1 Basic Models Fits

Further to Pinheiro and Bates (1994), several simple LME models are constructed for the blood pressure data. This data set is the subject of a method comparison study in Bland and Altman (1999).

1.1 Implementing the Mixed Models Fits

They are implemented using the following R code, utilising the 'nlme' package. An analysis of variance is used to compare the model fits.

The R script:

```
fit1 = lme( BP ~ method, data = dat, random = ~1 | subject )
fit2 = update(fit1, random = ~1 | subject/method )
fit3 = update(fit1, random = ~method - 1 | subject )
#analysis of variance
anova(fit1,fit2,fit3)
```

1. Simplest workable model, allows differences between methods and incorporates a random intercept for each subject. For subject 1 we have

$$m{X}_i = \left(egin{array}{ccc} 1 & 0 \ 1 & 0 \ 1 & 1 \ 1 & 1 \ 1 & 1 \end{array}
ight), \quad m{eta} = \left(egin{array}{c} eta_0 \ eta_1 \end{array}
ight), \quad m{Z}_i = \left(egin{array}{c} 1 \ 1 \ 1 \ 1 \ 1 \ 1 \end{array}
ight), \quad m{b}_i = b$$

where E(b) = 0 and $var(b) = \psi$.

2.

$$m{Z}_i = \left(egin{array}{ccc} 1 & 0 \ 1 & 0 \ 1 & 0 \ 0 & 1 \ 0 & 1 \ 0 & 1 \end{array}
ight) & m{b}_i = \left(egin{array}{ccc} b_1 & 0 \ 0 & b_2 \end{array}
ight)$$

where $E(b_i) = 0$ and $var(\boldsymbol{b}) = \boldsymbol{\Psi}$.

The variance of error terms is a 6×6 matrix.

1.2 Model Fit 1

This is a simple model with no interactions. There is a fixed effect for each method and a random effect for each subject.

$$y_{ijk} = \beta_j + b_i + \epsilon_{ijk}, \quad i = 1, \dots, 2, j = 1, \dots, 85, k = 1, \dots, 3$$

$$b_i \sim \mathcal{N}(0, \sigma_b^2), \qquad \epsilon_i \sim \mathcal{N}(0, \sigma^2)$$

Linear mixed-effects model fit by REML

Data: dat

Log-restricted-likelihood: -2155.853

Fixed: BP ~ method

(Intercept) methodS 127.40784 15.61961

Random effects:

Formula: ~1 | subject (Intercept) Residual

StdDev: 29.39085 12.44454

Number of Observations: 510

Number of Groups: 85

1.3 Model Fit 2

This is a simple model, this time with an interaction effect. There is a fixed effect for each method. This model has random effects at two levels b_i for the subject, and another, b_{ij} , for the respective method within each subject.

$$y_{ijk} = \beta_j + b_i + b_{ij} + \epsilon_{ijk}, \qquad i = 1, \dots, 2, j = 1, \dots, 85, k = 1, \dots, 3$$

$$b_i \sim \mathcal{N}(0, \sigma_1^2), \qquad b_{ij} \sim \mathcal{N}(0, \sigma_2^2), \qquad \epsilon_i \sim \mathcal{N}(0, \sigma^2)$$

In this model, the random interaction terms all have the same variance σ_2^2 . These terms are assumed to be independent of each other, even within the same subject.

Linear mixed-effects model fit by REML

Data: dat

Log-restricted-likelihood: -2047.714

Fixed: BP ~ method

(Intercept) methodS

127.40784 15.61961

Random effects:

Formula: ~1 | subject

(Intercept)

StdDev: 28.28452

Formula: ~1 | method %in% subject

(Intercept) Residual

StdDev: 12.61562 7.763666

Number of Observations: 510

Number of Groups:

subject method %in% subject

85 170

1.4 Model Fit 3

This model is a more general model, compared to 'model fit 2'. This model treats the random interactions for each subject as a vector and allows the variance-covariance matrix for that vector to be estimated from the set of all positive-definite matrices. y_i is the entire response vector for the *i*th subject. X_i and Z_i are the fixed- and random-effects design matrices respectively.

$$y_i = X_i \beta + Z_i b_i + \epsilon_i, \qquad i = 1, \dots, 85$$

$$oldsymbol{Z_i} \sim \mathcal{N}(oldsymbol{0}, oldsymbol{\Psi}), \qquad oldsymbol{\epsilon_i} \sim \mathcal{N}(oldsymbol{0}, oldsymbol{\sigma^2}oldsymbol{\Lambda})$$

For the first subject the response vector, y_1 , is:

observation	BP	subject	method	replicate
1	100.00	1	J	1
86	106.00	1	J	2
171	107.00	1	J	3
511	122.00	1	S	1
596	128.00	1	S	2
681	124.00	1	S	3

The fixed effects design matrix $\boldsymbol{X_i}$ is given by:

(Intercept)	method S
1	0
1	0
1	0
1	1
1	1
1	1

The random effects design matrix $\boldsymbol{Z_i}$ is given by:

method J	method S
1	0
1	0
1	0
0	1
0	1
0	1

The following output was obtained.

Linear mixed-effects model fit by REML

Data: dat

Log-restricted-likelihood: -2047.582

Fixed: BP ~ method

(Intercept) methodS 127.40784 15.61961

Random effects:

Formula: ~method - 1 | subject

Structure: General positive-definite, Log-Cholesky parametrization

StdDev Corr

methodJ 30.455093 methdJ methodS 31.477237 0.835

Residual 7.763666

Number of Observations: 510

Number of Groups: 85

1.5 Extended LME model

The extended single level LME model relaxes the independence assumption, allowing heteroscedastic and correlated within group errors.

$$\epsilon_i = \mathcal{N}(0, \sigma^2 \Lambda_i) \tag{1}$$

 Λ_i are positive definite matrices. σ^2 is factored out of the matrix for computational reasons.

2 Variance functions

Variance functions are applied to LME models through the 'weights' argument. R supports several variance functions.

'varIdent' cosntructs a model with different variances per stratum.

2.1 Diagnostic plots

Diagnostic plots for identifying within-group heteroscedascity and assessing the adequacy of a variance function can also be used with 'nlme' objects.

References

Bland, J. and D. Altman (1999). Measuring agreement in method comparison studies. Statistical Methods in Medical Research 8(2), 135–160.

Pinheiro, J. and D. Bates (1994). *Mixed Effects Models in S and S plus* (2nd ed.). Reading, Massachusetts: Springer.