



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

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## Analysing Longitudinal Data II – Generalised Estimation Equations and Linear Mixed Effect Models: Treating Respiratory Illness and Epileptic Seizures

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### 13.1 Introduction

### 13.2 Methods for Non-normal Distributions

### 13.3 Analysis Using R: GEE

#### 13.3.1 *Beat the Blues Revisited*

To use the `gee` function, package `gee` (Carey et al., 2012) has to be installed and attached:

```
R> library("gee")
```

The `gee` function is used in a similar way to the `lme` function met in Chapter 12 with the addition of the features of the `glm` function that specify the appropriate error distribution for the response and the implied link function, and an argument to specify the structure of the working correlation matrix. Here we will fit an independence structure and then an exchangeable structure. The R code for fitting generalised estimation equations to the `BtheB_long` data (as constructed in Chapter 12) with identity working correlation matrix is as follows (note that the `gee` function assumes the rows of the *data.frame* `BtheB_long` to be ordered with respect to subjects):

```
R> osub <- order(as.integer(BtheB_long$subject))
R> BtheB_long <- BtheB_long[osub,]
R> btb_gee <- gee(bdi ~ bdi.pre + trt + length + drug,
+               data = BtheB_long, id = subject, family = gaussian,
+               corstr = "independence")
```

and with exchangeable correlation matrix:

```
R> btb_gee1 <- gee(bdi ~ bdi.pre + trt + length + drug,
+                 data = BtheB_long, id = subject, family = gaussian,
+                 corstr = "exchangeable")
```

The `summary` method can be used to inspect the fitted models; the results are shown in Figures 13.1 and 13.2.

---

```
R> summary(bt看_gee)

...
Model:
  Link:                Identity
  Variance to Mean Relation: Gaussian
  Correlation Structure: Independent
...

Coefficients:
              Estimate Naive S.E. Naive z Robust S.E. Robust z
(Intercept)    3.569      1.4833    2.41      2.2695    1.572
bdi_pre         0.582      0.0564   10.32      0.0916    6.355
trtBtheB       -3.237      1.1296   -2.87      1.7746   -1.824
length>6m       1.458      1.1380    1.28      1.4826    0.983
drugYes        -3.741      1.1766   -3.18      1.7827   -2.099

Estimated Scale Parameter: 79.3
...
```

---

**Figure 13.1** R output of the `summary` method for the `btb_gee` model (slightly abbreviated).

---

```
R> summary(bt看_gee1)

...
Model:
  Link:                Identity
  Variance to Mean Relation: Gaussian
  Correlation Structure: Exchangeable
...

Coefficients:
              Estimate Naive S.E. Naive z Robust S.E. Robust z
(Intercept)    3.023      2.3039    1.3122      2.2320    1.3544
bdi_pre         0.648      0.0823    7.8741      0.0835    7.7583
trtBtheB       -2.169      1.7664   -1.2281      1.7361   -1.2495
length>6m      -0.111      1.7309   -0.0643      1.5509   -0.0718
drugYes        -3.000      1.8257   -1.6430      1.7316   -1.7323

Estimated Scale Parameter: 81.7
...
```

---

**Figure 13.2** R output of the `summary` method for the `btb_gee1` model (slightly abbreviated).

### 13.3.2 Respiratory Illness

The baseline status, i.e., the status for `month == 0`, will enter the models as an explanatory variable and thus we have to rearrange the *data.frame* `respiratory` in order to create a new variable `baseline`:

```
R> data("respiratory", package = "HSAUR2")
R> resp <- subset(respiratory, month > "0")
R> resp$baseline <- rep(subset(respiratory, month == "0")$status,
+                       rep(4, 111))
```

```
R> resp$nstat <- as.numeric(resp$status == "good")
R> resp$month <- resp$month[, drop = TRUE]
```

The new variable `nstat` is simply a dummy coding for a poor respiratory status. Now we can use the data `resp` to fit a logistic regression model and GEE models with an independent and an exchangeable correlation structure as follows.

```
R> resp_glm <- glm(status ~ centre + trt + gender + baseline
+               + age, data = resp, family = "binomial")
R> resp_gee1 <- gee(nstat ~ centre + trt + gender + baseline
+               + age, data = resp, family = "binomial", id = subject,
+               corstr = "independence", scale.fix = TRUE,
+               scale.value = 1)
R> resp_gee2 <- gee(nstat ~ centre + trt + gender + baseline
+               + age, data = resp, family = "binomial", id = subject,
+               corstr = "exchangeable", scale.fix = TRUE,
+               scale.value = 1)
```

---

```
R> summary(resp_glm)
```

```
Call:
glm(formula = status ~ centre + trt + gender + baseline + age,
    family = "binomial", data = resp)
```

```
Deviance Residuals:
```

Min	1Q	Median	3Q	Max
-2.315	-0.855	0.434	0.895	1.925

```
Coefficients:
```

	Estimate	Std. Error	z	value	Pr(> z )
(Intercept)	-0.90017	0.33765	-2.67	0.0077	
centre2	0.67160	0.23957	2.80	0.0051	
trttrt	1.29922	0.23684	5.49	4.1e-08	
gendermale	0.11924	0.29467	0.40	0.6857	
baselinegood	1.88203	0.24129	7.80	6.2e-15	
age	-0.01817	0.00886	-2.05	0.0404	

```
(Dispersion parameter for binomial family taken to be 1)
```

```
Null deviance: 608.93 on 443 degrees of freedom
Residual deviance: 483.22 on 438 degrees of freedom
AIC: 495.2
```

```
Number of Fisher Scoring iterations: 4
```

---

**Figure 13.3** R output of the `summary` method for the `resp_glm` model.

The estimated treatment effect taken from the exchangeable structure GEE model is 1.299 which, using the robust standard errors, has an associated 95% confidence interval

```
R> se <- summary(resp_gee2)$coefficients["trttrt",
+                                       "Robust S.E."]
R> coef(resp_gee2)["trttrt"] +
+   c(-1, 1) * se * qnorm(0.975)
```

---

```
R> summary(resp_gee1)

...
Model:
  Link:                      Logit
  Variance to Mean Relation: Binomial
  Correlation Structure:     Independent
...

Coefficients:
              Estimate Naive S.E. Naive z Robust S.E. Robust z
(Intercept)  -0.9002    0.33765  -2.666    0.460   -1.956
centre2       0.6716    0.23957   2.803    0.357   1.882
trtttrt      1.2992    0.23684   5.486    0.351   3.704
gendermale    0.1192    0.29467   0.405    0.443   0.269
baselinegood  1.8820    0.24129   7.800    0.350   5.376
age          -0.0182    0.00886  -2.049    0.013  -1.397

Estimated Scale Parameter: 1
...
```

---

**Figure 13.4** R output of the `summary` method for the `resp_gee1` model (slightly abbreviated).

---

```
R> summary(resp_gee2)

...
Model:
  Link:                      Logit
  Variance to Mean Relation: Binomial
  Correlation Structure:     Exchangeable
...

Coefficients:
              Estimate Naive S.E. Naive z Robust S.E. Robust z
(Intercept)  -0.9002    0.4785  -1.881    0.460   -1.956
centre2       0.6716    0.3395   1.978    0.357   1.882
trtttrt      1.2992    0.3356   3.871    0.351   3.704
gendermale    0.1192    0.4176   0.286    0.443   0.269
baselinegood  1.8820    0.3419   5.504    0.350   5.376
age          -0.0182    0.0126  -1.446    0.013  -1.397

Estimated Scale Parameter: 1
...
```

---

**Figure 13.5** R output of the `summary` method for the `resp_gee2` model (slightly abbreviated).

```
[1] 0.612 1.987
```

These values reflect effects on the log-odds scale. Interpretation becomes simpler if we exponentiate the values to get the effects in terms of odds. This gives a treatment effect of 3.666 and a 95% confidence interval of

```
R> exp(coef(resp_gee2)["trtttrt"] +
+      c(-1, 1) * se * qnorm(0.975))
[1] 1.84 7.29
```

The odds of achieving a ‘good’ respiratory status with the active treatment is between about twice and seven times the corresponding odds for the placebo.

### 13.3.3 Epilepsy

Moving on to the count data in `epilepsy` from Table ??, we begin by calculating the means and variances of the number of seizures for all interactions between treatment and period:

```
R> data("epilepsy", package = "HSAUR2")
R> itp <- interaction(epilepsy$treatment, epilepsy$period)
R> tapply(epilepsy$seizure.rate, itp, mean)
```

<i>placebo.1</i>	<i>Progabide.1</i>	<i>placebo.2</i>	<i>Progabide.2</i>	<i>placebo.3</i>
9.36	8.58	8.29	8.42	8.79
<i>Progabide.3</i>	<i>placebo.4</i>	<i>Progabide.4</i>		
8.13	7.96	6.71		

```
R> tapply(epilepsy$seizure.rate, itp, var)
```

<i>placebo.1</i>	<i>Progabide.1</i>	<i>placebo.2</i>	<i>Progabide.2</i>	<i>placebo.3</i>
102.8	332.7	66.7	140.7	215.3
<i>Progabide.3</i>	<i>placebo.4</i>	<i>Progabide.4</i>		
193.0	58.2	126.9		

Some of the variances are considerably larger than the corresponding means, which for a Poisson variable may suggest that overdispersion may be a problem, see Chapter 7.

We can now fit a Poisson regression model to the data assuming independence using the `glm` function. We also use the GEE approach to fit an independence structure, followed by an exchangeable structure using the following R code:

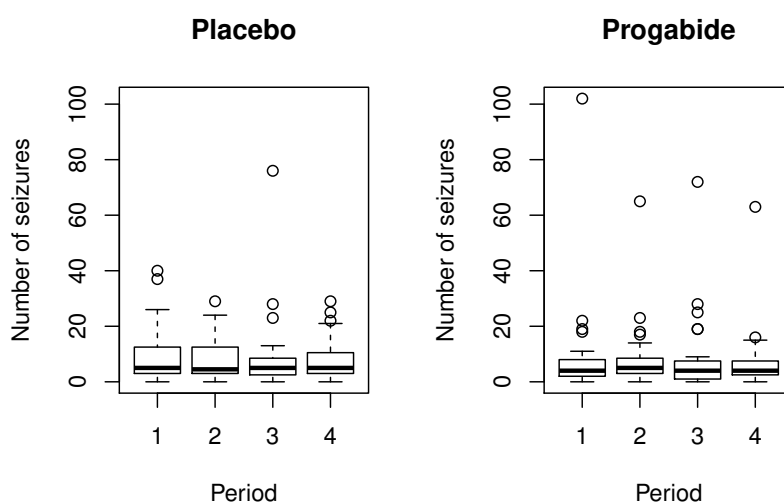
```
R> per <- rep(log(2), nrow(epilepsy))
R> epilepsy$period <- as.numeric(epilepsy$period)
R> names(epilepsy)[names(epilepsy) == "treatment"] <- "trt"
R> fm <- seizure.rate ~ base + age + trt + offset(per)
R> epilepsy_glm <- glm(fm, data = epilepsy, family = "poisson")
R> epilepsy_gee1 <- gee(fm, data = epilepsy, family = "poisson",
+   id = subject, corstr = "independence", scale.fix = TRUE,
+   scale.value = 1)
R> epilepsy_gee2 <- gee(fm, data = epilepsy, family = "poisson",
+   id = subject, corstr = "exchangeable", scale.fix = TRUE,
+   scale.value = 1)
R> epilepsy_gee3 <- gee(fm, data = epilepsy, family = "poisson",
+   id = subject, corstr = "exchangeable", scale.fix = FALSE,
+   scale.value = 1)
```

As usual we inspect the fitted models using the `summary` method, the results are given in Figures 13.8, 13.9, 13.10, and 13.11.

```

R> layout(matrix(1:2, nrow = 1))
R> ylim <- range(epilepsy$seizure.rate)
R> placebo <- subset(epilepsy, treatment == "placebo")
R> progabide <- subset(epilepsy, treatment == "Progabide")
R> boxplot(seizure.rate ~ period, data = placebo,
+         ylab = "Number of seizures",
+         xlab = "Period", ylim = ylim, main = "Placebo")
R> boxplot(seizure.rate ~ period, data = progabide,
+         main = "Progabide", ylab = "Number of seizures",
+         xlab = "Period", ylim = ylim)

```



**Figure 13.6** Boxplots of numbers of seizures in each two-week period post randomisation for placebo and active treatments.

### 13.4 Analysis Using R: Random Effects

As an example of using generalised mixed models for the analysis of longitudinal data with a non-normal response, the following logistic model will be fitted to the respiratory illness data

$$\begin{aligned} \text{logit}(P(\text{status} = \text{good})) = & \beta_0 + \beta_1 \text{treatment} + \beta_2 \text{time} + \beta_3 \text{gender} \\ & + \beta_4 \text{age} + \beta_5 \text{centre} + \beta_6 \text{baseline} + u \end{aligned}$$

where  $u$  is a subject-specific random effect.

The necessary R code for fitting the model using the `glmer` function from package **lme4** (Bates and Sarkar, 2012, Bates, 2005) is:

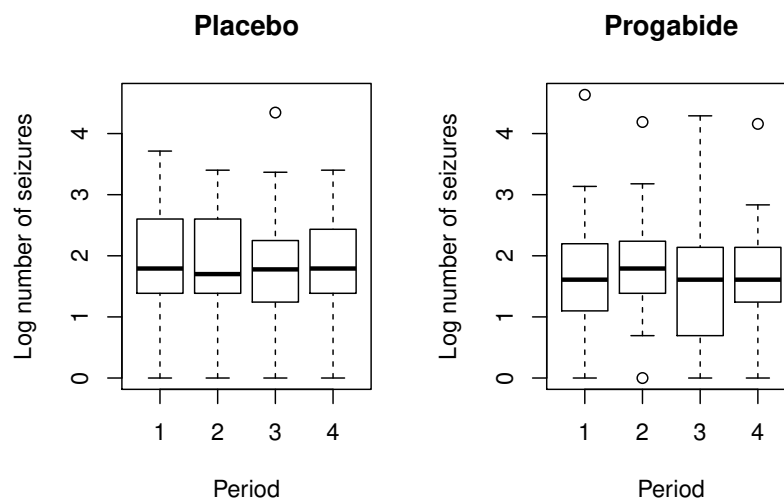
```
R> library("lme4")
```



```

R> layout(matrix(1:2, nrow = 1))
R> ylim <- range(log(epilepsy$seizure.rate + 1))
R> boxplot(log(seizure.rate + 1) ~ period, data = placebo,
+         main = "Placebo", ylab = "Log number of seizures",
+         xlab = "Period", ylim = ylim)
R> boxplot(log(seizure.rate + 1) ~ period, data = progabide,
+         main = "Progabide", ylab = "Log number of seizures",
+         xlab = "Period", ylim = ylim)

```



**Figure 13.7** Boxplots of log of numbers of seizures in each two-week period post randomisation for placebo and active treatments.

```

R> resp_lmer <- glmer(status ~ baseline + month +
+   trt + gender + age + centre + (1 | subject),
+   family = binomial(), data = resp)
R> exp(fixef(resp_lmer))

```

(Intercept)	baselinegood	month.L	month.Q
0.191	21.954	0.816	0.972
month.C	trttrt	gendermale	age
0.701	8.725	1.269	0.975
centre2			
2.825			

The significance of the effects as estimated by this random effects model and by the GEE model described in Section 13.3.2 is generally similar. But as expected from our previous discussion the estimated coefficients are substantially larger. While the estimated effect of treatment on a randomly sampled

---

```
R> summary(epilepsy_glm)

Call:
glm(formula = fm, family = "poisson", data = epilepsy)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-4.436  -1.403  -0.503   0.484  12.322

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.130616   0.135619  -0.96   0.3355
base         0.022652   0.000509  44.48 < 2e-16
age          0.022740   0.004024   5.65 1.6e-08
trtProgabide -0.152701   0.047805  -3.19  0.0014

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 2521.75  on 235  degrees of freedom
Residual deviance:  958.46  on 232  degrees of freedom
AIC: 1732

Number of Fisher Scoring iterations: 5
```

---

**Figure 13.8** R output of the `summary` method for the `epilepsy_glm` model.

---

```
R> summary(epilepsy_gee1)

...
Model:
Link:                      Logarithm
Variance to Mean Relation: Poisson
Correlation Structure:     Independent
...

Coefficients:
            Estimate Naive S.E. Naive z Robust S.E. Robust z
(Intercept)  -0.1306   0.135619  -0.963   0.36515  -0.358
base          0.0227   0.000509  44.476   0.00124  18.332
age           0.0227   0.004024   5.651   0.01158   1.964
trtProgabide -0.1527   0.047805  -3.194   0.17111  -0.892

Estimated Scale Parameter:  1
...
```

---

**Figure 13.9** R output of the `summary` method for the `epilepsy_gee1` model (slightly abbreviated).

individual, given the set of observed covariates, is estimated by the marginal model using GEE to increase the log-odds of being disease free by 1.299, the corresponding estimate from the random effects model is 2.166. These are not inconsistent results but reflect the fact that the models are estimating different parameters. The random effects estimate is conditional upon the patient's random effect, a quantity that is rarely known in practice. Were we to examine the log-odds of the average predicted probabilities with

---

```
R> summary(epilepsy_gee2)
```

```
...
Model:
  Link:                      Logarithm
  Variance to Mean Relation: Poisson
  Correlation Structure:     Exchangeable

...

Coefficients:
              Estimate Naive S.E. Naive z Robust S.E. Robust z
(Intercept)  -0.1306    0.200442  -0.652    0.36515   -0.358
base          0.0227    0.000753  30.093    0.00124   18.332
age           0.0227    0.005947   3.824    0.01158    1.964
trtProgabide -0.1527    0.070655  -2.161    0.17111   -0.892

Estimated Scale Parameter:  1
...
```

---

**Figure 13.10** R output of the `summary` method for the `epilepsy_gee2` model (slightly abbreviated).

---

```
R> summary(epilepsy_gee3)
```

```
...
Model:
  Link:                      Logarithm
  Variance to Mean Relation: Poisson
  Correlation Structure:     Exchangeable

...

Coefficients:
              Estimate Naive S.E. Naive z Robust S.E. Robust z
(Intercept)  -0.1306    0.4522  -0.289    0.36515   -0.358
base          0.0227    0.0017  13.339    0.00124   18.332
age           0.0227    0.0134   1.695    0.01158    1.964
trtProgabide -0.1527    0.1594  -0.958    0.17111   -0.892

Estimated Scale Parameter:  5.09
...
```

---

**Figure 13.11** R output of the `summary` method for the `epilepsy_gee3` model (slightly abbreviated).

and without treatment (averaged over the random effects) this would give an estimate comparable to that estimated within the marginal model.

---

```
R> summary(resp_lmer)
...
Fixed effects:
      Estimate Std. Error z value Pr(>|z|)
(Intercept)  -1.6546    0.7762   -2.13   0.033
baselinegood   3.0890    0.5986    5.16 2.5e-07
month.L       -0.2035    0.2796   -0.73   0.467
month.Q       -0.0282    0.2791   -0.10   0.919
month.C       -0.3557    0.2808   -1.27   0.205
trttrt        2.1662    0.5516    3.93 8.6e-05
gendermale     0.2384    0.6661    0.36   0.720
age           -0.0256    0.0199   -1.28   0.200
centre2        1.0385    0.5418    1.92   0.055
...
```

---

**Figure 13.12** R output of the `summary` method for the `resp_lmer` model (abbreviated).

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## Bibliography

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