

# BIOS 755: Linear Mixed Models II

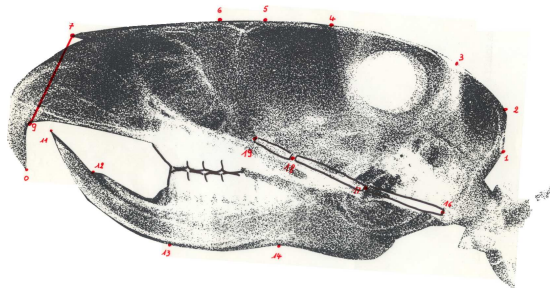
Alexander McLain

## Rat Data

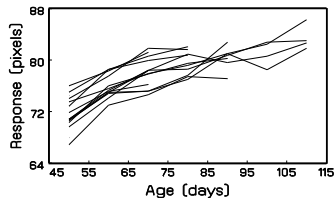
- ▶ Randomized experiment in which 50 male Wistar rats are randomized to:
  - ▶ Control (15 rats)
  - ▶ Low dose of Decapeptyl (18 rats)
  - ▶ High dose of Decapeptyl (17 rats) population.
- ▶ Question of interest: How does craniofacial growth depend on testosterone production?

## Rat Data

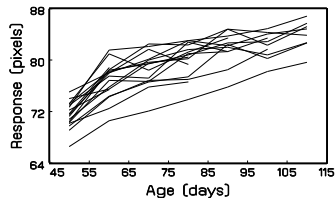
- ▶ Treatment starts at 45 days; measurements are taken every 10 days from day 50 on.
- ▶ The responses are distances (pixels) between well-defined points on x-ray pictures of the skull of each rat:



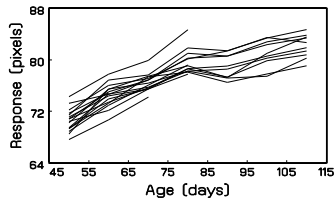
- ▶ We'll consider only one response: the height of the skull.
- ▶ Individual profiles: Control



Low dose



High dose



## Models under consideration

- Let's consider the model:

$$\begin{aligned} Y_{ij} &= (\beta_0 + b_{0i}) + (\beta_1 L_i + \beta_2 H_i + \beta_3 C_i + b_{1i})t_{ij} + \varepsilon_{ij} \\ &= \begin{cases} (\beta_0 + b_{0i}) + (\beta_1 + b_{1i})t_{ij} + \varepsilon_{ij}, & \text{if low dose} \\ (\beta_0 + b_{0i}) + (\beta_2 + b_{1i})t_{ij} + \varepsilon_{ij}, & \text{if high dose} \\ (\beta_0 + b_{0i}) + (\beta_3 + b_{1i})t_{ij} + \varepsilon_{ij}, & \text{if Control} \end{cases} \end{aligned}$$

Where the covariance of the random effects is

$$\mathbf{D} = \text{cov}(\mathbf{b}) = \begin{pmatrix} d_{11} & d_{12} \\ d_{12} & d_{22} \end{pmatrix}$$

## Linear Mixed representation

- ▶ What are the  $\mathbf{X}$  and  $\mathbf{Z}$  from the linear mixed model that corresponds to this model?
- ▶ What is the implied mean structure?
- ▶ What is the implied variance of  $Y_{ij}$ ?

## Linear Mixed representation

- What is the implied marginal Variance of  $Y_{ij}$ ?

$$\begin{aligned} \text{Var}(Y_{ij}) &= \begin{pmatrix} 1 & t_{ij} \end{pmatrix} \mathbf{D} \begin{pmatrix} 1 \\ t_{ij} \end{pmatrix} + \sigma^2 \\ &= (d_{11} + \sigma^2) + 2d_{12}t_{ij} + d_{22}t_{ij}^2 \end{aligned}$$

where

## Analysis

- ▶ The following model was fitted to the data

$$Y_{ij} = (\beta_0 + b_{1i}) + (\beta_1 L_i + \beta_2 H_i + \beta_3 C_i + b_{2i})t_{ij} + \varepsilon_{ij}$$

- ▶ The REML estimates obtained from PROC Mixed are:

Effect	Parameter	REMLE (s.e.)
Intercept	$\beta_0$	68.606 (0.325)
Time effects:		
Low dose	$\beta_1$	7.503 (0.228)
High dose	$\beta_2$	6.877 (0.231)
Control	$\beta_3$	7.319 (0.285)
Covariance of $b_i$ :		
var( $b_{1i}$ )	$d_{11}$	3.369 (1.123)
var( $b_{2i}$ )	$d_{22}$	0.000 ( — )
cov( $b_{1i}, b_{2i}$ )	$d_{12} = d_{21}$	0.090 (0.381)
Residual variance:		
var( $\varepsilon_{ij}$ )	$\sigma^2$	1.445 (0.145)
REML log-likelihood		-466.173



## Analysis

- ▶ This suggests that the REML likelihood could be further increased by allowing negative estimates for  $d_{22}$ .
- ▶ In SAS, this can be done by adding the option `nobound` to the PROC MIXED statement.

- ▶ Results:

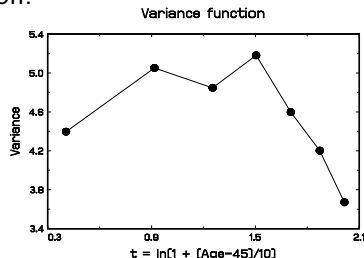
Effect	Parameter	Parameter restrictions for $\alpha$	
		$d_{ii} \geq 0, \sigma^2 \geq 0$	$d_{ii} \in \mathbb{R}, \sigma^2 \in \mathbb{R}$
		REMLE (s.e.)	REMLE (s.e.)
Intercept	$\beta_0$	68.606 (0.325)	68.618 (0.313)
Time effects:			
Low dose	$\beta_1$	7.503 (0.228)	7.475 (0.198)
High dose	$\beta_2$	6.877 (0.231)	6.890 (0.198)
Control	$\beta_3$	7.319 (0.285)	7.284 (0.254)
Covariance of $b_i$ :			
$\text{var}(b_{1i})$	$d_{11}$	3.369 (1.123)	2.921 (1.019)
$\text{var}(b_{2i})$	$d_{22}$	0.000 ( — )	-0.287 (0.169)
$\text{cov}(b_{1i}, b_{2i})$	$d_{12} = d_{21}$	0.090 (0.381)	0.462 (0.357)
Residual variance:			
$\text{var}(\varepsilon_{ij})$	$\sigma^2$	1.445 (0.145)	1.522 (0.165)
REML log-likelihood		-466.173	-465.193

## Meaning of a negative variance component

- Fitted variance function

$$\begin{aligned} \text{Var}(Y_{ij}) &= (\hat{d}_{11} + \hat{\sigma}^2) + 2\hat{d}_{12}t_{ij} + \hat{d}_{22}t_{ij}^2 \\ &= 4.443 + 0.924t - 0.287t_{ij}^2 \end{aligned}$$

- The suggested negative curvature in the variance function is supported by the sample variance function:



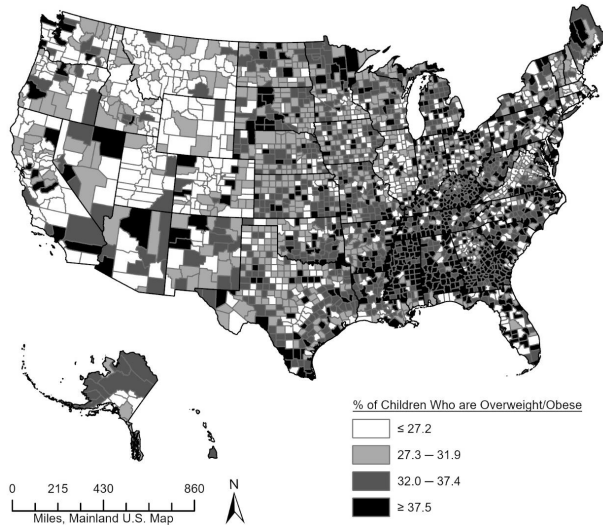
# INFERENCE FOR LINEAR MIXED MODELS

## Introduction

- ▶ In most applications, inference is focused on the fixed effects,  $\beta$ .
- ▶ However, in some studies we may want to predict (or “estimate”) subject-specific response profiles.
- ▶ Technically, because the  $\mathbf{b}_i$ ’s are random, we customarily talk of “predicting” the random effects rather than “estimating” them.
- ▶ The predicted random effects can be used to predict values for all levels in the data.

## Example: County level disease rates/summaries.

- ▶ The National Study of Children's Health (NSCH) gathers data from roughly 50K 2–17 year-old children at each survey.
- ▶ The NSCH variables include indicators of ADHD, ASD, and many other conditions.
- ▶ It also includes BMI percentile, and other continuous variables.
- ▶ A regression model with a random county level intercept was fitted.
- ▶ To predict (estimate) county level values, we needed to predict the value of the random effect.



## Conditional Expectation

- ▶ For a RE ANOVA model on  $Y_{i1}, Y_{i2}, \dots, Y_{in_i}$  we have

$$Y_{ij} = \mu + b_i + e_{ij}$$

with  $b_i \sim N(0, G)$  and  $e_i \sim N(0, \sigma^2)$ .

- ▶ Under this model, the predicted value of the random intercept is

$$E(b_i | Y_i) = \frac{n_i G}{n_i G + \sigma^2} (\bar{Y}_i - \mu)$$

where  $\text{Var}(b_i) = G$

## Best Linear Unbiased Predictor (BLUP)

- ▶ When  $\Sigma_i$  is known, the estimator for  $\beta$  can be obtained by using ML weighted least square. Then the prediction of  $\mathbf{b}_i$  is given by

$$\mathbf{G}\mathbf{Z}_i'\Sigma_i^{-1}(\mathbf{Y}_i - \mathbf{X}_i\hat{\beta}),$$

where

$$\Sigma_i = \text{var}(\mathbf{Y}_i) = \mathbf{Z}_i\mathbf{G}\mathbf{Z}_i' + \mathbf{R}_i$$

- ▶ This is known as the Best Linear Unbiased Predictor (or BLUP).



## Empirical BLUP

- ▶ In more general cases we use the Best Linear Unbiased Predictor (or BLUP) to predict the random effects.
- ▶ The formula for this is

$$\hat{\mathbf{b}}_i = \hat{\mathbf{G}} \mathbf{Z}_i' \hat{\Sigma}_i^{-1} (\mathbf{Y}_i - \mathbf{X}_i \hat{\boldsymbol{\beta}}),$$

is often referred to as the “Empirical BLUP” or the “Empirical Bayes” (EB) estimator.

- ▶ Furthermore, it can be shown that

$$\text{var}(\hat{\mathbf{b}}_i) = \mathbf{G} \mathbf{Z}_i' \Sigma_i^{-1} \mathbf{Z}_i \mathbf{G} - \mathbf{G} \mathbf{Z}_i' \Sigma_i^{-1} \mathbf{X}_i \left( \sum_{i=1}^n \mathbf{X}_i' \Sigma_i^{-1} \mathbf{X}_i \right)^{-1} \mathbf{X}_i' \Sigma_i^{-1} \mathbf{Z}_i \mathbf{G}$$

## The BLUP Estimation of Individual Mean

- Finally, the  $i$ th subject's predicted response profile is,

$$\begin{aligned}\hat{\mathbf{Y}}_i &= \mathbf{X}_i\hat{\boldsymbol{\beta}} + \mathbf{Z}_i\hat{\mathbf{b}}_i \\ &= \mathbf{X}_i\hat{\boldsymbol{\beta}} + \mathbf{Z}_i\hat{\mathbf{G}}\mathbf{Z}_i'\hat{\boldsymbol{\Sigma}}_i^{-1}(\mathbf{Y}_i - \mathbf{X}_i\hat{\boldsymbol{\beta}}) \\ &= \left(\hat{\mathbf{R}}\hat{\boldsymbol{\Sigma}}^{-1}\right)\mathbf{X}_i\hat{\boldsymbol{\beta}} + \left(\mathbf{I} - \hat{\mathbf{R}}\hat{\boldsymbol{\Sigma}}_i^{-1}\right)\mathbf{Y}_i\end{aligned}$$

- That is, the  $i$ th subject's predicted response profile is a weighted combination of the population-averaged mean response profile,  $\mathbf{X}_i\hat{\boldsymbol{\beta}}$ , and the  $i$ th subject's observed response profile  $\mathbf{Y}_i$ .

## BLUP As a Weighted Average

- ▶ When the between-subject variability is greater than the within-subject variability, more weight is given to the  $i$ th subject's observed data  $\mathbf{Y}_i$ .
- ▶ One formulation of the predicted values can be written as

$$\hat{\mathbf{Y}}_i = W_i \mathbf{X}_i \hat{\beta}_i^{OLS} + (1 - W_i) \mathbf{X}_i \hat{\beta}$$

where

$$W_i = \frac{n_i D_{11}}{n_i D_{11} + \sigma^2}$$

## Example: Country level rates of malnutrition.

- ▶ Ending malnutrition is a key outcome in the Sustainable Development Goal (SDG)
- ▶ The 2nd SDG calls for achieving, by 2025, a reduction of stunting and wasting and halt the rise in overweight in children under 5 years of age.
- ▶ Monitoring countries' progress toward the achievement of their SDG targets is an important task, but data sparsity makes monitoring trends challenging.
- ▶ The model fitted for this analysis was

$$Y_{ijk} = \beta' \mathbf{X}_{ijk} + \mathbf{b}'_i \mathbf{B}_{ij} + \mathbf{b}'_{ij} \mathbf{B}_{ijk} + \epsilon_{ij}, \quad (1)$$

