

Multivariate Analysis for the Behavioral Sciences,
Second Edition (Chapman and Hall/CRC, 2019)

Examples of Chapter 9:
Analysis of Longitudinal Data II: Linear
Mixed Effects Models for Normal Response
Variables

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Examples

Table 9.1: Body Weights of Rats Recorded Over a 9-Week Period

```
library(tidyr); library(dplyr); library(ggplot2)

##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##   filter, lag
## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union
RATS <- read.table("data/rats.txt", header = TRUE, sep = '\t')

RATS <- within(RATS, {
  ID <- factor(ID)
  Group <- factor(Group)
})

glimpse(RATS)

## Observations: 16
## Variables: 13
## $ ID      <fct> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16
## $ Group   <fct> 1, 1, 1, 1, 1, 1, 1, 1, 2, 2, 2, 2, 3, 3, 3, 3
## $ WD1     <int> 240, 225, 245, 260, 255, 260, 275, 245, 410, 405, 445, 5...
## $ WD8     <int> 250, 230, 250, 255, 260, 265, 275, 255, 415, 420, 445, 5...
## $ WD15    <int> 255, 230, 250, 255, 255, 270, 260, 260, 425, 430, 450, 5...
## $ WD22    <int> 260, 232, 255, 265, 270, 275, 270, 268, 428, 440, 452, 5...
## $ WD29    <int> 262, 240, 262, 265, 270, 275, 273, 270, 438, 448, 455, 5...
## $ WD36    <int> 258, 240, 265, 268, 273, 277, 274, 265, 443, 460, 455, 5...
## $ WD43    <int> 266, 243, 267, 270, 274, 278, 276, 265, 442, 458, 451, 5...
## $ WD44    <int> 266, 244, 267, 272, 273, 278, 271, 267, 446, 464, 450, 5...
## $ WD50    <int> 265, 238, 264, 274, 276, 284, 282, 273, 456, 475, 462, 6...
## $ WD57    <int> 272, 247, 268, 273, 278, 279, 281, 274, 468, 484, 466, 6...
## $ WD64    <int> 278, 245, 269, 275, 280, 281, 284, 278, 478, 496, 472, 6...
```

Table 9.2

```
RATSL <- gather(RATS, key = WD, value = Weight, -ID, -Group) %>%
  mutate(Time = as.integer(substr(WD,3,4)))

glimpse(RATSL)

## Observations: 176
## Variables: 5
## $ ID      <fct> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, ...
## $ Group   <fct> 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 2, 2, 2, 3, 3, 3, 3, 1, 1, 1...
## $ WD      <chr> "WD1", "WD1", "WD1", "WD1", "WD1", "WD1", "WD1", "WD1", "...
## $ Weight  <int> 240, 225, 245, 260, 255, 260, 275, 245, 410, 405, 445, ...
## $ Time    <int> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 8, 8, 8...

head(RATSL); tail(RATSL)

##   ID Group  WD Weight Time
## 1  1     1 WD1    240    1
## 2  2     1 WD1    225    1
## 3  3     1 WD1    245    1
## 4  4     1 WD1    260    1
## 5  5     1 WD1    255    1
## 6  6     1 WD1    260    1

##   ID Group  WD Weight Time
## 171 11     2 WD64    472   64
## 172 12     2 WD64    628   64
## 173 13     3 WD64    525   64
## 174 14     3 WD64    559   64
## 175 15     3 WD64    548   64
## 176 16     3 WD64    569   64
```

Figure 9.1

```
p1 <- ggplot(RATSL, aes(x = Time, y = Weight, group = ID))
p2 <- p1 + geom_text(aes(label = Group))
p3 <- p2 + scale_x_continuous(name = "Time (days)", breaks = seq(0, 60, 10))
p4 <- p3 + scale_y_continuous(name = "Weight (grams)")
p5 <- p4 + theme_bw()
p6 <- p5 + theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank())
p6
```

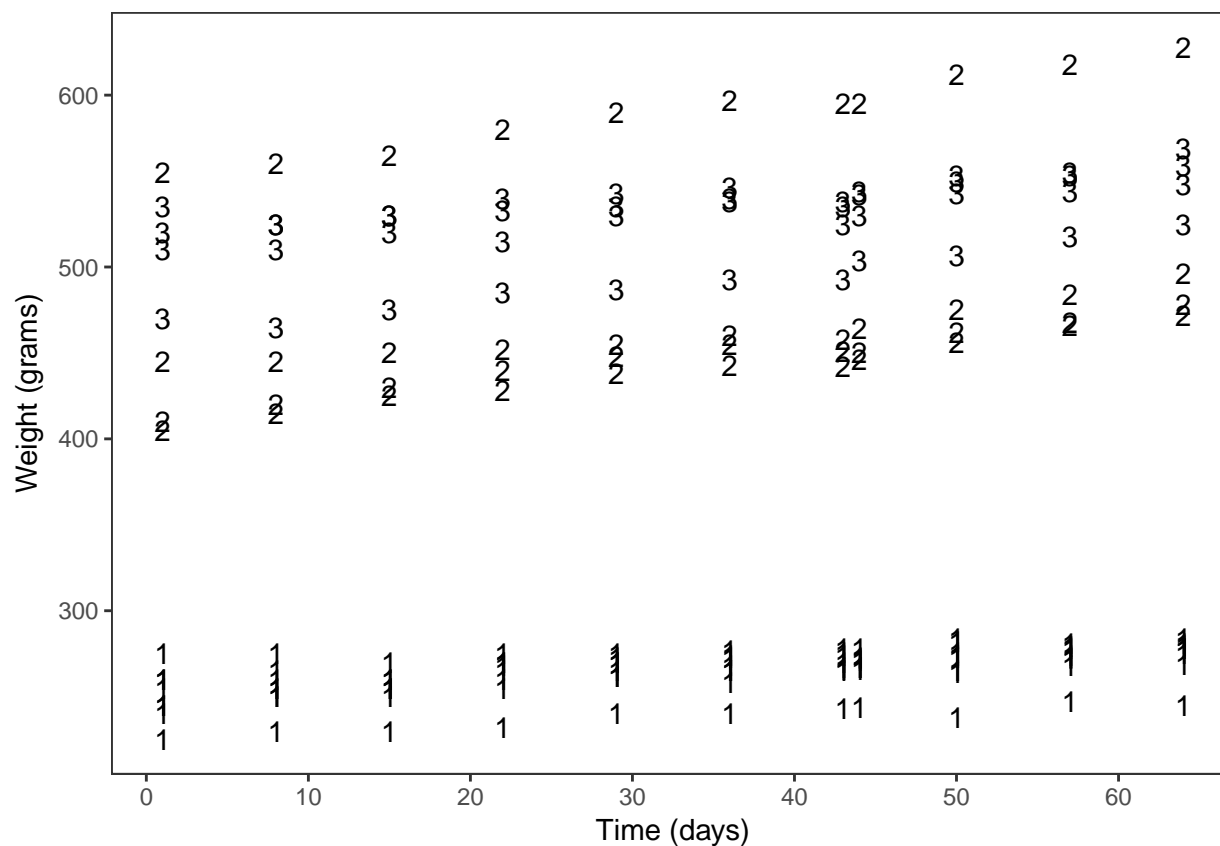


Table 9.3

```
RATS_reg <- lm(Weight ~ Time + Group, data = RATSL)
summary(RATS_reg)

##
## Call:
## lm(formula = Weight ~ Time + Group, data = RATSL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -60.643 -24.017   0.697  10.837 125.459
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  244.0689     5.7725  42.281 < 2e-16 ***
## Time          0.5857     0.1331   4.402 1.88e-05 ***
## Group2       220.9886     6.3402  34.855 < 2e-16 ***
## Group3       262.0795     6.3402  41.336 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 34.34 on 172 degrees of freedom
## Multiple R-squared:  0.9283, Adjusted R-squared:  0.9271
## F-statistic: 742.6 on 3 and 172 DF,  p-value: < 2.2e-16
# dummies (in Table) vs summary output: D1 = Group2, D2 = Group3
```

Figure 9.2

```
p1 <- ggplot(RATSL, aes(x = Time, y = Weight, group = ID))
p2 <- p1 + geom_line(aes(linetype = Group))
p3 <- p2 + scale_x_continuous(name = "Time (days)", breaks = seq(0, 60, 10))
p4 <- p3 + scale_y_continuous(name = "Weight (grams)")
p5 <- p4 + theme_bw() + theme(legend.position = "top")
p6 <- p5 + theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank())
p6
```

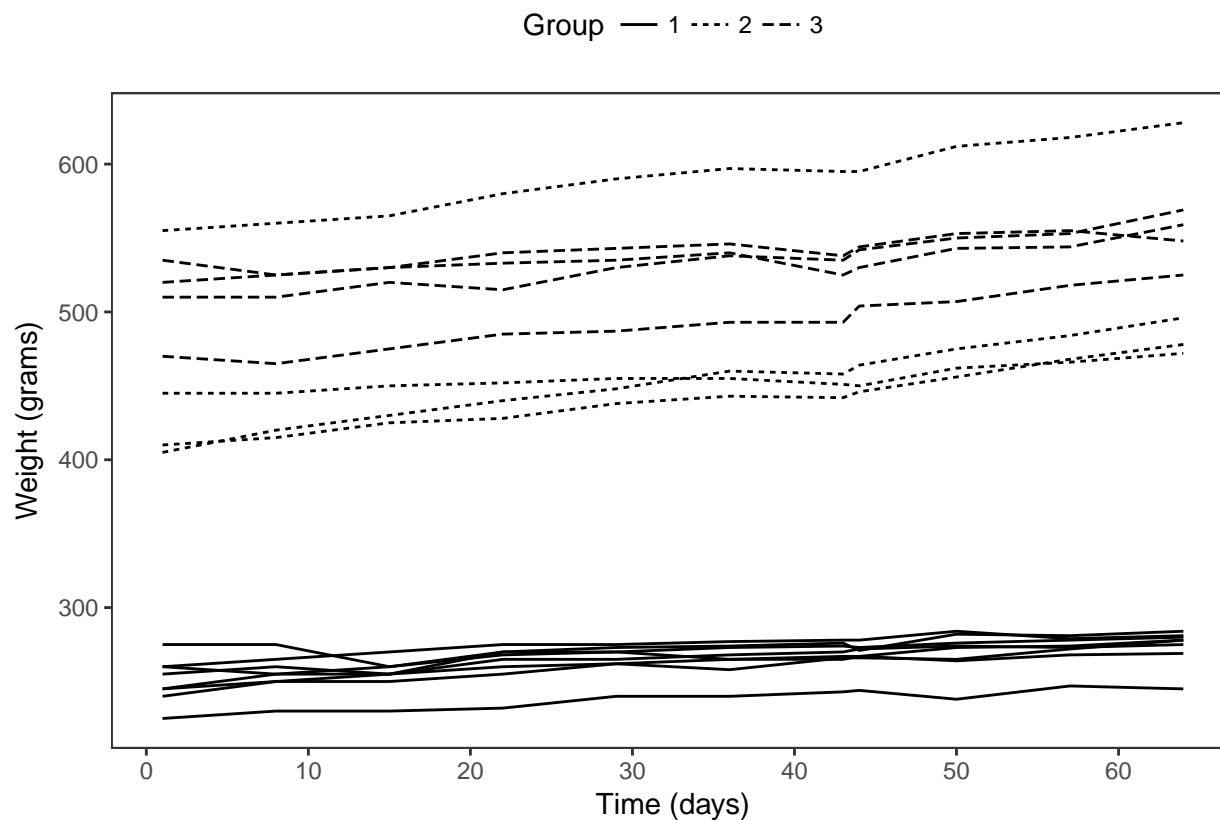


Figure 9.3

```
pairs(RATS[, 3:13], cex = 0.7)
```

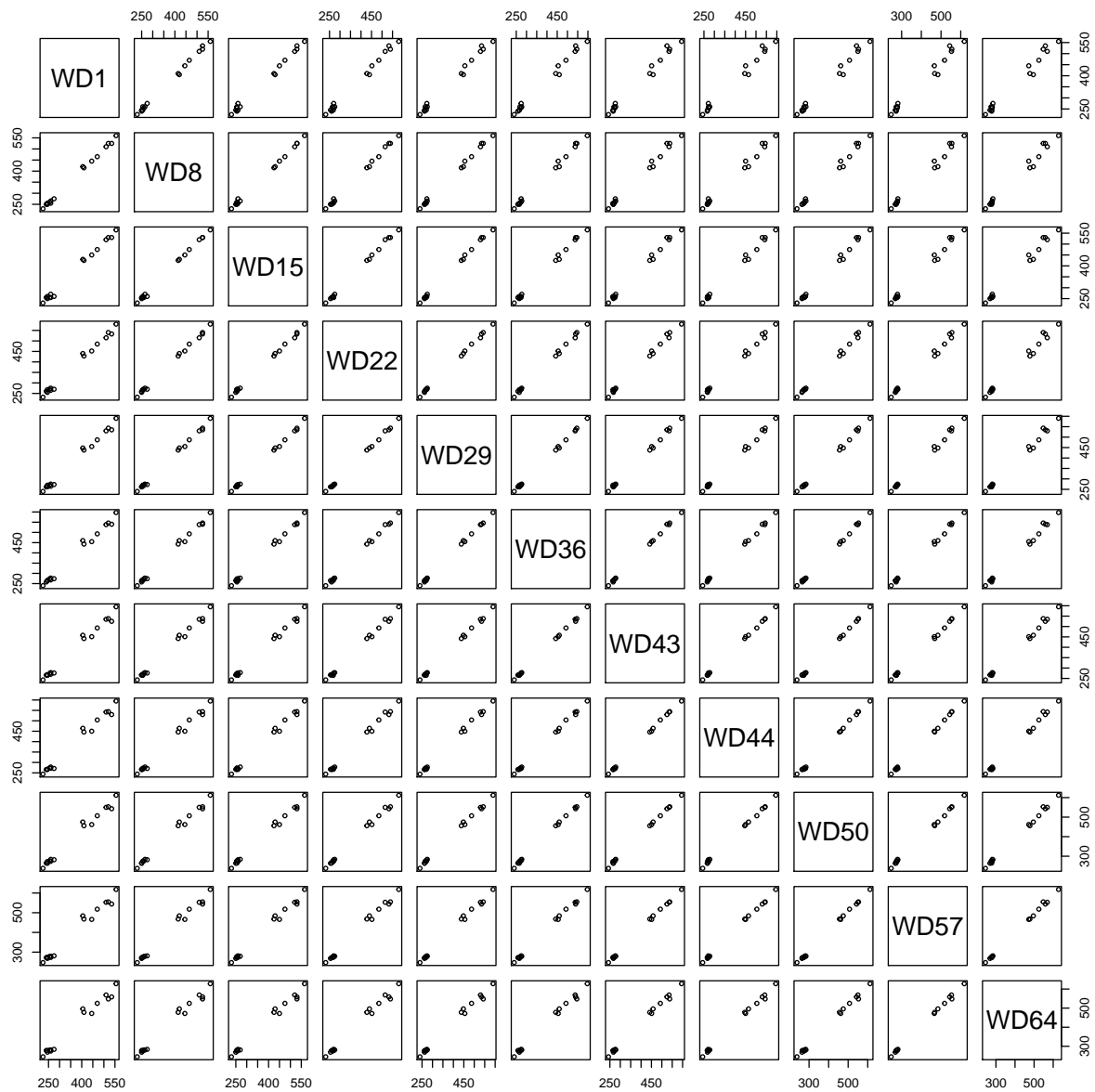


Table 9.4

```
library("lme4")

## Loading required package: Matrix
##
## Attaching package: 'Matrix'
## The following object is masked from 'package:tidyr':
##
##     expand
RATS_ref <- lmer(Weight ~ Time + Group + (1 | ID), data = RATSL, REML = FALSE)
summary(RATS_ref)

## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: Weight ~ Time + Group + (1 | ID)
## Data: RATSL
##
##      AIC      BIC   logLik deviance df.resid
## 1333.2   1352.2   -660.6   1321.2     170
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.5386 -0.5581 -0.0494  0.5693  3.0990
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## ID      (Intercept)  1085.92   32.953
## Residual                    66.44    8.151
## Number of obs: 176, groups: ID, 16
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept) 244.06890   11.73107   20.80
## Time         0.58568    0.03158   18.54
## Group2      220.98864   20.23577   10.92
## Group3      262.07955   20.23577   12.95
##
## Correlation of Fixed Effects:
##      (Intr) Time   Group2
## Time   -0.090
## Group2 -0.575  0.000
## Group3 -0.575  0.000  0.333

# dummies (in Table) vs summary output: D1 = Group2, D2 = Group3
```


Table 9.5

```
RATS_ref1 <- lmer(Weight ~ Time + Group + (Time | ID), data = RATSL, REML = FALSE)
summary(RATS_ref1)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
```

```
## Formula: Weight ~ Time + Group + (Time | ID)
```

```
## Data: RATSL
```

```
##
```

```
##      AIC      BIC   logLik deviance df.resid
```

```
##  1194.2   1219.6   -589.1   1178.2     168
```

```
##
```

```
## Scaled residuals:
```

```
##      Min       1Q   Median       3Q      Max
```

```
## -3.2261 -0.4322  0.0555  0.5638  2.8827
```

```
##
```

```
## Random effects:
```

```
## Groups   Name                Variance Std.Dev. Corr
```

```
## ID      (Intercept) 1140.5363 33.7718
```

```
##          Time          0.1122  0.3349  -0.22
```

```
## Residual          19.7456  4.4436
```

```
## Number of obs: 176, groups: ID, 16
```

```
##
```

```
## Fixed effects:
```

```
##              Estimate Std. Error t value
```

```
## (Intercept) 246.45727   11.81526  20.859
```

```
## Time          0.58568    0.08548   6.852
```

```
## Group2       214.58736   20.17983  10.634
```

```
## Group3       258.92732   20.17983  12.831
```

```
##
```

```
## Correlation of Fixed Effects:
```

```
##      (Intr) Time   Group2
```

```
## Time   -0.166
```

```
## Group2 -0.569  0.000
```

```
## Group3 -0.569  0.000  0.333
```

```
# dummies (in Table) vs summary output: D1 = Group2, D2 = Group3
```

```
anova(RATS_ref1, RATS_ref)
```

```
## Data: RATSL
```

```
## Models:
```

```
## RATS_ref: Weight ~ Time + Group + (1 | ID)
```

```
## RATS_ref1: Weight ~ Time + Group + (Time | ID)
```

```
##      Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
```

```
## RATS_ref  6 1333.2 1352.2 -660.58   1321.2
```

```
## RATS_ref1  8 1194.2 1219.6 -589.11   1178.2 142.94      2 < 2.2e-16 ***
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Table 9.6

```
RATS_ref2 <- lmer(Weight ~ Time * Group + (Time | ID), data = RATSL, REML = FALSE)
summary(RATS_ref2)
```

```
## Linear mixed model fit by maximum likelihood ['lmerMod']
```

```
## Formula: Weight ~ Time * Group + (Time | ID)
```

```
## Data: RATSL
```

```
##
```

```
##      AIC      BIC    logLik deviance df.resid
```

```
##  1185.9   1217.6   -582.9   1165.9     166
```

```
##
```

```
## Scaled residuals:
```

```
##      Min       1Q   Median       3Q      Max
```

```
## -3.2669 -0.4249  0.0726  0.6034  2.7513
```

```
##
```

```
## Random effects:
```

```
## Groups   Name                Variance Std.Dev. Corr
```

```
## ID       (Intercept) 1.107e+03 33.2763
```

```
##          Time         4.925e-02 0.2219  -0.15
```

```
## Residual                1.975e+01 4.4436
```

```
## Number of obs: 176, groups: ID, 16
```

```
##
```

```
## Fixed effects:
```

```
##              Estimate Std. Error t value
```

```
## (Intercept) 251.65165   11.80279  21.321
```

```
## Time         0.35964    0.08215   4.378
```

```
## Group2       200.66549   20.44303   9.816
```

```
## Group3       252.07168   20.44303  12.330
```

```
## Time:Group2   0.60584    0.14229   4.258
```

```
## Time:Group3   0.29834    0.14229   2.097
```

```
##
```

```
## Correlation of Fixed Effects:
```

```
##              (Intr) Time   Group2 Group3 Tm:Gr2
```

```
## Time         -0.160
```

```
## Group2       -0.577  0.092
```

```
## Group3       -0.577  0.092  0.333
```

```
## Time:Group2   0.092 -0.577 -0.160 -0.053
```

```
## Time:Group3   0.092 -0.577 -0.053 -0.160  0.333
```

```
# dummies (in Table) vs summary output: D1 = Group2, D2 = Group3
```

```
anova(RATS_ref1, RATS_ref2)
```

```
## Data: RATSL
```

```
## Models:
```

```
## RATS_ref1: Weight ~ Time + Group + (Time | ID)
```

```
## RATS_ref2: Weight ~ Time * Group + (Time | ID)
```

```
##      Df      AIC      BIC    logLik deviance  Chisq Chi Df Pr(>Chisq)
```

```
## RATS_ref1  8 1194.2 1219.6 -589.11   1178.2
```

```
## RATS_ref2 10 1185.9 1217.6 -582.93   1165.9 12.361      2  0.00207 **
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Figure 9.4

```
Fitted <- fitted(RATS_ref2)
RATSL <- RATSL %>% mutate(Fitted)

p1 <- ggplot(RATSL, aes(x = Time, y = Weight, group = ID))
p2 <- p1 + geom_line(aes(linetype = Group))
p3 <- p2 + scale_x_continuous(name = "Time (days)", breaks = seq(0, 60, 20))
p4 <- p3 + scale_y_continuous(name = "Weight (grams)")
p5 <- p4 + theme_bw() + theme(legend.position = "right") # "none" in the book
p6 <- p5 + theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank())
p7 <- p6 + ggtitle("Observed")
graph1 <- p7

p1 <- ggplot(RATSL, aes(x = Time, y = Fitted, group = ID))
p2 <- p1 + geom_line(aes(linetype = Group))
p3 <- p2 + scale_x_continuous(name = "Time (days)", breaks = seq(0, 60, 20))
p4 <- p3 + scale_y_continuous(name = "Weight (grams)")
p5 <- p4 + theme_bw() + theme(legend.position = "right")
p6 <- p5 + theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank())
p7 <- p6 + ggtitle("Fitted")
graph2 <- p7

graph1; graph2
```

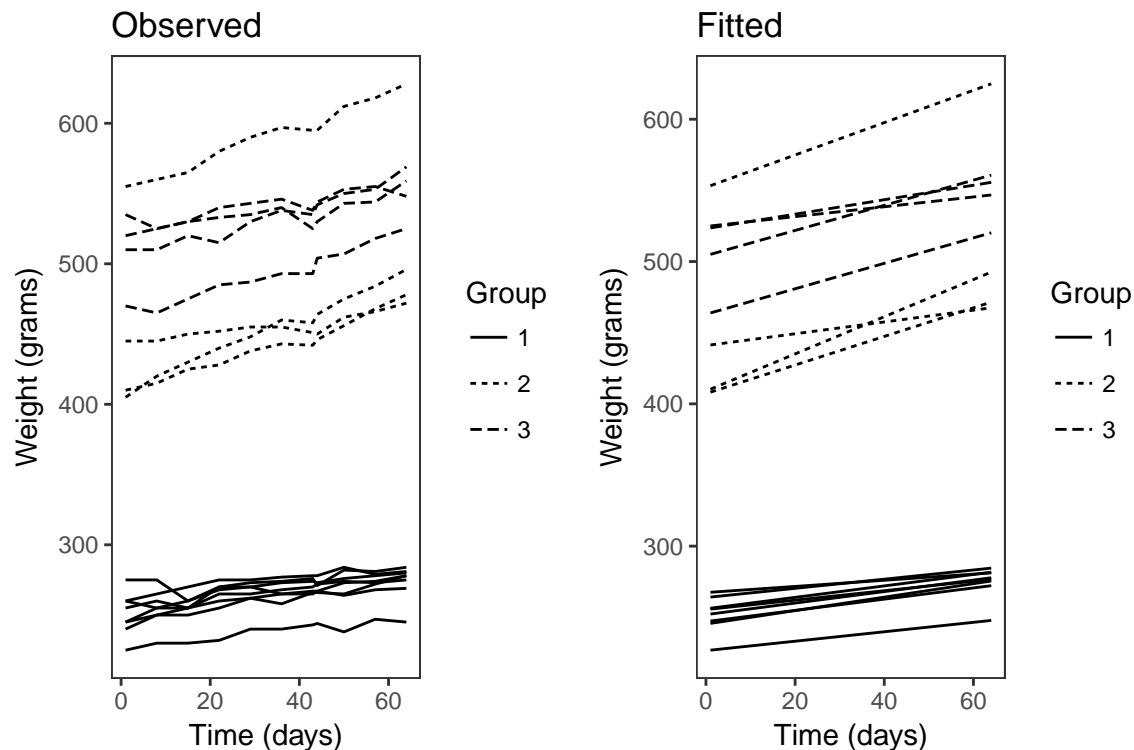


Table 9.7: Patients in Each Treatment Group of the “Beat the Blues” (BtB) Clinical Trial of CBT for Depression

```
library(tidyr); library(dplyr); library(ggplot2)

BtB <- read.table("data/BtB.txt", header = TRUE, sep = '\t')

# to make sure that the factor levels are logical (esp. Treatment):
BtB <- within(BtB, {
  Drug <- factor(Drug, levels=c("No", "Yes")) # default
  Length <- factor(Length, levels=c("<6m", ">6m")) # default
  Treatment <- factor(Treatment, levels=c("TAU", "BtheB")) # NOT default!
})

glimpse(BtB); head(BtB); tail(BtB)
```

```
## Observations: 100
## Variables: 9
## $ Subject    <int> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 1...
## $ Drug       <fct> No, Yes, Yes, No, Yes, Yes, Yes, No, Yes, Yes, No, Y...
## $ Length     <fct> >6m, >6m, <6m, >6m, >6m, <6m, <6m, >6m, <6m, >6m, >6...
## $ Treatment  <fct> TAU, BtheB, TAU, BtheB, BtheB, BtheB, TAU, TAU, Bthe...
## $ BDIpre     <int> 29, 32, 25, 21, 26, 7, 17, 20, 18, 20, 30, 49, 26, 3...
## $ BDI2m      <int> 2, 16, 20, 17, 23, 0, 7, 20, 13, 5, 32, 35, 27, 26, ...
## $ BDI4m      <int> 2, 24, NA, 16, NA, 0, 7, 21, 14, 5, 24, NA, 23, 36, ...
## $ BDI6m      <int> NA, 17, NA, 10, NA, 0, 3, 19, 20, 8, 12, NA, NA, 27,...
## $ BDI8m      <int> NA, 20, NA, 9, NA, 0, 7, 13, 11, 12, 2, NA, NA, 22, ...

##   Subject Drug Length Treatment BDIpre BDI2m BDI4m BDI6m BDI8m
## 1      1   No   >6m      TAU      29      2      2    NA    NA
## 2      2  Yes   >6m    BtheB      32     16     24     17     20
## 3      3  Yes   <6m      TAU      25     20     NA     NA     NA
## 4      4   No   >6m    BtheB      21     17     16     10      9
## 5      5  Yes   >6m    BtheB      26     23     NA     NA     NA
## 6      6  Yes   <6m    BtheB       7      0      0      0      0

##   Subject Drug Length Treatment BDIpre BDI2m BDI4m BDI6m BDI8m
## 95      95   No   >6m    BtheB      16     11      4      2      3
## 96      96  Yes   >6m    BtheB      16     16     10     10      8
## 97      97  Yes   <6m      TAU      28     NA     NA     NA     NA
## 98      98   No   >6m    BtheB      11     22      9     11     11
## 99      99   No   <6m      TAU      13      5      5      0      6
## 100     100  Yes   <6m      TAU      43     NA     NA     NA     NA
```

Figure 9.5

```
# Convert data to long form, including the baseline BDI measurement:
BtBL0 <- gather(BtB, key = Visit, value = BDI, BDIpre, BDI2m, BDI4m, BDI6m, BDI8m)

glimpse(BtBL0); head(BtBL0); tail(BtBL0)

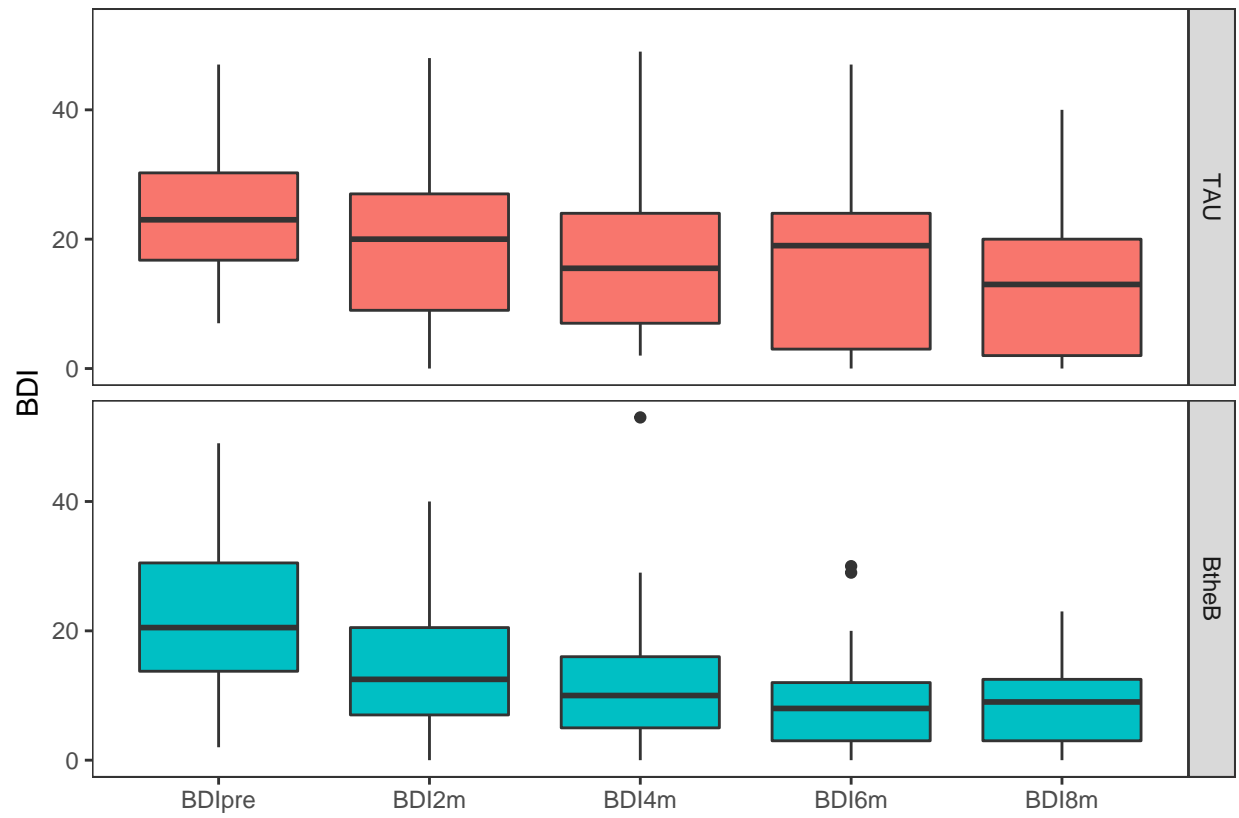
## Observations: 500
## Variables: 6
## $ Subject    <int> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 1...
## $ Drug       <fct> No, Yes, Yes, No, Yes, Yes, Yes, No, Yes, Yes, No, Y...
## $ Length     <fct> >6m, >6m, <6m, >6m, >6m, <6m, <6m, >6m, <6m, >6m, >6...
## $ Treatment  <fct> TAU, BtheB, TAU, BtheB, BtheB, BtheB, TAU, TAU, Bthe...
## $ Visit      <chr> "BDIpre", "BDIpre", "BDIpre", "BDIpre", "BDIpre", "B...
## $ BDI        <int> 29, 32, 25, 21, 26, 7, 17, 20, 18, 20, 30, 49, 26, 3...

##   Subject Drug Length Treatment Visit BDI
## 1         1   No    >6m      TAU BDIpre 29
## 2         2  Yes    >6m    BtheB BDIpre 32
## 3         3  Yes    <6m      TAU BDIpre 25
## 4         4   No    >6m    BtheB BDIpre 21
## 5         5  Yes    >6m    BtheB BDIpre 26
## 6         6  Yes    <6m    BtheB BDIpre 7

##   Subject Drug Length Treatment Visit BDI
## 495       95   No    >6m    BtheB BDI8m 3
## 496       96  Yes    >6m    BtheB BDI8m 8
## 497       97  Yes    <6m      TAU BDI8m NA
## 498       98   No    >6m    BtheB BDI8m 11
## 499       99   No    <6m      TAU BDI8m 6
## 500      100  Yes    <6m      TAU BDI8m NA

p1 <- ggplot(BtBL0, aes(x = factor(Visit), y = BDI, fill = Treatment))
p2 <- p1 + geom_boxplot()
p3 <- p2 + facet_grid(Treatment ~ ., labeller = label_parsed)
p4 <- p3 + theme_bw() + theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank())
p5 <- p4 + theme(legend.position = "none")
p6 <- p5 + scale_x_discrete(name = "", limits = c("BDIpre", "BDI2m", "BDI4m", "BDI6m", "BDI8m")) # BDIpre
p6

## Warning: Removed 120 rows containing non-finite values (stat_boxplot).
```



```
# p7 <- p6 + scale_fill_grey(start = 1, end = 1) # B&W in the book
# p7
```

Figure 9.6

```
pairs(BtB[, -c(1:4)], cex = 0.8, cex.labels = 1.0)
```

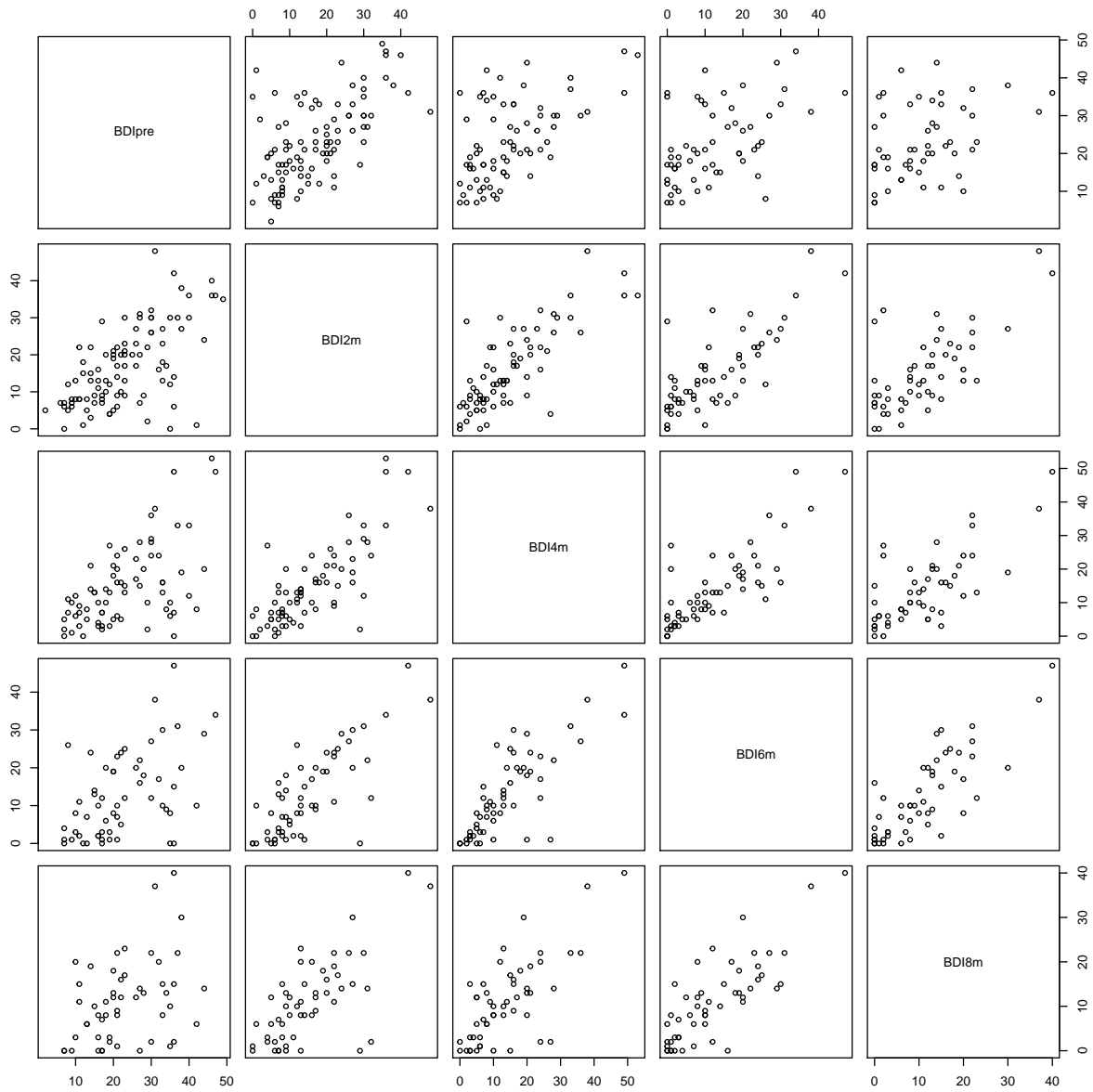


Table 9.8

```
# Convert data to long form for the analyses, adding Time:
BtBL <- gather(BtB, key = Visit, value = BDI, BDI2m, BDI4m, BDI6m, BDI8m) %>%
  mutate(Time = as.integer(substr(Visit, 4, 4)))

glimpse(BtBL); head(BtBL); tail(BtBL)

## Observations: 400
## Variables: 8
## $ Subject    <int> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 1...
## $ Drug       <fct> No, Yes, Yes, No, Yes, Yes, Yes, No, Yes, Yes, No, Y...
## $ Length     <fct> >6m, >6m, <6m, >6m, >6m, <6m, <6m, >6m, <6m, >6m, >6...
## $ Treatment  <fct> TAU, BtheB, TAU, BtheB, BtheB, BtheB, TAU, TAU, Bthe...
## $ BDIpre     <int> 29, 32, 25, 21, 26, 7, 17, 20, 18, 20, 30, 49, 26, 3...
## $ Visit      <chr> "BDI2m", "BDI2m", "BDI2m", "BDI2m", "BDI2m", "BDI2m"...
## $ BDI        <int> 2, 16, 20, 17, 23, 0, 7, 20, 13, 5, 32, 35, 27, 26, ...
## $ Time       <int> 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2...

##   Subject Drug Length Treatment BDIpre Visit BDI Time
## 1      1   No   >6m      TAU      29 BDI2m   2    2
## 2      2  Yes   >6m     BtheB     32 BDI2m  16    2
## 3      3  Yes   <6m      TAU     25 BDI2m  20    2
## 4      4   No   >6m     BtheB     21 BDI2m  17    2
## 5      5  Yes   >6m     BtheB     26 BDI2m  23    2
## 6      6  Yes   <6m     BtheB      7 BDI2m   0    2

##   Subject Drug Length Treatment BDIpre Visit BDI Time
## 395     95   No   >6m     BtheB     16 BDI8m   3    8
## 396     96  Yes   >6m     BtheB     16 BDI8m   8    8
## 397     97  Yes   <6m      TAU     28 BDI8m  NA    8
## 398     98   No   >6m     BtheB     11 BDI8m  11    8
## 399     99   No   <6m      TAU     13 BDI8m   6    8
## 400    100  Yes   <6m      TAU     43 BDI8m  NA    8

BtB_fit0 <- lm(BDI ~ BDIpre + Time + Treatment + Drug + Length, data = BtBL, na.action = na.omit)
summary(BtB_fit0)

##
## Call:
## lm(formula = BDI ~ BDIpre + Time + Treatment + Drug + Length,
##     data = BtBL, na.action = na.omit)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -24.202  -5.312   0.011   5.295  27.778
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    7.88307    1.78049   4.427 1.38e-05 ***
## BDIpre          0.57237    0.05486  10.433 < 2e-16 ***
## Time           -0.96081    0.23263  -4.130 4.82e-05 ***
## TreatmentBtheB -3.35397    1.09832  -3.054 0.00248 **
## DrugYes        -3.54601    1.14469  -3.098 0.00215 **
## Length>6m       1.75308    1.10850   1.581 0.11492
```



```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 8.654 on 274 degrees of freedom
## (120 observations deleted due to missingness)
## Multiple R-squared:  0.3978, Adjusted R-squared:  0.3868
## F-statistic: 36.2 on 5 and 274 DF,  p-value: < 2.2e-16
```

Table 9.9

```
library("lme4")

BtB_fit1 <- lmer(BDI ~ BDIPre + Time + Treatment + Drug + Length + (1 | Subject),
               data = BtBL, na.action = na.omit)
summary(BtB_fit1)

## Linear mixed model fit by REML ['lmerMod']
## Formula: BDI ~ BDIPre + Time + Treatment + Drug + Length + (1 | Subject)
## Data: BtBL
##
## 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
## BDIPre         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) BDIPre Time   TrtmBB DrugYs
## BDIPre       -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
```

```
BtB_fit2 <- lmer(BDI ~ BDIPre + Time + Treatment + Drug + Length + (Time | Subject),
               data = BtBL, na.action = na.omit)
summary(BtB_fit2)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## BDI ~ BDIPre + Time + Treatment + Drug + Length + (Time | Subject)
## Data: BtBL
##
## REML criterion at convergence: 1865.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.3271 -0.4641 -0.0813  0.3687  3.5399
##
## Random effects:
## Groups Name Variance Std.Dev. Corr
## Subject (Intercept) 50.5609  7.1106
## Time 0.2317  0.4814 -0.09
## Residual 23.8676  4.8854
## Number of obs: 280, groups: Subject, 97
##
## Fixed effects:
## Estimate Std. Error t value
## (Intercept) 5.94390 2.29859 2.586
## BDIPre 0.64439 0.07927 8.129
## Time -0.69950 0.15616 -4.480
## TreatmentBtheB -2.48582 1.70778 -1.456
## DrugYes -2.88745 1.76478 -1.636
## Length>6m 0.09736 1.67236 0.058
##
## Correlation of Fixed Effects:
## (Intr) BDIPre Time TrtmBB DrugYs
## BDIPre -0.680
## Time -0.250 0.019
## TretmntBthB -0.388 0.120 0.020
## DrugYes -0.076 -0.233 -0.021 -0.324
## Length>6m -0.244 -0.237 -0.036 0.000 0.159
```

```
anova(BtB_fit2, BtB_fit1)
```

```
## refitting model(s) with ML (instead of REML)
## Data: BtBL
## Models:
## BtB_fit1: BDI ~ BDIPre + Time + Treatment + Drug + Length + (1 | Subject)
## BtB_fit2: BDI ~ BDIPre + Time + Treatment + Drug + Length + (Time | Subject)
## Df AIC BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## BtB_fit1 8 1886.6 1915.7 -935.31 1870.6
## BtB_fit2 10 1889.8 1926.2 -934.90 1869.8 0.8161 2 0.665
```