X_i$  design matrix describing structural component
- ▷  $V_i$  covariance matrix describing the correlation structure

## 3.1 The Linear Mixed Model (cont'd)

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- **Alternative intuitive approach:** Each subject in the population has her own subject-specific mean response profile over time

## 3.1 The Linear Mixed Model (cont'd)



## 3.1 The Linear Mixed Model (cont'd)

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- The evolution of each subject in time can be described by a linear model

$$y_{ij} = \tilde{\beta}_{i0} + \tilde{\beta}_{i1}t_{ij} + \varepsilon_{ij}, \quad \varepsilon_{ij} \sim \mathcal{N}(0, \sigma^2),$$

where

- ▷  $y_{ij}$  the  $j$ th response of the  $i$ th subject
- ▷  $\tilde{\beta}_{i0}$  is the intercept and  $\tilde{\beta}_{i1}$  the slope for subject  $i$
- **Assumption:** Subjects are randomly sampled from a population  $\Rightarrow$  subject-specific regression coefficients are also sampled from a population of regression coefficients

$$\tilde{\beta}_i \sim \mathcal{N}(\beta, D)$$

## 3.1 The Linear Mixed Model (cont'd)

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- We can reformulate the model as

$$y_{ij} = (\beta_0 + b_{i0}) + (\beta_1 + b_{i1})t_{ij} + \varepsilon_{ij},$$

where

- ▷  $\beta$ s are known as the *fixed effects*
- ▷  $b_i$ s are known as the *random effects*

- In accordance for the random effects we assume

$$b_i = \begin{bmatrix} b_{i0} \\ b_{i1} \end{bmatrix} \sim \mathcal{N}(0, D)$$

## 3.1 The Linear Mixed Model (cont'd)

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- Put in a general form

$$\begin{cases} y_i = X_i\beta + Z_ib_i + \varepsilon_i, \\ b_i \sim \mathcal{N}(0, D), \quad \varepsilon_i \sim \mathcal{N}(0, \sigma^2 \mathbf{I}_{n_i}), \end{cases}$$

with

- ▷  $X$  design matrix for the fixed effects  $\beta$
- ▷  $Z$  design matrix for the random effects  $b_i$
- ▷  $b_i$  and  $\varepsilon_i$  are assumed independent

## 3.2 Interpretation

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- Fixed and random effects:
  - ▷  $\beta_j$  denotes the change in the average  $y_i$  when  $x_j$  is increased by one unit
  - ▷  $b_i$  are interpreted in terms of how a subset of the regression parameters for the  $i$ th subject deviates from those in the population
- Advantageous feature: population + subject-specific predictions
  - ▷  $\beta$  describes mean response changes in the population
  - ▷  $\beta + b_i$  describes individual response trajectories



## 3.2 Interpretation (cont'd)

- Example: We fit a linear mixed model for the AIDS dataset assuming
  - ▷ different average longitudinal evolutions per treatment group (**fixed part**)
  - ▷ random intercepts & random slopes (**random part**)

$$\left\{ \begin{array}{l} \sqrt{\text{CD4}}_{ij} = \beta_0 + \beta_1 \text{Time}_{ij} + \beta_2 \{ \text{ddI}_i \times \text{Time}_{ij} \} + b_{i0} + b_{i1} \text{Time}_{ij} + \varepsilon_{ij}, \\ b_i \sim \mathcal{N}(0, D), \quad \varepsilon_{ij} \sim \mathcal{N}(0, \sigma^2) \end{array} \right.$$

- Note: We did not include a main effect for treatment due to randomization

## 3.2 Interpretation (cont'd)

	Value	Std.Err.	<i>t</i> -value	<i>p</i> -value
$\beta_0$	7.189	0.222	32.359	< 0.001
$\beta_1$	-0.163	0.021	-7.855	< 0.001
$\beta_2$	0.028	0.030	0.952	0.342

- No evidence of differences in the average longitudinal evolutions between the two treatments

## 3.2 Interpretation (cont'd)

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- Interaction & nonlinear terms: As we have seen in the previous chapter (see pp. 59–71), often
  - ▷ the effect of some predictors may be nonlinear (e.g., time effect), and/or
  - ▷ the effect of some predictors on the outcome may be influenced from other predictors (e.g., different average longitudinal evolutions per treatment group)
- In such cases, we need to consider more elaborate models that contain terms to capture these features, namely
  - ▷ polynomials or splines to model nonlinearities
  - ▷ interaction effects

## 3.2 Interpretation (cont'd)

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- When such terms are included in the model, the interpretation of the parameters can become quite complicated
- To understand a complex mixed model we can visualize it using **effect plots**
- Example: We fit a model to the PBC dataset for serum bilirubin that contains
  - ▷ *fixed effects:*
    - \* nonlinear time effect with splines, main effect of sex, age and baseline prothrombin
    - \* interaction effects of sex with nonlinear time, age and baseline prothrombin
  - ▷ *random effects:* nonlinear time effect

## 3.2 Interpretation (cont'd)

- The model has the form:

$$\begin{aligned} \log(\text{serBilir}_{ij}) = & \beta_0 + \beta_1 N(\text{Time}_{ij})_1 + \beta_2 N(\text{Time}_{ij})_2 + \beta_3 \text{Female}_i + \beta_4 \text{Age}_i + \\ & \beta_5 \text{basePro}_i + \beta_6 \{\text{Female}_i \times \text{Age}_i\} + \\ & \beta_7 \{\text{Female}_i \times \text{basePro}_i\} + \beta_8 \{\text{Female}_i \times N(\text{Time}_{ij})_1\} + \\ & \beta_9 \{\text{Female}_i \times N(\text{Time}_{ij})_2\} + b_{i0} + b_{i1} N(\text{Time}_{ij})_1 + \\ & b_{i2} N(\text{Time}_{ij})_2 + \varepsilon_{ij} \end{aligned}$$

where

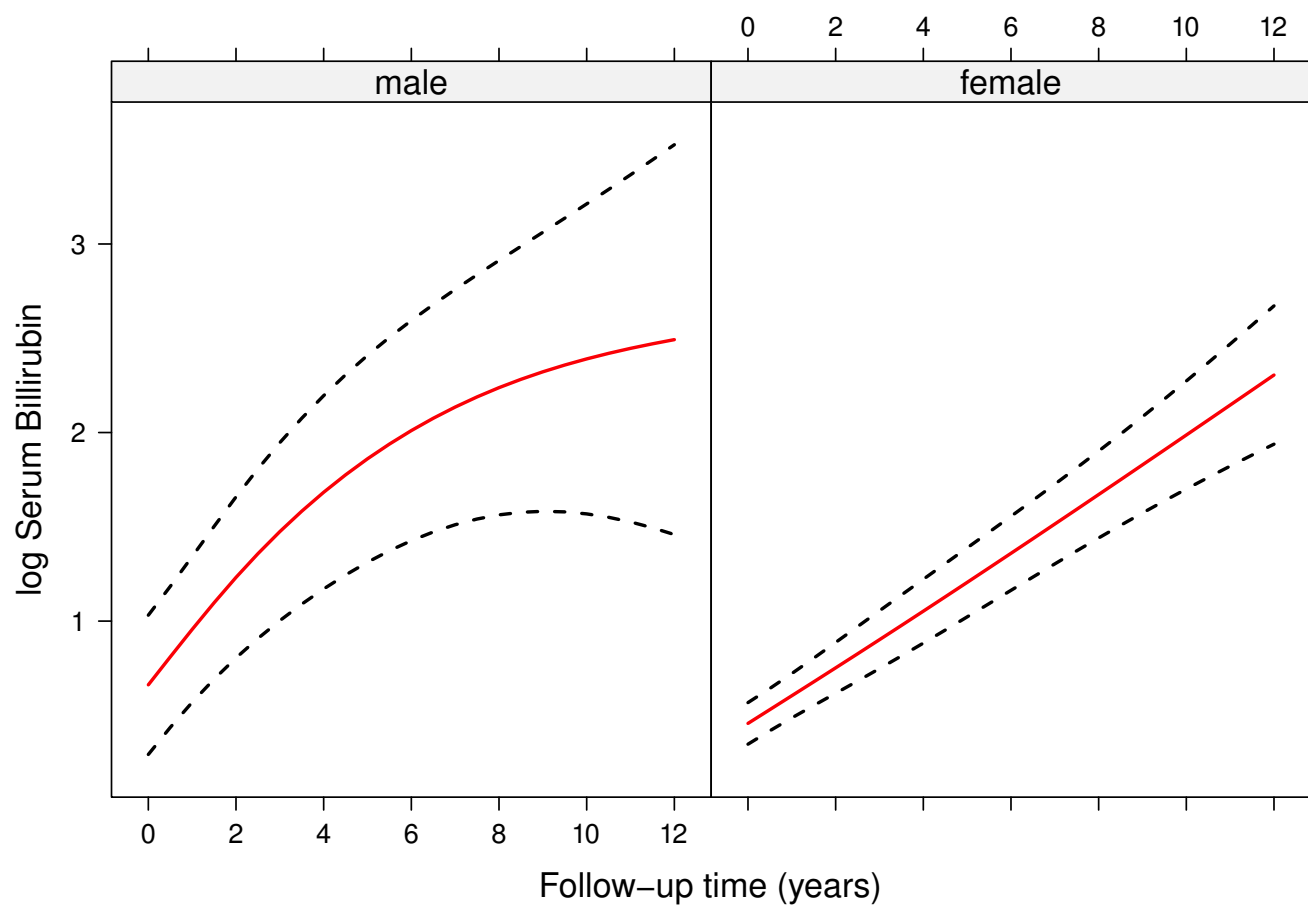
- ▷ the terms  $N(\text{Time}_{ij})_1$  and  $N(\text{Time}_{ij})_2$  denote the basis for a natural spline with two degrees of freedom
- ▷  $b_i \sim \mathcal{N}(0, D)$  and  $\varepsilon_{ij} \sim \mathcal{N}(0, \sigma^2)$

## 3.2 Interpretation (cont'd)

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- In this model not all coefficients have a direct interpretation in isolation
- Hence to understand the model we depict
  - ▷ how the average longitudinal profiles evolve over time,
  - ▷ separately for males and females, and prothrombin time of 10.6 sec
  - ▷ for the average age of 49 years old
  - ▷ including also the corresponding 95% pointwise confidence intervals
  - ▷ (in the app different ages and prothrombin times can be selected)

## 3.2 Interpretation (cont'd)



## 3.3 Hierarchical vs Marginal

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- How do the random effects capture correlation:
  - ▷ Given the random effects, the measurements of each subject are independent (*conditional independence assumption*)

$$p(y_i | b_i) = \prod_{j=1}^{n_i} p(y_{ij} | b_i)$$

- ▷ Marginally (integrating out the random effects), the measurements of each subject are correlated

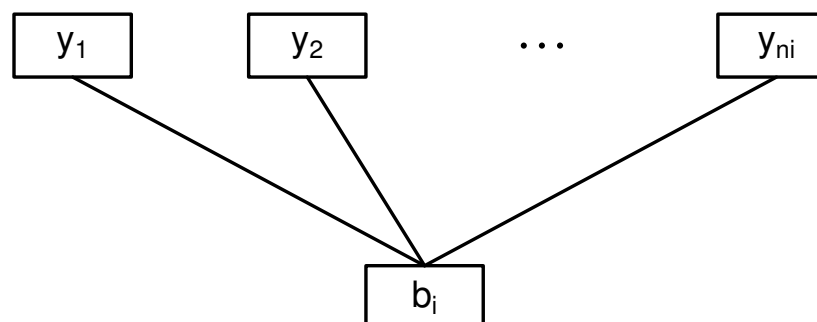
$$p(y_i) = \int p(y_i | b_i) p(b_i) db_i \quad \Rightarrow \quad y_i \sim \mathcal{N}(X_i\beta, Z_i D Z_i^\top + \sigma^2 \mathbf{I}_{n_i})$$



## 3.3 Hierarchical vs Marginal (cont'd)

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Graphical representation of the conditional independence assumption



### 3.3 Hierarchical vs Marginal (cont'd)

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- Hence, with random effects we again model the correlations in the repeated measurements of each subject
- Notes: In using random effects for modeling the covariance matrix
  - ▷ The more random effects we include the more flexibly we capture the correlations
  - ▷ By using random effects (other than random intercept alone) we also directly allow for heteroscedasticity (i.e., non-constant variances in time)
  - ▷ Nevertheless, we do assume a particular type of structure for the correlations and the variances – they are **not** allowed completely free
  - ▷ Random effects work equally well with balanced or unbalanced data

## 3.3 Hierarchical vs Marginal (cont'd)

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- Let's try the app...

## 3.3 Hierarchical vs Marginal (cont'd)

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- Hierarchical formulation

- ▷ a model for  $y_i$  given  $b_i$ , and a model for  $b_i$
- ▷  $D$  is the covariance matrix of the random effects  $\Rightarrow$  **needs to be positive definite**

- Marginal formulation

- ▷ a model for  $y_i$ , and a specific form of the marginal covariance matrix  

$$V_i = Z_i D Z_i^\top + \sigma^2 I_{n_i}$$
- ▷ only  $V_i$  needs to be positive definite
- ▷  $V_i$  **can be positive definite without  $D$  being positive definite**

## 3.3 Hierarchical vs Marginal (cont'd)

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**The hierarchical model implies the marginal one,  
not vice versa**

- A simple example: Random-intercepts model

$$\begin{cases} y_{ij} = \beta_0 + \beta_1 t_{ij} + b_{i0} + \varepsilon_{ij}, \\ b_{i0} \sim \mathcal{N}(0, \sigma_b^2), \quad \varepsilon_{ij} \sim \mathcal{N}(0, \sigma^2). \end{cases}$$

## 3.3 Hierarchical vs Marginal (cont'd)



### 3.3 Hierarchical vs Marginal (cont'd)

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- Implied marginal covariance matrix has the form

$$V_i = \sigma_b^2 \mathbf{1}_{n_i} \mathbf{1}_{n_i}^\top + \sigma^2 \mathbf{I}_{n_i}$$

it assumes

- ▷ constant variance  $\sigma_b^2 + \sigma^2$  over time, and
- ▷ equal positive correlation  $\rho = \sigma_b^2 / (\sigma_b^2 + \sigma^2)$  between the measurements of any two time points (aka *intra-class correlation*)
- ▷ it is known as the *compound symmetric* covariance matrix

### 3.3 Hierarchical vs Marginal (cont'd)

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- Note that we could also have a compound symmetric covariance matrix with negative intra-class correlation
  - ▷ such a matrix could never have come from a mixed model

Random intercepts **imply** compound symmetry  
but  
Compound symmetry **does not imply** random intercepts



### 3.3 Hierarchical vs Marginal (cont'd)

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- What are the implications of this?
- Statistical software that fit mixed models under ML actually fit the implied marginal model
  - ▷ we can construct examples where two mixed models have exactly the same implied marginal model
  - ▷ based on the fitted model we **cannot** say under which model the data have been generated
- We can only do it under a Bayesian approach (because there we actually fit the hierarchical model)

## 3.4 Estimation

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- Fixed effects: For known marginal covariance matrix  $V_i = Z_i D Z_i^\top + \sigma^2 I_{n_i}$ , the fixed effects are estimated using generalized least squares

$$\hat{\beta} = \left( \sum_{i=1}^n X_i^\top V_i^{-1} X_i \right)^{-1} \sum_{i=1}^n X_i^\top V_i^{-1} y_i$$

- Variance Components: The unique parameters in  $V_i$  are estimated based on either maximum likelihood (ML) or restricted maximum likelihood (REML)
  - ▷ REML provides unbiased estimates for the variance components in small samples

## 3.4 Estimation (cont'd)

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- Two-step iterative procedure
  - ▷ Step 0: Set initial values for  $D$  and  $\sigma^2$
  - ▷ Step 1: Calculate the covariance matrix  $\hat{V}_i^{it=k}$  and following the fixed effects  $\hat{\beta}^{it=k}$
  - ▷ Step 2: Update  $\hat{V}_i^{it=k+1}$  using REML or ML
  - ▷ Step 3: Check convergence criterion, if not satisfied return to Step 1

Steps 1–3 are repeated until convergence is attained

## 3.4 Estimation (cont'd)

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- Estimation of random effects

- ▷ based on a fitted mixed model, estimates for the random effects are based on the posterior distribution:

$$p(b_i | y_i; \theta) = \frac{p(y_i | b_i; \theta) p(b_i; \theta)}{p(y_i; \theta)}$$

$$\propto p(y_i | b_i; \theta) p(b_i; \theta),$$

in which  $\theta$  is replaced by its MLE  $\hat{\theta}$

## 3.4 Estimation (cont'd)

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- This is a whole distribution
  - ▷ in the linear mixed model we have seen, this posterior distribution has a closed-form:

$$[b_i \mid y_i; \theta] \sim \mathcal{N}\left\{DZ_i^\top V_i^{-1}(y_i - X_i\beta), DZ_i^\top K Z_i D\right\},$$

with

$$K = V_i^{-1} - V_i^{-1}X_i\left(\sum_{i=1}^n X_i^\top V_i^{-1}X_i\right)^{-1}X_i^\top V_i^{-1}$$

## 3.4 Estimation (cont'd)

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- To obtain estimates for the random effects we typically use measures of location from this posterior distribution (e.g., mean or mode)
- Due to the fact that in linear mixed models we obtain a normal distribution (in which the mean and mode coincide), we use as estimates of the random effects the means of these distributions

$$\hat{b}_i = DZ_i^\top V_i^{-1}(y_i - X_i\beta)$$

- These estimates are called the *empirical Bayes* estimates of the random effects

## 3.4 Estimation (cont'd)

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- Estimates of the random effects are very useful in prediction
  - ▷ in this context there is an important difference between the marginal models we have seen in Chapter 2 and the mixed models of this chapter
- In particular, the predictions from a marginal model are

$$\hat{y}_i^{\text{marg}} = X_i \hat{\beta}$$

whereas from the mixed model we obtain

$$\hat{y}_i^{\text{subj}} = X_i \hat{\beta} + Z_i \hat{b}_i$$

## 3.4 Estimation (cont'd)

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- The difference is that
  - ▷ from the marginal model we obtain predictions for the '*average*' patient having characteristics  $X_i$  (i.e., age, sex, etc.)
  - ▷ from the mixed model we obtain predictions for the '*average*' patient that has characteristics  $X_i$  and observed data  $y_i$  (i.e., they have a subject-specific nature)
  
- The predictions  $X_i\hat{\beta} + Z_i\hat{b}_i$  we obtain from the mixed model are called the *Best Linear Unbiased Predictions (BLUPs)*
  - ▷ 'linear' because they are a linear combination of  $\hat{\beta}$  and  $\hat{b}_i$
  - ▷ 'unbiased' because their average equals the true subject-specific mean
  - ▷ 'best' because they have the smallest variance of all linear predictors



## 3.4 Estimation (cont'd)

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- **Example:** To see an example of the difference between the marginal and subject-specific predictions, we compare the two sets of predictions for the complex linear mixed model we have seen in Section 3.2 (pp.156–159) for 16 randomly selected patients
  - ▷ **red lines** denote the marginal predictions,
  - ▷ **blue lines** denote the subject-specific predictions
  - ▷ **black circles** the observed data

## 3.4 Estimation (cont'd)



## 3.4 Estimation (cont'd)

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- We clearly observe that the subject-specific predictions are much closer to the data of each individual patient than the marginal ones

## 3.5 Mixed-Effects Models in R

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**R>** There are two primary packages in R for mixed models analysis:

▷ Package **nlme**

- \* fits linear & nonlinear mixed effects models, and marginal models for normal data
- \* allows for both random effects & correlated error terms
- \* several options for covariances matrices and variance functions

▷ Package **lme4**

- \* fits linear, nonlinear & generalized mixed effects models
- \* uses only random effects
- \* allows for nested and crossed random-effects designs

## 3.5 Mixed-Effects Models in R (cont'd)

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- R>** The basic function to fit linear mixed models in the **nlme** package is `lme()`, and has three basic arguments
- ▷ **fixed**: a formula specifying the response vector and the fixed-effects structure
  - ▷ **random**: a formula specifying the random-effects structure
  - ▷ **data**: a data frame containing all the variables

## 3.5 Mixed-Effects Models in R (cont'd)

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**R>** The data frame that contains all variables should be in the *long format*

Subject	y	time	gender	age
1	5.1	0.0	male	45
1	6.3	1.1	male	45
2	5.9	0.1	female	38
2	6.9	0.9	female	38
2	7.1	1.2	female	38
2	7.3	1.5	female	38
⋮	⋮	⋮	⋮	⋮

## 3.5 Mixed-Effects Models in R (cont'd)

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**R>** The code used to fit the linear mixed model for the AIDS dataset (pp.153) is as follows

```
lmeFit <- lme(CD4 ~ obstime + obstime:drug, data = aids,  
             random = ~ obstime | patient)
```

```
summary(lmeFit)
```

## 3.5 Mixed-Effects Models in R (cont'd)

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R> The same fixed-effects structure but only random intercepts

```
lme(CD4 ~ obstime + obstime:drug, data = aids,  
    random = ~ 1 | patient)
```

R> The same fixed-effects structure, random intercepts & random slopes, with a diagonal covariance matrix (using the `pdDiag()` function)

```
lme(CD4 ~ obstime + obstime:drug, data = aids,  
    random = list(patient = pdDiag(form = ~ obstime)))
```



## 3.5 Mixed-Effects Models in R (cont'd)

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- R>** The basic function to fit linear mixed models in the **lme4** package is `lmer()`, and has two basic arguments
- ▷ **formula**: a formula specifying the response vector, the fixed- and random-effects structure
  - ▷ **data**: a data frame containing all the variables
- R>** Again the data should be in the long format

## 3.5 Mixed-Effects Models in R (cont'd)

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**R>** The analogous code to fit the linear mixed model for the AIDS dataset (pp.153) is as follows

```
lmerFit <- lmer(CD4 ~ obstime + obstime:drug + (obstime | patient),  
               data = aids)
```

```
summary(lmerFit)
```

## 3.5 Mixed-Effects Models in R (cont'd)

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**R>** To fit the same model but with a diagonal matrix for the random effects the call becomes:

```
lmerFit2 <- lmer(CD4 ~ obstime + obstime:drug +  
                (obstime || patient),  
                data = aids)
```

```
summary(lmerFit2)
```

## 3.6 Nested and Crossed Random Effects\*

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- In the previous examples the primary type of correlated data we have seen is longitudinal data
  - ▷ correlations stems from the fact that we measure *the same* outcome repeatedly in time for each subject
- Another commonly encountered feature that induces correlation is clustering, e.g.,
  - ▷ patients are clustered within hospitals
  - ▷ children are clustered within schools or families
  - ▷ ...

## 3.6 Nested and Crossed Random Effects\* (cont'd)

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- **Example:** In the Glaucoma data we have a multilevel clustered design (see pp.11)
  - ▷ each location is nested within the hemifield
  - ▷ each hemifield is nested within the eye
  - ▷ each eye is nested within the patient

Measurements in the same cluster are expected to be **(positively)  
correlated**

## 3.6 Nested and Crossed Random Effects\* (cont'd)

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- To account for the correlations in each level of the multilevel structure we can include level-specific random effects
- Continuing in the Glaucoma data example, we focus (for simplicity) in the higher two levels, namely the patient and the eye
  - ▷ we fit a linear mixed model with a separate random effect per level

$$\left\{ \begin{array}{l} \text{VF}_{ijk} = \beta_0 + \beta_1 \text{Time}_{ijk} + b_i + u_{ij} + \varepsilon_{ijk} \\ b_i \sim \mathcal{N}(0, \sigma_{\text{patient}}^2), \quad u_{ij} \sim \mathcal{N}(0, \sigma_{\text{eye}}^2), \\ \varepsilon_{ijk} \sim \mathcal{N}(0, \sigma^2) \end{array} \right.$$

## 3.6 Nested and Crossed Random Effects\* (cont'd)

where

- ▷  $VF_{ijk}$  denotes the  $k$ -th visual field sensitivity measurement for the  $j$ -th eye of the  $i$ -th patient
- ▷  $Time_{ijk}$  denotes the corresponding time point this measurement was taken
- ▷  $b_i$  is the random effect for the patients – the measurements of the  $i$ -th patient are correlated because all these measurements share the *same* random effect  $b_i$
- ▷  $u_{ij}$  is the random effect for the eye within the patient – the measurements of the  $j$ -th eye of the  $i$ -th patient are more correlated than the measurements of the  $j'$ -th eye because they share the *same* random effect  $u_{ij}$

## 3.6 Nested and Crossed Random Effects\* (cont'd)

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- The estimated variance components from the Glaucoma data are:
  - ▷  $\sigma_{patient} = 4.3$
  - ▷  $\sigma_{eye} = 5.8$
  - ▷  $\sigma = 7.9$
  
- Based on these variance components we can compute the corresponding correlations, i.e.,
  - ▷ measurements in the same eye have correlation

$$\frac{\sigma_{patient}^2 + \sigma_{eye}^2}{\sigma_{patient}^2 + \sigma_{eye}^2 + \sigma^2} = 0.46$$



## 3.6 Nested and Crossed Random Effects\* (cont'd)

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▷ and measurements from different eyes

$$\frac{\sigma_{patient}^2}{\sigma_{patient}^2 + \sigma_{eye}^2 + \sigma^2} = 0.16$$

- It goes without saying, that if the correlations in the data are more complex, we could include additional random effects
- Example: Continuing in the Glaucoma example, by including only random intercepts terms we assume that the correlations are constant in time
  - ▷ as we have previously discussed, this may be a simplistic assumption for longitudinal data

## 3.6 Nested and Crossed Random Effects\* (cont'd)

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- We extend the model by including a random slopes terms in the patient level, i.e.,

$$\left\{ \begin{array}{l} \text{VF}_{ijk} = \beta_0 + \beta_1 \text{Time}_{ijk} + b_{i0} + b_{i1} \text{Time}_{ijk} + u_{ij} + \varepsilon_{ijk} \\ b_i \sim \mathcal{N}(0, D_{\text{patient}}), \quad u_{ij} \sim \mathcal{N}(0, \sigma_{\text{eye}}^2), \\ \varepsilon_{ijk} \sim \mathcal{N}(0, \sigma^2) \end{array} \right.$$

▷ now, in the patient level we have a covariance matrix  $D$

## 3.6 Nested and Crossed Random Effects\* (cont'd)

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- The estimated variance components from the Glaucoma data are:

- ▷  $\sigma_{patient,int} = 4.7$

- ▷  $\sigma_{patient,slp} = 0.4$

- ▷  $\text{corr}_{patient,int-slp} = -0.4$

- ▷  $\sigma_{eye} = 5.8$

- ▷  $\sigma = 7.8$

## 3.6 Nested and Crossed Random Effects\* (cont'd)

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- The examples we have seen so far in this section refer to settings in which the measurements of one level are *nested* within another level
  - ▷ due to this feature, the random effects we have used in the previous examples of the Glaucoma data are called *nested random effects*
- However, there are also settings in which we have different types of groupings of measurements that are not nested
  - ▷ in these cases we use *crossed random effects*

## 3.6 Nested and Crossed Random Effects\* (cont'd)

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- **Example:** One feature of visual field sensitivity measurements is that they exhibit the so-called *Global Visit Effect* (see pp.12)
  - ▷ in particular, for some visits some patients showed strangely low sensitivity to the stimuli
  - ▷ in the next visit, their sensitivity levels improved
  - ▷ it is not possible this low sensitivity to be due to Glaucoma because it is an irreparable disease
  - ▷ hence, the low sensitivity measurements are attributed to other reasons (e.g., tiredness)
- To capture this Global Visit Effect we can include a random effect for each visit
  - ▷ this random effect is **not** nested to the previously used random effects

## 3.6 Nested and Crossed Random Effects\* (cont'd)

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- Hence, our model now becomes

$$\left\{ \begin{array}{l} \text{VF}_{ijk} = \beta_0 + \beta_1 \text{Time}_{ijk} + b_i + \mathbf{v}_k + \varepsilon_{ijk} \\ b_i \sim \mathcal{N}(0, \sigma_{\text{patient}}^2), \quad \mathbf{v}_k \sim \mathcal{N}(0, \sigma_{\text{visit}}^2), \\ \varepsilon_{ijk} \sim \mathcal{N}(0, \sigma^2) \end{array} \right.$$

- The estimated variance components from the Glaucoma data are:
  - ▷  $\sigma_{\text{patient}} = 5.9$
  - ▷  $\sigma_{\text{visit}} = 0.8$
  - ▷  $\sigma = 8.9$

## 3.7 Mixed Models with Correlated Errors

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- We have seen two classes of models for longitudinal data, namely

▷ *Marginal Models*

$$y_i = X_i\beta + \varepsilon_i, \quad \varepsilon_i \sim \mathcal{N}(0, V_i), \quad \text{and}$$

▷ *Conditional Models*

$$\begin{cases} y_i = X_i\beta + Z_ib_i + \varepsilon_i, \\ b_i \sim \mathcal{N}(0, D), \quad \varepsilon_i \sim \mathcal{N}(0, \sigma^2 I_{n_i}) \end{cases}$$

## 3.7 Mixed Models with Correlated Errors (cont'd)

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- It is also possible to combine the two approaches and obtain a linear mixed model with correlated error terms

$$\begin{cases} y_i = X_i\beta + Z_ib_i + \varepsilon_i, \\ b_i \sim \mathcal{N}(0, D), \quad \varepsilon_i \sim \mathcal{N}(0, \Sigma_i), \end{cases}$$

where, as in marginal models, we can consider different forms for  $\Sigma_i$

- The corresponding marginal model is of the form

$$y_i \sim \mathcal{N}(X_i\beta, Z_iDZ_i^\top + \Sigma_i)$$



## 3.7 Mixed Models with Correlated Errors (cont'd)

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- Features
  - ▷ both  $b_i$  and  $\Sigma_i$  try to capture the correlation in the observed responses  $y_i$
  - ▷ this model does not assume conditional independence
- Choice between the two approaches is to a large extent philosophical
  - ▷ *Random Effects*: trajectory of a subject dictated by time-independent random effects  $\Rightarrow$  the shape of the trajectory is an inherent characteristic of this subject
  - ▷ *Serial Correlation*: attempts to more precisely capture features of the trajectory by allowing subject-specific trends to vary in time

## 3.7 Mixed Models with Correlated Errors (cont'd)

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Often in practice it is **not** possible to include both a serial correlation term and many random effects because of numerical problems

- **Example:** In the AIDS dataset we investigate the fit of a mixed model with exponential serial correlation and increasing number of random effects – in particular:
  - ▷ Model I: random intercepts
  - ▷ Model II: random intercepts & random slopes

the fixed-effects part includes linear and quadratic slopes and their interaction with treatment

## 3.7 Mixed Models with Correlated Errors (cont'd)

	Model I	Model II
Intercept	7.173	7.214
$\text{Time}_{ij}$	-0.247	-0.251
$\text{Time}_{ij}^2$	0.007	0.007
$\text{ddI}_i \times \text{Time}_{ij}$	0.186	0.154
$\text{ddI}_i \times \text{Time}_{ij}^2$	-0.013	-0.010

- We observe small differences in the estimated fixed effects

## 3.7 Mixed Models with Correlated Errors (cont'd)

	Model I	Model II
$\phi$	2.29	0.52
95% CI	(1.62; 3.23)	(0.08; 3.45)

- However, we observe a more profound effect in the estimated parameter of the exponential serial correlation structure
  - ▷ as we include more random effects, less information is available for estimating the serial correlation structure – note length of 95% CIs
- *Numerical problems:*
  - ▷ The model is fitted with the exponential serial correlation structure,
  - ▷ but if you instead tried the Gaussian serial correlation structure, then the models do not appropriately converge (Hessian matrix of the MLEs is not positive-definite)

## 3.8 Time-Varying Covariates\*

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- Up to now we have only included in mixed models covariates, which were fixed from baseline (except of course the time variable)
- However, often we may also be interested in assessing how a longitudinal outcome is associated with a covariate whose value changes over time
  - ▷ such covariates are called *time-varying covariates*
- **Example:** In the PBC dataset we are interested in the effect of prothrombin time on serum bilirubin – prothrombin time has also been collected longitudinally during follow-up

## 3.8 Time-Varying Covariates\* (cont'd)

---

- The handling of time-varying covariates poses some *important challenges*:
  1. Not always the longitudinal outcome and the time-varying covariate are collected at the same time points
  2. The longitudinal outcome at a particular time point  $t$  may depend not only on the value of the covariate at the same time point but also at other time points
  3. There are two types of time-varying covariates, *endogenous* and *exogenous*
    - ▷ a time-varying covariate is *exogenous* if its distribution at time  $t$  is conditionally independent of all preceding outcomes
    - ▷ a time-varying covariate is *endogenous* if it is not exogenous

## 3.8 Time-Varying Covariates\* (cont'd)

- The formal definitions of *exogenous* and *endogenous* time-varying covariates are:

$$p\{x_i(t) \mid \mathcal{H}_i^Y(t), \mathcal{H}_i^X(t)\} = p\{x_i(t) \mid \mathcal{H}_i^X(t)\}$$

$$p\{x_i(t) \mid \mathcal{H}_i^Y(t), \mathcal{H}_i^X(t)\} \neq p\{x_i(t) \mid \mathcal{H}_i^X(t)\}$$

where

- ▷  $\mathcal{H}_i^Y(t) = \{y_i(t_{i1}), \dots, y_i(t_{ik}); t_{ik} \leq t\}$  denotes the set of longitudinal measurements up to time  $t$
- ▷  $\mathcal{H}_i^X(t) = \{x_i(t_{i1}), \dots, x_i(t_{ik}); t_{ik} \leq t\}$  denotes the set of covariate measurements up to time  $t$

## 3.8 Time-Varying Covariates\* (cont'd)

- These features complicate postulating an appropriate model with such covariates
- A procedure to follow when working with time-varying covariates
  - ▷ Determine if the covariate is *endogenous* or *exogenous*
    - \* if it is exogenous, then
      - we can proceed by postulating a standard mixed (or marginal) model, and
      - the longitudinal outcome at time  $t$  can only be associated with past covariate measurements, i.e.,  $\mathcal{H}_i^X(t)$
    - \* if it is endogenous, then more complicated types of analysis are required (joint models or marginal structural models) that fall outside the scope of this course



## 3.8 Time-Varying Covariates\* (cont'd)

---

▷ Next, determine how to link the time-varying covariate to the longitudinal outcome (association structure)

\* the longitudinal outcome at  $t$  is associated to the covariate at which time points (the same, previous time points, etc.)

\* Note: If the scientific interest is focused on a particular type of association structure but in reality the longitudinal outcomes is differently associated to the time-varying covariate, then the estimated association of interest may be diluted (biased) unless a specific type of analysis is followed (a marginal model with independent error terms, i.e., linear regression and corrected standard errors using the sandwich estimator)

## 3.8 Time-Varying Covariates\* (cont'd)

- ▷ Depending on the chosen association structure in the previous step, and if the time-varying covariate is not measured at the same time points as the longitudinal outcome, then a form of interpolation may be required
- Example: In the PBC dataset we are interested in the effect of prothrombin time on serum bilirubin

$$\log(\text{serBilir}_{ij}) = \beta_0 + \beta_1 N(\text{Time}_{ij})_1 + \beta_2 N(\text{Time}_{ij})_2 + \beta_3 \text{Female}_i + \beta_4 \text{Age}_i + \beta_5 \text{Prothr}_{ij} + b_{i0} + b_{i1} N(\text{Time}_{ij})_1 + b_{i2} N(\text{Time}_{ij})_2 + \varepsilon_{ij}$$

the covariance matrix of the random effects is assumed to be diagonal

### 3.8 Time-Varying Covariates\* (cont'd)

	Value	Std.Err.	<i>t</i> -value	<i>p</i> -value
$\beta_0$	0.347	0.366	0.948	0.343
$\beta_1$	1.772	0.139	12.738	< 0.001
$\beta_2$	1.266	0.197	6.422	< 0.001
$\beta_3$	-0.233	0.184	-1.263	0.207
$\beta_4$	-0.000	0.006	-0.080	0.936
$\beta_5$	0.036	0.008	4.675	< 0.001

- Log serum bilirubin at time  $t$  is strongly related with the prothrombin time at the same time point – a unit increase of prothrombin time at follow-up time  $t$  increases the expected log serum bilirubin at the same follow-up time by 0.036

## 3.8 Time-Varying Covariates\* (cont'd)

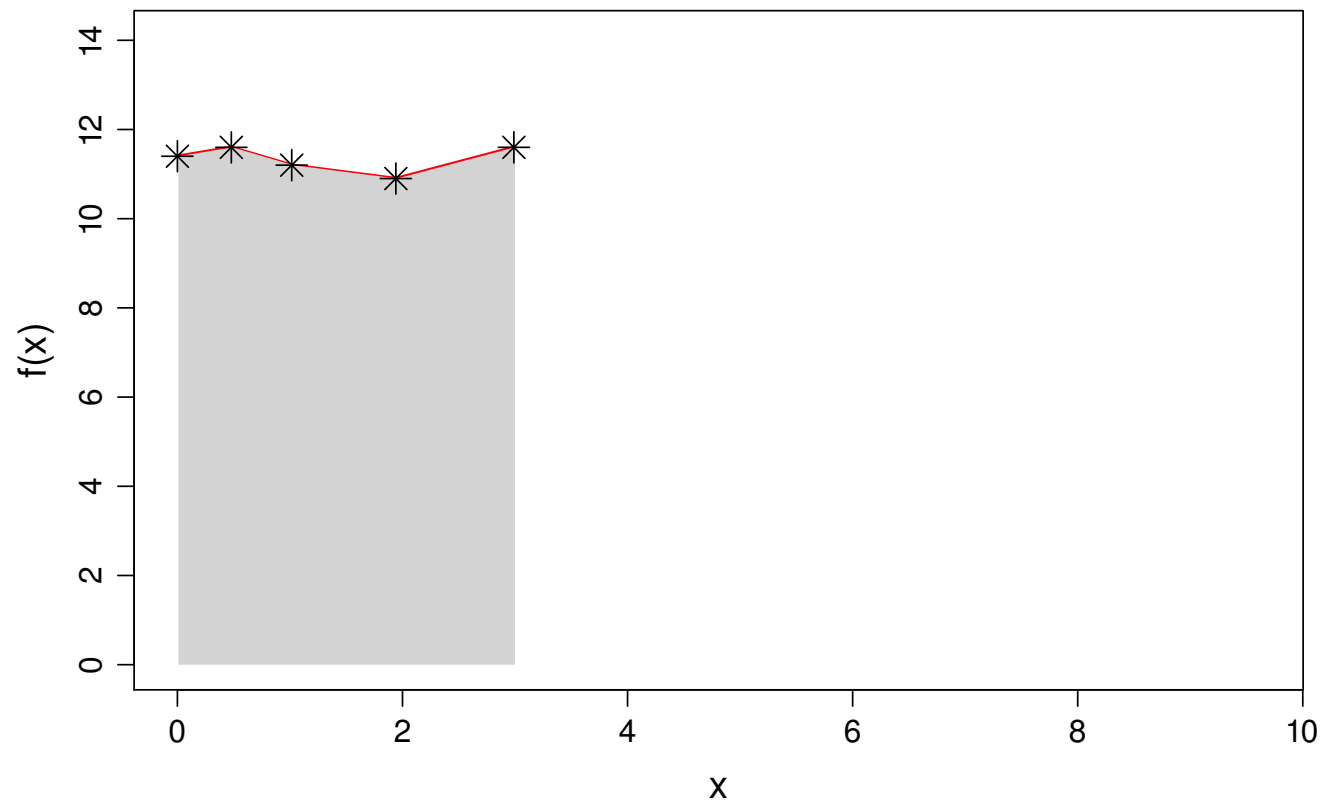
- We continue on the same example, but now we allow the log serum bilirubin at time  $t$  to be associated with the prothrombin time at previous time points as well – in particular:

$$\log(\text{serBilir}_{ij}) = \beta_0 + \beta_1 N(\text{Time}_{ij})_1 + \beta_2 N(\text{Time}_{ij})_2 + \beta_3 \text{Female}_i + \beta_4 \text{Age}_i + \beta_5 \text{CumProthr}_{ij} + b_{i0} + b_{i1} N(\text{Time}_{ij})_1 + b_{i2} N(\text{Time}_{ij})_2 + \varepsilon_{ij}$$

the covariance matrix of the random effects is assumed to be diagonal

- $\text{CumProthr}_{ij}$  denotes the cumulative effect of prothrombin time
  - ▷ for Patient 21 and at two different follow-up times this effect is:

## 3.8 Time-Varying Covariates\* (cont'd)



## 3.8 Time-Varying Covariates\* (cont'd)



## 3.8 Time-Varying Covariates\* (cont'd)

	Value	Std.Err.	<i>t</i> -value	<i>p</i> -value
$\beta_0$	0.728	0.361	2.015	0.044
$\beta_1$	1.700	0.159	10.686	< 0.001
$\beta_2$	1.256	0.210	5.974	< 0.001
$\beta_3$	-0.245	0.187	-1.311	0.191
$\beta_4$	-0.000	0.006	-0.007	0.995
$\beta_5$	0.009	0.004	2.462	0.014

- Log serum bilirubin at time  $t$  is strongly related with the cumulative prothrombin time up to the same time point – a unit increase of the cumulative prothrombin time up to follow-up time  $t$  increases the expected log serum bilirubin at the same follow-up time by 0.009

## 3.9 Model Building

---

- Mixed models consist of two parts, namely
  - ▷ *fixed effects* that describe how specific covariates influence the average longitudinal evolutions
  - ▷ *random effects* that describe how specific regression coefficients deviate from the overall mean described by the fixed effects
    - \* the random effects also model the correlations in the repeated measurements
- Interest can either be
  - ▷ on the fixed-effects part alone (e.g., does treatment influence the average evolutions) or
  - ▷ on both parts (e.g., to obtain subject specific predictions)



## 3.9 Model Building (cont'd)

---

- The general model building strategy we have seen in the previous chapter for marginal models also applies in the case of mixed models – more specifically:
  1. Put all the covariates of interest in the fixed-effects part, considering possible nonlinear terms and/or interactions between them – **do NOT** remove the ones that are not significant
  2. Then select an appropriate random-effects structure that adequately describes the correlations in the repeated measurements
    - \* typically we start from random intercepts and include each time an additional random effect term to see if we improve the fit (i.e., random slopes, quadratic random slopes, etc.)
    - \* you should be a bit anti-conservative, i.e., do not favor a simpler covariance matrix if the  $p$ -value is just non-significant

## 3.9 Model Building (cont'd)

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3. Finally, return to the mean part and exclude non significant covariates
  - \* first start by testing the nonlinear & interaction terms

## 3.10 Hypothesis Testing

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- Similarly to the marginal models of Chapter 2, in mixed models we can use standard inferential tools for performing hypothesis testing
  - ▷ Wald tests / t-tests / F-tests
  - ▷ Score tests
  - ▷ Likelihood ratio tests
- Following the model building strategy described above, we will again split the types of hypothesis tests in two parts:
  - ▷ first, describe how can we choose the appropriate covariance matrix, and
  - ▷ second, focus on hypothesis testing for the mean part of the model

## 3.10 Hypothesis Testing (cont'd)

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- **Hypothesis testing for  $V_i = Z_i D Z_i^\top + \sigma^2 I_{n_i}$ :** Assuming the same mean structure, we can fit a series of mixed models and choose the one that best describes the covariances
- In general, we distinguish between two cases
  - ▷ comparing two mixed models with *nested* covariance matrices
  - ▷ comparing two mixed models with *non-nested* covariance matrices
- **Note:** Model A is nested in Model B, when Model A is a special case of Model B
  - ▷ i.e., by setting some of the parameters of Model B at some specific value we obtain Model A

## 3.10 Hypothesis Testing (cont'd)

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- For **nested** models the preferable test for selecting  $V_i$  is the likelihood ratio test (LRT):

$$\text{LRT} = -2 \times \{\ell(\hat{\theta}_0) - \ell(\hat{\theta}_a)\} \sim \chi_p^2$$

where

- ▷  $\ell(\hat{\theta}_0)$  the value of the log-likelihood function under the null hypothesis, i.e., the special case model
  - ▷  $\ell(\hat{\theta}_1)$  the value of the log-likelihood function under the alternative hypothesis, i.e., the general model
  - ▷  $p$  denotes the number of parameters being tested
- 
- **Note:** Provided that the mean structure in the two models is the same, we can either compare the REML or ML likelihoods of the models (preferable is REML)

## 3.10 Hypothesis Testing (cont'd)

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Though, there is a **technical** complication when we compare nested mixed models for which one model has more random effects than the other

## 3.10 Hypothesis Testing (cont'd)

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- To illustrate the issue, consider the hypothesis test between the random intercepts and the random intercepts & random slopes models
  - ▷ random intercepts model

$$y_{ij} = X\beta + b_{i0} + \varepsilon_{ij}, \quad b_{i0} \sim \mathcal{N}(0, \sigma_{b_1}^2)$$

- ▷ random intercepts & random slopes model

$$y_{ij} = X\beta + b_{i0} + b_{i1}t + \varepsilon_{ij}, \quad b_{i0} \sim \mathcal{N}(0, D)$$

with

$$D = \begin{bmatrix} \sigma_{b_1}^2 & \sigma_{b_{12}} \\ \sigma_{b_{12}} & \sigma_{b_2}^2 \end{bmatrix}$$

## 3.10 Hypothesis Testing (cont'd)

---

- Hence, the hypotheses to be tested are

$$H_0 : \sigma_{b_2}^2 = \sigma_{b_{12}} = 0$$

$$H_a : \sigma_{b_2}^2 \neq 0 \text{ or } \sigma_{b_{12}} \neq 0$$

- What is the problem? The null hypothesis for  $\sigma_{b_2}^2$  is on the boundary of its corresponding parameter space
  - ▷ statistical tests derived from standard ML theory assume the  $H_0$  is an interior point of the parameter space
  - ▷ **the classical asymptotic  $\chi^2$  distribution for the likelihood ratio test statistic does not apply**



## 3.10 Hypothesis Testing (cont'd)

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- For simple settings (as the one above), it has been proposed to use a mixture of  $\chi^2$  distributions to derive  $p$ -values, namely
  - ▷ 50% from the  $\chi^2$  distribution with degrees of freedom the number of parameters being tested, and
  - ▷ 50% from the  $\chi^2$  distribution with degrees of freedom the number of parameters who are not on the boundary under  $H_0$
- Nonetheless, it has been suggested that this solution does not always work satisfactorily
  - ▷ e.g., see package **RLRsim** in R and the references therein

## 3.10 Hypothesis Testing (cont'd)

- **Example:** In the AIDS dataset we compare two mixed models with linear and quadratic slopes in the fixed effects, and in the random effects
  - ▷  $M_1$  : random intercepts & linear random slopes
  - ▷  $M_2$  : random intercepts, linear random slopes & quadratic random slopes
- Hence, the covariance matrices of the random effects under the two models are

$$M_1 : D = \begin{bmatrix} \sigma_{b_1}^2 & \sigma_{b_{12}} \\ \sigma_{b_{12}} & \sigma_{b_2}^2 \end{bmatrix} \quad \text{and} \quad M_2 : D = \begin{bmatrix} \sigma_{b_1}^2 & \sigma_{b_{12}} & \sigma_{b_{13}} \\ \sigma_{b_{12}} & \sigma_{b_2}^2 & \sigma_{b_{23}} \\ \sigma_{b_{13}} & \sigma_{b_{23}} & \sigma_{b_3}^2 \end{bmatrix}$$

## 3.10 Hypothesis Testing (cont'd)

---

- And, the hypotheses being tested are

$$H_0 : \sigma_{b_3}^2 = \sigma_{b_{13}} = \sigma_{b_{23}} = 0$$

$$H_a : \text{at least one different from zero}$$

- The likelihood ratio test gives:

	df	logLik	LRT	p-value	Mixture p-value
$M_1$	9	-3573.88			
$M_2$	12	-3570.71	6.34	0.0961	0.0690

## 3.10 Hypothesis Testing (cont'd)

---

- About the two  $p$ -values
  - ▷ The first  $p$ -value is based on the classic  $\chi^2$  distribution with degrees of freedom the number of parameters being tested, i.e., in this case 3
  - ▷ The second  $p$ -value is based on the mixture of  $\chi^2$  distributions with 3 degrees of freedom (i.e., the classic one) and 2 degrees of freedom (the number of parameters not on the boundary under  $H_0$ ), respectively
- We observe that the classic  $p$ -value is more conservative
  - ▷ as we have seen in the previous section (see pp.216), when choosing the appropriate random effects we should be more liberal, and hence the mixture of  $\chi^2$  distribution is to be preferred

## 3.10 Hypothesis Testing (cont'd)

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- When we have **non-nested** models we **cannot** use standard tests anymore
  - ▷ the alternative in this case is to use the information criteria AIC or BIC

When we compare two **non-nested** models we choose the model that has the **lowest** AIC/BIC value

## 3.10 Hypothesis Testing (cont'd)

---

- Example: In the PBC dataset we want to compare two mixed models with a spline effect of time and its interaction with sex in the fixed effects, and in the random effects
  - ▷  $M_1$  : random intercepts & linear random slopes, with an unstructured matrix for these random effects
  - ▷  $M_2$  : random intercepts, & nonlinear random slopes with splines, with a diagonal matrix for these random effects

In the fixed-effects part and in the random-effects part of model  $M_2$  : the splines are natural cubic splines with 2 internal knots

- These models are not nested and hence to compare them we use the AIC and BIC values

## 3.10 Hypothesis Testing (cont'd)

---

- The AIC and BIC values for the two models are:

	df	logLik	AIC	BIC
$M_1$	10	-1522.38	3064.75	3120.45
$M_2$	10	-1438.53	2897.06	2952.76

- ▷ Both AIC and BIC suggest that the model with the nonlinear random slopes is better than the model with the linear random slopes

## 3.10 Hypothesis Testing (cont'd)

---

- Notes: Hypothesis testing for the covariance matrix  $V_i$ 
  - ▷ The aforementioned procedures assume that the fixed-effects structure of the mixed models to be compared are the same
    - \* under this assumption we can compare mixed models fitted with the restricted maximum likelihood (REML) method
    - \* otherwise the models should be fitted with maximum likelihood (ML)
  - ▷ The AIC and BIC do not always select the same model – when they disagree
    - \* AIC typically selects the more elaborate model, whereas
    - \* BIC the more parsimonious model



## 3.10 Hypothesis Testing (cont'd)

---

- **Hypothesis testing for the regression coefficients  $\beta$ :** We assume that first a suitable choice for the covariance matrix has been made
- In the majority of the cases we compare nested models, and hence standard tests can be used
- We distinguish between two cases
  - ▷ tests for individual coefficients
  - ▷ tests for groups of coefficients

## 3.10 Hypothesis Testing (cont'd)

---

- Everything works in the same manner as we have seen for marginal models in Chapter 2 (see pp.108–111)
  - ▷ hence, we are not going to repeat the details here
- Example: We have fitted the following model to the Prothro dataset:

## 3.10 Hypothesis Testing (cont'd)

$$\left\{ \begin{array}{l} \text{pro}_{ij} = (\beta_0 + b_{i0}) + (\beta_1 + b_{i1})N(\text{Time}_{ij})_1 + (\beta_2 + b_{i2})N(\text{Time}_{ij})_2 + \\ (\beta_3 + b_{i3})N(\text{Time}_{ij})_3 + \beta_4 \text{predn}_i + \\ \beta_5 \{\text{predn}_i \times N(\text{Time}_{ij})_1\} + \beta_6 \{\text{predn}_i \times N(\text{Time}_{ij})_2\} + \\ \beta_7 \{\text{predn}_i \times N(\text{Time}_{ij})_3\} + \varepsilon_{ij} \\ b_i \sim \mathcal{N}(0, D) \quad D \text{ is a diagonal matrix,} \quad \varepsilon_{ij} \sim \mathcal{N}(0, \sigma^2) \end{array} \right.$$

- ▷ The terms  $N(\text{Time}_{ij})_1$ ,  $N(\text{Time}_{ij})_2$  and  $N(\text{Time}_{ij})_3$  denote the basis for a natural cubic spline with three degrees of freedom to model possible nonlinearities in the time effect

## 3.10 Hypothesis Testing (cont'd)

---

- We are interested in
  - ▷ the main effect of treatment,
  - ▷ the overall effect of time, and
  - ▷ the overall effect of treatment (i.e., main effect + interactions)
- Under the postulated model the main effect of treatment is given by parameter  $\beta_4$ , i.e.,

$$H_0 : \beta_4 = 0$$

$$H_a : \beta_4 \neq 0$$

- The output of the model gives: ...

## 3.10 Hypothesis Testing (cont'd)

	Value	Std.Err.	<i>t</i> -value	<i>p</i> -value
$\beta_0$	72.357	1.435	50.423	< 0.001
$\beta_1$	-12.131	3.953	-3.069	0.002
$\beta_2$	31.954	3.445	9.274	< 0.001
$\beta_3$	34.015	4.706	7.228	< 0.001
$\beta_4$	-4.154	2.057	-2.019	0.044
$\beta_5$	14.621	5.679	2.575	0.010
$\beta_6$	-7.809	5.040	-1.549	0.121
$\beta_7$	-3.253	7.177	-0.453	0.650

## 3.10 Hypothesis Testing (cont'd)

---

- Hence, a significant treatment effect at baseline (strange!)
  - ▷ the  $t$ -value in the output is the estimated coefficient divided by its standard error
- For the overall effect of time, we are interested in the hypothesis:

$$H_0 : \beta_1 = \beta_2 = \beta_3 = \beta_5 = \beta_6 = \beta_7 = 0$$

$$H_a : \text{at least one coefficient different from 0}$$

- To test this hypothesis we can use an F-test but appropriately constructing the contrasts matrix

## 3.10 Hypothesis Testing (cont'd)

---

- We obtain

$F$ -value	$df_1$	$df_2$	$p$ -value
23.555	6	1939	$< 0.0001$

▷ Hence, a significant overall time effect

## 3.10 Hypothesis Testing (cont'd)

---

- For the overall treatment effect, we obtain the hypothesis:

$$H_0 : \beta_4 = \beta_5 = \beta_6 = \beta_7 = 0$$

$$H_a : \text{at least one coefficient different from 0}$$

- This cannot be tested with an F-test because of technical reasons
  - ▷ the denominator degrees of freedom are not the same for the main effect and the terms involving time
- As an alternative we can use the likelihood ratio test
  - ▷ i.e., we compare the model we fitted with the model that only has the nonlinear effect of time in the fixed effects



## 3.10 Hypothesis Testing (cont'd)

---

- The likelihood ratio test gives

	df	logLik	AIC	BIC	LRT	p-value
without Treatment	9	−13240.53	26499.06	26553.02		
with Treatment	13	−13229.80	26485.59	26563.53	21.47	0.0003

▷ Hence, we obtain a significant overall treatment effect

## 3.11 Residuals

---

- As we have similarly done for marginal models in Chapter 2, before extracting conclusions from mixed models, we will first need to validate the underlying assumptions they make
- To do this we can use the residuals of the model
- In the setting of mixed models we have two types of residuals
  - ▷ *Marginal residuals*: These are based on the implied marginal model behind a linear mixed model (see pp.160)
  - ▷ *Conditional residuals*: These are based on the hierarchical representation of the mixed model and utilize the empirical Bayes estimates of the random effects (see pp.174)

## 3.11 Residuals (cont'd)

- The exact definitions are as follows:

▷ *Marginal residuals:*

$$\begin{cases} y_i &= X_i\beta + \varepsilon_i^*, \quad \varepsilon_i^* \sim \mathcal{N}(0, Z_i D Z_i^\top + \sigma^2 \mathbf{I}_{n_i}) \\ r_i^{marg} &= y_i - X_i \hat{\beta} \end{cases}$$

- ▷ These residuals predict the marginal errors  $\varepsilon_i^*$
- ▷ They can be used to
  - \* investigate misspecification of the mean structure  $X_i\beta$
  - \* validate the assumptions for the within-subjects covariance structure  $Z_i D Z_i^\top + \sigma^2 \mathbf{I}_{n_i}$

## 3.11 Residuals (cont'd)

---

▷ *Conditional residuals*

$$\begin{cases} y_i &= X_i\beta + Z_ib_i + \varepsilon_i, \quad b_i \sim \mathcal{N}(0, D), \quad \varepsilon_i \sim \mathcal{N}(0, \sigma^2 \mathbf{I}_{n_i}) \\ r_i^{cond} &= y_i - X_i\hat{\beta} - Z_i\hat{b}_i \end{cases}$$

- ▷ These residuals predict the conditional errors  $\varepsilon_i$
- ▷ They can be used to
  - \* investigate misspecification of the hierarchical mean structure  $X_i\beta + Z_ib_i$
  - \* validate the assumptions for the within-subjects variance structure  $\sigma^2$

## 3.11 Residuals (cont'd)

- **Example:** We evaluate the assumptions behind the following model fitted to the Prothro dataset:

$$\left\{ \begin{array}{l} \text{pro}_{ij} = (\beta_0 + b_{i0}) + (\beta_1 + b_{i1})N(\text{Time}_{ij})_1 + (\beta_2 + b_{i2})N(\text{Time}_{ij})_2 + \\ (\beta_3 + b_{i3})N(\text{Time}_{ij})_3 + \beta_4 \text{predn}_i + \beta_5 \{\text{predn}_i \times N(\text{Time}_{ij})_1\} + \\ \beta_6 \{\text{predn}_i \times N(\text{Time}_{ij})_2\} + \beta_7 \{\text{predn}_i \times N(\text{Time}_{ij})_3\} + \varepsilon_{ij}, \\ b_i \sim \mathcal{N}(0, \text{diag}\{D\}), \quad \varepsilon_{ij} \sim \mathcal{N}(0, \sigma^2) \end{array} \right.$$

$N(\cdot)$  denotes a natural cubic spline basis

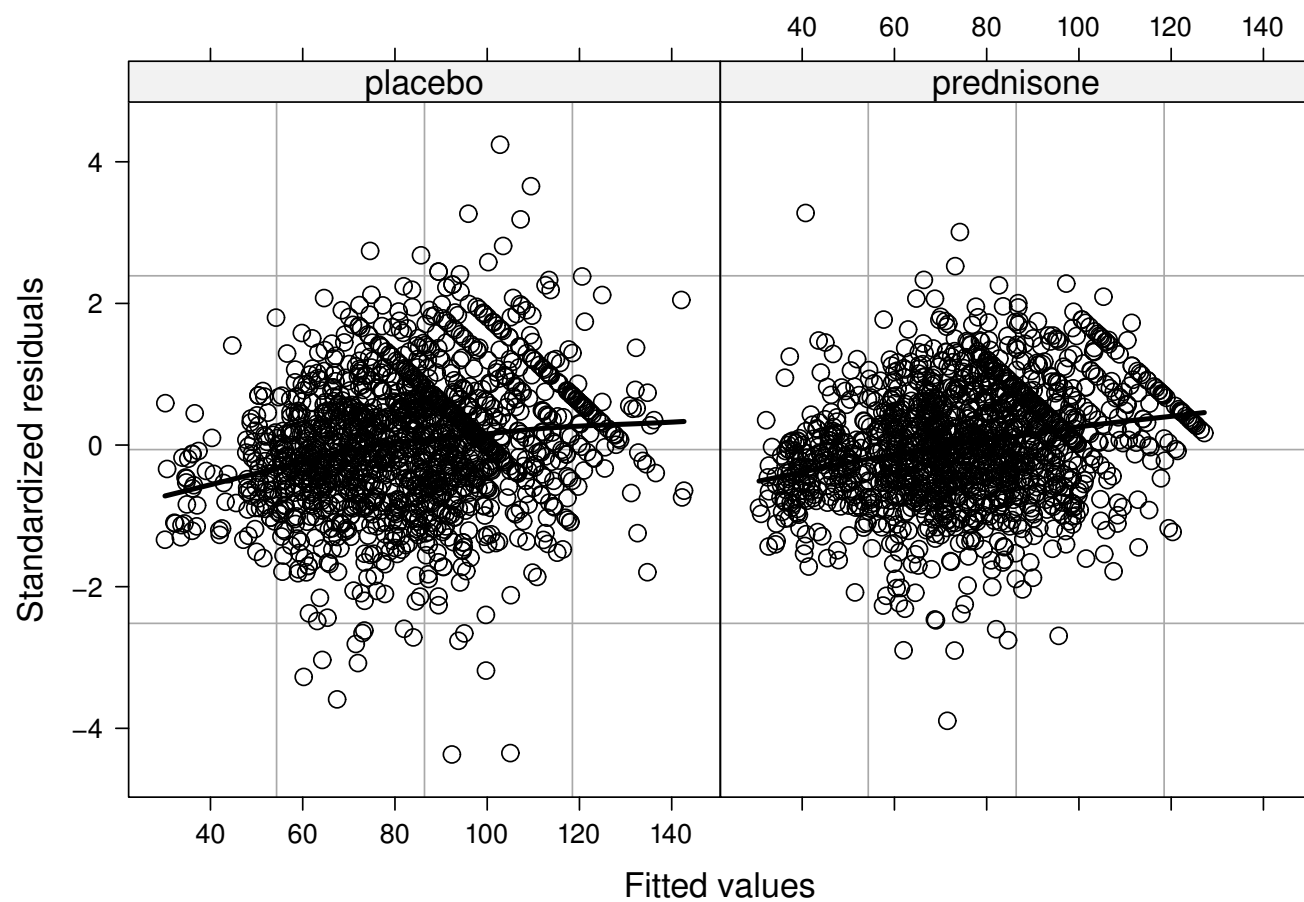
## 3.11 Residuals (cont'd)

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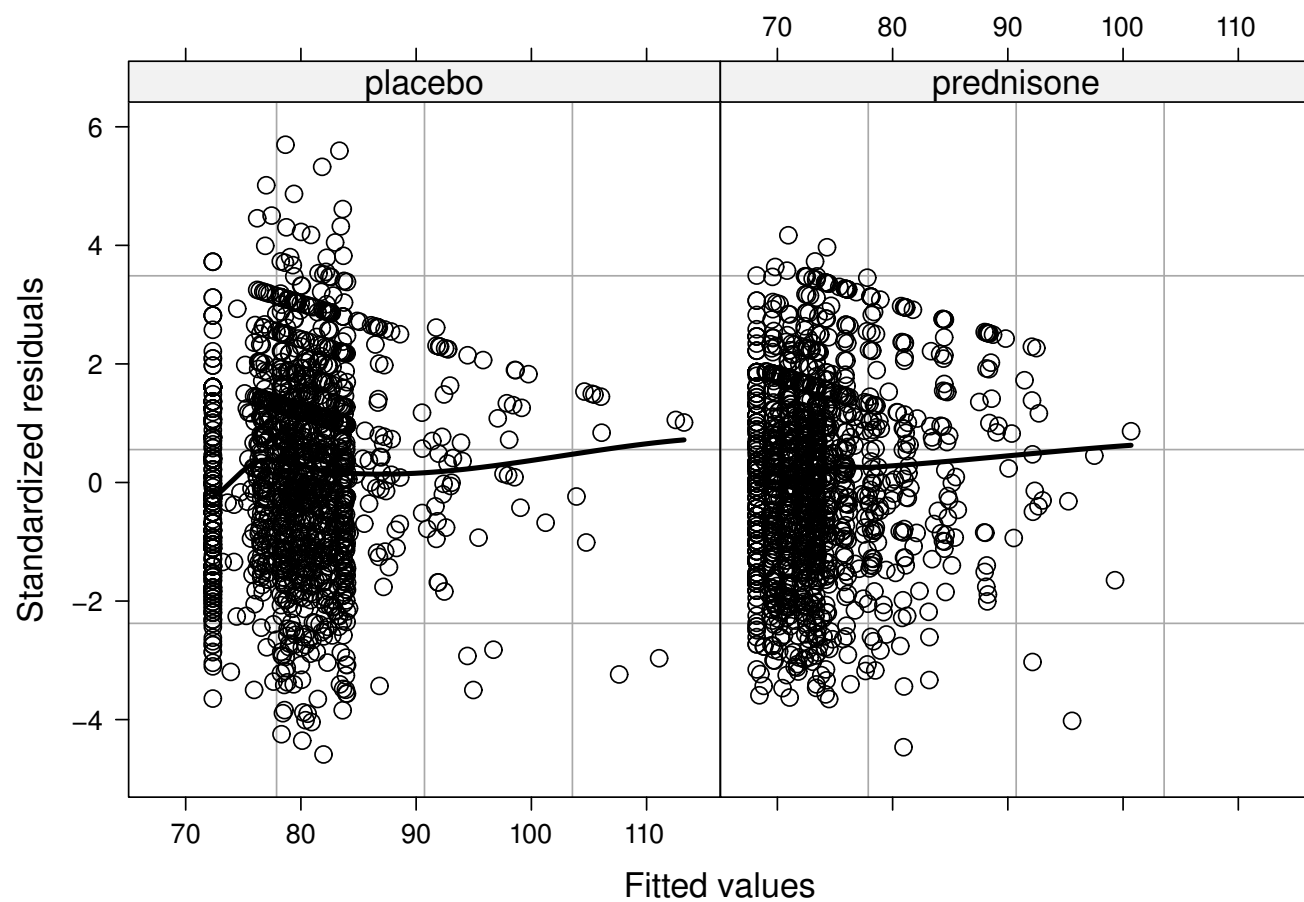
by plotting

- ▷ the standardized marginal residuals versus fitted values per treatment group
- ▷ the standardized conditional residuals versus fitted values per treatment group
- ▷ QQ-plot of the standardized marginal residuals
- ▷ QQ-plot of the standardized conditional residuals

## 3.11 Residuals (cont'd)

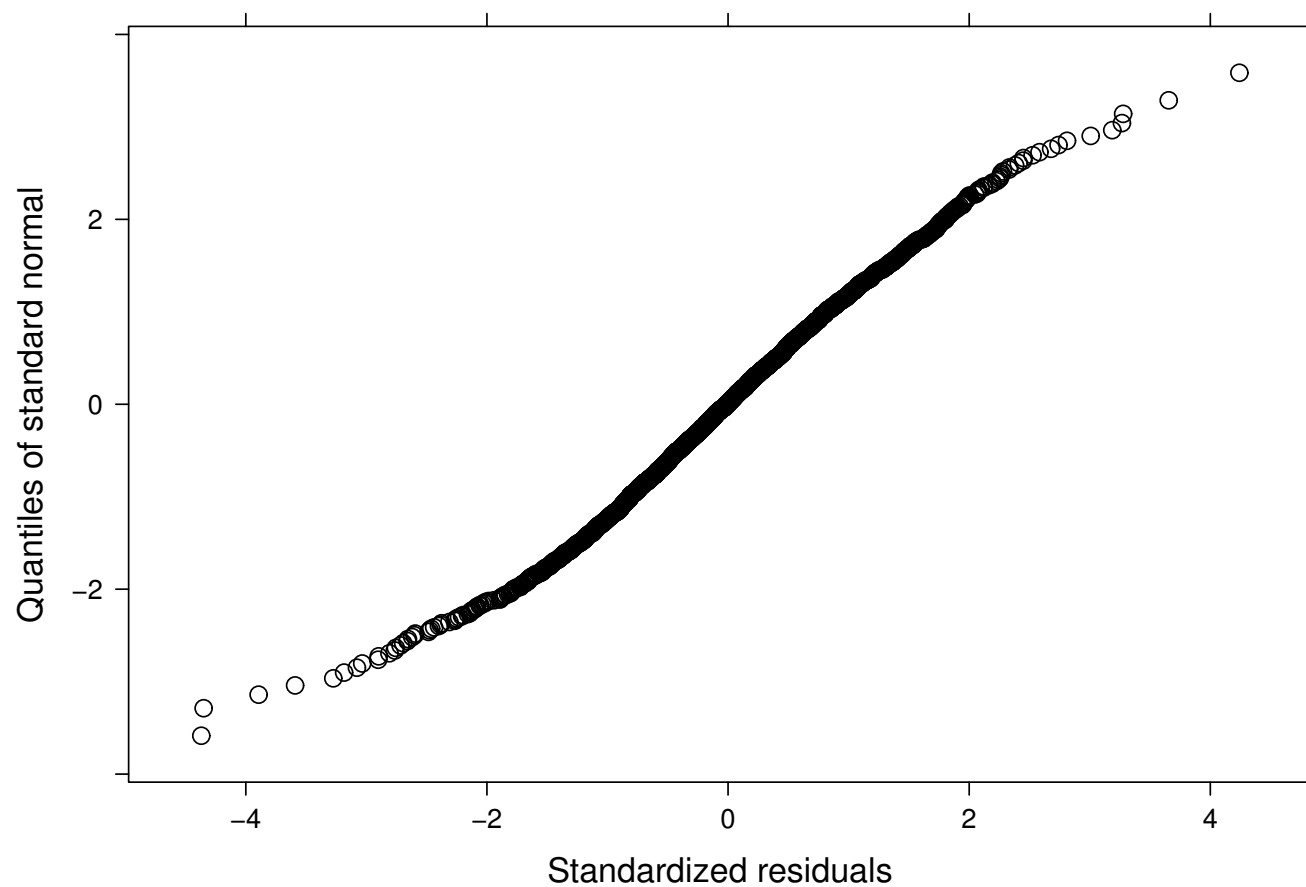


## 3.11 Residuals (cont'd)

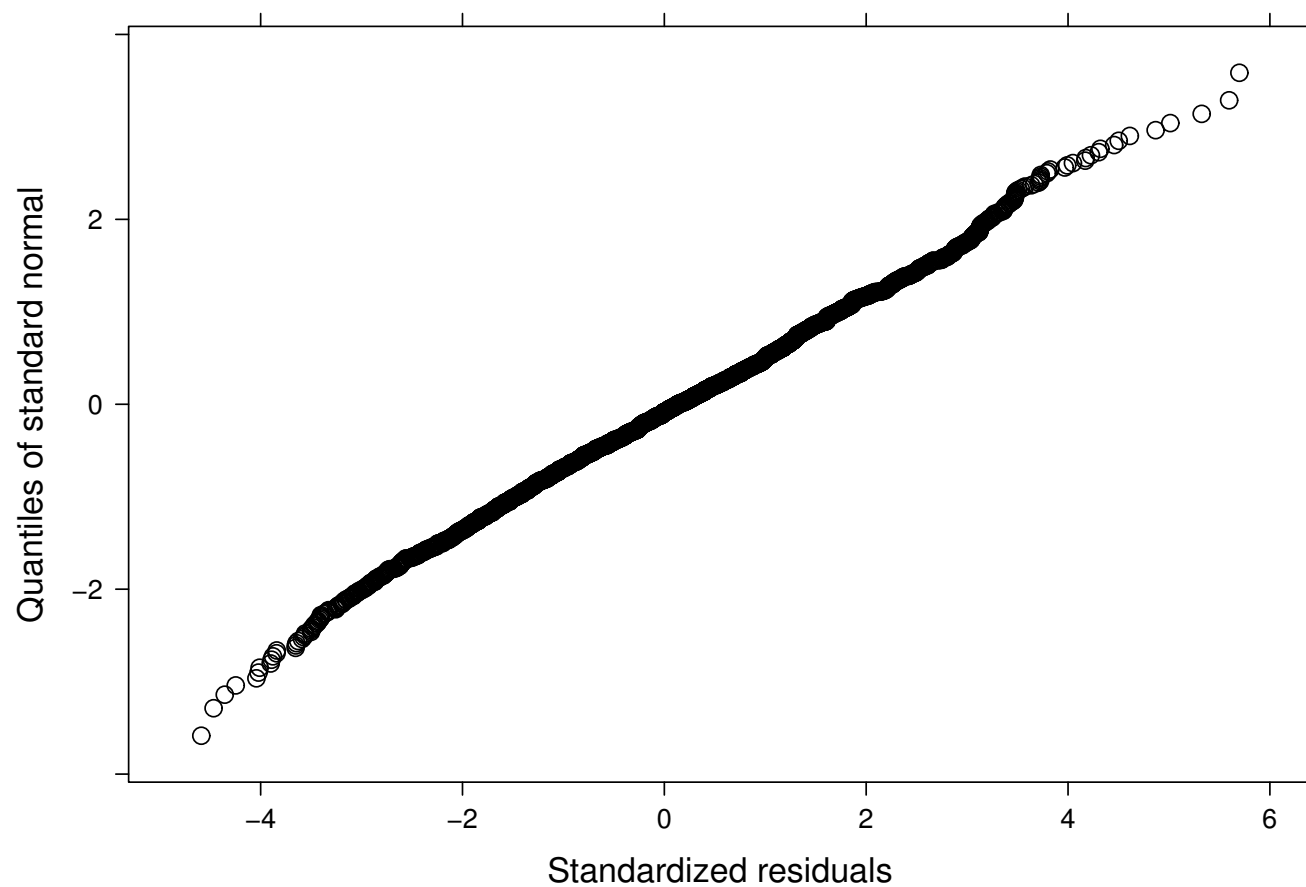




## 3.11 Residuals (cont'd)



## 3.11 Residuals (cont'd)



## 3.11 Residuals (cont'd)

---

- Observations
  - ▷ the plots of the residuals versus the fitted values do show a slightly systematic behavior
  - ▷ the QQ-plots do not show big discrepancies from normality

## 3.12 Review of Key Points

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- Mixed effects models constitute an alternative modeling framework for analyzing grouped/clustered data
  - ▷ basic idea: sample units in the same group/cluster share the same random effects
  - ▷ the random effects are *unobserved* variables that induce correlation
- From a practical viewpoint, mixed models provide a more flexible framework to model correlations when
  - ▷ we have unbalanced data and/or
  - ▷ the correlation structure has a complicated form (e.g., multilevel designs)

## 3.12 Review of Key Points (cont'd)

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- The random effects can be estimated using empirical Bayes methodology
  - ▷ mixed models provide subject-specific predictions that are more accurate than marginal predictions
- Mixed models can be extended to include correlated error terms
  - ▷ this is in the same spirit as the marginal models of Chapter 2
  - ▷ however, this extension often makes the model computationally unstable

## 3.12 Review of Key Points (cont'd)

---

- Hypothesis testing
  - ▷ for the covariance structure and for nested models likelihood ratio tests are most often used, for non-nested models AIC/BIC
  - ▷ for the mean structure  $t$  and  $F$  tests with appropriate degrees of freedom
- Residuals
  - ▷ standard residuals plots are used to check the model assumptions
  - ▷ marginal and conditional residuals available