

Chapter 5

Mixed Models for Discrete Data

5.1 Generalized Linear Mixed Models

- The previous chapter focused on the framework of Generalized Estimating Equations
 - ▷ this can be seen as the extension of the marginal models for continuous data of Chapter 2 to the setting of categorical longitudinal responses
- In this chapter we will see the analogue of linear mixed models for categorical data



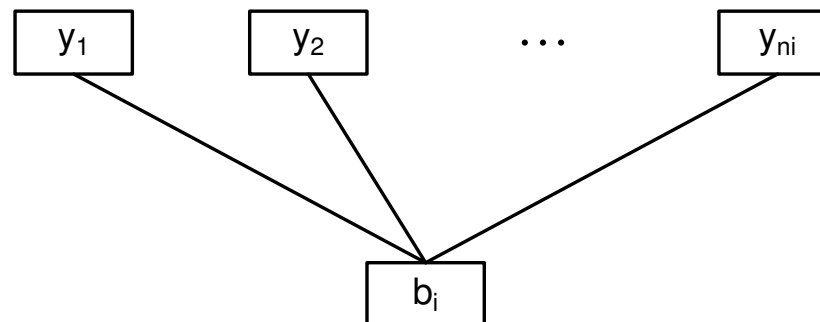
Generalized Linear Mixed Models (GLMMs)

5.1 Generalized Linear Mixed Models (cont'd)

- The intuitive idea behind GLMMs is the same as in linear mixed models, i.e.,
 - ▷ the correlation between the repeated categorical measurements is induced by unobserved random effects
 - ▷ in other words: the categorical longitudinal measurements of a subject are correlated because all of them share the *same* unobserved random effect (**conditional independence assumption**)

5.1 Generalized Linear Mixed Models (cont'd)

Graphical representation of the conditional independence assumption



5.1 Generalized Linear Mixed Models (cont'd)

- Similarly to Chapter 4, we will focus on clustered dichotomous/binary data
 - ▷ nonetheless, the same ideas and issues also apply to other categorical responses (e.g., Poisson, ordinal data, multinomial data, etc.)
- Suppose we have a binary outcome y_{ij}

$$y_{ij} = \begin{cases} 1, & \text{if subject } i \text{ has a positive response at measurement } j \\ 0, & \text{if subject } i \text{ has a negative response at measurement } j \end{cases}$$

5.1 Generalized Linear Mixed Models (cont'd)

- The generic mixed model for y_{ij} is a *Mixed-Effects Logistic Regression* and has the form:

$$\begin{cases} \log \frac{\pi_{ij}}{1 - \pi_{ij}} = x_{ij}^{\top} \beta + z_{ij}^{\top} b_i \\ b_i \sim \mathcal{N}(0, D) \end{cases}$$

where

- ▷ $\pi_{ij} = \Pr(y_{ij} = 1)$ the probability of a positive response
- ▷ x_{ij} a vector of fixed-effects covariates, with corresponding regression coefficients β
- ▷ z_{ij} a vector of random-effects covariates, with corresponding regression coefficients b_i

5.1 Generalized Linear Mixed Models (cont'd)

- More formally, we have the following three-part specification
 1. Conditional on the random effects b_i , the responses y_{ij} are independent and have a Bernoulli distribution with mean $E(y_{ij} | b_i) = \pi_{ij}$ and variance $\text{var}(y_{ij} | b_i) = \pi_{ij}(1 - \pi_{ij})$
 2. The conditional mean of y_{ij} depends upon fixed and random effects via the following expression:

$$\log \frac{\pi_{ij}}{1 - \pi_{ij}} = x_{ij}^\top \beta + z_{ij}^\top b_i$$

3. The random effects follow a multivariate normal distribution with mean zero and variance-covariance matrix D

5.1 Generalized Linear Mixed Models (cont'd)

- Notes: On the definition of GLMMs
 - ▷ The three-part specification of GLMMs corresponds to a full specification of the distribution of the outcome y_{ij} – this is in contrast to the GEE approach, which is a semi-parametric method
 - ▷ The mean and correlation structures are simultaneously defined using random effects
 - ⇒ As we will see next, this has direct and important implications with respect to the interpretation of the parameters

5.2 Interpretation

- Example: In the AIDS dataset, a very low CD4 count (less than 150 cells/mm^3) is an indicator for opportunistic infections
 - ▷ In the following analysis we dichotomize the CD4 cell counts from the AIDS dataset using this threshold
 - ▷ We fit a mixed effects logistic regression with
 - * *fixed effects*: time, treatment and their interaction
 - * *random effects*: random intercepts

5.2 Interpretation (cont'd)

- The model has the form:

$$\log \frac{\pi_{ij}}{1 - \pi_{ij}} = \beta_0 + \beta_1 \text{Time}_{ij} + \beta_2 \text{ddI}_i + \beta_3 \{\text{Time}_{ij} \times \text{ddI}_i\} + b_i, \quad b_i \sim \mathcal{N}(0, \sigma_b^2)$$

	Value	Std.Err.	z-value	p-value
β_0	5.080	0.362	14.028	< 0.001
β_1	0.136	0.041	3.329	0.001
β_2	-0.624	0.494	-1.262	0.207
β_3	-0.025	0.055	-0.459	0.646
σ_b	5.102			

5.2 Interpretation (cont'd)

- Interpretation of fixed effects

- ▷ At baseline for group ddC the log odds of a low CD4 cell count are on average $\beta_0 = 5.08$

- * 95% heterogeneity interval (**not** confidence interval):
 $(\beta_0 - 1.96\sigma_b ; \beta_0 + 1.96\sigma_b) = (-4.92 ; 15.08)$

- ▷ We translate the log odds to the probability scale: The probability of low CD4 cell count is $\exp(\beta_0) / \{1 + \exp(\beta_0)\} = 0.99382$

- * 95% heterogeneity interval:
 $(1/[1 + \exp\{-(\beta_0 - 1.96\sigma_b)\}] ; 1/[1 + \exp\{-(\beta_0 + 1.96\sigma_b)\}]) = (0.00725 ; 1)$

5.2 Interpretation (cont'd)

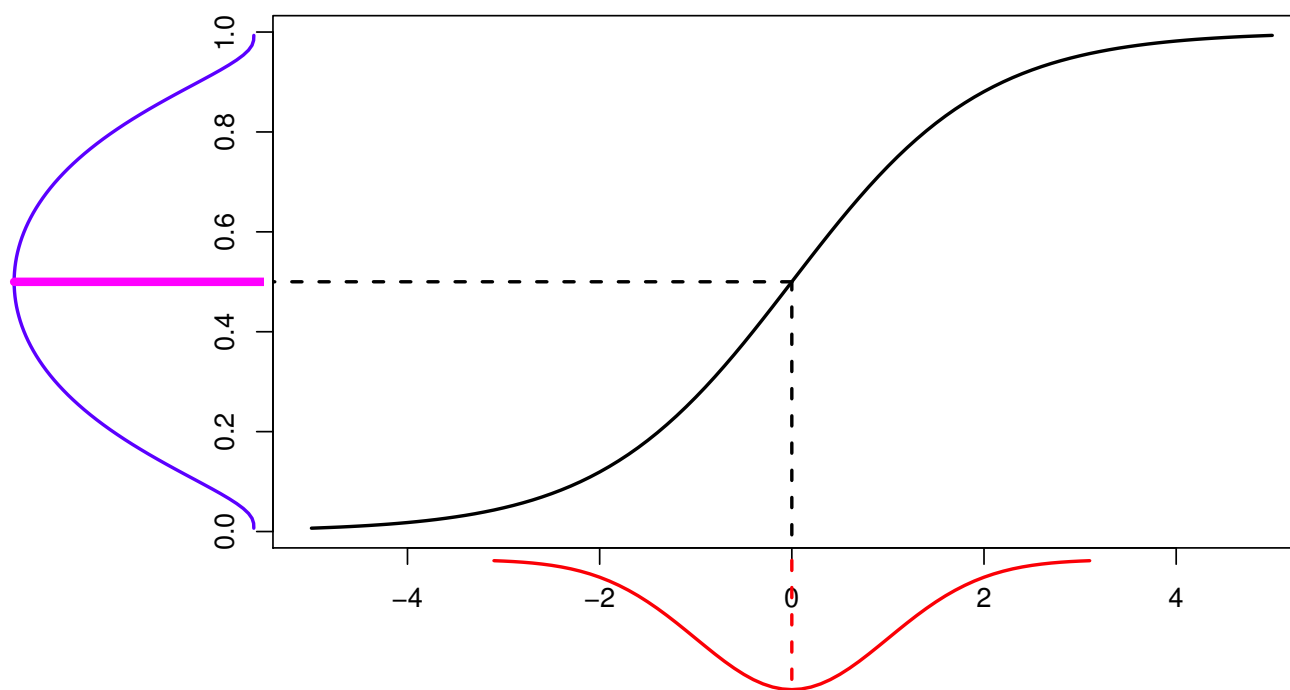
- When we compare the middle point of the transformed heterogeneity interval with the transformed intercept an **important** observation is made:
 - ▷ $\exp(\beta_0)/\{1 + \exp(\beta_0)\} = 0.99382$
 - ▷ mean of transformed interval = 0.50363

When we transform the fixed effects to the probability scale, they do not correspond to the average probability

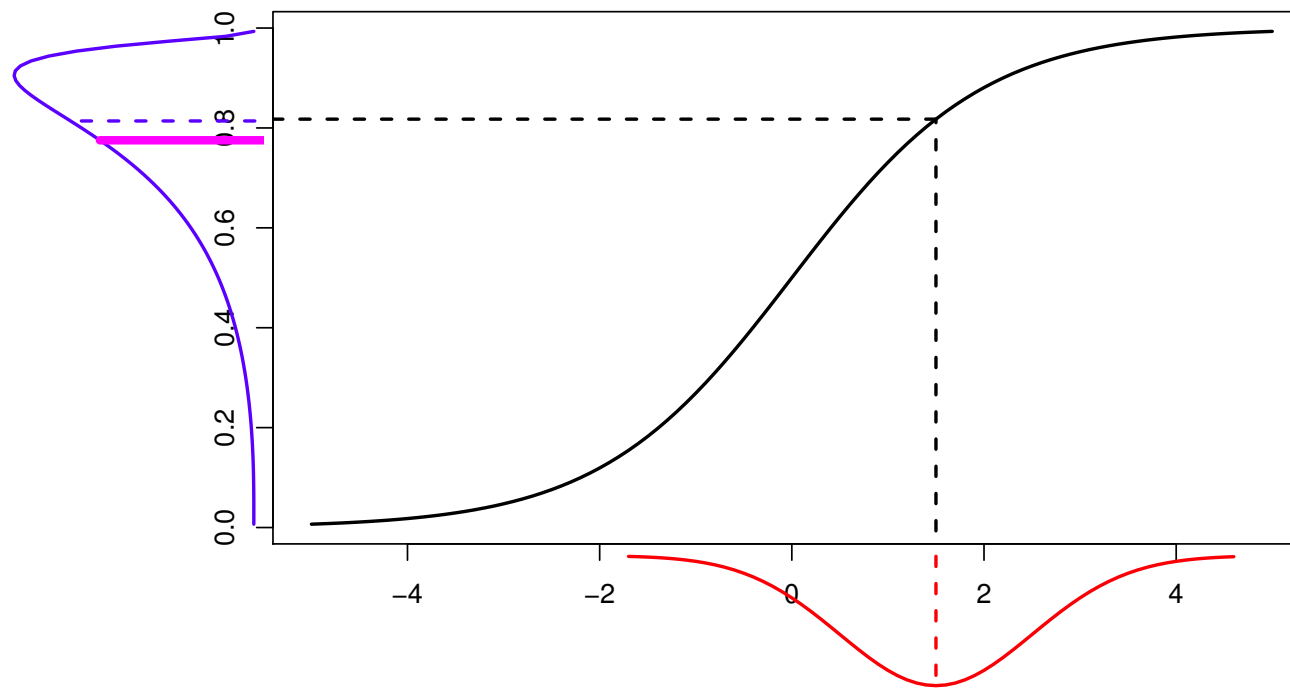
5.2 Interpretation (cont'd)

- Let's explain this issue graphically ...

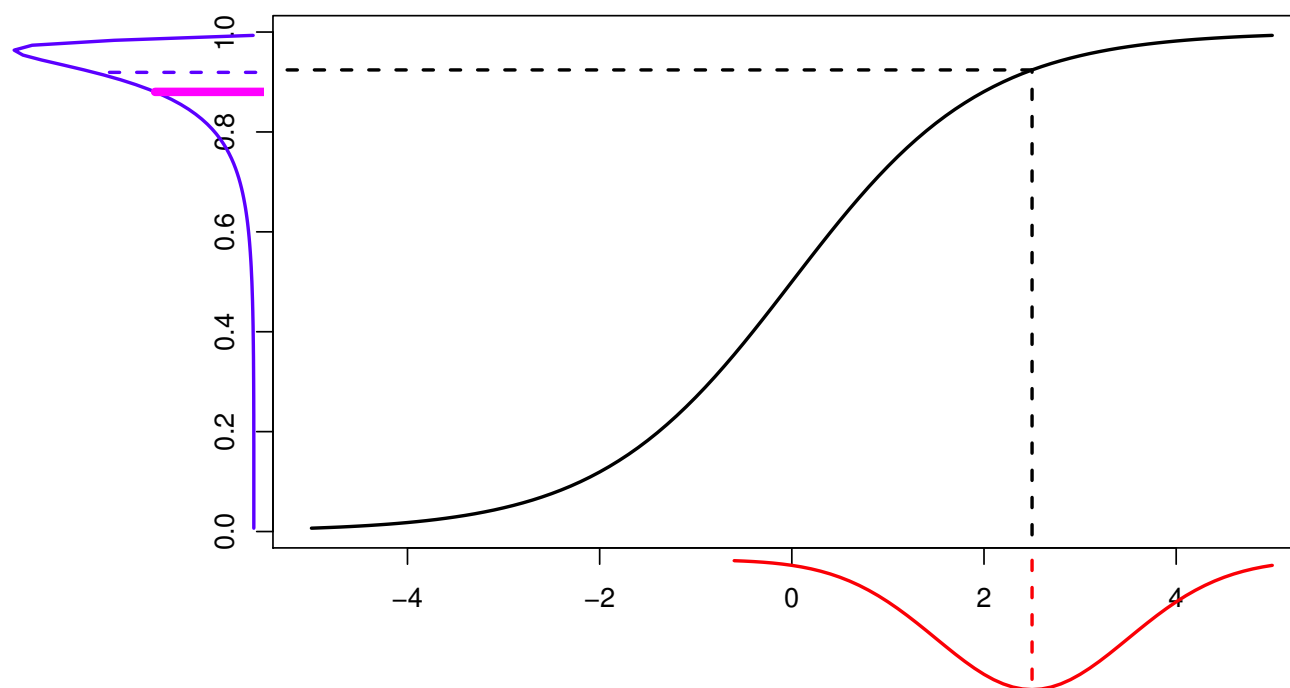
5.2 Interpretation (cont'd)



5.2 Interpretation (cont'd)



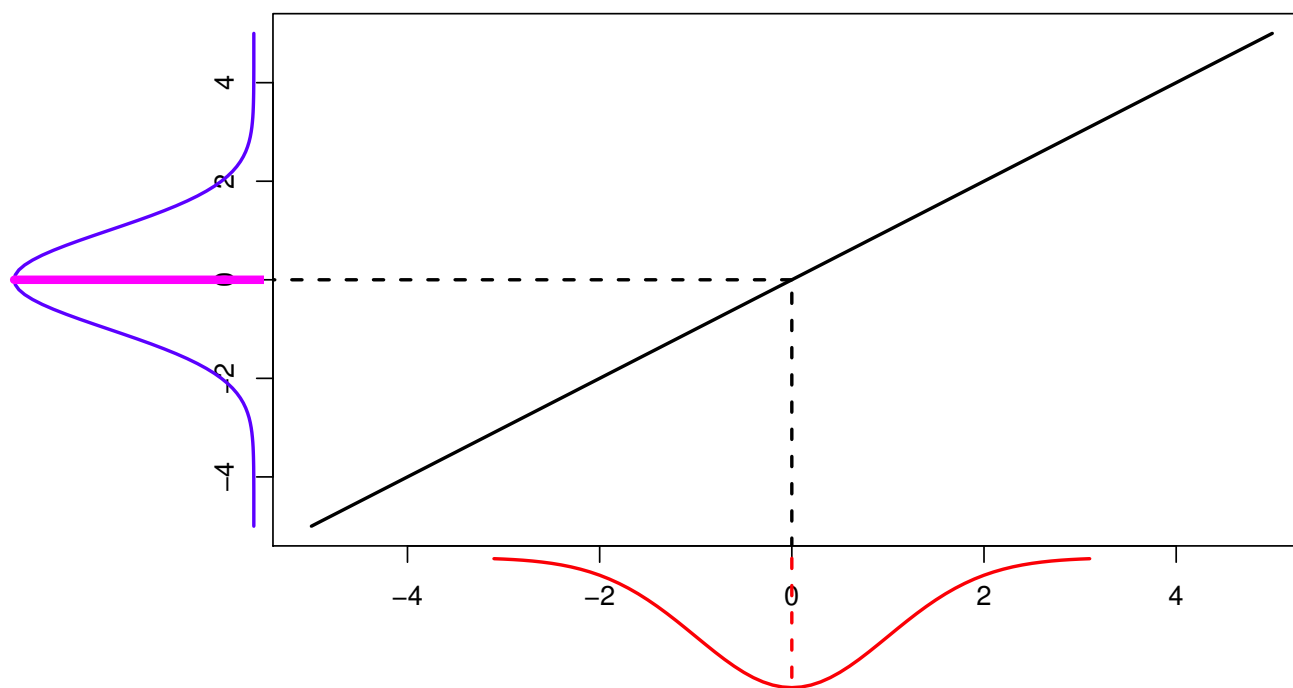
5.2 Interpretation (cont'd)



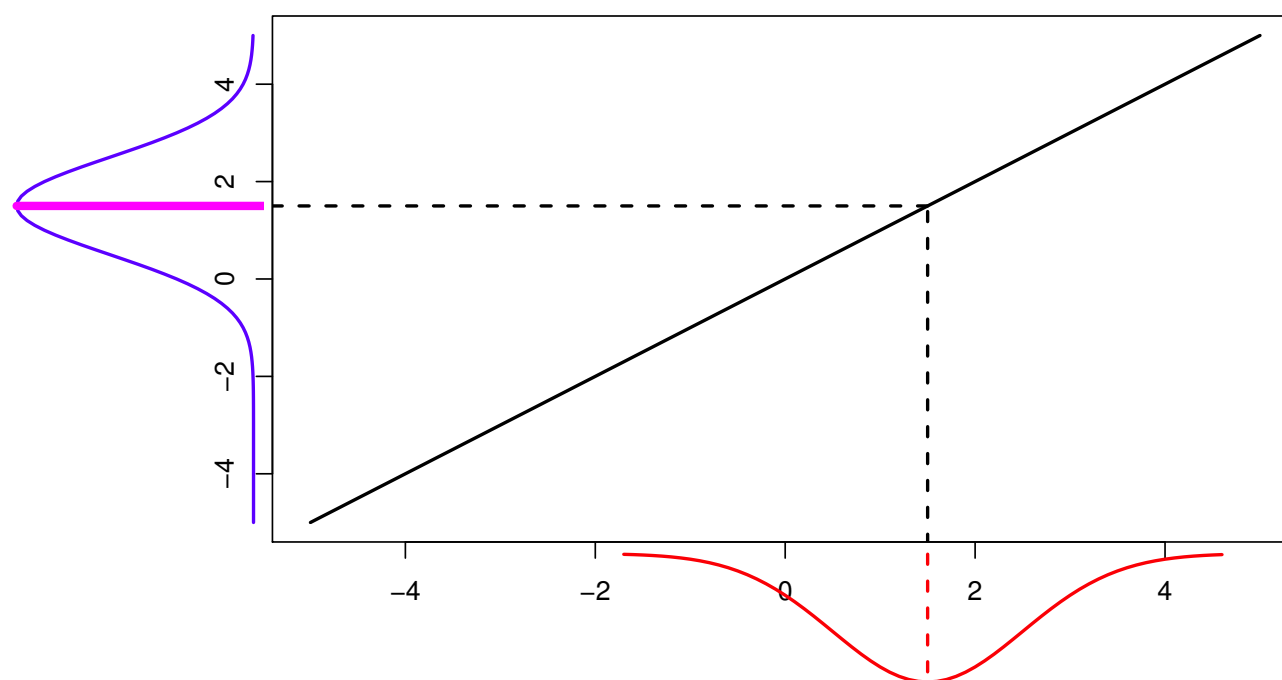
5.2 Interpretation (cont'd)

- We did not have this problem in the case of the linear mixed model because we did not have a link function
 - ▷ or to put it more precisely, the link function was the identity $g(x) = x$
- Let's see graphically again why for linear mixed models we do not have the same problem . . .

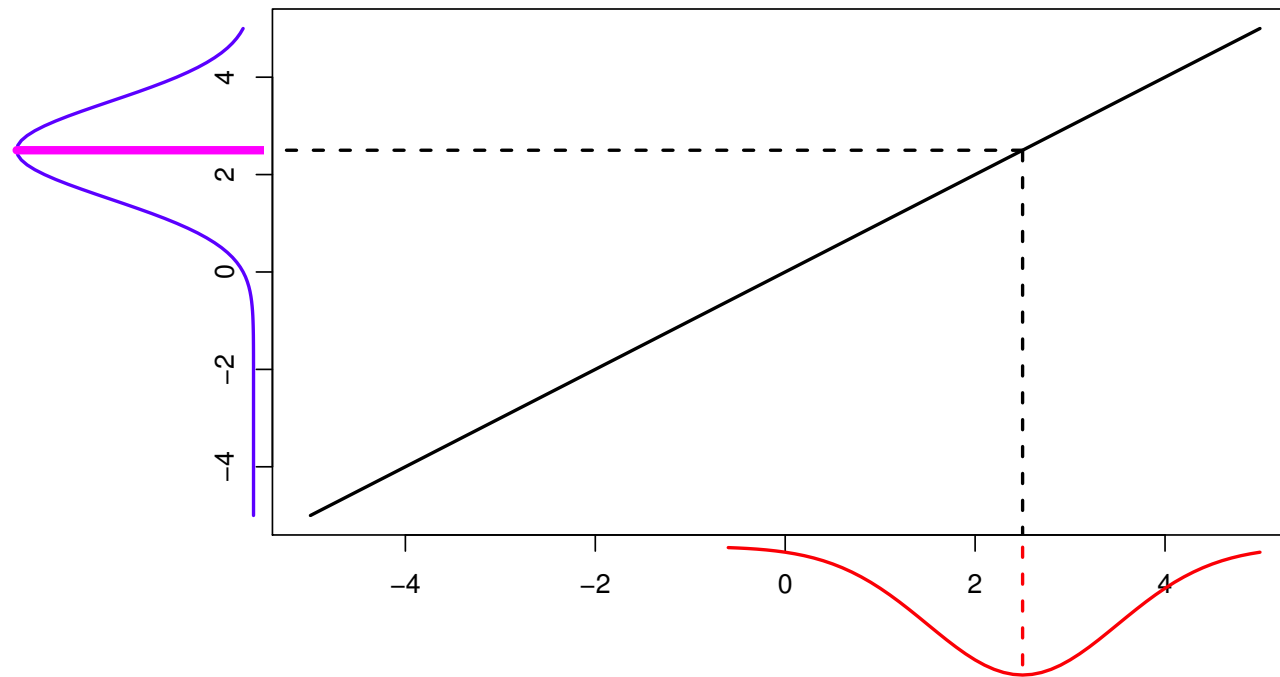
5.2 Interpretation (cont'd)



5.2 Interpretation (cont'd)



5.2 Interpretation (cont'd)



5.2 Interpretation (cont'd)

- The same complications also hold for the other fixed-effects coefficients of the logistic regression model
 - ▷ e.g., e^{β_1} does **not** have the interpretation of the *average* odds ratio for a month increase in follow-up
- Let's see why
 - ▷ say that we compare two patients at different follow-up times who both took ddC, Patient *i* at month m and Patient *i'* at month $m + 1$
 - ▷ the equation of the model for Patient *i* is:

$$\log \frac{\pi_{ij}}{1 - \pi_{ij}} = \beta_0 + \beta_1 \{\text{Time}_{ij} = m\} + b_i$$

5.2 Interpretation (cont'd)

▷ the equation of the model for Patient i' is:

$$\log \frac{\pi_{i'j}}{1 - \pi_{i'j}} = \beta_0 + \beta_1 \{\text{Time}_{ij} = m + 1\} + b_{i'}$$

▷ hence, the corresponding odds ratio is:

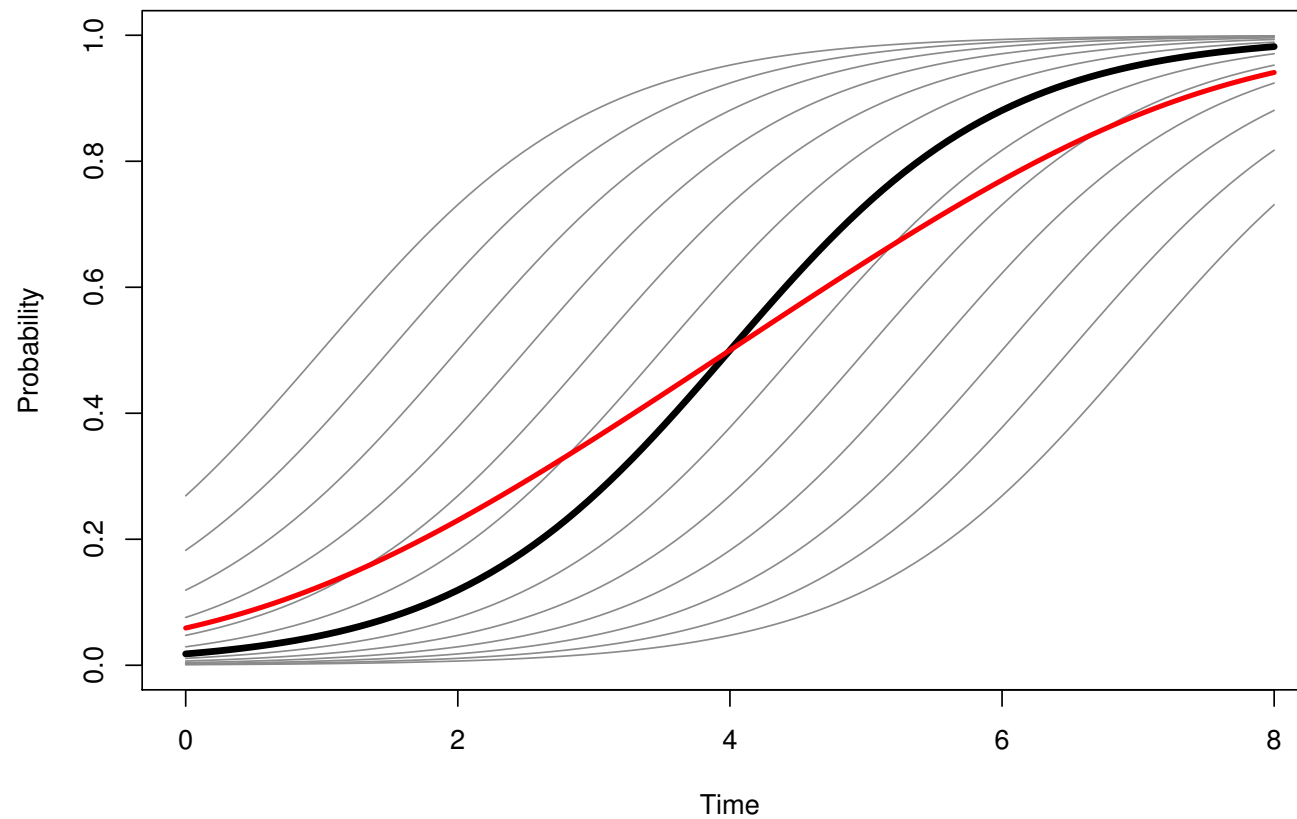
$$\text{log odds ratio: } \log \frac{\pi_{i'j}}{1 - \pi_{i'j}} - \log \frac{\pi_{ij}}{1 - \pi_{ij}} = \beta_1 + (b_{i'} - b_i) \Rightarrow$$

$$\text{odds ratio: } \frac{\pi_{i'j}/(1 - \pi_{i'j})}{\pi_{ij}/(1 - \pi_{ij})} = \exp\{\beta_1 + (b_{i'} - b_i)\} \neq \exp(\beta_1)$$

5.2 Interpretation (cont'd)

- Hence, the interpretation of e^{β_1} is not the odds ratio for unit increase of Time for all subjects, but rather for subjects with *the same random-effect value*
- To illustrate this again graphically, we depict the relationship between time and the probability of low CD4 cell counts
 - ▷ the grey lines depict 13 random subjects with increasing random effects
 - ▷ the black line corresponds to the subject with $b_i = 0$ (i.e., the mean individual)
⇒ This line is actually $1/[1 + \exp\{-(\beta_0 + \beta_1 \text{Time}_{ij})\}]$
 - ▷ the red line that crosses the 13 lines denotes the average longitudinal evolution of the probability of low CD4 cells counts across subjects

5.2 Interpretation (cont'd)



5.2 Interpretation (cont'd)

- To summarize:
 - ▷ The fixed-effects regression coefficients are interpreted in terms of the effects of covariates on changes in an *individual's* transformed mean response, while holding the remaining covariates fixed
 - ▷ Because the components of the fixed effects β , have interpretations that depend upon holding b_i (the i -th subject's random effects) fixed, they are often referred to as *subject-specific* regression coefficients
 - ▷ As a result, GLMMs are most useful when the main scientific objective is to make inferences about individuals rather than population averages
 - ▷ Population averages are the targets of inference in marginal models (i.e., GEE)

5.2 Interpretation (cont'd)

Hence, contrary to the marginal and mixed effects model for continuous data (Chapters 2 & 3), the regression coefficients from marginal models for discrete data **do not** have the same interpretation as the corresponding coefficients from mixed effects models

5.2 Interpretation (cont'd)

- **Nonetheless**, for the special case of random intercepts, there is a closed-form expression to obtain the marginal regression coefficients from the subject-specific ones, i.e.,

$$\beta^M = \frac{\beta^{SS}}{\sqrt{1 + 0.346\sigma_b^2}}$$

where

- ▷ β^M denotes the marginal coefficients
- ▷ β^{SS} denotes the subject-specific coefficients
- ▷ σ_b^2 denotes the variance of the random intercepts

5.2 Interpretation (cont'd)

- **However**, this formula only works for random intercepts, and cannot be used in models with more random effects
- An alternative solution has been recently proposed to overcome this issue,
 - ▷ in particular the marginal coefficients β^M are obtained as the solution to the equation

$$\beta^M = (X^\top X)^{-1} X^\top \text{logit}(\pi^M)$$

where

- * X is the design matrix of the fixed effects
- * $\pi_i^M = \int \text{expit}(x_i^\top \beta^{SS} + z_i^\top b_i) p(b_i) db_i$ are the marginal probabilities derived from the mixed model and the subject-specific coefficients

5.2 Interpretation (cont'd)

- The marginal probabilities can be obtained using a Monte Carlo sampling procedure
 - ▷ for each row of the design matrix X , we generate a random sample of subjects with random effects values coming from the normal distribution $\mathcal{N}(0, \hat{D})$, where \hat{D} denotes the estimated covariance matrix of the random effects
 - ▷ for each of these simulated subjects we calculate the probability of $Y = 1$
 - ▷ we take as an estimate of the marginal probability the mean of the calculated probabilities of the simulated subjects

5.2 Interpretation (cont'd)

- **Example:** We continue on the previous example from the AIDS dataset (see pp.316) and we compute the corresponding marginal regression coefficients

Subject-specific					Marginal			
	Value	Std.Err.	z-value	p-value	Value	Std.Err.	z-value	p-value
β_0	5.080	0.362	14.028	< 0.001	1.560	0.136	11.492	< 0.001
β_1	0.136	0.041	3.329	0.001	0.046	0.015	3.165	0.002
β_2	-0.624	0.494	-1.262	0.207	-0.201	0.161	-1.252	0.210
β_3	-0.025	0.055	-0.459	0.646	-0.010	0.020	-0.475	0.635
σ_b	5.102							

5.2 Interpretation (cont'd)

- We observe considerable differences between the two sets of parameters
 - ▷ the subject-specific odds ratio for a unit increase over time for a specific ddC patients is 1.15 (95% CI: 1.06; 1.24),
 - ▷ whereas the corresponding marginal odds ratio averaged over all ddC patients equals 1.048 (95% CI: 1.018; 1.078)
 - ▷ note that the lower limit of the 95% CI for the subject-specific odds ratio almost equals the upper limit of the 95% CI for the marginal odds ratio
⇒ *the confidence intervals just overlap*

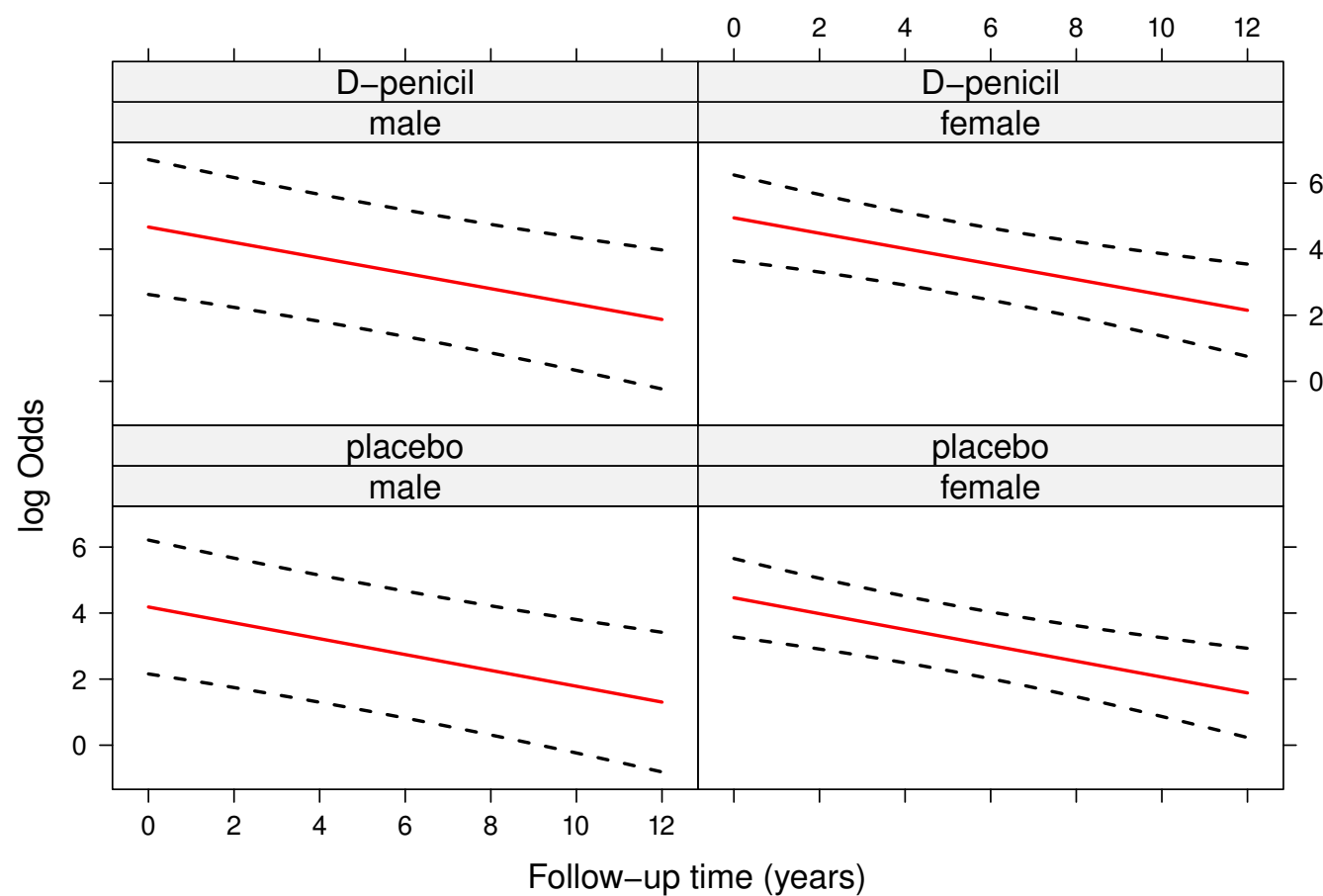
5.2 Interpretation (cont'd)

- As we have previously seen, effect plots can be used to effectively communicate complex models
 - ▷ especially in GLMMs, these plots also can be used to depict the marginal average evolutions (i.e., even if the fixed effects coefficients have a subject-specific interpretation, we can still calculate the marginal means)
- **Example:** In the PBC dataset we are interested in the probability of having excess serum cholesterol levels
 - ▷ we include the main effects of time, drug, age & sex
 - ▷ the interaction effect between time and drug, and the interaction effect between age and sex

5.2 Interpretation (cont'd)

- In the following figure we depict the log odds ratio as a function of time, separately for each combination of the randomized treatment and sex, for the average/median patient
 - ▷ average/median patient is the one with random effects values equal to zero

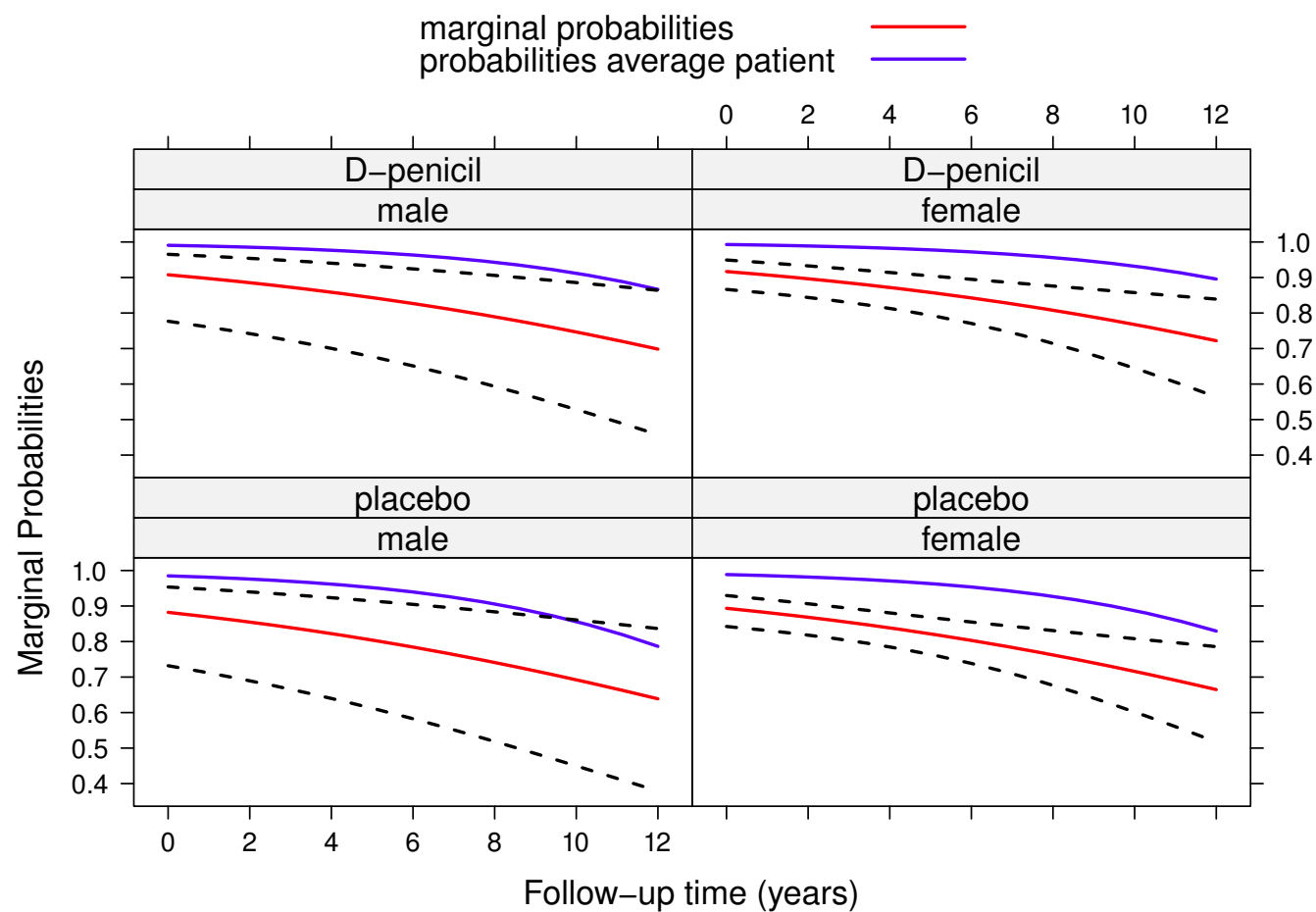
5.2 Interpretation (cont'd)



5.2 Interpretation (cont'd)

- In the following figure we depict the marginal probabilities, as a function for time, separately for each combination of randomized treatment and sex
 - ▷ contrary to the previous figure, these probabilities are averaged over the patients
 - ▷ they are obtained using the marginalized coefficients, presented in pp.336
 - ▷ to see the difference, the blue line corresponds to the probabilities of the average patient

5.2 Interpretation (cont'd)



5.2 Interpretation (cont'd)

- Calculation of 95% confidence intervals for the estimated marginal probabilities is based on an additional Monte Carlo scheme

5.3 Estimation

- The estimation of GLMMs is based on the same principles as in marginal and mixed models for continuous data
 - ▷ i.e., we have a full specification of the distribution of the data (contrary to GEE), and hence we can use *maximum likelihood*
- Nevertheless, there is an important complication in GLMMs

The fitting of GLMMs is a computationally challenging task!

5.3 Estimation (cont'd)

- Even though the nature of this problem is of rather computational/technical nature, we will need to discuss it in more detail ...
- What is the problem?
 - ▷ The log-likelihood expression for GLMMs has the same form as in linear mixed models (see pp.160)

$$\ell(\theta) = \sum_{i=1}^n \log \int p(y_i | b_i; \theta) p(b_i; \theta) db_i$$

where θ are the parameters of the model

5.3 Estimation (cont'd)

- In linear mixed effects models both terms in the integrand

- ▷ $p(y_i \mid b_i; \theta)$

- ▷ $p(b_i; \theta)$

are densities of (multivariate) normal distributions, and also because y_i and b_i are linearly related

In linear mixed effects models the integral in the log-likelihood expression **has a closed-form solution** (i.e., we can compute it on paper)

5.3 Estimation (cont'd)

- In GLMMs the two terms of the integrand denote densities of different distributions – e.g., in mixed effects logistic regression
 - ▷ $p(y_i | b_i; \theta) \Rightarrow$ Bernoulli distribution
 - ▷ $p(b_i; \theta) \Rightarrow$ multivariate normal distribution

The implication is that

In GLMMs the same integral does not have a closed-form solution

5.3 Estimation (cont'd)

- To overcome this problem two general types of solutions have been proposed in the literature
 - ▷ *Approximation of the integrand*: this entails approximating the product inside the integral (i.e., $\{p(y_i | b_i; \theta)p(y_i | b_i; \theta)\}$) by a multivariate normal distribution for which the integral has a closed-form solution
 - * Penalized Quasi Likelihood (PQL)
 - * Laplace approximation
 - ▷ *Approximation of the integral*: this entails approximating the whole integral (i.e., $\int p(y_i | b_i; \theta)p(y_i | b_i; \theta)db_i$) by a sum
 - * Gaussian Quadrature & adaptive Gaussian Quadrature
 - * Monte Carlo & MCMC (Bayesian approach)

5.3 Estimation (cont'd)

From the two alternatives, methods that rely on approximation of the integral have been shown to be superior

- Though they are (much) more computationally demanding – they have a parameter that controls the accuracy of the approximation:
 - ▷ in Gaussian quadrature rules it is the number of quadrature points (*adaptive Gaussian quadrature with 1 point is equivalent to the Laplace approximation*)
 - ▷ in Monte Carlo/MCMC approaches it is the number of samples

5.3 Estimation (cont'd)

- **Example:** We continue on the AIDS example, but we now treat the time variable as a factor (i.e., categorical) – the model has the form:

$$\log \frac{\pi_{ij}}{1 - \pi_{ij}} = \beta_0 + \beta_1 \{\text{Time}_{ij} = 2\} + \beta_2 \{\text{Time}_{ij} = 6\} + \beta_3 \{\text{Time}_{ij} = 12\} + \beta_4 \{\text{Time}_{ij} = 18\} + b_i$$

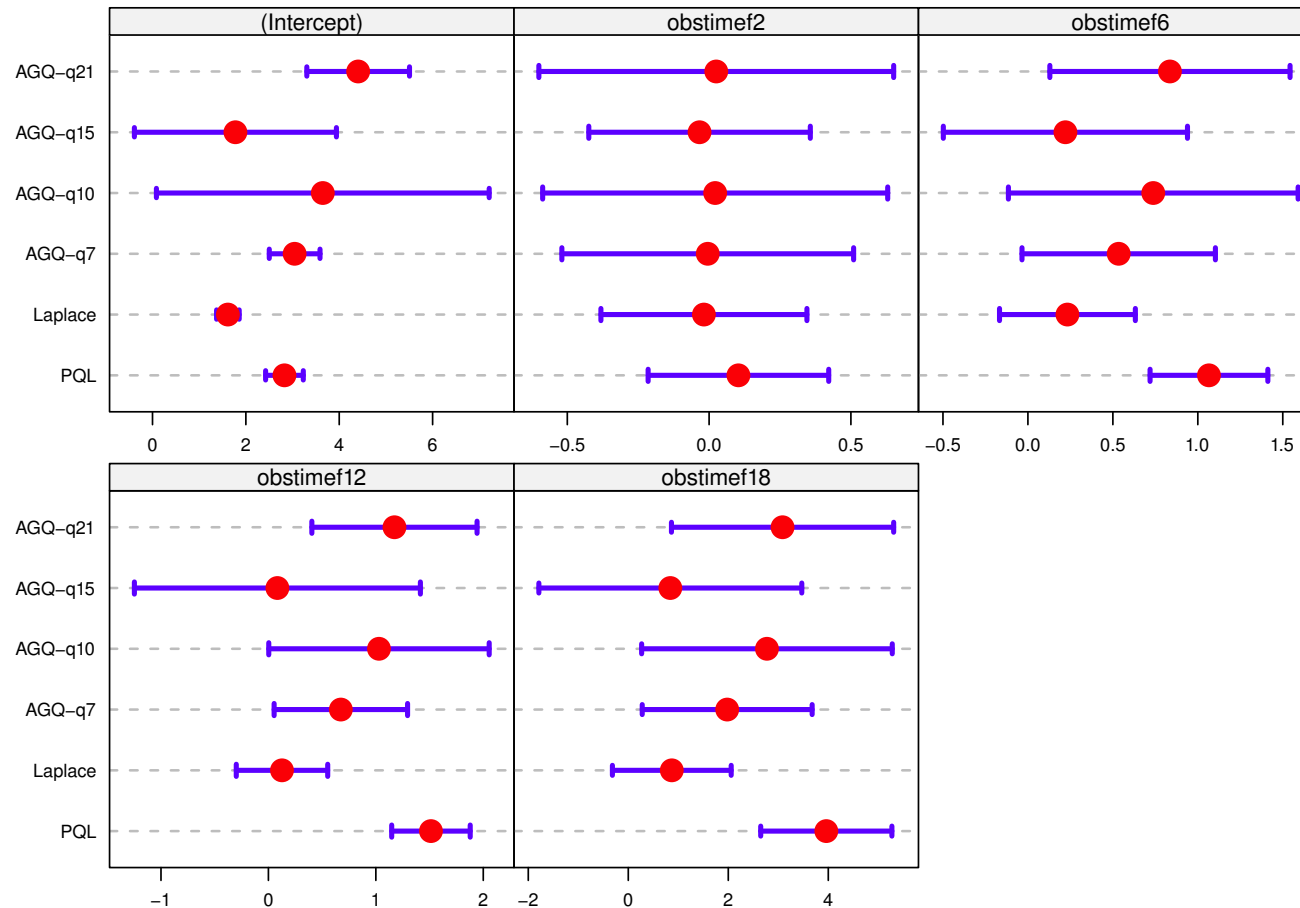
where

- ▷ $\pi_{ij} = \Pr(\text{CD4}_{ij} < 150)$
- ▷ $\{\text{Time}_{ij} = 2\}$ denotes the dummy variable for month 2, $\{\text{Time}_{ij} = 6\}$ the dummy variable for month 6, and so on

5.3 Estimation (cont'd)

- We have fitted this model using
 - ▷ PQL
 - ▷ Laplace approximation (adaptive Gaussian quadrature with 1 point)
 - ▷ adaptive Gaussian quadrature with 5, 10, 15 and 21 points
- The following figure depicts the estimated fixed effect coefficients under each approximation with corresponding 95% CIs

5.3 Estimation (cont'd)



5.3 Estimation (cont'd)

- We observe considerable differences between
 - ▷ PQL & Laplace (approximation of the integrand), and
 - ▷ adaptive Gaussian quadrature (approximation of the integral)
- In general, PQL and Laplace will work better as the data get more 'continuous', i.e.,
 - ▷ in Bernoulli data as the number of repeated measurements increases *considerably*
 - ▷ in Binomial data as the number of trials increases
 - ▷ in Poisson data as the rate increases

5.3 Estimation (cont'd)

- Estimation of the random effects proceeds in a similar manner as in linear mixed models (see pp.172–179)
 - ▷ 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 θ is replaced by its MLE $\hat{\theta}$

5.3 Estimation (cont'd)

- This is a whole distribution
 - ▷ to obtain estimates for the random effects we typically use measures of location from this posterior distribution (e.g., mean or mode)
 - ▷ as an estimate of the dispersion of the random effect we use the variance of the local curvature around the mode of the posterior distribution

- Contrary to linear mixed models in which this distribution has a closed-form, in GLMMs for categorical responses this is not the case
 - ▷ calculation of the above mentioned measures of location and dispersion is achieved using numerical algorithms

5.4 GLMMs in R

- R>** In R there are several packages to fit GLMMs – in this course we are going to see **lme4** and **GLMMadaptive**
- The function that fits GLMMs in **lme4** is `glmer()` – this has similar syntax as the `lmer()` function that fits linear mixed models, namely
 - ▷ `formula`: a formula specifying the response vector, the fixed- and random-effects structure
 - ▷ `data`: a data frame containing all the variables
 - ▷ `family`: a `family` object specifying the distribution of the outcome and the link function
 - ▷ `nAGQ`: the number of quadrature points

5.4 GLMMs in R (cont'd)

R> The following code fits a mixed effects logistic regression for abnormal serum cholesterol from the PBC dataset with random intercepts and 15 quadrature points for the adaptive Gauss-Hermite rule

```
glmmFit <- glmer(serCholD ~ year * drug + (1 | id),  
                 family = binomial(), data = pbc2, nAGQ = 15)  
  
summary(glmmFit)
```

5.4 GLMMs in R (cont'd)

- R>** The function that fits GLMMs in **GLMMadaptive** is `mixed_model()`; its basic arguments are
- ▷ `fixed`: a formula specifying the response vector, and the fixed-effects part of the model
 - ▷ `random`: a formula specifying the random-effects part
 - ▷ `data`: a data frame containing all the variables
 - ▷ `family`: a `family` object specifying the distribution of the outcome and the link function
 - ▷ `nAGQ`: the number of quadrature points

R> More info & examples available at:
<https://drizopoulos.github.io/GLMMadaptive/>

5.4 GLMMs in R (cont'd)

R> To fit the same model for the PBC data as we did above with `glmer()` the code is:

```
glmmFit <- mixed_model(fixed = serCholD ~ year * drug,  
  random = ~ 1 | id, family = binomial(), data = pbc2, nAGQ = 15)  
  
summary(glmmFit)
```

5.4 GLMMs in R (cont'd)

- Differences between `glmer()` (package **lme4**) and `mixed_model()` (package **GLMMadaptive**)
 - ▷ `glmer()` only provides the adaptive Gaussian quadrature rule for the random intercepts case, whereas `mixed_model()` uses this integration method with several random terms.
 - ▷ `mixed_model()` currently only handles a single grouping factor for the random effects, i.e., you cannot fit nested or crossed random effects, whereas such designs can be fitted with `glmer()`
 - ▷ `mixed_model()` can fit zero-inflated Poisson and negative binomial data, allowing for random effects in the zero part

5.5 Model Building

- Model building for GLMMs proceeds in the same manner as for linear mixed models, i.e.,
 - ▷ we start with an elaborate specification of the fixed-effects structure that contains all the variables we wish to study, and potential nonlinear and interactions terms
 - ▷ following we build-up the random-effects structure, starting from random intercepts, next including also random slopes, quadratic slopes, etc.
 - * in each step we perform likelihood ratio tests to see whether including the additional random effect improves the fit of the model
 - ▷ having chosen the random-effects structure, we return to the fixed effects and check whether the specification can be simplified
 - * again we first start by testing the complex terms (i.e., interactions and nonlinear terms), and then we continue to drop explanatory variables, if required

5.5 Model Building (cont'd)

- **Nevertheless**, quite often, and especially for dichotomous data, extending the random-effects structure may lead to numerical/computational problems
 - ▷ this is because dichotomous data contain the least amount of information
- Hence, for dichotomous data and when we have few to moderate number of repeated measurements per subject, we often can only fit random intercepts models

5.6 Hypothesis Testing

- Having fitted a GLMM with maximum likelihood, testing of either the fixed- or random-effects structure proceeds in a similar manner as in linear mixed models
- **Important difference:** in GLMMs we do not have REML we always work with full maximum likelihood
 - ▷ when we want to test the random-effects, the fixed-effects structure is also allowed to be different (though comparing nested models is a requirement for using the standard tests)

5.6 Hypothesis Testing (cont'd)

- **Example:** In the PBC dataset and for the dichotomous longitudinal outcome excess serum cholesterol levels (defined as before as above the threshold of 210 mg/dL), we fit a model that postulates
 - ▷ *fixed effects*:
 - * main effects of time, treatment, and sex
 - * interaction effects between time and treatment, and between drug and sex
 - ▷ *random effects*: random intercepts

We are interested in testing whether the model can be simplified by dropping the interaction terms

5.6 Hypothesis Testing (cont'd)

- The models under the two hypotheses are:

$$\left\{ \begin{array}{l} H_0 : \log \frac{\pi_{ij}}{1 - \pi_{ij}} = \beta_0 + \beta_1 \text{Time}_{ij} + \beta_2 \text{D-penicil}_i + \beta_3 \text{Female}_i + b_i \\ H_a : \log \frac{\pi_{ij}}{1 - \pi_{ij}} = \beta_0 + \beta_1 \text{Time}_{ij} + \beta_2 \text{D-penicil}_i + \beta_3 \text{Female}_i + \\ \quad \beta_4 \{ \text{Time}_{ij} \times \text{D-penicil}_i \} + \beta_5 \{ \text{Female}_i \times \text{D-penicil}_i \} + b_i \end{array} \right.$$

where $\pi_{ij} = \Pr(\text{serChol}_{ij} > 210)$

5.6 Hypothesis Testing (cont'd)

- With respect to coefficients:

$$\begin{cases} H_0 : \beta_4 = \beta_5 = 0 \\ H_a : \text{at least one different from 0} \end{cases}$$

	df	logLik	AIC	BIC	LRT	p-value
H_0		-353.59	717.17	735.76		
H_a	2	-353.33	720.66	720.66	0.51	0.7750

- The result suggests that the interaction terms do not seem to improve the fit of the model

5.6 Hypothesis Testing (cont'd)

- Similarly to previous chapters, when we want to test non-nested models we can use information criteria, i.e., the AIC or the BIC

5.7 Review of Key Points

- GLMMs are the analogue of linear mixed models for categorical data
 - ▷ we include random effects in the linear predictor to account for the correlations in the outcomes belonging to the same group/cluster

- Features of GLMMs
 - ▷ these models provide a complete specification of the distribution of the grouped/longitudinal outcome – contrary to GEE, which is a semi-parametric method
 - ▷ interpretation of parameters is conditional on the random effects – contrary to GEE, which provide coefficients with a marginal interpretation

5.7 Review of Key Points (cont'd)

- Features of GLMMs
 - ▷ estimation of GLMMs is more complex, and requires careful choice of numerical algorithms
 - ▷ **they provide valid inferences under MAR – contrary to GEE, which only provide valid inferences under MCAR**
- Model building and hypothesis testing works in the same way as in the previous models we have seen