

**A Handbook of Statistical Analyses  
Using R**

---

Brian S. Everitt and Torsten Hothorn



# 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"))
```

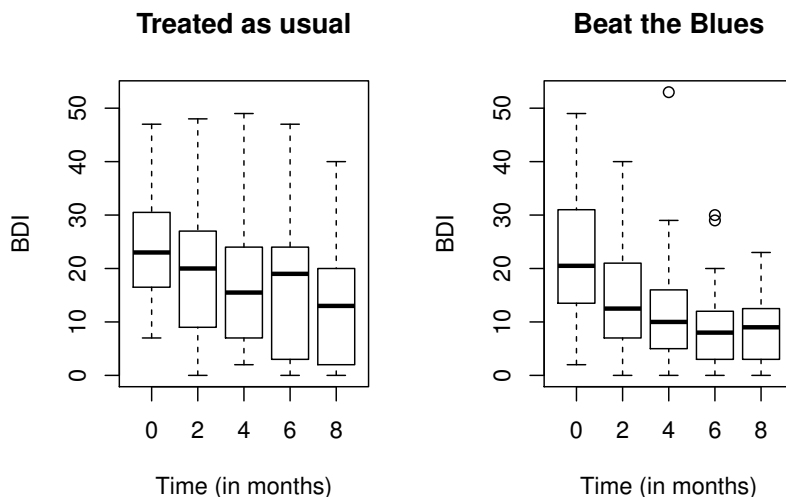
|      | <i>drug</i> | <i>length</i> | <i>treatment</i> | <i>bdi.pre</i> | <i>subject</i> | <i>time</i> | <i>bdi</i> |
|------|-------------|---------------|------------------|----------------|----------------|-------------|------------|
| 1.2m | No          | >6m           | TAU              | 29             | 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         |
| 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

```

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.

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,
+   REML = FALSE, na.action = na.omit)
R> BtheB_lmer2 <- lmer(bdi ~ bdi.pre + time + treatment + drug +
+   length + (time | subject), data = BtheB_long,
+   REML = FALSE, 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 maximum likelihood ['lmerMod']
Formula:
bdi ~ bdi.pre + time + treatment + drug + length + (1 | subject)
Data: BtheB_long
```

|  | AIC    | BIC    | logLik | deviance | df.resid |
|--|--------|--------|--------|----------|----------|
|  | 1886.6 | 1915.7 | -935.3 | 1870.6   | 272      |

```
Scaled residuals:
      Min       1Q   Median       3Q      Max
-2.7608 -0.4809 -0.0957  0.4022  3.7431
```

```
Random effects:
Groups   Name             Variance Std.Dev.
subject (Intercept)  48.30    6.950
Residual                25.13    5.013
Number of obs: 280, groups: subject, 97
```

```
Fixed effects:
              Estimate Std. Error t value
(Intercept)   5.94366    2.24922   2.643
bdi.pre        0.63819    0.07759   8.225
time          -0.71702    0.14606  -4.909
treatmentBtheB -2.37308    1.66375  -1.426
drugYes       -2.79784    1.72000  -1.627
length>6m     0.25635    1.63219   0.157
```

```
Correlation of Fixed Effects:
      (Intr) bdi.pr time  trtmBB drugYs
bdi.pre   -0.678
time      -0.264  0.023
trtmntBtheB -0.389  0.121  0.022
drugYes   -0.071 -0.237 -0.025 -0.323
length>6m -0.238 -0.242 -0.043  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 Eigen and S4*, 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.