

**A Handbook of Statistical Analyses  
Using R — 2nd Edition**

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

## 12.1 Introduction

## 12.2 Analysing Longitudinal Data

## 12.3 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, 2012, 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:

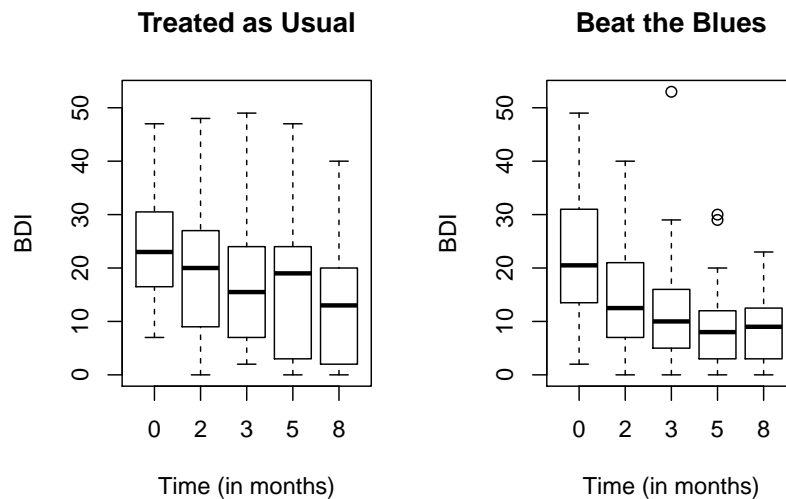
```
R> data("BtheB", package = "HSAUR2")
R> BtheB$subject <- factor(rownames(BtheB))
R> nobs <- nrow(BtheB)
R> BtheB_long <- reshape(BtheB, idvar = "subject",
+   varying = c("bdi.2m", "bdi.3m", "bdi.5m", "bdi.8m"),
+   direction = "long")
R> BtheB_long$time <- rep(c(2, 3, 5, 8), rep(nobs, 4))
such that 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
1.3m	No	>6m	TAU	29	1	3	2
2.3m	Yes	>6m	BtheB	32	2	3	24
3.3m	Yes	<6m	TAU	25	3	3	NA
1.5m	No	>6m	TAU	29	1	5	NA
2.5m	Yes	>6m	BtheB	32	2	5	17
3.5m	Yes	<6m	TAU	25	3	5	NA
1.8m	No	>6m	TAU	29	1	8	NA

```

R> data("BtheB", package = "HSAUR2")
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, 3, 5, 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, 3, 5, 8),
+          ylim = ylim)

```



**Figure 12.1** Boxplots for the repeated measures by treatment group for the `BtheB` data.

2.8m	Yes	>6m	<i>BtheB</i>	32	2	8	20
3.8m	Yes	<6m	<i>TAU</i>	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 6 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   Chisq Chi Df Pr(>Chisq)
BtheB_lmer1  8 1887.5 1916.6 -935.75
BtheB_lmer2 10 1891.0 1927.4 -935.52  0.4542    2    0.7969
```

The `summary` method for *lmer* objects doesn't print *p*-values for Gaussian mixed models because the degrees of freedom of the *t* reference distribution are not obvious. However, one can rely on the asymptotic normal distribution for computing univariate *p*-values for the fixed effects using the `cfstest` function from package **multcomp**. The asymptotic *p*-values are given in Figure~12.3.

We can check the assumptions of the final model fitted to the **BtheB** data, i.e., the normality of the random effect terms and the residuals, by first using the `ranef` method to *predict* the former and the `residuals` method to calculate the differences between the observed data values and the fitted values, and then using normal probability plots on each. How the random effects are predicted is explained briefly in Section~???. The necessary R code to obtain the effects, residuals and plots is shown with Figure~12.4. There appear to be no large departures from linearity in either plot.

---

```
R> summary(BtheB_lmer1)
```

*Linear mixed model fit by maximum likelihood*  
*Formula: bdi ~ bdi.pre + time + treatment + drug + length + (1 | subject)*  
*Data: BtheB\_long*

AIC	BIC	logLik	deviance	REMLdev
1887	1917	-935.7	1871	1867

Random effects:

Groups	Name	Variance	Std.Dev.
subject	(Intercept)	48.777	6.9841
Residual		25.140	5.0140

Number of obs: 280, groups: subject, 97

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	5.59244	2.24232	2.494
bdi.pre	0.63967	0.07789	8.213
time	-0.70477	0.14639	-4.814
treatmentBtheB	-2.32912	1.67026	-1.394
drugYes	-2.82497	1.72674	-1.636
length>6m	0.19712	1.63823	0.120

Correlation of Fixed Effects:

	(Intr)	bdi.pr	time	trtmBB	drugYs
bdi.pre	-0.682				
time	-0.238	0.020			
tretmntBthB	-0.390	0.121	0.018		
drugYes	-0.073	-0.237	-0.022	-0.323	
length>6m	-0.243	-0.242	-0.036	0.002	0.157

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**Figure 12.2** R output of the linear mixed-effects model fit for the **BtheB** data.

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```
R> cftest(BtheB_lmer1)
```

```
Simultaneous Tests for General Linear Hypotheses
```

```
Fit: lmer(formula = bdi ~ bdi.pre + time + treatment + drug + length +
(1 | subject), data = BtheB_long, REML = FALSE, na.action = na.omit)
```

```
Linear Hypotheses:
```

	Estimate	Std. Error	z value	Pr(> z )
(Intercept) == 0	5.59244	2.24232	2.494	0.0126
bdi.pre == 0	0.63967	0.07789	8.213	2.22e-16
time == 0	-0.70477	0.14639	-4.814	1.48e-06
treatmentBtheB == 0	-2.32912	1.67026	-1.394	0.1632
drugYes == 0	-2.82497	1.72674	-1.636	0.1018
length>6m == 0	0.19712	1.63823	0.120	0.9042

(Univariate p values reported)

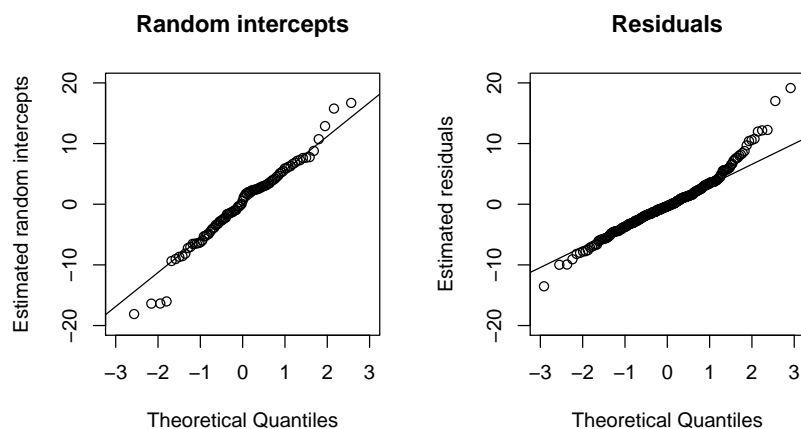
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**Figure 12.3** R output of the asymptotic  $p$ -values for linear mixed-effects model fit for the **BtheB** data.

```

R> layout(matrix(1:2, ncol = 2))
R> qint <- ranef(BtheB_lmer1)$subject[["(Intercept)"]]
R> qres <- residuals(BtheB_lmer1)
R> qqnorm(qint, ylab = "Estimated random intercepts",
+        xlim = c(-3, 3), ylim = c(-20, 20),
+        main = "Random intercepts")
R> qqline(qint)
R> qqnorm(qres, xlim = c(-3, 3), ylim = c(-20, 20),
+        ylab = "Estimated residuals",
+        main = "Residuals")
R> qqline(qres)

```



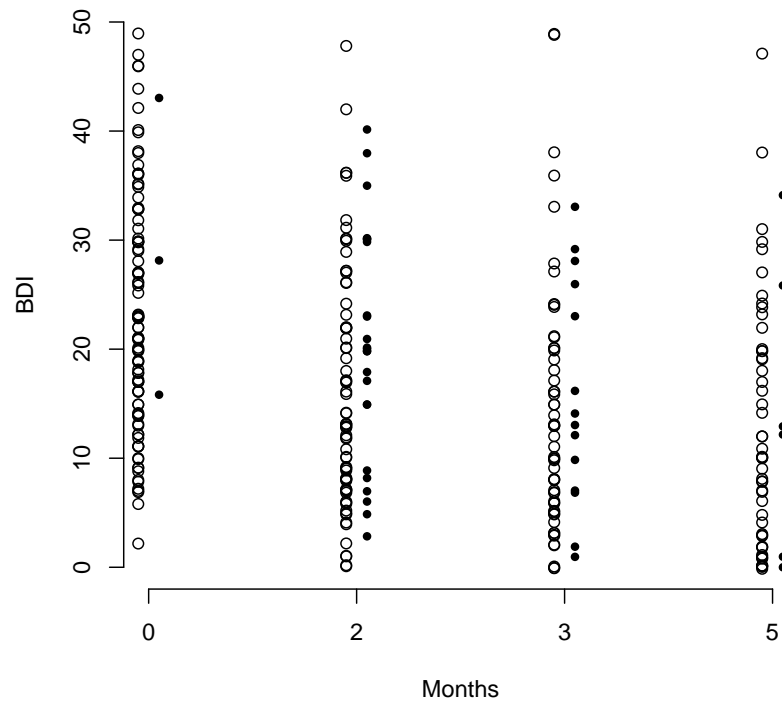
**Figure 12.4** Quantile-quantile plots of predicted random intercepts and residuals for the random intercept model `BtheB_lmer1` fitted to the `BtheB` data.



```

R> bdi <- BtheB[, grep("bdi", names(BtheB))]
R> plot(1:4, rep(-0.5, 4), type = "n", axes = FALSE,
+       ylim = c(0, 50), xlab = "Months", ylab = "BDI")
R> axis(1, at = 1:4, labels = c(0, 2, 3, 5))
R> axis(2)
R> for (i in 1:4) {
+   dropout <- is.na(bdi[,i + 1])
+   points(rep(i, nrow(bdi)) + ifelse(dropout, 0.05, -0.05),
+          jitter(bdi[,i]), pch = ifelse(dropout, 20, 1))
+ }

```



**Figure 12.5** Distribution of BDI values for patients that do (circles) and do not (bullets) attend the next scheduled visit.



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## Bibliography

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- 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. (2012), ***lme4**: Linear Mixed-Effects Models Using *S4* Classes*, URL <http://CRAN.R-project.org/package=lme4>, R package version 0.999375-42.
- Pinheiro, J.~C. and Bates, D.~M. (2000), *Mixed-Effects Models in S and S-PLUS*, New York, USA: Springer-Verlag.