A Handbook of Statistical Analyses Using R

Brian S. Everitt and Torsten Hothorn

CHAPTER 10

Analysing Longitudinal Data I: Computerised Delivery of Cognitive Behavioural Therapy–Beat the Blues

10.1 Introduction

10.2 Analysing Longitudinal Data

10.3 Analysis Using R

We shall fit both random intercept and random intercept and slope models to the data including the baseline BDI values (`pre.bdi`), `treatment` group, `drug` and `length` as fixed effect covariates. Linear mixed effects models are fitted in R by using the `lmer` function contained in the *lme4* package (Bates and Sarkar, 2006, Pinheiro and Bates, 2000, Bates, 2005), but an essential first step is to rearrange the data from the 'wide form' in which they appear in the `BtheB` data frame into the 'long form' in which each separate repeated measurement and associated covariate values appear as a separate row in a *data.frame*. This rearrangement can be made using the following code:

```
R> data("BtheB", package = "HSAUR")
R> BtheB$subject <- factor(rownames(BtheB))
R> nobs <- nrow(BtheB)
R> BtheB_long <- reshape(BtheB, idvar = "subject",
+      varying = c("bdi.2m", "bdi.4m", "bdi.6m", "bdi.8m"),
+      direction = "long")
R> BtheB_long$time <- rep(c(2, 4, 6, 8), rep(nobs, 4))
```

such that the data are now in the form (here shown for the first three subjects)

```
R> subset(BtheB_long, subject %in% c("1", "2", "3"))
```

	drug	length	treatment	bdi.pre	subject	time	bdi
1.2m	No	>6m	TAU	29	1	2	2
2.2m	Yes	>6m	BtheB	32	2	2	16
3.2m	Yes	<6m	TAU	25	3	2	20
1.4m	No	>6m	TAU	29	1	4	2
2.4m	Yes	>6m	BtheB	32	2	4	24
3.4m	Yes	<6m	TAU	25	3	4	NA
1.6m	No	>6m	TAU	29	1	6	NA
2.6m	Yes	>6m	BtheB	32	2	6	17
3.6m	Yes	<6m	TAU	25	3	6	NA
1.8m	No	>6m	TAU	29	1	8	NA

```
R> data("BtheB", package = "HSAUR")
R> layout(matrix(1:2, nrow = 1))
R> ylim <- range(BtheB[,grep("bdi", names(BtheB))],
+                na.rm = TRUE)
R> tau <- subset(BtheB, treatment == "TAU")[,
+      grep("bdi", names(BtheB))]
R> boxplot(tau, main = "Treated as usual", ylab = "BDI",
+          xlab = "Time (in months)", names = c(0, 2, 4, 6, 8),
+          ylim = ylim)
R> btheb <- subset(BtheB, treatment == "BtheB")[,
+      grep("bdi", names(BtheB))]
R> boxplot(btheb, main = "Beat the Blues", ylab = "BDI",
+          xlab = "Time (in months)", names = c(0, 2, 4, 6, 8),
+          ylim = ylim)
```

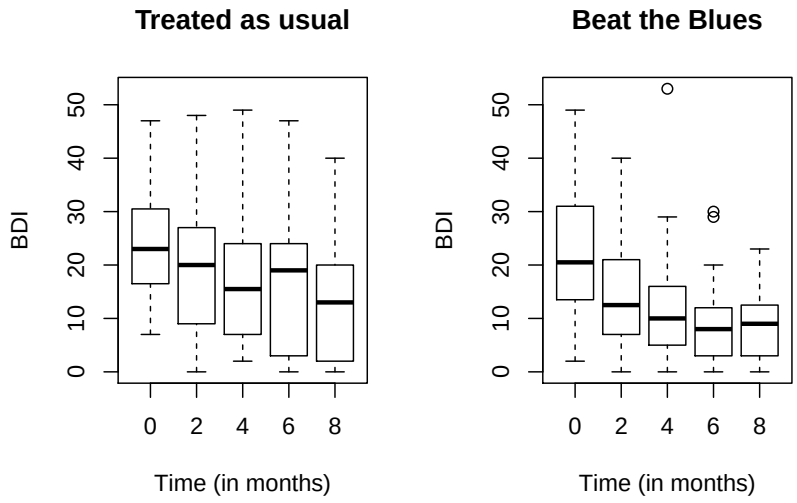

Figure 10.1 Boxplots for the repeated measures by treatment group for the `BtheB` data.

```
2.8m  Yes    >6m     BtheB      32       2    8  20
3.8m  Yes    <6m       TAU      25       3    8  NA
```

The resulting *data.frame* `BtheB_long` contains a number of missing values and in applying the `lmer` function these will be dropped. But notice it is only the missing values that are removed, *not* participants that have at least one missing value. All the available data is used in the model fitting process. The `lmer` function is used in a similar way to the `lm` function met in Chapter **??** with the addition of a random term to identify the source of the repeated

measurements, here `subject`. We can fit the two models (??) and (??) and test which is most appropriate using

```
R> library("lme4")
R> BtheB_lmer1 <- lmer(bdi ~ bdi.pre + time + treatment + drug +
+      length + (1 | subject), data = BtheB_long,
+      method = "ML", na.action = na.omit)
R> BtheB_lmer2 <- lmer(bdi ~ bdi.pre + time + treatment + drug +
+      length + (time | subject), data = BtheB_long,
+      method = "ML", na.action = na.omit)
R> anova(BtheB_lmer1, BtheB_lmer2)
```

```
Data: BtheB_long
Models:
BtheB_lmer1: bdi ~ bdi.pre + time + treatment + drug + length + (1 | subject)
BtheB_lmer2: bdi ~ bdi.pre + time + treatment + drug + length + (time | subject)
            Df    AIC    BIC  logLik deviance  Chisq Chi Df
BtheB_lmer1  8 1886.6 1915.7 -935.31   1870.6
BtheB_lmer2 10 1889.8 1926.2 -934.90   1869.8 0.8161      2
            Pr(>Chisq)
BtheB_lmer1
BtheB_lmer2      0.665
```

```
R> summary(BtheB_lmer1)

Linear mixed model fit by REML ['lmerMod']
Formula:
bdi ~ bdi.pre + time + treatment + drug + length + (1 | subject)
   Data: BtheB_long

REML criterion at convergence: 1866.1

Scaled residuals:
    Min      1Q  Median      3Q     Max
-2.7501 -0.4755 -0.0934  0.4001  3.7377

Random effects:
 Groups   Name        Variance Std.Dev.
 subject  (Intercept) 51.44    7.172
 Residual             25.27    5.027
Number of obs: 280, groups:  subject, 97

Fixed effects:
              Estimate Std. Error t value
(Intercept)    5.92148    2.30586   2.568
bdi.pre        0.63888    0.07961   8.025
time          -0.71353    0.14664  -4.866
treatmentBtheB -2.35900    1.70841  -1.381
drugYes       -2.78885    1.76594  -1.579
length>6m      0.23810    1.67537   0.142

Correlation of Fixed Effects:
            (Intr) bdi.pr time   trtmBB drugYs
bdi.pre     -0.679
time        -0.258  0.023
tretmntBthB -0.389  0.121  0.022
drugYes     -0.072 -0.236 -0.025 -0.323
length>6m   -0.239 -0.241 -0.042  0.002  0.158
```

Figure 10.2 R output of the linear mixed-effects model fit for the `BtheB` data.

Bibliography

Bates, D. (2005), "Fitting linear mixed models in R," *R News*, 5, 27–30, URL http://CRAN.R-project.org/doc/Rnews/.

Bates, D. and Sarkar, D. (2006), *lme4: Linear Mixed-Effects Models Using S4 Classes*, URL http://CRAN.R-project.org, R package version 0.99875-8.

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