SOLUTIONS MANUAL

FOR

Korosteleva, O. (2018). *Advanced Regression Models with SAS and R*, CRC Press

By

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CHAPTER 1

EXERCISE 1.1. Show that the normal distribution belongs to the exponential family of distributions.

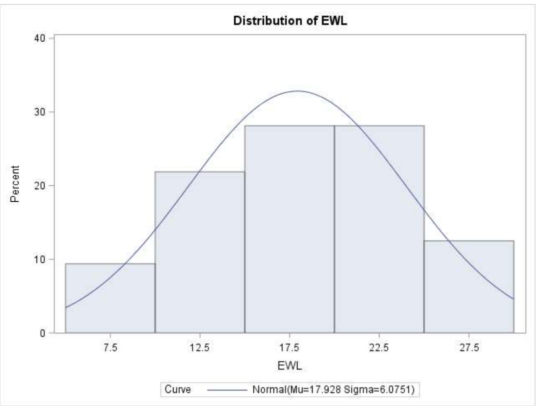
$f(y,\mu,\sigma^2)=\frac{1}{\sqrt{2\pi\sigma^2}}\exp\left\{-\frac{(y-\mu)^2}{2\sigma^2}\right\}=\exp\left\{-\frac{1}{2}\ln(2\pi\sigma^2)-\frac{1}{2\sigma^2}(y^2-2y\mu+\mu^2)\right\}$. Let $\theta=\mu$ and $\phi=\sigma^2$. Then, we can write $f(y,\theta,\phi)=\exp\left\{-\frac{1}{2}\ln(2\pi\phi\,)-\frac{1}{2\phi}\,(y^2-2y\theta+\theta^2\,)\right\}$

$=\exp\left\{\frac{y\theta-\frac{\theta^2}{2}}{\phi}-\frac{1}{2}\ln(2\pi\phi)-\frac{y^2}{2\phi}\right\}=\exp\left\{\frac{y\theta-c(\theta)}{\phi}+h(y,\phi)\right\}$ where $c(\theta)=\frac{\theta^2}{2}$, and

$$h(y,\phi)=-\frac{1}{2}\ln(2\pi\phi)-\frac{y^2}{2\phi}.$$

EXERCISE 1.2. (a) Verify normality of the response variable, then fit the linear regression model to the data. State the fitted model. Give estimates for all parameters.
In SAS:

```
data weightloss;
input drug$ age gender$ EWL @@;
cards;
A 49 F 14.2  A 54 M 25.4  A 37 F 14.1  A 43 F 20.0  A 57  M 11.7 A 48 M 16.6
A 34 F 15.9  A 51 F 17.4  A 54 F 22.8  A 45 F 16.7  A 36  M 12.7 A 57 M 15.0
A 44 M 8.4   A 56 M 11.2  A 44 M 17.3  A 47 M 20.5  A 44  F 6.7  B 52 F 29.4
B 51 M 21.9  B 44 F 23.6  B 53 F 23.8  B 55 M 7.4   B 30  F 23.1 B 47 M 16.8
B 26 M 14.1  B 56 F 24.6  B 28 F 17.8  B 34 M 27.8  B 43  M 10.6 B 55 M 26.8
B 52 F 15.7  B 54 F 23.7
;

/*running normality check*/
proc univariate;
 var EWL;
  histogram/normal;
run;
```



```
   Goodness-of-Fit Tests for Normal Distribution
Test                  Statistic       p Value
Kolmogorov-Smirnov D    0.10216310 Pr > D    >0.150
Cramer-von Mises   W-Sq 0.05103595 Pr > W-Sq >0.250
Anderson-Darling   A-Sq 0.28788730 Pr > A-Sq >0.250
```

Based on the large p-values of the normality tests and the histogram, we can conclude that the response variable follows a normal distribution.

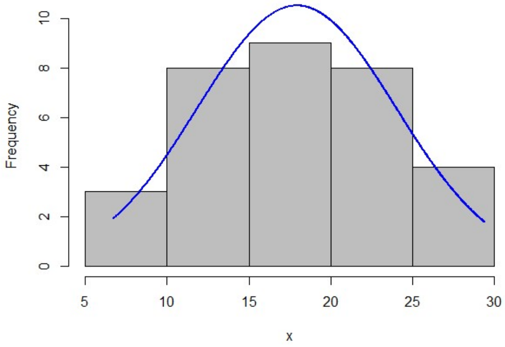
```
/*fitting general linear model*/
proc genmod;
 class drug(ref='A') gender;
  model EWL = drug age gender / dist=normal link=identity;
run;
```

```
Log Likelihood -98.4395

                Analysis Of Maximum Likelihood Parameter Estimates
Parameter    DF Estimate Standard    Wald 95% Confidence        Wald Chi- Pr > ChiSq
                            Error          Limits                 Square
Intercept    1   9.2146   5.3301     -1.2322      19.6614           2.99     0.0838
drug       B 1   4.8103   1.8697      1.1456       8.4749           6.62     0.0101
drug       A 0   0.0000   0.0000      0.0000       0.0000            .          .
age          1   0.1102   0.1067     -0.0988       0.3192           1.07     0.3015
gender     F 1   2.7235   1.8664     -0.9346       6.3815           2.13     0.1445
gender     M 0   0.0000   0.0000      0.0000       0.0000            .          .
Scale        1   5.2451   0.6556      4.1054       6.7012
```

The fitted model is $\hat{E}(EWL) = 9.2146 + 4.8103 \cdot drugB\ + 0.1102 \cdot age + 2.7235 \cdot female$, and $\hat{\sigma} = 5.2451$.

In R:

```
weightloss.data<- read.csv(file="C:/<insert path>/Exercise1.2Data.csv", header =
TRUE, sep = ",")

#running normality check
library(rcompanion)
plotNormalHistogram(weightloss.data$EWL)
```



```
shapiro.test(weightloss.data$EWL)
```

```
Shapiro-Wilk normality test

W = 0.97424, p-value = 0.6234
```

```
#specifying reference levels
drug.rel<- relevel(weightloss.data$drug, ref="A")
gender.rel<- relevel(weightloss.data$gender, ref="M")

#fitting general linear model
summary(fitted.model<- glm(EWL ~ drug.rel + age + gender.rel, data =
weightloss.data, family=gaussian(link=identity)))
```

```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   9.2146     5.6981   1.617   0.1171
drug.relB     4.8103     1.9988   2.407   0.0229
age           0.1102     0.1140   0.967   0.3420
gender.relF   2.7235     1.9952   1.365   0.1831
```

```
#outputting estimated sigma
sigma(fitted.model)
```

```
5.607257
```

(b) Which regression coefficients turn out to be significant at the 5%? Discuss goodness of fit of the model.

Drug B is the only significant predictor in the model at the 5% significance level since the corresponding p-value is the only one under 0.05.

In SAS:

```
/*checking model fit*/
proc genmod;
 model EWL = / dist=normal link=identity;
run;
```

```
Log Likelihood -102.6326
```

```
data deviance_test;
 deviance = -2*(-102.6326 - (-98.4395));
  pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance     pvalue
  8.3862   0.038669
```

The p-value for the deviance test is less than 0.05, indicating a good fit of the model. The R code and output are:

```
#checking model fit
null.model<- glm(EWL ~ 1, data=weightloss.data, family=gaussian(link=identity))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
8.386158
```

```
print(p.value<- pchisq(deviance, df=3, lower.tail=FALSE))
```

```
0.03867005
```

(c) Is one of the drugs more efficient for weight loss than the other? Interpret all estimated significant coefficients.

The estimated average EWL for subjects taking drug B is 4.8103 percent higher than that for subjects taking drug A, keeping all the other predictors fixed. It means that drug B is more efficient than drug A.

(d) According to the model, what is the predicted percent decrease in excess body weight for a 35-year old male who is taking drug A?

The predicted percent decrease in excess body weight for a 35-year old male who is taking drug A is computed by hand as: $EWL^0 = 9.2146 + 0.1102 \cdot 35 = 13.0716$.

In SAS:

```
 /*using fitted model for prediction*/
data predict;
 input drug$ age gender$;
cards;
A 35 M
;

data weightloss;
 set weightloss predict;
run;

proc genmod;
 class drug gender;
  model EWL = drug age gender / dist=normal link=identity;
   output out=outdata p=pEWL;
run;

proc print data=outdata (firstobs=33) noobs;
var pEWL;
run;
```

```
   pEWL
13.0718
```

In R:

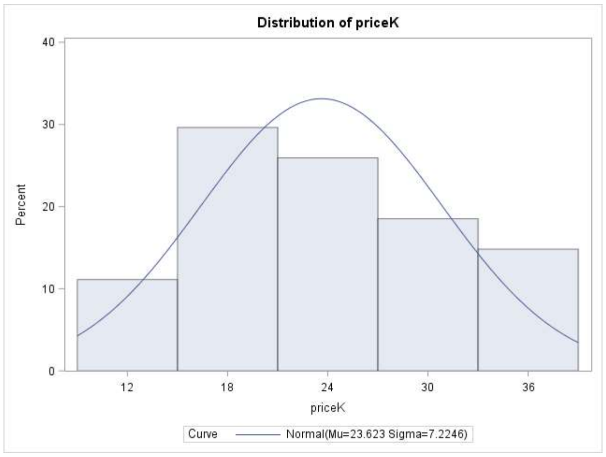
```
#using fitted model for prediction
print(predict(fitted.model, data.frame(drug.rel="A", age=35, gender.rel="M")))
```

```
13.7178
```

EXERCISE 1.3. (a) Reduce the car price by the factor of 1000. Check that the distribution of the price is normal. Fit a general linear regression model to predict the price of a car. Write down the fitted model, specifying all estimated parameters.

In SAS:

```
data carsales;
input bodystyle$ 1-9 country$ hwy doors leather$ price @@;
priceK=price/1000;
cards;
coupe     USA     26 4 no  17445  coupe     USA     40 4 no  23500
coupe     USA     35 2 no  19600  coupe     Germany 37 4 no  23400
coupe     Germany 25 4 no  24100  coupe     Germany 24 2 no  12400
coupe     Japan   26 2 no  13300  coupe     Japan   27 4 no  15550
coupe     Japan   20 4 yes 29345  hatchback USA     30 2 no  12540
hatchback USA     39 4 no  17595  hatchback USA     38 2 no  17300
hatchback Germany 38 4 no  17800  hatchback Germany 32 4 no  22500
hatchback Germany 34 4 no  20300  hatchback Japan   38 4 yes 27300
hatchback Japan   38 2 yes 23300  hatchback Japan   38 2 yes 29300
sedan     USA     29 4 no  32000  sedan     USA     25 2 yes 34200
sedan     USA     33 4 yes 33395  sedan     Germany 40 4 no  22850
sedan     Germany 23 2 yes 36000  sedan     Germany 25 4 no  19900
sedan     Japan   40 4 yes 36700  sedan     Japan   35 4 yes 31600
sedan     Japan   37 4 no  24600
run;

/*running normality check*/
proc univariate;
 var priceK;
  histogram/normal;
run;
```



```
  Goodness-of-Fit Tests for Normal Distribution
Test                  Statistic       p Value
Kolmogorov-Smirnov D    0.11287889 Pr > D    >0.150
Cramer-von Mises   W-Sq 0.05867848 Pr > W-Sq >0.250
Anderson-Darling   A-Sq 0.37263698 Pr > A-Sq >0.250
```

P-values for the normality tests are all in excess of 0.05, indicating that normality holds. The histogram also displays a distribution close to bell-shaped.

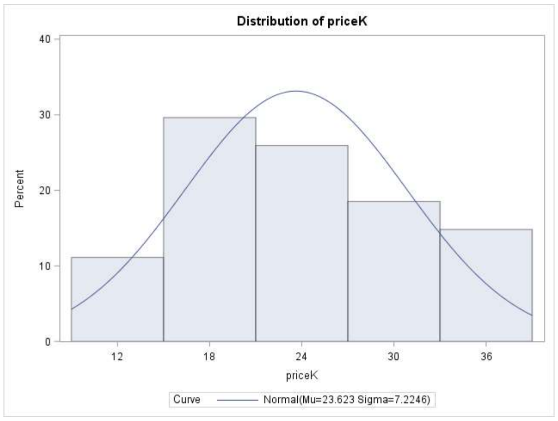
```
/*fitting general linear model*/
proc genmod;
 class bodystyle(ref='hatchback') country(ref='Japan') leather(ref='no');
  model priceK=bodystyle country hwy doors leather/dist=normal link=identity;
run;
```

```
Log Likelihood -67.2613

                Analysis Of Maximum Likelihood Parameter Estimates
Parameter           DF Estimate Standard  Wald 95% Confidence   Wald Chi- Pr > ChiSq
                                   Error        Limits             Square
Intercept            1   5.1353   4.6900   -4.0570   14.3276        1.20     0.2735
bodystyle coupe      1   2.2698   1.6836   -1.0301    5.5696        1.82     0.1776
bodystyle sedan      1   6.4107   1.5477    3.3772    9.4441       17.16     <.0001
bodystyle hatchback  0   0.0000   0.0000    0.0000    0.0000           .          .
country   Germany    1   3.1959   1.6859   -0.1085    6.5002        3.59     0.0580
country   USA        1   3.2128   1.5780    0.1199    6.3058        4.15     0.0418
country   Japan      0   0.0000   0.0000    0.0000    0.0000           .          .
hwy                  1   0.1305   0.1117   -0.0884    0.3494        1.36     0.2427
doors                1   1.5554   0.6630    0.2560    2.8549        5.50     0.0190
leather   yes        1  12.1757   1.6217    8.9972   15.3541       56.37     <.0001
leather   no         0   0.0000   0.0000    0.0000    0.0000           .          .
Scale                1   2.9219   0.3976    2.2378    3.8150
```

The fitted model is $\hat{E}(priceK) = 5.1353 + 2.2698 \cdot coupe + 6.4107 \cdot sedan + 3.1959 \cdot Germany + 3.2128 \cdot USA + 0.1305 \cdot hwy + 1.5554 \cdot doors + 12.1757 \cdot leather,$ and $\hat{\sigma} = 2.9219.$

In R:

```
carsales.data<- read.csv(file="C:/<insert path>/Exercise1.3Data.csv",header=TRUE,
sep=',')

#rescaling price
priceK<- carsales.data$price/1000

#running normality check
library(rcompanion)
plotNormalHistogram(priceK)
```



```
shapiro.test(priceK)
```

```
Shapiro-Wilk normality test

W = 0.95482, p-value = 0.28
```

```
#specifying reference levels
bodystyle.rel<- relevel(carsales.data$bodystyle, ref="hatchback")
country.rel<- relevel(carsales.data$country, ref="Japan")
leather.rel<- relevel(carsales.data$leather, ref="no")

#fitting general linear model
summary(fitted.model<- glm(priceK ~ bodystyle.rel + country.rel + hwy + doors +
leather.rel, data=carsales.data, family=gaussian(link=identity)))
```

```
Coefficients:
                   Estimate Std. Error t value Pr(>|t|)
(Intercept)          5.1353     5.5909   0.919  0.36986
bodystyle.relcoupe   2.2698     2.0070   1.131  0.27216
bodystyle.relsedan   6.4107     1.8450   3.475  0.00254
country.relGermany   3.1959     2.0098   1.590  0.12829
country.relUSA       3.2128     1.8812   1.708  0.10394
hwy                  0.1305     0.1332   0.980  0.33937
doors                1.5554     0.7904   1.968  0.06384
leather.relyes      12.1757     1.9332   6.298 4.79e-06
```

```
#outputting estimated sigma
sigma(fitted.model)
```

```
3.483088
```

(b) How good is the model fit? Discuss significance of the regression coefficients.
The p-value in the deviance test is way below 0.05, indicating a good model fit. Significant variables are sedan body style and leather interior.

In SAS:

```
 /*checking model fit*/
proc genmod;
 model priceK = / dist=normal link=identity;
run;
```

```
 Log Likelihood -91.1942
```

```
data deviance_test;
 deviance = -2*(-91.1942 - (-67.2613));
  pvalue = 1 - probchi(deviance,7);
run;

proc print noobs;
run;
```

```
 deviance      pvalue
  47.8658   3.7823E-8
```

In R:

```
#checking model fit
null.model<- glm(priceK ~ 1, data=carsales.data, family=gaussian(link=identity))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
47.86586
```

```
print(p.value<- pchisq(deviance, df=7, lower.tail = FALSE))
```

```
3.78218e-08
```

(c) Interpret the estimates of those regression coefficients that differ significantly from zero.

As estimated, sedan costs on average \$6,410.70 more than a hatchback, under all other equal conditions. The estimated average price of a car with leather interior is \$12,175.70 larger compared to a car without leather interior.

(d) What is the predicted price of a sedan made in USA that has 4 doors, leather seats, and runs 30 mpg on highway?

The predicted price of a sedan that is made in USA, has 4 doors, leather seats, and runs 30 mpg on highway is calculated as: $price^0 = \$1{,}000(5.1353 + 6.4107 + 3.2128 + 0.1305 \cdot 30 + 1.5554 \cdot 4 + 12.1757) = \$37{,}071.10.$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input bodystyle$ country$ hwy doors leather$;
cards;
sedan USA 30 4 yes
;

data carsales;
 set carsales predict;
run;

proc genmod;
 class bodystyle country leather;
  model priceK = bodystyle country hwy doors leather / dist=normal link=identity;
   output out=outdata p=ppriceK;
run;

data final_prediction;
set outdata;
pprice=ppriceK*1000;
run;

proc print data=final_prediction (firstobs=28) noobs;
 var pprice;
run;
```

```
  pprice
37071.14
```

In R:

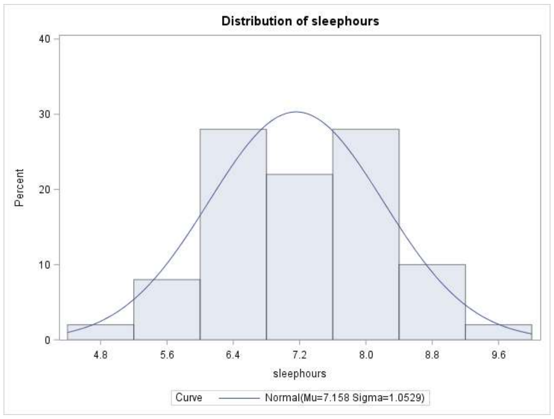
```
#using fitted model for prediction
prediction<- (predict(fitted.model, data.frame(bodystyle.rel='sedan', country.rel
='USA',hwy=30, doors=4, leather.rel='yes')))
print(prediction*1000)
```

```
37071.14
```

EXERCISE 1.4. (a) Show normality of the distribution of the number of hours of sleep per night. Regress the number of hours of sleep on all the given factors. Write explicitly what the fitted model is.

In SAS:

```
data sleep;
input age gender$ quiettime nchildren stresslevel jobstatus$ nactivities pastvac
sleephours @@;
cards;
62 F 60  1 5 unempl  1 15 7.7  28 F 15  1 6  unempl  5 11 5.3
50 M 15  0 5 unempl  1 19 6.4  36 M 60  1 6  full    1 21 7.7
56 F 50  0 3 part    4 5  7.6  48 M 180 0 5  full    0 6  6.4
55 M 40  0 8 full    8 23 7.0  26 F 80  0 7  student 9 8  8.3
44 M 180 1 3 part    6 20 9.6  49 F 5   0 7  unempl  5 15 5.5
29 M 60  2 5 student 5 7  7.7  56 M 10  1 4  unempl  4 17 5.7
46 F 40  1 7 part    3 3  7.4  41 F 5   2 6  full    9 10 6.2
22 M 15  0 8 full    4 3  6.3  36 F 45  2 5  part    8 14 7.5
54 F 120 1 8 part    7 10 8.5  42 F 60  3 1  full    9 11 6.3
58 F 5   1 7 full    1  17 5.3 33 M 100 2 1  full    9 5  8.3
50 F 2   2 6 full    3  12 5.1 59 M 30  2 5  full    2 6  6.9
32 M 30  1 8 full    5  9  6.9 50 M 60  2 8  part    8 13 8.0
56 F 10  0 3 unempl  7  7  6.1 42 F 240 0 1  part    8 21 8.8
58 F 10  2 7 full    9  4  6.2 57 F 15  1 6  full    2 16 6.3
30 F 30  0 2 full    8  9  8.3 54 M 20  2 8  full    6 7  6.5
57 M 45  2 4 full    7  18 7.5 45 F 120 0 9  part    2 13 6.6
33 F 40  1 6 unempl  9  24 7.0 56 F 120 0 5  part    2 20 8.7
59 F 60  2 9 part    4  19 8.1 41 M 60  2 3  student 2 3  7.5
62 M 40  0 1 unempl  0  2  8.6 29 M 15  1 7  unempl  3 20 6.3
34 F 30  0 7 unempl  9  0  6.6 32 F 20  3 7  unempl  2 8  7.8
46 F 20  2 3 unempl  9  18 7.9 45 M 60  0 2  unempl  0 22 9.0
23 M 45  0 6 part    4  12 7.6 38 M 60  4 5  full    3 5  7.8
45 M 30  0 5 unempl  9  7  6.8 63 F 40  0 6  unempl  5 5  7.3
27 F 120 0 4 student 1  16 7.3 30 F 45  0 7  part    8 10 7.7
34 F 5   3 6 full    0  4  6.0 62 M 10  0 10 part    8 11 6.0
;

/*running normality check*/
proc univariate;
 var sleephours;
  histogram/normal;
run;
```



```
Goodness-of-Fit Tests for Normal Distribution
Test               Statistic       p Value
Kolmogorov-Smirnov D    0.08733974 Pr > D    >0.150
Cramer-von Mises   W-Sq 0.06145088 Pr > W-Sq >0.250
Anderson-Darling   A-Sq 0.32815950 Pr > A-Sq >0.250
```

The normality tests (p-values > 0.05) as well as the bell-shaped histogram indicate normality of the response variable.

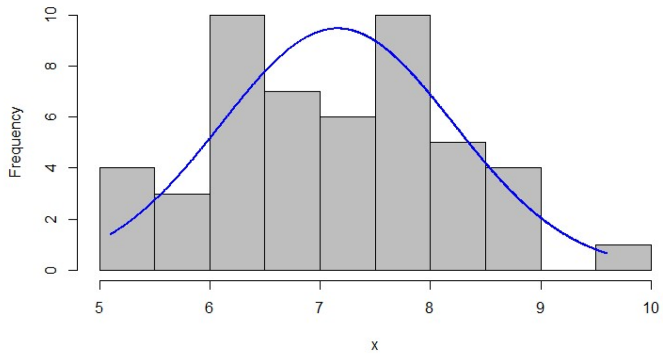
```
/*fitting general linear model*/
proc genmod;
 class gender(ref='F') jobstatus(ref='full');
  model sleephours = age gender quiettime nchildren stresslevel jobstatus
     nactivities pastvac / dist=normal link=identity;
run;
```

```
Log Likelihood -54.6201

                 Analysis Of Maximum Likelihood Parameter Estimates
Parameter           DF Estimate Standard  Wald 95% Confidence   Wald Chi- Pr > ChiSq
                                   Error        Limits             Square
Intercept            1   6.8260   0.7051    5.4440     8.2080       93.72     <.0001
age                  1  -0.0037   0.0093   -0.0218     0.0145        0.16     0.6932
gender      M        1   0.3568   0.2132   -0.0610     0.7747        2.80     0.0942
gender      F        0   0.0000   0.0000    0.0000     0.0000         .          .
quiettime            1   0.0074   0.0029    0.0018     0.0130        6.74     0.0095
nchildren            1   0.1204   0.1086   -0.0925     0.3334        1.23     0.2677
stresslevel          1  -0.1398   0.0536   -0.2450    -0.0347        6.80     0.0091
jobstatus   part     1   1.0484   0.3188    0.4235     1.6732       10.81     0.0010
jobstatus   student  1   0.6286   0.4358   -0.2255     1.4828        2.08     0.1492
jobstatus   unempl   1   0.3818   0.2857   -0.1781     0.9418        1.79     0.1814
jobstatus   full     0   0.0000   0.0000    0.0000     0.0000         .          .
nactivities          1   0.0204   0.0345   -0.0472     0.0879        0.35     0.5545
pastvac              1   0.0050   0.0170   -0.0282     0.0383        0.09     0.7663
Scale                1   0.7214   0.0721    0.5930     0.8776
```

The fitted model is
$\hat{E}(sleephours) = 6.8260 - 0.0037 \cdot age + 0.3568 \cdot male + 0.0074 \cdot quiettime + 0.1204 \cdot nchildren - 0.1398 \cdot stresslevel + 1.0484 \cdot parttime + 0.6286 \cdot student + 0.3818 \cdot unempl + 0.0204 \cdot nactivities + 0.0050 \cdot pastvac$, and $\hat{\sigma} = 0.7214$.

In R:

```
sleep.data<- read.csv(file="C:/<insert path>/Exercise1.4Data.csv", header=TRUE,
sep=',')

#running normality check
library(rcompanion)
plotNormalHistogram(sleep.data$sleephours)
```



```
shapiro.test(sleep.data$sleephours)

Shapiro-Wilk normality test

W = 0.98284, p-value = 0.6762

#specifying reference levels
gender.rel<- relevel(sleep.data$gender, ref="F")
jobstatus.rel<- relevel(sleep.data$jobstatus, ref="full")

#fitting general linear model
summary(fitted.model<- glm(sleephours ~ age + gender.rel + quiettime + nchildren
+ stresslevel + jobstatus.rel + nactivities + pastvac, data=sleep.data,
family=gaussian(link=identity)))

Coefficients:
                      Estimate Std. Error t value Pr(>|t|)
(Intercept)           6.826002   0.798388   8.550 1.78e-10
age                  -0.003656   0.010494  -0.348  0.72943
gender.relM           0.356815   0.241401   1.478  0.14741
quiettime             0.007421   0.003238   2.292  0.02738
nchildren             0.120419   0.123020   0.979  0.33368
stresslevel          -0.139828   0.060734  -2.302  0.02674
jobstatus.relpart     1.048386   0.360976   2.904  0.00603
jobstatus.relstudent  0.628623   0.493437   1.274  0.21021
jobstatus.relunempl   0.381840   0.323501   1.180  0.24501
nactivities           0.020373   0.039031   0.522  0.60465
pastvac               0.005046   0.019222   0.263  0.79430

#outputting estimated sigma
sigma(fitted.model)

0.8168443
```

(b) How good is the model fit? What beta coefficients are significantly different from zero at the 5% level of significance?

The p-value in the deviance test is smaller than 0.05, which indicates a good fit of the model. Significant variables at the 5% level are quiet time, stress level, and part-time employment status.

In SAS:

```
/*checking model fit*/
proc genmod;
 model sleephours = / dist=normal link=identity;
```

```
run;
```

```
Log Likelihood -73.0195
```

```
data deviance_test;
 deviance = -2*(-73.0195 - (-54.6201));
  pvalue = 1 - probchi(deviance,10);
run;

proc print noobs;
run;
```

```
deviance        pvalue
 36.7988    .000061312
```

In R:

```
#checking model fit
null.model<- glm(sleephours ~ 1, data=sleep.data, family=gaussian(link=identity))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
36.79887
```

```
print(p.value<- pchisq(deviance, df=10, lower.tail = FALSE))
```

```
6.131066e-05
```

(c) Interpret the estimated significant regression coefficients.

It is estimated that for each extra minute of quiet time, a person would get on average 0.0074 hours more sleep per night. For a unit increase in stress level, the estimated average number of hours of night sleep decrease by 0.1398. It is estimated that, on average, someone working part-time would get 1.0484 more hours of sleep compared to someone who is working full-time.

(d) Find the estimated number of hours of night's sleep that a 30-year old full-time mom of three children under the age of five has, if she gets 10 minutes a day for herself, walks to the park with her kids every day of the week, estimates her stress level as 7, and who hasn't gotten any vacation for one year.

Below we calculate the predicted number of hours of night's sleep that a 30-year old full-time mom of three children under the age of five has, if she gets 10 minutes a day for herself, walks to the park with her kids every day of the week, estimates her stress level as 7, and who hasn't gotten any vacation for one year.

$$
\begin{aligned}
sleephours^0 = {} & 6.8260 - 0.0037 \cdot 30 + 0.0074 \cdot 10 + 0.1204 \cdot 3 - 0.1398 \cdot 7 + 0.0204 \cdot 7 \\
& + 0.0050 \cdot 12 \ = \ 6.3744.
\end{aligned}
$$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input age gender$ quiettime nchildren stresslevel jobstatus$ nactivities pastvac;
cards;
30 F 10 3 7 full 7 12
```

```
;

data sleep;
 set sleep predict;
run;

proc genmod;
 class gender jobstatus;
  model sleephours = age gender quiettime nchildren stresslevel jobstatus
       nactivities pastvac / dist=normal link=identity;
   output out=outdata p=psleephours;
run;

proc print data=outdata (firstobs=51) noobs;
 var psleephours;
run;
```

```
psleephours
    6.37616
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(age=30, gender.rel='F', quiettime=10,
nchildren=3, stresslevel=7, jobstatus.rel='full', nactivities=7, pastvac=12)))
```

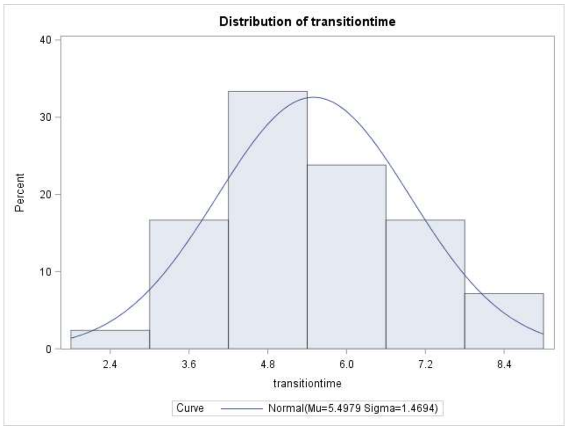
```
6.376164
```

EXERCISE 1.5. (a) Compute the total time spent on both transitions. Verify normality of the distribution of this variable, and fit a general linear regression model. Specify the fitted model.

In SAS:

```
data time;
input age gender$ run t1 bike t2 swim @@;
   transitiontime=t1+t2;
cards;
55 M 24.17  2.60  37.95 2.50  5.70  59 F 34.88  2.83  52.15 3.05  5.20
24 M 32.97  2.55  59.20 3.47  5.37  53 F 22.2   1.83  46.70 2.15  5.50
51 M 27.35  1.75  42.05 2.32  3.75  38 F  32.13 2.38  50.92 2.95  6.00
66 M 25.39  1.95  41.57 2.80  3.93  30 F 24.67  1.58  48.28 2.77  5.68
43 F 42.33  2.78  63.60 4.08  7.18  47 F 28.73  2.35  45.57 3.90  6.62
26 F 29.62  2.92  51.23 3.85  4.92  45 M 22.23  2.07  38.95 2.35  4.28
29 F 26.93  2.10  44.33 2.45  7.47  34 M 17.75  0.75  33.27 1.23  3.65
39 M 37.47  2.52  55.67 4.47  8.60  54 M 36.63  3.27  43.92 3.08  7.15
26 M 34.42  2.73  52.62 2.67  9.23  36 M 27.38  2.22  39.03 2.92  7.43
42 M 21.37  2.12  35.95 1.93  3.95  49 M 29.03  4.50  38.53 3.95  8.80
42 F 28.53  3.27  49.85 3.67  8.13  42 F 25.12  1.72  39.52 2.50  4.55
42 F 26.33  1.70  48.98 2.30  5.02  41 F 36.75  3.95  62.85 3.13  6.93
15 M 25.12  1.70  44.75 3.20  7.48  48 M 26.52  4.43  40.98 3.82  6.58
37 M 28.3   2.85  41.78 3.47  6.02  55 M 31.25  2.70  43.43 3.25  5.25
42 M 24.38  1.45  37.13 1.83  3.70  25 M 33.45  2.25  51.38 4.03  7.45
12 F 27.62  2.23  55.47 2.97  4.37  23 F 28.55  2.17  54.57 2.55  7.90
49 M 33.88  2.77  54.82 3.87  6.90  53 F 26.97  1.77  42.33 3.40  6.58
45 F 26.58  1.65  44.30 2.52  5.40  33 F 32.32  2.10  54.87 2.32  6.25
```

```
63 M 40.53  3.78  69.75 3.83  12.17 50 M 33.68  3.07  43.57 3.13  5.77
43 F 34.93  2.58  62.35 2.95  7.92  24 M 22.88  1.82  39.55 2.12  4.03
44 M 29.25  2.47  45.60 2.75  9.18  51 F 36.98  3.70  46.58 5.18  7.60
;

/*running normality check*/
proc univariate;
 var transitiontime;
  histogram/normal;
run;
```



```
   Goodness-of-Fit Tests for Normal Distribution
Test                  Statistic        p Value
Kolmogorov-Smirnov D    0.07499320 Pr > D    >0.150
Cramer-von Mises   W-Sq 0.03895414 Pr > W-Sq >0.250
Anderson-Darling   A-Sq 0.26390584 Pr > A-Sq >0.250
```

The p-values in the normality tests are above 0.05, which means that the response variable has a normal distribution. The histogram displays a bell-shaped curve, supporting the normality conclusion.

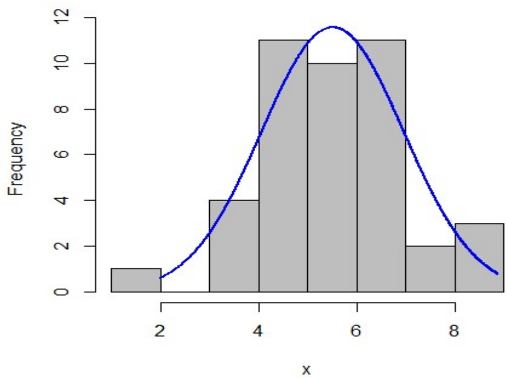
```
/*fitting general linear model*/
proc genmod;
 class gender;
  model transitiontime = age gender run bike swim / dist=normal link=identity;
run;
```

```
Log Likelihood -56.4150

                Analysis Of Maximum Likelihood Parameter Estimates
Parameter    DF Estimate Standard    Wald 95% Confidence        Wald Chi- Pr > ChiSq
                          Error          Limits                  Square
Intercept     1   0.5293   1.0253      -1.4803       2.5388         0.27     0.6057
age           1   0.0067   0.0128      -0.0184       0.0318         0.27     0.6032
gender     F  1   0.0961   0.3256      -0.5421       0.7343         0.09     0.7679
gender     M  0   0.0000   0.0000       0.0000       0.0000            .          .
run           1   0.1964   0.0500       0.0985       0.2943        15.46     <.0001
bike          1  -0.0565   0.0328      -0.1207       0.0078         2.97     0.0849
swim          1   0.2475   0.1024       0.0468       0.4483         5.84     0.0156
Scale         1   0.9271   0.1012       0.7486       1.1481
```

The fitted model is $\hat{E}(transitiontime) = 0.5293 + 0.0067 \cdot age + 0.0961 \cdot female + 0.1964 \cdot run - 0.0565 \cdot bike + 0.2475 \cdot swim$, and $\hat{\sigma} = 0.9271$.

In R:

```
time.data<- read.csv(file="C:/<insert path>/Exercise1.5Data.csv", header=TRUE,
sep=',')

#computing total transition time
transition.time<- time.data$t1 + time.data$t2

#running normality check
library(rcompanion)
plotNormalHistogram(transition.time)
```



```
shapiro.test(transition.time)

Shapiro-Wilk normality test

W = 0.97896, p-value = 0.6216

#specifying reference levels
gender.rel<- relevel(time.data$gender, ref="M")

#fitting general linear model
summary(fitted.model<- glm(transition.time ~ age + gender.rel + run + bike +
swim, data=time.data, family=gaussian(link=identity)))

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.529266   1.107464   0.478 0.635605
age          0.006659   0.013837   0.481 0.633232
gender.relF  0.096094   0.351716   0.273 0.786250
run          0.196405   0.053953   3.640 0.000849
bike        -0.056487   0.035412  -1.595 0.119427
swim         0.247544   0.110615   2.238 0.031507

#outputting estimated sigma
sigma(fitted.model)

1.001351
```

(b) Discuss the model fit. Are all the predictors in that model significant at the 5% significance level?

In SAS:

```
/*checking model fit*/
proc genmod;
 model transitiontime = / dist=normal link=identity;
run;
```

```
Log Likelihood -74.6263
```

```
data deviance_test;
 deviance = -2*(-74.6263 - (-56.4150));
  pvalue = 1 - probchi(deviance,5);
run;

proc print noobs;
run;
```

```
deviance      pvalue
 36.4226  .000000782
```

Since the p-value in the deviance test is tiny, the model has a good fit. The only significant predictors at the 5% level are run time and swim time.

In R:

```
#checking model fit
null.model<- glm(transition.time ~ 1, data=time.data,
family=gaussian(link=identity))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
36.42269
```

```
print(p.value<- pchisq(deviance, df=5, lower.tail = FALSE))
```

```
7.817128e-07
```

(c) Interpret only the estimated significant regression coefficients of this model.

The estimated average transition time increases by 0.1964 for a one-minute increase in run time. For a one-minute increase in swim time, the estimated average transition time increases by 0.2475.

(d) What is the predicted total time at transitions for the student, if his best result in 5-kilometer run is 27:32, 13-mile bike is 56:17, and 200-meter swim is 8:46?

Below we compute the predicted time at transitions for the 25-year-old student with a 27:32 run, 56:17 bike, and 8:46 swim. First we convert the times into minutes: 27+32/60=27.53, 56+17/60=56.28, and 8+46/60=8.77. The calculation is as follows: $transitiontime^0 = 0.5293 + 0.0067 \cdot 25 + 0.1964 \cdot 27.53 - 0.0565 \cdot 56.28 + 0.2475 \cdot 8.77 = 5.09$.

In SAS:

```
/*using fitted model for prediction*/
data predict;
```

```
input age gender$ run bike swim;
cards;
25 M 27.53 56.28 8.77
;
data time;
 set time predict;
run;

proc genmod;
 class gender;
  model transitiontime = age gender run bike swim / dist=normal link=identity;
   output out=outdata p=ptransitiontime;
run;

proc print data=outdata (firstobs=43) noobs;
 var ptransitiontime;
run;
```

```
ptransitiontime
        5.09465
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(age=25, gender.rel='M',  run=27.53,
bike=56.28, swim=8.77)))
```

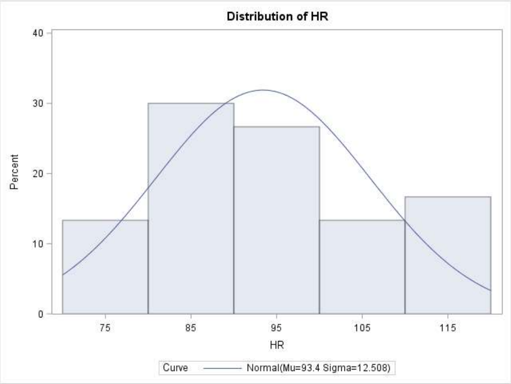
```
5.094653
```

EXERCISE 1.6. (a) Check that the measurements for the heart rate are coming from a normal distribution. Fit the regression model and specify all estimated parameters.

In SAS:

```
data heartrate;
length AQI $9.;
input age gender$ ethnicity$ BMI nmeds AQI$ HR @@;
cards;
48 F  Black    29.9 0 good      76   56 F White    22.9 3 unhealthy 112
67 F  White    23.4 1 good      94   82 M Black    29.7 0 good      92
64 F  White    31.4 3 good      97   58 M White    18.9 2 moderate  79
72 F  Black    25.2 0 moderate  114  70 F Black    25.9 1 moderate  115
54 M  Hispanic 29.6 0 moderate  80   57 F Hispanic 20.2 2 good      81
50 F  Black    23.9 1 unhealthy 97   59 F Hispanic 22.6 0 good      86
61 M  Hispanic 32.8 1 good      84   69 M Hispanic 24.1 2 unhealthy 94
65 F  Black    23.4 2 moderate  114  66 F Hispanic 27.8 3 good      82
74 M  White    32.4 1 moderate  97   66 M Hispanic 22.9 2 good      86
53 M  Hispanic 25.2 0 good      84   55 M Hispanic 24.6 0 moderate  94
73 F  Hispanic 24.8 3 moderate  105  45 F Hispanic 19.0 2 unhealthy 83
71 F  White    20.3 2 unhealthy 111  63 M Black    23.8 2 unhealthy 108
71 F  White    21.5 2 moderate  100  62 M Hispanic 27.4 3 good      79
44 F  Hispanic 17.2 0 unhealthy 86   49 M White    17.1 1 good      75
63 M  Black    28.0 2 good      91   65 F Hispanic 22.2 1 moderate  106
;

/*running normality check*/
```

```
proc univariate;
 var HR;
  histogram/normal;
run;
```



```
  Goodness-of-Fit Tests for Normal Distribution
Test                  Statistic         p Value
Kolmogorov-Smirnov D    0.15627802 Pr > D    0.061
Cramer-von Mises   W-Sq 0.09496306 Pr > W-Sq 0.129
Anderson-Darling   A-Sq 0.65250988 Pr > A-Sq 0.084
```

Based on the histograms and the large p-values, we can conclude that the heart rate follows a normal distribution.

```
/*fitting generallinear model*/
proc genmod;
 class gender ethnicity(ref='Hispanic') AQI(ref='good');
  model HR = age gender ethnicity BMI nmeds AQI / dist=normal link=identity;
run;
```

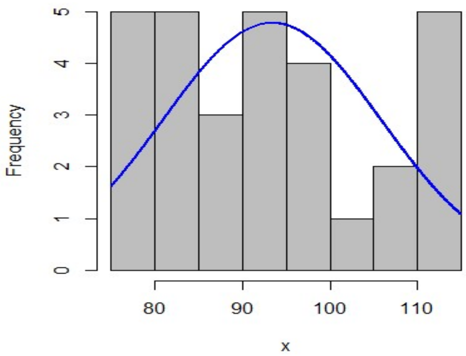
```
Log Likelihood -96.2779
```

```
                Analysis Of Maximum Likelihood Parameter Estimates
Parameter            DF Estimate Standard  Wald 95% Confidence   Wald Chi- Pr > ChiSq
                                 Error           Limits           Square
Intercept             1  38.0164  10.2408   17.9449    58.0879      13.78      0.0002
age                   1   0.6503   0.1472    0.3617     0.9389      19.51      <.0001
gender    F           1   7.1031   2.3608    2.4760    11.7303       9.05      0.0026
gender    M           0   0.0000   0.0000    0.0000     0.0000          .           .
ethnicity Black       1   7.5351   2.8956    1.8598    13.2104       6.77      0.0093
ethnicity White       1   2.2633   2.7895   -3.2041     7.7306       0.66      0.4172
ethnicity Hispanic    0   0.0000   0.0000    0.0000     0.0000          .           .
BMI                   1   0.0431   0.3225   -0.5890     0.6751       0.02      0.8938
nmeds                 1   0.4384   1.1919   -1.8976     2.7743       0.14      0.7130
AQI       moderate    1  10.8596   2.6942    5.5790    16.1402      16.25      <.0001
AQI       unhealthy   1  14.1674   3.1905    7.9142    20.4206      19.72      <.0001
AQI       good        0   0.0000   0.0000    0.0000     0.0000          .           .
Scale                 1   5.9914   0.7735    4.6520     7.7165
```

The fitted model is $\widehat{E}(HR) = 38.0164 + 0.6503 \cdot age + 7.1031 \cdot female + 7.5351 \cdot Black + 2.2633 \cdot White + 0.0431 \cdot BMI + 0.4384 \cdot nmeds + 10.8596 \cdot AQImoderate + 14.1674 \cdot AQIunhealthy$, and $\hat{\sigma} = 5.9914$.

In R:

```
hr.data<- read.csv(file="C:/<insert path>/Exercise1.6Data.csv", header=TRUE,
sep=',')

#running normality check
library(rcompanion)
plotNormalHistogram(hr.data$HR)
```



```
shapiro.test(hr.data$HR)
```

```
Shapiro-Wilk normality test

W = 0.93047, p-value = 0.05054
```

```
#specifying reference levels
gender.rel<- relevel(hr.data$gender, ref="M")
ethnicity.rel<- relevel(hr.data$ethnicity, ref="Hispanic")
AQI.rel<- relevel(hr.data$AQI, ref="good")

#fitting general linear model
summary(fitted.model<- glm(HR ~ age + gender.rel + ethnicity.rel + BMI + nmeds +
AQI.rel, data=hr.data, family=gaussian(link=identity)))
```

```
Coefficients:
                   Estimate Std. Error t value Pr(>|t|)
(Intercept)        38.01638   12.24005   3.106  0.00535
age                 0.65033    0.17599   3.695  0.00134
gender.relF         7.10311    2.82173   2.517  0.02002
ethnicity.relBlack  7.53509    3.46094   2.177  0.04102
ethnicity.relWhite  2.26328    3.33411   0.679  0.50466
BMI                 0.04306    0.38543   0.112  0.91210
nmeds               0.43836    1.42454   0.308  0.76133
AQI.relmoderate    10.85963    3.22023   3.372  0.00288
AQI.relunhealthy   14.16737    3.81333   3.715  0.00128
```

```
#outputting estimated sigma
sigma(fitted.model)
```

```
7.161087
```

(b) Discuss the goodness-of-fit of the model. What variables are significant predictors of heart rate at the 5% level of significance?

In SAS:

```
/*checking model fit*/
proc genmod;
 model HR = / dist=normal link=identity;
run;
```

```
Log Likelihood -117.8512
```

```
data deviance_test;
 deviance = -2*(-117.8512 - (-96.2779));
  pvalue = 1 - probchi(deviance,8);
run;

proc print noobs;
run;
```

```
deviance      pvalue
 43.1466  .000000824
```

Since the p-value in the deviance test is tiny, the model has a good fit. The significant predictors at the 5% level are age, gender, ethnicity level Black, and both levels of AQI.

In R:

```
#checking model fit
null.model<- glm(HR ~ 1, data=hr.data, family=gaussian(link=identity))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
43.14658
```

```
print(p.value<- pchisq(deviance, df=8, lower.tail=FALSE))
```

```
8.243212e-07
```

(c) Give interpretation of the estimated statistically significant regression coefficients.

As age increases by one year, the estimated average heart rate increases by 0.6503 beats per minute. The estimated average heart rate for females is 7.1031 beats per minute larger than that for males. The estimated average heart rate for Blacks is 7.5351 beats per minute larger than that for Hispanics. The estimated average heart rate for people living with moderate air quality is 10.8956 beats per minute larger than that for people living with good air quality. The estimated average heart rate for people living with moderate air quality is 14.1674beats per minute larger than that for people living with good air quality.

(d) Compute the predicted heart rate of a 50-year-old Hispanic male who has a BMI of 20, is not taking any heart medications, and resides in an area with a moderate air quality.

The predicted heart rate of a 50-year-old Hispanic male who has a BMI of 20, is not taking any heart medications, and resides in an area with a moderate air quality is computed as follows:

$$\widehat{HR}^0 = 38.0164 + 0.6503 \cdot 50 + 0.0431 \cdot 20 + 10.8596 \; = \; 82.253.$$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input age gender$ ethnicity$ BMI nmeds AQI$;
cards;
50 M Hispanic 20 0 moderate
;

data heartrate;
set heartrate predict;
run;

proc genmod;
 class gender ethnicity AQI;
  model HR = age gender ethnicity BMI nmeds AQI / dist=normal link=identity;
   output out=outdata p=pHR;
run;

proc print data=outdata (firstobs=31) noobs;
 var pHR;
run;
```

```
    pHR
82.2536
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(age=50, gender.rel='M',  ethnicity.rel='Hi
spanic', BMI=20, nmeds=0, AQI.rel='moderate')))
```

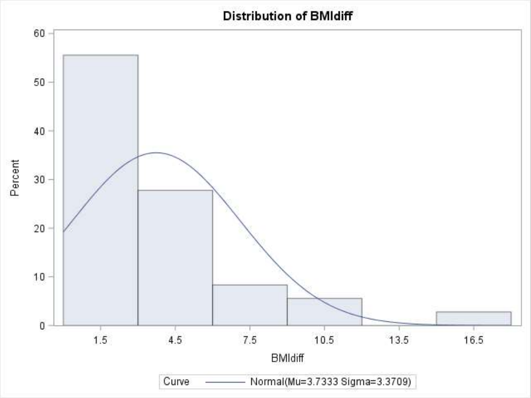
```
82.25361
```

CHAPTER 2

EXERCISE 2.1. (a) Is the decrease in BMI percentile (preBMI-postBMI) normally distributed? Plot a histogram and test for normality of the distribution.

In SAS:

```
data obesity;
input gender$ age group$ preBMI postBMI @@;
  BMIdiff=preBMI-postBMI;
   female=(gender='F');
    control=(group='Cx');
cards;
F 6  Cx 85.7 83.8  F 6  Cx 93.8 92.9  F 7 Cx 93.5 92.5   F 8  Cx 90.1 89.8
F 9  Tx 92.3 90.7  F 9  Tx 90.3 88.3  F 12 Cx 87.6 85.9  F 12 Cx 87.2 84.1
F 12 Tx 96.9 94.9  F 12 Tx 85.8 81.2  F 13 Cx 96.7 94.1  F 13 Cx 93.5 92.9
F 13 Tx 92.3 87.5  F 13 Tx 85.3 83.7  F 14 Tx 95.5 78.7  F 15 Cx 91.3 89.9
F 15 Tx 95.8 87.1  F 16 Tx 90.7 87.2  M 6  Cx 92.6 88.1  M 7  Cx 95.8 94.7
M 7  Cx 90.4 89.1  M 7  Cx 91.2 88.6  M 8  Tx 94.4 87.8  M 8  Tx 93.2 87.3
M 10 Cx 93.9 91.5  M 10 Tx 96.2 91.1  M 10 Tx 89.4 87.9  M 11 Tx 86.2 77.1
M 11 Tx 95.4 84.8  M 12 Cx 97.7 95.8  M 13 Tx 85.3 80.0  M 13 Tx 86.2 82.4
M 14 Cx 85.5 83.6  M 14 Cx 97.8 93.8  M 16 Cx 95.0 93.6  M 16 Tx 93.1 86.8
;

/*running normality check of response*/
proc univariate;
 var BMIdiff;
  histogram/normal;
run;
```

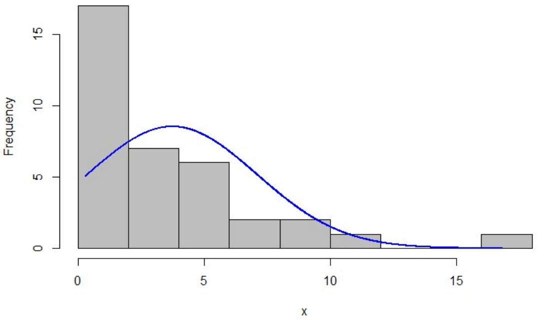


```
  Goodness-of-Fit Tests for Normal Distribution
Test                 Statistic        p Value
Kolmogorov-Smirnov D     0.18720025 Pr > D     <0.010
Cramer-von Mises   W-Sq  0.36512474 Pr > W-Sq <0.005
Anderson-Darling   A-Sq  2.15289200 Pr > A-Sq <0.005
```

Neither the histogram nor the normality tests support normality of the response. In fact, the distribution is right-skewed.

In R:

```
bmi.data<- read.csv(file="C:/<insert path>/Exercise2.1Data.csv",header=TRUE,
sep=',')

#creating the difference in BMI
BMIdiff<- bmi.data$preBMI-bmi.data$postBMI

#running normality check of response
library(rcompanion)
plotNormalHistogram(BMIdiff)
```



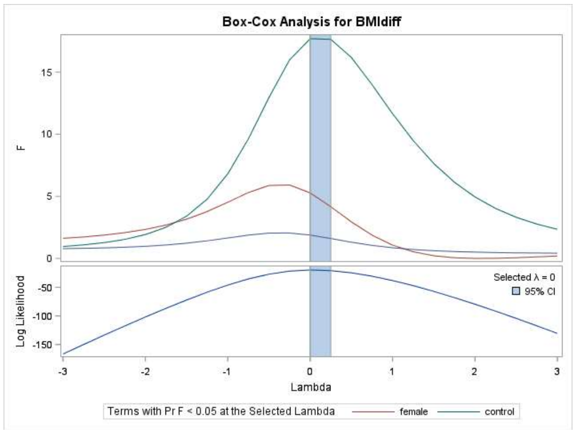
```
shapiro.test(BMIdiff)
```

```
Shapiro-Wilk normality test
W = 0.79159, p-value = 1.114e-05
```

(b) Find the optimal lambda for Box-Cox transformation. Transform the change in BMI percentile (find the appropriate transformation in Table 2.1), and show that the transformed variable is normally distributed. Plot the histogram and do a formal testing.

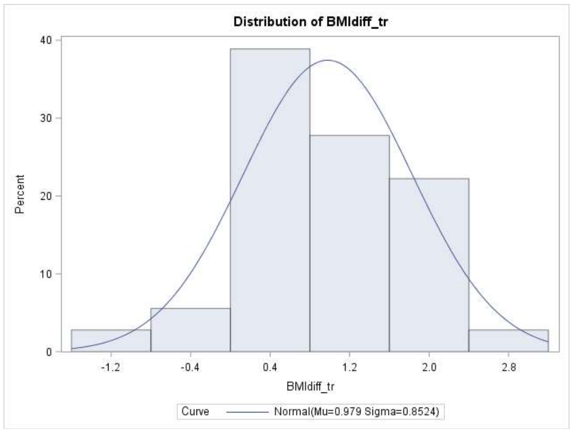
In SAS:

```
/*finding optimal lambda for Box-Cox transformation*/
proc transreg;
model BoxCox(BMIdiff) = identity(age female control);
run;
```



```
/*applying Box-Cox transformation with lambda=0*/
data obesity;
```

```
set obesity;
 BMIdiff_tr=log(BMIdiff);
run;

/*running normality check of transformed response*/
proc univariate;
 var BMIdiff_tr;
  histogram/normal;
run;
```



```
      Goodness-of-Fit Tests for Normal Distribution
 Test                 Statistic          p Value
 Kolmogorov-Smirnov  D     0.10351850  Pr > D     >0.150
 Cramer-von Mises    W-Sq  0.03884400  Pr > W-Sq  >0.250
 Anderson-Darling    A-Sq  0.22534295  Pr > A-Sq  >0.250
```

The optimal lambda for the Box-Cox transformation is $\lambda = 0$, which corresponds to the log-transformation. The log-transformed response variable has a normal distribution as backed up by a bell shape on the histogram and the large p-values in the normality tests.

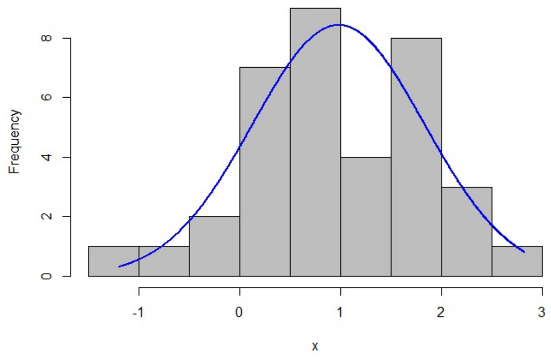
In R:

```
#creating indicator variables
female<- relevel(bmi.data$gender, ref="M")
control<- relevel(bmi.data$group, ref="Tx")

#finding optimal lambda for Box-Cox transformation
library(MASS)

BoxCox.fit<- boxcox(BMIdiff ~ age + female + control, data=bmi.data, lambda = 
seq(-3,3,1/4), interp = FALSE)
BoxCox.data<- data.frame(BoxCox.fit$x, BoxCox.fit$y)
ordered.data<- BoxCox.data[with(BoxCox.data, order(-BoxCox.fit.y)),]
ordered.data[1,]
```

```
BoxCox.fit.x BoxCox.fit.y

           0    -46.71658
```

```
#applying Box-Cox transformation with lambda=0
BMIdiff.tr<- log(BMIdiff)

#running normality check of transformed response
```

```
library(rcompanion)
plotNormalHistogram(BMIdiff.tr)
```



```
shapiro.test(BMIdiff.tr)
```

```
Shapiro-Wilk normality test
W = 0.9877, p-value = 0.9532
```

(c) Fit the general regression model to the Box-Cox tranformed change in BMI percentile. Does this model have a good fit?

In SAS:

```
/*fitting general linear model to transformed response*/
proc genmod;
 model BMIdiff_tr = age female control / dist=normal link=identity;
run;
```

```
 Log Likelihood -33.2950

                Analysis Of Maximum Likelihood Parameter Estimates
 Parameter DF Estimate Standard    Wald 95% Confidence        Wald Chi- Pr > ChiSq
                          Error          Limits                  Square
 Intercept  1   1.1438   0.4333      0.2945       1.9930           6.97     0.0083
 age        1   0.0501   0.0344     -0.0174       0.1176           2.12     0.1457
 female     1  -0.4986   0.2047     -0.8998      -0.0975           5.94     0.0148
 control    1  -0.9384   0.2103     -1.3506      -0.5262          19.91     <.0001
 Scale      1   0.6101   0.0719      0.4843       0.7687
```

The fitted model is $\hat{E}\ (\ln BMIdiff) = 1.1438 + 0.0501 \cdot age - 0.4986 \cdot female - 0.9384 \cdot control,$ and $\hat{\sigma} = 0.6101.$

```
/*checking model fit*/
proc genmod;
 model BMIdiff_tr = / dist=normal link=identity;
run;
```

```
 Log Likelihood -44.8268
```

```
data deviance_test;
 deviance = -2*(-44.8268 - (-33.2950));
```

```
  pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance      pvalue
 23.0636  .000039169
```

Based on the small p-value in the deviance test, the model for the log-transformed response fits the data well.

In R:

```
#fitting general linear model to transformed response

summary(fitted.model<- glm(BMIdiff.tr ~ age + female + control, data=bmi.data,
family=gaussian(link=identity)))
```

```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  1.14375    0.45959   2.489 0.018218
age          0.05008    0.03651   1.372 0.179731
femaleF     -0.49862    0.21708  -2.297 0.028317
controlCx   -0.93835    0.22307  -4.207 0.000195
```

```
#outputting estimated sigma

sigma(fitted.model)
```

```
0.6471448
```

```
#checking model fit

null.model<- glm(BMIdiff.tr ~ 1, family=gaussian(link=identity))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
23.06361
```

```
print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))
```

```
3.916872e-05
```

(d) What predictors are significant at the 5% level? Write the interpretation of the estimated regression coefficients for the significant predictors only.

Gender and group are significant predictors. The estimated mean of log-transformed reduction in BMI percentile is 0.4986 units larger in females than in males. The estimated average log-transformed decrease in BMI percentile for the control group participants is 0.9384 units smaller than that for participants in the intervention group (conclusion: intervention works).

(e) Predict change in BMI percentile for a 9-year old girl in the control group.

To predict the change in BMI percentile for a 9-year old girl in the control group, we calculate:

$$BMIdiff^0 = \exp(1.1438 + 0.0501 \cdot 9 - 0.4986 - 0.9384) = 1.1708.$$

In SAS:

```
data predict;
input age female control;
cards;
9 1 1
;

data obesity;
set obesity predict;
run;

proc genmod;
 model BMIdiff_tr = age female control / dist=normal link=identity;
  output out=outdata p=pBMIdiff_tr;
run;

data outdata;
set outdata;
 pBMIdiff=exp(pBMIdiff_tr);
run;

proc print data=outdata(firstobs=37) noobs;
 var pBMIdiff;
run;
```

```
pBMIdiff
 1.17061
```

In R:

```
#using fitted model for prediction
pred.BMIdiff.tr<- predict(fitted.model, data.frame(female='F', age=9,
control='Cx'))
print(exp(pred.BMIdiff.tr))
```

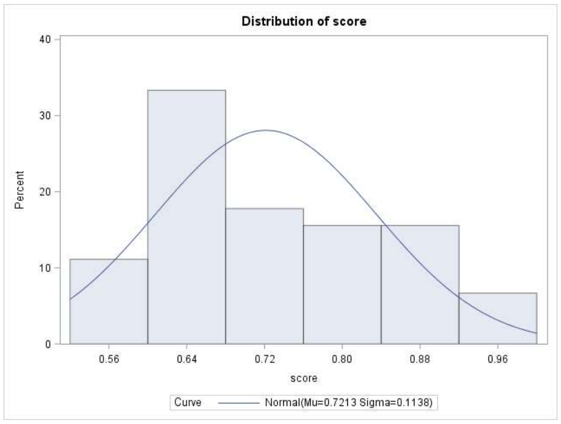
```
1.170609
```

EXERCISE 2.2. (a) Construct a histogram of the score. Does the distribution look normal? Perform the test for normality. Draw conclusion.

In SAS:

```
data QI;
length desgn $6.;
input desgn$ wrkyrs priorQI$ score @@;
 nurse=(desgn='nurse');
  doctor=(desgn='doctor');
    priorQIyes=(priorQI='yes');
      score=score/100;
cards;
nurse  16 yes 63  nurse  9  yes 93  nurse  8  yes 74
nurse  1  no  69  nurse  5  no  67  nurse  3  no  66
nurse  24 no  86  nurse  4  no  74  nurse  1  no  88
nurse  24 no  84  nurse  3  no  97  doctor 2  yes 88
doctor 5  yes 78  doctor 26 yes 82  doctor 3  no  57
doctor 3  no  88  doctor 15 no  78  doctor 4  no  65
doctor 25 no  78  staff  3  yes 62  staff  21 no  55
staff  8  no  62  staff  11 no  67  nurse  8  yes 62
```

```
nurse  22 yes 68  nurse  4  no  93  nurse  6  no  77
nurse  2  no  59  nurse  20 no  64  nurse  2  no  70
nurse  3  no  63  nurse  16 no  65  nurse  18 no  73
nurse  15 no  76  doctor 2  yes 85  doctor 7  yes 91
doctor 2 yes  69  doctor 20 no  66  doctor 13 no  55
doctor 8  no  62  doctor 14 no  61  staff  9  yes 57
staff  11 yes 69  staff  19 no  64  staff  17 no  76
;

/*running normality check of response*/
proc univariate;
 var score;
  histogram/normal;
run;
```

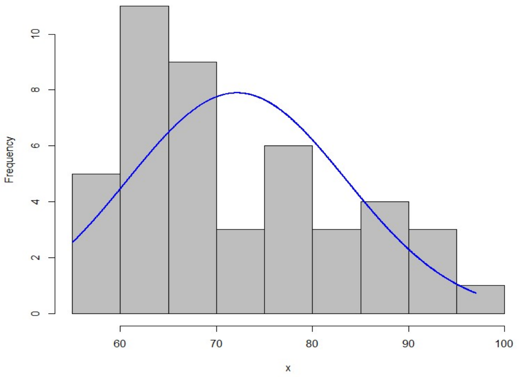


```
  Goodness-of-Fit Tests for Normal Distribution
Test                  Statistic        p Value
Kolmogorov-Smirnov D    0.14185097 Pr > D    0.023
Cramer-von Mises   W-Sq 0.14986260 Pr > W-Sq 0.023
Anderson-Darling   A-Sq 0.88141925 Pr > A-Sq 0.023
```

The histogram shows a right-skewed distribution. The normality tests support the conclusion that the distribution is not normal, since the p-values are below 0.05.

In R:

```
jobscore.data<- read.csv(file="C:/<insert path>/Exercise2.2Data.csv",
header=TRUE, sep=',')

#running normality check of response
library(rcompanion)

plotNormalHistogram(jobscore.data$score)
```



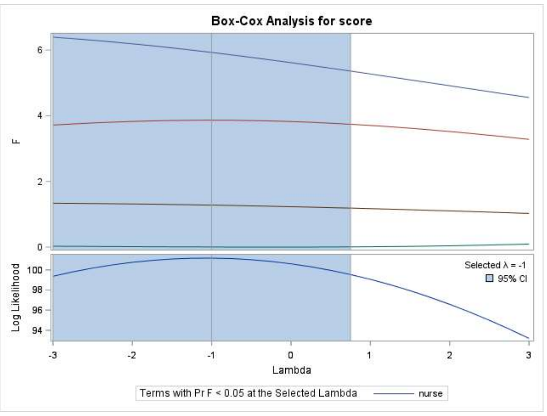
```
shapiro.test(jobscore.data$score)
```

```
Shapiro-Wilk normality test

W = 0.94357, p-value = 0.02913
```

(b) Transform the score variable using a meaningful Box-Cox transformation and assure that it is now normally distributed by plotting the histogram and doing normality testing.

In SAS:

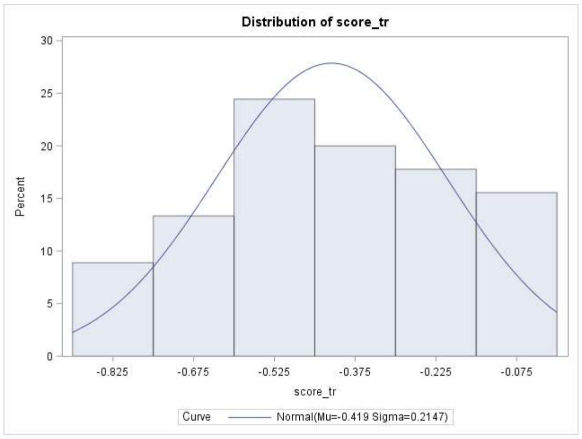
```
/*finding optimal lambda for Box-Cox transformation*/
proc transreg;
 model BoxCox(score) = identity(nurse doctor wrkyrs priorQIyes);
run;
```



The optimal lambda for the Box-Cox transformation is $\lambda = -1$, which corresponds to the inverse transformation. The inverse-transformed response variable has a normal distribution as can be seen from the histogram and the large p-values in the normality tests.

```
/*applying Box-Cox transformation with lambda=-1*/
data qi;
set qi;
 score_tr=1-(1/score);
run;

/*running normality check of transformed response*/
proc univariate;
 var score_tr;
  histogram/normal;
```

```
run;
```



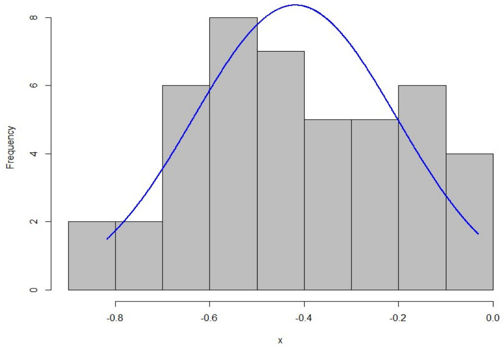
```
  Goodness-of-Fit Tests for Normal Distribution
Test                 Statistic       p Value
Kolmogorov-Smirnov D    0.08928583 Pr > D    >0.150
Cramer-von Mises   W-Sq 0.07051371 Pr > W-Sq >0.250
Anderson-Darling   A-Sq 0.44867900 Pr > A-Sq >0.250
```

In R:

```
#creating indicator variables and rescaling score
desgn.rel<- relevel(jobscore.data$desgn, ref="staff")
priorQI.rel<- relevel(jobscore.data$priorQI, ref="no")
score<- jobscore.data$score/100

#finding optimal lambda for Box-Cox transformation
library(MASS)
BoxCox.fit<- boxcox(score ~ desgn.rel + wrkyrs + priorQI.rel,
data=jobscore.data, lambda=seq(-3,3,1/4), interp = FALSE)
BoxCox.data<- data.frame(BoxCox.fit$x, BoxCox.fit$y)
ordered.data<- BoxCox.data[with(BoxCox.data, order(-BoxCox.fit.y)),]
ordered.data[1,]
```

```
BoxCox.fit.x BoxCox.fit.y

          -1     2.940242
```

```
#applying Box-Cox transformation with lambda=-1
score.tr<- 1-(1/score)

#running normality check of transformed response
plotNormalHistogram(score.tr)
```



```
shapiro.test(score.tr)
```

```
Shapiro-Wilk normality test

W = 0.96606, p-value = 0.2073
```

(c) Run the general linear regression model on the transformed score. What predictors are significant at the 0.05 level?

In SAS:

```
/*fitting general linear model to transformed response*/
proc genmod;
 model score_tr = nurse doctor wrkyrs priorQIyes / dist=normal link=identity;
run;
```

```
Log Likelihood 9.5061

Analysis Of Maximum Likelihood Parameter Estimates
Parameter  DF Estimate Standard Wald 95% Confidence      Wald Chi-      Pr > ChiSq
                       Error    Limits                   Square
Intercept  1  -0.6093  0.0888   -0.7833      -0.4353     47.11          <.0001
nurse      1  0.2122   0.0822   0.0511       0.3733      6.67           0.0098
doctor     1  0.1799   0.0863   0.0108       0.3490      4.35           0.0371
wrkyrs     1  0.0002   0.0039   -0.0073      0.0078      0.00           0.9497
priorQIyes 1  0.0773   0.0644   -0.0490      0.2035      1.44           0.2304
Scale      1  0.1959   0.0206   0.1593       0.2408
```

The fitted model is $\hat{E}\left(1-\frac{1}{score}\right) = -0.6093 + 0.2122 \cdot nurse + 0.1799 \cdot doctor + 0.0002 \cdot wrkyrs + 0.0773 \cdot priorQIyes,$ and $\hat{\sigma} = 0.1959$. Judging by p-values, nurse and doctor are significant predictors.

In R:

```
#fitting general linear model to transformed response
summary(fitted.model<- glm(score.tr ~ desgn.rel + wrkyrs + priorQI.rel,
data=jobscore.data, family=gaussian(link = identity)))
```

```
Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)     -0.609290   0.094150  -6.471 1.03e-07
desgn.reldoctor  0.179873   0.091507   1.966   0.0563
desgn.relnurse   0.212200   0.087173   2.434   0.0195
```

```
wrkyrs          0.000243   0.004086   0.059   0.9529
priorQI.relyes  0.077263   0.068323   1.131   0.2649
```

```
#outputting estimated sigma
sigma(fitted.model)
```

```
0.2077762
```

(d) Interpret the estimates of the significant beta coefficients. Does the model fit the data well? Conduct the chi-squared deviance test.

The estimated mean inverse transformed score for nurses is 0.2122 points above that for staff, and for doctors it is 0.1799 points above that for staff.

The model doesn't really fit the data well, as seen from the large p-value of the deviance test given below.

In SAS:

```
/*checking model fit*/
proc genmod;
 model score_tr = / dist=normal link=identity;
run;
```

```
Log Likelihood 5.8777
```

```
data deviance_test;
 deviance = -2*(5.8777 - 9.5061);
 pvalue = 1 - probchi(deviance,4);
run;

proc print noobs;
run;
```

```
deviance  pvalue
7.2568   0.12292
```

In R:

```
#checking model fit
null.model<- glm(score.tr ~ 1, family = gaussian(link=identity))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
7.256887
```

```
print(p.value<- pchisq( deviance, df=4, lower.tail = FALSE))
```

```
0.1229198
```

(e) Predict the score for a nurse who has worked at the center for seven years and who had previously been a co-PI on a grant that involved quality assurance component.

We calculate $score^0 = 100 \cdot (1—(0.6093 + 0.2122 + 0.0002 \cdot 7 + 0.0773))^{-1} = 75.84951$.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input nurse doctor wrkyrs priorQIyes;
cards;
1 0 7 1
;

data QI;
set QI predict;
run;

proc genmod;
 model score_tr = nurse doctor wrkyrs priorQIyes / dist=normal link=identity;
  output out=outdata p=pscore_tr;
run;

data outdata;
set outdata;
 pscore=100/(1-pscore_tr);
run;

proc print data=outdata (firstobs=46) noobs;
 var pscore;
run;
```

```
pscore

75.8653
```

In R:

```
#using fitted model for prediction
pscore.tr<- predict(fitted.model, data.frame(desgn.rel='nurse', wrkyrs=7,
priorQI.rel='yes'))
print(100/(1-pscore.tr))
```

```
75.86528
```

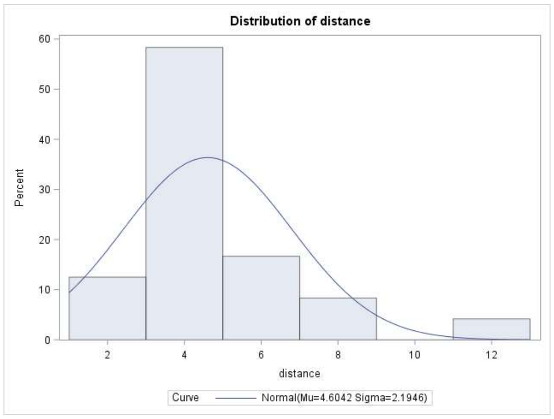
EXERCISE 2.3. (a) Are the distances normally distributed? Plot the histogram, do the testing. Explain.

In SAS:

```
data distance;
input gender$ prior_expr$ self_eval distance @@;
male=(gender='M');
priorexpr_yes=(prior_expr='yes');
cards;
F no  2  1.9   F no  2  2.1  F yes 8  3.8  F yes 4 3.0
M no  5  4.2   F yes 10 8.2  F no  3  3.1  F no  4 2.4
F no  5  4.6   M yes 6  8.7  F no  6  4.7  M yes 7 4.2
F no  7  4.4   F yes 3  3.1  M yes 10 6.4  F yes 4 3.2
F no  6  5.1   M no  10 5.9  F no  6  5.0  M yes 3 3.6
F no  7  4.4   M yes 10 11.2 F yes 3  3.0  M yes 7  4.3
;

/*running normality check of response*/
proc univariate;
 var distance;
  histogram/normal;
```

```
run;
```

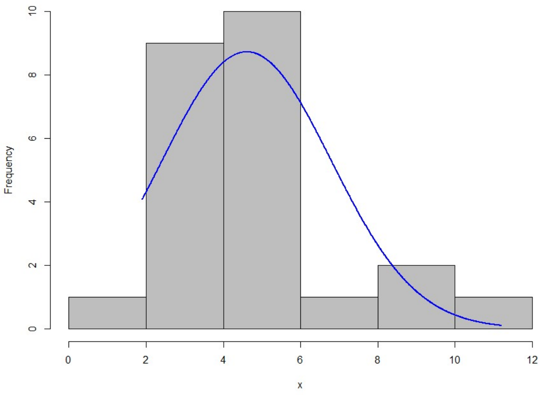
The distribution of distances is skewed to the right as depicted on the histogram. The normality tests give a small p-value indicating that the distribution is not normal.



```
Goodness-of-Fit Tests for Normal Distribution
Test               Statistic       p Value
Kolmogorov-Smirnov D    0.20229147 Pr > D    0.012
Cramer-von Mises   W-Sq 0.19637956 Pr > W-Sq 0.005
Anderson-Darling   A-Sq 1.14009053 Pr > A-Sq <0.005
```

In R:

```
distance.data<- read.csv(file="C:/<insert path>/Exercise2.3Data.csv", 
header=TRUE, sep=',')

#running normality check of response
library(rcompanion)
plotNormalHistogram(distance.data$distance)
```



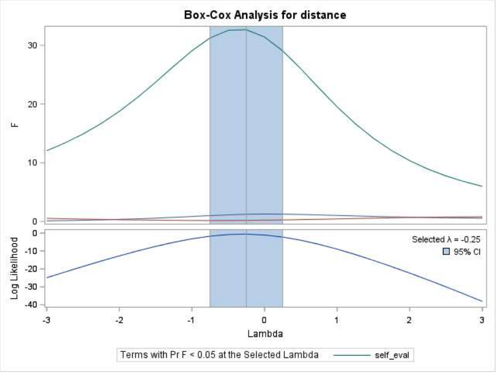
```
shapiro.test(distance.data$distance)
```

```
Shapiro-Wilk normality test

W = 0.86065, p-value = 0.00347
```

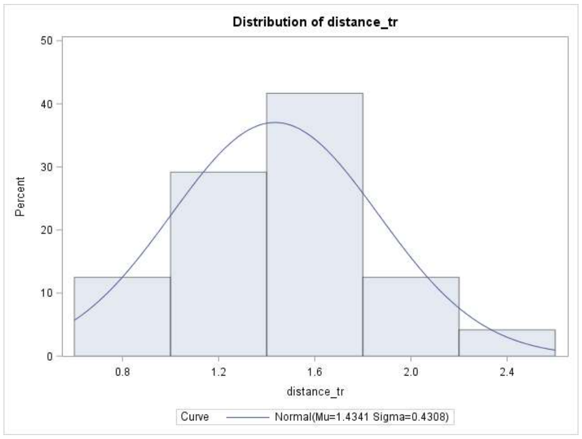
(b) Create indicator variables male and prior yes (existing prior experience), and use them to find a meaningful Box-Cox transformation that would transform the distance into a normally distributed variable. Prove its normality.

In SAS:

```
/*finding optimal lambda for Box-Cox transformation*/
proc transreg;
 model BoxCox(distance) = identity(male  priorexpr_yes  self_eval);
run;
```



```
/*applying Box-Cox transformation with lambda=0*/
data distance;
set distance;
 distance_tr=log(distance);
run;

/*running normality check of transformed response*/
proc univariate;
 var distance_tr;
  histogram/normal;
run;
```



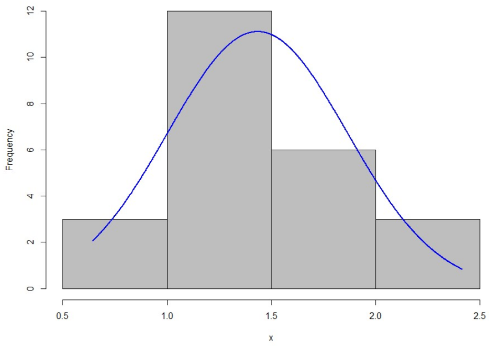
```
Goodness-of-Fit Tests for Normal Distribution
Test               Statistic      p Value
Kolmogorov-Smirnov D    0.11690632 Pr > D    >0.150
Cramer-von Mises   W-Sq 0.05030901 Pr > W-Sq >0.250
Anderson-Darling   A-Sq 0.29858732 Pr > A-Sq >0.250
```

In R:

```
#creating indicator variables
gender.rel<- relevel(distance.data$gender, ref="F")
priorexpr.rel<- relevel(distance.data$priorexpr, ref="no")

#finding optimal lambda for Box-Cox transformation
library(MASS)
BoxCox.fit<- boxcox(distance ~ gender.rel + priorexpr.rel + selfeval,
data=distance.data, lambda=seq(-3,3,1/4), interp = FALSE)
BoxCox.data<- data.frame(BoxCox.fit$x, BoxCox.fit$y)
ordered.data<- BoxCox.data[with(BoxCox.data, order(-BoxCox.fit.y)),]
ordered.data[1,]
```

```
BoxCox.fit.x BoxCox.fit.y

       -0.25    -2.144156
```

```
#applying Box-Cox transformation with lambda=0
distance.tr<- log(distance.data$distance)

#running normality check of transformed response
plotNormalHistogram(distance.tr)
```



```
shapiro.test(distance.tr)
```

```
Shapiro-Wilk normality test

W = 0.97326, p-value = 0.7472
```

(c) Fit the general linear regression model to the transformed distance. Show that the model has a good fit. Discuss significance of predictors.

In SAS:

```
/*fitting general linear model to transformed response*/
proc genmod;
 model distance_tr = male priorexpr_yes self_eval / dist=normal link=identity;
run;
```

```
Log Likelihood 1.4688
```

```
Analysis Of Maximum Likelihood Parameter Estimates
Parameter     DF Estimate Standard Wald 95% Confidence     Wald Chi-     Pr > ChiSq
                          Error    Limits                  Square
Intercept     1  0.6437   0.1206   0.4073       0.8800     28.49         <.0001
male          1  0.1402   0.1140   -0.0833      0.3637     1.51          0.2189
priorexpr_yes 1  0.0504   0.0995   -0.1446      0.2454     0.26          0.6125
self_eval     1  0.1249   0.0204   0.0851       0.1648     37.69         <.0001
Scale         1  0.2276   0.0329   0.1715       0.3020
```

```
/*checking model fit*/
proc genmod;
 model distance_tr = / dist=normal link=identity;
run;
```

```
Log Likelihood -13.3323
```

```
data deviance_test;
 deviance = -2*(-13.3323 - (1.4688));
 pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance    pvalue
29.6022  .000001673
```

Since the p-value is tiny, the model has a good fit. Self-evaluation is the only significant predictor.

In R:

```
#fitting general linear model for transformed response
summary(fitted.model<- glm(distance.tr ~ gender.rel + priorexpr.rel
+ selfeval, data=distance.data, family=gaussian(link=identity)))
```

```
Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)       0.64370    0.13210   4.873 9.21e-05
gender.relM       0.14018    0.12491   1.122    0.275
priorexpr.relyes  0.05040    0.10900   0.462    0.649
selfeval          0.12494    0.02229   5.604 1.74e-05
```

```
#outputting estimated sigma
sigma(fitted.model)
```

```
0.2493296
```

```
#checking model fit
null.model<- glm(distance.tr ~ 1, data=distance.data,
family = gaussian(link=identity))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
29.60224
```

```
print(p.value<- pchisq(deviance,3,lower.tail=FALSE))
```

```
1.673199e-06
```

(d) Give interpretation for the estimates of the statistically significant regression coefficients. Use alpha=0.05.

As the self-evaluation score increases by one unit, the estimated mean log-transformed distance increases by 0.1249.

(e) Write down the final model that can be used for prediction of distance. Predict the distance that a woman with no prior experience would bike, if she is moderately confident about her abilities with the self-assessment value of 5.

The fitted model is $\hat{E}\ (\ln(distance)) = 0.6437 + 0.1402 \cdot male + 0.0504 \cdot priorexperyes + 0.1249\ \cdot selfeval,$ and $\hat{\sigma} = 0.2276$.

The predicted value is computed as follows: $distance^0 = \exp(0.6437 + 0.1249 \cdot 5) = 3.5544$.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input male priorexpr_yes self_eval;
cards;
0 0 5
;

data distance;
set distance predict;
run;

proc genmod;
 model distance_tr = male priorexpr_yes self_eval / dist=normal link=identity;
  output out=outdata p=pdistance_tr;
run;

data outdata;
set outdata;
pdistance=exp(pdistance_tr);
run;

proc print data=outdata (firstobs=25) noobs;
 var pdistance;
run;
```

```
pdistance
  3.55522
```

In R:

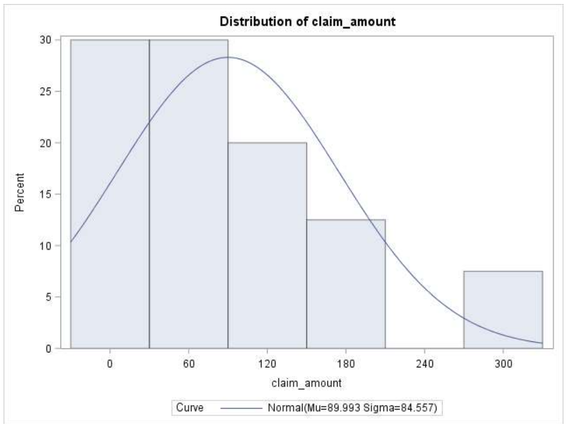
```
#using fitted model for prediction
pdistance.tr<- predict(fitted.model, data.frame(gender.rel='F',
priorexpr.rel='no', selfeval=5))
print(exp(pdistance.tr))
```

```
3.555221
```

EXERCISE 2.4. (a) Plot a histogram and carry out statistical tests for normality of the distribution of claim amounts. Transform the variable via a Box-Cox transformation to achieve normality. Show that the transformed variable is normally distributed.

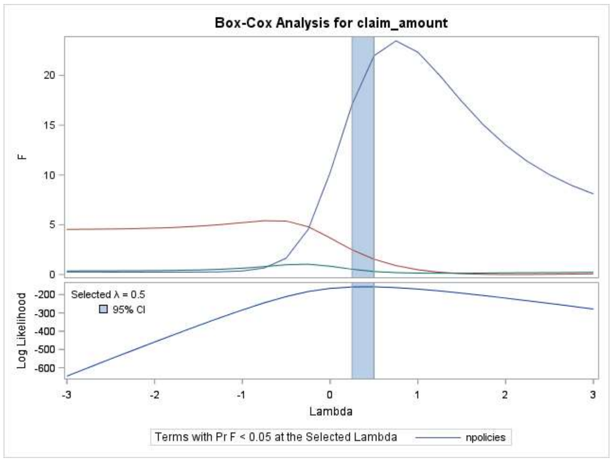
In SAS:

```
data claims;
input npolicies yrswithfirm percopenclaims claim_amount @@;
npoliciesK=npolicies/1000;
cards;
12318 4  16 19.9   29777  4   15 200.5  36980 10 12 308.5
18055 4  20 24.4   16505  20  27 48.7   19049 11 14 51.0
37112 20 26 163.2  22338  16  35 7.1    32349 16 25 1.5
26626 1  21 81.0   28547  11  17 91.0   33268 5  21 147.5
29045 13 29 63.9   18622  7   10 8.5    22784 12 11 27.0
39612 23 26 296.6  28423  7   12 129.0  17020 6  30 26.0
36930 7  24 98.6   37152  15  26 103.5  29629 9  35 107.4
32319 6  19 78.9   27103  23  25 0.3    23704 2  28 6.1
20432 21 16 58.4   30899  16  12 19.5   19052 10 23 46.9
37823 12 19 325.6  24269  14  31 5.7    23103 22 14 71.2
25556 4  32 29.3   15878  11  12 34.4   36772 17 13 50.6
19475 1  34 107.5  29241  8   29 180.2  36821 7  33 158.7
47309 11 12 124.0  15381  2   25 41.9   39857 13 11 195.0
34790 7  18 60.7
;

/*running normality check of response*/
proc univariate;
 var claim_amount;
  histogram/normal;
run;
```

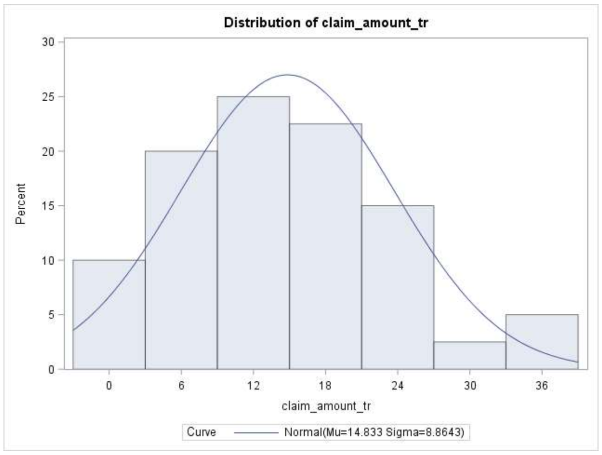


```
Goodness-of-Fit Tests for Normal Distribution
Test               Statistic       p Value
Kolmogorov-Smirnov D    0.14617911 Pr > D    0.030
Cramer-von Mises   W-Sq 0.26260150 Pr > W-Sq <0.005
Anderson-Darling   A-Sq 1.70664028 Pr > A-Sq <0.005
```

```
/*finding optimal lambda for Box-Cox transformation*/
proc transreg;
 model BoxCox(claim_amount) = identity(npoliciesK yrswithfirm percopenclaims);
run;
```



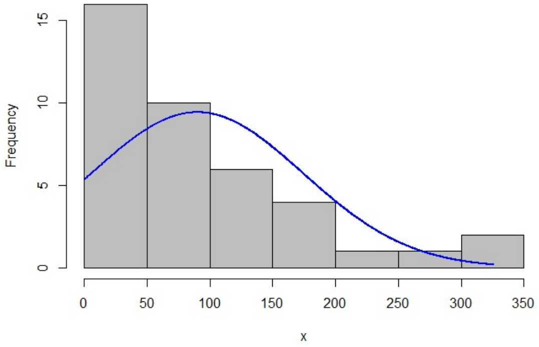
```
/*applying Box-Cox transformation with lambda=0.5*/
data claims;
set claims;
 claim_amount_tr = 2*(claim_amount**(0.5)-1);
run;

/*running normality check of transformed response*/
proc univariate;
 var claim_amount_tr;
  histogram/normal;
run;
```



```
Goodness-of-Fit Tests for Normal Distribution
Test               Statistic       p Value
Kolmogorov-Smirnov D    0.06321834 Pr > D    >0.150
Cramer-von Mises   W-Sq 0.02560195 Pr > W-Sq >0.250
Anderson-Darling   A-Sq 0.21938379 Pr > A-Sq >0.250
```

In R:

```
claims.data<- read.csv(file="C:/<insert path>/Exercise2.4Data.csv", header=TRUE,
sep=',')

#running normality check of response
library(rcompanion)
plotNormalHistogram(claims.data$claimamount)
```



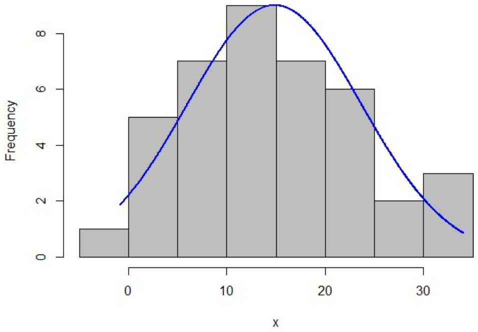
```
shapiro.test(claims.data$claimamount)
```

```
Shapiro-Wilk normality test

W = 0.85595, p-value = 0.0001259
```

```
#rescaling npolicies
npoliciesK<- claims.data$npolicies/1000

#finding optimal lambda for Box-Cox transformation
library(MASS)
BoxCox.fit<- boxcox(claimamount ~ npoliciesK + yrswithfirm + percopenclaims,
data=claims.data, interp = FALSE)
BoxCox.data<- data.frame(BoxCox.fit$x, BoxCox.fit$y)
ordered.data<- BoxCox.data[with(BoxCox.data, order(-BoxCox.fit.y)),]
ordered.data[1,]
```

```
BoxCox.fit.x BoxCox.fit.y

         0.4    -72.77094
```

```
#applying Box-Cox transformation with lambda=0.5
claimamount.tr<- 2*(sqrt(claims.data$claimamount)-1)

#running normality check of transformed response
plotNormalHistogram(claimamount.tr)
```



```
shapiro.test(claimamount.tr)
```

```
Shapiro-Wilk normality test

W = 0.97601, p-value = 0.5445
```

(b) Fit a linear regression model, relating the transformed claim amounts to all the other variables. Which variables are significant predictors at the 5% level?

In SAS:

```
/*fitting general linear model to transformed response*/
proc genmod;
 model claimamount_tr = npoliciesK yrswithfirm percopenclaims / dist=normal
link=identity;
run;
```

```
Log Likelihood -133.7181

Analysis Of Maximum Likelihood Parameter Estimates
Parameter      DF Estimate Standard Wald 95% Confidence     Wald Chi-     Pr > ChiSq
                           Error    Limits                  Square
Intercept      1  0.6928   5.2239   -9.5459     10.9314     0.02          0.8945
npoliciesK     1  0.6624   0.1341   0.3996      0.9251      24.41         <.0001
yrswithfirm    1  -0.2338  0.1786   -0.5838     0.1163      1.71          0.1905
percopenclaims 1  -0.0825  0.1419   -0.3607     0.1956      0.34          0.5609
Scale          1  6.8484   0.7657   5.5007      8.5262
```

The fitted model is

$\hat{E}\ \left(2\left(\sqrt{claimamount}-1\right)\right) = 0.6928 + 0.6624 \cdot npoliciesK - 0.2338 \cdot yrswithfirm -$ $0.0825\ \cdot peropenclaims,$ and $\hat{\sigma}$ = Scale = 6.8484.

At the 5% level, only number of policies is a significant predictor.

In R:

```
#fitting general linear model to transformed response
summary(fitted.model<- glm(claimamount.tr ~ npoliciesK + yrswithfirm +
percopenclaims, data=claims.data, family=gaussian(link=identity)))
```

```
Coefficients:
               Estimate Std. Error t value Pr(>|t|)
(Intercept)     0.69275    5.50646   0.126    0.901
npoliciesK      0.66236    0.14130   4.688 3.89e-05
yrswithfirm    -0.23379    0.18826  -1.242    0.222
percopenclaims -0.08254    0.14961  -0.552    0.585
```

```
#outputting estimated sigma
sigma(fitted.model)
```

```
7.218831
```

(c) Assess the model fit. Interpret estimated significant regression coefficients.

In SAS:

```
/*checking model fit*/
proc genmod;
```

```
 model claimamount_tr = / dist=normal link=identity;
run;
```

```
Log Likelihood -143.5324
```

```
data deviance_test;
 deviance = -2*(-143.5324 - (-133.7181));
 pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance      pvalue
 19.6286  .000202641
```

The model has a good fit since the p-value is very small.

In R:

```
checking model fit
null.model<- glm(claimamount.tr ~ 1, data=claims.data,
family=gaussian(link=identity))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
19.62872
```

```
print(p.value<- pchisq(deviance,3,lower.tail=FALSE))
```

```
0.0002026295
```

As the number of policies increases by one thousand, the estimated mean square root-transformed claim amount increases by 0.0007.

(d) Compute the predicted amount of aggregate claims for a company with 15,500 policy holders, that has been buying policies at this firm for the past three years, and that still has 15% of outstanding claims from the previous year.

The predicted value is evaluated as follows: $claimamount^0 = \left(\frac{1}{2}(0.6928 + 0.66236 \cdot 15.5 - 0.2338 \cdot 3 - 0.0825 \ \cdot 15) + 1\right)^2 = 30.36.$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input npoliciesK yrswithfirm percopenclaims;
cards;
15.5 3 15
;

data claims;
set claims predict;
run;

proc genmod;
 model claim_amount_tr = npoliciesK yrswithfirm percopenclaims / dist=normal
  link=identity;
  output out=outdata p=pclaim_amount_tr;
run;

data outdata;
set outdata;
 pclaim_amount=((pclaim_amount_tr/2)+1)**2;
run;

proc print data=outdata (firstobs=41);
 var pclaim_amount;
run;
```

```
pclaim_amount
      30.3600
```

In R:

```
#using fitted model for prediction
pclaim.amount.tr<- predict(fitted.model, data.frame(npoliciesK=15.5,
yrswithfirm=3, percopenclaims=15))
print((pclaim.amount.tr/2+1)**2)
```

```
30.36
```

EXERCISE 2.5. Show that a gamma distribution with density defined by (2.3) belongs to the exponential family of distributions. Conclude that the gamma regression is a generalized linear regression. Give its link function.

$$f_Y(y;\alpha,\beta)=\frac{y^{\alpha-1}}{\Gamma(\alpha)\beta^{\alpha}}e^{-\frac{y}{\beta}}=\exp\left\{-\frac{y}{\beta}-\alpha\ln\beta+(\alpha-1)\ln y-\ln\Gamma(\alpha)\right\}$$

$$=\exp\left\{\frac{y\left(-\frac{1}{\alpha\beta}\right)-\ln\beta}{\frac{1}{\alpha}}+(\alpha-1)\ln y-\ln\Gamma(\alpha)\right\}.$$

If we let $\theta=-\frac{1}{\alpha\beta}$ and $\phi=\frac{1}{\alpha}$, we can write $\ln\beta=\ln\left(-\frac{1}{\alpha\theta}\right)=\ln(-\frac{1}{\theta})+\ln\frac{1}{\alpha}=\ln(-\frac{1}{\theta})+\ln\phi$, and thus, we obtain

$$f_Y(y;\alpha,\beta)=\exp\left\{\frac{y\theta-\ln(-\frac{1}{\theta})+\ln\phi}{\phi}+\left(\frac{1}{\phi}-1\right)\ln y-\ln\Gamma\left(\frac{1}{\phi}\right)\right\}.$$

Letting $c(\theta)=\ln(-\frac{1}{\theta})$, and $h(y,\phi)=\frac{\ln\phi}{\phi}+\left(\frac{1}{\phi}-1\right)\ln y-\ln\Gamma\left(\frac{1}{\phi}\right)$, we obtain the form of a density that belongs to the exponential family of distributions (1.3). Thus, a gamma regression is a generalized linear regression. According to (2.4), the mean response is modeled via a log-link function.

EXERCISE 2.6. (a) Fit the gamma regression model with the log link function. Write down the fitted model. Check

its goodness of fit.

In SAS:

```
data obesity;
input gender$ age group$ preBMI postBMI @@;
    BMIdiff=preBMI-postBMI;
cards;
F 6  Cx 85.7 83.8  F 6  Cx 93.8 92.9  F 7  Cx 93.5 92.5  F 8  Cx 90.1 89.8
F 9  Tx 92.3 90.7  F 9  Tx 90.3 88.3  F 12 Cx 87.6 85.9  F 12 Cx 87.2 84.1
F 12 Tx 96.9 94.9  F 12 Tx 85.8 81.2  F 13 Cx 96.7 94.1  F 13 Cx 93.5 92.9
F 13 Tx 92.3 87.5  F 13 Tx 85.3 83.7  F 14 Tx 95.5 78.7  F 15 Cx 91.3 89.9
F 15 Tx 95.8 87.1  F 16 Tx 90.7 87.2  M 6  Cx 92.6 88.1  M 7  Cx 95.8 94.7
M 7  Cx 90.4 89.1  M 7  Cx 91.2 88.6  M 8  Tx 94.4 87.8  M 8  Tx 93.2 87.3
M 10 Cx 93.9 91.5  M 10 Tx 96.2 91.1  M 10 Tx 89.4 87.9  M 11 Tx 86.2 77.1
M 11 Tx 95.4 84.8  M 12 Cx 97.7 95.8  M 13 Tx 85.3 80.0  M 13 Tx 86.2 82.4
M 14 Cx 85.5 83.6  M 14 Cx 97.8 93.8  M 16 Cx 95.0 93.6  M 16 Tx 93.1 86.8
;

/*fitting gamma regression model*/
proc genmod;
 class gender(ref='F') group(ref='Cx');
  model BMIdiff = gender age group / dist=gamma link=log;
run;
```

```
Log Likelihood -69.3482

Analysis Of Maximum Likelihood Parameter Estimates
Parameter    DF Estimate Standard Wald 95% Confidence      Wald Chi-     Pr > ChiSq
                         Error    Limits                   Square
Intercept    1  -0.0442  0.4154   -0.8584       0.7700     0.01          0.9153
gender     M 1  0.3862   0.2052   -0.0160       0.7884     3.54          0.0598
gender     F 0  0.0000   0.0000   0.0000        0.0000     .             .
age          1  0.0470   0.0349   -0.0214       0.1154     1.82          0.1777
group     Tx 1  0.9870   0.2104   0.5747        1.3994     22.01         <.0001
group     Cx 0  0.0000   0.0000   0.0000        0.0000     .             .
Scale        1  2.8805   0.6435   1.8591        4.4629
```

The fitted model is $\hat{E}(BMIdiff) = \exp(-0.0442 + 0.3862 \cdot male + 0.0470 \cdot age + 0.9870 \cdot Tx)$, and $\hat{\alpha} = \frac{1}{2.8805} = 0.3472$.

```
/*checking model fit*/
proc genmod;
 model BMIdiff = / dist=gamma link=log;
run;
```

```
Log Likelihood -81.2031
```

```
data deviance_test;
```

```
 deviance = -2*(-81.2031 - (-69.3482));
 pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance      pvalue
 23.7098  .000028719
```

The model has a good fit since the p-value is very small.

In R:

```
bmi.data<- read.csv(file="C:/<insert path>/Exercise2.1Data.csv", header=TRUE,
sep=',')

#creating the difference in BMI
BMIdiff<- bmi.data$preBMI-bmi.data$postBMI

#fitting gamma regression model
summary(fitted.model<- glm(BMIdiff ~ gender + age + group, data=bmi.data,
family=Gamma(link=log)))
```

```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.04415    0.45077  -0.098 0.922581
genderM      0.38624    0.22749   1.698 0.099250
age          0.04703    0.03826   1.229 0.227963
groupTx      0.98701    0.23376   4.222 0.000187

Dispersion parameter for Gamma family taken to be 0.4599244
```

```
#checking model fit
null.model<- glm(BMIdiff ~ 1, data=bmi.data, family=Gamma(link=log))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
23.83593
```

```
print(p.value<- pchisq(deviance,3,lower.tail = FALSE))
```

```
2.70297e-05
```

(b) What variables are significant predictors in this model? Use the 5% significance level.

Only group is a significant predictor.

(c) Interpret estimated significant regression coefficients.

Estimated average decrease in BMI percentile for patients in the intervention group is $\exp\{0.9870\} \cdot 100\% = 268.32\%$ of that for patients in the control group.

(d) Predict change in BMI percentile for a 9-year old girl in the control group. Compare the prediction with the one obtained in Exercise 2.1.

We calculate the predicted value as follows:

$BMIdiff^0 = \exp(-0.0442 + 0.0470 \cdot 9)$=1.4605.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input gender$ age group$;
cards;
F 9 Cx
;

data obesity;
set obesity predict;
run;

proc genmod;
 class gender(ref='F') group(ref='Cx');
  model BMIdiff = gender age group / dist=gamma link=log;
   output out=outdata p=pBMIdiff;
run;

proc print data=outdata (firstobs=37);
 var pBMIdiff;
run;
```

```
pBMIdiff
 1.46106
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(gender='F', age=9, group='Cx'),
type="response"))
```

```
1.461058
```

EXERCISE 2.7. (a) Fit the gamma regression model with the log link function. Present the fitted model and discuss its goodness-of-fit.

In SAS:

```
data QI;
length desgn $6.;
input desgn$ wrkyrs priorQI$ score @@;
score=score/100;
cards;
nurse  16 yes 63  nurse  9  yes 93  nurse  8  yes 74
nurse  1  no  69  nurse  5  no  67  nurse  3  no  66
nurse  24 no  86  nurse  4  no  74  nurse  1  no  88
nurse  24 no  84  nurse  3  no  97  doctor 2  yes 88
doctor 5  yes 78  doctor 26 yes 82  doctor 3  no  57
doctor 3  no  88  doctor 15 no  78  doctor 4  no  65
doctor 25 no  78  staff  3  yes 62  staff  21 no  55
staff  8  no  62  staff  11 no  67  nurse  8  yes 62
nurse  22 yes 68  nurse  4  no  93  nurse  6  no  77
nurse  2  no  59  nurse  20 no  64  nurse  2  no  70
nurse  3  no  63  nurse  16 no  65  nurse  18 no  73
nurse  15 no  76  doctor 2  yes 85  doctor 7  yes 91
doctor 2  yes 69  doctor 20 no  66  doctor 13 no  55
doctor 8  no  62  doctor 14 no  61  staff  9  yes 57
staff  11 yes 69  staff  19 no  64  staff  17 no  76
;

/*fitting gamma regression model*/
proc genmod;
 class desgn(ref='staff') priorQI(ref='no');
  model score=desgn wrkyrs priorQI/dist=gamma link=log;
run;
```

```
Log Likelihood 39.1840

Analysis Of Maximum Likelihood Parameter Estimates
Parameter        DF Estimate Standard Wald 95% Confidence      Wald Chi-    Pr > ChiSq
                             Error    Limits                   Square
Intercept        1  -0.4624  0.0640   -0.5880    -0.3369       52.14        <.0001
desgn     doctor 1  0.1340   0.0625   0.0115     0.2564        4.60         0.0320
desgn     nurse  1  0.1540   0.0595   0.0375     0.2706        6.71         0.0096
desgn     staff  0  0.0000   0.0000   0.0000     0.0000        .            .
wrkyrs           1  -0.0002  0.0028   -0.0056    0.0052        0.01         0.9290
priorQI   yes    1  0.0532   0.0470   -0.0389    0.1454        1.28         0.2575
priorQI   no     0  0.0000   0.0000   0.0000     0.0000        .            .
Scale            1  49.8543  10.4753  33.0256    75.2584
```

The fitted model is $\hat{E}(score) = 100 \cdot \exp\{-0.4624 + 0.1340 \cdot doctor + 0.1540 \cdot nurse - 0.0002 \cdot wrkyrs + 0.0532 \cdot priorQIyes\}$, and $\hat{\alpha} = \frac{1}{49.8543} = 0.020058$.

The model doesn't really fit the data well because the p-value for the deviance test is larger than 0.05.

```
/*checking model fit*/
proc genmod;
 model score = / dist=gamma link=log;
run;
```

```
Log Likelihood 35.5289
```

```
data deviance_test;
 deviance = -2*(35.5289 - 39.1840);
 pvalue = 1 - probchi(deviance,4);
run;

proc print noobs;
run;
```

```
deviance   pvalue
7.3102     0.12038
```

In R:

```
jobscore.data<- read.csv(file="C:/<insert path>/Exercise2.2Data.csv",
header=TRUE, sep=',')

#rescaling values and setting references
desgn.rel<- relevel(jobscore.data$desgn, ref="staff")
priorQI.rel<- relevel(jobscore.data$priorQI, ref="no")
score<- jobscore.data$score/100

#fitting gamma regression model
summary(fitted.model<- glm(score ~ desgn.rel + wrkyrs + priorQI.rel,
data=jobscore.data, family=Gamma(link=log)))
```

```
Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
(Intercept)      4.1427297  0.0686964  60.305   <2e-16
desgn.reldoctor  0.1339899  0.0667675   2.007   0.0516
desgn.relnurse   0.1540443  0.0636050   2.422   0.0201
wrkyrs          -0.0002455  0.0029813  -0.082   0.9348
priorQI.relyes   0.0532444  0.0498513   1.068   0.2919

Dispersion parameter for Gamma family taken to be 0.02298337
```

```
#checking model fit
null.model<- glm(score ~ 1, data=jobscore.data, family=Gamma(link=log))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
7.310283
```

```
print(p.value<- pchisq(deviance,4,lower.tail=FALSE))
```

```
0.1203719
```

(b) Discuss significance of the beta coefficients. Interpret the estimated significant coefficients.

Indicators of doctor and nurse are significant at the 5% level. The estimated mean score for doctors is $\exp(0.1340) \cdot 100\% = 114.34\%$ of that for staff. The estimated mean score for nurses is $\exp(0.1540) \cdot 100\% = 116.65\%$ of that for staff.

(c) Predict the score for a nurse who has worked at the center for seven years and who had previously been a co-PI on a grant that involved quality assurance component. Compare that predicted score to the one obtained in Exercise 2.2.

The predicted value is calculated as: $score^0 = 100 \cdot \exp(-0.4624 + 0.1540 - 0.0002 \cdot 7 + 0.0532) = 77.3678$. The predicted score in Exercise 2.2 is 75.8653 which is smaller than what we predict here.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input desgn$ wrkyrs priorQI$;
cards;
nurse 7 yes
;
```

```
data QI;
set QI predict;
run;

proc genmod;
 class desgn(ref='staff') priorQI(ref='no');
  model score = desgn wkryrs priorQI / dist=gamma link=log;
   output out=outdata p=pscore;
run;

data outdata;
set outdata;
 pscore=pscore*100;
run;

proc print data=outdata (firstobs=46) noobs;
 var pscore;
run;
```

```
pscore
77.3468
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(desgn.rel='nurse', wrkyrs=7,
priorQI.rel='yes'), type="response"))
```

```
77.34687
```

EXERCISE 2.8. (a) Write out explicitly the estimated model. Check goodness of fit of this model.

In SAS:

```
data distance;
input gender$ prior_expr$ self_eval distance @@;
cards;
F no  2  1.9   F no  2  2.1  F yes 8  3.8  F yes 4 3.0  M no  5 4.2
F yes 10 8.2   F no  3  3.1  F no  4  2.4  F no  5 4.6  M yes 6 8.7
F no  6  4.7   M yes 7  4.2  F no  7  4.4  F yes 3 3.1  M yes 10 6.4
F yes 4  3.2   F no  6  5.1  M no  10 5.9  F no  6 5.0  M yes 3 3.6
F no  7  4.4   M yes 10 11.2 F yes 3  3.0  M yes 7 4.3
;

/*fitting gamma regression model*/
proc genmod;
 class gender(ref='F') prior_expr(ref='no');
  model distance = gender prior_expr self_eval / dist=gamma link=log;
run;
```

```
Log Likelihood -33.4006
```

```
Analysis Of Maximum Likelihood Parameter Estimates
Parameter      DF Estimate Standard Wald 95% Confidence     Wald Chi-     Pr > ChiSq
                           Error    Limits                  Square
Intercept       1 0.6494   0.1241   0.4060      0.8927      27.36         <.0001
gender      M   1 0.1652   0.1156   -0.0614     0.3918      2.04          0.1531
gender      F   0 0.0000   0.0000   0.0000      0.0000      .             .
prior_expr yes  1 0.0571   0.1026   -0.1440     0.2583      0.31          0.5778
prior_expr no   0 0.0000   0.0000   0.0000      0.0000      .             .
self_eval       1 0.1266   0.0208   0.0859      0.1672      37.19         <.0001
Scale           1 18.9200  5.4143   10.7978     33.1517
```

The fitted model is $\hat{E}(distance) = \exp\left\{0.6494 + 0.1652 \cdot male + 0.0571 \cdot prior_{expr_{yes}} + 0.1266 \cdot self_{eval}\right\}$, and $\hat{\alpha} = \frac{1}{18.92} = 0.052854$. This model fits well as indicated by a small p-value in the deviance test.

```
/*checking model fit*/
proc genmod;
 model distance = / dist=gamma link=log;
run;
```

```
Log Likelihood -48.6416
```

```
data deviance_test;
 deviance = -2*(-48.6416 - (-33.4006));
 pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance      pvalue
  30.482  .000001093
```

In R:

```
distance.data<- read.csv(file="C:/<insert path>/Exercise2.3Data.csv",header=TRUE,
sep=',')

#setting reference variables
gender.rel<- relevel(distance.data$gender, ref="F")
priorexpr.rel<- relevel(distance.data$priorexpr, ref="no")

#fitting gamma regression
summary(fitted.model<- glm(distance ~ gender.rel + priorexpr.rel + selfeval,
data=distance.data, family=Gamma(link=log)))
```

```
Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)       0.64936    0.13858   4.686 0.000142
gender.relM       0.16515    0.13104   1.260 0.222054
priorexpr.relyes  0.05713    0.11435   0.500 0.622822
selfeval          0.12656    0.02339   5.411 2.69e-05

Dispersion parameter for Gamma family taken to be 0.06841251
```

```
#checking model fit
null.model<- glm(distance ~ 1, data=distance.data, family=Gamma(link=log))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
30.492
```

```
print(p.value<- pchisq(deviance,3,lower.tail=FALSE))
```

```
1.087373e-06
```

(b) Which predictors would really influence the response, if changed? Give interpretation of the estimated significant regression coefficients.

Self-evaluation score is the only significance predictor. If self-evaluation score increases by one, the estimated mean distance increases by $(\exp(0.1266) - 1) \cdot 100\% = 13.49\%$.

(c) Predict the distance that a woman with no prior experience would bike, if she is moderately confident about her abilities with the self-assessment value of 5. Compare your answer to the one obtained in Exercise 2.3.

Predicted distance is $distance^0 = \exp(0.6494 + 0.1266 \cdot 5) = 3.6053$. In Exercise 2.3, the predicted value is 3.5544, which is smaller than the one in this exercise.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input  gender$ prior_expr$ self_eval;
cards;
F no 5
;

data distance;
set distance predict;
run;

proc genmod;
 class gender(ref='F') prior_expr(ref='no');
  model distance = gender prior_expr self_eval / dist=gamma link=log;
   output out=outdata p=pdistance;
run;

proc print data=outdata (firstobs=25) noobs;
 var pdistance;
run;
```

```
pdistance
  3.60448
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(gender.rel='F', priorexpr.rel='no',
selfeval=5), type="response"))
```

```
3.604477
```

EXERCISE 2.9. (a) Run the gamma regression and write the predicted model. What variables are significant predictors of the claim amount? Compare to the model in Exercise 2.4.

In SAS:

```
data claims;
input npolicies yrswithfirm percopenclaims claim_amount @@;
npoliciesK=npolicies/1000;
cards;
12318 4  16 19.9   29777  4   15 200.5  36980 10 12 308.5
18055 4  20 24.4   16505  20  27 48.7   19049 11 14 51.0
37112 20 26 163.2  22338  16  35 7.1    32349 16 25 1.5
26626 1  21 81.0   28547  11  17 91.0   33268 5  21 147.5
29045 13 29 63.9   18622  7   10 8.5    22784 12 11 27.0
39612 23 26 296.6  28423  7   12 129.0  17020 6  30 26.0
36930 7  24 98.6   37152  15  26 103.5  29629 9  35 107.4
32319 6  19 78.9   27103  23  25 0.3    23704 2  28 6.1
20432 21 16 58.4   30899  16  12 19.5   19052 10 23 46.9
37823 12 19 325.6  24269  14  31 5.7    23103 22 14 71.2
25556 4  32 29.3   15878  11  12 34.4   36772 17 13 50.6
19475 1  34 107.5  29241  8   29 180.2  36821 7  33 158.7
47309 11 12 124.0  15381  2   25 41.9   39857 13 11 195.0
34790 7  18 60.7
;

/*fitting gamma regression model*/
proc genmod;
 model claim_amount = npoliciesK yrswithfirm percopenclaims / dist=gamma
    link=log;
run;
```

```
Log Likelihood -211.7158

                 Analysis Of Maximum Likelihood Parameter Estimates
Parameter      DF Estimate Standard  Wald 95% Confidence      Wald Chi- Pr > ChiSq
                           Error          Limits               Square
Intercept       1   2.4656  0.6775      1.1376     3.7936       13.24     0.0003
npoliciesK      1   0.0764  0.0169      0.0432     0.1096       20.38     <.0001
yrswithfirm     1  -0.0186  0.0216     -0.0610     0.0238        0.74     0.3897
percopenclaims  1  -0.0037  0.0187     -0.0403     0.0330        0.04     0.8444
Scale           1   1.2907  0.2597      0.8701     1.9147
```

The fitted model is $\hat{E}(claim\ amount) = \exp\left(2.4656 + 0.0764 \cdot \frac{npolicies}{1000} - 0.0186 \cdot yearwithfirm - 0.0037 \cdot percentopenclaims\right)$ and $\hat{\alpha} = \frac{1}{1.2907} = 0.7748$. Only number of policies is significant at the 5% level, which is the same as in the model in Exercise 2.4.

In R:

```
claims.data<- read.csv(file="C:/<insert path>/Exercise2.4Data.csv", header=TRUE,
sep=',')
```

```
#rescaling npolicies
npoliciesK<- claims.data$npolicies/1000

#fitting gamma regression
summary(fitted.model<- glm(claimamount ~ npoliciesK + yrswithfirm +
percopenclaims, data=claims.data, family=Gamma(link=log)))
```

```
Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)     2.465581   0.529342   4.658 4.25e-05
npoliciesK      0.076404   0.013584   5.625 2.21e-06
yrswithfirm    -0.018610   0.018098  -1.028    0.311
percopenclaims -0.003667   0.014382  -0.255    0.800

Dispersion parameter for Gamma family taken to be 0.4815732
```

(b) Interpret estimates of the significant beta coefficients. How good is the model fit?
When the number of policies increases by one thousand, the estimated mean claim amount increases by $(\exp\{0.0764\}-1)\cdot 100\% = 7.94\%$. The fit of the model is good since the p-value is tiny.

In SAS:

```
/*checking model fit*/
proc genmod;
 model claim_amount = / dist=gamma link=log;
run;
```

```
Log Likelihood -219.9272
```

```
data deviance_test;
 deviance = -2*(-219.9272 - (-211.7158));
 pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance      pvalue
 16.4228  .000928679
```

In R:

```
#checking model fit
null.model<- glm(claimamount~ 1, data=claims.data, family=Gamma(link=log))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
16.67906
```

```
print(p.value<- pchisq(deviance,3,lower.tail=FALSE))
```

```
0.0008226888
```

(c) Obtain the predicted amount of aggregate claims for a company with 15,500 policy holders, that has been buying policies at this firm for the past three years, and that still has 15% of outstanding claims from the previous year. Compare the result with the one computed in Exercise 2.4.

The prediction as done by hand yields: $claim\ amount^0 = \exp\left(2.4656 + 0.0764 \cdot \frac{15500}{1000} - 0.0186 \cdot 3 - 0.0037 \cdot 15\right) = 34.4153$. In Exercise 2.4, the predicted claim amount is 30.36 which is much less.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input npoliciesK yrswithfirm percopenclaims;
cards;
15.5 3 15
;
data claims;
set claims predict;
run;

proc genmod;
  model claim_amount = npoliciesK yrswithfirm percopenclaims / dist=gamma
    link=log;
  output out=outdata p=pclaim_amount;
run;

proc print data=outdata (firstobs=41) noobs;
 var pclaim_amount;
run;
```

```
pclaim_amount
      34.4327
```

In R:

```
#using fitted model for prediction
print(pred.claims<- predict(fitted.model, type='response',
data.frame(npoliciesK=15.5, yrswithfirm=3, percopenclaims=15)))
```

```
34.43248
```

CHAPTER 3

EXERCISE 3.1. Show that the probability mass function of a Bernoulli(π) random variable belongs to the exponential family of distributions. Conclude that the logistic, probit, and complement log-log models are special cases of the generalized linear regression. Specify the respective link functions.

$$f_Y(y;\alpha,\beta) = \pi^y(1-\pi)^{1-y} = \exp\{y\ln\pi + (1-y)\ln(1-\pi)\}$$

$$= \exp\left\{y\ln\frac{\pi}{1-\pi} + \ln(1-\pi)\right\} = \exp\{y\cdot\theta - c(\theta)\}$$

where $\theta = \ln\frac{\pi}{1-\pi}$ and $c(\theta) = -\ln(1-\pi) = -\ln\left(1-\frac{e^\theta}{1+e^\theta}\right) = \ln\left(1+e^\theta\right)$. Thus, Bernoulli($\pi$) belongs to the exponential family of distributions with the location parameter $\theta = \ln\frac{\pi}{1-\pi}$ and dispersion parameter $\phi = 1$. Thus, logistic, probit, and complementary log-log models belong to the class of generalized linear models with the link functions logit, probit, and complementary log-log, respectively.

EXERCISE 3.2. (a) Fit a binary logistic model. Write down the fitted model. Discuss significance of predictor variables, and goodness of fit of the model. Use $\alpha = 0.05$.

In SAS:

```
/*fitting logistic model*/
data psoriasis;
input gender$ age medication$ relief @@;
cards;
M 37 A 1  F 24 A 1  F 15 A 1  M 31 B 1  F 39 B 1  M 31 B 1
M 20 A 1  M 32 A 1  M 30 A 1  F 24 B 0  M 17 B 0  F 33 B 1
M 24 A 1  M 32 A 1  F 27 A 1  M 16 A 1  F 33 A 1  F 28 A 0
M 51 B 1  F 35 B 0  M 16 B 0  F 25 A 0  M 18 A 1  F 19 A 1
M 39 B 1  M 38 B 1  M 37 B 1  F 24 B 0  F 39 B 0  F 33 B 0
;

proc genmod;
```

```
 class gender(ref='F') medication(ref='B');
  model relief(event='1') = gender age medication / dist=binomial link=logit;
run;
```

```
Log Likelihood -10.5042


AIC  29.0084
AICC 30.6084
BIC  34.6132
```

```
                 Analysis Of Maximum Likelihood Parameter Estimates
Parameter    DF Estimate Standard   Wald 95% Confidence      Wald Chi- Pr > ChiSq
                           Error          Limits                Square
Intercept     1  -6.7992  3.1143     -12.9031    -0.6953          4.77     0.0290
gender     M  1   3.1713  1.4710       0.2883     6.0544          4.65     0.0311
gender     F  0   0.0000  0.0000       0.0000     0.0000             .          .
age           1   0.1713  0.0869       0.0010     0.3416          3.89     0.0487
medication A  1   3.8164  1.5462       0.7860     6.8469          6.09     0.0136
medication B  0   0.0000  0.0000       0.0000     0.0000             .          .
```

The fitted model is $\ln\frac{\hat{P}(relief)}{1-\hat{P}(relief)} = -6.7992 + 3.1713 \cdot male + 0.1713 \cdot age + 3.8164 \cdot medication\ A.$ Gender, age, and medication type are all significant predictors at the 5% level.

```
/*checking model fit*/
proc genmod;
 model relief = / dist=binomial link=logit;
run;
```

```
Log Likelihood -18.3259
```

```
data deviance_test;
 deviance = -2*(-18.3259 - (-10.5042));
 pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance      pvalue
15.6434   .001341753
```

The model has a good find as follows from the small p-value (<0.05) in the deviance test.

In R:

```
#fitting logistic model
psoriasis.data<- read.csv(file='C:/<insert path>/Exercise3.2Data.csv',
header=TRUE, sep=',')

#setting reference categories
gender.rel<- relevel(psoriasis.data$gender, ref="F")
medication.rel<- relevel(psoriasis.data$medication, ref="B")
```

```
#running the model
summary(fitted.model<- glm(relief ~ gender.rel + age + medication.rel,
data=psoriasis.data,family=binomial(link=logit)))
```

```
Coefficients:
                Estimate Std. Error z value Pr(>|z|)
(Intercept)     -6.79921    3.11430  -2.183   0.0290
gender.relM      3.17132    1.47097   2.156   0.0311
age              0.17131    0.08691   1.971   0.0487
medication.relA  3.81641    1.54617   2.468   0.0136

AIC: 29.008
```

```
#computing AICC
p<-4
n<-30
print(AICC<- -2*logLik(fitted.model)+2*p*n/(n-p-1))
```

```
30.60842
```

```
#outputting BIC
BIC(fitted.model)
```

```
34.6132
```

```
#checking model fit
null.model<- glm(relief ~ 1, data=psoriasis.data, family=binomial(link=logit))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
15.64344
```

```
print(p.value<- pchisq(deviance,3,lower.tail = FALSE))
```

```
0.001341726
```

(b) Give interpretation of the estimated significant regression coefficients.

The estimated odds in favor of relief from psoriasis for male patients are $\exp(3.1713)\cdot 100\% = 2{,}383.85\%$ of those for female patients. As age increases by one year, the estimated odds increase by $(\exp(0.1713)-1)\cdot 100\% = 18.68\%$. The estimated odds for patients taking medication A are $\exp(3.8164)\cdot 100\% = 4{,}544.03\%$ of those for patients taking medication B.

(c) Find the predicted probability of relief from psoriasis for a 50-year old woman who is administered the medication A treatment.

The predicted probability is computed as:

$$P^0(relief) = \frac{\exp(-6.7992+0.1713\cdot 50+3.8164)}{1+\mathrm{e}\quad(-6.7992+0.1713\cdot 50+3.8164)} = 0.99625.$$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input gender$ age medication$;
cards;
F 50 A
```

```
;
run;

data psoriasis;
set psoriasis predict;
run;

proc genmod;
 class gender medication;
  model relief(event='1') = gender age medication / dist=binomial link=logit;
   output out=outdata p=presponse;
run;

proc print data=outdata (firstobs=31) noobs;
 var presponse;
run;
```

```
presponse
  0.99625
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, type='response', data.frame(gender.rel='F', age=50,
medication.rel='A')))
```

```
0.9962508
```

(d) Repeat parts (a)-(c) but fit a probit model. Compare the results.

In SAS:

```
/*fitting probit model*/
data psoriasis;
input gender$ age medication$ relief @@;
cards;
M 37 A 1  F 24 A 1  F 15 A 1  M 31 B 1  F 39 B 1  M 31 B 1  M 20 A 1
M 32 A 1  M 30 A 1  F 24 B 0  M 17 B 0  F 33 B 1  M 24 A 1  M 32 A 1
F 27 A 1  M 16 A 1  F 33 A 1  F 28 A 0  M 51 B 1  F 35 B 0  M 16 B 0
F 25 A 0  M 18 A 1  F 19 A 1  M 39 B 1  M 38 B 1  M 37 B 1  F 24 B 0
F 39 B 0  F 33 B 0
;

proc genmod;
 class gender(ref='F') medication(ref='B');
  model relief(event='1') = gender age medication / dist=binomial link=probit;
run;
```

```
Log Likelihood -10.3775

AIC  28.7549
AICC 30.3549
BIC  34.3597
```

```
                Analysis Of Maximum Likelihood Parameter Estimates
Parameter    DF Estimate Standard   Wald 95% Confidence      Wald Chi- Pr > ChiSq
                          Error          Limits               Square
Intercept     1  -4.0783  1.8291     -7.6633     -0.4932        4.97     0.0258
gender      M 1   1.9230  0.8477      0.2615      3.5846        5.15     0.0233
gender      F 0   0.0000  0.0000      0.0000      0.0000         .          .
age           1   0.1026  0.0514      0.0019      0.2033        3.99     0.0458
medication A  1   2.2335  0.8595      0.5490      3.9181        6.75     0.0094
medication B  0   0.0000  0.0000      0.0000      0.0000         .          .
```

The fitted model is $\Phi^{-1}\big(\hat{P}(relief)\big) = -4.0783 + 1.9230 \cdot male + 0.1026 \cdot age + 2.2335 \cdot medication\ A$. All the three predictors are significant at the 5% level (the same as in the logistic model).

```
/*checking model fit*/
proc genmod;
 model relief = / dist=binomial link=probit;
run;
```

```
Log Likelihood -18.3259
```

```
data deviance_test;
 deviance = -2*(-18.3259 - (-10.3775));
 pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance      pvalue
 15.8968  .001190587
```

The p-value in the deviance test is less than 0.05, thus the model fits the data well (the same as the logistic model).

The estimated regression coefficients are interpreted as follows. The z-score of estimated probability of relief from psoriasis for male patients is larger than that for female patients by 1.9230. As age increases by one year, the z-score of the estimated probability of relief increases by 0.1026. The z-score for estimated probability of relief for medication A patients is larger than that for medication B patients by 2.2335.

The predicted value is obtained as: $P^0(relief) = \Phi(-4.0783 + 0.1026 \cdot 50 + 2.2335) = \Phi(3.2852) = 0.99949$. This predicted value is slightly larger than that in the logistic model.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input gender$ age medication$;
cards;
F 50 A
;
run;

data psoriasis;
```

```
set psoriasis predict;
run;

proc genmod;
 class gender medication;
  model relief(event='1') = gender age medication / dist=binomial link=probit;
   output out=outdata p=presponse;
run;

proc print data=outdata (firstobs=31) noobs;
 var presponse;
run;
```

```
presponse
  0.99949
```

In R:

```
#fitting probit model
psoriasis.data<- read.csv(file='C:/<insert path>/Exercise3.2Data.csv',
header=TRUE, sep=',')

#setting reference categories
gender.rel<- relevel(psoriasis.data$gender, ref="F")
medication.rel<- relevel(psoriasis.data$medication, ref="B")

#fitting the model
summary(fitted.model<- glm(relief ~ gender.rel + age + medication.rel,
data=psoriasis.data,family=binomial(link=probit)))
```

```
Coefficients:
                  Estimate Std. Error z value Pr(>|z|)
(Intercept)       -4.07825    1.76524  -2.310  0.02087
gender.relM       1.92301    0.80597   2.386  0.01703
age               0.10260    0.04969   2.065  0.03892
medication.relA   2.23351    0.85603   2.609  0.00908

AIC: 28.755
```

```
#computing AICC
p<-4
n<-30
print(AICC<- -2*logLik(fitted.model)+2*p*n/(n-p-1))
```

```
30.35491
```

```
#outputting BIC
BIC(fitted.model)
```

```
34.3597
```

```
#checking model fit
null.model<- glm(relief ~ 1, data=psoriasis.data, family=binomial(link=probit))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
15.89695
```

```
print(p.value<- pchisq(deviance,3,lower.tail = FALSE))
```

```
0.001190503
```

```
#using fitted model for prediction
print(predict(fitted.model, type='response', data.frame(gender.rel='F', age=50,
medication.rel='A')))
```

```
0.9994907
```

(e) Repeat parts (a)-(c), fitting a complementary log-log model. Compare the results with the previous two models. Which of the three models has a better fit?

In SAS:

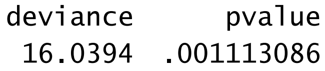
```
/*fitting complementary log-log model*/
data psoriasis;
input gender$ age medication$ relief @@;
cards;
M 37 A 1  F 24 A 1  F 15 A 1  M 31 B 1  F 39 B 1  M 31 B 1  M 20 A 1
M 32 A 1  M 30 A 1  F 24 B 0  M     17 B 0  F 33 B 1
M 24 A 1  M 32 A 1  F 27 A 1  M 16 A 1  F 33 A 1  F 28 A 0
M 51 B 1  F 35 B 0  M 16 B 0  F 25 A 0  M 18 A 1  F 19 A 1
M 39 B 1  M 38 B 1  M 37 B 1  F 24 B 0  F 39 B 0  F 33 B 0
;

proc genmod;
 class gender(ref='F') medication(ref='B');
  model relief(event='1') = gender age medication / dist=binomial link=cloglog;
run;
```

```
Log Likelihood -10.3062

AIC  28.6125
AICC 30.2125
BIC  34.2173

                Analysis Of Maximum Likelihood Parameter Estimates
Parameter    DF Estimate Standard    Wald 95% Confidence       Wald Chi- Pr > ChiSq
                            Error          Limits                 Square
Intercept     1  -4.7318   2.1937     -9.0313      -0.4324          4.65     0.0310
gender      M 1   2.1558   0.9651      0.2643       4.0473          4.99     0.0255
gender      F 0   0.0000   0.0000      0.0000       0.0000             .          .
age           1   0.1069   0.0596     -0.0099       0.2236          3.22     0.0728
medication A  1   2.2361   0.9386      0.3964       4.0757          5.68     0.0172
medication B  0   0.0000   0.0000      0.0000       0.0000             .          .
```

The fitted model is $1 - \hat{P}(relief) = \exp(-\exp(-4.7318 + 2.1558 \cdot male + 0.1069 \cdot age + 2.2361 \cdot medication\ A))$. Gender and medication type are significant at the 5% level, whereas age is not significant. This is different from the logistic and probit models.

```
/*checking model fit*/
proc genmod;
 model relief = / dist=binomial link=logit;
run;

data deviance_test;
 deviance = -2*(-18.3259 - (-10.3062));
 pvalue = 1 - probchi(deviance,3);
run;
```

```
proc print noobs;
run;
```



```
deviance      pvalue
 16.0394  .001113086
```

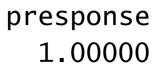
The complementary log-log model fits the data well since the p-value is very small.

Next, we interpret the estimated beta coefficients for the significant predictors. For male patients, the estimated probability of no relief from psoriasis is that for female patients raised to the power $\exp(2.1558) = 8.63$. The estimated probability of no relief for patients taking medication A is that for patients taking medication B raised to the power $\exp(2.2361) = 9.36$. It means that the estimated probability of no relief for males (medication A patients) is much smaller than that for females (medication B patients). This is in accordance with the logistic and probit models.

The predicted value in this model is derived as: $P^0(relief) = 1 - \exp(-\exp(-4.7318 + 0.1069 \cdot 50 + 2.2361)) = 0.99999997$. This predicted value is larger than those in the logistic and probit models.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input gender$ age medication$;
cards;
F 50 A
;

data psoriasis;
set psoriasis predict;
run;

proc genmod;
 class gender medication;
  model relief(event='1') = gender age medication / dist=binomial link=cloglog;
   output out=outdata p=presponse;
run;

proc print data=outdata (firstobs=31) noobs;
 var presponse;
run;
```



```
presponse
  1.00000
```

In R:

```
#fitting complementary log-log model
psoriasis.data<- read.csv(file='C:/<insert path>/Exercise3.2Data.csv',
header=TRUE, sep=',')

#setting reference categories
gender.rel<- relevel(psoriasis.data$gender, ref="F")
```

```
medication.rel<- relevel(psoriasis.data$medication, ref="B")

#running the model
summary(fitted.model<- glm(relief ~ gender.rel + age + medication.rel,
data=psoriasis.data,family=binomial(link=cloglog)))


Coefficients:
                Estimate Std. Error z value Pr(>|z|)
(Intercept)     -4.73174    2.12142  -2.230   0.0257
gender.relM      2.15577    0.87247   2.471   0.0135
age              0.10686    0.05708   1.872   0.0612
medication.relA  2.23606    0.96039   2.328   0.0199

AIC: 28.612
#computing AICC
p<-4
n<-30
print(AICC<- -2*logLik(fitted.model)+2*p*n/(n-p-1))

30.21248

#outputting BIC
BIC(fitted.model)

34.21727

#checking model fit
null.model<- glm(relief ~ 1, data=psoriasis.data, family=binomial(link=cloglog))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))

16.03937

print(p.value<- pchisq(deviance,3,lower.tail = FALSE))

0.0011131

#using fitted model for prediction
print(predict(fitted.model, type='response', data.frame(gender.rel='F', age=50,
medication.rel='A')))

1
```

As we can see, the complementary log-log model has the smallest values in the AIC, AICC, and BIC criteria, thus has the best fit.

	logistic	probit	cloglog
AIC	29.0084	28.7549	28.6125
AICC	30.6084	30.3549	30.2125
BIC	34.6132	34.3597	34.2173

EXERCISE 3.3. (a) Fit a binary logistic model to the data. What predictors turn out to be significant at the 5% level? How good is the fit of the model?

In SAS:

```
/*fitting logistic model*/
data novel;
input success$ cover$ methods$ novels$ years @@;
cards;
yes   yes   one  many    18  no  no  one  first   7
no    yes   none several 10  yes yes many many    6
no    yes   none several 1   no  no  one  several 1
no    no    one  first   11  yes no  one  several 19
yes   yes   none first   5   no  no  none many    2
no    no    one  several 10  no  no  many many    9
yes   no    many several 6   yes yes many many    8
no    no    one  several 12  no  no  none many    2
yes   no    none several 17  yes yes many first   10
yes   no    none several 7   no  no  one  first   12
no    yes   none several 7   no  yes none many    4
no    no    one  several 9   yes no  many several 13
yes   yes   none first   6   no  no  none many    2
yes   yes   one  several 7   yes yes many many    17
yes   yes   many first   18  yes yes one  several 17
no    yes   none several 9   no  no  one  several 11
yes   yes   many first   17  no  no  many many    1
no    no    many many    6   no  yes none several 1
yes   yes   many first   6   yes yes one  many    4
no    yes   none many    7   no  no  one  first   12
no    no    one  several 7   yes yes one  several 9
no    no    one  several 8   no  no  one  several 2
;

proc genmod;
 class cover(ref='no') methods(ref='none') novels(ref='many');
  model success(event='yes') = cover methods novels years / dist=binomial
    link=logit;
run;
```

```
Log Likelihood -16.0357

AIC  46.0714
AICC 49.1825
BIC  58.5607

                Analysis Of Maximum Likelihood Parameter Estimates
Parameter         DF Estimate Standard  Wald 95% Confidence     Wald Chi- Pr > ChiSq
                              Error          Limits              Square
Intercept          1  -6.8762  2.3656    -11.5127    -2.2397       8.45     0.0037
cover     yes      1   3.5238  1.3120      0.9522     6.0954       7.21     0.0072
cover     no       0   0.0000  0.0000      0.0000     0.0000        .          .
methods   many     1   3.9286  1.7918      0.4168     7.4404       4.81     0.0283
methods   one      1   0.7008  1.1914     -1.6344     3.0360       0.35     0.5564
methods   none     0   0.0000  0.0000      0.0000     0.0000        .          .
novels    first    1   1.8768  1.5784     -1.2168     4.9703       1.41     0.2344
novels    several  1   1.3992  1.3254     -1.1986     3.9969       1.11     0.2911
novels    many     0   0.0000  0.0000      0.0000     0.0000        .          .
years              1   0.2907  0.1269      0.0420     0.5394       5.25     0.0220
```

The fitted model has the form: $\ln\frac{\hat{P}(success)}{1-\hat{P}(success)} = -6.8762 + 3.5238 \cdot catchy\ cover + 3.9286 \cdot many\ methods + 0.7008 \cdot one\ method + 1.8768 \cdot first\ novel + 1.3992 \cdot several\ novels + 0.2907 \cdot years.$

The significant at the 5% level are: catchy cover, many promotional methods, and years the publisher was in business.

```
/*checking model fit*/

proc genmod;
  model success = / dist=binomial link=logit;
run;
```

```
Log Likelihood -30.0881
```

```
data deviance_test;
 deviance = -2*(-30.0881 - (-16.0357));
 pvalue = 1 - probchi(deviance,6);
run;

proc print noobs;
run;
```

```
deviance      pvalue
 28.1048  .000089787
```

The fit of this mode is very good as indicated by the tiny p-value in the deviance test.

In R:

```
#fitting logistic model
novel.data<- read.csv(file='C:/<insert path>/Exercise3.3Data.csv',
header=TRUE, sep=',')

#setting reference categories
cover.rel<- relevel(novel.data$cover, ref="no")
methods.rel<- relevel(novel.data$methods, ref="none")
novels.rel<- relevel(novel.data$novels, ref="many")

#fitting the model
summary(fitted.model<- glm(success~ cover.rel + methods.rel + novels.rel
+ years, data=novel.data,family=binomial(link=logit)))
```

```
Coefficients:
                  Estimate Std. Error z value Pr(>|z|)
(Intercept)        -6.8762     2.3656  -2.907  0.00365
cover.relyes        3.5238     1.3120   2.686  0.00724
methods.relmany     3.9286     1.7917   2.193  0.02834
methods.relone      0.7008     1.1914   0.588  0.55642
novels.relfirst     1.8768     1.5784   1.189  0.23442
novels.relseveral   1.3992     1.3254   1.056  0.29113
years               0.2907     0.1269   2.291  0.02198

AIC: 46.071
```

```
#computing AICC
```

```
p<-7
n<-44
print(AICC<- -2*logLik(fitted.model)+2*p*n/(n-p-1))
```

```
49.18253
```

```
#outputting BIC
BIC(fitted.model)
```

```
58.56075
```

```
#checking model fit
null.model<- glm(success ~ 1, data=novel.data, family=binomial(link=logit))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
28.10479
```

```
print(p.value<- pchisq(deviance,6,lower.tail = FALSE))
```

```
8.97874e-05
```

(b) Give interpretation of the estimated significant beta coefficients.

The estimated odds in favor of financial success for a novel with catchy cover are $\exp(3.5238) \cdot 100\% = 3{,}391.31\%$ of those for a novel without a catchy cover. The estimated odds for a publisher with many promotional methods are $\exp(3.9286) \cdot 100\% = 5{,}083.58\%$ of those for a publisher with no promotional methods. For every additional year a publisher was in business prior to publication of a novel, the estimated odds in favor of financial success of the novel increase by $(\exp(0.2907) - 1) \cdot 100\% = 33.74\%$.

(c) Suppose a newly established publishing house prints a novel by some previously unknown author, and doesn't advertise the publication. Find the estimated probability that this novel is successful financially, if it has an extremely catchy cover.

The predicted value is calculated as follows: $P^0(success) = \frac{\exp(-6.876 \quad .5238 \quad .8768)}{1+\exp(-6.8762+3.5238+\ .8768)} = 0.18609$.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input cover$ methods$ novels$ years;
cards;
yes none first 0
;
run;

data novel;
set novel predict;
run;

proc genmod;
 class cover methods novels;
  model success(event='yes') = cover methods novels years / dist=binomial
     link=logit;
   output out=outdata p=psuccess;
run;
```

```
proc print data=outdata (firstobs=45) noobs;
 var psuccess;
run;
```

```
psuccess
 0.18609
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, type='response', data.frame(cover.rel='yes',
methods.rel='none', novels.rel='first', years=0)))
```

```
0.186086
```

(f) Redo parts (a) through (c), fitting a probit model.

In SAS:

```
/*fitting probit model*/
data novel;
input success$ cover$ methods$ novels$ years @@;
cards;
yes   yes   one  many    18  no  no  one  first   7
no    yes   none several 10  yes yes many many    6
no    yes   none several 1   no  no  one  several 1
no    no    one  first   11  yes no  one  several 19
yes   yes   none first   5   no  no  none many    2
no    no    one  several 10  no  no  many many    9
yes   no    many several 6   yes yes many many    8
no    no    one  several 12  no  no  none many    2
yes   no    none several 17  yes yes many first   10
yes   no    none several 7   no  no  one  first   12
no    yes   none several 7   no  yes none many    4
no    no    one  several 9   yes no  many several 13
yes   yes   none first   6   no  no  none many    2
yes   yes   one  several 7   yes yes many many    17
yes   yes   many first   18  yes yes one  several 17
no    yes   none several 9   no  no  one  several 11
yes   yes   many first   17  no  no  many many    1
no    no    many many    6   no  yes none several 1
yes   yes   many first   6   yes yes one  many    4
no    yes   none many    7   no  no  one  first   12
no    no    one  several 7   yes yes one  several 9
no    no    one  several 8   no  no  one  several 2
;

proc genmod;
 class cover(ref='no') methods(ref='none') novels(ref='many');
  model success(event='yes') = cover methods novels years / dist=binomial
link=probit;
run;
```

```
Log Likelihood -16.2531

AIC  46.5062
```

```
AICC 49.6173
BIC  58.9955

                Analysis Of Maximum Likelihood Parameter Estimates
Parameter           DF Estimate Standard  Wald 95% Confidence    Wald Chi- Pr > ChiSq
                                   Error        Limits             Square
Intercept            1  -3.6827   1.1644   -5.9648    -1.4006       10.00     0.0016
cover     yes        1   1.8841   0.6447    0.6205     3.1477        8.54     0.0035
cover     no         0   0.0000   0.0000    0.0000     0.0000         .          .
methods   many       1   2.0626   0.9293    0.2412     3.8841        4.93     0.0265
methods   one        1   0.2483   0.6293   -0.9850     1.4816        0.16     0.6932
methods   none       0   0.0000   0.0000    0.0000     0.0000         .          .
novels    first      1   0.9553   0.8852   -0.7796     2.6901        1.16     0.2805
novels    several    1   0.7903   0.7415   -0.6630     2.2436        1.14     0.2865
novels    many       0   0.0000   0.0000    0.0000     0.0000         .          .
years                1   0.1623   0.0679    0.0291     0.2955        5.71     0.0169
```

The fitted model can be written as: $\Phi^{-1}\big(\hat{P}(success)\big) = -3.6827 + 1.8841 \cdot catchy\ cover + 2.0626 \cdot many\ methods + 0.2483 \cdot one\ method + 0.9553 \cdot first\ novel + 0.7903 \cdot several\ novels + 0.1623 \cdot years.$

The significant at the 5% level are: catchy cover, many promotional methods, and years the publisher was in business. The same as in the logistic model.

```
/*checking model fit*/
proc genmod;
  model success = / dist=binomial link=probit;
run;
```

```
Log Likelihood -30.0881
```

```
data deviance_test;
 deviance = -2*(-30.0881 - (-16.2531));
 pvalue = 1 - probchi(deviance,6);
run;

proc print noobs;
run;
```

```
deviance      pvalue
   27.67  .000108405
```

The probit model fits the data very well since the p-value is tiny. The estimated regression coefficients for significant predictors yield the following interpretation. The z-score for the estimated probability of financial success for a novel with a catchy cover is 1.8841 units larger than that for a novel without a catchy cover. The z-score for the estimated probability of success of a novel for publishing houses with many promotional methods exceeds by 2.0626 that for publishing houses with no promotional methods. As the number of years in business increases by one, the z-score increases by 0.1623.

Both, the logistic and probit models agree on the direction of influence of the significant predictors on the estimated probability of success.

The predicted probability is obtained as: $P^0(relief) = \Phi(-3.6827 + 1.8841 + 0.9553) = \Phi(-0.8433) = 0.19953$. This prediction exceeds that in the logistic model.
In SAS:

```
/*using fitted model for prediction*/
data predict;
input cover$ methods$ novels$ years;
cards;
yes none first 0
;
run;

data novel;
set novel predict;
run;

proc genmod;
 class cover methods novels;
  model success(event='yes') = cover methods novels years / dist=binomial
    link=probit;
   output out=outdata p=psuccess;
run;

proc print data=outdata (firstobs=45) noobs;
 var psuccess;
run;
```

```
psuccess
 0.19953
```

In R:

```
#fitting probit model
novel.data<- read.csv(file='C:/<insert path>/Exercise3.3Data.csv',
header=TRUE, sep=',')

#setting reference categories
cover.rel<- relevel(novel.data$cover, ref="no")
methods.rel<- relevel(novel.data$methods, ref="none")
novels.rel<- relevel(novel.data$novels, ref="many")

#running the model
summary(fitted.model<- glm(success~ cover.rel + methods.rel + novels.rel + years,
data=novel.data,family=binomial(link=probit)))
```

```
Coefficients:
                  Estimate Std. Error z value Pr(>|z|)
(Intercept)       -3.68266    1.20990  -3.044  0.00234
cover.relyes       1.88408    0.67751   2.781  0.00542
methods.relmany    2.06258    0.94055   2.193  0.02831
methods.relone     0.24823    0.67040   0.370  0.71118
novels.relfirst    0.95527    0.87638   1.090  0.27570
novels.relseveral  0.79030    0.72763   1.086  0.27742
years              0.16230    0.06649   2.441  0.01465

AIC: 46.506
```

```
#computing AICC
```

```
p<-7
n<-44
print(AICC<- -2*logLik(fitted.model)+2*p*n/(n-p-1))
```

```
49.6173
```

```
#outputting BIC
BIC(fitted.model)
```

```
58.99552
```

```
#checking model fit
null.model<- glm(success ~ 1, data=novel.data, family=binomial(link=probit))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
27.67002
```

```
print(p.value<- pchisq(deviance,6,lower.tail = FALSE))
```

```
0.000108404
```

```
#using fitted model for prediction
print(predict(fitted.model, type='response', data.frame(cover.rel='yes',
methods.rel='none', novels.rel='first', years=0)))
```

```
0.1995286
```

(g) Redo parts (a) through (c) with the complementary log-log model. How good is the model fit compared to the logistic and probit models?

In SAS:

```
/*fitting complementary log-log model*/
data novel;
input success$ cover$ methods$ novels$ years @@;
cards;
yes   yes   one  many    18  no  no  one  first   7
no    yes   none several 10  yes yes many many    6
no    yes   none several 1   no  no  one  several 1
no    no    one  first   11  yes no  one  several 19
yes   yes   none first   5   no  no  none many    2
no    no    one  several 10  no  no  many many    9
yes   no    many several 6   yes yes many many    8
no    no    one  several 12  no  no  none many    2
yes   no    none several 17  yes yes many first   10
yes   no    none several 7   no  no  one  first   12
no    yes   none several 7   no  yes none many    4
no    no    one  several 9   yes no  many several 13
yes   yes   none first   6   no  no  none many    2
yes   yes   one  several 7   yes yes many many    17
yes   yes   many first   18  yes yes one  several 17
no    yes   none several 9   no  no  one  several 11
yes   yes   many first   17  no  no  many many    1
no    no    many many    6   no  yes none several 1
yes   yes   many first   6   yes yes one  many    4
no    yes   none many    7   no  no  one  first   12
no    no    one  several 7   yes yes one  several 9
no    no    one  several 8   no  no  one  several 2
;
```

```
proc genmod;
 class cover(ref='no') methods(ref='none') novels(ref='many');
  model success(event='yes') = cover methods novels years / dist=binomial
    link=cloglog;
run;
```

```
Log Likelihood -15.3985

AIC  44.7971
AICC 47.9082
BIC  57.2864

                  Analysis Of Maximum Likelihood Parameter Estimates
Parameter          DF Estimate Standard  Wald 95% Confidence    Wald Chi- Pr > ChiSq
                                  Error         Limits             Square
Intercept           1  -6.1473   2.0929    -10.2493   -2.0453        8.63     0.0033
cover     yes       1   2.8126   1.0659      0.7235    4.9017        6.96     0.0083
cover     no        0   0.0000   0.0000      0.0000    0.0000          .          .
methods   many      1   3.4196   1.5548      0.3722    6.4670        4.84     0.0279
methods   one       1   0.8348   0.9811     -1.0882    2.7578        0.72     0.3949
methods   none      0   0.0000   0.0000      0.0000    0.0000          .          .
novels    first     1   1.8391   1.4227     -0.9492    4.6275        1.67     0.1961
novels    several   1   1.2622   1.1214     -0.9358    3.4602        1.27     0.2604
novels    many      0   0.0000   0.0000      0.0000    0.0000          .          .
years               1   0.2187   0.1029      0.0171    0.4204        4.52     0.0335
```

The fitted model has the form$1-\hat{P}(success)=\exp(-\exp(-6.1473+2.8126\cdot catchy\ cover+3.4196\cdot many\ methods+0.8348\cdot one\ method+1.8391\cdot first\ novel+1.2622\cdot several\ novels+0.2187\cdot years))$. The significant at the 5% level predictors are the same as in the logistic and probit models. Namely, catchy cover, many promotional methods, and years the publisher was in business.

```
/*checking model fit*/
proc genmod;
  model success = / dist=binomial link=cloglog;
run;
```

```
Log Likelihood -30.0881
```

```
data deviance_test;
 deviance = -2*(-30.0881 - (-15.3985));
 pvalue = 1 - probchi(deviance,6);
run;

proc print noobs;
run;
```

```
deviance      pvalue
 29.3792  .000051563
```

The model fits the data very well as indicated by the tiny p-value. The interpretation of the estimated significant regression coefficients goes as follows: The estimated probability of financial failure for a novel with a catchy cover is that of a novel without a catchy cover raised to the power $\exp(2.8126)=16.65$. The estimated probability of financial failure of a novel for publishing houses with many promotional methods that for publishing houses with no promotional methods raised to the power $\exp(3.4196) = 30.56$. For every additional year in the publishing house was in business, the estimated probability of failure is raised to the power $\exp(0.2187) = 1.24$.

This interpretation is in agreement with the ones given in the logistic and probit models (in the same direction and roughly magnitude).

The prediction in this model is calculated as: $P^0(success) = 1 - \exp(-\exp(-6.1473 + 2.8126 + 1.8391)) = 0.200776$. This predicted value is larger than those obtained through logistic and probit modeling.
In SAS:

```
/*using fitted model for prediction*/
data predict;
input cover$ methods$ novels$ years;
cards;
yes none first 0
;
run;

data novel;
set novel predict;
run;

proc genmod;
 class cover methods novels;
  model success(event='yes') = cover methods novels years / dist=binomial
link=cloglog;
   output out=outdata p=psuccess;
run;

proc print data=outdata (firstobs=45) noobs;
 var psuccess;
run;
```

```
psuccess
 0.20078
```

In R:

```
#fitting complementary log-log model
novel.data<- read.csv(file='C:/<insert path>/Exercise3.3Data.csv',
header=TRUE, sep=',')

#setting reference categories
cover.rel<- relevel(novel.data$cover, ref="no")
methods.rel<- relevel(novel.data$methods, ref="none")
novels.rel<- relevel(novel.data$novels, ref="many")

#running the model
summary(fitted.model<- glm(success~ cover.rel + methods.rel + novels.rel + years,
data=novel.data,family=binomial(link=cloglog)))
```

```
Coefficients:
                  Estimate Std. Error z value Pr(>|z|)
(Intercept)       -6.14718    1.98767  -3.093  0.00198
cover.relyes       2.81247    0.96108   2.926  0.00343
```

```
methods.relmany    3.41940    1.37735   2.483  0.01304
methods.relone     0.83463    0.86156   0.969  0.33267
novels.relfirst    1.83906    1.30348   1.411  0.15828
novels.relseveral  1.26216    1.02470   1.232  0.21805
years              0.21874    0.09438   2.318  0.02047
```

```
AIC: 44.797
```

```
#computing AICC
p<-7
n<-44
print(AICC<- -2*logLik(fitted.model)+2*p*n/(n-p-1))
```

```
47.9082
```

```
#outputting BIC
BIC(fitted.model)
```

```
57.28642
```

```
#checking model fit
null.model<- glm(success ~ 1, data=novel.data, family=binomial(link=cloglog))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
29.37912
```

```
print(p.value<- pchisq(deviance,6,lower.tail = FALSE))
```

```
5.156521e-05
```

```
#using fitted model for prediction
print(predict(fitted.model, type='response', data.frame(cover.rel='yes',
methods.rel='none', novels.rel='first', years=0)))
```

```
0.2007672
```

To see which of the three models fits the data the best, we compare the AIC, AICC, and BIC values. For convenience, we repeat them below.

	logistic	probit	cloglog
AIC	46.0714	46.5062	44.7971
AICC	49.1825	49.6173	47.9082
BIC	58.5607	58.9955	57.2864

The complementary log-log model has smaller values in all the three criteria, thus has a better fit.

EXERCISE 3.4. (a) Run the binary logistic model, regressing on all the predictors. Identify variables that are significant predictors of loan default at the 5% level of significance. Analyze the model fit.

In SAS:

```
/*fitting logistic model*/
```

```
data loan;
input LTV age income$ default$ @@;
cards;
70 41 low  no   70 25 high yes  65 48 low  no   65 48 high no
60 32 high yes  50 48 high no   55 53 low  no   85 38 high yes
80 43 low  yes  50 33 low  no   60 42 low  no   90 23 low  yes
80 31 high no   70 37 high no   40 39 high no   80 40 low  no
70 52 high no   80 29 low  yes  40 44 low  no   80 36 high no
90 47 high no   80 29 high no   70 24 low  yes  30 42 high no
50 33 low  no   80 36 low  no   75 54 low  no   75 29 high yes
70 38 low  no   60 35 low  no   95 30 low  yes  80 34 low  yes
75 43 low  yes  75 47 high no   85 47 low  yes
;

proc genmod;
 class income(ref='high');
  model default(event='yes') = LTV age income / dist=binomial link=logit;
run;
```

```
Log Likelihood -14.2347

AIC  36.4693
AICC 37.8027
BIC  42.6907

                Analysis Of Maximum Likelihood Parameter Estimates
Parameter      DF Estimate Standard  Wald 95% Confidence      Wald Chi- Pr > ChiSq
                              Error          Limits             Square
Intercept       1  -3.0087   4.0955    -11.0356      5.0183       0.54     0.4626
LTV             1   0.1059   0.0512      0.0054      0.2063       4.27     0.0388
age             1  -0.1616   0.0731     -0.3049     -0.0182       4.88     0.0272
income    low   1   1.1162   1.0249     -0.8926      3.1250       1.19     0.2761
income    high  0   0.0000   0.0000      0.0000      0.0000          .          .
```

The fitted model is written as: $\ln\frac{\hat{P}(default)}{1-\hat{P}(default)} = -3.0087 + 0.1059 \cdot LTV - 0.1616 \cdot age + 1.1162 \cdot low\ income$. LTV and age are significant at the 5% level.

```
/*checking model fit*/
proc genmod;
  model default = / dist=binomial link=logit;
run;
```

```
Log Likelihood -22.5019
```

```
data deviance_test;
 deviance = -2*(-22.5019 - (-14.2347));
 pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance     pvalue
 16.5344  .000880948
```

The model fit is excellent as shown by the small p-value in the deviance test.

In R:

```
#fitting logistic model
rate.data<- read.csv(file='C:/<insert path>/Exercise3.4Data.csv', header=TRUE,
sep=',')

#running the model
summary(fitted.model<- glm(default ~ LTV + age + income, data=rate.data,
family=binomial(link=logit)))

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -3.00869    4.09545  -0.735   0.4626
LTV          0.10586    0.05124   2.066   0.0388
age         -0.16157    0.07314  -2.209   0.0272
incomelow    1.11619    1.02490   1.089   0.2761


AIC: 36.469

#computing AICC
p<-4
n<-35
print(AICC<- -2*logLik(fitted.model)+2*p*n/(n-p-1))

37.80266

#outputting BIC
BIC(fitted.model)

42.69072

#checking model fit
null.model<- glm(default ~ 1, data=rate.data, family=binomial(link=logit))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))

16.53454

print(p.value<- pchisq(deviance,3,lower.tail = FALSE))

0.0008808876
```

(b) Interpret the estimated significant beta coefficients. What is your suggestion in order for the bank to decrease the default rate of home equity loans?

As loan-to-value ratio increases by one, the estimated odds in favor or default increase by $(\exp(0.1059)-1)\cdot 100\% = 11.17\%$. As the age of a client increases by one year, the estimated odds in favor of default change by $(\exp(-0.1616)-1)\cdot 100\% = -14.92\%$, that is, decrease by 14.92%. To decrease the default rate, the bank might want to give loans with smaller loan-to-value ratio, and/or give loans to older clients.

(c) Give a point estimate for the probability of loan default if LTV ratio is 50%, and the borrower is a 50-year old men with high income.

The predicted probability is computed as: $P^0(default) = \frac{\exp(-3.0087+\ .1059\cdot 50-0.1616\cdot 50)}{1+\exp(-3.0087+\ .1059\cdot 50-0.1616\cdot 50)} =$ 0.0030374.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input LTV age income$;
cards;
50 50 high
;
run;

data loan;
set loan predict;
run;

proc genmod;
 class income;
  model default(event='yes') = LTV age income / dist=binomial link=logit;
   output out=outdata p=pdefault;
run;

proc print data=outdata (firstobs=36) noobs;
 var pdefault;
run;
```

```
  pdefault
.003035760
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, type='response', data.frame(LTV=50, age=50,
income='high')))
```

```
0.00303576
```

(d) Repeat the previous parts, fitting a probit model. How different are the results?

In SAS:

```
/*fitting probit model*/
data loan;
input LTV age income$ default$ @@;
cards;
70 41 low  no   70 25 high yes  65 48 low  no   65 48 high no
60 32 high yes  50 48 high no   55 53 low  no   85 38 high yes
80 43 low  yes  50 33 low  no   60 42 low  no   90 23 low  yes
80 31 high no   70 37 high no   40 39 high no   80 40 low  no
70 52 high no   80 29 low  yes  40 44 low  no   80 36 high no
90 47 high no   80 29 high no   70 24 low  yes  30 42 high no
50 33 low  no   80 36 low  no   75 54 low  no   75 29 high yes
70 38 low  no   60 35 low  no   95 30 low  yes  80 34 low  yes
75 43 low  yes  75 47 high no   85 47 low  yes
;

proc genmod;
 class income(ref='high');
  model default(event='yes') = LTV age income / dist=binomial link=probit;
run;
```

```
Log Likelihood -14.0867

AIC  36.1733
AICC 37.5067
BIC  42.3947

                 Analysis Of Maximum Likelihood Parameter Estimates
Parameter      DF Estimate Standard   Wald 95% Confidence       Wald Chi- Pr > ChiSq
                              Error          Limits                Square
Intercept       1  -1.6059   2.3230    -6.1589      2.9472          0.48      0.4894
LTV             1   0.0620   0.0287     0.0057      0.1183          4.67      0.0308
age             1  -0.0987   0.0431    -0.1832     -0.0141          5.24      0.0221
income    low   1   0.6392   0.5932    -0.5234      1.8019          1.16      0.2812
income    high  0   0.0000   0.0000     0.0000      0.0000             .           .
```

The fitted model is $\Phi^{-1}\big(\hat{P}(default)\big) = -1.6059 + 0.0620 \cdot LTV - 0.0987 \cdot age + 0.6392 \cdot low\ income$. Significant at the 5% level are LTV and age, the same as in the logistic model.

```
/*checking model fit*/
proc genmod;
  model default = / dist=binomial link=probit;
run;
```

```
Log Likelihood -22.5019
```

```
data deviance_test;
 deviance = -2*(-22.5019 - (-14.0867));
 pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance      pvalue
 16.8304  .000765830
```

The probit model fits the data well because the p-value is very small. The significant estimated coefficients are interpreted as follows. For a one-percent increase in the loan-to-value ratio, the z-score of the estimated probability of default increases by 0.0620 units. If age of a client increases by one year, the z-score of the estimated probability of default decreases by 0.0987 units. The same direction is observed in the logistic model.

The predicted probability of default in this model is equal to $P^0(default) = \Phi(-1.6059 + 0.0620 \cdot 50 - 0.0987 \cdot 50) = \Phi(-3.4409) = 0.0002899$. This probability is a magnitude smaller than that obtained in the logistic regression.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input LTV age income$;
cards;
50 50 high
;
```

```
run;

data loan;
set loan predict;
run;

proc genmod;
 class income;
  model default(event='yes') = LTV age income / dist=binomial link=probit;
   output out=outdata p=pdefault;
run;

proc print data=outdata (firstobs=36) noobs;
 var pdefault;
run;
```

```
  pdefault
.000292304
```

In R:

```
#fitting probit model
rate.data<- read.csv(file='C:/<insert path>/Exercise3.4Data.csv', header=TRUE,
sep=',')

#running the model
summary(fitted.model<- glm(default ~ LTV + age + income, data=rate.data,
family=binomial(link=probit)))
```

```
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -1.60587    2.34383  -0.685   0.4933
LTV          0.06200    0.02853   2.173   0.0297
age         -0.09865    0.04121  -2.394   0.0167
incomelow    0.63924    0.59365   1.077   0.2816

AIC: 36.173
```

```
#computing AICC
p<-4
n<-35
print(AICC<- -2*logLik(fitted.model)+2*p*n/(n-p-1))
```

```
37.50665
```

```
#outputting BIC
BIC(fitted.model)
```

```
42.39471
```

```
#checking model fit
null.model<- glm(default ~ 1, data=rate.data, family=binomial(link=probit))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
16.83055
```

```
print(p.value<- pchisq(deviance,3,lower.tail = FALSE))
```

```
0.0007657748
```

```
#using fitted model for prediction
```

```
print(predict(fitted.model, type='response', data.frame(LTV=50, age=50,
income='high')))
```

```
0.0002923167
```

(e) Redo parts (a)-(c) with a complementary log-log model. Discuss differences between the three models, if any. Which model fits the data the best?

In SAS:

```
/*fitting complementary log-log model*/
data loan;
input LTV age income$ default$ @@;
cards;
70 41 low  no   70 25 high yes  65 48 low  no   65 48 high no
60 32 high yes  50 48 high no   55 53 low  no   85 38 high yes
80 43 low  yes  50 33 low  no   60 42 low  no   90 23 low  yes
80 31 high no   70 37 high no   40 39 high no   80 40 low  no
70 52 high no   80 29 low  yes  40 44 low  no   80 36 high no
90 47 high no   80 29 high no   70 24 low  yes  30 42 high no
50 33 low  no   80 36 low  no   75 54 low  no   75 29 high yes
70 38 low  no   60 35 low  no   95 30 low  yes  80 34 low  yes
75 43 low  yes  75 47 high no   85 47 low  yes
;

proc genmod;
 class income(ref='high');
  model default(event='yes') = LTV age income / dist=binomial link=cloglog;
run;
```

```
Log Likelihood -14.2179

AIC  36.4358
AICC 37.7691
BIC  42.6572

                Analysis Of Maximum Likelihood Parameter Estimates
Parameter      DF Estimate Standard   Wald 95% Confidence      Wald Chi- Pr > ChiSq
                              Error         Limits               Square
Intercept       1  -2.6814   3.5174    -9.5754      4.2125         0.58     0.4459
LTV             1   0.0790   0.0416    -0.0026      0.1605         3.60     0.0578
age             1  -0.1225   0.0555    -0.2314     -0.0137         4.87     0.0273
income    low   1   0.8907   0.7346    -0.5491      2.3305         1.47     0.2253
income    high  0   0.0000   0.0000     0.0000      0.0000            .          .
```

The fitted complementary log-log model can be written as $1 - \hat{P}(default) = \exp(-\exp(-2.6814 + 0.0790 \cdot LTV - 0.1225 \cdot age + 0.8907 \cdot low\ income))$. Age is a significant predictor at the 5% significance level, whereas LTV is only marginally significant at this level. This is different from what we have seen in the two previous models.

```
/*checking model fit*/
proc genmod;
  model default = / dist=binomial link=cloglog;
run;
```

```
Log Likelihood -22.5019
```

```
data deviance_test;
 deviance = -2*(-22.5019 - (-14.2179));
 pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance     pvalue
  16.568  .000867061
```

The complementary log-log model has a very good fit to the data since the p-value is very small.

As age of a client increases by one year, the probability of no default is raised into the power $\exp(-0.1225) = 0.8847$, that is the probability of no default increases. This agrees with our findings in the logistic and probit models.

The predicted probability is calculated as: $P^0(default) = 1 - \exp(-\exp(-2.6814 + 0.0790 \cdot 50 - 0.1225 \cdot 50)) = 0.007748$. This probability is larger than those predicted by the logistic and probit models.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input LTV age income$;
cards;
50 50 high
;
run;

data loan;
set loan predict;
run;

proc genmod;
 class income;
  model default (event='yes') = LTV age income / dist=binomial link=cloglog;
   output out=outdata p=pdefault;
run;

proc print data=outdata (firstobs=36) noobs;
 var pdefault;
run;
```

```
  pdefault
.007713442
```

In R:

```
#fitting complementary log-log model
rate.data<- read.csv(file='C:/<insert path>/Exercise3.4Data.csv',
header=TRUE, sep=',')

#running the model
summary(fitted.model<- glm(default ~ LTV + age + income, data=rate.data,
family=binomial(link=cloglog)))
Coefficients:
```

```
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -2.68156    3.27613  -0.819   0.4131
LTV          0.07896    0.04114   1.919   0.0550
age         -0.12254    0.05111  -2.398   0.0165
incomelow    0.89073    0.72016   1.237   0.2161
AIC: 36.436
```

```
#computing AICC
p<-4
n<-35
print(AICC<- -2*logLik(fitted.model)+2*p*n/(n-p-1))
```

```
37.7691
```

```
#outputting BIC
BIC(fitted.model)
```

```
42.65716
```

```
#checking model fit
null.model<- glm(default ~ 1, data=rate.data, family=binomial(link=cloglog))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
16.56811
```

```
print(p.value<- pchisq(deviance,3,lower.tail = FALSE))
```

```
0.0008670163
```

```
#using fitted model for prediction
print(predict(fitted.model, type='response', data.frame(LTV=50, age=50,
income='high')))
```

```
0.007713725
```

The probit model has the smallest AIC, AICC, and BIC values and therefore has the best fit.

	logistic	probit	cloglog
AIC	36.4693	36.1733	36.4358
AICC	37.8027	37.5067	37.7691
BIC	42.6907	42.3947	42.6572

EXERCISE 3.5. (a) Model the probability of being a cardiac patient via the binary logistic regression. Write the fitted model explicitly. Discuss the goodness of fit of the model and significance of the regression coefficients. Assume $\alpha = 0.01$ for all tests.

In SAS:

```
/*fitting logistic model*/
data cardiac;
input group A W @@;
cards;
```

```
1 8 2  1 1 2  1 2 1  1 4 0  1 2 7  1 6 3  1 2 8  1 1 9
1 3 0  1 0 2  1 3 2  1 2 7  1 2 7  1 2 8  1 6 0  1 3 5
1 1 0  1 7 1  1 4 3  1 2 4  1 5 3  1 7 1  1 8 1  1 0 6
0 0 9  0 2 1  0 0 8  0 1 3  0 3 1  0 1 4  0 0 8  0 1 6
0 0 9  0 2 2  0 4 4  0 0 6  0 3 2  0 1 2  0 2 5  0 4 0
0 8 1  0 2 7  0 0 10 0 0 5  0 0 6  0 2 1  0 0 7  0 0 6
;
proc genmod;
 model group(event='1') = A W / dist=binomial link=logit;
run;
```

```
Log Likelihood -29.0551

AIC  64.1102
AICC 64.6557
BIC  69.7238

                Analysis Of Maximum Likelihood Parameter Estimates
Parameter DF Estimate Standard    Wald 95% Confidence        Wald Chi- Pr > ChiSq
                      Error           Limits                   Square
Intercept  1  -1.1160   0.8896       -2.8596      0.6276          1.57     0.2097
A          1   0.4378   0.1989        0.0480      0.8276          4.85     0.0277
W          1   0.0277   0.1257       -0.2188      0.2741          0.05     0.8260
```

The fitted logistic model is $\ln\frac{\hat{P}(cardiac)}{1-\hat{P}(cardiac)} = -1.1160 + 0.4378 \cdot \#\, of\ arches + 0.0277 \cdot \#\, of\ whorls$. Number of arches is a significant predictor at the 5% level.

```
/*checking model fit*/
proc genmod;
 model group = / dist=binomial link=logit;
run;
```

```
Log Likelihood -33.2711
```

```
data deviance_test;
 deviance = -2*(-33.2711 - (-29.0551));
 pvalue = 1 - probchi(deviance,2);
run;

proc print noobs;
run;
```

```
deviance   pvalue
   8.432  0.014758
```

The model fits the data reasonably well, since the p-value is smaller than 0.05.

In R:

```
#fitting logistic model
cardiac.data<- read.csv(file='C:/<insert path>/Exercise3.5Data.csv',
header=TRUE, sep=',')

#running the model
summary(fitted.model<- glm(group ~ A + W, data=cardiac.data,
family=binomial(link=logit)))
```

```
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -1.11602    0.88961  -1.255   0.2097
A            0.43778    0.19888   2.201   0.0277
W            0.02765    0.12574   0.220   0.8260

AIC: 64.11
```

```
#computing AICC
p<-3
n<-48
print(AICC<- -2*logLik(fitted.model)+2*p*n/(n-p-1))
```

```
64.65568
```

```
#outputting BIC
BIC(fitted.model)
```

```
69.72383
```

```
#checking model fit
null.model<- glm(group ~ 1, data=cardiac.data, family=binomial(link=logit))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
8.4319
```

```
print(p.value<- pchisq(deviance,2,lower.tail = FALSE))
```

```
0.0147583
```

(b) Interpret the estimated significant regression coefficients. For which fingerprint pattern the fitted probability is the largest? For which, the lowest?

If the number of arches increased by one, the estimated odds in favor of a cardiac disease would increase by $(\exp(0.4378) - 1) \cdot 100\% = 54.93\%$. A person with all ten arches has the highest estimated probability $\hat{P}(cardiac) = \frac{\exp(-1.1160+0.4378\cdot 10)}{1+\exp(-1.1160+0.4378\cdot 10)} = 0.9631$. A person with all ten loops has the lowest estimated probability $\hat{P}(cardiac) = \frac{\exp(-1.1160)}{1+\exp(-1.1160)} = 0.2468$.

(c) Suppose the model is used to predict the probability of being a cardiac patient in a male with the dermatoglyphics reading L-L-W-W-A-W-A-L-LW. What is this predicted probability?

The predicted probability for this person is $P^0(cardiac) = \frac{\exp(-1.1160+0.4378\cdot 2+0.0277\cdot 4)}{1+\exp(-1.1160+0.4378\cdot 2+0.0277\cdot 4)} = 0.4676$.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input A W;
cards;
2 4
;
run;

data cardiac;
```

```
set cardiac predict;
run;

proc genmod;
 model group(event='1') = A W / dist=binomial link=logit;
  output out=outdata p=pcardiac;
run;

proc print data=outdata (firstobs=49) noobs;
 var pcardiac;
run;
```

```
pcardiac
 0.46758
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, type='response', data.frame(A=2, W=4)))
```

```
0.4675796
```

(h) In parts (a)-(c), fit a probit model. Compare results.

In SAS:

```
/*fitting probit model*/
data cardiac;
input group A W @@;
cards;
1 8 2  1 1 2  1 2 1  1 4 0  1 2 7  1 6 3  1 2 8  1 1 9
1 3 0  1 0 2  1 3 2  1 2 7  1 2 7  1 2 8  1 6 0  1 3 5
1 1 0  1 7 1  1 4 3  1 2 4  1 5 3  1 7 1  1 8 1  1 0 6
0 0 9  0 2 1  0 0 8  0 1 3  0 3 1  0 1 4  0 0 8  0 1 6
0 0 9  0 2 2  0 4 4  0 0 6  0 3 2  0 1 2  0 2 5  0 4 0
0 8 1  0 2 7  0 0 10 0 0 5  0 0 6  0 2 1  0 0 7  0 0 6
;

proc genmod;
 model group(event='1') = A W / dist=binomial link=probit;
run;
```

```
Log Likelihood -29.1509

AIC  64.3018
AICC 64.8473
BIC  69.9154

                 Analysis Of Maximum Likelihood Parameter Estimates
Parameter DF Estimate Standard    Wald 95% Confidence          Wald Chi- Pr > ChiSq
                         Error          Limits                    Square
Intercept  1  -0.6300   0.5189      -1.6471       0.3871           1.47     0.2248
A          1   0.2490   0.1061       0.0409       0.4570           5.50     0.0190
W          1   0.0105   0.0760      -0.1385       0.1594           0.02     0.8904
```

The fitted probit model looks like $\Phi^{-1}\left(\hat{P}(cardiac)\right) = -0.6300 + 0.2490 \cdot \#\, of\ arches + 0.0105 \cdot \#\, of\ whorls$. Only the number of arches is a significant predictor, which is similar to what the logistic model gives.

```
/*checking model fit*/
proc genmod;
 model group = / dist=binomial link=probit;
run;
```

```
Log Likelihood -33.2711
```

```
data deviance_test;
 deviance = -2*(-33.2711 - (-29.1509));
 pvalue = 1 - probchi(deviance,2);
run;

proc print noobs;
run;
```

```
deviance    pvalue
  8.2404  0.016241
```

The probit models fits the data reasonably well, at the 5% level. If the number of arches increased by one, the z-score of the estimated probability of a cardiac disease would increase by 0.2490.
The predicted probability in this model is $P^0(cardiac) = \Phi(-0.6300 + 0.2490 \cdot 2 + 0.0105 \cdot 4) = \Phi(-0.09) = 0.4641$. This prediction is a tiny bit smaller than the one produced by the logistic model.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input A W;
cards;
2 4
;
run;

data cardiac;
set cardiac predict;
run;

proc genmod;
 model group(event='1') = A W / dist=binomial link=probit;
  output out=outdata p=pcardiac;
run;

proc print data=outdata (firstobs=49) noobs;
 var pcardiac;
run;
```

```
pcardiac
 0.46408
```

In R:

```
#fitting probit model
cardiac.data<- read.csv(file='C:/<insert path>/Exercise3.5Data.csv',
header=TRUE, sep=',')
```

```
#running the model
summary(fitted.model<- glm(group ~ A + W, data=cardiac.data,
family=binomial(link=probit)))
```

```
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.62995    0.53497  -1.178   0.2390
A            0.24895    0.11125   2.238   0.0252
W            0.01047    0.07694   0.136   0.8918
AIC: 64.302
```

```
#computing AICC
p<-3
n<-48
print(AICC<- -2*logLik(fitted.model)+2*p*n/(n-p-1))
```

```
64.84727
```

```
#outputting BIC
BIC(fitted.model)
```

```
69.91541
```

```
#checking model fit
null.model<- glm(group ~ 1, data=cardiac.data, family=binomial(link=probit))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
8.240317
```

```
print(p.value<- pchisq(deviance,2,lower.tail = FALSE))
```

```
0.01624194
```

```
#using fitted model for prediction
print(predict(fitted.model, type='response', data.frame(A=2, W=4)))
```

```
0.4640763
```

(e) Fit the complementary log-log model instead of the logistic model in (a) through (c). Do the models differ? Which of the three models should be preferred?

In SAS:

```
/*fitting complementary log-log model*/
data cardiac;
input group A W @@;
cards;
1 8 2  1 1 2  1 2 1  1 4 0  1 2 7  1 6 3  1 2 8  1 1 9
1 3 0  1 0 2  1 3 2  1 2 7  1 2 7  1 2 8  1 6 0  1 3 5
1 1 0  1 7 1  1 4 3  1 2 4  1 5 3  1 7 1  1 8 1  1 0 6
0 0 9  0 2 1  0 0 8  0 1 3  0 3 1  0 1 4  0 0 8  0 1 6
0 0 9  0 2 2  0 4 4  0 0 6  0 3 2  0 1 2  0 2 5  0 4 0
0 8 1  0 2 7  0 0 10 0 0 5  0 0 6  0 2 1  0 0 7  0 0 6
;

proc genmod;
 model group(event='1') = A W / dist=binomial link=cloglog;
run;
```

```
Log Likelihood -29.5236

AIC  65.0471
AICC 65.5926
BIC  70.6607

                Analysis Of Maximum Likelihood Parameter Estimates
Parameter DF Estimate Standard    Wald 95% Confidence          Wald Chi- Pr > ChiSq
                       Error           Limits                   Square
Intercept  1  -1.0392   0.6424       -2.2984      0.2199           2.62     0.1057
A          1   0.2382   0.1039        0.0345      0.4419           5.25     0.0219
W          1   0.0167   0.0971       -0.1735      0.2070           0.03     0.8631
```

We write the fitted model $1-\hat{P}(cardiac)=\exp(-\exp(-1.0392+0.2382\cdot \#\, of\ arches+0.0167\cdot \#\, of\ whorls))$. The number of arches is the only significant predictor, as concurs with the previous two models.

```
/*checking model fit*/
proc genmod;
 model group = / dist=binomial link=cloglog;
run;
```

```
Log Likelihood -33.2711
```

```
data deviance_test;
 deviance = -2*(-33.2711 - (-29.5236));
 pvalue = 1 - probchi(deviance,2);
run;

proc print noobs;
run;
```

```
deviance   pvalue
   7.495  0.023577
```

The model has a good fit at the 5% level of significance. If the number of arches increased by one, the estimated probability of no cardiac disease would be raised to the power $\exp(0.2382)=1.27$, that is, the probability of no cardiac disease would decrease, which is in agreement with the previous two models. The predicted probability is found as $P^0(cardiac)=1-\exp(-\exp(-1.0392+0.2382\cdot 2+0.0167\cdot 4))=0.4561$.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input A W;
cards;
2 4
;
run;

data cardiac;
set cardiac predict;
run;

proc genmod;
```

```
 model group(event='1') = A W / dist=binomial link=cloglog;
  output out=outdata p=pcardiac;
run;

proc print data=outdata (firstobs=49) noobs;
 var pcardiac;
run;
```

```
pcardiac
 0.45612
```

In R:

```
#fitting complementary log-log model
cardiac.data<- read.csv(file='C:/<insert path>/Exercise3.5Data.csv',
header=TRUE, sep=',')

#running the model
summary(fitted.model<- glm(group ~ A + W, data=cardiac.data,
family=binomial(link=cloglog)))
```

```
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -1.03922    0.62874  -1.653   0.0984
A            0.23818    0.10916   2.182   0.0291
W            0.01674    0.09199   0.182   0.8556

AIC: 65.047
```

```
#computing AICC
p<-3
n<-48
print(AICC<- -2*logLik(fitted.model)+2*p*n/(n-p-1))
```

```
65.59256
```

```
#outputting BIC
BIC(fitted.model)
```

```
70.66071
```

```
#checking model fit
null.model<- glm(group ~ 1, data=cardiac.data, family=binomial(link=cloglog))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
7.495025
```

```
print(p.value<- pchisq(deviance,2,lower.tail = FALSE))
```

```
0.02357632
```

```
#using fitted model for prediction
print(predict(fitted.model, type='response', data.frame(A=2, W=4)))
```

```
0.45612
```

Using the AIC, AICC, and BIC criteria, we see that the logistic regression has the smallest values and thus should be preferred.

	logistic	probit	cloglog

AIC	64.1102	64.3018	65.0471
AICC	64.6557	64.8473	65.5926
BIC	69.7238	69.9154	70.6607

CHAPTER 4

EXERCISE 4.1. (a) Run the cumulative logit model and specify the fitted model. Discuss the model fit. What predictors are significant at the 5% level? Interpret the estimated significant regression coefficients. Predict the probabilities of each admission status for a person whose GPA is 3.1 and GMAT score is 550.

In SAS:

```
/*fitting cumulative logit model*/
data admission;
input GPA GMAT status$ @@;
cards;
2.96 596 admit     3.14 473 admit     3.22 482 admit     3.29 527 admit
3.69 505 admit     2.46 693 admit     3.03 626 admit     3.19 663 admit
3.63 447 admit     3.59 588 admit     3.30 563 admit     3.78 591 admit
3.44 692 admit     3.48 528 admit     3.47 552 admit     3.35 520 admit
2.89 543 admit     2.28 523 admit     3.21 530 admit     3.58 564 admit
3.33 565 admit     2.80 444 border    3.13 416 border    2.89 431 border
3.01 471 border    2.91 446 border    2.75 546 border    2.73 467 border
3.12 463 border    3.08 440 notadmit  3.01 453 notadmit  3.03 414 notadmit
3.04 446 notadmit  2.89 485 notadmit  2.79 490 notadmit  2.54 446 notadmit
2.43 425 notadmit  2.20 474 notadmit  3.36 531 notadmit  2.57 542 notadmit
2.36 482 notadmit  3.66 420 notadmit
;

proc genmod;
 model status = GPA GMAT / dist=multinomial link=cumlogit;
run;
```

```
Log Likelihood -27.5443

AIC  63.0887
AICC 64.1698
BIC  70.0394

                 Analysis Of Maximum Likelihood Parameter Estimates
Parameter  DF Estimate Standard    Wald 95% Confidence          Wald Chi- Pr > ChiSq
                          Error           Limits                  Square
Intercept1  1 -23.3903   5.8569     -34.8697     -11.9109          15.95     <.0001
Intercept2  1 -21.8526   5.6696     -32.9647     -10.7404          14.86     0.0001
GPA         1   3.1194   1.1913       0.7845       5.4543           6.86     0.0088
GMAT        1   0.0278   0.0084       0.0113       0.0442          10.90     0.0010
```

The fitted model is $\frac{\hat{P}(admit)}{1-\hat{P}(admit)}=\exp(-23.3903+3.1194\cdot GPA+0.0278\cdot GMAT)$, and $\frac{\hat{P}(admit\ or\ borderline)}{\hat{P}(not\ admit)}=\exp(-21.8526+3.1194\cdot GPA+0.0278\cdot GMAT)$. Both GPA and GMAT score are significant predictors. As GPA increases by one point, the estimated odds in favor of more towards admission increase by $(\exp(3.1194)-1)\cdot 100\%=2{,}163.28\%$. As GMAT score increases by one point, the estimated odds in favor of more towards admission increase by $(\exp(0.0278) - 1) \cdot 100\% = 2.819\%$.

```
/*checking model fit*/
proc genmod;
 model status = / dist=multinomial link=cumlogit;
run;
```

```
Log Likelihood -43.0673
```

```
data deviance_test;
 deviance = -2*(-43.0673 - (-27.5443));
 pvalue = 1 - probchi(deviance,2);
run;

proc print noobs;
run;
```

```
deviance      pvalue
  31.046  .000000181
```

Due to the small p-value of the deviance test, the model has a good fit.

To predict probabilities of admit, border line, and not admit for a person whose GPA is 3.1 and GMAT score is 550 we do the follow calculations:

$$P^0(admit) = \frac{\exp\big(-23.3903 + (3.1194)(3.1) + (0.0278)(550)\big)}{1 + \exp\big(-23.3903 + (3.1194)(3.1) + (0.0278)(550)\big)} = 0.827761,$$

$$P^0(admit\ or\ borderline) = \frac{\exp(-21.8526 + (3.1194)(3.1) + (0.0278)(550))}{1 + \exp\big((-21.8526 + (3.1194)(3.1) + (0.0278)(550)\big)}$$
$$= 0.957203,$$

from where $P^0(not\ admit) = 1 - 0.957203 = 0.042797$, and $P^0(borderline) = 0.957203 - 0.827761$ =0.129442.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input GPA GMAT;
cards;
3.1 550
;

data admission;
set admission predict;
run;

proc genmod;
 model status = GPA GMAT / dist=multinomial link=cumlogit;
  output out=outdata p=pstatus;
run;

proc print data=outdata (firstobs=85) noobs;
 var _level_ pstatus;
run;
```

```
_LEVEL_ pstatus
admit   0.82419
border  0.95618
```

In R:

```
#fitting cumulative logit model
admission.data<- read.csv(file='C:/<insert path>/Exercise4.1Data.csv',
header= TRUE, sep=',')

#rescaling predictor
GMAT.res<- admission.data$GMAT/100

#running the model
library(ordinal)
summary(fitted.model<- clm(status ~ GPA + GMAT.res, data=admission.data,
link="logit"))
```

```
AIC
63.09

Coefficients:
         Estimate Std. Error z value Pr(>|z|)
GPA       -3.1194     1.1913  -2.618 0.008833
GMAT.res  -2.7755     0.8406  -3.302 0.000961

Threshold coefficients:
                Estimate Std. Error z value
admit|border     -23.390      5.857  -3.994
border|notadmit  -21.853      5.670  -3.854
```

```
#computing AICC
p<- 4
n<- 42
print(AICC<- -2*logLik(fitted.model)+2*p*n/(n-p-1))
```

```
64.16976
```

```
#outputting BIC
BIC(fitted.model)
```

```
70.03935
```

```
#checking model fit
null.model<- clm(status ~ 1, data=admission.data, link="logit")
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
31.04588
```

```
print(p.value<- pchisq(deviance, df=2, lower.tail = FALSE))
```

```
1.813312e-07
```

```
#using fitted model for prediction
print(predict(fitted.model, type='prob', data.frame(GPA=3.1, GMAT.res=5.50)))
```

```
    admit    border   notadmit
```

```
0.8241952 0.1319818 0.04382299
```

(b) Redo part (a), fitting the cumulative probit model.

In SAS:

```
/*fitting cumulative probit model*/
data admission;
input GPA GMAT status$ @@;
cards;
2.96 596 admit     3.14 473 admit     3.22 482 admit     3.29 527 admit
3.69 505 admit     2.46 693 admit     3.03 626 admit     3.19 663 admit
3.63 447 admit     3.59 588 admit     3.30 563 admit     3.78 591 admit
3.44 692 admit     3.48 528 admit     3.47 552 admit     3.35 520 admit
2.89 543 admit     2.28 523 admit     3.21 530 admit     3.58 564 admit
3.33 565 admit     2.80 444 border    3.13 416 border    2.89 431 border
3.01 471 border    2.91 446 border    2.75 546 border    2.73 467 border
3.12 463 border    3.08 440 notadmit  3.01 453 notadmit  3.03 414 notadmit
3.04 446 notadmit  2.89 485 notadmit  2.79 490 notadmit  2.54 446 notadmit
2.43 425 notadmit  2.20 474 notadmit  3.36 531 notadmit  2.57 542 notadmit
2.36 482 notadmit  3.66 420 notadmit
;

proc genmod;
 model status = GPA GMAT / dist=multinomial link=cumprobit;
run;
```

```
Log Likelihood -27.5930

AIC   63.1860
AICC  64.2271
BIC   70.1367

                Analysis Of Maximum Likelihood Parameter Estimates
Parameter   DF Estimate Standard    Wald 95% Confidence        Wald Chi- Pr > ChiSq
                           Error          Limits                  Square
Intercept1  1 -13.6033   3.0779     -19.6359     -7.5707          19.53     <.0001
Intercept2  1 -12.7243   3.0012     -18.6065     -6.8421          17.98     <.0001
GPA         1   1.7356   0.6222       0.5162      2.9550           7.78     0.0053
GMAT        1   0.0165   0.0046       0.0076      0.0255          13.09     0.0003
```

The fitted model is of the form: $\hat{P}(admit) = \Phi(-13.6033 + 1.7356 \cdot GPA + 0.0165 \cdot GMAT)$, and $\hat{P}(admit\ or\ borderline) = \Phi(-12.7243 + 1.7356 \cdot GPA + 0.0165 \cdot GMAT)$.
Both GPA and GMAT are significant predictors. As GPA increases by one point, the z-scores of the estimated probabilities increase by 1.7356. For a unit-increase in GMAT, the z-score increases by 0.0165.

```
/*checking model fit*/
proc genmod;
 model status = / dist=multinomial link=cumprobit;
run;
```

```
Log Likelihood -43.0673
```

```
data deviance_test;
 deviance = -2*(-43.0673 - (-27.5930));
 pvalue = 1 - probchi(deviance,2);
run;

proc print noobs;
run;
```

```
deviance     pvalue
 30.9486  .000000190
```

The model has a very good fit which is evidenced by a tiny p-value in the deviance test. The predicted probabilities are found in the following manner: $P^0(admit) = \Phi(-13.6033 + 1.7356 \cdot 3.1 + 0.0165 \cdot 550) = 0.80291$, and $P^0(admit\ or\ borderline) = \Phi(-12.7243 + 1.7356 \cdot 3.1 + 0.0165 \cdot 550) = 0.958279$. Thus, $P^0(not\ admit) = 1 - 0.958279 = 0.041721$, and $P^0(borderline) = 0.958279 - 0.80291 = 0.15537$.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input GPA GMAT;
cards;
3.1 550
;

data admission;
set admission predict;
run;

proc genmod;
 model status = GPA GMAT / dist=multinomial link=cumprobit;
  output out=outdata p=pstatus;
run;

proc print data=outdata (firstobs=85) noobs;
 var _level_ pstatus;
run;
```

```
_LEVEL_ pstatus
admit   0.80985
border  0.96048
```

In R:

```
#fitting cumulative probit model
admission.data<- read.csv(file='C:/<insert path>/Exercise4.1Data.csv', header=
TRUE, sep=',')

#rescaling predictor
GMAT.res<- admission.data$GMAT/100

#running the model
library(ordinal)
summary(fitted.model<- clm(status ~ GPA + GMAT.res, data=admission.data,
link="probit"))
```

```
AIC
```

```
63.19

Coefficients:
         Estimate Std. Error z value Pr(>|z|)
GPA       -1.7356     0.6222  -2.790 0.005276
GMAT.res  -1.6546     0.4573  -3.618 0.000297

Threshold coefficients:
                Estimate Std. Error z value
admit|border     -13.603      3.078   -4.42
border|notadmit  -12.724      3.001   -4.24
```

```
#computing AICC
p<- 4
n<- 42
print(AICC<- -2*logLik(fitted.model)+2*p*n/(n-p-1))
```

```
64.26707
```

```
#outputting BIC
BIC(fitted.model)
```

```
70.13666
```

```
#checking model fit
null.model<- clm(status ~ 1, data=admission.data, link="probit")
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
30.94857
```

```
print(p.value<- pchisq(deviance, df=2, lower.tail = FALSE))
```

```
1.903718e-07
```

```
#using fitted model for prediction
print(predict(fitted.model, type='prob', data.frame(GPA=3.1, GMAT.res=5.50)))
```

```
    admit    border   notadmit
0.8098528 0.1506302 0.03951702
```

(c) Redo part (a), fitting the cumulative complementary log-log model.

In SAS:

```
/*fitting cumulative complementary log-log model*/
data admission;
input GPA GMAT status$ @@;
cards;
2.96 596 admit     3.14 473 admit     3.22 482 admit     3.29 527 admit
3.69 505 admit     2.46 693 admit     3.03 626 admit     3.19 663 admit
3.63 447 admit     3.59 588 admit     3.30 563 admit     3.78 591 admit
3.44 692 admit     3.48 528 admit     3.47 552 admit     3.35 520 admit
2.89 543 admit     2.28 523 admit     3.21 530 admit     3.58 564 admit
3.33 565 admit     2.80 444 border    3.13 416 border    2.89 431 border
3.01 471 border    2.91 446 border    2.75 546 border    2.73 467 border
3.12 463 border    3.08 440 notadmit  3.01 453 notadmit  3.03 414 notadmit
3.04 446 notadmit  2.89 485 notadmit  2.79 490 notadmit  2.54 446 notadmit
2.43 425 notadmit  2.20 474 notadmit  3.36 531 notadmit  2.57 542 notadmit
2.36 482 notadmit  3.66 420 notadmit
;
```

```
proc genmod;
 model status = GPA GMAT / dist=multinomial link=cumcll;
run;
```

```
Log Likelihood -29.4951
AIC    66.9901
AICC   68.0712
BIC    73.9408
```

```
                Analysis Of Maximum Likelihood Parameter Estimates
Parameter  DF Estimate Standard    Wald 95% Confidence        Wald Chi- Pr > ChiSq
                          Error          Limits                  Square
Intercept1  1 -13.1371   3.0594      -19.1335     -7.1407         18.44     <.0001
Intercept2  1 -12.2653   2.9885      -18.1228     -6.4079         16.84     <.0001
GPA         1   1.6479   0.6316        0.4099      2.8858          6.81     0.0091
GMAT        1   0.0152   0.0043        0.0068      0.0236         12.46     0.0004
```

The fitted model is $\hat{P}(admit) = 1 - \exp(-\exp(-13.1371 + 1.6479 \cdot GPA + 0.0152 \cdot GMAT))$ and $\hat{P}(admit\ or\ borderline) = 1 - \exp(-\exp(-12.2653 + 1.6479 \cdot GPA + 0.0152 \cdot GMAT))$. GPA and GMAT are both significant predictors. As GPA increases by one point, the estimated complementary probabilities are raised to the power $\exp(1.6479) = 5.196$. As GMAT score increases by one point, the estimated complementary probabilities are raised to the power $\exp(0.0152) = 1.015$.

```
/*checking model fit*/
proc genmod;
 model status = / dist=multinomial link=cumcll;
run;
```

```
Log Likelihood -43.0673
```

```
data deviance_test;
 deviance = -2*(-43.0673 - (-29.4951));
 pvalue = 1 - probchi(deviance,2);
run;

proc print noobs;
run;
```

```
deviance      pvalue
 27.1444  .000001275
```

This model has a very good fit because of the small p-value in the deviance test. To calculate the predicted probabilities, we write $P^0(admit) = 1 - \exp(-\exp(-13.1371 + 1.6479 \cdot 3.1 + 0.0152 \cdot 550)) = 0.751647$, and $P^0(admit\ or\ borderline) = 1 - \exp(-\exp(-12.2653 + 1.6479 \cdot 3.1 + 0.0152 \cdot 550)) = 0.964233$. Hence, $P^0(not\ admit) = 1 - 0.964233 = 0.035767$, and $P^0(borderline) = 0.964233 - 0.751647 = 0.212586$.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input GPA GMAT;
cards;
```

```
3.1 550
;

data admission;
set admission predict;
run;

proc genmod;
 model status = GPA GMAT / dist=multinomial link=cumcll;
  output out=outdata p=pstatus;
run;

proc print data=outdata (firstobs=85) noobs;
 var _level_ pstatus;
run;
```

```
_LEVEL_ pstatus
admit   0.74976
border  0.96358
```

In R:

```
#fitting cumulative complementary log-log model
admission.data<- read.csv(file='C:/<insert path>/Exercise4.1Data.csv', header=
TRUE, sep=',')

#rescaling predictor
GMAT.res<- admission.data$GMAT/100

#running the model
library(ordinal)
summary(fitted.model<- clm(status ~ GPA + GMAT.res, data=admission.data,
link="cloglog"))
```

```
AIC
66.99
Coefficients:
         Estimate Std. Error z value Pr(>|z|)
GPA       -1.6479     0.6316  -2.609 0.009081
GMAT.res  -1.5190     0.4303  -3.530 0.000415

Threshold coefficients:
                Estimate Std. Error z value
admit|border     -13.137      3.059  -4.294
border|notadmit  -12.265      2.989  -4.104
```

```
#computing AICC
p<- 4
n<- 42
print(AICC<- -2*logLik(fitted.model)+2*p*n/(n-p-1))
```

```
68.07119
```

```
#outputting BIC
BIC(fitted.model)
```

```
73.94079
```

```
#checking model fit
```

```
null.model<- clm(status ~ 1, data=admission.data, link="cloglog")
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
27.14445
```

```
print(p.value<- pchisq(deviance, df=2, lower.tail = FALSE))
```

```
1.275435e-06
```

```
#using fitted model for prediction
print(predict(fitted.model, type='prob', data.frame(GPA=3.1, GMAT.res=5.50)))
```

```
    admit    border   notadmit
0.7497578 0.2138205 0.03642168
```

(d) Which of the models obtained in parts (a)-(c) has the best fit?

By the AIC, AICC, and BIC criteria, we see that the cumulative logit regression has the smallest values and thus has the best fit.

	cumulative logit	cumulative probit	Cumulative cloglog
AIC	63.0887	63.1860	66.9901
AICC	64.1698	64.2671	68.0712
BIC	70.0394	70.1367	73.9408

EXERCISE 4.2. (a) Regress the satisfaction score on the other variables via the cumulative logit model. How good is the model fit? Which regression coefficients are significant at $\alpha = 0.05$? State the fitted model explicitly and interpret the estimated significant beta coefficients. Predict probabilities of each of the five levels of the satisfaction score for a caller who had been subscribed for 3 months, doesn't receive the magazine, and whose issue was resolved over the phone.

In SAS:

```
/*fitting cumulative logit model*/
data service;
input subscribed magazine$ resolved$ satisf @@;
cards;
5     yes   no    5  49 yes   no    5  56 no    no    3
13    yes   yes   5  27 no    yes   4  41 yes   yes   5
2     yes   yes   5  64 yes   yes   4  88 yes   yes   4
43    yes   yes   4  94 yes   no    4  8  no    no    1
9     yes   no    2  68 yes   no    4  5  no    yes   2
108   no    yes   3  21 yes   yes   4  25 yes   no    3
2     no    yes   4  11 no    no    2  98 yes   yes   5
11    no    yes   5  46 no    no    4  7  no    no    3
7     no    yes   5  9  yes   yes   5  17 no    no    2
8     no    yes   2  9  no    yes   1  95 no    no    4
60    no    yes   3  80 no    yes   4  2  yes   no    3
33    yes   yes   4  5  yes   no    3  7  no    no    1
;
```

```
proc genmod;
 class magazine(ref='yes') resolved(ref='yes');
  model satisf = subscribed magazine resolved / dist=multinomial link=cumlogit;
run;
```

```
Log Likelihood -47.0487

AIC  108.0974
AICC 112.0974
BIC  119.1820

                Analysis Of Maximum Likelihood Parameter Estimates
Parameter      DF Estimate Standard  Wald 95% Confidence       Wald Chi- Pr > ChiSq
                           Error           Limits              Square
Intercept1      1  -4.2359  0.9678     -6.1328      -2.3390       19.16     <.0001
Intercept2      1  -2.8298  0.8126     -4.4224      -1.2373       12.13     0.0005
Intercept3      1  -1.5740  0.7442     -3.0327      -0.1153        4.47     0.0344
Intercept4      1   0.3350  0.6708     -0.9797       1.6498        0.25     0.6175
subscribed      1  -0.0105  0.0097     -0.0295       0.0085        1.18     0.2776
magazine   no   1   1.9175  0.6771      0.5903       3.2447        8.02     0.0046
magazine   yes  0   0.0000  0.0000      0.0000       0.0000          .          .
resolved   no   1   1.4288  0.6559      0.1434       2.7143        4.75     0.0294
resolved   yes  0   0.0000  0.0000      0.0000       0.0000          .          .
```

The fitted model is of the form $\frac{\hat{P}(satisf=1)}{1-\hat{P}(satisf=1)} = \frac{\hat{P}(very\ dissatisfied)}{1-\hat{P}(very\ dissatisfied)} = \exp(-4.2359 - 0.0105 \cdot \#of\ months\ subscribed + 1.9175 \cdot no\ magazine + 1.4288 \cdot issue\ not\ resolved)$,
$\frac{\hat{P}(satisf=1\ or\ 2)}{1-\hat{P}(satisf=\ \ or\ 2)} = \frac{\hat{P}(very\ dissatisfied\ or\ dissatisfied)}{1-\hat{P}(very\ dissatisfied\ or\ dissatisfied)} = \exp(-2.8298 - 0.0105 \cdot \#of\ months\ subscribed + 1.9175 \cdot no\ magazine + 1.4288 \cdot issue\ not\ resolved)$,

$\frac{\hat{P}(satisf=1,2,or\ 3)}{1-\hat{P}(satisf=1,2,or\ 3)} = \frac{\hat{P}(very\ dissatisfied,\ \ dissatisfied,\ \ or\ neutral)}{\hat{P}(satisfied\ or\ very\ satisfied)} = \exp(-1.5740 - 0.0105 \cdot \#of\ months\ subscribed + 1.9175 \cdot no\ magazine + 1.4288 \cdot issue\ not\ resolved)$,

and $\frac{\hat{P}(satisf=1,2,3,or\ 4)}{1-\hat{P}(satisf=1,2,3,or\ 4)} = \frac{\hat{P}(very\ dissatisfied,\ \ dissatisfied,\ \ neutral,\ \ or\ satisfied\ )}{\hat{P}(very\ satisfied)} = \exp(0.3350 - 0.0105 \cdot \#of\ months\ subscribed + 1.9175 \cdot no\ magazine + 1.4288 \cdot issue\ not\ resolved)$.

Subscription to magazine and whether the issue was resolved are statistically significant at the 5% level. The number or months subscribed is not a significant predictor.

For the customers not receiving the magazine, the estimated odds are $\exp(1.9175) \cdot 100\% = 680.39\%$ of those for customer who receive the magazine. If the issue was not resolved, the estimated odds are $\exp(1.4288) \cdot 100\% = 417.37\%$ of those when the issue was resolved.

```
/*checking model fit*/
proc genmod;
 model satisf = / dist=multinomial link=cumlogit;
run;
```

```
Log Likelihood -54.4484
```

```
data deviance_test;
 deviance = -2*(-54.4484 - (-47.0487));
 pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance      pvalue
 14.7994  .001996353
```

The model has a very good fit as indicated by a small p-value. The predicted probabilities are obtained as follows. $P^0(satisf\ = 1) =\ P^0(very\ dissatisfied) = \frac{\exp(-4.2359-0.0105\cdot 3+1.9175)}{1+\exp(-4.2359-0.0105\cdot 3+1.9175)} = 0.087074,\ P^0(satisf\ = 1\ or\ 2) = P^0(very\ dissatisfied\ or\ dissatisfied) = \frac{\exp(-2.8298-0.0105\cdot 3+1.9175)}{1+\exp(-2.8298-0.0105\cdot 3+1.9175)} = 0.280133,\ P^0(satisf\ = 1, 2, or\ 3) = P^0(very\ dissatisfied, dissatisfied, or\ neutral) = \frac{\exp(-1.5740-0.0105\cdot 3+1.9175)}{1+\exp(-1.5740-0.0105\cdot 3+1.9175)} = 0.577373,$ and $P^0(satisf\ = 1, 2, 3, or\ 4) = P^0(very\ dissatisfied, dissatisfied, neutral, or\ satisfied) = \frac{\exp(0.3350-0.0105\cdot 3+1.9175)}{1+\exp(0.3350-0.0105\cdot 3+1.9175)} = 0.90212.$ From here, the predicted probabilities of each of the five levels of the satisfaction score are $P^0(very\ dissatisfied) = 0.087074,\ P^0(dissatisfied) = 0.280133 - 0.087074 = 0.19306,\ \ P^0(neutral) = 0.577373 - 0.280133 = 0.29724,$ $P^0(satisfied) = 0.90212 - 0.577373 = 0.324746,$ and $P^0(very\ satisfied) = 1 - 0.90212 = 0.09788.$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input subscribed magazine$ resolved$;
cards;
3 no yes
;

data service;
set service predict;
run;

proc genmod;
 class magazine resolved;
  model satisf = subscribed magazine resolved / dist=multinomial link=cumlogit;
    output out=outdata p=psatisf;
run;

proc print data=outdata (firstobs=145) noobs;
 var _level_ psatisf;
run;
```

```
_LEVEL_ psatisf
1       0.08707
2       0.28012
3       0.57736
4       0.90212
```

In R:

```
#fitting cumulative logit model
service.data<- read.csv(file='C:/<insert path>/Exercise4.2Data.csv', header=
TRUE, sep=',')

#making response a categorical variable
satisf.cat<- as.factor(service.data$satisf)

#specifying reference categories
magazine.rel<- relevel(service.data$magazine, ref="yes")
resolved.rel<- relevel(service.data$resolved, ref="yes")

#running the model
library(ordinal)
summary(fitted.model<- clm(satisf.cat ~ subscribed + magazine.rel
+ resolved.rel, data=service.data, link="logit"))
```

```
AIC
108.10


Coefficients:
                Estimate Std. Error z value Pr(>|z|)
subscribed      0.010516   0.009686   1.086  0.27760
magazine.relno -1.917509   0.677141  -2.832  0.00463
resolved.relno -1.428832   0.655864  -2.179  0.02937

Threshold coefficients:
    Estimate Std. Error z value
1|2  -4.2359     0.9678  -4.377
2|3  -2.8298     0.8126  -3.483
3|4  -1.5740     0.7442  -2.115
4|5   0.3350     0.6708   0.499
```

```
#computing AICC
p<-7
n<-36
print(AICC<- -2*logLik(fitted.model)+2*p*n/(n-p-1))
```

```
112.0974
```

```
#outputting BIC
BIC(fitted.model)
```

```
119.182
```

```
#checking model fit
null.model<- clm(satisf.cat ~ 1, data=service.data, link="logit")
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
14.7994
```

```
print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))
```

```
0.001996357
```

```
#using fitted model for prediction
print(predict(fitted.model, type='prob', data.frame(subscribed=3,
magazine.rel='no', resolved.rel='yes')))
```

```
         1         2         3         4          5
0.08706729 0.1930496 0.2972414 0.3247592 0.09788253
```

(b) Redo part (a), running the cumulative probit model.

In SAS:

```
/*fitting cumulative probit model*/
data service;
input subscribed magazine$ resolved$ satisf @@;
cards;
5     yes   no    5  49 yes   no    5  56 no    no    3
13    yes   yes   5  27 no    yes   4  41 yes   yes   5
2     yes   yes   5  64 yes   yes   4  88 yes   yes   4
43    yes   yes   4  94 yes   no    4  8  no    no    1
9     yes   no    2  68 yes   no    4  5  no    yes   2
108   no    yes   3  21 yes   yes   4  25 yes   no    3
2     no    yes   4  11 no    no    2  98 yes   yes   5
11    no    yes   5  46 no    no    4  7  no    no    3
7     no    yes   5  9  yes   yes   5  17 no    no    2
8     no    yes   2  9  no    yes   1  95 no    no    4
60    no    yes   3  80 no    yes   4  2  yes   no    3
33    yes   yes   4  5  yes   no    3  7  no    no    1
;

proc genmod;
 class magazine(ref='yes') resolved(ref='yes');
  model satisf = subscribed magazine resolved / dist=multinomial link=cumprobit;
run;
```

```
Log Likelihood -46.6927

AIC   107.3854
AICC  111.3854
BIC   118.4700

                  Analysis Of Maximum Likelihood Parameter Estimates
Parameter      DF Estimate Standard   Wald 95% Confidence      Wald Chi- Pr > ChiSq
                              Error         Limits                Square
Intercept1      1  -2.6005   0.5384    -3.6558    -1.5453          23.33     <.0001
Intercept2      1  -1.7878   0.4709    -2.7108    -0.8648          14.41     0.0001
Intercept3      1  -1.0295   0.4411    -1.8940    -0.1650           5.45     0.0196
Intercept4      1   0.1114   0.3933    -0.6596     0.8823           0.08     0.7771
subscribed      1  -0.0061   0.0057    -0.0173     0.0051           1.12     0.2892
magazine   no   1   1.2027   0.3885     0.4413     1.9641           9.58     0.0020
magazine   yes  0   0.0000   0.0000     0.0000     0.0000              .          .
resolved   no   1   0.8809   0.3783     0.1394     1.6224           5.42     0.0199
resolved   yes  0   0.0000   0.0000     0.0000     0.0000              .          .
```

The fitted model is written as $\hat{P}(very\ dissatisfied) = \Phi(-2.6005 - 0.0061 \cdot \#of\ months\ subscribed + 1.2027 \cdot no\ magazine + 0.8809 \cdot issue\ not\ resolved)$, $\hat{P}(very\ dissatisfied\ or\ dissatisfied) = \Phi(-1.7878 - 0.0061 \cdot \#of\ months\ subscribed + 1.2027 \cdot no\ magazine + 0.8809 \cdot issue\ not\ resolved)$, $\hat{P}(very\ dissatisfied, dissatisfied, or\ neutral) = \Phi(-1.0295 - 0.0061 \cdot \#of\ months\ subscribed + 1.2027 \cdot no\ magazine +$

$0.8809 \cdot issue\ not\ resolved$), and $\hat{P}(very\ dissatisfied, dissatistied, neutral, or\ satisfied) = \Phi(0.1114 - 0.0061 \cdot \#of\ months\ subscribed + 1.2027 \cdot no\ magazine + 0.8809 \cdot issue\ \ not\ resolved)$.

Subscription to magazine and whether the issue was resolved are statistically significant at the 5% level. The number or months subscribed is not a significant predictor.

For the customers not receiving the magazine, the z-scores of the estimated are 1.2027 points larger than those for customers who receive the magazine. The z-scores of the estimated probabilities for customers whose issue was not resolved are 0.8809 points larger than those for customers whose issue was resolved.

```
/*checking model fit*/
proc genmod;
 model satisf = / dist=multinomial link=cumprobit;
run;
```

```
Log Likelihood -54.4484
```

```
data deviance_test;
 deviance = -2*(-54.4484 - (-46.6927));
 pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance      pvalue
 15.5114  .001427894
```

The p-value is small, indicating a good model fit. The prediction is carried out as follows: $P^0(very\ dissatisfied) = \Phi(-2.6005 - 0.0061 \cdot 3 + 1.2027) = 0.078373$, $P^0(very\ dissatisfied\ or\ dissatisfied) = \Phi(-1.7878 - 0.0061 \cdot 3 + 1.2027) = 0.273121$, $P^0(very\ dissatisfied, dissatisfied, or\ neutral) = \Phi(-1.0295 - 0.0061 \cdot 3 + 1.2027) = 0.56155$, and $P^0(very\ dissatisfied, dissatistied, neutral, or\ satisfied) = \Phi(0.1114 - 0.0061 \cdot 3 + 1.2027) = 0.902478$. Therefore, for each individual level of the satisfaction score, the predicted probabilities are $P^0(very\ dissatisfied) = 0.078373$, $P^0(dissatisfied) = 0.273121 - 0.078373 = 0.194748$, $P^0(neutral) = 0.56155 - 0.273121 = 0.288429$, $P^0(satisfied) = 0.902478 - 0.56155 = 0.340928$, and $P^0(very\ satisfied) = 1 - 0.902478 = 0.097522$.

```
/*using fitted model for prediction*/
data predict;
input subscribed magazine$ resolved$;
cards;
3 no yes
;

data service;
set service predict;
run;

proc genmod;
 class magazine resolved;
  model satisf = subscribed magazine resolved / dist=multinomial link=cumprobit;
```

```
    output out=outdata p=psatisf;
run;

proc print data=outdata (firstobs=145) noobs;
 var _level_ psatisf;
run;
```

```
_LEVEL_ psatisf
1       0.07838
2       0.27315
3       0.56159
4       0.90249
```

In R:

```
#fitting cumulative probit model
service.data<- read.csv(file='C:/<insert path>/Exercise4.2Data.csv', header=
TRUE, sep=',')

#making response a categorical variable
satisf.cat<- as.factor(service.data$satisf)

#specifying reference categories
magazine.rel<- relevel(service.data$magazine, ref="yes")
resolved.rel<- relevel(service.data$resolved, ref="yes")

#running the model
library(ordinal)
summary(fitted.model<- clm(satisf.cat ~ subscribed + magazine.rel + resolved.rel,
data=service.data, link="probit"))
```

```
AIC
107.39

Coefficients:
                Estimate Std. Error z value Pr(>|z|)
subscribed      0.006061   0.005718   1.060  0.28919
magazine.relno -1.202678   0.388476  -3.096  0.00196
resolved.relno -0.880893   0.378313  -2.328  0.01989

Threshold coefficients:
    Estimate Std. Error z value
1|2  -2.6005     0.5384  -4.830
2|3  -1.7878     0.4709  -3.796
3|4  -1.0295     0.4411  -2.334
4|5   0.1114     0.3933   0.283
```

```
#computing AICC
p<-7
n<-36
print(AICC<- -2*logLik(fitted.model)+2*p*n/(n-p-1))
```

```
111.3854
```

```
#outputting BIC
BIC(fitted.model)
```

```
118.47
```

```
#checking model fit
null.model<- clm(satisf.cat ~ 1, data=service.data, link="probit")
```

```
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))

15.51138

print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))
0.001427906

#using fitted model for prediction
print(predict(fitted.model, type='prob', data.frame(subscribed=3,
magazine.rel='no', resolved.rel='yes')))

        1         2         3         4          5
0.0783845 0.1947673 0.2884392 0.3408959 0.09751309
```

(c) Redo part (a), running the cumulative complementary log-log model.

In SAS:

```
/*fitting cumulative complementary log-log model*/
data service;
input subscribed magazine$ resolved$ satisf @@;
cards;
5     yes   no    5  49 yes   no    5  56 no    no    3
13    yes   yes   5  27 no    yes   4  41 yes   yes   5
2     yes   yes   5  64 yes   yes   4  88 yes   yes   4
43    yes   yes   4  94 yes   no    4  8  no    no    1
9     yes   no    2  68 yes   no    4  5  no    yes   2
108   no    yes   3  21 yes   yes   4  25 yes   no    3
2     no    yes   4  11 no    no    2  98 yes   yes   5
11    no    yes   5  46 no    no    4  7  no    no    3
7     no    yes   5  9  yes   yes   5  17 no    no    2
8     no    yes   2  9  no    yes   1  95 no    no    4
60    no    yes   3  80 no    yes   4  2  yes   no    3
33    yes   yes   4  5  yes   no    3  7  no    no    1
;

proc genmod;
 class magazine(ref='yes') resolved(ref='yes');
  model satisf = subscribed magazine resolved / dist=multinomial link=cumcll;
run;
```

```
Log Likelihood -48.3651

AIC  110.7302
AICC 114.7302
BIC  121.8149

               Analysis Of Maximum Likelihood Parameter Estimates
Parameter      DF Estimate Standard  Wald 95% Confidence       Wald Chi- Pr > ChiSq
                              Error        Limits                 Square
Intercept1      1  -3.6044   0.7514    -5.0770     -2.1317        23.01     <.0001
Intercept2      1  -2.4709   0.5899    -3.6271     -1.3147        17.54     <.0001
Intercept3      1  -1.5993   0.5275    -2.6331     -0.5655         9.19     0.0024
Intercept4      1  -0.4294   0.4201    -1.2527      0.3939         1.05     0.3066
subscribed      1  -0.0030   0.0063    -0.0154      0.0094         0.22     0.6364
magazine   no   1   1.1422   0.4226     0.3140      1.9704         7.31     0.0069
magazine   yes  0   0.0000   0.0000     0.0000      0.0000            .          .
```

```
                  Analysis Of Maximum Likelihood Parameter Estimates
Parameter       DF Estimate Standard   Wald 95% Confidence       Wald Chi- Pr > ChiSq
                            Error          Limits                  Square
resolved   no   1   1.0099   0.4301      0.1670      1.8528          5.51     0.0189
resolved   yes  0   0.0000   0.0000      0.0000      0.0000             .          .
```

The fitted model is $\hat{P}(satisf = 1) = \hat{P}(very\ dissatisfied) = 1 - \exp(-\exp(-3.6044 - 0.0030 \cdot \#of\ months\ subscribed + 1.1422 \cdot no\ magazine + 1.0099 \cdot issue\ not\ resolved))$, $\hat{P}(very\ dissatisfied\ or\ dissatisfied) = 1 - \exp(-\exp(-2.4709 - 0.0030 \cdot \#of\ months\ subscribed + 1.1422 \cdot no\ magazine + 1.0099 \cdot issue\ not\ resolved))$, $\hat{P}(very\ dissatisfied, dissatisfied, or\ neutral) = 1 - \exp(-\exp(-1.5993 - 0.0030 \cdot \#of\ months\ subscribed + 1.1422 \cdot no\ magazine + 1.0099 \cdot issue\ not\ resolved))$, and $\hat{P}(very\ dissatisfied, dissatistied, neutral, or\ satisfied) = 1 - \exp(-\exp(-0.4294 - 0.0030 \cdot \#of\ months\ subscribed + 1.1422 \cdot no\ magazine + 1.0099 \cdot issue\ not\ resolved))$.

Significant predictors are substription to the magazine and whether the issue was resolved or not.

The estimated complementary probabilities for customers no don't receive the magazine are those for customers who receive the magazine raised to the power $\exp(1.1422) = 3.133655$. The estimated complementary probabilities for customers whose issues were not resolved are those for customers whose issue were resolved raised to the power $\exp(1.0099) = 2.745326$.

```
/*checking model fit*/
proc genmod;
 model satisf = / dist=multinomial link=cumcll;
run;
```

```
Log Likelihood -54.4484
```

```
data deviance_test;
 deviance = -2*(-54.4484 - (-48.3651));
 pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance      pvalue
 12.1666  .006833713
```

The model has a good fit, judging by the small p-value in the goodness-of-fit test. The predicted probabilities are: $P^0(very\ dissatisfied) = 1 - \exp(-\exp(-3.6044 - 0.0030 \cdot 3 + 1.1422)) = 0.081013$, $P^0(very\ dissatisfied\ or\ dissatisfied) = 1 - \exp(-\exp(-2.4709 - 0.0030 \cdot 3 + 1.1422)) = 0.230834$, $P^0(very\ dissatisfied, dissatisfied, or\ neutral) = 1 - \exp(-\exp(-1.5993 - 0.0030 \cdot 3 + 1.1422)) = 0.466045$, and $P^0(very\ dissatisfied, dissatistied, neutral, or\ satisfied) = 1 - \exp(-\exp(-0.4294 - 0.0030 \cdot 3 + 1.1422)) = 0.867533$.

The predicted probabilities for invidivual levels of the satisfaction score are:

$P^0(very\ dissatisfied) = 0.081013$, $P^0(dissatisfied) = 0.230834 - 0.081013 = 0.149821$,

$P^0(neutral) = 0.466045 - 0.230834 = 0.235211$, $P^0(satisfied) = 0.867533 - 0.466045 = 0401487$, and $P^0(very\ satisfied) = 1 - 0.867533 = 0.132467$.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input subscribed magazine$ resolved$;
cards;
3 no yes
;

data service;
set service predict;
run;

proc genmod;
 class magazine resolved;
  model satisf = subscribed magazine resolved / dist=multinomial link=cumcll;
    output out=outdata p=psatisf;
run;

proc print data=outdata (firstobs=145) noobs;
 var _level_ psatisf;
run;
```

```
_LEVEL_ psatisf
1       0.08101
2       0.23084
3       0.46604
4       0.86752
```

In R:

```
fitting cumulative complementary log-log model
service.data<- read.csv(file='C:/<insert path>/Exercise4.2Data.csv', header=
TRUE, sep=',')

#making response a categorical variable
satisf.cat<- as.factor(service.data$satisf)

#running the model
library(ordinal)
summary(fitted.model<- clm(satisf.cat ~ subscribed + magazine + resolved,
data=service.data, link="cloglog"))
```

```
AIC
110.73


Coefficients:
                Estimate Std. Error z value Pr(>|z|)
subscribed      0.002997   0.006339   0.473  0.63641
magazine.relno -1.142173   0.422566  -2.703  0.00687
resolved.relno -1.009893   0.430080  -2.348  0.01887

Threshold coefficients:
    Estimate Std. Error z value
1|2  -3.6044     0.7514  -4.797
```

```
2|3  -2.4709     0.5899  -4.189
3|4  -1.5993     0.5275  -3.032
4|5  -0.4294     0.4201  -1.022

#computing AICC
p<-7
n<-36
print(AICC<- -2*logLik(fitted.model)+2*p*n/(n-p-1))

114.7302
#outputting BIC
BIC(fitted.model)

121.8149

#checking model fit
null.model<- clm(satisf.cat ~ 1, data=service.data, link="cloglog")
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))

12.16653

print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))

0.006833923

#using fitted model for prediction
print(predict(fitted.model, type='prob', data.frame(subscribed=3, magazine='no',
resolved='yes')))

        1         2         3         4         5
0.0810142 0.1498225 0.2352053 0.4014798 0.1324782
```

(d) Discuss the relative fit of the models obtained in parts (a)-(c).

By the AIC, AICC, and BIC criteria, we see that the cumulative probit regression model has the smallest values and hence has the best fit. The cumulative complementary log-log model has the worse fit.

	cumulative logit	cumulative probit	Cumulative cloglog
AIC	108.0974	107.3854	110.7302
AICC	112.0974	111.3854	114.7302
BIC	119.1820	118.4700	121.8149

EXERCISE 4.3. (a) Categorize the amount spent into the three categories: '<$10,000 ', '$10,000-<$30,000', and '$30,000+'. Fit a cumulative logit model. Write down the fitted model, discuss its fit, and interpret estimated significant coefficients. Predict probabilities of each expenditure bracket for a company that has been in business for 4 years, and buys electronics from the supply corporation on the regular basis.

In SAS:

```
/*fitting cumulative logit model*/
data expense;
input inbusiness$ 1-9 firsttime$ type$ 15-25 amount;
cards;
< 1 year  yes stationary  5690
1-5 years yes stationary  14454
5+ years  yes electronics 20489
5+ years  no  stationary  13115
< 1 year  no  electronics 44885
< 1 year  no  electronics 28182
< 1 year  no  furniture   40982
< 1 year  no  stationary  10160
1-5 years no  furniture   51363
5+ years  yes electronics 29448
5+ years  no  stationary  2093
< 1 year  no  furniture   127133
1-5 years yes furniture   21593
< 1 year  no  furniture   220909
1-5 years  no electronics 17000
1-5 years yes electronics 22812
1-5 years yes electronics 13090
1-5 years no  electronics 24336
5+ years  yes stationary  452
< 1 year  yes stationary  3600
5+ years  yes furniture   2450
< 1 year  no  electronics 12230
5+ years  yes stationary  2451
1-5 years no  stationary  1110
< 1 year  yes electronics 69280
< 1 year  yes furniture   119613
< 1 year  no  electronics 21770
< 1 year  yes electronics 64160
< 1 year  no  furniture   78900
< 1 year  no  electronics 75095
5+ years  no  furniture   7450
5+ years  no  furniture   5200
< 1 year  no  furniture   32099
5+ years  no  electronics 1997
;

/*categorizing spending amount*/
data expense;
set expense;
length amount_cat $13;
if amount <10000 then amount_cat='1. <$10K';
if amount ge 10000 and amount < 30000 then amount_cat='2. $10K-<$30K';
if amount ge 30000 then amount_cat='3. $30K+';
run;

proc genmod;
 class inbusiness(ref='< 1 year') firsttime(ref='yes') type(ref='furniture');
  model amount_cat = inbusiness firsttime type / dist=multinomial link=cumlogit;
run;
```

```
Log Likelihood -22.7726

AIC  59.5452
AICC 63.8529
BIC  70.2297
```

```
                Analysis Of Maximum Likelihood Parameter Estimates
Parameter                DF Estimate Standard      Wald 95%          Wald Pr > ChiSq
                                        Error  Confidence Limits      Chi-
                                                                    Square
Intercept1                1  -4.8694   1.4721   -7.7546   -1.9842    10.94     0.0009
Intercept2                1  -1.2584   1.0212   -3.2599    0.7431     1.52     0.2178
inbusiness 1-5 years      1   1.6606   0.9266   -0.1554    3.4766     3.21     0.0731
inbusiness 5+ years       1   4.5406   1.3818    1.8323    7.2490    10.80     0.0010
inbusiness < 1 year       0   0.0000   0.0000    0.0000    0.0000        .          .
firsttime  no             1   0.1112   0.8040   -1.4647    1.6870     0.02     0.8900
firsttime  yes            0   0.0000   0.0000    0.0000    0.0000        .          .
type       electronics    1   0.7418   0.8609   -0.9454    2.4291     0.74     0.3888
type       stationary     1   3.8781   1.4425    1.0509    6.7053     7.23     0.0072
type       furniture      0   0.0000   0.0000    0.0000    0.0000        .          .
```

The fitted model is $\frac{\hat{P}(amount<\$10{,}000)}{1-\hat{P}(amount<\$10{,}000)} = \exp(-4.8694 + 1.6606 \cdot in\ business\ 1\ to\ 5\ years + 4.5406 \cdot in\ business\ \geq 5\ years + 0.1112 \cdot not\ first\ time + 0.7418 \cdot electronics + 3.8781 \cdot stationary)$, and $\frac{\hat{P}(amount<\$30{,}000)}{1-\hat{P}(amoun\quad \$30{,}000)} = \exp(-1.2584 + 1.6606 \cdot in\ business\ 1\ to\ 5\ years + 4.5406 \cdot in\ business\ \geq 5\ years + 0.1112 \cdot not\ first\ time + 0.7418 \cdot electronics + 3.8781 \cdot stationary)$.

Being in business for 5 or more years and purchasing stationary are significant predictors.

The estimated odds for companies that are in business for 5 or more years are $\exp(4.5406) \cdot 100\% = 9{,}374.703\%$ of those who are less than 1 year. The estimated odds for companies that purchase stationary are $\exp(3.8781) \cdot 100\% = 4{,}833.23\%$ of those for companies that purchase furnature.

```
/*checking model fit*/
proc genmod;
 model amount_cat = / dist=multinomial link=cumlogit;
run;
```

```
Log Likelihood -37.1492
```

```
data deviance_test;
 deviance = -2*(-37.1492 - (-22.7726));
 pvalue = 1 - probchi(deviance,5);
run;

proc print noobs;
run;
```

```
deviance     pvalue
 28.7532 .000025921
```

The model fits the data well as supported by the small magnitude of the p-value in the deviance test. As for predicted probabilities, they are derived as follows. The company we want to predict the probabilities for has been in business between 1 and 5 years, is not a first-time buyer, and purchases electronics. Therefore, $P^0(amount < \$10{,}000) = \frac{\exp(-4.8694+1.6606+0.1112+0.7418)}{1+\exp(-4.8694\quad .6606+0.1112+0.7418)} =$ 0.086606, and $P^0(amount < \$30{,}000) = \frac{\exp(-1.2584+\ .6606+0.1112+0.7418)}{1+\exp(-1.2584+1.6606+0.1112+0.7418)} = 0.778199.$

Thus, the predicted probabilities for each expenditure bracket are $P^0(amount < \$10{,}000) = 0.086606, P^0(\$10{,}000 \leq amount < \$30{,}000) = 0.778199 - 0.086606 = 0.691593$, and $P^0(amount \geq \$30{,}000) = 1 - 0.778199 = 0.221801.$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input inbusiness $ 1-9 firsttime$ type$ 14-24;
cards;
1-5 years no electronics
;

data expense;
set expense predict;
run;

proc genmod;
 class inbusiness firsttime type;
  model amount_cat = inbusiness firsttime type / dist=multinomial link=cumlogit;
   output out=outdata p=ptype;
run;

proc print data=outdata (firstobs=69) noobs;
var _level_ ptype;
run;
```

```
_LEVEL_         ptype
1. <$10K      0.08660
2. $10K-<$30K 0.77820
```

In R:

```
#fitting cumulative logit model
expense.data<- read.csv(file='C:/<insert path>/Exercise4.3Data.csv', header=
TRUE, sep=',')

#specifying reference categories
inbusiness.rel<- relevel(expense.data$inbusiness, ref="< 1 year")
firsttime.rel<- relevel(expense.data$firsttime, ref="yes")
type.rel<- relevel(expense.data$type, ref="furniture")

#categorizing response variable
amount.cat<- as.factor(ifelse(expense.data$amount < 10000, '1.<$10,000',
ifelse(expense.data$amount >= 30000, '3.$30,000+', '2.$10,000-<$30,000')))

#running the model
library(ordinal)
summary(fitted.model<- clm(amount.cat ~ inbusiness.rel + firsttime.rel
+ type.rel, data=expense.data, link="logit"))
```

```
AIC
59.55

Coefficients:
                        Estimate Std. Error z value Pr(>|z|)
inbusiness.rel1-5 years  -1.6606     0.9266  -1.792  0.07309
inbusiness.rel5+ years   -4.5406     1.3818  -3.286  0.00102
firsttime.relno          -0.1112     0.8040  -0.138  0.89003
type.relelectronics      -0.7418     0.8609  -0.862  0.38882
type.relstationary       -3.8781     1.4425  -2.689  0.00718

Threshold coefficients:
                              Estimate Std. Error z value
1.<$10,000|2.$10,000-<$30,000   -4.869      1.472  -3.308
2.$10,000-<$30,000|3.$30,000+   -1.258      1.021  -1.232
```

```
#computing AICC
p<- 7
n<- 34
print(AICC<- -2*logLik(fitted.model)+2*p*n/(n-p-1))
```

```
63.85288
```

```
#outputting BIC
BIC(fitted.model)
```

```
70.22971
```

```
#checking model fit
null.model<- clm(amount.cat ~ 1, data=expense.data, link="logit")
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
28.75325
```

```
print(p.value<- pchisq(deviance, df=5, lower.tail = FALSE))
```

```
2.592039e-05
```

```
#using fitted model for prediction
print(predict(fitted.model, type='prob', data.frame(inbusiness.rel='1-5 years',
firsttime.rel='no', type='electronics')))
```

```
1.<$10,000   2.$10,000-<$30,000   3.$30,000+
0.08660481            0.6915989    0.2217963
```

(b) Fit a cumulative probit model to the data, and answer the questions in part (a).

In SAS:

```
/*fitting cumulative probit model*/
data expense;
input inbusiness$ 1-9 firsttime$ type$ 15-25 amount;
cards;
< 1 year  yes stationary  5690
1-5 years yes stationary  14454
5+ years  yes electronics 20489
5+ years  no  stationary  13115
< 1 year  no  electronics 44885
< 1 year  no  electronics 28182
< 1 year  no  furniture   40982
< 1 year  no  stationary  10160
1-5 years no  furniture   51363
5+ years  yes electronics 29448
5+ years  no  stationary  2093
< 1 year  no  furniture   127133
1-5 years yes furniture   21593
< 1 year  no  furniture   220909
1-5 years  no electronics 17000
1-5 years yes electronics 22812
1-5 years yes electronics 13090
1-5 years no  electronics 24336
5+ years  yes stationary  452
< 1 year  yes stationary  3600
5+ years  yes furniture   2450
< 1 year  no  electronics 12230
5+ years  yes stationary  2451
1-5 years no  stationary  1110
< 1 year  yes electronics 69280
< 1 year  yes furniture   119613
< 1 year  no  electronics 21770
< 1 year  yes electronics 64160
< 1 year  no  furniture   78900
< 1 year  no  electronics 75095
5+ years  no  furniture   7450
5+ years  no  furniture   5200
< 1 year  no  furniture   32099
5+ years  no  electronics 1997
;

/*categorizing spending amount*/
data expense;
set expense;
length amount_cat $13;
if amount <10000 then amount_cat='1. <$10K';
if amount ge 10000 and amount < 30000 then amount_cat='2. $10K-<$30K';
if amount ge 30000 then amount_cat='3. $30K+';
run;

proc genmod;
 class inbusiness(ref='< 1 year') firsttime(ref='yes') type(ref='furniture');
  model amount_cat = inbusiness firsttime type / dist=multinomial link=cumprobit;
run;
```

```
Log Likelihood -22.8168

AIC  59.6336
AICC 63.9413
BIC  70.3181

                Analysis Of Maximum Likelihood Parameter Estimates
Parameter              DF Estimate Standard      Wald 95%             Wald Pr > ChiSq
                                      Error  Confidence Limits        Chi-
                                                                    Square
Intercept1              1  -2.7301   0.7096   -4.1208   -1.3393      14.80     0.0001
Intercept2              1  -0.7096   0.4827   -1.6557    0.2365       2.16     0.1416
inbusiness 1-5 years    1   0.9682   0.5508   -0.1113    2.0477       3.09     0.0788
inbusiness 5+ years     1   2.4398   0.6659    1.1347    3.7449      13.43     0.0002
inbusiness < 1 year     0   0.0000   0.0000    0.0000    0.0000          .          .
```

```
                  Analysis Of Maximum Likelihood Parameter Estimates
Parameter                DF Estimate Standard       Wald 95%           Wald Pr > ChiSq
                                     Error  Confidence Limits         Chi-
                                                                     Square
firsttime  yes            1   0.0503   0.4621   -0.8553    0.9560      0.01     0.9133
firsttime  no             0   0.0000   0.0000    0.0000    0.0000         .          .
type       electronics    1   0.4350   0.5216   -0.5874    1.4573      0.70     0.4043
type       stationary     1   2.0446   0.6890    0.6943    3.3950      8.81     0.0030
type       furniture      0   0.0000   0.0000    0.0000    0.0000         .          .
```

The fitted model can be written as:

as $\hat{P}(amount < \$10{,}000) = \Phi(-2.7301 + 0.9682 \cdot in\ business\ 1\ to\ 5\ years + 2.4398 \cdot in\ business\ \geq 5\ years + 0.0503 \cdot not\ first\ time + 0.4350 \cdot electronics + 2.0446 \cdot stationary)$, and $\hat{P}(amount < \$30{,}000) = \Phi(-0.7096 + 0.9682 \cdot in\ business\ 1\ to\ 5\ years + 2.4398 \cdot in\ business\ \geq 5\ years + 0.0503 \cdot not\ first\ time + 0.4350 \cdot electronics + 2.0446 \cdot stationary)$. Being in business for 5 or more years and purchasing stationary are significan predictors. The z-scores for the estimated probabilities for companies that have been in business for 5 or more years are larger by 2.4398 than those for companies that have been in business less than one year. The z-scores for the estimated probabilities for companies that purchase electronics are 2.0446 points larger than those for companies that purchase furniture.

```
/*checking model fit*/
proc genmod;
 model amount_cat = / dist=multinomial link=cumprobit;
run;
```

```
Log Likelihood -37.1492
```

```
data deviance_test;
 deviance = -2*(-37.1492 - (-22.8168));
 pvalue = 1 - probchi(deviance,5);
run;

proc print noobs;
run;
```

```
deviance      pvalue
 28.6648  .000026976
```

The model has an excellent fit as indicated by the small p-value in the deviance test. The predicted probabilities can be obtained as follows:

$P^0(amount < \$10{,}000) = \Phi(-2.7301 + 0.9682 + 0.0503 + 0.4350) = 0.100872$, and
$P^0(amount < \$30{,}000) = \Phi(-0.7096 + 0.9682 + 0.0503 + 0.4350) = 0.771532$.
The predicted probabilities for individual expenditure brackets are $P^0(amount < \$10{,}000) = 0.100872$, $P^0(\$10{,}000 \leq amount < \$30{,}000) = 0.771532 - 0.100872 = 0.67066$, and $P^0(amount \geq \$30{,}000) = 1 - 0.771532 = 0.228468$.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input inbusiness $ 1-9 firsttime$ type$ 14-24;
```

```
cards;
1-5 years no electronics
;
run;

data expense;
set expense predict;
run;

proc genmod;
 class inbusiness(ref='< 1 year') firsttime(ref='no') type(ref='furniture');
  model amount_cat = inbusiness firsttime type / dist=multinomial link=cumprobit;
   output out=outdata p=ptype;
run;

proc print data=outdata (firstobs=69) noobs;
var _level_ ptype;
run;
```

```
_LEVEL_          ptype
1. <$10K       0.09227
2. $10K-<$30K  0.75603
```

In R:

```
#fitting cumulative probit model
expense.data<- read.csv(file='C:/<insert path>/Exercise4.3Data.csv', header=
TRUE, sep=',')

#specifying reference categories
inbusiness.rel<- relevel(expense.data$inbusiness, ref="< 1 year")
firsttime.rel<- relevel(expense.data$firsttime, ref="yes")
type.rel<- relevel(expense.data$type, ref="furniture")

#categorizing response variable
amount.cat<- as.factor(ifelse(expense.data$amount < 10000, '1.<$10,000',
ifelse(expense.data$amount >= 30000, '3.$30,000+', '2.$10,000-<$30,000')))

#running the model
library(ordinal)
summary(fitted.model<- clm(amount.cat ~ inbusiness.rel + firsttime.rel
+ type.rel, data=expense.data, link="probit"))
```

```
AIC
59.63


Coefficients:
                        Estimate Std. Error z value Pr(>|z|)
inbusiness.rel1-5 years -0.96820    0.55078  -1.758 0.078772
inbusiness.rel5+ years  -2.43983    0.66588  -3.664 0.000248
firsttime.relyes        -0.05032    0.46208  -0.109 0.913289
type.relelectronics     -0.43497    0.52163  -0.834 0.404347
type.relstationary      -2.04464    0.68897  -2.968 0.003001

Threshold coefficients:
                                  Estimate Std. Error z value
1.<$10,000|2.$10,000-<$30,000  -2.7301     0.7096  -3.847
2.$10,000-<$30,000|3.$30,000+  -0.7096     0.4827  -1.470
```

```
#computing AICC
```

```
p<- 7
n<- 34
print(AICC<- -2*logLik(fitted.model)+2*p*n/(n-p-1))
```

```
63.94131
```

```
#outputting BIC
BIC(fitted.model)
```

```
70.31814
```

```
#checking model fit
null.model<- clm(amount.cat ~ 1, data=expense.data, link="probit")
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
28.66482
```

```
print(p.value<- pchisq(deviance, df=5, lower.tail = FALSE))
```

```
2.697567e-05
```

```
#using fitted model for prediction
print(predict(fitted.model, type='prob', data.frame(inbusiness.rel='1-5 years',
firsttime.rel='no', type.rel='electronics')))
```

```
1.<$10,000   2.$10,000-<$30,000   3.$30,000+
0.09227224             0.663757    0.2439708
```

(c) Repeat part (a) with a cumulative complementary log-log model.

In SAS:

```
/*fitting cumulative complementary log-log model*/
data expense;
input inbusiness$ 1-9 firsttime$ type$ 15-25 amount;
cards;
< 1 year  yes stationary  5690
1-5 years yes stationary  14454
5+ years  yes electronics 20489
5+ years  no  stationary  13115
< 1 year  no  electronics 44885
< 1 year  no  electronics 28182
< 1 year  no  furniture   40982
< 1 year  no  stationary  10160
1-5 years no  furniture   51363
5+ years  yes electronics 29448
5+ years  no  stationary  2093
< 1 year  no  furniture   127133
1-5 years yes furniture   21593
< 1 year  no  furniture   220909
1-5 years  no electronics 17000
1-5 years yes electronics 22812
1-5 years yes electronics 13090
1-5 years no  electronics 24336
5+ years  yes stationary  452
< 1 year  yes stationary  3600
5+ years  yes furniture   2450
< 1 year  no  electronics 12230
5+ years  yes stationary  2451
```

```
1-5 years no  stationary  1110
< 1 year  yes electronics 69280
< 1 year  yes furniture   119613
< 1 year  no  electronics 21770
< 1 year  yes electronics 64160
< 1 year  no  furniture   78900
< 1 year  no  electronics 75095
5+ years  no  furniture   7450
5+ years  no  furniture   5200
< 1 year  no  furniture   32099
5+ years  no  electronics 1997
;
/*categorizing spending amount*/
data expense;
set expense;
length amount_cat $13;
if amount <10000 then amount_cat='1. <$10K';
if amount ge 10000 and amount < 30000 then amount_cat='2. $10K-<$30K';
if amount ge 30000 then amount_cat='3. $30K+';
run;

proc genmod;
 class inbusiness(ref='< 1 year') firsttime(ref='no') type(ref='furniture');
  model amount_cat = inbusiness firsttime type / dist=multinomial link=cumcll;
run;
```

```
Log Likelihood -23.6537

AIC  61.3074
AICC 65.6151
BIC  71.9920

                Analysis Of Maximum Likelihood Parameter Estimates
Parameter              DF Estimate Standard     Wald 95%            Wald Pr > ChiSq
                                      Error  Confidence Limits      Chi-
                                                                  Square
Intercept1              1  -3.5603   0.9430   -5.4084   -1.7121    14.25     0.0002
Intercept2              1  -1.1928   0.5920   -2.3532   -0.0324     4.06     0.0439
inbusiness 1-5 years    1   1.2523   0.6415   -0.0049    2.5096     3.81     0.0509
inbusiness 5+ years     1   2.5159   0.8228    0.9033    4.1286     9.35     0.0022
inbusiness < 1 year     0   0.0000   0.0000    0.0000    0.0000       .           .
firsttime  yes          1   0.1249   0.5370   -0.9276    1.1774     0.05     0.8161
firsttime  no           0   0.0000   0.0000    0.0000    0.0000       .           .
type       electronics  1   0.5535   0.6549   -0.7302    1.8371     0.71     0.3981
type       stationary   1   1.9368   0.7914    0.3857    3.4879     5.99     0.0144
type       furniture    0   0.0000   0.0000    0.0000    0.0000       .           .
```

The fitted model is $\hat{P}(amount < \$10{,}000) = 1 - \exp(-\exp(-3.5603 + 1.2523 \cdot in\ business\ 1\ to\ 5\ years + 2.5159 \cdot in\ business\ \geq 5\ years + 0.1249 \cdot first\ time + 0.5535 \cdot electronics + 1.9368 \cdot stationary))$, and $\hat{P}(amount < \$30{,}000) = 1 - \exp(-\exp(-1.1928 + 1.2523 \cdot in\ business\ 1\ to\ 5\ years + 2.5159 \cdot in\ business\ \geq 5\ years + 0.1249 \cdot first\ time + 0.5535 \cdot electronics + 1.9368 \cdot stationary))$.

Being in business for 5 or more years and purchasing stationary are significant predictors.

The estimated complementary probabilities for companies that are in business for 5 or more years are those for companies that are in business for less than one year raised to the power $\exp(2.5159) = 12.37774.$ The estimated complementary probabilities for companies that purchase stationary are those for companies that purchase furniture raised to the power $\exp(1.9368) = 6.936519.$

```
/*checking model fit*/
proc genmod;
 model amount_cat = / dist=multinomial link=cumcll;
run;
```

```
Log Likelihood -37.1492
```

```
data deviance_test;
 deviance = -2*(-37.1492 - (-23.6537));
 pvalue = 1 - probchi(deviance,5);
run;

proc print noobs;
run;
```

```
deviance      pvalue
  26.991  .000057273
```

The fit of the model is very good since the p-value is very small. The predicted probabilities are computed as $P^0(amount < \$10{,}000) = 1 - \exp(-\exp(-3.5603 + 1.2523 + 0.5535)) = 0.158857$, and $P^0(amount < \$30{,}000) = 1 - \exp(-\exp(-1.1928 + 1.2523 + 0.5535)) = 0.842126$. Thus, the predicted probabilities for each expenditure bracket are $P^0(amount < \$10{,}000) = 0.158857,\ P^0(\$10{,}000 \leq amount < \$30{,}000) = 0.842126 - 0.158857 = 0.683269$, and $P^0(amount \geq \$30{,}000) = 1 - 0.842126 = 0.157874$.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input inbusiness $ 1-9 firsttime$ type$ 14-24;
cards;
1-5 years no electronics
;
run;

data expense;
set expense predict;
run;

proc genmod;
 class inbusiness firsttime type;
  model amount_cat = inbusiness firsttime type / dist=multinomial link=cumcll;
   output out=outdata p=ptype;
run;

proc print data=outdata (firstobs=69) noobs;
var _level_ ptype;
run;
```

```
_LEVEL_          ptype
1. <$10K       0.15886
```

```
_LEVEL_         ptype
2. $10K-<$30K 0.84213
```

In R:

```
#fitting cumulative complementary log-log model
expense.data<- read.csv(file='C:/<insert path>/Exercise4.3Data.csv', header=
TRUE, sep=',')

#specifying reference categories
inbusiness.rel<- relevel(expense.data$inbusiness, ref="< 1 year")
firsttime.rel<- relevel(expense.data$firsttime, ref="no")
type.rel<- relevel(expense.data$type, ref="furniture")

#categorizing response variable
amount.cat<- as.factor(ifelse(expense.data$amount < 10000, '1.<$10,000',
ifelse(expense.data$amount >= 30000, '3.$30,000+', '2.$10,000-<$30,000')))

#running the model
library(ordinal)
summary(fitted.model<- clm(amount.cat ~ inbusiness.rel + firsttime.rel
+ type.rel, data=expense.data, link="cloglog"))
```

```
AIC
61.31

Coefficients:
                        Estimate Std. Error z value Pr(>|z|)
inbusiness.rel1-5 years  -1.2523     0.6415  -1.952  0.05091
inbusiness.rel5+ years   -2.5159     0.8228  -3.058  0.00223
firsttime.relyes         -0.1249     0.5370  -0.233  0.81610
type.relelectronics      -0.5535     0.6549  -0.845  0.39808
type.relstationary       -1.9368     0.7914  -2.447  0.01439

Threshold coefficients:
                              Estimate Std. Error z value
1.<$10,000|2.$10,000-<$30,000   -3.560      0.943  -3.776
2.$10,000-<$30,000|3.$30,000+   -1.193      0.592  -2.015
```

```
#computing AICC
p<- 7
n<- 34
print(AICC<- -2*logLik(fitted.model)+2*p*n/(n-p-1))
```

```
65.61512
```

```
#outputting BIC
BIC(fitted.model)
```

```
71.99195
```

```
#checking model fit
null.model<- clm(amount.cat ~ 1, data=expense.data, link="cloglog")
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
26.99101
```

```
print(p.value<- pchisq(deviance, df=5, lower.tail = FALSE))
```

```
5.727298e-05
```

```
#using fitted model for prediction
```

```
print(predict(fitted.model, type='prob', data.frame(inbusiness.rel='1-5 years',
firsttime.rel='no', type.rel='electronics')))
```

```
1.<$10,000   2.$10,000-<$30,000   3.$30,000+
 0.1588638             0.683266    0.1578701
```

(d) Which of the three fitted models has the best fit?

Comparing the values for AIC, AICC, and BIC criteria, we determine that the cumulative logit model has the smallest values and thus has the best fit.

	cumulative logit	cumulative probit	Cumulative cloglog
AIC	59.5452	59.6336	61.3074
AICC	63.8529	63.9413	65.6151
BIC	70.2297	70.3181	71.9920

EXERCISE 4.4. (a) Assuming that the outcome is measured on the nominal scale, run the generalized logit model. Use the correct prediction as the reference category. Write down the fitted model explicitly.

In SAS:

```
/*fitting generalized logit model*/
data forecast;
input elevation water$ winddir windspeed outcome$ @@;
cards;
146  yes 270 2  FA  841  no 360 13  FA  672  yes 360 4  FA
312  no  250 5  FA  126  yes 170 8  FA  607  no  360 8  FA
748  no  270 15 FA  620  yes 290 5  FA  5431 no  200 2  FD
2181 yes 310 8  FD  645  yes 170 7  FD  433  no  270 6  FD
360  no  140 15 FD  4227 yes 200 2  FD  14   yes 150 7  C
1026 no  290 1  C   17   yes 180 2  C   20   yes 270 6  C
15   yes 0   3  C   1135 no  20  13 C   21   yes 30  8  C
98   no  140 8  C   36   yes 10  3  C   8    yes 270 10 C
26   yes 0   3  C   13   yes 170 9  C   9    yes 270 6  C
18   yes 200 12 C   96   no  200 8  C   60   yes 240 9  C
;

proc logistic;
 class water(ref='yes') / param=ref;
  model outcome(ref='C') = elevation water winddir windspeed / link=glogit;
run;
```

```
     Testing Global Null Hypothesis: BETA=0
Test                Chi-Square   DF  Pr > ChiSq
Likelihood Ratio       25.8630    8      0.0011
```

```
          Analysis of Maximum Likelihood Estimates
Parameter    outcome DF Estimate Standard Wald       Pr > ChiSq
                                 Error    Chi-Square
Intercept    FA      1  -7.7634  3.5821   4.6971     0.0302
Intercept    FD      1  -5.2150  3.0482   2.9270     0.0871
elevation    FA      1  0.00109  0.00195  0.3105     0.5774
elevation    FD      1  0.00299  0.00181  2.7306     0.0984
water     no FA      1  0.2216   1.3405   0.0273     0.8687
water     no FD      1  0.0499   1.5847   0.0010     0.9749
winddir      FA      1  0.0250   0.0120   4.3335     0.0374
winddir      FD      1  0.00756  0.00864  0.7668     0.3812
windspeed    FA      1  0.1116   0.1756   0.4038     0.5251
windspeed    FD      1  0.1420   0.1962   0.5237     0.4693
```

The fitted model has the form

$$\frac{\hat{P}(false\ alarm)}{\hat{P}(correct\ prediction)} = \exp(-7.7634 + 0.00109 \cdot elevation + 0.2216 \cdot not\ near\ water + 0.0250 \cdot wind\ direction + 0.1116 \cdot wind\ speed),$$

and

$$\frac{\hat{P}(failure\ to\ detect)}{\hat{P}(correct\ prediction)} = \exp(-5.2150 + 0.00299 \cdot elevation + 0.0499 \cdot not\ near\ water + 0.00756 \cdot wind\ direction + 0.1420 \cdot wind\ speed).$$

In R:

```
#fitting generalized logit model
forecast.data<- read.csv(file='C:/<insert path>/Exercise4.4Data.csv', header=
TRUE, sep=',')

#specifying reference categories
outcome.rel<- relevel(forecast.data$outcome, ref="C")
water.rel<- relevel(forecast.data$water, ref="yes")

#running the model
library(nnet)
summary(fitted.model<- multinom(outcome.rel ~ elevation + winddir + windspeed +
water.rel, data=forecast.data))

Coefficients:
   (Intercept)   elevation     winddir windspeed water.relno
FA   -7.764088 0.001089404 0.025033087 0.1116808  0.22092498
FD   -5.218338 0.002986672 0.007571138 0.1421470  0.04887474

#checking model fit
null.model<- multinom(outcome.rel ~ 1, data=forecast.data)
print(deviance<- deviance(null.model)-deviance(fitted.model))

25.86298

print(p.value<- pchisq(deviance, df=8, lower.tail = FALSE))
```

```
0.001108523
```

(b) How good is the model fit? Which variables are significant predictors at the 10% level of significance?

The model fits the data well since in the deviance test, the p-value = 0.0011 < 0.05. Wind direction is significant at the 5% (p-value=0.0374) as a predictor for odds in favor of false alarm against a correct prediction. Elevation is a significant predictor at the 10% level (p-value=0.0984) for odds in favor of failure to detect against a correct prediction.

(c) Give interpretation of the estimated significant coefficients.

As wind direction increases by one degree clockwise, the estimated odds in favor of false alarm against a correct prediction increase by $(\exp(0.0250) - 1) \cdot 100\% = 2.53\%$. As elevation increases by one foot, the estimated odds in favor of failure to detect against a correct prediction increase by $(\exp(0.00299) - 1) \cdot 100\% = 0.299\%$.

(d) Find predicted probabilities of each outcome of weather forecast for an airport that is located at 2,000 feet above the sea level, away from a large body of water, in the presence of wind at 5 knots blowing from the east.

The calculations below show how the predicted probabilities are computed.

$P^0(correct\ prediction) = (1 + \exp(-7.7634 + 0.00109 \cdot 2000 + 0.2216 + 0.0250 \cdot 90 + 0.1116 \cdot 5) + \exp(-5.2150 + 0.00299 \cdot 2000 + 0.0499 + 0.00756 \cdot 90 + 0.1420 \cdot 5))^{-1} = (1 + 0.077786 + 9.072973)^{-1} = 0.0985,$
$P^0(false\ alarm) = P^0(correct\ prediction) \cdot \exp(-7.7634 + 0.00109 \cdot 2000 + 0.2216 + 0.0250 \cdot 90 + 0.1116 \cdot 5) = 0.0985 \cdot 0.077786 = 0.0077$, and
$P^0(failure\ to\ detect) = P^0(correct\ prediction) \cdot \exp(-5.2150 + 0.00299 \cdot 2000 + 0.0499 + 0.00756 \cdot 90 + 0.1420 \cdot 5) = 0.0985 \cdot 9.072973 = 08938.$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input elevation water$ winddir windspeed;
cards;
2000 no 90 5
;

data forecast;
set forecast predict;
run;

proc logistic;
 class water;
  model outcome(ref='C') = elevation water winddir windspeed / link=glogit;
    output out=outdata p=poutcome;
run;

proc print data=outdata (firstobs=91) noobs;
 var _level_ poutcome;
run;
```

```
_LEVEL_ poutcome
C        0.09931
FA       0.00772
FD       0.89297
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, type='prob', data.frame(elevation=2000, winddir=90,
windspeed=5, water.rel='no')))
        C          FA         FD
0.09933447 0.00773318 0.89293235
```

EXERCISE 4.5. (a) Regress the ankle condition on age and gender by running the generalized logit regression model for the nominal response. Use “sprained” as the reference category.

In SAS:

```
/*fitting generalized logit model*/
data ankle;
input age gender$ condition$ @@;
cards;
7  female sprained  9  male   torn      11 male   broken
12 male   broken    8  male   torn      8  female torn
9  female broken    13 male   broken    13 male   torn
15 female sprained  16 female sprained  11 male   torn
12 male   broken    10 female sprained  9  female torn
8  male   sprained  8  female sprained  7  female torn
15 male   broken    17 male   broken    18 male   broken
18 female sprained  18 female torn      16 female torn
12 male   broken
;

proc logistic;
 class gender(ref='female') / param=ref;
  model condition(ref='sprained') = age gender / link=glogit;
run;
```

```
 Testing Global Null Hypothesis: BETA=0
Test             Chi-Square DF Pr > ChiSq
Likelihood Ratio 12.4676    4  0.0142

             Analysis of Maximum Likelihood Estimates
Parameter      condition DF Estimate Standard Wald       Pr > ChiSq
                                     Error    Chi-Square
Intercept      broken    1  -4.6675  3.1632   2.1773     0.1401
Intercept      torn      1  0.3343   1.6797   0.0396     0.8422
age            broken    1  0.2109   0.2024   1.0861     0.2973
age            torn      1  -0.0454  0.1379   0.1082     0.7422
gender    male broken    1  4.1963   1.6559   6.4216     0.0113
gender    male torn      1  1.5574   1.2735   1.4956     0.2213
```

In R:

```
#fitting generalized logit model
ankle.data<- read.csv(file='C:/<insert path>/Exercise4.5Data.csv', header= TRUE,
sep=',')

#specifying reference categories
condition.rel<- relevel(ankle.data$condition, ref="sprained")
gender.rel<- relevel(ankle.data$gender, ref="female")

#running the model
library(nnet)
summary(fitted.model<- multinom(condition.rel ~ age + gender.rel,
data=ankle.data))
```

```
Coefficients:
        (Intercept)         age gender.relmale
broken   -4.6658881  0.21077974       4.195560
torn      0.3352406 -0.04544743       1.556776
```

```
#checking model fit
summary(null.model<- multinom(condition.rel ~ 1, data=ankle.data))
print(deviance<- deviance(null.model)-deviance(fitted.model))
```

```
12.46759
```

```
print(p.value<- pchisq(deviance, df=4, lower.tail = FALSE))
```

```
0.01419266
```

(b) Write down the estimated model. Discuss its goodness-of-fit.

The fitted model is $\frac{\hat{P}(broken)}{\hat{P}(sprained)} = \exp(-4.6675 + 0.2109 \cdot age + 4.1963 \cdot male)$, and $\frac{\hat{P}(torn)}{\hat{P}(sprained)} = \exp(0.3343 - 0.0454 \cdot age + 1.5574 \cdot male)$.

The p-value for the deviance test is 0.0142 which is less than 0.05, indicating a good fit of the model.

(c) Interpret the estimates of the regression coefficients that significantly differ from zero.

The only statistically significant predictor is gender in the model for the odds of broken ankle vs. sprained one. The estimated odds for males are $\exp(4.1963) \cdot 100\% = 6{,}644.01\%$ of those for females.

(d) What are the predicted probabilities of each type of ankle injury for a 9-year-old girl?

The prediction is carried out as follows: $P^0(sprained) = (1 + \exp(-4.6675 + 0.2109 \cdot 9) + \exp(0.3343 - 0.0454 \cdot 9))^{-1} = (1 + 0.0627 + 0.9284)^{-1} = 0.5022$,
$P^0(broken) = P^0(sprained) \cdot \exp(-4.6675 + 0.2109 \cdot 9) = 0.5022 \cdot 0.0627 = 0.0315$, and
$P^0(torn) = P^0(sprained) \cdot \exp(0.3343 - 0.0454 \cdot 9) = 0.5022 \cdot 0.9284 = 0.4663$.

In SAS:

```
/*using fitted model for prediction*/
data predict;
```

```
input age gender$;
cards;
9 female
;

data ankle;
set ankle predict;
run;

proc logistic;
 class gender;
  model condition = age gender / link=glogit;
   output out=outdata p=pcondition;
run;

proc print data=outdata (firstobs=76) noobs;
 var _level_ pcondition;
run;
```

```
_LEVEL_  pcondition
broken      0.03148
sprained    0.50216
torn        0.46636
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, type='prob', data.frame(age=9, gender.rel='female')))
```

```
  sprained   broken     torn
0.50210809 0.03149866 0.46639325
```

EXERCISE 4.6. (a) Regress the communication status on the other variables. Treat it as a nominal variable. Use the zero level as reference. Write down the fitted model.

In SAS:

```
/*fitting generalized logit model*/

data datingsite;
input status agediff heightdiff drinking$ @@;
cards;
3  -3 -1 0  3  3  -2 1  3  2  -3 1  3   0  1 1  3 -5   0 1  3 -6  -6 1
3   2 -5 1  3  0  -4 1  3  4  -7 1  3  -1 -8 1  3 -5   1 1  3 -2   2 1
3  -6 -4 1  3 -7  -6 0  2 -5  -1 0  2 -18  0 1  2 -8   3 0  2  4   0 1
2  -4  2 1  2  1  -8 1  2  0  -7 1  2   4 -3 0  1  8  -7 1  1  1   0 1
1  11  0 0  1 -4  -7 0  1  7  -6 1  1  14 -6 1  1 -1  -8 0  1 -5  -4 0
1  -1 -7 0  1 -3  -8 1  1  8  -4 1  1   4 -5 1  0  3  -8 1  0  4   3 0
0  -6  3 0  0  2  -2 0  0  6   3 1  0   6  3 0
;

proc logistic;
 class drinking (ref='0') / param=ref;
 model status(ref='0') = agediff heightdiff drinking / link=glogit;
run;
```

```
 Testing Global Null Hypothesis: BETA=0
Test             Chi-Square DF Pr > ChiSq
Likelihood Ratio    29.3421  9     0.0006

          Analysis of Maximum Likelihood Estimates
Parameter    status DF Estimate Standard       Wald Pr > ChiSq
                                   Error Chi-Square
Intercept    1       1  -0.7248   0.9372     0.5982     0.4393
Intercept    2       1  -0.9584   1.0239     0.8761     0.3493
Intercept    3       1  -1.4013   1.0981     1.6285     0.2019
agediff      1       1   0.0652   0.1258     0.2689     0.6041
agediff      2       1  -0.2946   0.1429     4.2524     0.0392
agediff      3       1  -0.2717   0.1373     3.9140     0.0479
heightdiff   1       1  -0.5116   0.2083     6.0299     0.0141
heightdiff   2       1  -0.1767   0.1913     0.8535     0.3556
heightdiff   3       1  -0.2532   0.1843     1.8868     0.1696
drinking   1 1       1  -0.1375   1.3391     0.0105     0.9182
drinking   1 2       1   1.8911   1.4309     1.7466     0.1863
drinking   1 3       1   3.0551   1.4460     4.4638     0.0346
```

The fitted model is written as

$$\frac{\hat{P}(user\ sent\ message)}{\hat{P}(neither\ sent\ messages)} = \exp(-0.7248 + 0.0652 \cdot agediff - 0.5116 \cdot heightdiff$$
$$- 0.1375 \cdot same\ drinking\ preference),$$

$$\frac{\hat{P}(candidate\ sent\ message)}{\hat{P}(neither\ sent\ messages)} = \exp(-0.9584 - 0.2946 \cdot agediff - 0.1767 \cdot heightdiff$$
$$+ 1.8911 \cdot same\ drinking\ preference),$$

and

$$\frac{\hat{P}(exchanged\ messages)}{\hat{P}(neither\ sent\ messages)} = \exp(-1.4013 - 0.2717 \cdot agediff - 0.2532 \cdot heightdiff$$
$$+ 3.0551 \cdot same\ drinking\ preference).$$

In R:

```
#fitting generalized logit model
datingsite.data<- read.csv(file='C:/<insert path>/Exercise4.6Data.csv',
header= TRUE, sep=',')

#specifying reference categories
status.rel<- relevel(as.factor(datingsite.data$status), ref="0")

#running the model
library(nnet)
summary(fitted.model<- multinom(status.rel ~ agediff + heightdiff + drinking,
data=datingsite.data))
```

```
Coefficients:
  (Intercept)     agediff heightdiff  drinking
1  -0.7248097  0.06523868 -0.5116114 -0.137546
2  -0.9583625 -0.29461474 -0.1767453  1.891054
3  -1.4012291 -0.27171217 -0.2531624  3.055023
```

```
#checking model fit
summary(null.model<- multinom(status.rel ~ 1, data=datingsite.data))
print(deviance<- deviance(null.model)-deviance(fitted.model))
```

```
29.34211
```

```
print(p.value<- pchisq(deviance, df=9, lower.tail = FALSE))
```

```
0.0005672988
```

(b) Evaluate the goodness-of-fit of the model. What predictors are significant at the 5% level of significance?

The model fits the data well which follows from a small p-value in the deviance test.

Height difference is a significant predictor of odds in favor of user sending message as opposed to neither sending message. Age difference is significant in predicting odds of candidate sending message vs. neither sending message. Drinking preference is significant in predicting odds in favor of exchanged messages vs. neither sending message.

(c) Give interpretation of the estimated significant beta coefficients.

As the height difference between a user and candidate increases by one inch, the estimated odds in favor of user sending a message vs. neither side sending a message change by $(\exp(-0.5116) - 1) \cdot 100\% = -40.05\%$, that is, decrease by 40.05%. As the age difference between a user and candidate increases by one year, the estimated odds in favor of candidate sending message vs. neither sending message change by $(\exp(-0.2946) - 1) \cdot 100\% = -25.52\%$, that is, decrease by 25.52%. If user and candidate have the same drinking preferences, the estimated odds in favor of exchanged messages vs. neither sending messages are $\exp(3.0551) \cdot 100\% = 2{,}122.33\%$ of estimated odds for user and candidate with different drinking preferences.

(d) Use the fitted model to describe the situation when the user has low odds of contacting the candidate. When does the candidate have low odds of messaging the user? When do both have low odds of exchanging messages?

Based on the signs of the fitted regression coefficients, the user has low odds of messaging the candidate if she is much younger (large negative age difference), she is much taller (big positive height difference), and drinking preferences are the same. The candidate has low odds of messaging the user if she is much older (big positive age difference), if she is much taller (big positive height difference), and if they have different drinking preferences. The candidate and the user have low odds of exchanging messages if the user is much older (big positive age difference), she is much taller (big positive height difference), and they have different drinking preferences.

CHAPTER 5

EXERCISE 5.1. (a) Run the Poisson regression model. Discuss the significance of predictors at the 5% level of significance.

In SAS:

```
data defectives;
input ndefectives experience shift$ @@;
cards;
2 3.1 morning  5 2.1 morning  3 8.0 morning  3 7.6 morning  2 5.9 morning
2 4.0 morning  1 1.7 morning  0 1.8 morning  0 8.2 morning  1 8.1 morning
3 3.0 day      3 7.7 day      2 6.3 day      2 8.1 day      2 7.7 day
1 2.4 day      1 3.0 day      1 4.6 day      0 2.1 day      2 3.0 day
5 8.2 evening  4 4.0 evening  4 6.2 evening  3 2.9 evening  2 2.1 evening
2 1.9 evening  1 6.7 evening  1 3.4 evening  1 7.6 evening  6 5.1 night
4 3.2 night    4 7.6 night    4 2.5 night    3 6.2 night    3 2.0 night
5 4.0 night
;

/*fitting Poisson regression model*/
proc genmod;
 class shift(ref='day');
  model ndefectives = experience shift / dist=poisson link=log;
run;
```

```
Log Likelihood -3.6998

                Analysis Of Maximum Likelihood Parameter Estimates
Parameter          DF Estimate Standard  Wald 95% Confidence   Wald Chi- Pr > ChiSq
                                  Error         Limits            Square
Intercept           1   0.3571   0.3373    -0.3040    1.0183        1.12     0.2897
experience          1   0.0355   0.0471    -0.0568    0.1278        0.57     0.4507
shift      evening  1   0.4081   0.3198    -0.2188    1.0350        1.63     0.2019
shift      morning  1   0.1009   0.3342    -0.5541    0.7559        0.09     0.7627
shift      night    1   0.9067   0.3063     0.3064    1.5070        8.76     0.0031
shift      day      0   0.0000   0.0000     0.0000    0.0000           .          .
```

Only the night shift is a significant preditor.

In R:

```
defectives.data<- read.csv(file='C:/<insert path>/Exercise5.1Data.csv',
header= TRUE, sep=',')

shift.rel<- relevel(defectives.data$shift, ref="day")

#fitting Poisson Regression model
summary(fitted.model<- glm(ndefectives ~ experience + shift.rel,
data=defectives.data, family=poisson(link=log)))
```

```
Coefficients:
                 Estimate Std. Error z value Pr(>|z|)
(Intercept)       0.35714    0.33734   1.059  0.28973
experience        0.03552    0.04709   0.754  0.45066
shift.relevening  0.40813    0.31985   1.276  0.20195
shift.relmorning  0.10090    0.33419   0.302  0.76270
shift.relnight    0.90671    0.30630   2.960  0.00307
```

(b) Write down the estimated model. How good is the fit of the model?

The fitted model has rate $\hat{\lambda} = \exp(0.3571 + 0.0355 \cdot months\ of\ experence + 0.4081 \cdot evening\ shift + 0.1009 \cdot morning\ shift + 0.9067 \cdot night\ shift)$. This model has a good fit since the deviance test p-value is less than 0.05.

In SAS:

```
/*checking model fit*/
proc genmod;
 model ndefectives = / dist=poisson link=log;
run;
```

```
Log Likelihood -9.3440
```

```
data deviance;
 deviance = -2*(-9.3440 - (-3.6998));
 pvalue = 1 - probchi(deviance,4);
run;

proc print noobs;
run;
```

```
deviance    pvalue
 11.2884   0.023507
```

In R:

```
#checking model fit
null.model<- glm(ndefectives ~ 1, data=defectives.data,family=poisson(link=log))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
11.28837
```

```
print(p.value<- pchisq(deviance, df=4, lower.tail = FALSE))
```

```
0.02350729
```

(c) Give interpretation of the estimated significant coefficients.

During the night shift, the estimated average number of defective items is $\exp(0.9067) \cdot 100\% = 247.61\%$ of that during the day shift.

(d) Predict the number of defective items produced during a night shift by an operator with six months of experience.

The predicted number of defective items is $ndefectives^0 = \exp(0.3571 + 0.0355 \cdot 6 + 0.9067) =$ $= 4.3789$.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input experience shift$;
cards;
6 night
;

data defectives;
set defectives predict;
run;

proc genmod;
 class shift(ref='day');
  model ndefectives = experience shift / dist=poisson link=log;
   output out=outdata p=pndefectives;
run;
proc print data=outdata (firstobs=37) noobs;
 var pndefectives;
run;
```

```
pndefectives
     4.37963
```

In R:

```
#using fitted model for prediciton
print(predict(fitted.model, data.frame(experience=6, shift.rel='night'),
type='response'))
```

```
4.379627
```

EXERCISE 5.2. (a) Fit the Poisson model to the data and specify estimated parameters. What variables are statistically significant predictors of the number of car accidents? Use $\alpha = 0.05$.

In SAS;

```
data autoinsurance;
input naccidents gender$ age miles @@;
cards;
1 M 27 90   1 M 60 70   1 M 36 160  2 M 32 80   2 M 27 150  2 M 58 150
2 M 38 105  3 M 42 75   3 M 55 170  3 M 42 70   3 M 30 110  3 M 54 170
4 M 36 120  4 M 47 145  5 M 20 25   5 M 67 160  5 M 33 140  5 M 41 50
5 M 43 150  6 M 59 130  7 M 65 90   9 M 68 180  0 F 33 110  0 F 40 190
0 F 36 190  0 F 57 140  1 F 47 160  1 F 59 70   1 F 55 180  2 F 44 170
2 F 36 100  2 F 40 170  2 F 58 60   3 F 53 200  3 F 29 180  3 F 51 150
3 F 49 150  4 F 32 180  4 F 51 90   4 F 43 90   4 F 43 20   4 F 31 120
4 F 50 130  4 F 36 50   5 F 40 100  6 F 48 170  6 F 57 180  8 F 66 130
;
```

```
/*fitting Poisson regression model*/
proc genmod;
 class gender(ref='F');
  model naccidents = gender age miles / dist=poisson link=log;
run;
```

```
Log Likelihood 33.3456

                Analysis Of Maximum Likelihood Parameter Estimates
Parameter   DF Estimate Standard   Wald 95% Confidence      Wald Chi- Pr > ChiSq
                        Error          Limits                Square
Intercept    1   0.4492  0.3708     -0.2776     1.1759          1.47     0.2258
gender    M  1   0.2189  0.1609     -0.0965     0.5343          1.85     0.1738
gender    F  0   0.0000  0.0000      0.0000     0.0000             .          .
age          1   0.0171  0.0067      0.0039     0.0303          6.47     0.0110
miles        1  -0.0013  0.0018     -0.0048     0.0022          0.52     0.4712
```

The fitted model has the mean $\hat{\lambda} = exp(0.4492 + 0.2189 \cdot male + 0.0171 \cdot age - 0.0013 \cdot miles)$. Only age is a statistically significant predictor of the number of car accidents.

In R:

```
autoinsurance.data<- read.csv(file='C:/<insert path>/Exercise5.2Data.csv',
header=TRUE, sep=',')

gender.rel<- relevel(autoinsurance.data$gender, ref="F")

#fitting Poisson regression model
summary(fitted.model<- glm(naccidents ~ gender.rel + age + miles,
data=autoinsurance.data, family=poisson(link=log)))
```

```
Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.449155   0.370804   1.211    0.226
gender.relM  0.218899   0.160938   1.360    0.174
age          0.017103   0.006726   2.543    0.011
miles       -0.001283   0.001781  -0.721    0.471
```

(b) Check goodness-of-fit of the model.

The model fits the data well as indicated by a p-value below 0.05.

In SAS:

```
/*checking model fit*/
proc genmod;
 model naccidents = / dist=poisson link=log;
run;
```

```
Log Likelihood 29.0520
```

```
data deviance;
 deviance = -2*(29.0520 - 33.3456);
 pvalue = 1 - probchi(deviance,3);
run;
```

```
proc print noobs;
run;
```

```
deviance     pvalue
  8.5872   0.035314
```

In R:

```
#checking model fit
null.model<- glm(naccidents ~ 1, data=autoinsurance.data,
family=poisson(link=log))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
8.587217
```

```
print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))
```

```
0.03531361
```

(c) Interpret the estimated significant regression coefficients.

As policyholder's age increases by one year, the estimated average number of car accidents caused by the policyholder increases by $(\exp(0.0171) - 1) \cdot 100\% = 1.7247\%$.

(d) Give a predicted value of the total number of auto accidents caused by a 35-year-old woman who has driven a total of one hundred thousand miles.

The predicted number of auto accidents is derived as $naccidents^0 = exp(0.4492 + 0.0171 \cdot 35 - 0.0013 \cdot 100) = 2.5035$.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input gender$ age miles;
cards;
F 35 100
;

data autoinsurance;
set autoinsurance predict;
run;

proc genmod;
 class gender(ref='F');
  model naccidents = gender age miles / dist=poisson link=log;
   output out=outdata p=pnaccidents;
run;

proc print data=outdata (firstobs=49) noobs;
 var pnaccidents;
run;
```

```
pnaccidents
    2.50791
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(gender.rel='F', age=35, miles=100),
type='response'))

2.507913
```

EXERCISE 5.3. (a) Fit a Poisson regression model for the number of calls. Discuss the model fit.

In SAS:

```
data howlingsurvey;
input ncalls time$ windspeed water$ @@;
cards;
2 dusk  0 yes  2 dusk  1 yes  3 dusk  0 no
2 night 6 no   3 dusk  2 no   4 night 3 yes
5 dusk  1 yes  3 night 5 yes  4 night 5 yes
7 night 0 yes  1 dusk  6 yes  2 night 1 no
4 dusk  2 yes  6 night 2 yes  5 dusk  3 yes
2 night 3 yes  3 dusk  0 yes  0 dusk  3 no
1 dusk  3 yes  2 dusk  3 yes  7 night 2 yes
5 dusk  0 yes  2 night 0 yes  4 night 2 no
6 night 1 yes  3 night 3 yes  0 dusk  1 no
1 dusk  3 no   4 night 3 yes  1 dusk  0 yes
4 dusk  2 yes  1 dusk  2 yes
;

/*fitting Poisson regression model*/
proc genmod;
 class time(ref='dusk') water(ref='no');
  model ncalls = time windspeed water / dist=poisson link=log;
run;
```

```
Log Likelihood 19.7922

                  Analysis Of Maximum Likelihood Parameter Estimates
Parameter       DF Estimate Standard   Wald 95% Confidence      Wald Chi- Pr > ChiSq
                               Error          Limits               Square
Intercept        1   0.6052   0.2980      0.0212     1.1892          4.13     0.0423
time      night  1   0.5577   0.2083      0.1494     0.9659          7.17     0.0074
time      dusk   0   0.0000   0.0000      0.0000     0.0000             .          .
wind             1  -0.0991   0.0634     -0.2233     0.0251          2.45     0.1179
water     yes    1   0.5557   0.2814      0.0041     1.1073          3.90     0.0483
water     no     0   0.0000   0.0000      0.0000     0.0000             .          .
```

```
/*checking model fit*/
proc genmod;
 model ncalls = / dist=poisson link=log;
run;
```

```
Log Likelihood 12.8090
```

```
data deviance;
 deviance = -2*(12.8090 - 19.7922);
 pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance      pvalue
 13.9664  .002951247
```

The model has a very good fit due to a small p-value in the deviance test.

In R:

```
howlingsurvey.data<- read.csv(file='C:/<insert path>/Exercise5.3Data.csv',
header=TRUE, sep=',')

#reference levels
time.rel<- relevel(howlingsurvey.data$time, ref="dusk")
water.rel<- relevel(howlingsurvey.data$water, ref="no")

#fitting poisson regression model
summary(fitted.model<- glm(ncalls ~ time.rel + windspeed + water.rel,
data=howlingsurvey.data, family=poisson(link=log)))
```

```
Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    0.60517    0.29796   2.031  0.04225
time.relnight  0.55765    0.20827   2.678  0.00742
wind          -0.09909    0.06336  -1.564  0.11786
water.relyes   0.55568    0.28145   1.974  0.04834
```

```
#checking model fit
null.model<- glm(ncalls ~ 1, data=howlingsurvey.data,family = poisson(link=log))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
13.96632
```

```
print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))
```

```
0.002951363
```

(b) Specify the fitted model. Give estimates of all parameters. Which variables are significant at the 5%?

The fitted model has the rate $\hat{\lambda} = exp(0.6052 + 0.5577 \cdot night\ time - 0.0991 \cdot wind\ speed + 0.5557 \cdot\ water\ source)$. The night time and presense of water source are significant predictors.

(c) Give interpretation of estimated significant regression coefficients.

When a howling session is conducted at night time, the estimated mean number of calls is $exp(0.5577) \cdot 100\% = 174.67\%$ of that for a howling session conducted at dusk time. If there is a water source in the wilderness, the estimated mean number of calls is $exp(0.5557) \cdot 100\% = 174.32\%$ of that when there is no water source.

(d) What is the predicted number of wolves that would call back during a howling session conducted at dusk, in a wilderness with no water source, if the wind's speed is 5 mph?

The predicted value is evaluated as $ncalls^0 = exp(0.6052 - 0.0991 \cdot 5) = 1.11594.$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input time$ windspeed water$;
cards;
dusk 5 no
;

data howlingsurvey;
set howlingsurvey predict;
run;

proc genmod;
 class time(ref='dusk') water(ref='no');
  model ncalls = time windspeed water / dist=poisson link=log;
   output out=outdata p=pncalls;
run;

proc print data=outdata (firstobs=33) noobs;
 var pncalls;
run;
```

```
pncalls
1.11596
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(time.rel='dusk', windspeed=5,
water.rel='no'), type='response'))
```

```
1.115965
```

EXERCISE 5.4. (a) Model the number of defective items via the zero-truncated Poisson regression model. Display the fitted model. List the significant predictors.

In SAS:

```
data defectives;
input ndefectives experience shift$ @@;
cards;
2 3.1 morning  5 2.1 morning  3 8.0 morning  3 7.6 morning  2 5.9 morning
2 4.0 morning  1 1.7 morning  0 1.8 morning  0 8.2 morning  1 8.1 morning
3 3.0 day      3 7.7 day      2 6.3 day      2 8.1 day      2 7.7 day
1 2.4 day      1 3.0 day      1 4.6 day      0 2.1 day      2 3.0 day
5 8.2 evening  4 4.0 evening  4 6.2 evening  3 2.9 evening  2 2.1 evening
2 1.9 evening  1 6.7 evening  1 3.4 evening  1 7.6 evening  6 5.1 night
```

```
4 3.2 night    4 7.6 night    4 2.5 night    3 6.2 night    3 2.0 night
5 4.0 night
;

data defectives;
set defectives;
if ndefectives>0;
run;

proc format;
value $shiftfmt 'morning'='morning' 'day'='ref' 'evening'='evening'
                'night'='night';
run;

/*fitting zero-truncated Poisson model*/
proc fmm;
 class shift;
  model ndefectives = experience shift / dist=truncpoisson;
format shift $shiftfmt.;
run;
```

```
-2 Log Likelihood 99.3494

   Parameter Estimates for Truncated Poisson Model
Effect     shift   Estimate Standard z Value Pr > |z|
                               Error
Intercept            0.1920   0.4411    0.44   0.6633
experience          0.03355  0.05607    0.60   0.5495
shift      evening   0.4764   0.4062    1.17   0.2409
shift      morning   0.3648   0.4256    0.86   0.3914
shift      night     1.0631   0.3812    2.79   0.0053
shift      ref            0        .       .        .
```

In the fitted model, the estimated parameter $\hat{\lambda} = \exp(0.1920 + 0.03355 \cdot months\ of\ experence + 0.4764 \cdot evening\ shift + 0.3648 \cdot morning\ shift + 1.0631 \cdot night\ shift)$. Here only the indicator of the night shift is a significant predictor.
In R:

```
defectives.data<- read.csv(file='C:/<insert path>/Exercise5.1Data.csv', header=
TRUE, sep=',')

#eliminating zeros
defectives.data<- defectives.data[which(defectives.data$ndefectives != 0),]

#fitting zero-truncated Poisson model
library(VGAM)
summary(fitted.model<- vglm(ndefectives ~ experience + shift,
data=defectives.data, family = pospoisson()))
```

```
Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)   0.19203    0.44108   0.435  0.66330
experience    0.03355    0.05606   0.598  0.54951
shiftevening  0.47641    0.40615   1.173  0.24080
shiftmorning  0.36479    0.42558   0.857  0.39135
shiftnight    1.06314    0.38115   2.789  0.00528
```

(b) Discuss the model fit.

The p-value in the deviance test is below 0.05, which supports a good fit of the model.

In SAS:

```
/*checking model fit*/
proc fmm;
 model ndefectives = / dist=truncpoisson;
run;
```

```
-2 Log Likelihood 109.3
```

```
data deviance;
 deviance = 109.3 - 99.3494;
 pvalue = 1 - probchi(deviance,4);
run;

proc print noobs;
run;
```

```
deviance   pvalue
  9.9506  0.041268
```

In R:

```
#checking model fit
null.model<- vglm(ndefectives ~ 1, data=defectives.data, family = pospoisson())
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
9.904659
```

```
print((p.value<- pchisq(deviance, df=4, lower.tail = FALSE)))
```

```
0.04206469
```

(c) Interpret estimated significant coefficients.

During the night shift, the estimated average number of defective items is $\exp(1.0631) \cdot 100\% = 289.53\%$ of that during the day shift.

(d) Predict the number of defective items produced during a night shift by an operator with six months of experience.

The predicted number of defective items is

$$ndefectives^0 = \frac{\exp(0.1920+0.03355\cdot 6+1.0631)}{1-\exp(-\exp(0.1920+\ .03355\cdot 6+1.0631))} = 4.350361.$$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input experience shift$;
cards;
```

```
6 night
;

data defectives;
set defectives predict;
run;

proc fmm;
 class shift;
  model ndefectives = experience shift / dist=truncpoisson;
   output out=outdata pred=pndefectives;
run;

proc print data=outdata (firstobs=34) noobs;
 var pndefectives;
run;
```

```
pndefectives
     4.35042
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(experience=6, shift='night'),
type='response'))
```

```
4.350423
```

EXERCISE 5.5. In the setting of Exercise 5.2, remove those policyholders who caused no accidents. Run the zero-truncated Poisson regression model on the remaining data.

(a) Write down the fitted model. Are there any significant predictors at the 5% level?

In SAS:

```
data autoinsurance;
input naccidents gender$ age miles @@;
cards;
1 M 27 90   1 M 60 70   1 M 36 160  2 M 32 80   2 M 27 150  2 M 58 150
2 M 38 105  3 M 42 75   3 M 55 170  3 M 42 70   3 M 30 110  3 M 54 170
4 M 36 120  4 M 47 145  5 M 20 25   5 M 67 160  5 M 33 140  5 M 41 50
5 M 43 150  6 M 59 130  7 M 65 90   9 M 68 180  0 F 33 110  0 F 40 190
0 F 36 190  0 F 57 140  1 F 47 160  1 F 59 70   1 F 55 180  2 F 44 170
2 F 36 100  2 F 40 170  2 F 58 60   3 F 53 200  3 F 29 180  3 F 51 150
3 F 49 150  4 F 32 180  4 F 51 90   4 F 43 90   4 F 43 20   4 F 31 120
4 F 50 130  4 F 36 50   5 F 40 100  6 F 48 170  6 F 57 180  8 F 66 130
;

data autoinsurance;
set autoinsurance;
if naccidents>0;
run;

proc format;
```

```
value $genderfmt 'F'='ref' 'M'='M';
run;

/*fitting zero-truncated Poisson model*/
proc fmm;
 class gender;
  model naccidents = gender age miles / dist=truncpoisson;
format gender $genderfmt.;
run;
```

```
-2 Log Likelihood 168.2

  Parameter Estimates for Truncated Poisson Model
Effect    gender Estimate Standard z Value Pr > |z|
                             Error
Intercept          0.4869   0.3982    1.22   0.2213
gender    M       0.08270   0.1705    0.48   0.6277
gender    ref           0        .       .        .
age               0.01574 0.007256    2.17   0.0301
miles            -0.00020 0.001906   -0.11   0.9159
```

The fitted rate $\hat{\lambda} = \exp(0.4869 + 0.0827 \cdot male + 0.01574 \cdot age - 0.0002 \cdot miles)$. Only age is a significant predictor.

In R:

```
autoinsurance.data<- read.csv(file='C:/<insert path>/Exercise5.2Data.csv',
header=TRUE, sep=',')

#eliminating zeros
autoinsurance.data<- autoinsurance.data[which(autoinsurance.data$naccidents !=
0),]

#fitting zero-truncated Poisson model
library(VGAM)
summary(fitted.model<- vglm(naccidents ~ gender + age + miles,
data=autoinsurance.data, family = pospoisson()))
```

```
Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.4869342  0.3981630   1.223   0.2213
genderM      0.0826963  0.1705286   0.485   0.6277
age          0.0157404  0.0072558   2.169   0.0301
miles       -0.0002013  0.0019055  -0.106   0.9159
```

(b) Discuss the fit of the model.

The model doesn’t fit the data well because the p-value is in excess of 0.05.

In SAS:

```
/*checking model fit*/
proc fmm;
 model naccidents = / dist=truncpoisson;
run;
```

```
-2 Log Likelihood 173.2
```

```
data deviance;
 deviance = 173.2 - 168.2;
 pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance   pvalue
       5  0.17180
```

In R:

```
#checking model fit
null.model<- vglm(naccidents ~ 1, data=autoinsurance.data, family = pospoisson())
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
5.087076
```

```
print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))
```

```
0.1655309
```

(c) Interpret the estimated significant beta coefficients.

If the age of a policyholder increases by one year, the estimated mean number of car accidents caused by the policyholder increases by $(\exp(0.01574)-1)\cdot 100\% = 1.5865\%$.

(d) Give a predicted value of the total number of auto accidents caused by a 35-year-old woman who has driven a total of one hundred thousand miles.

The predicted number of car accidents is

$$naccidents^0 = \frac{\exp(0.4869+\ .01574\cdot 35-0.0002\cdot 100)}{1-\exp(-\exp(0.4869\quad .01574\cdot 35-0.0002\cdot 100))} = 2.962657.$$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input gender$ age miles;
cards;
F 35 100
;

data autoinsurance;
set autoinsurance predict;
run;

proc fmm;
```

```
 class gender;
  model naccidents = gender age miles / dist=truncpoisson;
   output out=outdata pred=pnaccidents;
run;

proc print data=outdata (firstobs=45) noobs;
 var pnaccidents;
run;
```

```
pnaccidents
    2.95245
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(gender='F', age=35, miles=100),
type='response'))
```

```
2.952453
```

EXERCISE 5.6. (a) Model the number of wolves through a zero-truncated Poisson regression model. Estimate all parameters. Are there any significant predictors at the 0.05 level?

In SAS:

```
data howlingsurvey;
input ncalls time$ windspeed water$ @@;
cards;
2 dusk  0 yes  2 dusk  1 yes  3 dusk  0 no   2 night 6 no   3 dusk  2 no
4 night 3 yes  5 dusk  1 yes  3 night 5 yes  4 night 5 yes  7 night 0 yes
1 dusk  6 yes  2 night 1 no   4 dusk  2 yes  6 night 2 yes  5 dusk  3 yes
2 night 3 yes  3 dusk  0 yes  0 dusk  3 no   1 dusk  3 yes  2 dusk  3 yes
7 night 2 yes  5 dusk  0 yes  2 night 0 yes  4 night 2 no   6 night 1 yes
3 night 3 yes  0 dusk  1 no   1 dusk  3 no   4 night 3 yes  1 dusk  0 yes
4 dusk  2 yes  1 dusk  2 yes
;

data howlingsurvey;
set howlingsurvey;
if (ncalls>0);
run;

proc format;
value $timefmt 'dusk'='ref' 'night'='night';
value $waterfmt 'no'='zref' 'yes'='yes';
run;

/*fitting zero-truncated Poisson model*/
proc fmm;
 class time water;
  model ncalls = time windspeed water / dist=truncpoisson;
format time $timefmt. water $waterfmt.;
run;
```

```
-2 Log Likelihood 104.6

    Parameter Estimates for Truncated Poisson Model
Effect    time  water Estimate Standard z Value Pr > |z|
                                  Error
Intercept               0.7345   0.3513    2.09   0.0366
time      night         0.5652   0.2291    2.47   0.0136
time      ref                0        .       .        .
windspeed              -0.1154  0.06949   -1.66   0.0969
water           yes     0.4085   0.3244    1.26   0.2080
water           zref         0        .       .        .
```

The fitted model has the rate $\hat{\lambda} = exp(0.7345 + 0.5652 \cdot night\ time - 0.1154 \cdot wind\ speed + 0.4085 \cdot\ water\ source)$. The night time is the only significant predictor at the 5% level.

In R:

```
howlingsurvey.data<- read.csv(file='C:/<insert path>/Exercise5.3Data.csv',
header=TRUE, sep=',')

#eliminating zeros
howlingsurvey.data<- howlingsurvey.data[which(howlingsurvey.data$ncalls != 0),]

#fitting zero=truncated Poisson model
library(VGAM)
summary(fitted.model<- vglm(ncalls ~ time + windspeed + water,
data=howlingsurvey.data, family=pospoisson()))

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.73449    0.35133   2.091   0.0366
timenight    0.56518    0.22907   2.467   0.0136
windspeed   -0.11538    0.06949  -1.660   0.0969
wateryes     0.40847    0.32443   1.259   0.2080
```

(b) Test the goodness-of-fit of the model.

The fit of the model is good because the p-value in the deviance test is below 0.05.
In SAS:

```
/*checking model fit*/
proc fmm;
 model ncalls = / dist=truncpoisson;
run;

-2 Log Likelihood 114.1

data deviance;
 deviance = 114.1 - 104.6;
 pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance   pvalue
     9.5  0.023331
```

In R:

```
#checking model fit
null.model<- vglm(ncalls ~ 1, data=howlingsurvey.data, family=pospoisson())
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
9.512972
```

```
print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))
```

```
0.02319376
```

(c) Give interpretation of the estimated significant regression coefficients.

When a howling session is conducted at night time, the estimated mean number of calls is $exp(0.5652)\cdot 100\% = 175.98\%$ of that for a howling session conducted at dusk time.

(d) Find the predicted number of wolves that would call back during a howling session conducted at dusk, in a wilderness with no water source, if the wind's speed is 5 mph.

The predicted value is $ncalls^0 = \frac{\exp(0.7345-0.1154\cdot 5)}{1-\exp(-\exp(0.7345- \ .1154\cdot 5))} = 1.69695.$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input time$ windspeed water$;
cards;
dusk 5 no
;

data howlingsurvey;
set howlingsurvey predict;
run;

proc fmm;
 class time water;
  model ncalls = time windspeed water / dist=truncpoisson;
   output out=outdata pred=pncalls;
run;

proc print data=outdata (firstobs=31) noobs;
 var pncalls;
run;
```

```
pncalls
1.69704
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(time='dusk', windspeed=5, water='no'),
type='response'))
```

```
1.697039
```

EXERCISE 5.7. Consider the zero-inflated Poisson regression model defined by (5.6) - (5.8).

(a) Show that the expected value of y is $E(y) = (1-\pi)\lambda$.

$$E(Y) = (1-\pi)\sum_{y=1}^{\infty} y \cdot \frac{\lambda^y e^{-y}}{y!} = (1-\pi)\sum_{y=0}^{\infty} y \cdot \frac{\lambda^y e^{-y}}{y!} = (1-\pi)\lambda.$$

(b) Prove that the estimated gamma coefficients in the expression for $\hat{\lambda}$ yield the same interpretation as in the Poisson regression model.

Since π and λ are modeled through a non-overlapping sets of predictors, when we interpret estimated gamma coefficients, we can assume that π has a fixed value. Therefore, if x_{m+1} is continuous, then $\exp(\hat{\gamma}_1)$ represents the ratio of the estimated expected values of y for $x_{m+1}+1$ and x_{m+1}:

$$\frac{\hat{E}(y)|_{x_{m+1}+1}}{\hat{E}(y)|_{x_{m+1}}} = \frac{(1-\pi)\hat{\lambda}|_{x_{m+1}+1}}{(1-\pi)\hat{\lambda}|_{x_{m+1}}} = \frac{\exp(\hat{\gamma}_0 + \hat{\gamma}_1(x_{m+1}+1) + \hat{\gamma}_2 x_{m+2} + \cdots + \hat{\gamma}_{k-m}x_k)}{\exp(\hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1} + \hat{\gamma}_2 x_{m+2} + \cdots + \hat{\gamma}_{k-m}x_k)}$$
$$= \exp(\hat{\gamma}_1).$$

If x_{m+1} is a 0-1 variable, then $\exp(\hat{\gamma}_1)$ represents the ratio of the estimated expected values of y for $x_{m+1} = 1$ and $x_{m+1} = 0$. Indeed,

$$\frac{\hat{E}(y)|_{x_{m+1}=1}}{\hat{E}(y)|_{x_{m+1}=0}} = \frac{(1-\pi)\hat{\lambda}|_{x_{m+1}=1}}{(1-\pi)\hat{\lambda}|_{x_{m+1}=0}} = \frac{\exp(\hat{\gamma}_0 + \hat{\gamma}_1 \cdot 1 + \hat{\gamma}_2 x_{m+2} + \cdots + \hat{\gamma}_{k-m}x_k)}{\exp(\hat{\gamma}_0 + \hat{\gamma}_1 \cdot 0 + \hat{\gamma}_2 x_{m+2} + \cdots + \hat{\gamma}_{k-m}x_k)} = \exp(\hat{\gamma}_1).$$

EXERCISE 5.8. (a) Fit the zero-inflated Poisson regression to model the number of runs in the previous two months. Check if pace is significantly associated with inflation of zeros. Write down the fitted model.

In SAS:

```
data races;
input nraces gender$ age run$ pace @@;
cards;
0 F 33 10K  10.04  5 M 26 Full 7.17   0 M 32 10K  11.14
3 F 27 5K   9.18   0 M 48 5K   7.52   4 F 47 10K  11.59
1 M 51 5K   9.44   2 F 49 5K   9.53   0 M 54 10K  8.48
3 F 27 5K   11.71  2 M 24 10K  7.56   0 F 14 5K   13.78
3 M 35 Full 7.34   0 M 50 5K   7.51   0 M 44 5K   8.92
6 F 37 5K   10.71  0 M 54 5K   8.72   2 F 51 10K  7.41
1 F 51 5K   12.28  4 F 35 10K  6.98   2 M 25 10K  12.01
3 M 34 5K   6.78   0 M 28 5K   11.66  0 F 39 10K  12.31
2 M 32 Full 6.58   5 F 44 Full 7.46   0 F 49 10K  11.11
2 M 52 Full 9.2    1 M 30 5K   6.41   1 M 43 10K  7.7
1 M 30 10K  10.01  0 M 53 5K   7.56   2 F 46 Full 8.34
0 F 28 5K   9.67   2 F 50 Full 10.07  2 F 54 5K   7.58
;
/*fitting zero-inflated Poisson model*/
proc genmod;
 class gender run(ref='5K');
  model nraces = gender age run/ dist=zip;
   zeromodel pace;
run;
```

```
Log Likelihood -15.1014
```

```
                 Analysis Of Maximum Likelihood Parameter Estimates
Parameter      DF Estimate Standard  Wald 95% Confidence      Wald Chi- Pr > ChiSq
                              Error         Limits              Square
Intercept       1   1.6313   0.5632     0.5274      2.7352        8.39     0.0038
gender    F     1   1.0230   0.3036     0.4280      1.6180       11.35     0.0008
gender    M     0   0.0000   0.0000     0.0000      0.0000           .          .
age             1  -0.0443   0.0148    -0.0733     -0.0153        8.98     0.0027
run       10K   1   0.1854   0.3608    -0.5218      0.8925        0.26     0.6074
run       Full  1   0.7547   0.3237     0.1203      1.3891        5.44     0.0197
run       5K    0   0.0000   0.0000     0.0000      0.0000           .          .

            Analysis Of Maximum Likelihood Zero Inflation Parameter Estimates
Parameter DF Estimate Standard    Wald 95% Confidence         Wald Chi- Pr > ChiSq
                         Error         Limits                   Square
Intercept  1  -8.7064   3.9941     -16.5346      -0.8782          4.75     0.0293
pace       1   0.7255   0.3628       0.0144       1.4366          4.00     0.0455
```

In the fitted regression model, the estimated parameters are $\hat{\pi} = \frac{\exp(-8.7064+\ .7255\cdot pace)}{1+\exp(-8.7064\quad .7255\cdot pace)}$, and $\hat{\lambda} = \exp(1.6313 + 1.0230 \cdot female - 0.0443 \cdot age + 0.1854 \cdot 10K + 0.7547 \cdot full\ marathon)$.
Pace is a significant predictor for the probability of a structural zero in the number of races in the past four months (that is, the probability of the first race ever), and gender and age significantly predict the average number of races.

In R:

```
races.data<-read.csv(file='C:/<insert path>/Exercise5.8Data.csv',
header = TRUE, sep=',')

#specifying reference levels
run.rel<- relevel(races.data$run, ref="5K")
gender.rel<- relevel(races.data$gender, ref="M")

#fitting zero-inflated Poisson model
library(pscl)
summary(fitted.model<- zeroinfl(nraces ~ gender.rel + age + run.rel | pace,
data=races.data))
```

```
Count model coefficients (poisson with log link):
             Estimate Std. Error z value Pr(>|z|)
(Intercept)   1.63134    0.56313   2.897 0.003769
gender.relF   1.02296    0.30360   3.369 0.000753
age          -0.04431    0.01478  -2.998 0.002719
run.rel10K    0.18539    0.36080   0.514 0.607359
run.relFull   0.75468    0.32369   2.331 0.019727

Zero-inflation model coefficients (binomial with logit link):
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -8.7064    3.9941   -2.18   0.0293
pace         0.7255    0.3628    2.00   0.0455
```

(b) Discuss the model fit.

The model has a good fit because the p-value is small.

In SAS:

```
/*checking model fit*/
proc genmod;
 model nraces = / dist=zip;
  zeromodel;
run;
```

```
Log Likelihood -24.8739
```

```
data deviance;
 deviance = -2*(-24.8739 - (-15.1014));
 pvalue = 1 - probchi(deviance, 5);
run;

proc print noobs;
run;
```

```
deviance      pvalue
  19.545  .001520755
```

In R:

```
#checking model fit
null.model<- zeroinfl(nraces ~ 1, data=races.data)
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
19.54518
```

```
print(p.value<- pchisq(deviance, df=5, lower.tail = FALSE))
```

```
0.001520639
```

(c) Interpret the estimated significant coefficients.

As the pace increases by one minute per mile, the estimated odds in favor of running the first race ever increase by $(\exp(0.7255)-1)\cdot 100\% = 106.58\%$. The average number of races run in the past four months for females is $\exp(1.0230)\cdot 100\% = 278.15\%$ of that for males. As age increases by one year, the average number of races run in the past four months changes by $(\exp(-0.0443)-1)\cdot 100\% = -4.33\%$, or decreases by 4.33%.

(d) Calculate the predicted number of races in the past four months for a female runner, aged 45, who ran at an average pace of 10 minutes per mile, if she ran 10K.

The predicted value is $nraces^0 = \frac{\exp(1.6313 \quad .0230-0.0443\cdot 45+0.1854)}{1+\exp(-8.7064+0.7255\cdot 10)} = 1.8884.$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input gender$ age run$ pace;
cards;
F 45 10K 10
;
```

```
data races;
set races predict;
run;

proc genmod;
 class gender run;
  model nraces = gender age run / dist=zip;
   zeromodel pace;
    output out=outdata p=pnraces;
run;

proc print data=outdata (firstobs=37) noobs;
 var pnraces;
run;
```

```
pnraces
1.88771
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(gender.rel='F', run.rel='10K', age=45,
pace=10)))
```

```
1.88771
```

EXERCISE 5.9. (a) Model these data using a zero-inflated Poisson regression with grade responsible for structural zeros, and homework and gender predicting the counting portion. Write the model explicitly, estimating all parameters. Which predictors are significant at the 5% significance level?

In SAS:

```
data readingclub;
input grade hw$ gender$ nbooks @@;
cards;
3 no  M 3  3 yes M 3  2 no  F 4  2 yes M 3  3 no  F 2  1 yes F 0  1 yes F 4
2 no  F 0  1 no  M 0  3 no  M 1  3 yes F 3  2 no  F 4  3 no  M 0  2 no  M 0
1 yes F 5  3 yes M 2  1 no  F 1  3 no  F 4  1 no  F 0  2 yes F 2  3 no  F 4
1 no  M 2  2 no  M 0  2 no  F 4  3 no  F 5  2 yes F 0  2 yes M 3  2 no  M 3
3 yes F 4  3 yes M 3  3 yes F 1  1 no  M 0  2 no  M 0  1 yes M 0  2 yes F 6
2 yes F 2  2 no  F 3  2 no  F 0  3 no  F 5  3 yes M 2  1 no  M 0  3 no  F 2
2 yes F 0  2 no  M 2  2 no  M 0  3 no  F 3  1 yes F 1  2 no  F 0  1 yes M 1
2 yes M 2
;
/*fitting zero-inflated Poisson model*/
proc genmod;
 class hw(ref='no') gender;
  model nbooks = hw gender / dist=zip;
   zeromodel grade;
run;
```

```
Log Likelihood -16.9395
```

```
                 Analysis Of Maximum Likelihood Parameter Estimates
Parameter     DF Estimate Standard   Wald 95% Confidence        Wald Chi- Pr > ChiSq
                          Error          Limits                  Square
Intercept      1   0.6308   0.2564       0.1283      1.1334          6.05     0.0139
hw        yes  1   0.0715   0.2200      -0.3598      0.5027          0.11     0.7453
hw        no   0   0.0000   0.0000       0.0000      0.0000             .          .
gender    F    1   0.4976   0.2455       0.0165      0.9788          4.11     0.0426
gender    M    0   0.0000   0.0000       0.0000      0.0000             .          .

         Analysis Of Maximum Likelihood Zero Inflation Parameter Estimates
Parameter DF Estimate Standard    Wald 95% Confidence           Wald Chi- Pr > ChiSq
                      Error           Limits                     Square
Intercept  1   1.4649   1.0651      -0.6227       3.5525             1.89     0.1690
grade      1  -1.2981   0.5616      -2.3988      -0.1975             5.34     0.0208
```

The fitted parameters are $\hat{\pi} = \frac{\exp(1.4649-1.2981\cdot grade)}{1+\exp(1.4649-1.2981\cdot grade)}$, and $\hat{\lambda} = \exp(0.6308 + 0.0715 \cdot part\ of\ hw + 0.4976 \cdot female)$. Grade level is a significant predictor of odds in favor of not turning in the list of books read, and gender is a significant predictor of the average number of books read.

In R:

```
readingclub.data<- read.csv(file='C:/<insert path>/Exercise5.9Data.csv',
header = TRUE, sep=',')

#setting reference levels
hw.rel<- relevel(readingclub.data$hw, ref="no")
gender.rel<- relevel(readingclub.data$gender, ref="M")

#fitting zero-inflated Poisson model
library(pscl)
summary(fitted.model<- zeroinfl(nbooks ~ hw.rel + gender.rel | grade,
data=readingclub.data))
```

```
Count model coefficients (poisson with log link):
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.63085    0.25643   2.460   0.0139
hw.relyes    0.07149    0.22003   0.325   0.7453
gender.relF  0.49765    0.24547   2.027   0.0426

Zero-inflation model coefficients (binomial with logit link):
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   1.4649     1.0651   1.375   0.1690
grade        -1.2981     0.5616  -2.312   0.0208
```

(b) Is it a reliable model? Present the quantitative argument for the goodness-of-fit of the model.

The model reliable because it has a good fit as indicated by a small p-value in the deviance test.

In SAS:

```
/*checking model fit*/
proc genmod;
```

```
 model nbooks = / dist=zip;
  zeromodel;
run;
```

```
Log Likelihood -22.4440
```

```
data deviance;
 deviance = -2*(-22.4440 - (-16.9395));
 pvalue = 1 - probchi(deviance, 3);
run;

proc print noobs;
run;
```

```
deviance   pvalue
  11.009  0.011677
```

In R:

```
#checking model fit
null.model<- zeroinfl(nbooks ~ 1, data=readingclub.data)
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
11.00896
```

```
print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))
```

```
0.01167754
```

(c) How are the estimated significant coefficients interpreted?

As the grade level increases by one, the estimated odds in favor of not turning in the list of books read change by $(\exp(-1.2981) - 1) \cdot 100\% = -72.70\%$, that is, decrease by 72.7%. The estimated average number of books read by females is $\exp(0.4976) \cdot 100\% = 164.48\%$ of that read by males.

(d) What is the predicted number of books read by a second-grade girl for whom the reading is part of the homework?

The predicted number of books is computed as $nbooks^0 = \frac{\exp(0.6308+0.0715+0.4976).}{1+\exp(1.4649- \ .2981\cdot 2)} = 2.510019.$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input grade hw$ gender$;
cards;
2 yes F
;

data readingclub;
set readingclub predict;
run;

proc genmod;
 class hw(ref='no') gender;
```

```
  model nbooks = hw gender / dist=zip;
   zeromodel grade;
    output out=outdata p=pnbooks;
run;

proc print data=outdata (firstobs=51) noobs;
 var pnbooks;
run;
```

```
pnbooks
2.51027
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(grade=2, gender.rel='F', hw.rel='yes')))
```

```
2.510273
```

EXERCISE 5.10. (a) Run a ZIP model with smoking predicting the probability of excess zeros. Fit the model, estimate the parameters. Discuss significance of predictors.

In SAS:

```
data healthsurvey;
input BMI age gender$ smoking$ nattacks @@;
cards;
25.1 61 F no  2  27.1 33 F yes 0  26.8 61 F no  1  23.9 53 F yes 1
26.9 59 M yes 2  18.8 45 F no  0  25.2 54 M yes 2  23.5 75 M yes 5
29.7 64 F no  3  24.5 55 F no  1  21.5 63 M yes 2  37.9 52 M no  0
22.6 43 M no  0  23.0 56 F no  1  28.1 50 F no  0  24.8 86 M yes 6
30.6 74 M yes 4  33.7 71 F yes 3  26.4 66 F yes 1  27.4 25 F no  0
28.6 50 F no  0  20.0 65 F yes 3  31.5 58 F no  2  25.8 64 M yes 5
38.3 56 F no  1  41.4 45 F no  0  31.2 26 F no  0  18.5 42 M yes 0
32.2 26 F no  0  23.9 65 F no  3  31.3 52 M no  2  25.6 32 F no  0
33.2 31 M no  0  23.8 60 M no  2  31.4 55 M no  1  34.0 53 F no  1
27.4 42 M no  3  20.6 61 F yes 2  28.3 64 M no  3  30.1 52 M yes 3
;

/*fitting zero-inflated Poisson model*/
proc genmod;
 class gender(ref='F') smoking(ref='yes');
  model nattacks = BMI gender / dist=zip;
   zeromodel age smoking;
run;
```

```
Log Likelihood -12.1919

                 Analysis Of Maximum Likelihood Parameter Estimates
Parameter     DF Estimate Standard   Wald 95% Confidence        Wald Chi- Pr > ChiSq
                             Error          Limits                 Square
Intercept      1   1.3685   0.9123     -0.4194       3.1565          2.25     0.1336
BMI            1  -0.0309   0.0338     -0.0972       0.0355          0.83     0.3617
gender    M    1   0.5667   0.2613      0.0545       1.0789          4.70     0.0301
```

```
                Analysis Of Maximum Likelihood Parameter Estimates
Parameter     DF Estimate Standard   Wald 95% Confidence       Wald Chi- Pr > ChiSq
                             Error         Limits                 Square
gender    F    0   0.0000   0.0000     0.0000       0.0000             .          .

         Analysis Of Maximum Likelihood Zero Inflation Parameter Estimates
Parameter     DF Estimate Standard   Wald 95% Confidence       Wald Chi- Pr > ChiSq
                             Error         Limits                 Square
Intercept      1  16.6073   7.0103     2.8673      30.3472          5.61     0.0178
age            1  -0.3640   0.1420    -0.6423      -0.0858          6.58     0.0103
smoking   no   1   1.0721   1.9415    -2.7333       4.8774          0.30     0.5808
smoking   yes  0   0.0000   0.0000     0.0000       0.0000             .          .
```

The fitted ZIP model has parameters $\hat{\pi} = \frac{\exp(16.6073- \ .3640\cdot age+1.0721\cdot doesn't smoke)}{1+\exp(16.6073-0.3640\cdot age+1.0721\cdot doesn't\ smoke)}$, and $\hat{\lambda} = \exp(1.3685 - 0.0309 \cdot BMI + 0.5667 \cdot male)$. Age is a significant predictor of odds in favor of excess zeros in the number of asthma attacks (never had an asthma attack), and gender is a significant predictor of the average number of asthma attacks.

In R:

```
healthsurvey.data<- read.csv(file='C:/<insert path>/Exercise5.10Data.csv',
header = TRUE, sep=',')

#setting reference levels
gender.rel<- relevel(healthsurvey.data$gender, ref="F")
smoking.rel<- relevel(healthsurvey.data$smoking, ref="yes")

#fitting zero-inflated Poisson model
library(pscl)
summary(fitted.model<- zeroinfl(nattacks ~ BMI + gender.rel | age + smoking.rel,
data=healthsurvey.data))
```

```
Count model coefficients (poisson with log link):
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  1.36855    0.91207   1.500   0.1335
BMI         -0.03087    0.03383  -0.912   0.3615
gender.relM  0.56670    0.26132   2.169   0.0301

Zero-inflation model coefficients (binomial with logit link):
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    16.6068     7.0060   2.370   0.0178
age            -0.3640     0.1419  -2.566   0.0103
smoking.relno   1.0721     1.9414   0.552   0.5808
```

(b) How good is the model fit?

The p-value is very small, thus the model has a good fit.

In SAS:

```
/*checking model fit*/
proc genmod;
 model nattacks = / dist=zip;
  zeromodel;
run;
```

```
Log Likelihood -30.1687
```

```
data deviance;
 deviance = -2*(-30.1687 - (-12.1919));
 pvalue = 1 - probchi(deviance,4);
run;

proc print noobs;
run;
```

```
deviance      pvalue
 35.9536  .000000296
```

In R:

```
#checking model fit
null.model<- zeroinfl(nattacks ~ 1, data=healthsurvey.data)
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
35.95365
```

```
print(p.value<- pchisq(deviance, df=4, lower.tail = FALSE))
```

```
2.957927e-07
```

(c) Interpret the estimates of the significant regression coefficients.

As age increases by one year, the estimated odds in favor of no asthma attacks ever change by $(\exp(-0.364)-1)\cdot 100\% = -30.51\%$, that is, decrease by 30.51%. The estimated mean number of asthma attacks for males is $\exp(0.5667)\cdot 100\% = 176.24\%$ of that for females.

(d) Calculate the predicted value for the number of severe asthma attacks for a male patient, aged 60, whose BMI is 21.2, and who is currently a smoker.

The predicted value is $nattacks^0 = \frac{\exp(1.3685-0.0309\cdot 21.2+0.5667)}{1+\exp(16.6073-\ .3640\cdot 60)} = 3.577968.$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input BMI age gender$ smoking$;
cards;
21.2 60 M yes
;

data healthsurvey;
set healthsurvey predict;
run;

proc genmod;
 class gender(ref='F') smoking(ref='yes');
  model nattacks = BMI gender / dist=zip;
   zeromodel age smoking;
    output out=outdata p=pnattacks;
```

```
run;

proc print data=outdata (firstobs=41) noobs;
 var pnattacks;
run;
```

```
pnattacks
  3.58072
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(BMI=21.2, age=60, gender.rel='M',
smoking.rel='yes')))
```

```
3.5807
```

EXERCISE 5.11. (a) Show that the expected value of the response variable in the hurdle Poisson model has the form $E(y|x_1, \dots, x_k) = \frac{(1-\pi)\lambda}{1-\exp(-\lambda)}$.

We write $E(y|x_1, \dots, x_k) = (1-\pi)\sum_{y=1}^{\infty} y \cdot \frac{\lambda^y e^{-\lambda}}{y!(1-e^{-\lambda})} = \frac{(1-\pi)}{(1-e^{-\lambda})}\sum_{y=0}^{\infty} y \cdot \frac{\lambda^y e^{-\lambda}}{y!} = \frac{(1-\pi)\lambda}{(1-e^{-\lambda})}$.

(b) Argue that the estimated regression coefficients in π and λ have the same interpretation as in a binary logistic and Poisson regression models, respectively.

The probability of $y = 0$ is modeled through the logistic function

$$\pi = \frac{\exp(\beta_0 + \beta_1 x_1 + \cdots + \beta_m x_m)}{1 + \exp(\beta_0 + \beta_1 x_1 + \cdots + \beta_m x_m)}$$

and thus, the estimated regression coefficients $\hat{\beta}_1, \dots, \hat{\beta}_m$ are interpreted the same way as in the binary logistic regression.

Now, lambda is modeled as $\lambda = exp(\gamma_0 + \gamma_1 x_{m+1} + \cdots + \gamma_{k-m} x_m)$ and $E(y|x_1, \dots, x_k) = \frac{(1-\pi)\lambda}{(1-e^{-\lambda})}$. Since the sets of predictors in π and λ are non-overlapping, when we interpret the estimated gamma coefficients, we can assume that π is constant. We also can assume that the denominator $1 - \exp(-\lambda)$ is negligibly small due to lambda being an exponential function itself. Therefore, the estimated gamma coefficients can be interpret the same way as in the Poisson regression model.

EXERCISE 5.12. (a) Run the hurdle Poisson regression to model the number of computers. Assume that if observations are positive, the number of computers is related to the number of books and periodicals, whereas the zero values are governed by expenditure per student. Write down the fitted model.

In SAS:

```
data libraries;
input ncomps nbooks njrnls budget @@;
cards;
0   8.2   0  0.00  19 11.7  10 16.45   0  2.0  0  5.29
13  8.2   8  23.5   5 30.0   2  6.33  16 14.1 15  7.20
12  9.5   0  3.07   6 21.8   0  4.00  12  9.0 11  4.39
22  5.0  20 17.07   0 15.7   4  1.82   7 19.3 66  9.09
6  20.8   2 10.49  28 11.0  30  0.47   0  9.3  0  0.06
11 12.7  14  0.00  17 15.6  14 22.22  22  9.0 16  0.00
32 18.3  23 22.22   0 12.0   5  0.17   6  8.8 12  7.14
1  14.0  60  1.83   5 12.5  32 24.66   7  3.0  5  7.07
3  16.3  40  12.0   1  6.5  40 13.85   3  8.5  4 18.22
4  10.0  20 30.49   7 18.0 100  0.81   0 11.5  2  0.61
3   9.1   0  9.19  13 10.4  36 25.67  36  7.5 55  7.89
0  19.7   8  1.00
;

/*fitting hurdle poisson model*/
proc fmm;
 model ncomps = nbooks njrnls / dist=truncpoisson;
   model+ / dist=constant;
     probmodel budget;
run;
```

```
-2 Log Likelihood 311.1


   Parameter Estimates for Truncated Poisson Model
Component Effect    Estimate Standard z Value Pr > |z|
                             Error
        1 Intercept   2.7338   0.1407   19.43   <.0001
        1 nbooks    -0.02574  0.01059   -2.43   0.0151
        1 njrnls    0.001832 0.002426    0.76   0.4502

     Parameter Estimates for Mixing Probabilities
Component Effect    Estimate Standard z Value Pr > |z|
                             Error
        1 Intercept  -0.4086   0.6625   -0.62   0.5374
        1 budget      0.4490   0.2174    2.07   0.0389
```

In the fitted hurdle Poisson model, the estimates of the parameters are: $\hat{\pi} = \frac{\exp(0.4086-0.4490\cdot budget)}{1+\exp(0.4086- \ .4490\cdot budget)}$ and $\hat{\lambda} = \exp(2.7338 - 0.02574 \cdot nbooks + 0.001832 \cdot njournals)$. Note that the estimated regression coefficients for $\hat{\pi}$ have to be taken with the opposite sign.

Budget is a significant predictor of odds in favor of no computers, and number of books in a significant predictor of the number of computers when they are present.

In R:

```
libraries.data<- read.csv(file='C:/<insert path>/Exercise5.12Data.csv',
header=TRUE, sep=',')

#fitting hurdle poisson model
```

```
library(pscl)
summary(fitted.model<- hurdle(ncomps ~ nbooks + njrnls | budget,
data=libraries.data, dist='poisson', zero.dist='binomial', link='logit'))
```

```
Count model coefficients (truncated poisson with log link):
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  2.733815   0.140691  19.431   <2e-16
nbooks      -0.025741   0.010592  -2.430   0.0151
njrnls       0.001832   0.002425   0.755   0.4500

Zero hurdle model coefficients (binomial with logit link):
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -0.4086     0.6625  -0.617   0.5374
budget        0.4490     0.2174   2.065   0.0389
```

(b) Discuss the model fit.

In the deviance test, the p-value is very small, hence the fit of the model is good.

In SAS:

```
/*checking model fit*/
proc fmm;
 model ncomps = / dist=truncpoisson;
  model+ / dist=constant;
  probmodel;
run;
```

```
-2 Log Likelihood 330.3
```

```
data deviance;
 deviance = 330.3 - 311.1;
 pvalue = 1 - probchi(deviance,3);

proc print noobs;
run;
```

```
deviance      pvalue
    19.2  .000248561
```

In R:

```
#checking model fit
null.model<- hurdle(ncomps ~ 1, data=libraries.data, dist='poisson',
zero.dist='binomial', link='logit')
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
19.21102
```

```
print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))
```

```
0.0002472598
```

(c) Interpret estimated significant parameters. State the practical conclusion.

As the budget increases by one dollar per student, the estimated odds in favor of no computers present change by $(\exp(-0.449)-1)\cdot 100\% = -36.17\%$, that is, decrease by 36.17%. As the number of books increases by one thousand, the estimated mean of positive number of computers changes by $(\exp(-0.02574)-1)\cdot 100\% = -2.54\%$, or decreases by 2.54%.

(d) What is the predicted number of computers in a library with 10,000 books, 25 periodicals, and annual budget of $15 per student?

The predicted value is

$$ncomputers^0 = \left(1-\frac{\exp(0.4086-0.4490\cdot 15)}{1+e\quad(0.4086\quad .4490\cdot 15)}\right)\frac{\exp(2.7338-\ .02574\cdot 10+0.001832\cdot 25)}{1-\exp(-\exp(.7338-\ .02574\cdot 10+0.001832\cdot 25))}$$
$$= 12.43378.$$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input nbooks njrnls budget;
cards;
10 25 15
;

data libraries;
set libraries predict;
run;

proc fmm;
 model ncomps = nbooks njrnls / dist=truncpoisson;
  model+ / dist=constant;
    probmodel budget;
  output out=outdata pred=pncomps;
run;

proc print data=outdata (firstobs=35) noobs;
 var pncomps;
run;
```

```
pncomps
12.4339
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(nbooks=10, njrnls=25, budget=15)))
```

```
12.43384
```

EXERCISE 5.13. (a) Fit the hurdle Poisson model to verify the hypotheses. Identify all parameters in the predicted model. Is the conclusion supportive of the research hypotheses?

In SAS:

```
data adherence;
input ndaysnomeds gender$ age nothermeds @@;
cards;
0 F 87 12  2 M 65 3   0 M 85 3  1 F 68 3  5 F 76 18  1 F 72 9  4 F 73 5
1 M 64 0   2 M 71 1   7 F 81 5  0 M 89 7  4 F 87 8   2 M 78 9  0 F 87 9
1 M 77 4   1 F 71 2   2 M 65 1  5 F 68 7  4 M 73 4   4 F 72 3  0 M 86 13
3 F 66 4   5 F 70 5   1 M 70 5  3 M 62 3    M 93 15  5 F 70 1  3 F 68 11
3 M 75 2   2 M 88 11
;

/*fitting hurdle poisson model*/
proc fmm;
 class gender;
  model ndaysnomeds = gender age / dist=truncpoisson;
   model+ / dist=constant;
   probmodel nothermeds;
run;
```

```
-2 Log Likelihood 104.5

      Parameter Estimates for Truncated Poisson Model
Component Effect    gender Estimate Standard z Value Pr > |z|
                                    Error
        1 Intercept        -1.0213   1.4841   -0.69   0.4913
        1 gender    F       0.7288   0.3049    2.39   0.0168
        1 gender    M            0        .       .        .
        1 age              0.02155  0.01995    1.08   0.2800

     Parameter Estimates for Mixing Probabilities
Component Effect     Estimate Standard z Value Pr > |z|
                              Error
        1 Intercept    3.0554   1.0511    2.91   0.0037
        1 nothermeds  -0.2288   0.1122   -2.04   0.0414
```

The fitted hurdle Possion model has the estimated parameters:

$\hat{\pi} = \frac{\exp(-3.055 \quad .2288 \cdot \#\ of\ othe \quad meds)}{1+\exp(-3.0554+ \ .2288 \cdot \#\ of\ other\ meds)}$ and $\hat{\lambda} = \exp(-1.0213 + 0.7288 \cdot female + 0.02155 \cdot age)$. Note that the estimated regression coefficients for $\hat{\pi}$ have to be taken with the opposite sign since SAS (as well as R) estimates the regression coefficients in $1 - \pi$.

Signifincant are the number of other medications as a predictor of π, and gender is significant as a predictor of λ. The research hypotheses are supposed to the extent that the regression coefficients have positive estimates thus women and older patients have higher mean positive response (even though age is not a significant factor), and number of other medications is positively associated with the odds in favor of zero response.

In R:

```
adherence.data<- read.csv(file='C:/<insert path>/Exercise5.13Data.csv',
header=TRUE, sep=',')

gender.rel<- relevel(adherence.data$gender, ref="M")
```

```
#fitting hurdle Poisson model
library(pscl)
summary(fitted.model<- hurdle(ndaysnomeds ~ gender.rel + age | nothermeds,
data=adherence.data, dist='poisson', zero.dist = 'binomial', link='logit'))
```

```
Count model coefficients (truncated poisson with log link):
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -1.02120    1.48329  -0.688   0.4912
gender.relF  0.72882    0.30489   2.390   0.0168
age          0.02155    0.01992   1.082   0.2794

Zero hurdle model coefficients (binomial with logit link):
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   3.0554     1.0511   2.907  0.00365
nothermeds   -0.2288     0.1122  -2.039  0.04144
```

(b) How good is the model fit?

The fit is good as the small p-value indicates.

In SAS:

```
/*checking model fit*/
proc fmm;
 model ndaysnomeds = / dist=truncpoisson;
  model+ / dist=constant;
  probmodel;
run;
```

```
-2 Log Likelihood 117.2
```

```
data deviance;
 deviance = 117.2 - 104.5;
 pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance      pvalue
    12.7  .005332402
```

In R:

```
#checking model fit
null.model<- hurdle(ndaysnomeds ~ 1, data=adherence.data, dist='poisson',
zero.dist='binomial', link='logit')
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
12.7902
```

```
print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))
```

```
0.005113002
```

(c) Give interpretation of estimated significant regression coefficients.

$\hat{\pi} = \frac{\exp(-3.0554+\ \ .2288\cdot\#\ of\ other\ meds)}{1+\exp(-3.0554+0.2288\cdot\#\ of\ other\ meds)}$ and $\hat{\lambda} = \exp(-1.0213 + 0.7288 \cdot female + 0.02155 \cdot age)$.

As the number of other medications increases by one, the estimated odds in favor of 100% adherence increase by $(\exp(0.2288) - 1) \cdot 100\% = 25.71\%$. The estimated mean positive number of days without the heart medication for women is $\exp(0.7288) \cdot 100\% = 207.26\%$ of that for men.

(d) Predict the number of days with missed heart medication for a 78-year-old male patient who is prescribed to take only that one medication.

The predicted value is $ndaysnomeds^0 = \left(1 - \frac{\exp(-3.0554)}{1+\exp(-3.0554)}\right) \frac{\exp(-1.0213+\ \ .02155\cdot 78)}{1-\exp(-\ ex\ \ (-1.0213+\ \ .02155\cdot 78))} = 2.159158$.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input gender$ age nothermeds;
cards;
M 78 0
;

data adherence;
set adherence predict;
run;

proc fmm;
 class gender;
  model ndaysnomeds = gender age / dist=truncpoisson;
   model+ / dist=constant;
     probmodel nothermeds;
    output out=outdata pred=pndaysnomeds;
run;

proc print data=outdata (firstobs=31) noobs;
 var pndaysnomeds;
run;
```

```
pndaysnomeds
     2.15893
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(gender.rel='M', age=78, nothermeds=0)))
```

```
2.158935
```

CHAPTER 6

EXERCISE 6.1. Consider a random experiment consisting of a sequence of independent trials each with outcomes of success or failure. And let p denote the probability of a success.
(a) Let X be the number of successes observed until the rth failure. The probabitity of a success is p. The distribution of X is negative binomial random variable with the probability mass function

$$P(X=x)=\binom{x+r-1}{x}p^x(1-p)^r, x=0,1,2,....$$

We can write this function as $P(X=x)=\exp\left(x\cdot\ln p+r\cdot\ln(1-p)+\ln\binom{x+r-1}{x}\right)$. If we let $\theta=\ln p$, we can rewrite this expression as $P(X=x)=\exp\left(x\cdot\theta+r\cdot\ln\left(1-e^{\theta}\right)+\ln\binom{x+r-1}{x}\right)$, which has the form as in (1.3) with $\phi=1,\ c(\theta)=-r\cdot\ln(1-e^{\theta})$, and $h(x,\phi)=\ln\binom{x+r-1}{x}$ and so this distribution belongs to the exponential familyof distributions.

(b) Substituting $p=\frac{\lambda}{r+\lambda}$, we get $P(X=x)=\binom{x+r-1}{x}\left(\frac{\lambda}{r+\lambda}\right)^x\left(1-\frac{\lambda}{r+\lambda}\right)^r=\left(\frac{r}{r+\lambda}\right)^r\binom{x+r-1}{x}\left(\frac{\lambda}{r+\lambda}\right)^x$

$=\left(\frac{r}{r+\lambda}\right)^r\frac{\Gamma(x+r)}{x!\Gamma(r)}\left(\frac{\lambda}{r+\lambda}\right)^x$, $x=0,1,2,....$ The mean is $E(X)=\frac{pr}{1-p}=\frac{\lambda r}{(r+\lambda)(1-\frac{\lambda}{r+\lambda})}=\frac{\lambda r}{r}=\lambda.$
The variance is $Var(X)=\frac{pr}{(1-p)^2}=\frac{\lambda r}{(r+\lambda)(1-\frac{\lambda}{r+\lambda})^2}=\frac{\lambda r(r+\lambda)}{r^2}=\lambda+\frac{\lambda^2}{r}.$

(c) We use the Stirling's formula $r!\simeq\sqrt{2\pi r}r^re^{-r}$ to write $\lim\limits_{r\longrightarrow\infty}\left(\frac{r}{r+\lambda}\right)^r\frac{\Gamma(x+r)}{x!\Gamma(r)}\left(\frac{\lambda}{r+\lambda}\right)^x=$
$\frac{\lambda^x}{x!}\lim\limits_{r\longrightarrow\infty}\frac{r^r}{(r+\lambda)^{r+x}}\frac{\sqrt{2\pi(x+r)}(x+r)^{x+r}e^{-(x+r)}}{\sqrt{2\pi r}r^re^{-r}}=\frac{\lambda^x}{x!}e^{-x}\lim\limits_{r\longrightarrow\infty}\frac{(x+r)^{x+r}}{(r+\lambda)^{r+x}}=\frac{\lambda^x}{x!}e^{-x}\lim\limits_{r\longrightarrow\infty}\left(1+\frac{x-\lambda}{r+\lambda}\right)^{r+\lambda+(x-\lambda)}=\frac{\lambda^x}{x!}e^{-x}e^{x-\lambda}=\frac{\lambda^x}{x!}e^{-\lambda}.$

EXERCISE 6.2. (a) Model mussel mortality via the negative binomial regression. Present the fitted model. What predictors turn out to be significant at the 5% level?

In SAS:

```
data mussels;
 input max_temp min_temp feeding_level$ ndead_mussels @@;
 cards;
77 60 high 0   88 59 high 1   78 62 high 1   85 60 high 2   78 61 high 0
89 63 high 0   92 62 high 2   75 58 high 0   80 59 med  1   90 61 med  2
74 63 med  4   92 62 med  6   83 62 med  8   75 63 med  3   76 61 med  2
86 62 med  1   92 62 low  2   89 64 low  3   96 68 low  19  86 62 low  7
74 61 low  3   88 62 low  12  97 63 low  9   91 61 low  7
;

/*fitting negative binomial model*/
proc genmod;
 class feeding_level(ref='high');
  model ndead_mussels = max_temp min_temp feeding_level / dist=negbin;
run;
```

```
Log Likelihood 72.2132

                Analysis Of Maximum Likelihood Parameter Estimates
Parameter          DF Estimate Standard  Wald 95% Confidence   Wald Chi- Pr > ChiSq
                                  Error        Limits            Square
Intercept           1 -11.4507   3.9298    -19.1529   -3.7485        8.49     0.0036
max_temp            1   0.0303   0.0224     -0.0136    0.0741        1.83     0.1764
min_temp            1   0.1418   0.0687      0.0072    0.2765        4.27     0.0389
feeding_level low   1   1.7786   0.4871      0.8239    2.7332       13.33     0.0003
feeding_level med   1   1.4125   0.4844      0.4632    2.3619        8.50     0.0035
feeding_level high  0   0.0000   0.0000      0.0000    0.0000           .          .
Dispersion          1   0.0940   0.1063      0.0103    0.8614
```

The fitted model has the estimated parameters $\hat{\lambda} = \exp(-11.4507 + 0.0303 \cdot maxtemp + 0.1418 \cdot mintemp + 1.7786 \cdot low\,feeding + 1.4125 \cdot high\,feeding)$ and $\hat{r} = \frac{1}{0.0940} = 10.6383$.
At the 5% level, minimum temperature and both feeding levels (low and medium) are significant predictors.

In R:

```
mussels.data<- read.csv(file='C:/<insert path>/Exercise6.2Data.csv',
header=TRUE, sep=',')

#specifying reference level
feeding.level.rel<- relevel(mussels.data$feeding.level, ref="high")

#fitting negative binomial model
library(MASS)

summary(fitted.model<- glm.nb(ndead.mussels ~ max.temp + min.temp
+ feeding.level.rel, data=mussels.data))

Coefficients:
                      Estimate Std. Error z value Pr(>|z|)
(Intercept)          -11.45070    3.98601  -2.873  0.00407
max.temp               0.03026    0.02222   1.361  0.17340
min.temp               0.14185    0.06925   2.048  0.04052
feeding.level.rellow   1.77858    0.48825   3.643  0.00027
feeding.level.relmed   1.41255    0.48347   2.922  0.00348

Theta:  10.6
```

(b) How good it the model fit?

The p-values is very small, so it can be concluded that the model fits the data well.

In SAS:

```
/*fitting negative binomial model*/
proc genmod;
 class feeding_level;
  model ndead_mussels = max_temp min_temp feeding_level / dist=negbin;
run;
```

```
Log Likelihood 58.5757
```

```
data deviance;
 deviance = -2*(58.5757 - 72.2132);
 pvalue = 1 - probchi(deviance,4);
run;

proc print noobs;
run;
```

```
deviance     pvalue
  27.275 .000017489
```

In R:

```
#checking model fit
null.model<- glm.nb(ndead.mussels ~ 1, data = mussels.data)
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
27.27491
```

```
print(p.value<- pchisq(deviance, df=4, lower.tail = FALSE))
```

```
1.749015e-05
```

(c) How would you interpret the estimated significant coefficients?

If the minimum temperature increases by one degree, the estimated mean number of dead mussels increases by $(\exp(0.1418) - 1) \cdot 100\% = 15.23\%$. The estimated mean number of dead mussels for low-fed specimens is $\exp(1.7786) \cdot 100\% = 592.16\%$ of that for high-fed specimens, and for medium-fed ones, it is $\exp(1.4125) \cdot 100\% = 410.62\%$ of those with high feeding regimen.

(d) Predict the number of dead mussels that were fed a high level of food, and were located in an area with the maximum temperature of 75 degrees and minimum temperature of 60 degrees.

The predicted value is computed as $ndeadmussels^0 = \exp(-11.4507 + 0.0303 \cdot 75 + 0.1418 \cdot 60) = 0.5116$.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input max_temp min_temp feeding_level$;
cards;
75 60 high
;

data mussels;
set mussels predict;
run;

proc genmod;
 class feeding_level;
  model ndead_mussels = max_temp min_temp feeding_level / dist=negbin;
```

```
   output out=outdata p=pndead_mussels;
run;

proc print data=outdata (firstobs=25) noobs;
 var pndead_mussels;
run;
```

```
pndead_mussels
       0.51132
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(max.temp=75, min.temp=60,
feeding.level.rel='high'), type='response'))
```

```
0.5113223
```

EXERCISE 6.3. (a) Is the negative binomial regression appropriate in modeling the amount of weekly allowance? Fit the model and discuss significance of the predictor variables.

In SAS:

```
data daily_allowance;
input age gender$ job$ allowance @@;
cards;
15 M yes 0  18 F yes 3  18 M yes 3  14 F no  6
16 F yes 2  17 F yes 1  18 F yes 1  15 F no  4
16 M yes 1  16 F no  9  16 M no  3  16 M no  10
16 F yes 0  14 M no  9  17 M yes 1  15 M no  0
15 M no  12 18 M no  3  15 M no  4  18 M yes 0
15 F no  8  15 M no  5  15 M no  5  14 M no  4
16 F yes 3  17 M no  2  18 M yes 2  17 F yes 11
15 M no  6  16 M no  12
;

/*fitting negative binomial model*/
proc genmod;
 class gender job;
  model allowance = age gender job / dist=negbin;
run;
```

```
Log Likelihood 81.7552

                Analysis Of Maximum Likelihood Parameter Estimates
Parameter      DF Estimate Standard  Wald 95% Confidence      Wald Chi- Pr > ChiSq
                              Error         Limits               Square
Intercept       1  -0.1297   2.6095     -5.2442     4.9849         0.00     0.9604
age             1   0.0359   0.1506     -0.2593     0.3311         0.06     0.8116
gender     F    1   0.4523   0.3192     -0.1733     1.0779         2.01     0.1565
gender     M    0   0.0000   0.0000      0.0000     0.0000            .          .
job        no   1   1.2630   0.4257      0.4286     2.0974         8.80     0.0030
job        yes  0   0.0000   0.0000      0.0000     0.0000            .          .
```

```
                 Analysis Of Maximum Likelihood Parameter Estimates
Parameter      DF Estimate Standard   Wald 95% Confidence       Wald Chi- Pr > ChiSq
                              Error          Limits                Square
Dispersion      1   0.3037   0.1550       0.1117     0.8258
```

In the fitted model, the estimated parameters $\hat{\lambda} = \exp(-0.1297 + 0.0359 \cdot age + 0.4523 \cdot female + 1.2630 \cdot no\ job)$ and $\hat{r} = \frac{1}{0.3037} = 3.2927$. Only the indicator of no job is significant at the 5% level.

In R:

```
allowance.data<- read.csv(file='C:/<insert path>/Exercise6.3Data.csv',
header=TRUE, sep=',')

#specifying reference levels
gender.rel<- relevel(allowance.data$gender, ref="M")
job.rel<- relevel(allowance.data$job, ref="yes")

#fitting negative binomial model
library(MASS)
summary(fitted.model<- glm.nb(allowance ~ age + gender.rel + job.rel,
data=allowance.data))
```

```
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -0.1297     2.3982  -0.054  0.95688
age           0.0359     0.1387   0.259  0.79570
gender.relF   0.4523     0.3067   1.475  0.14033
job.relno     1.2630     0.3937   3.208  0.00134

Theta:  3.29
```

b) How good is the model fit?

The p-value in the deviance test is below 0.05, indicating a good fit.

In SAS:

```
/*checking model fit*/
proc genmod;
 model allowance = / dist=negbin;
run;
```

```
Log Likelihood 75.8189
```

```
data deviance;
 deviance = -2*(75.8189 - 81.7552);
 pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance     pvalue
 11.8726 .007832568
```

In R:

```
#checking model fit
null.model<- glm.nb(allowance ~ 1, data=allowance.data)
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
11.87264
```

```
print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))
```

```
0.00783244
```

(c) Interpret the estimated significant regression coefficients.

The estimated average weekly allowance for students who haven't held a summer job is $\exp(1.2630) \cdot 100\% = 353.6\%$ than that for students who held a summer job.

(d) Predict the amount of weekly allowance for a male student, age 16, who hasn't held a summer job.

The predicted amount of weekly allowance is $allowance^0 = \exp(-0.1297 + 0.0359 \cdot 16 + 1.2630) = 5.5163$ or \$27.58.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input age gender$ job$;
cards;
16 M no
;

data daily_allowance;
set daily_allowance predict;
run;

proc genmod;
 class gender job;
  model allowance = age gender job / dist=negbin;
   output out=outdata p=pallowance;
run;

proc print data=outdata (firstobs=31) noobs;
 var pallowance;
run;
```

```
pallowance
   5.51684
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(age=16, gender.rel='M',  job.rel='no'),
type='response'))
```

```
5.516843
```

EXERCISE 6.4. (a) Argue that a zero-truncated negative binomial regression would be appropriate to model the number of rented kayaks. Fit the model. Discuss significance of predictors.

In SAS:

```
data statepark;
 input nkayaks partysize routelength camped$ @@;
 cards;
6  12 1  yes  2 4  3  yes  3 7  12 no   2 6  3  no   1  3  2 no
2  7  6  yes  2 4  2  no   1 3  6  yes  3 9  12 yes  5  10 4 no
1  2  1  no   2 6  12 yes  4 9  4  no   1 3  2  no   3  7  2 no
7  14 3  no   2 7  12 no   2 6  12 no   3 18 6  yes  2  4  1 yes
2  4  4  yes  4 9  12 yes  3 10 2  no   1 2  3  no   12 12 4 no
10 12 12 yes  2 7  6  yes  3 8  12 no   7 14 3  no   1  3  6 yes
;

/*fitting zero-truncated negative binomial model*/
proc fmm;
 class camped;
  model nkayaks = partysize routelength camped / dist=truncnegbin;
run;
```

```
-2 Log Likelihood 96.4664

Parameter Estimates for Truncated Negative Binomial Model
Effect          camped Estimate Standard z Value Pr > |z|
                                   Error
Intercept               -0.8576   0.5795   -1.48   0.1389
partysize                0.1833  0.04275    4.29   <.0001
routelength             0.02644  0.03529    0.75   0.4537
camped          no       0.2731   0.3045    0.90   0.3698
camped          yes           0        .       .        .
Scale Parameter          0.1116   0.1073
```

There are no zeros and variability is larger than for Poisson distribution, therefore zero-truncated negative binomial model should be appropriate. The fitted model has the estimated parameters $\hat{\lambda} = \exp(-0.8576 + 0.1833 \cdot party\ size + 0.02644 \cdot route\ length + 0.2731 \cdot no\ camping)$ and $\hat{r} = \frac{1}{0.1116} = 8.9606$. Only party size is a significant predictor.

In R:

```
statepark.data<- read.csv(file='C:/<insert path>/Exercise6.4Data.csv', header =
TRUE, sep=',')

#specifying reference level
camped.rel<- relevel(statepark.data$camped, ref="yes")

#fitting zero-truncated negative binomial model
library(VGAM)
summary(fitted.model<- vglm(nkayaks ~ partysize + routelength + camped.rel,
data=statepark.data, family=posnegbinomial()))
```

```
Coefficients:
               Estimate Std. Error z value Pr(>|z|)
(Intercept):1 -0.85770    0.55260  -1.552    0.121
(Intercept):2  2.19308    1.15141      NA       NA
partysize      0.18331    0.03440   5.329 9.89e-08
routelength    0.02644    0.03582   0.738    0.460
camped.relno   0.27304    0.29855   0.915    0.360
```

$\hat{r} = \exp(2.19308) = 8.962776.$

(b) Discuss model fit.

In the deviance test, the p-value is very small, suggesting that the model has a good fit.

In SAS:

```
/*checking model fit*/
proc fmm;
 model nkayaks = / dist=truncnegbin;
run;
```

```
2 Log Likelihood 121.1
```

```
data deviance;
 deviance = 121.1 - 96.4664;
 pvalue= 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance     pvalue
 24.6336 .000018418
```

In R:

```
#checking model fit
null.model<- vglm(nkayaks ~ 1, data=statepark.data, family=posnegbinomial())
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
24.63644
```

```
print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))
```

```
1.839315e-05
```

(c) Interpret the estimated significant regression coefficients, whatever are possible to interpret.

Interpretation is traditionally omitted due to complexity of the expression for the expected value.

(d) Predict the number of rented kayaks for a party of 5 people who plan to take a 6-hour route and to camp overnight.

The predicted value is $nkayaks^0 = \frac{\exp(-0.8576+0.1833\cdot 5+0.02644\cdot 6)}{1-(1+\text{ex }(-0.8576+\ .1833\cdot 5+0.02644\cdot 6)/8.9606)^{-8.9606}} = 1.8073.$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input partysize routelength camped$;
cards;
5 6 yes
;

data statepark;
set statepark predict;
run;

proc fmm;
 class camped;
  model nkayaks = partysize routelength camped / dist=truncnegbin;
   output out=outdata pred=pnkayaks;
run;

proc print data=outdata (firstobs=31) noobs;
 var pnkayaks;
run;
```

```
pnkayaks
 1.80725
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(partysize=5,routelength=6,
camped.rel='yes'), type='response'))
```

```
1.807214
```

EXERCISE 6.5. (a) Run the zero-truncated negative binomial model to regress the number of new videos on the other variables. Write the predicted model. What predictors turn out to be significant at the 5% level?

In SAS:

```
data vlogs;
length type $10;
input nnewvideos nvideos nsubscr nviews type$  @@;
cards;
3  81  3.9  205.8 lifeadvice  4  188 27   213.6 fashion
1  55  10.1 176.8 products    4  123 14.4 59.7  science
1  65  5    508.7 lifeadvice  2  118 3.5  280.6 comedy
3  119 4.7  25.7  fashion     1  47  4.4  135.8 products
2  405 58   423.6 comedy      4  160 10.9 212.8 science
4  123 1.3  204.1 fashion     1  96  1.1  449   comedy
2  44  2.7  217.7 fashion     1  71  8    12.3  lifeadvice
4  190 6.7  433.3 lifeadvice  1  59  9.5  90.4  science
1  36  9.2  423.9 products    3  511 92.5 158.4 products
2  112 4.2  225.7 products    4  156 32.4 140.8 comedy
```

```
3  212 1.3  121.1 products    4  86  4.2  160.2 fashion
12 517 85.4 163.7 lifeadvice  7  100 8      91.5  news
9  130 2.8  38.9  lifeadvice  2  34  2.4  151.9 fashion
30 396 7.6  118.4 comedy      12 52  0.9  617.2 lifeadvice
9  43  7.7  542.6 comedy      22 304 2.6  150.5 news
10 430 1.4  242.1 comedy      2  76  15.2 106.7 fashion
2  53 3.6   121.1 fashion     9  98  1    160.2 news
19 56 4.7   163.7 news        4  102 0.9  91.5  fashion
2 43  0.5   38.9  fashion     14 81  3.2  151.9 products
4 86  3.2   118.4 products    10 90  2.6  617.2 products
;

proc format;
value $typefmt 'fashion'='zref_fashion';
run;

/*fitting zero-truncated poisson model*/
proc fmm;
 class type;
  model nnewvideos = nvideos nsubscr nviews type / dist=truncnegbin;
format type $typefmt.;
run;
```

```
-2 Log Likelihood 191.9

  Parameter Estimates for Truncated Negative Binomial Model
Effect          type         Estimate Standard z Value Pr > |z|
                                         Error
Intercept                      0.3626   0.3995   0.91   0.3640
nvideos                      0.004948 0.001676   2.95   0.0032
nsubscr                      -0.02072 0.009700  -2.14   0.0326
nviews                       0.000955 0.000947   1.01   0.3132
type            comedy         0.3338   0.5390   0.62   0.5357
type            lifeadvice     0.5773   0.4984   1.16   0.2467
type            news           1.5310   0.5000   3.06   0.0022
type            products       0.3360   0.4561   0.74   0.4613
type            science       0.01012   0.6614   0.02   0.9878
type            Zref_fashion        0        .      .        .
Scale Parameter                0.4648   0.2165
```

The fitted model has the estimated parameters $\hat{\lambda} = \exp(0.3626 + 0.004948 \cdot nvideos - 0.02072 \cdot nsubscr + 0.000955 \cdot nviews + 0.3338 \cdot comedy + 0.5773 \cdot life\ advice + 1.5310 \cdot news + 0.3360 \cdot products + 0.01012 \cdot science)$ and $\hat{r} = \frac{1}{0.4648} = 2.1515$. At the 5% significance level, the significant predictors are total number of videos, number of subscribers, and the type of videos "news".

In R:

```
vlogs.data<- read.csv(file='C:/<insert path>/Exercise6.5Data.csv', header=TRUE,
sep=',')

#specifying reference level
type.rel<- relevel(vlogs.data$type, ref="fashion")

#fitting zero-truncated negative binomial model
```

```
library(VGAM)
summary(fitted.model<- vglm(nnewvideos ~ nvideos + nsubscr + nviews + type.rel,
data=vlogs.data, family = posnegbinomial()))
```

```
Coefficients:
                     Estimate Std. Error z value Pr(>|z|)
(Intercept):1       0.3625437  0.3899071   0.930  0.35246
(Intercept):2       0.7660984  0.4623516   1.657  0.09753
nvideos             0.0049484  0.0016068   3.080  0.00207
nsubscr            -0.0207244  0.0094039  -2.204  0.02754
nviews              0.0009554  0.0010078   0.948  0.34314
type.relcomedy      0.3336973  0.5483930   0.609  0.54286
type.rellifeadvice  0.5772579  0.4939778   1.169  0.24257
type.relnews        1.5310712  0.5050049   3.032  0.00243
type.relproducts    0.3359591  0.4596850   0.731  0.46487
type.relscience     0.0101134  0.6663842   0.015  0.98789
```

$\hat{r} = \exp(0.76660984) = 2.152457.$

(b) Does the model have a good fit?

The fit of the model is good, as supported by a small p-value in the deviance test.

In SAS:

```
/*checking model fit*/
proc fmm;
 model nnewvideos = / dist=truncnegbin;
run;
```

```
-2 Log Likelihood 212.8
```

```
data deviance;
 deviance = 212.8 - 191.9;
 pvalue = 1 - probchi(deviance,8);
run;

proc print noobs;
run;
```

```
deviance      pvalue
    20.9  .007417868
```

In R:

```
#checking model fit
null.model<- vglm(nnewvideos ~ 1, data = vlogs.data, family=posnegbinomial())
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
20.89688
```

```
print(p.value<- pchisq(deviance, df=8, lower.tail = FALSE))
```

```
0.007426463
```

(c) Interpret estimated signifficant regression coefficients, if possible.

Interpretation is not possible for this regression.

(d) Find the predicted number of new videos for a vlogger who posted a total of 87 videos on popular science, has 50,000 subscribers, and 254,000 views.

The predicted number of new videos is computed as:

$$nnewvideos^0 = \frac{\exp(0.3626 \quad .004948\cdot 87-0.02072\cdot 50+0.000955\cdot 254+0.01012)}{1-(1+\exp(0.3626+0.004948\cdot 87-0.02072\cdot 50+0.000955\cdot 254+ \quad .01012)/2.1515)^{-2.1515}}$$
$$= 1.793459.$$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input nvideos nsubscr nviews type$;
cards;
87 50 254 science
;

data vlogs;
set vlogs predict;
run;

proc fmm;
 class type;
  model nnewvideos = nvideos nsubscr nviews type / dist=truncnegbin;
   output out=outdata pred=pnnewvideos;
run;

proc print data=outdata (firstobs=41) noobs;
 var pnnewvideos;
run;
```

```
pnnewvideos
    1.79337
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(nvideos=87, nsubscr=50, nviews=254,
type.rel='science'), type='response'))
```

```
1.793339
```

EXERCISE 6.6. (a) Fit a zero-inflated negative binomial regression to model the number of claims made in the past five years. Model the probability of structural absence of claims as a function of the number of claims made in the previous five years. Model the positive responses as related to age and gender. What predictors are significant at the 5% level?

In SAS:

```
data insurance;
input nclaimspast5ys nclaimsprev5ys age gender$ @@;
cards;
1 1 39 M  1 2 66 M  7 0 56 M  3  4 43 F  4 1 42 F  4  2 52 M  0 0 39 F
4 6 68 M  6 1 41 F  0 1 54 F  4  2 50 F  6 4 57 M  5  4 47 F  1 2 43 M
1 1 36 M  1 2 55 F  5 5 57 F  8  5 53 M  0 1 72 M  0  1 67 F  8 3 69 F
0 2 70 M  7 2 70 M  3 1 54 F  2  1 38 M  3 1 50 F  0  1 62 M  8 2 54 M
0 0 59 M  0 1 61 F  0 0 69 F  8  3 57 F  0 0 57 M  12 5 72 F  0 2 42 M
6 2 42 F  7 2 66 M  7 4 53 M  6  0 52 M  3 3 57 F
;

/*fitting zero-inflated poisson model*/
proc genmod;
 class gender;
  model nclaimspast5ys = age gender / dist=zinb;
   zeromodel nclaimsprev5ys;
run;
```

```
Log Likelihood -82.0185

                Analysis Of Maximum Likelihood Parameter Estimates
Parameter    DF Estimate Standard     Wald 95% Confidence        Wald Chi- Pr > ChiSq
                            Error           Limits                  Square
Intercept     1  -0.1080   0.5354       -1.1574      0.9414           0.04     0.8401
age           1   0.0297   0.0092        0.0116      0.0477          10.40     0.0013
gender     F  1   0.1279   0.1842       -0.2332      0.4889           0.48     0.4876
gender     M  0   0.0000   0.0000        0.0000      0.0000              .          .
Dispersion    1   0.0309   0.0725        0.0003      3.0534

        Analysis Of Maximum Likelihood Zero Inflation Parameter Estimates
Parameter       DF Estimate Standard    Wald 95% Confidence      Wald Chi- Pr > ChiSq
                               Error          Limits                Square
Intercept        1   0.8826   0.7204     -0.5294      2.2947          1.50     0.2205
nclaimsprev5ys   1  -1.3297   0.5397     -2.3876     -0.2718          6.07     0.0138
```

The estimated parameters of the fitted model are $\hat{\pi} = \frac{\exp(0.8826 - 1.3297 \cdot nclaimsprev\qquad)}{1+\exp(0.8826-1.3297 \cdot nclaimsprev5ys)}$, $\hat{\lambda} = \exp(-0.1080 + 0.0297 \cdot age + 0.1279 \cdot female)$, and $\hat{r} = \frac{1}{0.0309} = 32.36246$.
Number of claims in the previous five years is a significant predictor of π, while age is a significant predictor of λ.

In R:

```
insurance.data<- read.csv(file='C:/<insert path>/Exercise6.6Data.csv',
header=TRUE, sep=',')

#specifying reference level
gender.rel<- relevel(insurance.data$gender, ref="M")

#fitting zero-inflated negative binomial model
library(pscl)
summary(fitted.model<- zeroinfl(nclaimspast5ys ~ age + gender.rel |
nclaimsprev5ys, data=insurance.data, dist='negbin'))
```

```
Count model coefficients (negbin with log link):
             Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.108006   0.536028  -0.201  0.84031
age          0.029678   0.009213   3.221  0.00128
gender.relF  0.127864   0.184205   0.694  0.48760
Log(theta)   3.475381   2.344614   1.482  0.13827

Zero-inflation model coefficients (binomial with logit link):
               Estimate Std. Error z value Pr(>|z|)
(Intercept)      0.8826     0.7204   1.225   0.2205
nclaimsprev5ys  -1.3297     0.5397  -2.464   0.0138

Theta = 32.3101
```

(b) Interpret the estimated significant coefficients.

As the number of claims in the previous five years increases by one, the estimated odds in favor of no claim in the past five years change by $(\exp(-1.3297) - 1) \cdot 100\% = -73.5443\%$, that is, decrease by 73.5443%. As the age of a policyholder increases by one year, the estimated average number of claims in the past five hears increases by $(\exp(0.0297) - 1) \cdot 100\% = 3.014544\%$.

(c) How good is the model fit? Give a quantitative answer.

In the deviance test, the p-value is very small, thus, the model has a good fit.

In SAS:

```
/*checking model fit*/
proc genmod;
 model nclaimspast5ys = / dist=zinb;
  zeromodel;
run;
```

```
Log Likelihood -92.1407
```

```
/*checking model fit*/
proc genmod;
 model nclaimspast5ys = / dist=zinb;
  zeromodel;
run;

data deviance;
 deviance = -2*(-92.1407 - (-82.0185));
 pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance      pvalue
 20.2444  .000151052
```

In R:

```
#checking model fit
null.model<- zeroinfl(nclaimspast5ys ~ 1, data=insurance.data, dist='negbin')
```

```
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
20.2445
```

```
print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))
```

```
0.0001510455
```

(d) What is the predicted number of claims made in the past five years by a 55-year-old female policyholder who has made no claims in the previous five years?

The predicted number of claims is $claims^0 = \frac{\exp(-0.1080+\ .0297\cdot 55+0.1279)}{1+\exp(0.8826)} = 1.528956.$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input nclaimsprev5ys age gender$;
cards;
0 55 F
;

data insurance;
set insurance predict;
run;

proc genmod;
 class gender;
   model nclaimspast5ys = age gender / dist=zinb;
   zeromodel nclaimsprev5ys;
       output out=outdata p=pnclaimspast5ys;
run;

proc print data=outdata (firstobs=41) noobs;
 var pnclaimspast5ys;
run;
```

```
pnclaimspast5ys
        1.52697
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(nclaimsprev5ys=0, age=55,
gender.rel='F')))
```

```
1.526969
```

EXERCISE 6.7. (a) Fit a zero-inflated negative binomial model, regressing the probability of structural zeros of DMFT index on age. Regress positive observations of DMFT index on gender and levels of oral hygiene. Write down the predicted model. Discuss significance of predictors at the 5% significance level.

In SAS:

```
data dental;
input DMFTindex   age   gender $ oralhygiene $ @@;
cards;
0  28 F high  2 30 F med   0 26 F high  15 55 M high  8  40 F med
2  19 M med   0 24 F med   8 77 F low   5  48 F high  3  21 F med
11 59 M med   9 50 M high  1 24 F med   0  26 M med   1  23 F high
2  24 F med   1 21 M low   2 40 M med   0  31 F med   11 29 M low
0  20 F high  0 25 F high  1 22 F high  7  37 M med   2  56 F med
15 63 M high  0 21 M med   5 55 F high  0  25 F high  2  68 M low
4  25 M med   6 59 F low   9 58 F med   0  37 M med   0  18 M high
16 73 M med   3 23 M med   8 65 M med
;

/*fitting zero-inflated negative binomial model*/
proc genmod;
 class gender(ref='F') oralhygiene(ref='med');
  model DMFTindex = oralhygiene gender / dist=zinb;
   zeromodel age;
run;
```

```
Log Likelihood -88.8603


                 Analysis Of Maximum Likelihood Parameter Estimates
Parameter        DF Estimate Standard  Wald 95% Confidence     Wald Chi- Pr > ChiSq
                                Error        Limits               Square
Intercept         1   1.2352   0.2762      0.6938    1.7766       20.00     <.0001
oralhygiene high  1   0.2468   0.3623     -0.4633    0.9569        0.46     0.4957
oralhygiene low   1   0.1577   0.4125     -0.6508    0.9662        0.15     0.7022
oralhygiene med   0   0.0000   0.0000      0.0000    0.0000           .          .
gender      M     1   0.6655   0.3130      0.0521    1.2789        4.52     0.0335
gender      F     0   0.0000   0.0000      0.0000    0.0000           .          .
Dispersion        1   0.4268   0.2007      0.1698    1.0729

         Analysis Of Maximum Likelihood Zero Inflation Parameter Estimates
Parameter DF Estimate Standard    Wald 95% Confidence          Wald Chi- Pr > ChiSq
                         Error          Limits                    Square
Intercept  1   2.1073   1.4259     -0.6874        4.9019           2.18     0.1394
age        1  -0.1013   0.0507     -0.2007       -0.0018           3.98     0.0460
```

The estimated parameters of the fitted model are $\hat{\pi} = \frac{\exp(2.1073\quad .1013 \cdot age)}{1+\text{ex}\ \ (2.1073-0.1013 \cdot age)}$, $\hat{\lambda} = \exp(1.2352 + 0.2468 \cdot high\ oral\ hygiene + 0.1577 \cdot low\ oral\ hygiene + 0.6655 \cdot male)$, and $\hat{r} = \frac{1}{0.4268} = 2.343018$.

Age is a significant predictor of π, and gender is a significant predictor of λ.

In R:

```
dental.data<- read.csv(file='C:/<insert path>/Exercise6.7Data.csv', header =
TRUE, sep=',')
```

```
#specifying reference levels
gender.rel<- relevel(dental.data$gender, ref="F")
oralhygiene.rel<- relevel(dental.data$oralhygiene, ref="med")

#fitting zero-inflated negative binomial model
library(pscl)
summary(fitted.model<- zeroinfl(DMFTindex ~ gender.rel + oralhygiene.rel | age,
data=dental.data, dist='negbin'))
```

```
Count model coefficients (negbin with log link):
                    Estimate Std. Error z value Pr(>|z|)
(Intercept)           1.2352     0.2762   4.472 7.75e-06
gender.relM           0.6655     0.3130   2.126  0.0335
oralhygiene.relhigh   0.2468     0.3623   0.681  0.4957
oralhygiene.rellow    0.1577     0.4125   0.382  0.7022

Zero-inflation model coefficients (binomial with logit link):
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  2.10729    1.42547   1.478   0.1393
age         -0.10126    0.05073  -1.996   0.0459 *

Theta = 2.3429
```

(b) Analyze the fit of the model.

The p-value in the deviance test is less than 0.05, indicating a goo fit of the model.

In SAS:

```
/*checking model fit*/
proc genmod;
 model DMFTindex = / dist=zinb;
  zeromodel;
run;
```

```
Log Likelihood -95.2421
```

```
data deviance;
 deviance = -2*(-95.2421 - (-88.8603));
  pvalue = 1 - probchi(deviance,4);
run;

proc print noobs;
run;
```

```
deviance    pvalue
 12.7636  0.012491
```

In R:

```
#checking model fit
null.model<- zeroinfl(DMFTindex ~ 1, data=dental.data, dist='negbin')
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
12.76369
```

```
print(p.value<- pchisq(deviance, df=4, lower.tail = FALSE))
```

```
0.01249009
```

(c) Give interpretation of the estimated signifficant coefficients.

As age increases by one year, the estimated odds in favor of the zero value of the DMFT index change by $(\exp(-0.1013) - 1) \cdot 100\% = -9.63381\%$, or decrease by 9.63%. The estimated mean value of the DMFT index for males is $\exp(0.6655) \cdot 100\% = 194.5463\%$ of that for females.

(d) Find the predicted value of the DMFT index for a man, aged 28, with a high level of oral hygiene.

The predicted value is computed as follows:

$$DMFT\ index^0 = \frac{\exp(1.2352 + 0.2468 + 0.6655)}{1 + \exp(2.1073 - 0.1013 \cdot 28)} = 5.776951.$$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input age gender$ oralhygiene$;
cards;
28 M high
;

data dental;
set dental predict;
run;

proc genmod;
 class gender(ref='F') oralhygiene(ref='med');
  model DMFTindex = oralhygiene gender / dist=zinb;
   zeromodel age;
    output out=outdata p=pDMFTindex;
run;

proc print data=outdata (firstobs=39) noobs;
 var pDMFTindex;
run;
```

```
pDMFTindex
   5.77492
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(age=28, gender.rel='M',
oralhygiene.rel='high')))
```

```
5.774924
```

EXERCISE 6.8. (a) Fit a hurdle negative binomial regression to model the number of claims made in the past five years. Model the probability of zero claims as a function of the number of claims

made in the previous five years. Model the positive responses as related to age and gender. Write down the fitted model explicitly. What predictors are significant at the 5% level?
In SAS:

```
data insurance;
input nclaimspast5ys nclaimsprev5ys age gender$ @@;
cards;
1 1 39 M  1 2 66 M  7 0 56 M  3 4 43 F  4 1 42 F  4  2 52 M  0 0 39 F
4 6 68 M  6 1 41 F  0 1 54 F  4 2 50 F  6 4 57 M  5  4 47 F  1 2 43 M
1 1 36 M  1 2 55 F  5 5 57 F  8 5 53 M  0 1 72 M  0  1 67 F  8 3 69 F
0 2 70 M  7 2 70 M  3 1 54 F  2 1 38 M  3 1 50 F  0  1 62 M  8 2 54 M
0 0 59 M  0 1 61 F  0 0 69 F  8 3 57 F  0 0 57 M  12 5 72 F  0 2 42 M
6 2 42 F  7 2 66 M  7 4 53 M  6 0 52 M  3 3 57 F
;

/*fitting hurdle negative binomial model*/
proc fmm;
 class gender;
  model nclaimspast5ys = age gender / dist=truncnegbin;
   model+ / dist=constant;
   probmodel nclaimsprev5ys;
run;
```

```
-2 Log Likelihood 163.4

 Parameter Estimates for Truncated Negative Binomial Model
Effect          gender  Estimate Standard z Value Pr > |z|
                                 Error
Intercept               -0.1879  0.5726   -0.33   0.7428
age                     0.03093  0.009793 3.16    0.0016
gender          F       0.1253   0.1936   0.65    0.5173
gender          M       0        .        .       .
Scale Parameter         0.04455  0.08328

  Parameter Estimates for Mixing Probabilities
Effect         Estimate Standard z Value Pr > |z|
                        Error
Intercept      -0.8814  0.7050   -1.25   0.2112
nclaimsprev5ys 1.2816   0.5071   2.53    0.0115
```

The estimated parameters of the fitted model are $\hat{\pi} = \frac{\exp(0.8814 - 1.2816 \cdot nclaimsprev5ys)}{1 + \exp(0.88214 \quad .2816 \cdot nclaimsprev5ys)}$, $\hat{\lambda} = \exp(-0.1879 + 0.03093 \cdot age + 0.1253 \cdot female)$, and $\hat{r} = \frac{1}{0.04455} = 22.44669$.
Number of claims in the previous five years is a significant predictor of π, while age is a significant predictor of λ.

In R:

```
insurance.data<- read.csv(file='C:/<insert path>/Exercise6.6Data.csv',
header=TRUE, sep=',')

#specifying reference level
gender.rel<- relevel(insurance.data$gender, ref="M")

#fitting hurdle negative binomial model
```

```
library(pscl)
summary(fitted.model<- hurdle(nclaimspast5ys ~ age + gender.rel | nclaimsprev5ys,
data=insurance.data,  dist='negbin', zero.dist = 'binomial', link='logit'))
```

```
Count model coefficients (truncated negbin with log link):
             Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.187878   0.573901  -0.327  0.74339
age          0.030928   0.009815   3.151  0.00163
gender.relF  0.125341   0.193554   0.648  0.51726

Zero hurdle model coefficients (binomial with logit link):
               Estimate Std. Error z value Pr(>|z|)
(Intercept)     -0.8814     0.7050  -1.250   0.2112
nclaimsprev5ys   1.2816     0.5071   2.527   0.0115

Theta: count = 22.4472
```

(b) Discuss goodness-of-fit of the model.

The model has a good fit which is supported by the small p-value in the deviance test.
In SAS:

```
/*checking model fit*/
proc fmm;
 model nclaimspast5ys = / dist=truncnegbin;
  model+ / dist=constant;
   probmodel;
run;
```

```
-2 Log Likelihood 184.3
```

```
data deviance;
 deviance = 184.3 - 163.4;
 pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance      pvalue
    20.9  .000110432
```

In R:

```
#checking model fit
null.model<- hurdle(nclaimspast5ys ~ 1, data=insurance.data, dist='negbin',
zero.dist='binomial', link='logit')
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
20.90545
```

```
print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))
```

```
0.0001101446
```

(c) Interpret the estimated significant coefficients. What is the direction of the relationships?

No interpretation of estimated regression coefficients is possible for hurdle models.

(d) Find the predicted number of claims made in the past five years by a 55-year-old female policyholder who has made no claims in the previous five years.

The predicted value is calculated as follows:

$$claims^0 = \frac{(1+\exp(0.8814))^{-1}\exp(-0.1879+0.03093\cdot 55+0.1253)}{1-(1+\exp(-0.1879+0.03093\cdot 55+0.1253)/22.44669)^{-22.44669}} = 1.522482.$$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input nclaimsprev5ys age gender$;
cards;
0 55 F
;

data insurance;
set insurance predict;
run;

proc fmm;
class gender;
  model nclaimspast5ys = age gender / dist=truncnegbin;
   model+ / dist=constant;
   probmodel nclaimsprev5ys;
       output out=outdata pred=pnclaimspast5ys;
run;

proc print data=outdata (firstobs=41) noobs;
 var pnclaimspast5ys;
run;
```

```
pnclaimspast5ys
        1.52243
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(nclaimsprev5ys=0,  age=55,
gender.rel='F')))
```

```
1.522423
```

EXERCISE 6.9. (a) Fit a hurdle negative binomial regression model. Specify the fitted model. Does it support the researchers' hypotheses? Discuss significance of predictor variables at the 5% significance level.

In SAS:

```
data sportsmedicine;
input ngameinjuries gender$ nsports npracticeinjuries @@;
cards;
0 M 2 2  0  M 1 1  1 F 2 3  1 F 1 0  2  F 1 1  0 F 2 1  0 M 1 0
6 M 2 3  7  M 1 5  2 M 2 4  8 M 3 1  10 M 2 2  4 M 1 7  0 F 1 1
2 M 2 2  2  F 2 0  0 F 2 0  1 F 2 2  2  M 2 3  0 M 1 0  3 M 2 4
5 F 1 4  0  M 2 0  7 M 3 4  7 F 2 3  3  F 3 4  8 M 1 2  3 F 3 5
7 M 3 6  12 M 2 5
;

proc format;
value $genderfmt 'F'='ref';
run;

/*fitting hurdle negative binomial model*/
proc fmm;
 class gender;
  model ngameinjuries = gender nsports / dist=truncnegbin;
   model+ / dist=constant;
    probmodel npracticeinjuries;
format gender $genderfmt.;
run;
```

```
-2 Log Likelihood 118.9

Parameter Estimates for Truncated Negative Binomial Model
Effect          gender  Estimate Standard z Value Pr > |z|
                                  Error
Intercept                 0.7247   0.4761    1.52   0.1280
gender          M         0.8873   0.3251    2.73   0.0063
gender          ref            0        .       .        .
nsports                  0.08047   0.1985    0.41   0.6852
Scale Parameter           0.1713   0.1530

   Parameter Estimates for Mixing Probabilities
Effect             Estimate Standard z Value Pr > |z|
                             Error
Intercept           -1.1574   0.8030  -1.44   0.1495
npracticeinjuries    1.3498   0.5401   2.50   0.0124
```

The estimated parameters of the fitted hurdle model are $\hat{\pi} = \frac{\exp(1.1574- \ .3498 \cdot npracticeinjuries)}{1+\exp(1.1574- \ .3498 \cdot npracticeinjuries)}$, $\hat{\lambda} = \exp(0.7247 + 0.8873 \cdot male + 0.08047 \cdot nsports)$, and $\hat{r} = \frac{1}{0.1713} = 5.837712$. Number of injuries during practice is a significant predictor of π, whereas gender is a significant predictor of λ.

In R:

```
sportsmedicine.data<- read.csv(file='C:/<insert path>/Exercise6.9Data.csv',
header=TRUE, sep=',')
library(pscl)
```

```
#specifying reference level
gender.rel<- relevel(sportsmedicine.data$gender, ref="F")

#fitting hurdle negative binomial model
summary(fitted.model<- hurdle(ngameinjuries ~ gender.rel +
nsports|npracticeinjuries, data=sportsmedicine.data, dist='negbin',
zero.dist='binomial', link='logit'))
```

```
Count model coefficients (truncated negbin with log link):
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.72465    0.47606   1.522  0.12796
gender.relM  0.88730    0.32510   2.729  0.00635
nsports      0.08047    0.19854   0.405  0.68525


Zero hurdle model coefficients (binomial with logit link):
                  Estimate Std. Error z value Pr(>|z|)
(Intercept)        -1.1574     0.8030  -1.441   0.1495
npracticeinjuries   1.3498     0.5401   2.499   0.0124

Theta: count = 5.8374
```

(b) Analyze the model fit.

The p-value in the deviance test is very small which means that the fit is very good.

In SAS:

```
/*checking model fit*/
proc fmm;
 model ngameinjuries = / dist=truncnegbin;
  model+ / dist=constant;
   probmodel;
run;
```

```
-2 Log Likelihood 140.2
```

```
data deviance;
 deviance = 140.2 - 118.9;
 pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance      pvalue
    21.3  .000091203
```

In R:

```
#checking model fit
null.model<- hurdle(ngameinjuries ~ 1, data=sportsmedicine.data, dist='negbin',
zero.dist = 'binomial', link='logit')
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
21.23368
```

```
print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))
```

```
9.414351e-05
```

(c) Give interpretation of the estimated signifficant coefficients.

Interpretation of estimated regression coefficients in the hurdle negative binomial model is traditionally omitted.

(d) Calculate the predicted number of injuries for a male athlete who throughout his college years has participated in two sports, and who has received one minor injury during practice games.

$$ninjuries^0 = \frac{(1+\exp(1.1574-1.3498))^{-1}\exp(0.7247+0.8873+0.08047\cdot 2)}{1-(1+\exp(0.7247+0.8873+0.08047\cdot 2)\,/5.837712)^{-5.837712}} = 3.282386.$$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input gender$ nsports npracticeinjuries;
cards;
M 2 1
;

data sportsmedicine;
set sportsmedicine predict;
run;

proc fmm;
 class gender;
  model ngameinjuries = gender nsports / dist=truncnegbin;
   model+ / dist=constant;
    probmodel npracticeinjuries;
       output out=outdata pred=pngameinjuries;
  format gender $genderfmt.;
run;

proc print data=outdata (firstobs=31) noobs;
 var pngameinjuries;
run;
```

```
pngameinjuries
       3.28221
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(gender.rel='M',  nsports=2,
npracticeinjuries=1)))
```

```
3.282217
```

CHAPTER 7

EXERCISE 7.1.

$$E(X) = \int_0^1 \frac{y^{\mu\phi}(1-y)^{(1-\mu)\phi-1}}{B(\mu\phi,(1-\mu)\phi)}\,dx = \frac{B(\mu\phi+1,(1-\mu)\phi)}{B(\mu\phi,(1-\mu)\phi)}$$

$$= \frac{\Gamma(\mu\phi+1)\Gamma((1-\mu)\phi)}{\Gamma(\phi+1)} \cdot \frac{\Gamma(\phi)}{\Gamma(\mu\phi)\Gamma\big((1-\mu)\phi\big)} = \frac{\mu\phi}{\phi} = \mu.$$

$$Var(X) = \int_0^1 \frac{y^{\mu\phi+}\ (1-y)^{(1-\mu)\phi-1}}{B(\mu\phi,(1-\mu)\phi)}\,dx\ -\ \mu^2 = \frac{B(\mu\phi+2,(1-\mu)\phi)}{B(\mu\phi,(1-\mu)\phi)}\ -\ \mu^2$$

$$= \frac{\Gamma(\mu\phi+2)\Gamma((1-\mu)\phi)}{\Gamma(\phi+2)} \cdot \frac{\Gamma(\phi)}{\Gamma(\mu\phi)\Gamma\big((1-\mu)\phi\big)}\ -\ \mu^2 = \frac{(\mu\phi+1)\mu\phi}{(\phi+1)\phi}\ -\ \mu^2 = \frac{\mu(1-\mu)}{1+\phi}.$$

EXERCISE 7.2. (a) Model the proportion of birds per flock that successfully reach the winter grounds. To avoid small estimates of the regression coefficients, convert mass into kilograms, wingspan into meters, and the distance, into thousands of kilometers. Write out the fitted model explicitly. Which predictors are significant at the 5% level?

In SAS:

```
data birdsmigration;
input mass wingspan distance nringed nmigrated @@;
cards;
811  67  1680 70  8    261  33  2137 113 75   398  48  2159 100 51
114  56  1204 145 113  119  53  1673 72  28   151  30  543  87  71
176  70  1414 116 109  184  45  2296 90  68   250  42  1511 52  42
505  24  741  74  63   551  17  1434 114 105  716  51  2116 98  58
735  119 2171 98  35   1233 108 2442 69  13   1315 98  2061 61  38
1633 72  1955 81  24   1736 119 1297 71  70   2019 101 930  112 105
2476 100 2312 95  37
;

/*rescaling predictors and computing response*/
data birdsmigration;
set birdsmigration;
mass=mass/1000;
wingspan=wingspan/100;
distance=distance/1000;
propsuccess=nmigrated/nringed;
run;

/*fitting beta regression model*/
proc glimmix;
 model propsuccess = mass wingspan distance / dist=beta link=logit solution;
run;
```

```
-2 Log Likelihood -12.81
```

```
             Parameter Estimates
Effect    Estimate Standard DF t Value Pr > |t|
                     Error
Intercept   2.7830   0.8642 15    3.22   0.0057
mass      -0.01502   0.4027 15   -0.04   0.9707
wingspan   0.04487   0.8796 15    0.05   0.9600
distance   -1.3186   0.4368 15   -3.02   0.0086
Scale       4.1727   1.2775  .       .        .
```

The fitted beta regression model has the estimated parameters

$$\hat{\mu} = \frac{\exp(2.7830 \quad .01502 \cdot mass + 0.04487 \cdot wingspan - 1.3186 \cdot distance)}{1+e \quad (2.7830 - 0.01502 \cdot mass + 0.04487 \cdot wingspan - \quad .3186 \cdot distance)}, \text{ and } \hat{\phi} = 4.1727.$$

Only distance is a significant predictor at the 5% level.

In R:

```
birdsmigration.data<- read.csv(file='C:/<insert path>/Exercise7.2Data.csv',
header=TRUE, sep=',')

#rescaling predictors and computing response
mass<- birdsmigration.data$mass/1000
wingspan<- birdsmigration.data$wingspan/100
distance<- birdsmigration.data$distance/1000
propsuccess<- birdsmigration.data$nmigrated/birdsmigration.data$nringed

#fitting beta model
library(betareg)
summary(fitted.model<- betareg(propsuccess ~ mass + wingspan + distance,
link='logit'))
```

```
Coefficients (mean model with logit link):
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  2.78304    0.78201   3.559 0.000373
mass        -0.01502    0.41088  -0.037 0.970848
wingspan     0.04487    0.93935   0.048 0.961901
distance    -1.31857    0.42237  -3.122 0.001797

(phi)    4.173
```

(b) Analyze the model fit.

The model has a reasonably good fit since the p-value < 0.05.

In SAS:

```
/*checking model fit*/
proc glimmix;
 model propsuccess = / dist=beta link=logit;
run;
```

```
2 Log Likelihood -4.25
```

```
data deviance;
 deviance = -4.25 - (-12.81);
 pvalue = 1 - probchi(deviance, 3);
run;

proc print noobs;
run;
```

```
deviance    pvalue
    8.56   0.035751
```

In R:

```
#checking model fit
null.model<- betareg(propsuccess ~ 1, link='logit')
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
8.55842
```

```
print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))
```

```
0.03577627
```

(c) Give interpretation of the estimated significant parameters.

As the distance increases by one thousand miles, the estimated ratio of the mean proportion of successfully migrated birds and the mean proportion of those that didn't migrate successfully changes by $(\exp(-1.3186)-1)\cdot 100\% = -73.249\%$, or decreases by 73.249%.

(d) Predict the number of birds that successfully reach the winter grounds for a flock of 70 birds with average mass of 600 grams, average wingspan of 65 centimeters, that travel a distance of 1650 kilometers.

The predicted proportion is found as:

$$nbirds^0 = 70\cdot\frac{\exp(2.7830-0.01502\cdot 0.6+0.04487\cdot 0.65-1.3186\cdot 1.65)}{1+\text{ex}\ \ (2.7830-\ \ .01502\cdot 0.6+0.04487\cdot 0.65-1.3186\cdot 1.65)} = (70)(0.651914) = 45.63398.$$

Only distance is a significant predictor at the 5% level.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input mass wingspan distance nringed;
cards;
0.6 0.65 1.65 70
;

data birdsmigration;
set birdsmigration predict;
run;

proc glimmix;
 model propsuccess = mass wingspan distance / dist=beta link=logit solution;
```

```
   output out=outdata pred(ilink)=ppropsuccess;
run;

data outdata;
 set outdata;
  pbirds = 70*ppropsuccess;
run;

proc print data=outdata (firstobs=20) noobs;
 var pbirds;
run;
```

```
 pbirds
45.6355
```

In R:

```
#using fitted model for prediction
print(70*predict(fitted.model, data.frame(mass=.6, wingspan=.65, distance=1.65,
nringed=70)))
```

```
45.63551
```

EXERCISE 7.3. (a) Model the proportion of hospitalized ER patients. Write down the fitted model. What factors are significant predictors? Use $\alpha = 0.05$.

In SAS:

```
data hospitals;
input perc_hospitalized location $ type $ nbeds @@;
prophospitalized=perc_hospitalized/100;
cards;
17 rural private 56   39 rural public  144  38 urban public  61
48 rural public  186  30 rural private 132  25 urban private 589
5  urban public  53   4  rural private 73   48 rural private 154
4  urban public  38   26 rural private 318  15 urban public  35
28 urban private 184  34 urban private 173  31 urban public  63
4  urban public  91   6  urban public  77   39 urban private 237
41 urban private 56   45 rural public  43   13 urban public  64
42 rural public  193  28 urban private 363  31 urban public  600
48 rural public  468  41 rural public  311  9  urban public  65
13 urban private 44   44 urban public  479  16 rural public  72
;

/*fitting beta regression model*/
proc glimmix;
 class location type(ref='private');
  model prophospitalized = location type nbeds / dist=beta link=logit solution;
run;
```

```
-2 Log Likelihood -41.58
```

```
                         Parameter Estimates
Effect    location type    Estimate Standard DF t Value Pr > |t|
                                     Error
Intercept                   -1.6735   0.2951 26   -5.67   <.0001
location  rural              0.5633   0.2526 26    2.23   0.0346
location  urban                   0        .  .       .        .
type               public   0.01165   0.2572 26    0.05   0.9642
type               private        0        .  .       .        .
nbeds                      0.002117 0.000707 26    3.00   0.0060
Scale                        9.8079   2.4611  .       .        .
```

The estimated parameters in the fitted model are

$$\hat{\mu}=\frac{\exp(-1.6735\quad .5633\cdot rural\quad .01165\cdot public+0.002117\cdot nbeds)}{1+\exp(-1.6735+0.5633\cdot rural+0.01165\cdot public+0.002117\cdot nbeds)},\text{ and }\hat{\phi}=9.8079.$$

Locations and number of beds are significant predictors at the 5% significance level.

In R:

```
hospitals.data<- read.csv(file='C:/<insert path>/Exercise7.3Data.csv',
header=TRUE, sep=',')

#computing response and specifying reference levels
prophospitalized<- hospitals.data$perchospitalized/100
location.rel<- relevel(hospitals.data$location, ref="urban")
type.rel<- relevel(hospitals.data$type, ref="private")

#fitting beta regression model
library(betareg)
summary(fitted.model<- betareg(prophospitalized ~ location.rel
+ type.rel + nbeds, data=hospitals.data, link='logit'))
```

```
Coefficients (mean model with logit link):
                    Estimate Std. Error z value Pr(>|z|)
(Intercept)       -1.6735254  0.2787233  -6.004 1.92e-09
location.relrural  0.5632707  0.2494671   2.258  0.02395
type.relpublic     0.0116530  0.2511991   0.046  0.96300
nbeds              0.0021170  0.0007219   2.933  0.00336

(phi)    9.808
```

(b) How good is the model fit?

The p-value is below 0.05, hence the fit is good.

In SAS:

```
/*checking model fit*/
proc glimmix;
 model prophospitalized = / dist=beta link=logit;
run;
```

```
2 Log Likelihood -30.58
```

```
data deviance;
 deviance = -30.58 - (-41.58);
 pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance    pvalue
      11  0.011726
```

In R:

```
#checking model fit
null.model<- betareg(prophospitalized ~ 1, data=hospitals.data, link='logit')
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
11.00244
```

```
print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))
```

```
0.01171267
```

(c) Interpret estimated significant regression coeficients.

For rural hospitals, the estimated ratio of the mean proportion of hospitalized ER patients and the mean proportion of non-hospitalized ones is $\exp(0.5633)\cdot 100\% = 175.6459\%$ of that for urban hospitals. As the number of beds increases by one, this estimated ratio increases by $(\exp(0.0002117)-1)\cdot 100\% = 0.211924\%$.

(d) Give the predicted proportion of hospitalized ER patients for a rural public hospital with 50 beds.

The predicted propotions is

$$prophospitalized^0 = \frac{\exp(-1.6735+0.5633+0.01165+0.002117\cdot 50)}{1+\exp(-1.6735+0.5633+0.01165+0.002117\cdot 50)} = 0.270379.$$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input location$ type$ nbeds;
cards;
rural public 50
;

data hospitals;
set hospitals predict;
run;

proc glimmix;
 class location type
  model prophospitalized = location type nbeds / dist=beta link=logit solution;
```

```
    output out=outdata pred(ilink)= pprophospitalized;
run;

proc print data=outdata (firstobs=31) noobs;
 var pprophospitalized;
run;
```

```
pprophospitalized
          0.27037
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(location.rel='rural', type.rel='public',
nbeds=50)))
```

```
0.270369
```

EXERCISE 7.4. (a) Use the beta regression to model proportion of by-catch. Convert depth to kilometers. Write down the fitted model.

In SAS:

```
data fishing;
input distance method $ depth percbycatch @@;
depth=depth/1000;
propbycatch= percbycatch/100;
cards;
120 trawl    250 14  115 trawl    150 6   70  trawl    300 24
130 trawl    150 6   90  seine    200 56  15  seine    350 32
15  seine    150 13  20  seine    350 23  15  longline 200 10
40  longline 150 7   115 trawl    300 8   160 trawl    200 10
160 trawl    200 10  50  trawl    150 15  10  seine    150 16
25  seine    200 22  15  seine    300 21  40  longline 100 21
60  longline 200 4   50  longline 150 17
;

/*fitting beta regression model*/
proc glimmix;
 class method;
  model propbycatch = distance method depth / dist=beta link=logit solution;
run;
```

```
-2 Log Likelihood -49.20

                  Parameter Estimates
Effect    method   Estimate Standard DF t Value Pr > |t|
                               Error
Intercept           -3.0476   0.8723 15   -3.49   0.0033
distance           0.006016 0.005386 15    1.12   0.2815
method    longline   0.5096   0.5864 15    0.87   0.3985
method    seine      1.4661   0.6348 15    2.31   0.0356
method    trawl           0        .  .       .        .
```

```
                   Parameter Estimates
Effect    method   Estimate Standard DF t Value Pr > |t|
                               Error
depth                1.5862   1.8090 15    0.88   0.3944
Scale               22.2401   7.0741  .       .        .
```

The estimated parameters in the fitted beta regression model are

$$\hat{\mu} = \frac{\exp(-3.0476+\ .006016\cdot distance+\ .5096\cdot longline+1.4661\cdot seine+1.5862\cdot depth)}{1+\exp(-3.0476+0.006016\cdot distance+\ .5096\cdot longline+1.4661\cdot seine+1.5862\cdot depth)},$$

and $\hat{\phi} = 22.2401$.

Fishing with a seine is the only significant predictor at the 5% significance level.

In R:

```
fishing.data<- read.csv(file='C:/<insert path>/Exercise7.4Data.csv',
header= TRUE, sep=',')

#computing response, rescaling and specifying reference level
propbycatch<- fishing.data$percbycatch/100
depthK<- fishing.data$depth/1000
method.rel<- relevel(fishing.data$method, ref="trawl")

#fitting beta regression model
library(betareg)
summary(fitted.model<- betareg(propbycatch ~ distance + method.rel
+ depthK, data=fishing.data, link='logit'))
```

```
Coefficients (mean model with logit link):
                   Estimate Std. Error z value Pr(>|z|)
(Intercept)       -3.047625   0.744117  -4.096 4.21e-05
distance           0.006016   0.004383   1.373   0.1699
method.rellongline 0.509570   0.505675   1.008   0.3136
method.relseine    1.466084   0.480930   3.048   0.0023
depthK             1.586194   1.827014   0.868   0.3853

(phi)   22.240
```

(b) Discuss significance of predictor variables and model fit.

The p-value is below 0.05, indicating a good fit.

In SAS:

```
/*checking model fit*/
proc glimmix;
 model propbycatch = / dist=beta link=logit;
run;
```

```
-2 Log Likelihood -38.25
```

```
data deviance;
 deviance = -38.25 - (-49.20);
 pvalue = 1 - probchi(deviance,4);
run;
```

```
proc print noobs;
run;
```

```
deviance   pvalue
   10.95  0.027132
```

In R:

```
#checking model fit
null.model<- betareg(propbycatch ~ 1, data=fishing.data, link='logit')
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
10.95303
```

```
print(p.value<- pchisq(deviance, df=4, lower.tail = FALSE))
```

```
0.02709695
```

(c) Give interpretation of the estimates of the regression coefficients for the significant predictors.

For purse seining method of fishing, the estimated ratio of the mean proportion of by-catch and the mean proportion of intended fish is $\exp(1.4661)\cdot 100\% = 433.2306\%$ of that for trawling method of fishing.

(d) Find the predicted percent of by-catch for a trawler that fishes 80 nautical miles off shore at the depth of 250 meters.

The predicted percent of by-catch can be computed as

$$\textit{prop by-catch}^0 = \frac{\exp(-3.0476+\ .006016\cdot 80+1.5862\cdot 0.25)}{1+\exp(-3.0476+0.006016\cdot 80+1.5862\cdot 0.25)} = 0.102498, \text{ or } 10.2498\%.$$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input distance method$ depth;
cards;
80 trawl 0.25
;

data fishing;
set fishing predict;
run;

proc glimmix;
 class method;
  model propbycatch = distance method depth / dist=beta link=logit;
    output out=outdata pred(ilink)=ppropbycatch;
run;

proc print data=outdata (firstobs=21) noobs;
 var ppropbycatch;
run;
```

```
pпропbycatch
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(distance=80, method.rel='trawl',
depthK=0.25)))

0.1024961
```

EXERCISE 7.5. (a) Fit the zero-inflated beta regression model to the proportion of houses. Regress the probability of zero on age of subdivision. To achieve model convergence, normalize the average price and number of houses by a factor of 100. Discuss significance of the predictors at the 5% level.

In SAS:

```
data realestate;
input percsold avgprice nhouses age @@;
avgprice=avgprice/100;
nhouses=nhouses/100;
propsold=percsold/100;
cards;
0    455 69  21  0    316 244 24  36.4 210 236 31  50 557 183 16
33.3 232 73  6   50   626 230 20  27.3 343 60  14  80 246 201 17
42.9 631 217 11  0    630 222 42  71.4 356 85  22  25 481 240 16
50   181 197 42  20   264 235 19  87.5 297 88  17  80 308 223 15
75   159 84  13  0    147 54  37  44.4 704 199 18  0  593 119 38
20   738 156 8   55.6 256 206 34  85.7 345 38  22  50 450 158 7
0    491 239 27  28.6 441 103 15  88.9 212 222 18  50 574 56  35
33.3 647 138 35  0    630 18  60
;

/*fitting zero-inflated beta regression model*/
proc nlmixed
parms b0=0.1 b1=0.1 g0=0.1 g1=0.1 g2=0.1 phi=0.1;
 pi0=exp(b0+b1*age)/(1+exp(b0+b1*age));
 mu=exp(g0+g1*avgprice+g2*nhouses)/(1+exp(g0+g1*avgprice+g2*nhouses));
 if(propsold=0) then loglikelihood=log(pi0);
  else loglikelihood=log(1-pi0)+lgamma(phi)-lgamma(mu*phi)-lgamma((1-mu)*phi)+
(mu*phi-1)*log(propsold)+((1-mu)*phi-1)*log(1-propsold);
   model propsold ~ general(loglikelihood);
run;
```

```
-2 Log Likelihood 11.1

                              Parameter Estimates
Parameter Estimate Standard DF t Value Pr > |t| 95% Confidence Limits Gradient
                      Error
b0         -4.5161   1.5570 30   -2.90   0.0069   -7.6959    -1.3363  4.25E-6
b1          0.1247  0.05093 30    2.45   0.0204   0.02068     0.2287 0.000209
g0          1.1639   0.5537 30    2.10   0.0441   0.03307     2.2948  5.63E-6
```

```
                              Parameter Estimates
Parameter Estimate Standard DF t Value Pr > |t| 95% Confidence Limits Gradient
                   Error
g1         -0.2002  0.09321 30   -2.15   0.0399    -0.3906   -0.00989 9.205E-6
g2         -0.1679   0.2442 30   -0.69   0.4970    -0.6667     0.3308 -5.58E-6
phi         5.4911   1.4991 30    3.66   0.0010     2.4294     8.5527 -2.61E-6
```

In the fitted model, the estimated parameters are

$\hat{\pi}_0 = \frac{\exp(-4.5161+\ .1247\cdot age)}{1+e\quad(-4.5161+0.1247\cdot age)}$, $\hat{\mu} = \frac{\exp(1.1639-\ .2002\cdot avgprice-\ .1679\cdot nhouses)}{1+\exp(1.1639-0.2002\cdot avgprice-0.1679\cdot nhouses)}$, and $\hat{\phi} = 5.4911$.

Age is a significant predictor of π_0, and average house price is a significant predictor of μ.

In R:

```
realestate.data<- read.csv(file='C:/<insert path>/Exercise7.5Data.csv',
header= TRUE, sep=',')

#computing response and rescaling predictors
realestate.data$propsold<- realestate.data$percsold/100
realestate.data$avgprice.res<- realestate.data$avgprice/100
realestate.data$nhouses.res<- realestate.data$nhouses/100

#fitting zero-inflated beta regression model
library(gamlss)
summary(fitted.model<- gamlss(propsold ~ avgprice.res + nhouses.res,
mu.link='logit', nu.formula = ~ age, nu.link='logit', data=realestate.data,
family = BEZI))
```

```
Mu Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)   1.16393    0.55373   2.102   0.0462
avgprice.res -0.20024    0.09321  -2.148   0.0420
nhouses.res  -0.16791    0.24421  -0.688   0.4983

Sigma Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)    1.703      0.273   6.238  1.9e-06


Nu Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -4.51609    1.55696  -2.901  0.00785
age          0.12468    0.05093   2.448  0.02205
```

(b) Present the fitted model. Does this model have a decent fit?

The model has a good fit since the p-value is small.

In SAS:

```
/*checking model fit*/
proc nlmixed;
parms b0=0.1 g0=0.1 phi=0.1;
 pi0=exp(b0)/(1+exp(b0));
 mu=exp(g0)/(1+exp(g0));
```

```
  if(propsold=0) then loglikelihood=log(pi0);
   else loglikelihood=log(1-pi0)+lgamma(phi)-lgamma(mu*phi)-lgamma((1-mu)*phi)+
(mu*phi-1)*log(propsold)+((1-mu)*phi-1)*log(1-propsold);
model propsold ~ general(loglikelihood);
run;
```

```
-2 Log Likelihood 25.2
```

```
data deviance;
 deviance = 25.2 - 11.1;
 pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance      pvalue
    14.1  .002772148
```

In R:

```
#checking model fit
null.model<- gamlss(propsold ~ 1, mu.link='logit', nu.formula= ~ 1,
nu.link='logit', data=realestate.data, family=BEZI)
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
14.12085
```

```
print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))
```

```
0.002745187
```

(c) Interpret parameter estimates for statistically significant predictors.

As age of subdivision increases by one year, the odds in favor of zero houses sold increase by $(\exp(0.1247)-1)\cdot 100\% = 13.28086\%$. As the average price of houses in a subdivision increases by one hundred thousand dollars, the ratio $\frac{\hat{\mu}}{1-\hat{\mu}}$ changes by $(\exp(-0.2002)-1)\cdot 100\% = -18.1433\%$, that is, decreases by 18.1433%.

(d) What is the model prediction for percent houses sold for a subdivision with 300 houses, built 50 years ago, and where houses are sold, on average, for $450,000?

The predicted value is

$propsold^0 = (1+\exp(-4.5161+0.1247\cdot 50))^{-1}\cdot\frac{\exp(1.1639-0.2002\cdot 4.5-0.1679\cdot 3)}{1+\exp(1.1639-\ .2002\cdot 4.5-0.1679\cdot 3)} = 0.066903$, or 6.6903%.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input avgprice nhouses age;
cards;
```

```
4.5 3 50
;

data realestate;
set realestate predict;
run;

proc nlmixed;
parms b0=0.1 b1=0.1 g0=0.1 g1=0.1 g2=0.1 phi=0.1;
 pi0=exp(b0+b1*age)/(1+exp(b0+b1*age));
 mu=exp(g0+g1*avgprice+g2*nhouses)/(1+exp(g0+g1*avgprice+g2*nhouses));
 if(propsold=0) then loglikelihood=log(pi0);
  else loglikelihood=log(1-pi0)+lgamma(phi)-lgamma(mu*phi)-lgamma((1-mu)*phi)+
(mu*phi-1)*log(propsold)+((1-mu)*phi-1)*log(1-propsold);
   model propsold ~ general(loglikelihood);
    predict (1-pi0)*mu out=outdata;
run;

proc print data=outdata (firstobs=31) noobs;
 var Pred;
run;
```

```
    Pred
0.066949
```

In R:

```
#using fitted model for prediction
param.pred<- predictAll(fitted.model, newdata=data.frame(avgprice.res=4.5,
nhouses.res=3, age=50), type='response')
print((1-param.pred$nu)*param.pred$mu)
```

```
0.06694997
```

EXERCISE 7.6. (a) Model the proportion of first-place trophies using a zero-inflated beta regression. Use the number of pupils to predict the probability of zero. Specify the fitted model. Use alpha of 0.05 to determine significance of regression coefficients.

In SAS:

```
data martialarts;
input ntrophies nfirstplaces nyears nblackbelts npupils @@;
propfirst=nfirstplaces/ntrophies;
cards;
21 7  5 1 96  12 3  5 2 59  21 10 5  2 71   23 4  3  2 94   11 1  1 3 53
20 9  6 4 52  15 4  6 2 61  28 16 13 5 104  19 8  3  4 95   4  0  1 1 27
6  0  1 1 45  19 12 7 5 42  21 7  4  3 86   32 24 11 6 151  5  0  3 1 78
23 9  5 2 81  8  0  3 2 35  21 13 15 3 89   12 3  6  3 39   11 0  3 2 40
12 7  5 2 81  22 13 7 4 148 10 3  8  3 128  20 0  2  2 42   19 2  3 1 39
14 2  2 3 105
;

/*fitting zero-inflated beta regression model*/
proc nlmixed;
parms b0=0.1 b1=0.1 g0=0.1 g1=0.1 g2=0.1 phi=0.1;
pi0=exp(b0+b1*npupils)/(1+exp(b0+b1*npupils));
```

```
mu=exp(g0+g1*nyears+g2*nblackbelts)/(1+exp(g0+g1*nyears+g2*nblackbelts));
if(propfirst=0) then loglikelihood=log(pi0);
else loglikelihood=log(1-pi0)+lgamma(phi)-lgamma(mu*phi)-lgamma((1-mu)*phi)
+(mu*phi-1)*log(propfirst)+((1-mu)*phi-1)*log(1-propfirst);
model propfirst ~ general(loglikelihood);
run;
```

```
-2 Log Likelihood -11.6

                              Parameter Estimates
Parameter Estimate Standard DF t Value Pr > |t| 95% Confidence Limits Gradient
                   Error
b0           2.9956   1.7966 26    1.67   0.1074    -0.6973     6.6885 5.469E-7
b1         -0.07133  0.03457 26   -2.06   0.0492    -0.1424   -0.00027 -0.00074
g0          -1.9445   0.3233 26   -6.01   <.0001    -2.6091    -1.2798 0.000089
g1           0.1274  0.03938 26    3.23   0.0033    0.04643     0.2083 0.000318
g2           0.2268   0.1060 26    2.14   0.0420   0.008854     0.4447 0.000364
phi         14.9642   4.6039 26    3.25   0.0032     5.5008    24.4277 -1.22E-6
```

In the fitted model, the estimated parameters are

$$\hat{\pi}_0 = \frac{\exp(2.9956-0.07133 \cdot npupils)}{1+\exp(2.9956-0.07133 \cdot npupils)}, \quad \hat{\mu} = \frac{\exp(-1.9445+0.1274 \cdot nyears+0.2268 \cdot nblackbelts)}{1+\exp(-1.9445+0.1274 \cdot nyears \quad .2268 \cdot nblackbelts)},$$

and $\hat{\phi} = 14.9642$.

All predictors are significant at the 5% level. Number of pupils is a significant predictor of π_0, and both number of years and number of blackbelt instructors are significant predictors of μ.

In R:

```
martialarts.data<- read.csv(file='C:/<insert path>/Exercise7.6Data.csv',
header=TRUE, sep=',')

#computing the response variable
martialarts.data$propfirst<-
martialarts.data$nfirstplaces/martialarts.data$ntrophies

#fitting zero-inflated beta regression model
library(gamlss)
summary(fitted.model<- gamlss(propfirst ~ nyears + nblackbelts, mu.link='logit',
nu.formula = ~ npupils, nu.link='logit', data=martialarts.data, family=BEZI))
```

```
Mu Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -1.94446    0.32335  -6.014 7.03e-06
nyears       0.12740    0.03938   3.235  0.00415
nblackbelts  0.22669    0.10602   2.138  0.04502

Sigma Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   2.7057     0.3077   8.795 2.62e-08

Nu Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  2.99552    1.79441   1.669    0.111
npupils     -0.07133    0.03452  -2.066    0.052
```

(b) Discuss the model fit. Present the fitted model.
The p-value is tiny indicating a very good model fit.

In SAS:

```
/*checking model fit*/
proc nlmixed;
parms b0=0.1 g0=0.1 phi=0.1;
pi0=exp(b0)/(1+exp(b0));
mu=exp(g0)/(1+exp(g0));
if(propfirst=0) then loglikelihood=log(pi0);
else loglikelihood=log(1-pi0)+lgamma(phi)-lgamma(mu*phi)-lgamma((1-mu)*phi)
+(mu*phi-1)*log(propfirst)+((1-mu)*phi-1)*log(1-propfirst);
model propfirst ~ general(loglikelihood);
run;
```

```
-2 Log Likelihood 15.8
```

```
data deviance;
 deviance = 15.8 - (-11.6);
 pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance      pvalue
    27.4  .000004853
```

In R:

```
#checking model fit
null.model<- gamlss(propfirst ~ 1, mu.link='logit', nu.formula = ~ 1,
nu.link='logit', data=martialarts.data, family=BEZI)
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
27.38556
```

```
print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))
```

```
4.887314e-06
```

(c) Interpret the estimates of significant regression coefficients.

As the number of pupils increases by one, the estimated odds in favor of no first-place trophies change by $(\exp(-0.07133)-1)\cdot 100\% = -6.88454\%$, that is, decrease by 6.88454%. As the studio's age increases by one year, the ratio $\frac{\hat{\mu}}{1-\hat{\mu}}$ increases by $(\exp(0.1274)-1)\cdot 100\% = 13.58713\%$. As the number of blackbelt instructors increases by one, the ratio $\frac{\hat{\mu}}{1-\hat{\mu}}$ increases by $(\exp(0.2268)-1)\cdot 100\% = 25.45789\%$.

(d) Predict the proportion of first-place trophies won by a studio that has been around for 10 years, has 85 students and three black-belt instructors.

The predicted proportion is

$$prop^0 = (1+\exp(2.9956-0.07133\cdot 85))^{-1}\cdot\frac{\exp(-1.9445\quad .1274\cdot 10+0.2268\cdot 3)}{1+\exp(-1.9445+\quad .1274\cdot 10+0.2268\cdot 3)} = 0.48013.$$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input nyears nblackbelts npupils;
cards;
10 3 85
;

data martialarts;
set martialarts predict;
run;

proc nlmixed;
parms b0=0.1 b1=0.1 g0=0.1 g1=0.1 g2=0.1 phi=0.1;
pi0=exp(b0+b1*npupils)/(1+exp(b0+b1*npupils));
mu=exp(g0+g1*nyears+g2*nblackbelts)/(1+exp(g0+g1*nyears+g2*nblackbelts));
if(propfirst=0) then loglikelihood=log(pi0);
else loglikelihood=log(1-pi0)+lgamma(phi)-lgamma(mu*phi)-lgamma((1-mu)*phi)
+(mu*phi-1)*log(propfirst)+((1-mu)*phi-1)*log(1-propfirst);
model propfirst ~ general(loglikelihood);
predict(1-pi0)*mu out=outdata;
run;

proc print data=outdata (firstobs=27) noobs;
 var Pred;
run;
```

```
   Pred
0.48004
```

In R:

```
#using fitted model for prediction
param.pred<- predictAll(fitted.model, newdata=data.frame(nyears=10,
nblackbelts=3, npupils=85), type='response')
print((1-param.pred$nu)*param.pred$mu)
```

```
0.4800583
```

EXERCISE 7.7. (a) Fit a one-inflated beta regression to model the proportion of survived trees. Regress the probability of one on amount of precipitation and wind speed. Discuss significance of the predictors at 5% and 10% significance levels.

In SAS:

```
data trees;
input nplanted nsurvived pestcontrol fertilization precipitation windspeed @@;
propsurvived=nsurvived/nplanted;
cards;
125 125 3 1 18 9.6   115 68  0 0 8  13.4  250 101 1 1 17 12.8
```

```
95  85  2 2 22 10    140 48  3 1 15 15.1  75  75  3 2 27 6.3
185 163 3 3 15 12.3  20  9   3 0 18 9.4   110 83  3 1 24 13.1
80  80  0 1 18 7.8   120 117 4 1 20 9.3   90  56  5 1 15 13.9
30  30  3 0 33 8.6   90  81  4 1 23 7.7   140 119 3 1 18 11.8
70  9   3 0 32 8.4   75  71  3 3 20 13.4  150 102 5 0 16 9.7
90  73  4 1 15 9.7   160 151 6 1 18 7.8   100 46  3 1 20 12.3
85  85  4 1 22 6.8   120 85  2 1 19 6.6   180 53  3 1 29 9.4
45  12  0 1 9  13.1  35  35  1 0 7  9.4
;

/*fitting one-inflated beta regression model*/
proc nlmixed;
parms b0=0.1 b1=0.1 b2=0.1 g0=0.1 g1=0.1 g2=0.1 phi=0.1;
pi1=exp(b0+b1*precipitation+b2*windspeed)/(1+exp(b0+b1*precipitation+b2*windspeed
));
mu=exp(g0+g1*pestcontrol+g2*fertilization)/(1+exp(g0+g1*pestcontrol+g2*fertilizat
ion));
if (propsurvived=1) then loglikelihood=log(pi1);
 else loglikelihood=log(1-pi1)+lgamma(phi)-lgamma(mu*phi)-lgamma((1-mu)*phi)
 +(mu*phi-1)*log(propsurvived)+((1-mu)*phi-1)*log(1-propsurvived);
model propsurvived ~ general(loglikelihood);
run;
```

```
2 Log Likelihood 3.8

                          Parameter Estimates
Parameter Estimate Standard DF t Value Pr > |t| 95% Confidence Limits Gradient
                   Error
b0          6.9100   4.2974 26    1.61   0.1199   -1.9235    15.7435 -3.25E-7
b1        -0.04206  0.09075 26   -0.46   0.6469   -0.2286     0.1445 -0.00003
b2         -0.7822   0.3775 26   -2.07   0.0483   -1.5582   -0.00632  -3.3E-6
g0         -1.1091   0.5643 26   -1.97   0.0601   -2.2690    0.05083 0.000013
g1          0.3234   0.1364 26    2.37   0.0254   0.04312     0.6038 0.000035
g2          0.7332   0.2822 26    2.60   0.0152    0.1532     1.3133 0.000010
phi         4.9777   1.5005 26    3.32   0.0027    1.8934     8.0620 -7.19E-7
```

In the fitted model, the estimated parameters are

$$\hat{\pi}_1 = \frac{\exp(6.91 - 0.04206 \cdot precipitation - 0.7822 \cdot windspeed)}{1 + \exp(6.91 - 0.04206 \cdot precipitation - 0.7822 \cdot windspeed)},$$

$$\hat{\mu} = \frac{\exp(-1.1091 + \ .3234 \cdot pestcontrol + 0.7332 \cdot fertilization)}{1 + \exp(-1.1091 + 0.3234 \cdot pestcontrol + \ .7332 \cdot fertilization)}, \text{ and } \hat{\phi} = 4.9777.$$

At the 5% level, windspeed is a significant predictor of π_1, and both pestcontrol and fertilization are significant predictors of μ.

In R:

```
trees.data<- read.csv(file='C:/<insert path>/Exercise7.7Data.csv',
header=TRUE, sep=',')

#computing response variable
trees.data$propsurvived<- trees.data$nsurvived/trees.data$nplanted
```

```
#fitting one-inflated beta model
library(gamlss)
summary(fitted.model<- gamlss(propsurvived ~ pestcontrol + fertilization,
mu.link='logit', nu.formula = ~ precipitation + windspeed, nu.link='logit',
data=trees.data, family=BEOI))
```

```
Mu Coefficients:
               Estimate Std. Error t value Pr(>|t|)
(Intercept)     -1.1080     0.5642  -1.964   0.0643
pestcontrol      0.3233     0.1364   2.371   0.0285
fertilization    0.7327     0.2821   2.597   0.0177

Sigma Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)    1.6048     0.3015   5.323 3.88e-05

Nu Coefficients:
               Estimate Std. Error t value Pr(>|t|)
(Intercept)     6.91004    4.29740   1.608   0.1243
precipitation -0.04206    0.09075  -0.463   0.6483
windspeed     -0.78224    0.37748  -2.072   0.0521 .
```

(b) Present the fitted model and discuss its fit.

The deviance test produces the p-value below 0.05, which indicates a good fit of the model.

In SAS:

```
/*checking model fit*/
proc nlmixed;
parms b0=0.1 g0=0.1 phi=0.1;
pi1=exp(b0)/(1+exp(b0));
mu=exp(g0)/(1+exp(g0));
if (propsurvived=1) then loglikelihood=log(pi1);
 else loglikelihood=log(1-pi1)+lgamma(phi)-lgamma(mu*phi)-lgamma((1-mu)*phi)
 +(mu*phi-1)*log(propsurvived)+((1-mu)*phi-1)*log(1-propsurvived);
model propsurvived ~ general(loglikelihood);
run;
```

```
-2 Log Likelihood 22.2
```

```
data deviance;
 deviance = 22.2 - 3.8;
 pvalue = 1 - probchi(deviance,4);
run;

proc print noobs;
run;
```

```
deviance     pvalue
    18.4 .001030602
```

In R:

```
#checking model fit
null.model<- gamlss(propsurvived ~ 1, mu.link='logit', nu.formula=~1,
nu.link='logit', data=trees.data, family=BEOI)
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
18.4455
```

```
print(p.value<- pchisq(deviance, df=4, lower.tail = FALSE))
```

```
0.001009668
```

(c) Interpret the estimated significant parameters.

As the windspeed increases by one mph, the estimated odds in favor of 100% survival of trees change by $(\exp(-0.7822)-1)\cdot 100\% = -54.2601373\%$, that is, decrease by 54.26%. As the frequency of pest control increases by one, the ratio $\frac{\hat{\mu}}{1-\hat{\mu}}$ increases by $(\exp(0.3234)-1)\cdot 100\% = 38.1818\%$. As the frequency of fertilization increases by one, the ratio $\frac{\hat{\mu}}{1-\hat{\mu}}$ increases by $(\exp(0.7332)-1)\cdot 100\% = 108.1732\%$.

(d) Parks and Recreation Department employees are considering planting 100 trees in a hard to reach area where neither pest control nor soil fertilization would be feasible. They are trying to decide between an area with lower precipitation (2 inches) and stronger winds (12.5mph), and an area with higher precipitation (25 in) and lower winds (6 mph). Which of the two areas would you recommend to use based on predicted proportion of trees that would survive for two years?

Predicted proportions of survived trees for the two areas are

$prop_1^0 = (1+\exp(6.91-0.04206\cdot 2-0.7822\cdot 12.5))^{-1}\Big(\exp(6.91-0.04206\cdot 2-0.7822\cdot 12.5)+\frac{\exp(-1.1091)}{1+\exp(-1.1091)}\Big) = 0.285381$,
and $prop_2^0 = (1+\exp(6.91-0.04206\cdot 25-0.7822\cdot 6))^{-1}\Big(\exp(6.91-0.04206\cdot 25-0.7822\cdot 6)+\frac{\exp(-1.1091)}{1+\exp(-1.1091)}\Big) = 0.821255$.

The second area (with higher precipitation and lower winds) has a higher predicted proportion of survived trees.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input pestcontrol fertilization precipitation windspeed;
cards;
0 0 2 12.5
0 0 25 6
;

data trees;
set trees predict;
run;

proc nlmixed;
parms b0=0.1 b1=0.1 b2=0.1 g0=0.1 g1=0.1 g2=0.1 phi=0.1;
pi1=exp(b0+b1*precipitation+b2*windspeed)/(1+exp(b0+b1*precipitation+b2*windspeed
));
mu=exp(g0+g1*pestcontrol+g2*fertilization)/(1+exp(g0+g1*pestcontrol+g2*fertilizat
ion));
```

```
if (propsurvived=1) then loglikelihood=log(pi1);
 else loglikelihood=log(1-pi1)+lgamma(phi)-lgamma(mu*phi)-lgamma((1-mu)*phi)
 +(mu*phi-1)*log(propsurvived)+((1-mu)*phi-1)*log(1-propsurvived);
model propsurvived ~ general(loglikelihood);
predict pi1+(1-pi1)*mu out=outdata;
run;

proc print data=outdata (firstobs=27) noobs;
 var Pred;
run;
```

```
   Pred
0.28537
0.82123
```

In R:

```
#using fitted model for prediction
param1<- predictAll(fitted.model, newdata = data.frame(pestcontrol=0,
fertilization=0, precipitation=2, windspeed=12.5), type='response')
param2<- predictAll(fitted.model, newdata = data.frame(pestcontrol=0,
fertilization=0, precipitation=25, windspeed=6), type='response')
print(param1$nu+(1-param1$nu)*param1$mu)
print(param2$nu+(1-param2$nu)*param2$mu)
```

```
0.2855535
0.8212778
```

EXERCISE 7.8. (a) Fit a one-inflated beta regression to model the proportion of completed sales, regressing the probability of one on the number of years of experience a salesperson has accrued. Use the significance level of 0.05. Write down the fitted model.

In SAS:

```
data sales;
input gender $ expyr bonus propsales @@;
female=(gender='F');
cards;
F 1  1.1  0.67  M 11 0.5  1     M 4  1.1  0.9   M 2  1.6  0.93
F 2  0.7  0.49  F 4  1.05 0.88  M 1  1.6  0.96  F 2  1.2  0.67
M 2  1.6  0.94  M 7  1.4  0.77  F 4  1.55 1     F 4  0.9  0.51
F 8  0.95 0.59  F 2  1.2  0.65  F 13  0.6 1     F 8  0.9  0.54
M 4  0.6  0.63  F 17 2.4  1     F 3  1.6  1     F 2  1.4  0.88
F 4  1.05 0.85  F 8  1.4  1     M 4  1.35 0.95  F 3  1    0.83
F 18 1.25 1     M 4  0.4  0.66
;

/*fitting one-inflated beta regression model*/
proc nlmixed;
parms b0=0.1 b1=0.1 g0=0.1 g1=0.1 g2=0.1 phi=0.1;
pi1=exp(b0+b1*expyr)/(1+exp(b0+b1*expyr));
mu=exp(g0+g1*female+g2*bonus)/(1+exp(g0+g1*female+g2*bonus));
if (propsales=1) then loglikelihood= log(pi1);
else loglikelihood=log(1-pi1)+lgamma(phi)-lgamma(mu*phi)-lgamma((1-mu)*phi)
 +(mu*phi-1)*log(propsales)+((1-mu)*phi-1)*log(1-propsales);
model propsales ~ general(loglikelihood);
```

```
run;
```

```
-2 Log Likelihood -22.6

                              Parameter Estimates
Parameter Estimate Standard DF t Value Pr > |t| 95% Confidence Limits Gradient
                   Error
b0         -3.7949   1.2965 26   -2.93   0.0070    -6.4598    -1.1300 7.533E-7
b1          0.4619   0.1933 26    2.39   0.0244    0.06453     0.8593 7.801E-6
g0         -0.3537   0.4533 26   -0.78   0.4423    -1.2854     0.5781 0.000015
g1         -0.7029   0.2599 26   -2.70   0.0119    -1.2371    -0.1686 0.000014
g2          1.8148   0.4038 26    4.49   0.0001     0.9848     2.6448 0.000021
phi        19.1898   6.1927 26    3.10   0.0046     6.4605    31.9192 3.494E-8
```

The fitted parameters are

$$\hat{\pi}_1 = \frac{\exp(-3.7949 + 0.4619 \cdot years\ of\ experience)}{1 + \exp(-3.7949 + 0.4619 \cdot years\ of\ experience)},$$

$$\hat{\mu} = \frac{\exp(-0.3537- \ \ .7029 \cdot female + +1.8148 \cdot bonus)}{1+\text{ex}\ \ (-0.3537 \quad .7029 \cdot female + +1.8148 \cdot bonus)},\ \text{and } \hat{\phi} = 19.1898.$$

At the 5% level, all predictors are significant: years of experience is a significant predictor of π_1, and gender and bonus amount are significant predictors of μ.

In R:

```
sales.data<- read.csv(file='C:/<insert path>/Exercise7.8Data.csv',
header=TRUE, sep=',')

#specifying reference level
sales.data$gender.rel<- relevel(sales.data$gender, ref="M")

#fitting one-inflated beta model
library(gamlss)
summary(fitted.model<- gamlss(propsales ~ gender.rel + bonus, mu.link='logit',
nu.formula = ~ expyr, nu.link='logit', data=sales.data, family=BEOI))
```

```
Mu Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -0.3532     0.4533  -0.779 0.445044
gender.relF  -0.7023     0.2599  -2.702 0.013712
bonus         1.8137     0.4038   4.492 0.000223

Sigma Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   2.9540     0.3228   9.151 1.38e-08

Nu Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -3.7949     1.2964  -2.927  0.00833
expyr         0.4619     0.1933   2.389  0.02684
```

(b) How good is the model fit?
The p-value is minuscule, which suggests a very good fit of the model.

In SAS:

```
/*checking model fit*/
proc nlmixed data=sales;
parms b0=0.1 g0=0.1 phi=0.1;
pi1=exp(b0)/(1+exp(b0));
mu=exp(g0)/(1+exp(g0));
if (propsales=1) then loglikelihood= log(pi1);
else loglikelihood=log(1-pi1)+lgamma(phi)-lgamma(mu*phi)-lgamma((1-mu)*phi)
 +(mu*phi-1)*log(propsales)+((1-mu)*phi-1)*log(1-propsales);
model propsales~general(loglikelihood);
run;
```

```
-2 Log Likelihood 9.6
```

```
data deviance;
 deviance = 9.6 - (-22.6);
 pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance      pvalue
32.2      .000000475
```

In R:

```
#checking model fit
null.model<- gamlss(propsales ~ 1, mu.link='logit', nu.formula = ~ 1,
nu.link='logit', data=sales.data, family=BEOI)
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
32.16519
```

```
print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))
```

```
4.830298e-07
```

(c) Interpret the estimated significant regression coefficients.

As the number of years of experience of a salesperson increases by one, the estimated odds in favor of 100% successful sales increase by $(\exp(0.4619)-1)\cdot 100\% = 58.70866\%$. For a female salesperson, the ratio $\frac{\hat{\mu}}{1-\hat{\mu}}$ is $\exp(-0.7029)\cdot 100\% = 49.51473\%$ of that for a male salesperson. As the amount of bonus increases by one thousand dollars, the ratio $\frac{\hat{\mu}}{1-\hat{\mu}}$ increases by $(\exp(1.8148)-1)\cdot 100\% = 513.9848\%$.

(d) Predict the proportion of completed sales for a salesman with 3 years of work experience and who received $1,500 in bonuses the previous year.

$$propsales^0 = (1+\exp(-3.7949+0.4619\cdot 3))^{-1}\left(\exp(-3.7949+0.4619\cdot 3) + \frac{\exp(-0.3537+1.8148\cdot 1.5)}{1+\exp(-0.3537+1.8148\cdot 1.5)}\right) = 0.921454.$$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input female expyr bonus;
cards;
0 3 1.5
;

data sales;
set sales predict;
run;

proc nlmixed;
parms b0=0.1 b1=0.1 g0=0.1 g1=0.1 g2=0.1 phi=0.1;
pi1=exp(b0+b1*expyr)/(1+exp(b0+b1*expyr));
mu=exp(g0+g1*female+g2*bonus)/(1+exp(g0+g1*female+g2*bonus));
if (propsales=1) then loglikelihood= log(pi1);
else loglikelihood=log(1-pi1)+lgamma(phi)-lgamma(mu*phi)-lgamma((1-mu)*phi)
 +(mu*phi-1)*log(propsales)+((1-mu)*phi-1)*log(1-propsales);
model propsales ~ general(loglikelihood);
predict pi1+(1-pi1)*mu out=outdata;
run;

proc print data=outdata (firstobs=27) noobs;
 var Pred;
run;
```

```
   Pred
0.92146
```

In R:

```
#using fitted model for prediction
param<- predictAll(fitted.model, newdata = data.frame(expyr=3, gender.rel='M',
bonus=1.5), type='response')
print(param$nu+(1-param$nu)*param$mu)
```

```
0.9213704
```

EXERCISE 7.9. (a) Fit the beta regression with inflated zeros and ones to model the germination rate. Regress parameter μ on altitude normalized by a factor of 1000, ν on EC, and τ on soil temperature. Specify the fitted model. Determine significance of regression coefficients at 5% and 10% levels.

In SAS:

```
data lab;
input EC soiltemp altitude germrate @@;
altitudeK=altitude/1000;
```

```
cards;
2.7 67 4368 0     1.1 67 1689 1     1.8   69 3156 0.87
1.6 67 4884 0.58  2.4 66 4926 0     1.6   63 3854 0.23
2.3 67 5146 0     1.2 64 2202 0.48  1.1   62 2759 0.82
1.9 62 2774 0.61  1.5 71 5927 0.19  1.7   61 827  0.93
2.8 62 3631 0     2.5 64 4229 0.17  1.8   69 2933 0.47
1.8 63 6110 0.32  1.5 67 461  1     2.5   67 5269 0
1.7 74 197  1     1.6 65 607  1     2.6   67 5263 0.16
1.2 69 651  1     1.7 65 863  0.8   1.5   62 4386 0.23
1.7 68 165  1     1.7 62 234  0.73
;

/*fitting zero-one-inflated beta model*/
proc nlmixed;
parms b0=0.1 b1=0.1 g0=0.1 g1=0.1 z0=0.1 z1=0.1 phi=0.1;
mu=exp(b0+b1*altitudeK)/(1+exp(b0+b1*altitudeK));
nu=exp(g0+g1*EC);
tau=exp(z0+z1*soiltemp);
pi0=nu/(1+nu+tau);
pi1=tau/(1+nu+tau);
if(germrate=0) then loglikelihood=log(pi0);
if(germrate=1) then loglikelihood=log(pi1);
if(germrate>0 and germrate<1) then loglikelihood=
log(1-pi0-pi1)+lgamma(phi)-lgamma(mu*phi)-lgamma((1-mu)*phi)+(mu*phi-
1)*log(germrate)
+((1-mu)*phi-1)*log(1-germrate);
model germrate ~ general(loglikelihood);
run;
```

```
-2 Log Likelihood 17.6

                          Parameter Estimates
Parameter Estimate Standard DF t Value Pr > |t| 95% Confidence Limits Gradient
                   Error
b0          1.6634   0.4713 26    3.53   0.0016      0.6946    2.6323  -7.9E-6
b1         -0.4791   0.1262 26   -3.80   0.0008     -0.7385   -0.2197 -0.00002
g0        -13.7160   6.1607 26   -2.23   0.0349    -26.3795   -1.0525 1.974E-7
g1          5.8628   2.5790 26    2.27   0.0315      0.5616   11.1640  1.34E-6
z0        -24.8615  12.9149 26   -1.93   0.0652    -51.4086    1.6855 -8.01E-7
z1          0.3599   0.1926 26    1.87   0.0729    -0.03588    0.7558 -0.00005
phi         6.5607   2.2800 26    2.88   0.0079      1.8741   11.2474 -1.11E-7
```

The fitted parameters in the fitted model are

$$\hat{\mu} = \hat{E}(y\,|0 < y < 1) = \frac{\exp(1.6634 - 0.4791 \cdot altitudeK)}{1 + \exp(1.6634 - 0.4791 \cdot altitudeK)},$$
$$\hat{\pi}_0 = \frac{\hat{\nu}}{1 + \hat{\nu} + \hat{\tau}}, \quad \text{and} \quad \hat{\pi}_1 = \frac{\hat{\tau}}{1 + \hat{\nu} + \hat{\tau}} \ ,$$

where $\hat{\nu} = \frac{\hat{P}(y=0)}{\hat{P}(0<y<1)} = \exp(-13.716 + 5.8628 \cdot EC)$, and $\hat{\tau} = \frac{\hat{P}(y=1)}{\hat{P}(0<y<1)} = \exp(-24.8615 + 0.3599 \cdot soiltemp)$.

At the 5% level, altitudeK is a significant predictor of μ and EC is a significant predictor of ν. Soil temperature is a significant predictor of τ at the 10% level.

In R:

```
lab.data<- read.csv(file='C:/<insert path>/Exercise7.9Data.csv', header=TRUE,
sep=',')

#rescaling variable
lab.data$altitudeK<- lab.data$altitude/1000

#fitting zero-one-inflated beta model
library(gamlss)
summary(fitted.model<- gamlss(germrate ~ altitudeK,  mu.link='logit', nu.formula
= ~ EC, nu.link='log', tau.formula = ~ soiltemp, tau.link='log', data=lab.data,
family=BEINF))
```

```
Mu Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   1.6631     0.4713   3.529  0.00224
altitudeK    -0.4790     0.1262  -3.796  0.00122

Sigma Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -0.5594     0.2370  -2.361   0.0291

Nu Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -13.716      6.161  -2.226   0.0383
EC             5.863      2.579   2.273   0.0348

Tau Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -24.8615    12.9583  -1.919   0.0702
soiltemp      0.3599     0.1932   1.863   0.0780
```

(b) Discuss the model fit.

The tiny p-value indicates a very good model fit.

In SAS:

```
/*checking model fit*/
proc nlmixed;
parms b0=0.1 g0=0.1 z0=0.1 phi=0.1;
mu=exp(b0)/(1+exp(b0));
nu=exp(g0);
tau=exp(z0);
pi0=nu/(1+nu+tau);
pi1=tau/(1+nu+tau);
if(germrate=0) then loglikelihood=log(pi0);
if(germrate=1) then loglikelihood=log(pi1);
if(germrate>0 and germrate<1) then loglikelihood=
log(1-pi0-pi1)+lgamma(phi)-lgamma(mu*phi)-lgamma((1-mu)*phi)+(mu*phi-
1)*log(germrate)
+((1-mu)*phi-1)*log(1-germrate);
model germrate ~ general(loglikelihood);
run;
```

```
-2 Log Likelihood 49.2
```

```
data deviance;
```

```
 deviance = 49.2 - 17.6;
 pvalue = 1 - probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance      pvalue
    31.6  .000000635
```

In R:

```
#checking model fit
null.model<- gamlss(germrate ~ 1, mu.link='logit', nu.formula = ~ 1,
nu.link='log', tau.formula = ~ 1, tau.link='log', data=lab.data, family=BEINF)
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
31.5888
```

```
print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))
```

```
6.389023e-07
```

(c) Give interpretation of the estimated significant regression coefficients.

As the plot altitude increases by one thousand feet, the ratio $\frac{\hat{\mu}}{1-\hat{\mu}}$ changes by $(\exp(-0.4791)-1)\cdot 100\% = -38.0659\%$, that is, decreases by 38.0659%. For a one-unit increase in EC, the estimated odds in favor of $y=0$ against $0<y<1$ increase by $(\exp(5.8628)-1)\cdot 100\% = 35{,}070.75\%$. For a one-degree increase in soil temperature, the estimated odds in favor of $y=1$ against $0<y<1$ increase by $(\exp(0.3599)-1)\cdot 100\% = 43.31861\%$.

(d) Use the fitted model to predict the germination rate for a plot with EC of 1.5 mS/cm^2, soil temperature of 68°F, and altitude of 950 feet.

The predicted germination rate is computed as

$$germrate^0 = \left(\exp(-24.8615+0.3599\cdot 68) + \frac{\exp(1.6634-0.4791\cdot 0.95)}{1+\exp(1.6634-0.4791\cdot 0.95)}\right)\times$$

$$\times\,(1+\exp(-13.716+5.8628\cdot 1.5)+\exp(-24.8615+0.3599\cdot 68))^{-1} = 0.859213.$$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input EC soiltemp altitudeK;
cards;
1.5 68 0.95
;

data lab;
set lab predict;
run;

proc nlmixed;
```

```
parms b0=0.1 b1=0.1 g0=0.1 g1=0.1 z0=0.1 z1=0.1 phi=0.1;
mu=exp(b0+b1*altitudeK)/(1+exp(b0+b1*altitudeK));
nu=exp(g0+g1*EC);
tau=exp(z0+z1*soiltemp);
pi0=nu/(1+nu+tau);
pi1=tau/(1+nu+tau);
if(germrate=0) then loglikelihood=log(pi0);
if(germrate=1) then loglikelihood=log(pi1);
if(germrate>0 and germrate<1) then loglikelihood=
log(1-pi0-pi1)+lgamma(phi)-lgamma(mu*phi)-lgamma((1-mu)*phi)+(mu*phi-
1)*log(germrate)
+((1-mu)*phi-1)*log(1-germrate);
model germrate ~ general(loglikelihood);
predict (tau+mu)/(1+nu+tau) out=outdata;
run;

proc print data=outdata (firstobs=27) noobs;
 var Pred;
run;
```

```
   Pred
0.85938
```

In R:

```
#using fitted model for prediction
param<- predictAll(fitted.model, newdata = data.frame(EC=1.5, soiltemp=68,
altitudeK=0.95), type='response')
print((param$tau+param$mu)/(1+param$nu+param$tau))
```

```
0.8593549
```

EXERCISE 7.10. (a) Regress the proportion of games played, using the zero-one-inflated beta model. Regress μ on vertical jump and number of bench press repetitions, ν on broad jump, and τ on BMI and forty-yard dash. What predictors are significant at the 5% level?

In SAS:

```
data football;
input BMI fortyyd vertical broad bench propgames @@;
cards;
31.1 4.58 35   108 20 0     28.5 4.70 30.5 115 21 1
32.4 4.39 36   116 18 0     30.8 4.67 33   121 15 0.87
29.6 4.41 33   116 26 0.47  30.0 4.56 38   122 21 0.8
31.3 4.50 35   119 29 0.8   29.4 4.49 31.5 115 18 0.33
28.1 4.37 34.5 130 21 0.53  31.0 4.52 33.5 128 25 0.87
29.7 4.57 31.5 124 18 0.73  27.6 4.62 38.5 118 15 1
29.5 4.60 32   121 15 0.47  30.7 4.40 34.5 113 22 0.47
29.4 4.73 34   114 15 0.6   29.1 4.57 35   111 19 0.87
30.6 4.60 30.5 114 24 0.47  29.3 4.55 36   115 17 0.87
28.1 4.59 35.5 109 14 0.87  31.7 4.62 37   121 19 0.8
29.7 4.73 34   118 21 1     30.7 4.80 34   114 15 0.33
28.8 4.37 36   121 19 0.73  30.7 4.68 34   105 14 0
```

```
30.7 4.64 33   116 21 0.47  30.3 4.50 35.5 115 25 0.6
30.0 4.48 34   119 20 0.67  28.6 4.59 36   123 17 1
30.8 4.43 34   117 18 0.53  27.7 4.51 33   117 20 0.73
30.7 4.50 38   114 18 1     28.1 4.59 36   115 17 0.93
29.3 4.61 32   113 20 0     27.9 4.64 33   118 23 1
29.7 4.67 41   124 21 1     29.9 4.48 35   111 18 0
32.0 4.51 33.5 116 25 0.67  29.6 4.37 37   115 24 0.93
32.9 4.55 33   122 27 0.47  27.6 4.67 33.5 118 26 1
30.4 4.55 32   109 17 0.73  31.4 4.50 38   121 18 0.67
;

/*fitting zero-one-inflated beta model*/
proc nlmixed;
parms b0=.1 b1=.1 b2=.1 g0=.1 g1=.1 z0=.1 z1=.1 z2=.1 phi=.1;
mu=exp(b0+b1*vertical+b2*bench)/(1+exp(b0+b1*vertical+b2*bench));
nu=exp(g0+g1*broad);
tau=exp(z0+z1*BMI+z2*fortyyd);
pi0=nu/(1+nu+tau);
pi1=tau/(1+nu+tau);
if (propgames=0) then loglikelihood=log(pi0);
if(propgames=1) then loglikelihood=log(pi1);
if(propgames>0 and propgames<1) then loglikelihood=
log(1-pi0-pi1)+lgamma(phi)-lgamma(mu*phi)-lgamma((1-mu)*phi)+(mu*phi-
1)*log(propgames)
+((1-mu)*phi-1)*log(1-propgames);
model propgames ~ general(loglikelihood);
run;
```

```
2 Log Likelihood 13.6

                          Parameter Estimates
Parameter Estimate Standard DF t Value Pr > |t| 95% Confidence Limits Gradient
                   Error
b0         -6.3365   2.4421 42   -2.59   0.0130    -11.2649    -1.4081 -6.57E-7
b1          0.2141  0.06943 42    3.08   0.0036     0.07398     0.3542 0.000011
b2        -0.01399  0.03066 42   -0.46   0.6504    -0.07586    0.04787 0.000086
g0         45.5487  19.0286 42    2.39   0.0212      7.1474    83.9500 -6.54E-6
g1         -0.4147   0.1691 42   -2.45   0.0184     -0.7560   -0.07346 -0.00072
z0        -27.0077  26.3559 42   -1.02   0.3114    -80.1960    26.1806 0.000024
z1         -1.0664   0.4812 42   -2.22   0.0322     -2.0374   -0.09530 0.000706
z2         12.4225   5.7433 42    2.16   0.0363      0.8321    24.0129 0.000110
phi         8.6232   2.1696 42    3.97   0.0003      4.2447    13.0016 1.258E-6
```

The fitted parameters in the fitted model are

$$\hat{\mu} = \hat{E}(y\,|0<y<1) = \frac{\exp(-6.3365 + 0.2141 \cdot vertical\ jump - 0.01399 \cdot bench\ press)}{1+\exp(-6.3365 + 0.2141 \cdot vertical\ jump - 0.01399 \cdot bench\ press)},$$

$$\hat{\pi}_0 = \frac{\hat{\nu}}{1+\hat{\nu}+\hat{\tau}}, \quad \text{and} \quad \hat{\pi}_1 = \frac{\hat{\tau}}{1+\hat{\nu}+\hat{\tau}},$$

where $\hat{\nu} = \frac{\hat{P}(y=0)}{\hat{P}(0<y<1)} = \exp(45.5487 - 0.4147 \cdot broad\ jump)$, and $\hat{\tau} = \frac{\hat{P}(y=1)}{\hat{P}(0<y<1)} = \exp(-27.0077 - 1.0664 \cdot BMI + 12.4225 \cdot \textit{forty-yard dash})$.

At the 5% level, vertical jump is a significant predictor of μ, broad jump is a significant predictor of ν, and BMI and forty-yard dash are significant predictors of τ.

In R:

```
football.data<- read.csv(file='C:/<insert path>/Exercise7.10Data.csv',
header=TRUE, sep=',')

#fitting zero-one-inflated beta model
library(gamlss)
summary(fitted.model<- gamlss(propgames ~ vertical + bench, mu.link='logit',
nu.formula = ~ broad, nu.link='log',tau.formula = ~ BMI + fortyyd, tau.link
='log', data=football.data, family=BEINF))
```

```
Mu Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -6.33600    2.44008  -2.597  0.01395
vertical     0.21407    0.06938   3.086  0.00409
bench       -0.01399    0.03066  -0.456  0.65117

Sigma Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -0.7429     0.1665  -4.463  8.9e-05

Nu Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  45.5488    18.5894   2.450   0.0197
broad        -0.4148     0.1652  -2.511   0.0171


Tau Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -27.0077    26.3530  -1.025   0.3129
BMI          -1.0664     0.4808  -2.218   0.0336
fortyyd      12.4225     5.7375   2.165   0.0377
```

(b) Analyze the fit of the model.

The model has a very good fit, since the p-value in the deviance test is very small.

In SAS:

```
/*checking model fit*/
proc nlmixed;
parms b0=.1 g0=.1 z0=.1 phi=.1;
mu=exp(b0)/(1+exp(b0));
nu=exp(g0);
tau=exp(z0);
pi0=nu/(1+nu+tau);
pi1=tau/(1+nu+tau);
if (propgames=0) then loglikelihood=log(pi0);
if(propgames=1) then loglikelihood=log(pi1);
if(propgames>0 and propgames<1) then loglikelihood=
log(1-pi0-pi1)+lgamma(phi)-lgamma(mu*phi)-lgamma((1-mu)*phi)+(mu*phi-
1)*log(propgames)
+((1-mu)*phi-1)*log(1-propgames);
model propgames ~ general(loglikelihood);
run;
```

```
-2 Log Likelihood 47.3
```

```
data deviance;
 deviance = 47.3 - 13.6;
 pvalue = 1 - probchi(deviance,5);
run;

proc print noobs;
run;
```

```
deviance      pvalue
    33.7  .000002732
```

In R:

```
#checking model fit
null.model<- gamlss(propgames ~ 1, mu.link='logit', nu.formula = ~ 1,
nu.link='log', tau.formula = ~ 1, tau.link='log', data=football.data,
family= BEINF)
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
33.66176
```

```
print(p.value<- pchisq(deviance, df=5, lower.tail = FALSE))
```

```
2.780153e-06
```

(c) Give interpretation of the estimated significant coefficients.

As the vertical jump increases by one inch, the ratio $\frac{\hat{\mu}}{1-\hat{\mu}}$ increases by $(\exp(0.2141)-1)\cdot 100\% = 23.87465\%$. For a one-inch increase in broad jump, the estimated odds in favor of $y = 0$ against $0 < y < 1$ change by $(\exp(-0.4147)-1)\cdot 100\% = -33.9462\%$, that is, decrease by 33.9462%. For a one-unit increase in BMI, the estimated odds in favor of $y = 1$ against $0 < y < 1$ change by $(\exp(-1.0664)-1)\cdot 100\% = -65.5754\%$, that is, decrease by 65.5754%. For a one-second increase in forty-dash run, the estimated odds in favor of $y = 1$ against $0 < y < 1$ increase by $(\exp(12.4225)-1)\cdot 100\% = 24{,}832{,}557.66\%$.

(d) Predict the proportion of games that a new player will play, if his BMI is 27.8 kg/m^2, forty-dash run is 4.67 seconds, vertical jump is 32 inches, broad jump is 117 inches, and bench press is 16 repetitions.

The predicted proportion of games is

$$propgames^0 = \Bigg(\exp(-27.0077 - 1.0664\cdot 27.8 + 12.4225\cdot 4.67) + \frac{\exp(-6.3365 + 0.2141\cdot 32 - 0.01399\cdot 16)}{1+\exp(-6.3365 + 0.2141\cdot 32 - 0.01399\cdot 16)}\Bigg)\times$$

$$\times\left(1+\exp(45.5487 - 0.4147\cdot 117) + \exp(-27.0077 - 1.0664\cdot 27.8 + 12.4225\cdot 4.67)\right)^{-1}$$

$$= 0.903133.$$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input BMI fortyyd vertical broad bench;
cards;
27.8 4.67 32 117 16
;

data football;
set football predict;
run;

proc nlmixed;
parms b0=.1 b1=.1 b2=.1 g0=.1 g1=.1 z0=.1 z1=.1 z2=.1 phi=.1;
mu=exp(b0+b1*vertical+b2*bench)/(1+exp(b0+b1*vertical+b2*bench));
nu=exp(g0+g1*broad);
tau=exp(z0+z1*BMI+z2*fortyyd);
pi0=nu/(1+nu+tau);
pi1=tau/(1+nu+tau);
if (propgames=0) then loglikelihood=log(pi0);
if(propgames=1) then loglikelihood=log(pi1);
if(propgames>0 and propgames<1) then loglikelihood=
log(1-pi0-pi1)+lgamma(phi)-lgamma(mu*phi)-lgamma((1-mu)*phi)+(mu*phi-
1)*log(propgames)
+((1-mu)*phi-1)*log(1-propgames);
model propgames ~ general(loglikelihood);
predict (tau+mu)/(1+nu+tau) out=outdata;
run;

proc print data=outdata (firstobs=43) noobs;
 var Pred;
run;
```

```
   Pred
0.90325
```

In R:

```
#using fitted model for prediction
param<- predictAll(fitted.model, newdata = data.frame(BMI=27.8, fortyyd=4.67,
vertical=32, broad=117, bench=16), type='response')
print((param$tau+param$mu)/(1+param$nu+param$tau))
```

```
0.9032484
```

CHAPTER 8

EXERCISE 8.1. (a) For any $i \neq i'$, $Cov(y_{ij}, y_{i'j'}) = Cov(\beta_0 + \beta_1 x_{1ij} + \cdots + \beta_k x_{kij} + \beta_{k+1} t_j + u_{1i} + u_{2i} t_j + \varepsilon_{ij},\ \beta_0 + \beta_1 x_{1i'j'} + \cdots + \beta_k x_{ki'j'} + \beta_{k+1} t_{j'} + u_{1i'} + u_{2i'} t_{j'} + \varepsilon_{i'j'}) = Cov(u_{1i} + u_{2i} t_j + \varepsilon_{ij},\ u_{1i'} + u_{2i'} t_{j'} + \varepsilon_{i'j'}) = Cov(u_{1i}, u_{1i'}) + Cov(u_{1i}, u_{2i'}) t_{j'} + Cov(u_{1i}, \varepsilon_{i'j'}) + Cov(u_{2i}, u_{1i'}) t_j + Cov(u_{2i}, u_{2i'}) t_j t_{j'} + Cov(u_{2i}, \varepsilon_{i'j'}) t_j + Cov(\varepsilon_{ij}, u_{1i'}) + Cov(\varepsilon_{ij}, u_{2i'}) t_{j'} + Cov(\varepsilon_{ij},\ \varepsilon_{i'j'}) = 0$.

(b) For any given i and $j \neq j'$, $Cov(y_{ij}, y_{ij'}) = Cov(\beta_0 + \beta_1 x_{1i} + \cdots + \beta_k x_{kij} + \beta_{k+1} t_j + u_{1i} + u_{2i} t_j + \varepsilon_{ij},\ \beta_0 + \beta_1 x_{1ij'} + \cdots + \beta_k x_{kij'} + \beta_{k+1} t_{j'} + u_{1i} + u_{2i} t_{j'} + \varepsilon_{ij'}) = Cov(u_{1i} + u_{2i} t_j + \varepsilon_{ij},\ u_{1i} + u_{2i} t_{j'} + \varepsilon_{ij'}) = Cov(u_{1i}, u_{1i}) + Cov(u_{1i}, u_{2i}) t_{j'} + Cov(u_{1i}, \varepsilon_{ij'}) + Cov(u_{2i}, u_{1i}) t_j + Cov(u_{2i}, u_{2i}) t_j t_{j'} + Cov(u_{2i}, \varepsilon_{ij'}) t_j + Cov(\varepsilon_{ij}, u_{1i}) + Cov(\varepsilon_{ij}, u_{2i}) t_{j'} + Cov(\varepsilon_{ij}, \varepsilon_{ij'})$ $= Var(u_{1i}) + +Cov(u_{1i}, u_{2i})(t_j + t_{j'}) + Var(u_{2i}) t_j t_{j'} = \sigma^2_{u_1} + \sigma_{u_1 u_2}(t_j + t_{j'}) + \sigma^2_{u_2} t_j t_{j'}$.

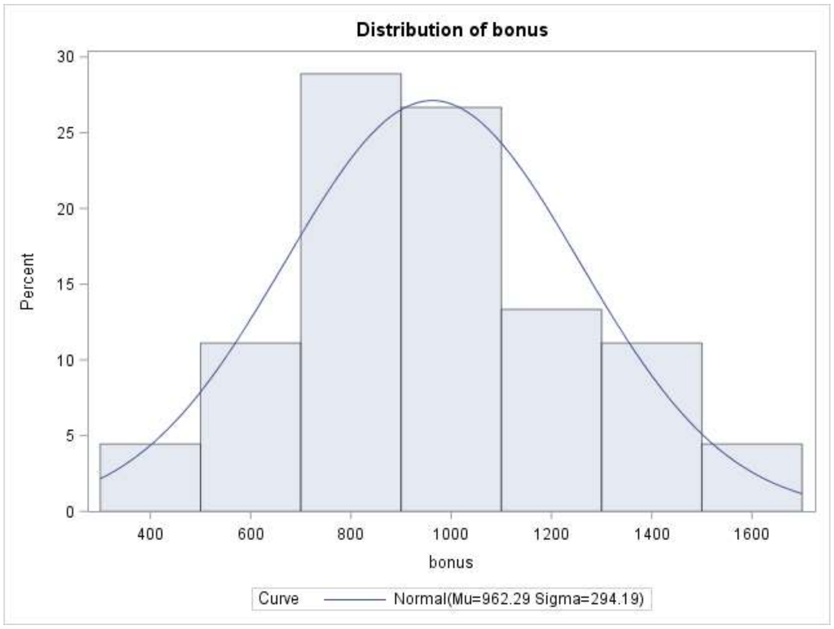
(c) The response variable $y_{ij} = \beta_0 + \beta_1 x_{1ij} + \cdots + \beta_k x_{kij} + \beta_{k+1} t_j + u_{1i} + u_{2i} t_j + \varepsilon_{ij}$ has a normal distribution as the sum of normal random variables. Its mean is $E(y_{ij}) = E(\beta_0 + \beta_1 x_{1ij} + \cdots + \beta_k x_{kij} + \beta_{k+1} t_j + u_{1i} + u_{2i} t_j + \varepsilon_{ij}) = \beta_0 + \beta_1 x_{1ij} + \cdots + \beta_k x_{kij} + \beta_{k+1} t_j + E(u_{1i}) + E(u_{2i}) t_j + E(\varepsilon_{ij}) = \beta_0 + \beta_1 x_{1ij} + \cdots + \beta_k x_{kij} + \beta_{k+1} t_j$, and the variance is $Var(y_{ij}) = Var(\beta_0 + \beta_1 x_{1ij} + \cdots + \beta_k x_{kij} + \beta_{k+1} t_j + u_{1i} + u_{2i} t_j + \varepsilon_{ij}) = Var(u_{1i} + u_{2i} t_j + \varepsilon_{ij}) = Var(u_{1i}) + 2Cov(u_{1i}, u_{2i}) t_j + Var(u_{2i}) t_j^2 + 2Cov(u_{1i}, \varepsilon_{ij}) + 2Cov(u_{2i}, \varepsilon_{ij}) t_j + Var(\varepsilon_{ij}) = \sigma^2_{u_1} + 2\sigma_{u_1 u_2} t_j + \sigma^2_{u_2} t_j^2 + \sigma^2$.

EXERCISE 8.2. (a) Carry out tests for normality of the bonus and plot the histogram. Is this variable normally distributed?

In SAS:

```
data deptstore;
input id totalyears status$ bonus18 bonus19 bonus20 @@;
cards;
1  16 full 1482 1508 1543  2  7  part 673  710  895
3  11 full 933  1351 1440  4  8  part 844  958  1196
5  6  part 564  790  815   6  5  full 601  708  780
7  6  part 775  822  902   8  17 full 1209 1297 1475
9  12 full 929  1008 1255  10 9  full 983  1013 1111
11 11 full 909  1004 1084  12 6  part 387  853  999
13 4  part 476  530  627   14 6  full 780  843  925
15 10 full 717  1200 1399
;

/*creating longform dataset*/
```

```
data longform;
set deptstore;
  array y[3] (1.8 1.9 2.0);
 array b[3] bonus18-bonus20;
  do i=1 to 3;
    year=y[i];
    bonus=b[i];
     output;
  end;
keep id totalyears status year bonus;
run;

/*checking normality of response*/
proc univariate;
 var bonus;
 histogram bonus/normal;
run;
```



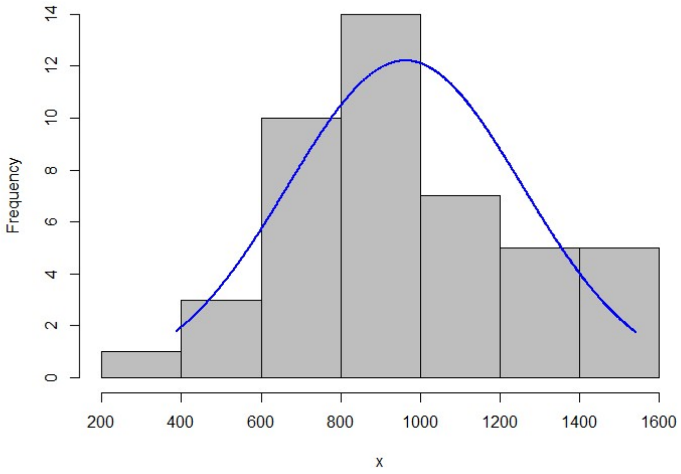
```
  Goodness-of-Fit Tests for Normal Distribution
Test                 Statistic       p Value
Kolmogorov-Smirnov D    0.12045943 Pr > D    0.098
Cramer-von Mises   W-Sq 0.08690779 Pr > W-Sq 0.168
Anderson-Darling   A-Sq 0.51592849 Pr > A-Sq 0.189
```

The histogram is roughly bell shaped, and the normality tests all have p-values above 0.05, indicating a normal distrubition of bonus.

In R:

```
deptstore.data<- read.csv(file='C:/<insert path>/Exercise8.2Data.csv',
header=TRUE, sep=',')

#creating longform dataset
library(reshape2)
longform.data<- melt(deptstore.data, id.vars=c('id','totalyears','status'),
variable.name='bonus.year', value.name='bonus')
```

```
year<- ifelse(longform.data$bonus.year=='bonus18',1.8,
ifelse(longform.data$bonus.year=='bonus19',1.9,2.0))

#checking normality of response
library(rcompanion)
plotNormalHistogram(longform.data$bonus)
```



```
shapiro.test(longform.data$bonus)
```

```
Shapiro-Wilk normality test

W = 0.96686, p-value = 0.222
```

(a) Fit a random slope and intercept model regressing bonus on years with the company, status, and year (scaled by a factor of 10). Does the model fit the data well?

In SAS:

```
/*fitting random slope and intercept model*/
proc mixed covtest;
 class status;
  model bonus = totalyears status year / solution;
   random intercept year / subject=id type=un;
run;
```

```
         Covariance Parameter Estimates
Cov Parm Subject Estimate Standard Z Value  Pr Z
                           Error
UN(1,1)  id       2249551  1204315    1.87 0.0309
UN(2,1)  id      -1194782   637878   -1.87 0.0611
UN(2,2)  id        636730   338378    1.88 0.0299
Residual          4608.43  1682.76    2.74 0.0031

              Solution for Fixed Effects
Effect     status Estimate Standard DF t Value Pr > |t|
                            Error
Intercept         -2246.11   457.20 12   -4.91   0.0004
totalyears         58.8982   8.2368 15    7.15   <.0001
status     full    53.9643  63.3473 15    0.85   0.4077
```

```
              Solution for Fixed Effects
Effect     status Estimate Standard DF t Value Pr > |t|
                              Error
status     part          0        . .       .        .
year              1394.67   240.44 14    5.80   <.0001


Null Model Likelihood Ratio Test
 DF    Chi-Square     Pr > ChiSq
  3         10.93         0.0121
```

The deviance test has the p-value below 0.05, which confirms the model's good fit. Also, the parameters of the random-effect terms are significant at the 5% level. The covariance between the random slope and intercept is marginally significant with the p-value of 0.0611. So, using the random slope and intercept model is justified.

In R:

```
#creating reference level
status.rel<- relevel(longform.data$status, ref="part")

#fitting random slope and intercept model
library(nlme)
summary(fitted.model<- lme(bonus ~ totalyears + status.rel + year,
random = ~ 1 + year | id, data=longform.data))
```

```
Random effects:
                StdDev   Corr
(Intercept) 1499.85877  (Intr)
year         797.95782  -0.998
Residual      67.88526

Fixed effects:
                    Value  Std.Error  DF   t-value  p-value
(Intercept)     -2246.1138  457.2023  29 -4.912735    0.000
totalyears         58.8982    8.2368  12  7.150631    0.000
status.relfull     53.9643   63.3473  12  0.851879    0.411
year             1394.6667  240.4381  29  5.800523    0.000
```

```
intervals(fitted.model)
```

```
 Random Effects:
                          lower           est.          upper
sd((Intercept))        891.8860755     1499.8587688     2522.2686935
sd(year)               476.3219559      797.9578238     1336.7779518
cor((Intercept),year)   -0.9995787       -0.9983042       -0.9931881
```

```
#checking model fit
null.model<- glm(bonus ~ totalyears + status.rel + year, data=longform.data)
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

45.81206

```
print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))
'
```

6.218073e-10

(c) Write down the fitted model, specifying all estimated parameters. What predictors are significant at the 5% significance level?

The fitted model has the form $\hat{E}(bonus) = -2246.11 + 58.8982 \cdot total\ years + 53.9643 \cdot full\text{-}time\ employee + 1394.67 \cdot year/10$. The other parameters have estimates $\hat{\sigma}_{u_1}^2 = 2249551, \hat{\sigma}_{u_2}^2 = 636730, \hat{\sigma}_{u_1 u_2} = -1194782,$ and $\hat{\sigma}^2 = 4608.43.$
Total years with the company and year are significant predictors at the 5% level.

(d) Give interpretation of the estimated significant regression coefficients.

As the total number of years with the company increases by one, the average bonus increases by \$58.8982. As year increases by one, the average bonus increases by \$1394.67/10=\$139.467.

(e) According to the fitted model, what is the predicted bonus in 2021 for a full-time employee who has been with the company for 7 years?

The predicted value is $bonus^0 = -2246.11 + 58.8982 \cdot 7 + 53.9643 + 1394.67 \cdot \frac{21}{10} =$ \$1,148.949.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input id totalyears status$ year;
cards;
21 7 full 2.1
;

data longform;
set longform predict;
run;

proc mixed covtest;
 class status;
  model bonus = totalyears status year / solution outpm=outdata;
   random intercept year / subject=id type=un;
run;

proc print data=outdata (firstobs=46) noobs;
 var Pred;
run;
```

```
   Pred
1148.94
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(status.rel='full', totalyears=7,
year=2.1), level=0))
```

```
1148.938
```

EXERCISE 8.3. (a) Create a long-form data set.

In SAS:

```
data orthoclinic;
input id gender$ age doctor$ length1 length2 length3 score1 score2 score3 @@;
cards;
101 F 78 A 25 20 25 7.1  7.5  7.6  102 F 63 A 30 30 40 5.5 5.8 6.1
103 F 62 A 10 15 10 10.0 10.0 9.8  104 F 71 B 15 15 40 7.8 7.3 7.5
105 M 68 A 40 60 40 3.5  3.5  3.0  106 F 63 A 25 15 20 8.5 8.7 8.8
107 F 60 B 25 35 25 6.7  5.7  6.5  108 F 70 A 20 20 20 9.0 8.3 8.2
109 F 57 A 30 20 15 8.4  7.8  8.1  110 F 59 B 25 30 15 7.1 7.4 7.9
111 M 62 A 50 30 70 3.0  3.2  2.6  112 M 58 A 20 15 45 6.1 6.8 6.9
113 M 75 A 25 35 30 5.7  5.6  4.7  114 M 76 B 35 50 25 4.9 5.4 5.2
115 F 75 A 15 20 25 8.2  8.9  8.2  116 M 57 A 45 30 40 4.6 3.9 3.2
117 F 68 A 35 25 40 3.8  4.8  5.3  118 M 65 B 40 40 25 3.9 3.9 4.7
119 F 67 B 20 15 30 6.5  7.2  6.6  120 F 60 B 25 15 15 7.3 7.1 7.8
121 F 67 A 15 20 15 7.7  8.0  8.3  122 F 57 B 10 15 15 9.8 9.2 8.6
123 M 62 B 55 60 75 3.4  2.7  2.3  124 M 71 A 20 30 25 7.1 6.6 7.4
125 M 71 B 15 15 20 8.8  9.1  9.3  126 M 64 A 25 30 30 5.6 6.3 6.3
127 M 51 A 35 40 30 5.1  4.6  3.9  128 F 70 B 35 25 15 6.8 7.1 7.6
129 M 61 A 35 40 50 5.5  5.2  4.8  130 M 62 B 60 40 65 3.7 3.4 2.4
131 F 68 A 20 35 35 5.3  5.6  4.9  132 F 68 B 35 30 15 7.2 6.2 5.6
133 M 64 B 40 20 30 5.4  4.9  4.5  134 F 76 B 30 45 25 5.5 4.7 4.6
135 F 78 B 25 20 15 7.6  8.3  9.2
;

/*creating longform dataset*/
data longform;
set orthoclinic;
 array l[3] length1-length3;
 array s[3] score1-score3;
  do visit=1 to 3;
  length=l[visit];
  score=s[visit];
   output;
    end;
keep id gender age doctor visit length score;
run;
```

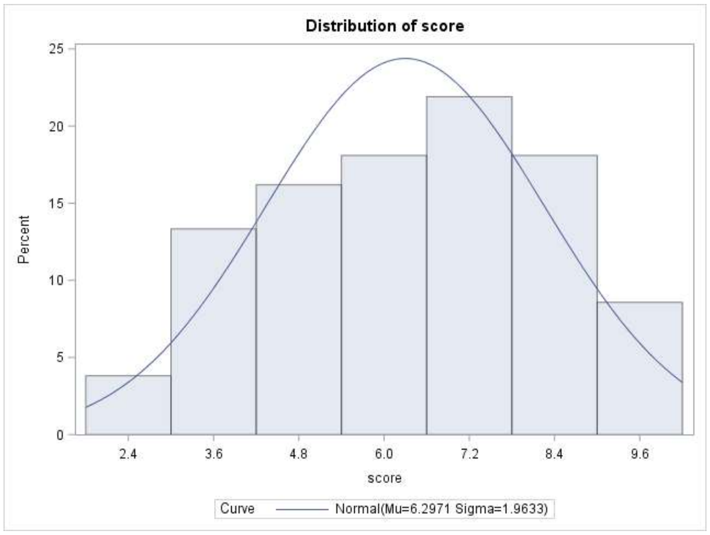
In R:

```
orthoclinic.data<- read.csv(file='C:/<insert path>/Exercise8.3Data.csv',
header=TRUE, sep=',')

#creating longform dataset
library(reshape2)
data1<- melt(orthoclinic.data[,c('id','gender','age','doctor','length1',
'length2','length3')],id.vars=c('id','gender','age','doctor'),
variable.name='length.visit',value.name='length')
data2<- melt(orthoclinic.data[,c('score1','score2','score3')],
variable.name='score.visit', value.name='score')
longform.data<- cbind(data1,data2)
visit<- ifelse(longform.data$score.visit=='score1',1,
ifelse(longform.data$score.visit=='score2',2,3))
```

(b) Confirm that the quality of service is normally distributed by plotting a histogram and conducting normality tests.

In SAS:

```
/*checking normality of response*/
proc univariate;
 var score;
  histogram score/normal;
run;
```

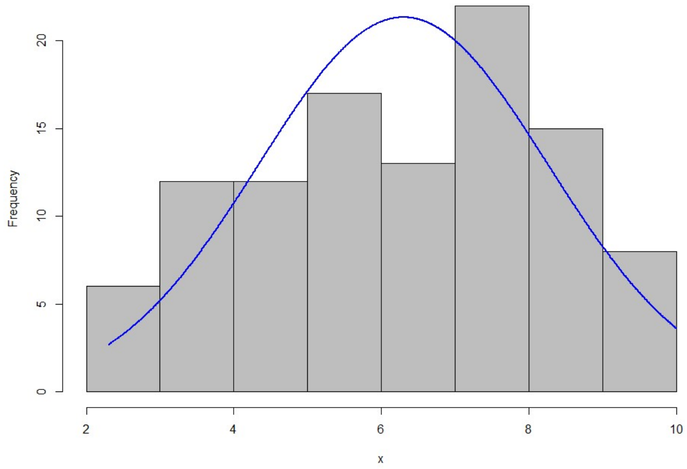


```
  Goodness-of-Fit Tests for Normal Distribution
Test                 Statistic        p Value
Kolmogorov-Smirnov D     0.08727378 Pr > D     0.048
Cramer-von Mises   W-Sq 0.10666743 Pr > W-Sq 0.093
Anderson-Darling   A-Sq 0.64603497 Pr > A-Sq 0.092
```

The p-values in the normality tests are above 0.05, indicating a normal distribution. The histogram is approximately bell-shaped.

In R:

```
#plotting histogram and checking normality
library(rcompanion)
plotNormalHistogram(longform.data$score)
```



```
shapiro.test(longform.data$score)
```

```
Shapiro-Wilk normality test

W = 0.97598, p-value = 0.05332
```

(c) Fit a random slope and intercept model to regress the quality of service scores on all the predictor variables. Discuss the model fit.

In SAS:

```
/*fitting random slope and intercept model*/
proc mixed covtest;
 class gender doctor;
  model score = gender age doctor length visit / solution;
   random intercept visit / subject=id type=un;
run;
```

```
         Covariance Parameter Estimates
Cov Parm Subject Estimate Standard Z Value   Pr Z
                             Error
UN(1,1)  id        2.2772   0.6365    3.58 0.0002
UN(2,1)  id       -0.1369   0.1277   -1.07 0.2835
UN(2,2)  id        0.1376  0.04432    3.10 0.0010
Residual          0.08137  0.01984    4.10 <.0001


                 Solution for Fixed Effects
Effect    gender doctor Estimate Standard DF t Value Pr > |t|
                                    Error
Intercept                 5.2216   2.5708 31    2.03   0.0509
gender    F               2.0847   0.5199 34    4.01   0.0003
gender    M                    0        .  .       .        .
age                     0.002997  0.03854 34    0.08   0.9385
doctor           A        0.1585   0.5085 34    0.31   0.7572
doctor           B             0        .  .       .        .
length                  -0.01051 0.004784 34   -2.20   0.0349
visit                   -0.04610  0.07144 34   -0.65   0.5230
```

```
Null Model Likelihood Ratio Test
  DF    Chi-Square    Pr > ChiSq
   3         93.29        <.0001
```

The model has a good fit since the p-value of the deviance test is below 0.05.

In R:

```
#specifying reference levels
gender.rel<- relevel(longform.data$gender, ref="M")
doctor.rel<- relevel(longform.data$doctor, ref="B")

#fitting random slope and intercept model
library(nlme)
summary(fitted.model<- lme(score ~ gender.rel + age + doctor.rel
+ length + visit, random = ~ 1 + visit | id, data=longform.data))
```

```
Random effects:
            StdDev    Corr
(Intercept) 1.5090310 (Intr)
visit       0.3709390 -0.245
Residual    0.2852501
Fixed effects:
                Value Std.Error DF   t-value p-value
(Intercept)  5.221580 2.5707920 68  2.031117  0.0462
gender.relF  2.084700 0.5198854 31  4.009921  0.0004
age          0.002997 0.0385434 31  0.077755  0.9385
doctor.relA  0.158469 0.5084557 31  0.311668  0.7574
length      -0.010510 0.0047844 68 -2.196820  0.0314
visit       -0.046100 0.0714364 68 -0.645336  0.5209
```

```
intervals(fitted.model)
```

```
Random Effects:
                           lower       est.     upper
sd((Intercept))        1.1473569  1.5090310    1.9847134
sd(visit)              0.2705064  0.3709390    0.5086597
cor((Intercept),visit) -0.5845323 -0.2446523    0.1682708
```

```
#checking model fit
null.model<- glm(score ~ gender.rel + age + doctor.rel + length + visit,
data=longform.data)
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
72.63075
```

```
print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))
```

```
1.166255e-15
```

(d) What parameters of the random terms are significant at the 5% level? Are the scores for each patient correlated?

At the 5% level, variances of the random slope, intercept, and random error are significant. The covariance between the intercept and slope is not significant. The scores for each patient are correlated and the use of mixed-effects model is justified.

(e) What fixed-effects variables are significant predictors at the 5% significance level? Write down the fitted model.

Gender and length of visit are significant predictors of score at the 5% level. The fitted model is $\hat{E}(score) = 5.2216 + 2.0847 \cdot female + 0.002997 \cdot age + 0.1585 \cdot doctor\ A - 0.01051 \cdot visit\ length - 0.04610 \cdot visit\ number$. The other parameters have estimates $\hat{\sigma}_{u_1}^2 = 2.2772, \hat{\sigma}_{u_2}^2 = 0.1376, \hat{\sigma}_{u_1 u_2} = -0.1369,$ and $\hat{\sigma}^2 = 0.08137$.

(f) Interpret the estimates of the significant regression coefficients.

The estimated mean score for female patients is 2.0847 points larger than that for male patients. As the length of doctor's visit increases by one minute, the estimated mean score decreases by 0.01051 points.

(g) Predict the quality of service score that would be given by a 55-year-old male patient on his fourth visit to Dr. A with a 30-minute appointment.

Prediction is done according the following calculation: $score^0 = 5.2216 + 0.002997 \cdot 55 + 0.1585 - 0.01051 \cdot 30 - 0.04610 \cdot 4 = 5.045235$.
In SAS:

```
/*using fitted model for prediction*/
data predict;
input id gender$ age doctor$ length visit;
cards;
136 M 55 A 30 4
;

data longform;
set longform predict;
run;

proc mixed covtest;
 class gender doctor;
  model score = gender age doctor length visit / outpm=outdata;
   random intercept visit / subject=id type=un;
run;

proc print data=outdata (firstobs=106) noobs;
 var Pred;
run;
```

```
   Pred
5.04517
```

In R:

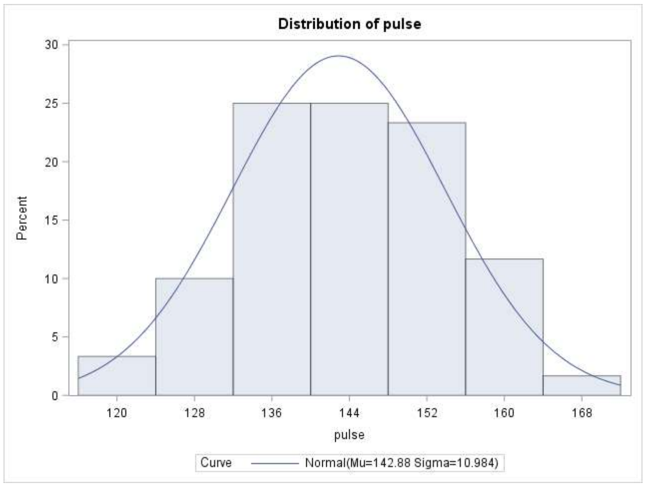
```
#using fitted model for prediction
print(predict(fitted.model, data.frame(id=136,gender.rel='M',age=55,
doctor.rel='A',length=30,visit=4),level=0))
```

```
5.045167
```

EXERCISE 8.4. (a) Check that pulse has normal distribution. Construct a histogram and conduct normality tests.

In SAS:

```
data fitness;
input id gender$ age oxygen1 runtime1 pulse1 oxygen2 runtime2 pulse2
oxygen3 runtime3 pulse3;
cards;
1  F 39 37.4 11.4 151 36.6 17.8 158 36.1 15.4 152
2  M 42 60.1 11.5 121 59.0 9.6  131 58.2 9.0  143
3  F 34 44.6 9.6  138 39.8 9.3  148 38.8 9.1  144
4  M 36 51.9 10.5 125 53.4 9.8  135 50.4 9.6  163
5  F 45 40.8 13.1 142 39.5 12.4 151 38.5 12.7 133
6  M 37 45.4 10.3 133 40.6 11.9 145 40.2 11.2 141
7  F 49 45.3 13.1 135 40.6 12.1 148 39.7 11.5 157
8  F 47 44.8 12.1 135 40.1 12.3 148 39.0 11.9 151
9  M 50 48.7 12.6 131 42.3 11.0 143 44.3 10.5 150
10 M 34 45.8 10.8 132 40.9 11.8 144 41.1 11.1 160
11 M 35 50.4 9.6  129 45.9 10.4 137 44.8 10.4 138
12 M 48 50.5 12.9 125 48.6 10.3 135 49.0 9.8  132
13 F 50 44.8 14.0 135 40.3 13.1 148 39.5 12.6 163
14 F 53 39.4 12.7 145 39.3 14.1 154 37.0 12.8 148
15 M 44 46.1 11.0 132 40.9 11.3 144 41.1 10.8 148
16 F 32 39.2 9.1  146 38.7 9.7  158 36.7 10.2 170
17 M 39 54.3 9.4  123 55.1 9.7  132 57.4 9.4  162
18 F 33 39.4 11.6 144 39.4 12.7 154 37.4 12.7 155
19 M 33 47.9 10.1 132 42.2 11.2 143 42.6 10.6 140
20 M 46 49.2 11.2 130 43.9 10.8 141 44.7 10.5 142
;

/*creating longform dataset*/
data longform;
set fitness;
 array o[3] oxygen1-oxygen3;
 array r[3] runtime1-runtime3;
 array p[3] pulse1-pulse3;
  do condition=1 to 3;
  oxygen=o[condition];
  runtime=r[condition];
  pulse=p[condition];
  output;
   end;
keep id gender age oxygen runtime pulse condition;
run;

/*checking normality of response*/
proc univariate;
 var pulse;
  histogram pulse/normal;
run;
```

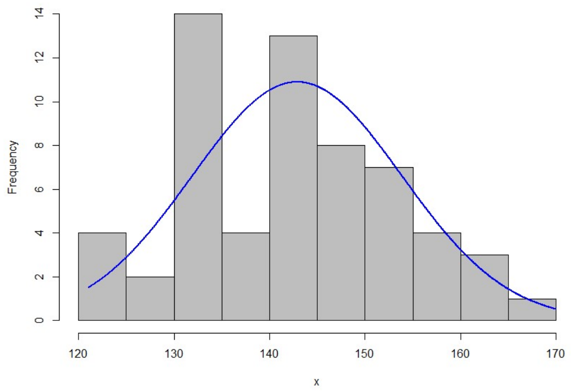


```
  Goodness-of-Fit Tests for Normal Distribution
Test                 Statistic       p Value
Kolmogorov-Smirnov D    0.09686645 Pr > D    >0.150
Cramer-von Mises   W-Sq 0.05033026 Pr > W-Sq >0.250
Anderson-Darling   A-Sq 0.32350837 Pr > A-Sq >0.250
```

A normal distribution is supported by the normality tests with the p-values in excess of 0.05. The histogram is roughly bell-shaped.

In R:

```
fitness.data<- read.csv(file='C:/<insert path>/Exercise8.4Data.csv',
header=TRUE, sep=',')

#creating longform dataset
library(reshape2)
data1<- melt(fitness.data[,c('id','gender','age','oxygen1','oxygen2','oxygen3')],
id.vars=c('id','gender','age'),variable.name='oxygen.cond',value.name='oxygen')
data2<- melt(fitness.data[,c('runtime1','runtime2','runtime3')],variable.name=
'runtime.cond',value.name='runtime')
data3<- melt(fitness.data[,c('pulse1','pulse2','pulse3')],variable.name=
'pulse.cond',value.name='pulse')
longform.data<- cbind(data1,data2,data3)
condition<- ifelse(longform.data$pulse.cond=='pulse1',1,
ifelse(longform.data$pulse.cond=='pulse2',2,3))

#checking normality of response
library(rcompanion)
plotNormalHistogram(longform.data$pulse)
```



```
shapiro.test(longform.data$pulse)
```

```
Shapiro-Wilk normality test

W = 0.98398, p-value = 0.6173
```

(b) Run a random slope and intercept regression model for pulse. Discuss the model fit.

In SAS:

```
/*fitting random slope and intercept model*/
proc mixed covtest;
 class gender;
  model pulse = gender age oxygen runtime condition / solution;
   random intercept condition / subject=id type=un;
run;
```

```
         Covariance Parameter Estimates
Cov Parm Subject Estimate Standard Z Value   Pr Z
                          Error
UN(1,1)  id       37.5141 32.7975    1.14 0.1264
UN(2,1)  id      -38.6973 20.9652   -1.85 0.0649
UN(2,2)  id       33.0452 14.6562    2.25 0.0121
Residual          21.0330  6.7194    3.13 0.0009
```

```
              Solution for Fixed Effects
Effect    gender Estimate Standard DF t Value Pr > |t|
                          Error
Intercept          172.88   8.7340 17   19.79   <.0001
gender    F        4.7249   1.4230 18    3.32   0.0038
gender    M             0        .  .       .        .
age               -0.1747   0.1019 18   -1.71   0.1038
oxygen            -0.9634   0.1325 18   -7.27   <.0001
runtime            0.4824   0.5270 18    0.92   0.3721
condition          6.0839   1.4984 19    4.06   0.0007
```

```
Null Model Likelihood Ratio Test
 DF     Chi-Square      Pr > ChiSq
  3          28.24          <.0001
```

The model fits the data well as indicated by the small p-value in the deviance test.

In R:

```
#specifying reference level
gender.rel<- relevel(longform.data$gender, ref="M")

#fitting random slope and intercept model
library(nlme)
summary(fitted.model<- lme(pulse ~ gender.rel + age + oxygen + runtime
+ condition, random = ~ 1 + condition | id, control= lmeControl(opt='optim'),
data=longform.data))
```

```
Random effects:
            StdDev   Corr
(Intercept) 8.007742 (Intr)
condition   6.091466 -0.999
Residual    3.938579

Fixed effects:
                Value Std.Error DF   t-value p-value
(Intercept) 169.71035 10.731555 37 15.814143  0.0000
gender.relF   4.78210  1.856487 17  2.575887  0.0196
age          -0.19789  0.124495 17 -1.589534  0.1304
oxygen       -0.90924  0.167780 37 -5.419243  0.0000
runtime       0.61422  0.591748 37  1.037967  0.3060
condition     6.19390  1.531663 37  4.043907  0.0003
```

```
intervals(fitted.model)
```

```
Random Effects:
                               lower       est.     upper
sd((Intercept))             4.945192  8.0077424 12.966926
sd(condition)               4.130192  6.0914661  8.984077
cor((Intercept),condition) -1.000000 -0.9992616  0.798489
```

```
#checking model fit
null.model<- glm(pulse ~ gender.rel + age + oxygen + runtime + condition,
data=longform.data)
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
29.29234
```

```
print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))
```

```
1.944012e-06
```

Note that is this exercise, SAS and R give slightly different estimates of the model parameters.

(c) Specify the fitted model. What parameters of the random-effects terms are significant at the 5% level? At the 10% level? What fixed-effects terms are significant at the 5% level?

The fitted model in SAS is $\hat{E}(pulse) = 172.88 + 4.7249 \cdot female - 0.1747 \cdot age - 0.9634 \cdot oxygen + 0.4824 \cdot runtime + 6.0839 \cdot condition.$ The estimates of the other model parameters are $\hat{\sigma}_{u_1}^2 = 37.5141, \hat{\sigma}_{u_2}^2 = 33.0452, \hat{\sigma}_{u_1 u_2} = -38.6973,$ and $\hat{\sigma}^2 = 21.033.$

The fitted model in R is $\hat{E}(pulse) = 169.71035 + 4.7821 \cdot female - 0.19789 \cdot age - 0.90924 \cdot oxygen + 0.61422 \cdot runtime + 6.1939 \cdot condition$. The estimates of the other model parameters are $\hat{\sigma}_{u_1} = 8.009942,\ \hat{\sigma}_{u_2} = 6.091466, \hat{\rho}_{u_1 u_2} = -0.999,$ and $\hat{\sigma} = 3.938579$.

At the 5% level, the variance of the random slope is significant. At the 10%, the covariance between the random intercept and slope is significant. As for the fixed-effects terms, gender, oxygen intake, and running condition are significant predictors.

(d) Interpret the estimated regression coefficients for the significant fixed-effects terms.

For female runners, the estimated average pulse is 4.78 points larger than that for male runners. As oxygen intake increases by one unit, the estimated mean pulse decreases by 0.96 (0.91) points. As the condition number increases by one, the estimated mean pulse increases by 6.08 (6.19) points.

(e) Predict an average heart rate for a 36-year-old woman who is running on a treadmill, if her oxygen intake is 40.2 units, and her run time is 10.3 minutes per mile.

The following calculations yield the predicted value. Using the model fitted in SAS,

$$pulse^0 = 172.88 + 4.7249 - 0.1747 \cdot 36 - 0.9634 \cdot 40.2 + 0.4824 \cdot 10.3 + 6.0839 = 143.6396.$$

Using the model fitted in R, $pulse^0 = 169.71035 + 4.7821 - 0.19789 \cdot 36 - 0.90924 \cdot 40.2 + 0.61422 \cdot 10.3 + 6.1939 = 143.3373$.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input id gender$ age oxygen runtime condition;
cards;
21 F 36 40.2 10.3 1
;

data longform;
set longform predict;
run;

proc mixed covtest;
 class gender;
  model pulse = gender age oxygen runtime condition / outpm=outdata;
   random intercept condition / subject=id type=un;
run;

proc print data=outdata (firstobs=61) noobs;
 var Pred;
run;
```

```
Pred
143.643
```

In R:

```
#using fitted model for prediction
```

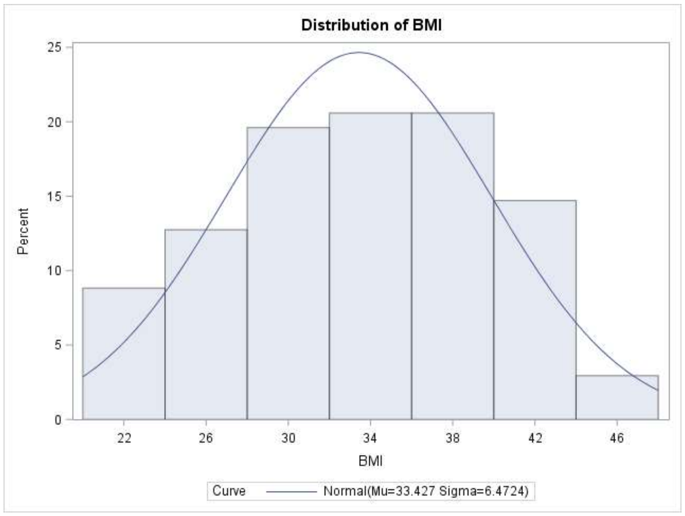
```
print(predict(fitted.model, data.frame(id=21, gender.rel='F', age=36,
oxygen=40.2, runtime=10.3, condition=1),level=0))
```

```
143.3374
```

EXERCISE 8.5. (a) Verify normality of the response variable BMI by plotting the histogram and carrying out normality tests.

In SAS:

```
data weightloss;
input id group$ gender$ aexercise aBMI bexercise bBMI cexercise cBMI @@;
cards;
1  Int F 0  42.4 50 40.0 120 36.8  2  Int F 15 32.9 20 30.6 25  28.6
3  Int M 10 32.0 30 30.8 30  26.1  4  Int M 20 26.1 80 25.5 80  21.1
5  Int F 0  27.5 20 26.4 20  22.5  6  Int F 30 40.4 75 38.3 180 32.1
7  Int M 15 33.5 50 28.2 50  25.8  8  Int F 15 35.2 35 34.8 90  30.6
9  Int F 0  39.5 55 37.1 50  35.3  10 Int M 20 27.3 30 26.3 30  22.6
11 Int M 0  46.9 50 43.5 50  40.3  12 Int M 20 34.4 80 32.2 85  28.1
13 Int F 0  34.2 60 31.0 65  26.8  14 Int F 45 26.5 30 24.6 30  20.8
15 Int F 0  29.6 20 28.2 20  24.9  16 Int F 10 31.2 80 29.3 50  28.6
17 Cnt F 0  29.3 25 28.9 30  26.3  18 Cnt M 20 45.9 10 43.1 15  42.9
19 Cnt M 0  41.5 20 38.8 30  39.9  20 Cnt F 30 33.3 25 33.4 35  33.2
21 Cnt M 15 31.1 35 30.9 0   30.9  22 Cnt F 10 43.3 35 43.6 30  44.5
23 Cnt M 15 35.5 0  36.5 5   35.3  24 Cnt F 10 42.4 15 43.4 50  42.3
25 Cnt F 20 37.0 30 36.6 45  35.5  26 Cnt M 0  37.8 30 35.7 45  34.3
27 Cnt F 20 23.7 10 23.1 0   23.7  28 Cnt F 10 38.7 15 20.4 25  20.1
29 Cnt F 0  41.2 15 41.2 55  39.7  30 Cnt F 30 30.2 35 29.9 5   29.4
31 Cnt M 10 38.4 20 38.1 30  37.0  32 Cnt F 10 37.5 15 37.4 5   36.8
33 Cnt M 30 34.5 10 34.4 20  33.9  34 Cnt M 15 37.6 35 36.2 25  36.0
;

/*creating longform dataset*/
data longform;
set weightloss;
 array m[3] (0 1 3);
 array e[3] aexercise bexercise cexercise;
 array b[3] aBMI bBMI cBMI;
  do i=1 to 3;
  month=m[i];
  exercise=e[i];
  BMI=b[i];
  output;
  end;
keep id group gender exercise BMI month;
run;

/*checking normality of response*/
proc univariate;
 var BMI;
  histogram BMI/normal;
run;
```

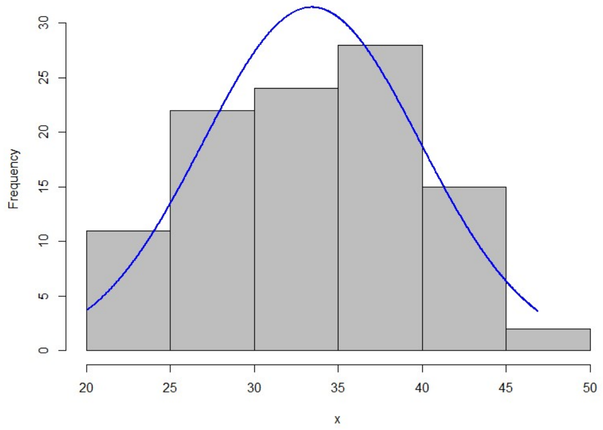


```
  Goodness-of-Fit Tests for Normal Distribution
Test                  Statistic        p Value
Kolmogorov-Smirnov D    0.04908222 Pr > D    >0.150
Cramer-von Mises   W-Sq 0.05735715 Pr > W-Sq >0.250
Anderson-Darling   A-Sq 0.37849800 Pr > A-Sq >0.250
```

On the graph we see a roughly bell-shaped histogram. In addition, the p-values in the normality tests are above 0.05, supporting normality of BMI.

In R:

```
weightloss.data<- read.csv(file='C:/<insert path>/Exercise8.5Data.csv',
header=TRUE, sep=',')

#creating longform dataset
library(reshape2)
data1<- melt(weightloss.data[,c('id','group','gender','aexercise','bexercise',
'cexercise')], id.vars=c('id','group','gender'),variable.name='exercise.visit',
value.name='exercise')
data2<- melt(weightloss.data[,c('aBMI','bBMI','cBMI')],variable.name=
'BMI.visit',value.name='BMI')
longform.data<- cbind(data1,data2)
month<- ifelse(longform.data$BMI.visit=='aBMI',0,
ifelse(longform.data$BMI.visit=='bBMI',1,3))

#checking normality of response
library(rcompanion)
plotNormalHistogram(longform.data$BMI)
```



```
shapiro.test(longform.data$BMI)
```

```
Shapiro-Wilk normality test

W = 0.98317, p-value = 0.2216
```

(b) Fit the random slope and intercept model. How good is the model fit?

In SAS:

```
/*fitting random slope and intercept model*/
proc mixed covtest;
 class group gender(ref='F');
  model BMI = group gender exercise month / solution;
   random intercept month / subject=id type=un;
run;
```

```
         Covariance Parameter Estimates
Cov Parm Subject Estimate Standard Z Value   Pr Z
                             Error
UN(1,1)  id       29.2800   8.1566    3.59 0.0002
UN(2,1)  id        2.5538   1.2409    2.06 0.0396
UN(2,2)  id        0.3306   0.3190    1.04 0.1501
Residual           3.4357   0.8496    4.04 <.0001
```

```
                Solution for Fixed Effects
Effect    group gender Estimate Standard DF t Value Pr > |t|
                                   Error
Intercept                34.5855   1.5561 31   22.23   <.0001
group     Cnt             1.1961   1.8719 33    0.64   0.5273
group     Int                  0        .  .       .        .
gender          M         1.2370   1.8969 33    0.65   0.5189
gender          F              0        .  .       .        .
exercise                -0.03974  0.01121 33   -3.54   0.0012
month                    -0.8445   0.2029 33   -4.16   0.0002
```

```
Null Model Likelihood Ratio Test
 DF    Chi-Square    Pr > ChiSq
  3        115.71        <.0001
```

The model has a very good fit because of a very small p-value in the deviance test.

In R:

```
#specifying reference levels
group.rel<- relevel(longform.data$group, ref="Int")
gender.rel<- relevel(longform.data$gender, ref="F")

#fitting random slope and intercept model
library(nlme)
summary(fitted.model<- lme(BMI ~ group.rel + gender.rel + exercise + month,
random = ~ 1 + month | id, data=longform.data))
```

```
Random effects:
            StdDev    Corr
(Intercept) 5.4112519 (Intr)
month       0.5749658 0.821
Residual    1.8535182

Fixed effects:
               Value   Std.Error  DF   t-value  p-value
 (Intercept)  34.58554 1.5561343 66 22.225291  0.0000
group.relCnt  1.19608  1.8719456 31  0.638949  0.5275
gender.relM   1.23698  1.8969761 31  0.652082  0.5192
exercise     -0.03974  0.0112112 66 -3.544454  0.0007
month        -0.84454  0.2028822 66 -4.162726  0.0001
```

```
intervals(fitted.model)
```

```
Random Effects:
                            lower      est.     upper
sd((Intercept))         4.1184307 5.4112519 7.1099041
sd(month)               0.2234017 0.5749658 1.4797814
cor((Intercept),month) -0.9626376 0.8207878 0.9996312
```

```
#checking model fit
null.model<- glm(BMI ~ gender.rel + group.rel + exercise + month,
data=longform.data)
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
115.6489
```

```
print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))
```

```
6.67375e-25
```

(c) Present the fitted model and specify all estimated parameters. Discuss significance of the parameters at the 5% significance level.

The fitted model is of the form $\hat{E}(BMI) = 34.5855 + 1.1961 \cdot control + 1.237 \cdot male - 0.03974 \cdot exercise - 0.8445 \cdot month.$ The estimates of the other model parameters are $\hat{\sigma}^2_{u_1} = 29.28, \hat{\sigma}^2_{u_2} = 0.3306, \hat{\sigma}_{u_1 u_2} = 2.5538,$ and $\hat{\sigma}^2 = 3.4357.$
At the 5% level of significance, length of daily exercise and month are significant predictors, and the variance of the random intercept and the covariance between intercept and slope are significant, validating the need for random-effect terms in the model.

(d) Give interpretation of the estimated significant beta coefficients. Is the intervention efficient?

As the length of daily exercise increases by one minute, the estimated average BMI decreases by 0.03974 units. It is estimated that the average BMI decreases by 0.8445 units for every additional month in the study.

(e) Compute the predicted BMI at 3 months for an intervention group female participant, if she exercises for 1 hour every day.

Predicted BMI is $BMI^0 = 34.5855 - 0.03974 \cdot 60 - 0.8445 \cdot 3 = 29.6676$.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input id group$ gender$ exercise month;
cards;
35 Int F 60 3
;

data longform;
set longform predict;
run;

proc mixed covtest;
 class group gender;
  model BMI = group gender exercise month / outpm=outdata;
   random intercept month / subject=id type=un;
run;

proc print data=outdata (firstobs=103) noobs;
 var Pred;
run;
```

```
   Pred
29.6676
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(id=35, gender.rel='F', group.rel='Int',
exercise=60, month=3),level=0))
```

```
29.66766
```

EXERCISE 8.6. Consider the data in Exercise 8.2. Answer the questions below.

(a) Fit random slope and intercept models with unstructured, Toeplitz, spatial power, autoregressive, compound symmetric, and independent covariance matrices for error terms. Present the AIC, AICC, and BIC criteria values for those models that converge. If the random slope and intercept model doesn't converge, try to fit a random intercept-only model.

In SAS:

```
data deptstore;
input id totalyears status$ bonus18 bonus19 bonus20 @@;
cards;
1  16 full 1482 1508 1543  2  7  part 673  710  895
3  11 full 933  1351 1440  4  8  part 844  958  1196
5  6  part 564  790  815   6  5  full 601  708  780
7  6  part 775  822  902   8  17 full 1209 1297 1475
9  12 full 929  1008 1255  10 9  full 983  1013 1111
11 11 full 909  1004 1084  12 6  part 387  853  999
13 4  part 476  530  627   14 6  full 780  843  925
15 10 full 717  1200 1399
;

/*creating longform dataset*/
data longform;
set deptstore;
  array y[3] (1.8 1.9 2.0);
 array b[3] bonus18-bonus20;
  do i=1 to 3;
    year=y[i];
    bonus=b[i];
     output;
  end;
keep id totalyears status year bonus;
run;

 /*fitting random slope and intercept model with
 unstructured covariance matrix of error terms*/
 proc mixed covtest;
  class status;
   model bonus = totalyears status year / solution;
    random intercept year / subject=id type=un;
    repeated / subject=id type=un;
 run;
```

```
        Fit Statistics
AIC (Smaller is Better)  566.3
AICC (Smaller is Better) 572.1
BIC (Smaller is Better)  572.7
```

```
/*fitting random slope and intercept model with
Toeplitz covariance matrix of error terms*/
proc mixed covtest;
 class status;
  model bonus = totalyears status year / solution;
   random intercept year / subject=id type=un;
   repeated / subject=id type=toep;
run;
```

```
        Fit Statistics
AIC (Smaller is Better)  524.4
AICC (Smaller is Better) 526.9
BIC (Smaller is Better)  528.6
```

```
/*fitting random slope and intercept model with
spatial power covariance matrix of error terms*/
```

```
proc mixed covtest;
 class status;
  model bonus = totalyears status year / solution;
   random intercept year / subject=id type=un;
   repeated / subject=id type=sp(pow)(year) r;
run;
```

```
WARNING: Did not converge.
```

```
/*fitting random intercept-only model with spatial
power covariance matrix of error terms*/
proc mixed covtest;
 class status;
  model bonus = totalyears status year / solution;
   random intercept / subject=id type=un;
   repeated / subject=id type=sp(pow)(year);
run;
```

```
        Fit Statistics
AIC (Smaller is Better)  518.3
AICC (Smaller is Better) 518.6
BIC (Smaller is Better)  519.7
```

```
/*fitting random slope and intercept model with
autoregressive covariance matrix of error terms*/
proc mixed covtest;
 class status;
  model bonus = totalyears status year / solution;
   random intercept year / subject=id type=un;
   repeated /subject=id type=ar(1);
run;
```

```
        Fit Statistics
AIC (Smaller is Better)  520.4
AICC (Smaller is Better) 521.6
BIC (Smaller is Better)  523.3
```

```
/*fitting random slope and intercept model with
compound symmetric covariance matrix of error terms*/
proc mixed covtest;
 class status;
  model bonus = totalyears status year / solution;
   random intercept year / subject=id type=un;
   repeated / subject=id type=cs;
run;
```

```
        Fit Statistics
AIC (Smaller is Better)  523.3
AICC (Smaller is Better) 525.0
BIC (Smaller is Better)  526.9
```

```
/*fitting random slope and intercept model with
independent covariance matrix of error terms*/
proc mixed covtest;
 class status;
  model bonus = totalyears status year / solution;
   random intercept year / subject=id type=un;
```

```
run;
```

```
       Fit Statistics
AIC (Smaller is Better)  521.3
AICC (Smaller is Better) 522.4
BIC (Smaller is Better)  524.1
```

In R:

```
deptstore.data<- read.csv(file='C:/<insert path>/Exercise8.2Data.csv',
header=TRUE, sep=',')

#creating longform dataset
library(reshape2)
longform.data<- melt(deptstore.data, id.vars=c('id','totalyears','status'),
variable.name='bonus.year', value.name='bonus')
year<- ifelse(longform.data$bonus.year=='bonus18',1.8,
ifelse(longform.data$bonus.year=='bonus19',1.9,2.0))

#rescaling response and creating reference level
status.rel<- relevel(longform.data$status, ref="part")

#fitting random slope and intercept model with
#unstructured covariance matrix of error terms
library(nlme)
summary(un.fitted.model<- lme(bonus ~ totalyears + status.rel + year,
random = ~ 1 + year | id, data=longform.data, correlation=corSymm(),
weights=varIdent(form = ~ id | year)))
```

```
    AIC      BIC
529.393 551.6694
```

```
#computing AICC
n<- 45
p<- 14
print(AICC<- -2*logLik(un.fitted.model)+2*p*n/(n-p-1))
```

```
545.393
```

```
#fitting random slope and intercept model with
#Toeplitz covariance matrix of error terms
summary(toep.fitted.model<- lme(bonus ~ totalyears + status.rel + year,
random = ~ 1 + year| id, data=longform.data,
correlation=corARMA(form = ~ 1 | id, p=1, q=1)))
```

```
    AIC      BIC
532.5445 549.6802
```

```
#computing AICC
p<-11
print(AICC<- -2*logLik(toep.fitted.model)+2*p*n/(n-p-1))
```

```
542.5445
```

```
#fitting random slope and intercept model with
#spatial power covariance matrix of error terms
summary(sppow.fitted.model<- lme(bonus ~ totalyears + status.rel + year,
random = ~ 1 + year | id, data=longform.data,
correlation=corCAR1(form = ~ 1 | id)))
```

```
      AIC      BIC
 532.8405 548.2627
```

```
#computing AICC
p<- 10
print(AICC<- -2*logLik(sppow.fitted.model)+2*p*n/(n-p-1))
```

```
 541.3111
```

```
#fitting random intercept-only model with
#spatial power covariance matrix of error terms
summary(sppowint.fitted.model<- lme(bonus ~ totalyears + status.rel + year,
random = ~ 1 | id, data=longform.data,
correlation=corCAR1(form = ~ 1 | id)))
```

```
     AIC      BIC
 528.8405 540.8355
```

```
#computing AICC
p<- 8
print(AICC<- -2*logLik(sppowint.fitted.model)+2*p*n/(n-p-1))
```

```
 534.8405
```

```
#fitting random slope and intercept model with
#autoregressive covariance matrix of error terms
summary(ar.fitted.model<- lme(bonus ~ totalyears + status.rel + year,
random = ~ 1 + year | id, data=longform.data,
correlation=corAR1(form = ~ 1 | id)))
```

```
      AIC      BIC
 532.8405 548.2627
```

```
#computing AICC
p<- 10
print(AICC<- -2*logLik(ar.fitted.model)+2*p*n/(n-p-1))
```

```
 541.3111
```

```
#fitting random slope and intercept model with
#compound symmetric covariance matrix of error terms
summary(cs.fitted.model<- lme(bonus ~ totalyears + status.rel + year,
random = ~ 1 + year | id, data=longform.data,
correlation=corCompSymm(form = ~ 1 | id)))
```

```
      AIC      BIC
 531.3133 546.7355
```

```
#computing AICC
p<- 10
print(AICC<- -2*logLik(cs.fitted.model)+2*p*n/(n-p-1))
```

```
 539.7839
```

```
fitting random slope and intercept model with
#independent covariance matrix of error terms
summary(ind.fitted.model<- lme(bonus ~ totalyears + status.rel+ year,
random = ~ 1 + year | id, data=longform.data))
```

```
      AIC      BIC
 529.3133 543.0219
 #computing AICC
 p<- 8
 print(AICC<- -2*logLik(ind.fitted.model)+2*p*n/(n-p-1))
```

```
533.3133
```

(b) Find the optimal model with respect to the AIC, AICC, and BIC criteria, and answer questions (c)-(e) in Exercise 8.2, using the best-fitted model.

For the models fitted in SAS, the one with the smallest AIC, AICC, and BIC is the random intercept-only model with the spatial power covariance matrix of the error terms. The values are summarized below.

	UN	Toeplitz	Sp Power Intercept	AR	CS	Ind
AIC	566.3	524.4	518.3	520.4	523.3	521.3
AICC	572.1	526.9	518.6	521.6	525	522.4
BIC	572.7	528.6	519.7	523.3	526.9	524.1

For the models fitted in R, according to the AICC criterion, the optimal model is the one with the independent covariance matrix of the error terms. The random intercept-only model with a spatial power covariance structure has the best fit according to the AIC and BIC criteria. The values are summed up here:

	UN	Toeplitz	Sp Power	Sp Power Intercept	AR	CS	Ind
AIC	529.4	532.5	532.8	528.8	532.8	531.3	529.3
AICC	545.4	542.5	541.3	534.8	541.3	539.8	533.3
BIC	551.7	549.7	548.3	540.8	548.3	546.7	543.0

Finally, we answer questions (c)-(e) in Exercise 8.2, using the best-fitted model.

In SAS:

```
/*fitting random intercept-only model with spatial
power covariance matrix of error terms*/
proc mixed covtest;
 class status;
  model bonus = totalyears status year / solution;
   random intercept / subject=id type=un;
   repeated / subject=id type=sp(pow)(year) r;
run;
```

```
 Estimated R Matrix for Subject 1
   Row      Col1    Col2       Col3
     1     17533   10081    5184.54
     2     10081   17533      10081
     3   5184.54   10081      17533
```

```
         Covariance Parameter Estimates
Cov Parm Subject Estimate Standard Z Value   Pr Z
                          Error
UN(1,1)  id             0        .       .      .
SP(POW)  id      -0.00652  0.01657   -0.39 0.6938
Residual            17533  5112.34    3.43 0.0003

              Solution for Fixed Effects
Effect     status Estimate Standard DF t Value Pr > |t|
                           Error
Intercept         -2255.12   391.89 12   -5.75   <.0001
totalyears         60.0189   9.0505 29    6.63   <.0001
status     full    47.2877  69.6058 29    0.68   0.5023
status     part          0        . .        .        .
year               1394.67   202.89 29    6.87   <.0001
```

The fitted model is $\hat{E}(bonus) = -2255.12 + 60.0189 \cdot total\ years + 47.2877 \cdot$ *full-time employee* $+ 1394.67 \cdot year/10$. The random intercept has estimated variance of zero, that is, the mixed-effect terms are non-existent. The estimated covariance matrix of the error terms is block diagonal, with 15 blocks of the form $\begin{pmatrix} 17533 & 10081 & 5184.54 \\ 10081 & 17533 & 10081 \\ 5184.54 & 10081 & 17533 \end{pmatrix}$.

Total years with the company and the year the bonus was recorded are significant predictors of bonus. As the total number of years with the company increases by one, the estimated average bonus increases by $60.0189. Every year, the estimated average increase in bonus is $139.467.

In R:

```
#fitting random intercept-only model with
#spatial power covariance matrix of error terms
summary(sppowint.fitted.model<- lme(bonus ~ totalyears + status.rel + year,
random = ~ 1 | id, data=longform.data, correlation=corCAR1(form = ~ 1 | id)))

Random effects:
        (Intercept) Residual
StdDev:  0.01464535 130.9026

      Phi
0.5467992

Fixed effects:
                    Value Std.Error DF   t-value  p-value
(Intercept)    -2253.4538  386.4705 29 -5.830856   0.0000
totalyears        59.8379    8.9004 12  6.723065   0.0000
status.relfull    48.2277   68.4510 12  0.704558   0.4945
year            1394.6667  200.1013 29  6.969804   0.0000

intervals(sppowint.fitted.model)


 Random Effects:
                      lower       est.        upper
sd((Intercept)) 1.224958e-49 0.01464535 1.750969e+45

getVarCov(sppowint.fitted.model, type='conditional')

Conditional variance covariance matrix
        1       2       3
```

```
1 17135.0  9369.7  5123.3
2  9369.7 17135.0  9369.7
3  5123.3  9369.7 17135.0
```

To predict the amount of bonus in 2021 for a full-time employee who has been with the company for 7 years, we compute $bonus^0 = -2255.12 + 60.0189 \cdot 7 + 47.2877 + 1394.67 \cdot 2.1 = \$1{,}141.107$.

In SAS:

```
data predict;
input id totalyears status$ year;
cards;
21 7 full 2.1
;

data longform;
set longform predict;
run;

proc mixed covtest;
 class status;
  model bonus = totalyears status year / outpm=outdata;
   random intercept / subject=id type=un;
   repeated / subject=id type=sp(pow)(year);
run;

proc print data=outdata (firstobs=46) noobs;
 var Pred;
run;
```

```
   Pred
1141.10
```

In R:

```
print(predict(sppowint.fitted.model, data.frame(totalyears=7, status.rel='full',
year=2.1), level=0))
```

```
1142.439
```

EXERCISE 8.7. For the data in Exercise 8.3,
(a) Fit random slope and intercept models with unstructured, Toeplitz, spatial power, autoregressive, compound symmetric, and independent covariance matrices for error terms, whichever converge. Try to fit a random intercept-only model if convergence criteria are not met.

In SAS:

```
data orthoclinic;
input id gender$ age doctor$ length1 length2 length3 score1 score2 score3 @@;
cards;
101 F 78 A 25 20 25 7.1  7.5  7.6  102 F 63 A 30 30 40 5.5 5.8 6.1
103 F 62 A 10 15 10 10.0 10.0 9.8  104 F 71 B 15 15 40 7.8 7.3 7.5
```

```
105 M 68 A 40 60 40 3.5  3.5  3.0  106 F 63 A 25 15 20 8.5 8.7 8.8
107 F 60 B 25 35 25 6.7  5.7  6.5  108 F 70 A 20 20 20 9.0 8.3 8.2
109 F 57 A 30 20 15 8.4  7.8  8.1  110 F 59 B 25 30 15 7.1 7.4 7.9
111 M 62 A 50 30 70 3.0  3.2  2.6  112 M 58 A 20 15 45 6.1 6.8 6.9
113 M 75 A 25 35 30 5.7  5.6  4.7  114 M 76 B 35 50 25 4.9 5.4 5.2
115 F 75 A 15 20 25 8.2  8.9  8.2  116 M 57 A 45 30 40 4.6 3.9 3.2
117 F 68 A 35 25 40 3.8  4.8  5.3  118 M 65 B 40 40 25 3.9 3.9 4.7
119 F 67 B 20 15 30 6.5  7.2  6.6  120 F 60 B 25 15 15 7.3 7.1 7.8
121 F 67 A 15 20 15 7.7  8.0  8.3  122 F 57 B 10 15 15 9.8 9.2 8.6
123 M 62 B 55 60 75 3.4  2.7  2.3  124 M 71 A 20 30 25 7.1 6.6 7.4
125 M 71 B 15 15 20 8.8  9.1  9.3  126 M 64 A 25 30 30 5.6 6.3 6.3
127 M 51 A 35 40 30 5.1  4.6  3.9  128 F 70 B 35 25 15 6.8 7.1 7.6
129 M 61 A 35 40 50 5.5  5.2  4.8  130 M 62 B 60 40 65 3.7 3.4 2.4
131 F 68 A 20 35 35 5.3  5.6  4.9  132 F 68 B 35 30 15 7.2 6.2 5.6
133 M 64 B 40 20 30 5.4  4.9  4.5  134 F 76 B 30 45 25 5.5 4.7 4.6
135 F 78 B 25 20 15 7.6  8.3  9.2
;

/*creating longform dataset*/
data longform;
set orthoclinic;
 array l[3] length1-length3;
 array s[3] score1-score3;
  do visit=1 to 3;
  length=l[visit];
  score=s[visit];
   output;
    end;
keep id gender age doctor visit length score;
run;

/*fitting random slope and intercept model with
unstructured covariance matrix of error terms*/
proc mixed covtest;
 class gender doctor;
  model score = gender age doctor length visit / solution;
   random intercept visit / subject=id type=un;
   repeated / subject=id type=un;
run;
```

```
        Fit Statistics
AIC (Smaller is Better)  266.8
AICC (Smaller is Better) 268.4
BIC (Smaller is Better)  279.2
```

```
/*fitting random slope and intercept model with
Toeplitz covariance matrix of error terms*/
proc mixed covtest;
 class gender doctor;
  model score = gender age doctor length visit / solution;
   random intercept visit / subject=id type=un;
    repeated / subject=id type=toep;
run;
```

```
WARNING: Did not converge.
```

```
/*fitting random intercept-only model with
Toeplitz covariance matrix of error terms*/
proc mixed covtest;
```

```
 class gender doctor;
  model score = gender age doctor length visit / solution;
   random intercept / subject=id type=un;
    repeated / subject=id type=toep;
run;
```

```
        Fit Statistics
AIC (Smaller is Better)  261.5
AICC (Smaller is Better) 261.9
BIC (Smaller is Better)  267.7
```

```
/*fitting random slope and intercept model with
spatial power covariance matrix of error terms*/
proc mixed covtest;
 class gender doctor;
  model score = gender age doctor length visit / solution;
   random intercept visit / subject=id type=un;
   repeated / subject=id type=sp(pow)(visit);
run;
```

```
WARNING: Did not converge.
```

```
/*fitting random intercept-only model with
spatial power covariance matrix of error terms*/
proc mixed covtest;
 class gender doctor;
  model score = gender age doctor length visit / solution;
   random intercept / subject=id type=un;
   repeated / subject=id type=sp(pow)(visit);
run;
```

```
        Fit Statistics
AIC (Smaller is Better)  258.6
AICC (Smaller is Better) 258.7
BIC (Smaller is Better)  261.7
```

```
/*fitting random slope and intercept model with
autoregressive covariance matrix of error terms*/
proc mixed covtest;
 class gender doctor;
  model score = gender age doctor length visit / solution;
   random intercept visit / subject=id type=un;
   repeated / subject=id type=ar(1);
run;
```

```
WARNING: Did not converge.
```

```
/*fitting random intercept-only model with
autoregressive covariance matrix of error terms*/
proc mixed covtest;
 class gender doctor;
  model score = gender age doctor length visit / solution;
   random intercept / subject=id type=un;
   repeated / subject=id type=ar(1);
run;
```

```
        Fit Statistics
AIC (Smaller is Better)  258.6
AICC (Smaller is Better) 258.7
```

```
        Fit Statistics
BIC (Smaller is Better)  261.7
```

```
/*fitting random slope and intercept model with
compound symmetric covariance matrix of error terms*/
proc mixed covtest;
 class gender doctor;
  model score = gender age doctor length visit / solution;
   random intercept visit / subject=id type=un;
   repeated / subject=id type=cs;
run;
```

```
        Fit Statistics
AIC (Smaller is Better)  261.1
AICC (Smaller is Better) 261.7
BIC (Smaller is Better)  268.8
```

```
/*fitting random slope and intercept model with
independent covariance matrix of error terms*/
proc mixed covtest;
 class gender doctor;
  model score = gender age doctor length visit / solution;
   random intercept visit / subject=id type=un;
run;
```

```
        Fit Statistics
AIC (Smaller is Better)  259.1
AICC (Smaller is Better) 259.5
BIC (Smaller is Better)  265.3
```

In R:

```
orthoclinic.data<- read.csv(file='C:/<insert path>/Exercise8.3Data.csv',
header=TRUE, sep=',')

#creating longform dataset
library(reshape2)
data1<- melt(orthoclinic.data[,c('id','gender','age','doctor', 'length1',
'length2', 'length3')], id.vars=c('id','gender','age','doctor'), variable.name
='length.visit',value.name='length')
data2<- melt(orthoclinic.data[,c('score1','score2','score3')], variable.name
='score.visit', value.name='score')
longform.data<- cbind(data1,data2)
visit<- ifelse(longform.data$score.visit=='score1',1,
ifelse(longform.data$score.visit=='score2',2,3))

#specifying reference levels
gender.rel<- relevel(longform.data$gender, ref="M")
doctor.rel<- relevel(longform.data$doctor, ref="B")

#fitting random slope and intercept model with
#untructured covariance matrix of error terms
library(nlme)
summary(un.fitted.model<- lme(score ~ gender.rel + age + doctor.rel + length +
visit, random = ~ 1 + visit | id, control= lmeControl(opt='optim'),
data=longform.data, correlation=corSymm(), weights=varIdent(form=~id|length)))
```

The model doesn't converge.

```
#fitting random intercept-only model with
#untructured covariance matrix of error terms
library(nlme)
summary(un.fitted.model<- lme(score ~ gender.rel + age + doctor.rel + length +
visit, random = ~ 1 | id, control= lmeControl(opt='optim'),
data=longform.data,correlation=corSymm(), weights=varIdent(form=~id|length)))
```

The model doesn't converge.

```
#fitting random slope and intercept model with
#Toeplitz covariance matrix of error terms
summary(toep.fitted.model<- lme(score ~ gender.rel + age + doctor.rel + length +
visit, random = ~ 1 + visit | id, data=longform.data,
correlation = corARMA(form = ~ 1 | id, p=1, q=1)))
```

```
      AIC      BIC
 274.9041 306.0456
```

```
#computing AICC
n<-105
p<- 12
print(AICC<- -2*logLik(toep.fitted.model)+2*p*n/(n-p-1))
```

```
278.2954
```

```
#fitting random slope and intercept model with
#spatial power covariance matrix of error terms
summary(sppow.fitted.model<- lme(score ~ gender.rel + age + doctor.rel + length +
visit, random = ~ 1 + visit| id, data=longform.data,
correlation=corCAR1(form = ~ 1 | id)))
```

```
     AIC      BIC
273.0585 301.6048
```

```
#computing AICC
p<- 11
print(AICC<- -2*logLik(sppow.fitted.model)+2*p*n/(n-p-1))
```

```
275.8972
```

```
#fitting random slope and intercept model with
#autoregressive covariance matrix of error terms
summary(ar.fitted.model<- lme(score ~ gender.rel + age + doctor.rel + length +
visit, random = ~ 1 + visit| id, data=longform.data,
correlation=corAR1(form = ~ 1 | id)))
```

```
     AIC      BIC
272.9041 301.4504
```

```
#computing AICC
p<- 11
print(AICC<- -2*logLik(ar.fitted.model)+2*p*n/(n-p-1))
```

```
275.7428
```

```
#fitting random intercept-only model with
#autoregressive covariance matrix of error terms
```

```
summary(arint.fitted.model<- lme(score ~ gender.rel + age + doctor.rel + length +
visit, random = ~ 1 | id, data=longform.data, correlation=corAR1(form = ~ 1 |
id)))
getVarCov(arint.fitted.model, type='conditional')

    AIC      BIC
272.612 295.9681

#computing AICC
p<- 9
print(AICC<- -2*logLik(arint.fitted.model)+2*p*n/(n-p-1))

274.5067

#fitting random slope and intercept model with
#compound symmetric covariance matrix of error terms
summary(cs.fitted.model<- lme(score ~ gender.rel + age + doctor.rel + length +
visit, random = ~ 1 + visit | id, data=longform.data,
correlation=corCompSymm(form = ~ 1 | id)))

     AIC      BIC
273.0585 301.6048

#computing AICC
p<- 11
print(AICC<- -2*logLik(cs.fitted.model)+2*p*n/(n-p-1))

275.8972

#fitting random slope and intercept model with
#independent covariance matrix of error terms
summary(ind.fitted.model<- lme(score ~ gender.rel + age + doctor.rel + length +
visit, random = ~ 1 + visit | id, data=longform.data))

     AIC      BIC
271.0585 297.0097

#computing AICC
p<- 10
print(AICC<- -2*logLik(ind.fitted.model)+2*p*n/(n-p-1))

273.3989
```

(b) Which of the fitted models has the best fit according to the AIC, AICC, and BIC criteria?

In SAS, spatial power (the same as autoregressive) model has the best fit. The AIC, AICC, and BIC values are given in the table below.

	UN	**Toeplitz**	**Sp Power Intercept**	**AR Intercept**	**CS**	**Ind**
AIC	266.8	261.5	258.6	258.6	261.1	259.1
AICC	268.4	261.9	258.7	258.7	261.7	259.5
BIC	279.2	267.7	261.7	261.7	268.8	265.3

According to R, the model with an independent structure has a better fit, but the next candidate is the random intercept-only autoregressive model. Note that in R, spatial power and autoregressive models are different (due possibly to dubious model convergence).

	Toeplitz	**Sp Power**	**AR**	**AR Intercept**	**CS**	**Ind**
AIC	274.9	273.1	272.9	272.6	273.1	271.1
AICC	278.3	275.9	275.7	274.5	275.9	273.4
BIC	306.0	301.6	301.5	296.0	301.6	297.0

(c) Answer parts (e)-(g) in Exercise 8.3 as applied to the best fitted model.

In SAS:

```
/*fitting random intercept-only model with
autoregressive covariance matrix of error terms*/
proc mixed covtest;
 class gender doctor;
  model score = gender age doctor length visit / solution;
   random intercept / subject=id type=un;
   repeated / subject=id type=ar(1) r;
run;
```

```
Estimated R Matrix for Subject 1
  Row     Col1     Col2     Col3
    1   2.4954   2.3447   2.2031
    2   2.3447   2.4954   2.3447
    3   2.2031   2.3447   2.4954

          Covariance Parameter Estimates
Cov Parm Subject Estimate Standard Z Value   Pr Z
                           Error
UN(1,1)  id             0        .       .      .
AR(1)    id        0.9396  0.01817   51.72 <.0001
Residual           2.4954   0.6142    4.06 <.0001

                  Solution for Fixed Effects
Effect    gender doctor Estimate Standard DF t Value Pr > |t|
                                  Error
Intercept                 4.6863   2.6628 31    1.76   0.0883
gender    F               2.2297   0.5389 68    4.14   <.0001
gender    M                    0        .  .       .        .
age                      0.01012  0.03984 68    0.25   0.8002
doctor           A        0.1670   0.5250 68    0.32   0.7513
doctor           B             0        .  .       .        .
length                  -0.01130 0.005149 68   -2.19   0.0317
visit                   -0.04559  0.06470 68   -0.70   0.4834
```

The fitted model has the form is $\hat{E}(score) = 4.6863 + 2.2297 \cdot female + 0.01012 \cdot age + 0.167 \cdot doctor\ A - 0.0113 \cdot visit\ length - 0.04559 \cdot visit\ number$. The estimated variance of the random intercept is zero, and the fitted covariance matrix of the error terms is block diagonal, with 35 blocks of the form $\begin{pmatrix} 2.4954 & 2.3447 & 2.2031 \\ 2.3447 & 2.4954 & 2.3447 \\ 2.2031 & 2.3447 & 2.4954 \end{pmatrix}$. Gender and visit length are significant predictors of score at the 5% level. For female patients, the estimated average score is 2.2297 points higher than that for male patients. As visit length increases by one minute, the estimated mean score decreases by 0.0113.

In R:

```
#fitting random intercept-only model with
#autoregressive covariance matrix of error terms
summary(arint.fitted.model<- lme(score ~ gender.rel + age + doctor.rel + length
+ visit, random = ~ 1 | id, data=longform.data, correlation=corAR1(form = ~ 1 |
id)))
```

```
Random effects:
        (Intercept) Residual
StdDev: 0.0005791566  1.57967

      Phi
0.9396084

Fixed effects:
                Value Std.Error DF   t-value p-value
(Intercept)  4.686268 2.6627508 68  1.759935  0.0829
gender.relF  2.229715 0.5388793 31  4.137689  0.0002
age          0.010122 0.0398445 31  0.254043  0.8011
doctor.relA  0.167042 0.5250427 31  0.318150  0.7525
length      -0.011298 0.0051494 68 -2.194026  0.0317
visit       -0.045594 0.0647041 68 -0.704658  0.4834
```

```
intervals(arint.fitted.model)
```

```
Random Effects:
                       lower         est.        upper
sd((Intercept)) 7.847905e-63 0.0005791566 4.274037e+55
```

```
getVarCov(arint.fitted.model, type='conditional')
```

```
Conditional variance covariance matrix
       1      2      3
1 2.4954 2.3447 2.2031
2 2.3447 2.4954 2.3447
3 2.2031 2.3447 2.4954
```

To predict the quality of service score that would be given by a 55-year-old male patient on his fourth visit to Dr. A with a 30-minute appointment, we do the following calculations:

$$score^0 = 4.6863 + 0.01012 \cdot 55 + 0.167 - 0.0113 \cdot 30 - 0.04559 \cdot 4 = 4.88854.$$

In SAS:

```
data predict;
input id gender$ age doctor$ length visit;
cards;
136 M 55 A 30 4
;

data longform;
set longform predict;
run;

proc mixed covtest;
 class gender doctor;
  model score = gender age doctor length visit / outpm=outdata;
   random intercept / subject=id type=un;
   repeated / subject=id type=ar(1);
run;
```

```
proc print data=outdata (firstobs=106) noobs;
 var Pred;
run;
```

```
   Pred
4.88872
```

In R:

```
print(predict(arint.fitted.model, data.frame(id=136, gender.rel='M', age=55,
doctor.rel='A', length=30, visit=4), level=0))
```

```
4.88872
```

EXERCISE 8.8. Use the data in Exercise 8.4 to do the following analysis:
(a) Output AIC, AICC, and BIC values for random slope and intercept (or random intercept-only) models with unstructured, Toeplitz, spatial power, autoregressive, compound symmetric, and independent covariance structures for the error terms.

In SAS:

```
data fitness;
input id gender$ age oxygen1 runtime1 pulse1 oxygen2 runtime2 pulse2
oxygen3 runtime3 pulse3;
cards;
1  F 39 37.4 11.4 151 36.6 17.8 158 36.1 15.4 152
2  M 42 60.1 11.5 121 59.0 9.6  131 58.2 9.0  143
3  F 34 44.6 9.6  138 39.8 9.3  148 38.8 9.1  144
4  M 36 51.9 10.5 125 53.4 9.8  135 50.4 9.6  163
5  F 45 40.8 13.1 142 39.5 12.4 151 38.5 12.7 133
6  M 37 45.4 10.3 133 40.6 11.9 145 40.2 11.2 141
7  F 49 45.3 13.1 135 40.6 12.1 148 39.7 11.5 157
8  F 47 44.8 12.1 135 40.1 12.3 148 39.0 11.9 151
9  M 50 48.7 12.6 131 42.3 11.0 143 44.3 10.5 150
10 M 34 45.8 10.8 132 40.9 11.8 144 41.1 11.1 160
11 M 35 50.4 9.6  129 45.9 10.4 137 44.8 10.4 138
12 M 48 50.5 12.9 125 48.6 10.3 135 49.0 9.8  132
13 F 50 44.8 14.0 135 40.3 13.1 148 39.5 12.6 163
14 F 53 39.4 12.7 145 39.3 14.1 154 37.0 12.8 148
15 M 44 46.1 11.0 132 40.9 11.3 144 41.1 10.8 148
16 F 32 39.2 9.1  146 38.7 9.7  158 36.7 10.2 170
17 M 39 54.3 9.4  123 55.1 9.7  132 57.4 9.4  162
18 F 33 39.4 11.6 144 39.4 12.7 154 37.4 12.7 155
19 M 33 47.9 10.1 132 42.2 11.2 143 42.6 10.6 140
20 M 46 49.2 11.2 130 43.9 10.8 141 44.7 10.5 142
;

/*creating longform dataset*/
data longform;
set fitness;
 array o[3] oxygen1-oxygen3;
 array r[3] runtime1-runtime3;
 array p[3] pulse1-pulse3;
  do condition=1 to 3;
  oxygen=o[condition];
  runtime=r[condition];
  pulse=p[condition];
  output;
   end;
keep id gender age oxygen runtime pulse condition;
run;

/*fitting random slope and intercept model with
unstructured covariance matrix of error terms*/
proc mixed covtest;
 class gender;
  model pulse = gender age oxygen runtime condition /solution;
   random intercept condition / subject=id type=un;
   repeated / subject=id type=un;
run;
```

```
        Fit Statistics
AIC (Smaller is Better)  338.0
AICC (Smaller is Better) 342.1
BIC (Smaller is Better)  346.9
```

```
/*fitting random slope and intercept model with
Toeplitz coveriance matrix of error terms*/
proc mixed covtest;
 class gender;
  model pulse = gender age oxygen runtime condition / solution;
   random intercept condition / subject=id type=un;
   repeated / subject=id type=toep;
run;
```

```
        Fit Statistics
AIC (Smaller is Better)  375.7
AICC (Smaller is Better) 376.5
BIC (Smaller is Better)  379.6
```

```
/*fitting random slope and intercept model with
spatial power covariance matrix of error terms*/
proc mixed covtest;
 class gender;
  model pulse = gender age oxygen runtime condition / solution;
   random intercept condition / subject=id type=un;
   repeated / subject=id type=sp(pow)(condition);
run;
```

```
WARNING: Did not converge.
```

```
/*fitting random intercept-only model with
spatial power covariance matrix of error terms*/
proc mixed covtest;
 class gender;
  model pulse = gender age oxygen runtime condition / solution;
   random intercept / subject=id type=un;
   repeated / subject=id type=sp(pow)(condition);
run;
```

```
        Fit Statistics
AIC (Smaller is Better)  399.3
AICC (Smaller is Better) 399.5
```

```
        Fit Statistics
BIC (Smaller is Better)  401.3
```

```
/*fitting random slope and intercept model with
autoregressive covariance matrix of error terms*/
proc mixed covtest;
 class gender;
  model pulse = gender age oxygen runtime condition / solution;
   random intercept condition / subject=id type=un;
   repeated / subject=id type=ar(1);
run;
```

```
WARNING: Did not converge.
```

```
/*fitting random intercept-only model with
autoregressive covariance matrix of error terms*/
proc mixed covtest;
 class gender;
  model pulse = gender age oxygen runtime condition / solution;
   random intercept / subject=id type=un;
   repeated / subject=id type=ar(1);
run;
```

```
        Fit Statistics
AIC (Smaller is Better)  399.3
AICC (Smaller is Better) 399.5
BIC (Smaller is Better)  401.3
```

```
/*fitting random slope and intercept model with
compound symmetric covariance matrix of error terms*/
proc mixed covtest;
 class gender;
  model pulse = gender age oxygen runtime condition / solution;
   random intercept condition / subject=id type=un;
   repeated / subject=id type=cs;
run;
```

```
        Fit Statistics
AIC (Smaller is Better)  377.8
AICC (Smaller is Better) 379.1
BIC (Smaller is Better)  382.8
```

```
/*fitting random slope and intercept model with
independent covariance matrix of error terms*/
proc mixed covtest;
 class gender;
  model pulse = gender age oxygen runtime condition / solution;
   random intercept condition / subject=id type=un;
run;
```

```
        Fit Statistics
AIC (Smaller is Better)  375.8
AICC (Smaller is Better) 376.6
BIC (Smaller is Better)  379.8
```

In R:

```
fitness.data<- read.csv(file='C:/<insert path>/Exercise8.4Data.csv',
header=TRUE, sep=',')

#creating longform dataset
library(reshape2)
data1<- melt(fitness.data[,c('id','gender','age','oxygen1','oxygen2','oxygen3')],
id.vars=c('id','gender','age'),variable.name='oxygen.cond',value.name='oxygen')
data2<- melt(fitness.data[,c('runtime1','runtime2','runtime3')],variable.name=
'runtime.cond',value.name='runtime')
data3<- melt(fitness.data[,c('pulse1','pulse2','pulse3')],variable.name=
'pulse.cond',value.name='pulse')
longform.data<- cbind(data1,data2,data3)
condition<- ifelse(longform.data$pulse.cond=='pulse1',1,
ifelse(longform.data$pulse.cond=='pulse2',2,3))

#specifying reference level
gender.rel<- relevel(longform.data$gender, ref="M")

#fitting random slope and intercept model with
#unstructured covariance matrix of error terms
library(nlme)
ctrl<- control= lmeControl(opt='optim')
summary(un.fitted.model<- lme(pulse ~ gender.rel + age + oxygen + runtime +
condition, random = ~ 1 + condition | id, control=ctrl, data=longform.data,
correlation=corSymm(), weights=varIdent(form = ~ id | condition)))
```

```
     AIC      BIC
353.7616 383.5964
```

```
#computing AICC
n<- 102
p<- 15
print(AICC<- -2*logLik(un.fitted.model)+2*p*n/(n-p-1))
```

```
359.343
```

```
#fitting random slope and intercept model with
#Toeplitz covariance matrix of error terms
summary(toep.fitted.model<- lme(pulse ~ gender.rel + age + oxygen + runtime
+ condition, random = ~ 1 + condition | id, control=ctrl, data=longform.data,
correlation = corARMA(form = ~ 1 | id, p=1, q=1)))
```

```
     AIC      BIC
391.9006 415.7684
```

```
#computing AICC
p<- 12
print(AICC<- -2*logLik(toep.fitted.model)+2*p*n/(n-p-1))
```

```
395.4062
```

```
#fitting random slope and intercept model with
#spatial power covariance matrix of error terms
summary(sppow.fitted.model<- lme(pulse ~ gender.rel + age + oxygen + runtime
+ condition, random = ~ 1 + condition | id, control=ctrl, data=longform.data,
correlation=corCAR1(form = ~ condition | id)))
```

```
     AIC      BIC
393.2069 415.0857
```

```
#computing AICC
p<- 11
print(AICC<- -2*logLik(sppow.fitted.model)+2*p*n/(n-p-1))
```

```
396.1402
```

```
#fitting random slope and intercept model with
#autoregressive covariance matrix of error terms
summary(ar.fitted.model<- lme(pulse ~ gender.rel + age + oxygen + runtime
+ condition, random = ~ 1 + condition | id, control=ctrl, data=longform.data,
correlation=corAR1(form = ~ 1 | id)))
```

```
     AIC      BIC
389.9551 411.8339
```

```
#computing AICC
p<- 11
print(AICC<- -2*logLik(ar.fitted.model)+2*p*n/(n-p-1))
```

```
392.8884
```

```
#fitting random slope and intercept model with
#compound symmetric covariance matrix of error terms
summary(cs.fitted.model<- lme(pulse ~ gender.rel + age + oxygen + runtime +
condition, random = ~ 1 + condition | id, control=ctrl, data=longform.data,
correlation=corCompSymm(form = ~ 1 | id)))
```

```
     AIC      BIC
389.8923 411.7711
```

```
#computing AICC
p<- 11
print(AICC<- -2*logLik(cs.fitted.model)+2*p*n/(n-p-1))
```

```
392.8256
```

```
#fitting random slope and intercept model with
#independent covariance matrix of error terms
summary(ind.fitted.model<- lme(pulse ~ gender.rel + age + oxygen + runtime +
condition, random = ~ 1 + condition | id, control=ctrl, data=longform.data))
```

```
     AIC      BIC
391.2189 411.1088
```

```
#computing AICC
p<- 10
print(AICC<- -2*logLik(ind.fitted.model)+2*p*n/(n-p-1))
```

```
393.6365
```

(b) Find the best-fitted model according to the AIC, AICC, and BIC criteria.

For the models fitted in SAS, the fitting criteria values are summarized in this table:

	UN	**Toeplitz**	**Sp Power Intercept**	**AR Intercept**	**CS**	**Ind**
AIC	338.0	375.7	399.3	399.3	377.8	375.8

AICC	342.1	376.5	399.5	399.5	379.1	376.6
BIC	346.9	379.6	401.3	401.3	382.8	379.8

For the models fitted in R, the values are as follows:

	UN	**Toeplitz**	**Sp Power**	**AR**	**CS**	**Ind**
AIC	353.8	391.9	393.2	390.0	389.9	391.2
AICC	359.3	395.4	396.1	392.9	392.8	393.6
BIC	383.6	415.8	415.1	411.8	411.8	411.1

The best-fitted model is the one with the unstructured covariance matrix of the error terms.

(c) Answer questions (c)-(e) in Exercise 8.4 for the model that fits the data the best.

In SAS:

```
/*fitting random slope and intercept model with
unstructured covariance matrix of error terms*/
proc mixed covtest;
 class gender;
  model pulse = gender age oxygen runtime condition / solution;
   random intercept condition / subject=id type=un;
   repeated / subject=id type=un r;
run;
```

```
Estimated R Matrix for Subject 1
 Row      Col1     Col2       Col3
   1    9.1604   8.4295   -11.3659
   2    8.4295   8.3031    -4.5490
   3  -11.3659  -4.5490     136.29

          Covariance Parameter Estimates
Cov Parm Subject Estimate Standard Z Value   Pr Z
                             Error
UN(1,1)  id        1.4266   219.42    0.01 0.4974
UN(2,1)  id       -1.8318   103.12   -0.02 0.9858
UN(2,2)  id        1.8059  49.2454    0.04 0.4854
UN(1,1)  id        9.1604  61.8377    0.15 0.4411
UN(2,1)  id        8.4295  12.7894    0.66 0.5098
UN(2,2)  id        8.3031        0       .      .
UN(3,1)  id      -11.3659  43.9102   -0.26 0.7958
UN(3,2)  id       -4.5490        0       .      .
UN(3,3)  id        136.29        0       .      .

               Solution for Fixed Effects
Effect     gender Estimate Standard DF t Value Pr > |t|
                              Error
Intercept           158.98   5.8430 17   27.21   <.0001
gender     F        6.6365   1.4390 18    4.61   0.0002
gender     M             0        . .        .        .
age                -0.1260  0.08944 18   -1.41   0.1759
```

```
              Solution for Fixed Effects
Effect    gender Estimate Standard DF t Value Pr > |t|
                             Error
oxygen            -0.6393  0.09872 18   -6.48   <.0001
runtime           -0.2299   0.1656 18   -1.39   0.1822
condition          9.0253   0.4501 19   20.05   <.0001
```

The fitted model has the estimated mean response $\hat{E}(pulse) = 158.98 + 6.6365 \cdot female - 0.126 \cdot age - 0.6393 \cdot oxygen - 0.2299 \cdot runtime + 9.0253 \cdot condition$. The estimated parameters for the random-effect terms are $\hat{\sigma}^2_{u_1} = 1.4266, \hat{\sigma}^2_{u_2} = 1.8059, \hat{\sigma}_{u_1 u_2} = -1.8318$, and the estimated covariance matrix of the error terms is block diagonal, with 20 blocks of the form $\begin{pmatrix} 9.1604 & 8.4295 & -11.3659 \\ 8.4295 & 8.3031 & -4.5490 \\ -11.3659 & -4.5490 & 136.29 \end{pmatrix}$. Gender, oxygen, and condition number are significant predictors of pulse. For female runners, the estimated average pulse is 6.6365 points higher than that for male runners. As oxygen intake increases by one unit, the estimated average pulse decreases by 0.6393 points. As the condition number increases by one, the estimated average pulse increases by 9.0253 points.

In R:

```
#fitting random intercept-only model with
#autoregressive covariance matrix of error terms
summary(arint.fitted.model<- lme(score ~ gender.rel + age + doctor.rel + length
+ visit, random = ~ 1 | id, data=longform.data, correlation=corAR1(form = ~ 1 |
id)))
```

```
Random effects:
              StdDev       Corr
(Intercept) 3.1670814167 (Intr)
condition   0.4693058637 -1
Residual    0.0004034296

Fixed effects:
                Value Std.Error DF   t-value p-value
(Intercept) 160.73185  6.200000 37 25.924492  0.0000
gender.relF   7.72051  1.424442 17  5.420026  0.0000
age          -0.12855  0.089524 17 -1.435918  0.1692
oxygen       -0.71493  0.098789 37 -7.236946  0.0000
runtime      -0.02773  0.176549 37 -0.157056  0.8761
condition     8.71834  0.468003 37 18.628799  0.0000
```

```
getVarCov(arint.fitted.model, type='conditional')
```

```
Conditional variance covariance matrix
           1          2          3
1 1.6276e-07 5.2205e-03 3.2633e-04
2 5.2205e-03 1.6745e+02 1.0472e+01
3 3.2633e-04 1.0472e+01 2.5288e+00
```

To predict an average heart rate for a 36-year-old woman who is running on a treadmill, if her oxygen intake is 40.2 units, and her run time is 10.3 minutes per mile, wo do the following calculations:

$$pulse^0 = 158.98 + 6.6365 - 0.126 \cdot 36 - 0.6393 \cdot 40.2 - 0.2299 \cdot 10.3 + 9.0253 = 142.047.$$

In SAS:

```
data predict;
input id gender$ age condition oxygen runtime;
cards;
21 F 36 1 40.2 10.3
;
run;
data longform;
set longform predict;
run;

proc mixed covtest;
 class gender;
  model pulse = gender age oxygen runtime condition / outpm=outdata;
   random intercept condition / subject=id type=un;
   repeated / subject=id type=un r;
run;

proc print data=outdata (firstobs=61) noobs;
 var Pred;
run;
```

```
   Pred
142.041
```

In R:

```
print(predict(un.fitted.model, data.frame(id=21, gender.rel='F', age=36,
oxygen=40.2, runtime=10.3, condition=1), level=0))
```

```
143.5173
```

EXERCISE 8.9. Take the data presented in Exercise 8.5.
(a) For BMI, fit the random slope and intercept regression models (or random intercept-only models) with unstructured, Toeplitz, spatial power, autoregressive, compound symmetric, and independent covariance structures for the error terms.

In SAS:

```
data weightloss;
input id group$ gender$ aexercise aBMI bexercise bBMI cexercise cBMI @@;
cards;
1  Int F 0  42.4 50 40.0 120 36.8  2  Int F 15 32.9 20 30.6 25  28.6
3  Int M 10 32.0 30 30.8 30  26.1  4  Int M 20 26.1 80 25.5 80  21.1
5  Int F 0  27.5 20 26.4 20  22.5  6  Int F 30 40.4 75 38.3 180 32.1
7  Int M 15 33.5 50 28.2 50  25.8  8  Int F 15 35.2 35 34.8 90  30.6
9  Int F 0  39.5 55 37.1 50  35.3  10 Int M 20 27.3 30 26.3 30  22.6
11 Int M 0  46.9 50 43.5 50  40.3  12 Int M 20 34.4 80 32.2 85  28.1
13 Int F 0  34.2 60 31.0 65  26.8  14 Int F 45 26.5 30 24.6 30  20.8
15 Int F 0  29.6 20 28.2 20  24.9  16 Int F 10 31.2 80 29.3 50  28.6
17 Cnt F 0  29.3 25 28.9 30  26.3  18 Cnt M 20 45.9 10 43.1 15  42.9
19 Cnt M 0  41.5 20 38.8 30  39.9  20 Cnt F 30 33.3 25 33.4 35  33.2
21 Cnt M 15 31.1 35 30.9 0   30.9  22 Cnt F 10 43.3 35 43.6 30  44.5
23 Cnt M 15 35.5 0  36.5 5   35.3  24 Cnt F 10 42.4 15 43.4 50  42.3
25 Cnt F 20 37.0 30 36.6 45  35.5  26 Cnt M 0  37.8 30 35.7 45  34.3
27 Cnt F 20 23.7 10 23.1 0   23.7  28 Cnt F 10 38.7 15 20.4 25  20.1
29 Cnt F 0  41.2 15 41.2 55  39.7  30 Cnt F 30 30.2 35 29.9 5   29.4
```

```
31 Cnt M 10 38.4 20 38.1 30  37.0  32 Cnt F 10 37.5 15 37.4 5   36.8
33 Cnt M 30 34.5 10 34.4 20  33.9  34 Cnt M 15 37.6 35 36.2 25  36.0
;

/*creating longform dataset*/
data longform;
set weightloss;
 array m[3] (0 1 3);
 array e[3] aexercise bexercise cexercise;
 array b[3] aBMI bBMI cBMI;
  do i=1 to 3;
  month=m[i];
  exercise=e[i];
  BMI=b[i];
  output;
  end;
keep id group gender exercise BMI month;
run;

/*fitting random slope and intercept model with
unstructured covariance matrix of error terms*/
proc mixed covtest;
 class group(ref='Cnt') gender(ref='F');
  model BMI = group gender exercise month / solution;
   random intercept month / subject=id type=un;
   repeated / subject=id type=un;
run;
```

```
        Fit Statistics
AIC (Smaller is Better)  522.6
AICC (Smaller is Better) 524.2
BIC (Smaller is Better)  534.8
```

```
/*fitting random slope and intercept model with
Toeplitz covariance matrix of error terms*/
proc mixed covtest;
 class group(ref='Cnt') gender(ref='F');
  model BMI = group gender exercise month / solution;
   random intercept month / subject=id type=un;
   repeated / subject=id type=toep;
run;
```

```
        Fit Statistics
AIC (Smaller is Better)  538.7
AICC (Smaller is Better) 539.4
BIC (Smaller is Better)  546.4
```

```
/*fitting random slope and intercept model with
spatial power covariance matrix of error terms*/
proc mixed covtest;
 class group(ref='Cnt') gender(ref='F');
  model BMI = group gender exercise month / solution;
   random intercept month / subject=id type=un;
   repeated / subject=id type=sp(pow)(month);
run;
```

```
        Fit Statistics
AIC (Smaller is Better)  516.8
AICC (Smaller is Better) 517.5
```

```
        Fit Statistics
BIC (Smaller is Better)  524.4
```

```
/*fitting random slope and intercept model with
autoregressive matrix of error terms*/
proc mixed covtest;
 class group(ref='Cnt') gender(ref='F');
  model BMI = group gender exercise month / solution;
   random intercept month / subject=id type=un;
   repeated / subject=id type=ar(1);
run;
```

```
        Fit Statistics
AIC (Smaller is Better)  536.7
AICC (Smaller is Better) 537.2
BIC (Smaller is Better)  542.9
```

```
/*fitting random slope and intercept model with
compound symmetric covariance matrix of error terms*/
proc mixed data=longform covtest;
 class group(ref='Cnt') gender(ref='F');
  model BMI = group gender exercise month / solution;
   random intercept month / subject=id type=un;
   repeated / subject=id type=cs;
run;
```

```
        Fit Statistics
AIC (Smaller is Better)  544.2
AICC (Smaller is Better) 544.9
BIC (Smaller is Better)  551.8
```

```
/*fitting random slope and intercept model with
independent covariance matrix of error terms*/
proc mixed data=longform covtest;
 class group(ref='Cnt') gender(ref='F');
  model BMI = group gender exercise month / solution;
   random intercept month / subject=id type=un;
run;
```

```
        Fit Statistics
AIC (Smaller is Better)  542.2
AICC (Smaller is Better) 542.6
BIC (Smaller is Better)  548.3
```

In R:

```
weightloss.data<- read.csv(file='C:/<insert path>/Exercise8.5Data.csv',
header=TRUE, sep=',')

#creating longform dataset
library(reshape2)
data1<- melt(weightloss.data[,c('id','group','gender','aexercise','bexercise',
'cexercise')], id.vars=c('id','group','gender'),variable.name='exercise.visit',
value.name='exercise')
data2<- melt(weightloss.data[,c('aBMI','bBMI','cBMI')],variable.name=
'BMI.visit',value.name='BMI')
longform.data<- cbind(data1,data2)
month<- ifelse(longform.data$BMI.visit=='aBMI',0,
ifelse(longform.data$BMI.visit=='bBMI',1,3))

#specifying reference levels
group.rel<- relevel(longform.data$group, ref="Int")
gender.rel<- relevel(longform.data$gender, ref="M")

#fitting random slope and intercept model with
#unstructured covariance matrix of error terms
library(nlme)
ctrl <- lmeControl(opt="optim")
summary(un.fitted.model<- lme(BMI ~ group.rel + gender.rel + exercise + month,
random = ~ 1 + month | id, control=ctrl, data=longform.data, correlation =
corSymm(), weights=varIdent(form=~id|month)))
```

```
     AIC      BIC
534.5973 570.6433
```

```
#computing AICC
n<- 102
p<- 14
print(AICC<- -2*logLik(un.fitted.model)+2*p*n/(n-p-1))
```

```
539.4249
```

```
#fitting random slope and intercept model with
#Toeplitz covariance matrix of error terms
summary(toep.fitted.model<- lme(BMI ~ group.rel + gender.rel + exercise
+ month, random = ~ 1 + month | id, control=ctrl, data=longform.data,
correlation = corARMA(form=~1|id, p=1, q=1)))
```

```
     AIC      BIC
553.4601 581.7819
```

```
#computing AICC
p<- 11
print(AICC<- -2*logLik(toep.fitted.model)+2*p*n/(n-p-1))
```

```
556.3935
```

```
#fitting random slope and intercept model with
#spatial power covariance matrix of error terms
summary(sppow.fitted.model<- lme(BMI ~ group.rel + gender.rel + exercise
+ month, random = ~ 1 + month | id, control=ctrl, data=longform.data,
correlation=corCAR1(form=~month|id)))
```

```
     AIC      BIC
554.2215 579.9686
```

```
#computing AICC
p<- 10
print(AICC<- -2*logLik(sppow.fitted.model)+2*p*n/(n-p-1))
```

```
556.6391
```

```
#fitting random slope and intercept model with
#autoregressive covariance matrix of error terms
summary(ar.fitted.model<- lme(BMI ~ group.rel + gender.rel + exercise
+ month, random = ~ 1 + month | id, control=ctrl, data=longform.data,
correlation=corAR1(form=~1|id)))
```

```
     AIC      BIC
551.595 577.3421

#computing AICC
p<-10
print(AICC<- -2*logLik(ar.fitted.model)+2*p*n/(n-p-1))

554.0126

#fitting random slope and intercept model with
#compound symmetric covariance matrix of error terms
summary(cs.fitted.model<- lme(BMI ~ group.rel + gender.rel + exercise
+ month, random = ~ 1 + month | id, control=ctrl, data=longform.data,
correlation=corCompSymm(form=~1|id)))

      AIC     BIC
554.2019 579.949

#computing AICC
p<-10
print(AICC<- -2*logLik(cs.fitted.model)+2*p*n/(n-p-1))

556.6194

#fitting random slope and intercept model with
#independent covariance matrix of error terms
summary(ind.fitted.model<- lme(BMI ~ group.rel + gender.rel + exercise
+ month, random = ~ 1 + month | id, control=ctrl, data=longform.data))

      AIC      BIC
552.2045 575.3769

#computing AICC
p<-9
print(AICC<- -2*logLik(ind.fitted.model)+2*p*n/(n-p-1))

554.161
```

(b) Which of the models has the best fit according to AIC, AICC, and BIC criteria?

According to SAS, the model with spatial power covariance structure has the best fit with respect to AIC, AICC, and BIC criteria. The values are summed up in this table:

	UN	**Toeplitz**	**Sp Power**	**AR**	**CS**	**Ind**
AIC	522.6	538.7	516.8	536.7	544.2	542.2
AICC	524.2	539.4	517.5	537.2	544.9	542.6
BIC	534.8	546.4	524.4	542.9	551.8	548.3

In R, however, the best-fitted model is the one with the unstructured covariance matrix of the error terms.

	UN	**Toeplitz**	**Sp Power**	**AR**	**CS**	**Ind**

AIC	534.6	553.5	554.2	551.6	554.2	552.2
AICC	539.4	556.4	556.6	554.0	556.6	554.2
BIC	570.6	581.8	580.0	577.3	579.9	575.4

(c) For the best-fitted model, do the analysis for questions (c) through (e) in Exercise 8.5.

In SAS:

```
/*fitting random slope and intercept model with
spatial power covariance matrix of error terms*/
proc mixed covtest;
 class group(ref='Cnt') gender(ref='F');
  model BMI = group gender month exercise / solution;
   random intercept month / subject=id type=un;
   repeated / subject=id type=sp(pow)(month) r;
run;
```

```
Estimated R Matrix for Subject 1
 Row      Col1      Col2      Col3
   1    2.8277   -2.4537   -1.8476
   2   -2.4537    2.8277    2.1292
   3   -1.8476    2.1292    2.8277

           Covariance Parameter Estimates
Cov Parm Subject Estimate Standard Z Value   Pr Z
                             Error
UN(1,1)  id       41.9237  13.4965    3.11 0.0009
UN(2,1)  id        3.7666   1.2958    2.91 0.0037
UN(2,2)  id        0.3456   0.1817    1.90 0.0286
SP(POW)  id       -0.8677  0.05390  -16.10 <.0001
Residual           2.8277   0.6943    4.07 <.0001

                   Solution for Fixed Effects
Effect    group gender Estimate Standard DF t Value Pr > |t|
                                   Error
Intercept                32.5252   1.5195 31   21.40   <.0001
group     Int             4.6343   1.5858 33    2.92   0.0062
group     Cnt                  0        .  .       .        .
gender           M        2.6890   1.6155 33    1.66   0.1055
gender           F             0        .  .       .        .
exercise               -0.04509 0.006957 33   -6.48   <.0001
month                    -0.7853   0.1395 33   -5.63   <.0001
```

The fitted model has the estimated mean response $\hat{E}(BMI) = 32.5252 + 4.6343 \cdot intervention + 2.689 \cdot male - 0.04509 \cdot length\ of\ exercise - 0.7853 \cdot month$. The estimated parameters for the random-effect terms are $\hat{\sigma}^2_{u_1} = 41.9237, \hat{\sigma}^2_{u_2} = 0.3456, \hat{\sigma}_{u_1 u_2} = 3.7666$, and the estimated covariance matrix of the error terms is block diagonal, with 34 blocks of the form $\begin{pmatrix} 2.8277 & -2.4537 & -1.8476 \\ -2.4537 & 2.8277 & 2.1292 \\ -1.8476 & 2.1292 & 2.8277 \end{pmatrix}$. Group, exercise, and month are significant predictors of BMI.

For the intervention group, the estimated average BMI is 4.6343 points above that in the control group. As the length of daily exercise increases by one minute, the estimated average BMI decreases by 0.04509 units. It is estimated that the average BMI decreases by 0.7853 units for every additional month in the study.

Predicted BMI at 3 months for an intervention group female participant who exercises for 1 hour every day is $BMI^0 = 32.5252 + 4.6343 - 0.04509 \cdot 60 - 0.7853 \cdot 3 = 32.0982.$

In SAS:

```
data predict;
input id group$ gender$ exercise month;
cards;
35 Int F 60 3
;

data longform;
set longform predict;
run;

proc mixed covtest;
 class group(ref='Cnt') gender(ref='F');
  model BMI = group gender exercise month / outpm=outdata;
   random intercept month / subject=id type=un;
   repeated / subject=id type=sp(pow)(month);
run;

proc print data=outdata (firstobs=103) noobs;
 var Pred;
run;
```

```
   Pred
32.0980
```

In R:

```
#fitting random slope and intercept model with
#unstructured covariance matrix of error terms
summary(un.fitted.model<- lme(BMI ~ group.rel + gender.rel + exercise
+ month, random = ~ 1 + month | id, control=ctrl, data=longform.data,
correlation = corSymm(), weights=varIdent(form = ~ id | month)))
```

```
Random effects:
            StdDev    Corr
(Intercept) 6.5901276 (Intr)
month       0.7815193 0.722
Residual    2.4238856

Fixed effects:
                Value Std.Error DF   t-value p-value
(Intercept)  32.25341 1.5309623 66 21.067411  0.0000
group.relInt  5.07648 1.5803999 31  3.212151  0.0031
gender.relM   2.81462 1.6128551 31  1.745119  0.0909
exercise     -0.04517 0.0068294 66 -6.613932  0.0000
month        -0.78606 0.1397604 66 -5.624341  0.0000
```

```
getVarCov(un.fitted.model, type='conditional')
```

```
Conditional variance covariance matrix
          1           2           3
1  5.8744000 -1.73220000 -1.0604e-03
```

```
2 -1.7322000  0.51077000  3.1279e-04
3 -0.0010604  0.00031279  2.0430e-07
```

The fitted model in R is $\hat{E}(BMI) = 32.25341 + 5.07648 \cdot intervention + 2.81462 \cdot male - 0.04517 \cdot length\ of\ exercise - 0.78606 \cdot month$. The estimates of the other model parameters are $\hat{\sigma}_{u_1} = 6.5898132,\ \hat{\sigma}_{u_2} = 0.7815473, \hat{\rho}_{u_1u_2} = 0.722,$ and the covariance matrix is

$$\begin{pmatrix} 5.8744 & -1.7322 & -0.0010604 \\ -1.7322 & 0.51077 & 0.00031279 \\ -0.0010604 & 0.00031279 & 0.0000002 \end{pmatrix}$$

. Group, length of exercise, and month are significant predictors of the response. For the intervention group, the estimated average BMI is 5.07648 points higher than for the control group. As the length of daily exercise increases by one minute, the estimated average BMI decreases by 0.04517 units. It is estimated that the average BMI decreases by 0.78605 units for every additional month in the study.

Predicted BMI at 3 months for an intervention group female participant who exercises for 1 hour every day is $BMI^0 = 32.25341 + 5.07648 - 0.04517 \cdot 60 - 0.78605 \cdot 3 = 32.2615.$

In R:

```
print(predict(un.fitted.model, data.frame(id=35, group.rel='Int', gender.rel='F',
exercise=60, month=3), level=0))
```

```
32.2611
```

EXERCISE 8.10. Returning to the data in Exercise 8.2, answer the following questions:
(a) Fit the GEE models with unstructured, Toeplitz (in SAS only), autoregressive, compound symmetric, and independent working correlation matrices.

In SAS:

```
 data deptstore;
input id totalyears status$ bonus18 bonus19 bonus20 @@;
cards;
1  16 full 1482 1508 1543  2  7  part 673  710  895
3  11 full 933  1351 1440  4  8  part 844  958  1196
5  6  part 564  790  815   6  5  full 601  708  780
7  6  part 775  822  902   8  17 full 1209 1297 1475
9  12 full 929  1008 1255  10 9  full 983  1013 1111
11 11 full 909  1004 1084  12 6  part 387  853  999
13 4  part 476  530  627   14 6  full 780  843  925
15 10 full 717  1200 1399
;

/*creating longform dataset*/
data longform;
set deptstore;
  array y[3] (1.8 1.9 2.0);
 array b[3] bonus18-bonus20;
  do i=1 to 3;
    year=y[i];
    bonus=b[i];
     output;
  end;
keep id totalyears status year bonus;
run;

/*fitting GEE model with unstructured working correlation matrix*/
proc genmod;
 class id status;
  model bonus = totalyears status year;
   repeated subject = id / type=un;
run;
```

```
WARNING: Iteration limit exceeded.
```

```
/*fitting GEE model with Toeplitz working correlation matrix*/
proc genmod;
 class id status;
  model bonus = totalyears status year;
   repeated subject = id / type=mdep(2);
run;
```

```
QIC 51.4667
```

```
/*fitting GEE model with autoregressive working correlation matrix*/
proc genmod;
 class id status;
  model bonus = totalyears status year;
   repeated subject = id / type=ar;
run;
```

```
QIC 51.6428
```

```
/*fitting GEE model with compound symmetric working correlation matrix*/
proc genmod;
 class id status;
  model bonus = totalyears status year;
   repeated subject = id / type=cs;
run;
```

```
QIC 52.0199
```

```
/*fitting GEE model with independent working correlation matrix*/
proc genmod;
 class id status;
  model bonus = totalyears status year;
   repeated subject = id / type=ind;
run;
```

```
QIC 52.0199
```

In R:

```
deptstore.data<- read.csv(file='C:/<insert path>/Exercise8.2Data.csv',
header=TRUE, sep=',')

#creating longform dataset
library(reshape2)
longform.data<- melt(deptstore.data, id.vars=c('id','totalyears','status'),
variable.name='bonus.year', value.name='bonus')
year<- ifelse(longform.data$bonus.year=='bonus18',1.8,
ifelse(longform.data$bonus.year=='bonus19',1.9,2.0))
```

```
#creating reference level
status.rel<- relevel(longform.data$status, ref="part")

library(geepack)
library(MuMIn)
#fitting GEE model with unstructured working correlation matrix
summary(un.fitted.model<- geeglm(bonus ~ totalyears + status.rel + year,
data=longform.data, id=id, family=gaussian(link='identity'),
corstr='unstructured'))
QIC(un.fitted.model)
```

```
The model doesn't converge.
```

```
#fitting GEE model with autoregressive working correlation matrix
summary(ar.fitted.model<- geeglm(bonus ~ totalyears + status.rel + year,
data=longform.data, id=id, family=gaussian(link='identity'), corstr='ar1'))
QIC(ar.fitted.model)
```

```
 QIC
52.6
```

```
#fitting GEE model with compound symmetric working correlation matrix
summary(cs.fitted.model<- geeglm(bonus ~ totalyears + status.rel + year,
data=longform.data, id=id, family=gaussian(link='identity'),
corstr='exchangeable'))
QIC(cs.fitted.model)
```

```
 QIC
52.6
```

```
#fitting GEE model with independent working correlation matrix
summary(ind.fitted.model<- geeglm(bonus ~ totalyears + status.rel + year,
data=longform.data, id=id, family=gaussian(link='identity'),
corstr='independence'))
QIC(ind.fitted.model)
```

```
 QIC
52.6
```

(c) Find the best model using the QIC criterion.

In SAS, the best-fitted model is the one with the Toeplitz working correlation matrix.

	Toep	**AR**	**CS**	**Ind**
QIC	51.4667	51.6428	52.0199	52.0199

R fits autoregressive, compound symmetric, and independent models, and all three models have the same parameter estimates.

(c) For the model that fits the data the best, answer questions (c)-(e) in Exercise 8.2.

In SAS:

```
/*fitting GEE model with Toeplitz working correlation matrix*/
proc genmod;
 class id status;
  model bonus = totalyears status year;
```

```
   repeated subject = id / type=mdep(2) corrw;
run;
```

```
Working Correlation Matrix
        Col1   Col2    Col3
Row1  1.0000 0.5021 -0.1012
Row2  0.5021 1.0000  0.5021
Row3 -0.1012 0.5021  1.0000
```

```
                 Analysis Of GEE Parameter Estimates
                  Empirical Standard Error Estimates
Parameter       Estimate Standard 95% Confidence Limits     Z Pr > |Z|
                            Error
Intercept       -2266.63 444.1249   -3137.10   -1396.16 -5.10   <.0001
totalyears       61.2667   7.8293    45.9214    76.6119  7.83   <.0001
status     full  40.8062  52.8054   -62.6905   144.3030  0.77   0.4397
status     part   0.0000   0.0000     0.0000     0.0000     .        .
year            1394.667 232.2850   939.3964   1849.937  6.00   <.0001
```

The fitted model is $\hat{E}(bonus) = -2266.63 + 61.2667 \cdot total\ years + 40.8062 \cdot full - time\ employee + 1394.667 \cdot year/10$. The working correlation matrix is $\begin{pmatrix} 1 & 0.5021 & -0.1012 \\ 0.5021 & 1 & 0.5021 \\ -0.1012 & 0.5021 & 1 \end{pmatrix}$. Total number of years with the company and year are significant predictors of bonus. As the total number of years increases by one, the estimated average bonus increases by \$61.2667. It is estimated that, on average, bonus amount increases by \$139.4667 every year.

The predicted bonus in 2021 for a full-time employee who has been with the company for 7 years is computed as follows: $bonus^0 = -2266.63 + 61.2667 \cdot 7 + 40.8062 + 1394.667 \cdot 2.1 =$ \$1,131.844.

In SAS:

```
data predict;
input id totalyears status$ year;
cards;
21 7 full 2.1
;

data longform;
set longform predict;
run;

proc genmod;
 class id status;
  model bonus = totalyears status year;
   repeated subject = id / type=mdep(2);
    output out=outdata p=pbonus;
run;

proc print data=outdata (firstobs=46) noobs;
 var pbonus;
run;
```

```
 pbonus
1131.84
```

In R:

```
#fitting GEE model with autoregressive working correlation matrix
summary(ar.fitted.model<- geeglm(bonus ~ totalyears + status.rel + year,
data=longform.data, id=id, family=gaussian(link='identity'), corstr='ar1'))

Coefficients:
               Estimate Std.err   Wald Pr(>|W|)
(Intercept)     -2247.0   424.0  28.08  1.2e-07
totalyears         59.1     5.5 115.49  < 2e-16
status.relfull     51.9    39.2   1.75     0.19
year             1394.7   223.9  38.81  4.7e-10

Estimated Correlation Parameters:
      Estimate
alpha        0
```

The fitted model is $\hat{E}(bonus) = -2247.0 + 59.1 \cdot total\ years + 51.9 \cdot full - time\ employee + 1394.7 \cdot year/10$. The working correlation matrix is $\begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix}$. Total number of years with the company and year are significant predictors of bonus. As the total number of years increases by one, the estimated average bonus increases by \$59.1. It is estimated that, on average, bonus amount increases by \$139.47 every year.

The predicted bonus in 2021 for a full-time employee who has been with the company for 7 years is computed as follows: $bonus^0 = -2247.0 + 59.1 \cdot 7 + 51.9 + 1394.7 \cdot 2.1 = \$1{,}147.47.$

In R:

```
print(predict(ar.fitted.model, data.frame(totalyears=7, status.rel='full',
year=2.1)))

1148
```

EXERCISE 8.11. For the data in Exercise 8.3,
(a) Fit the generalized estimating equations models with unstructured, Toeplitz (if using SAS), autoregressive, compound symmetric, and independent working correlation matrices.

In SAS:

```
data orthoclinic;
input id gender$ age doctor$ length1 length2 length3 score1 score2 score3 @@;
cards;
101 F 78 A 25 20 25 7.1  7.5  7.6  102 F 63 A 30 30 40 5.5 5.8 6.1
103 F 62 A 10 15 10 10.0 10.0 9.8  104 F 71 B 15 15 40 7.8 7.3 7.5
105 M 68 A 40 60 40 3.5  3.5  3.0  106 F 63 A 25 15 20 8.5 8.7 8.8
107 F 60 B 25 35 25 6.7  5.7  6.5  108 F 70 A 20 20 20 9.0 8.3 8.2
109 F 57 A 30 20 15 8.4  7.8  8.1  110 F 59 B 25 30 15 7.1 7.4 7.9
111 M 62 A 50 30 70 3.0  3.2  2.6  112 M 58 A 20 15 45 6.1 6.8 6.9
113 M 75 A 25 35 30 5.7  5.6  4.7  114 M 76 B 35 50 25 4.9 5.4 5.2
115 F 75 A 15 20 25 8.2  8.9  8.2  116 M 57 A 45 30 40 4.6 3.9 3.2
117 F 68 A 35 25 40 3.8  4.8  5.3  118 M 65 B 40 40 25 3.9 3.9 4.7
119 F 67 B 20 15 30 6.5  7.2  6.6  120 F 60 B 25 15 15 7.3 7.1 7.8
```

```
121 F 67 A 15 20 15 7.7  8.0  8.3  122 F 57 B 10 15 15 9.8 9.2 8.6
123 M 62 B 55 60 75 3.4  2.7  2.3  124 M 71 A 20 30 25 7.1 6.6 7.4
125 M 71 B 15 15 20 8.8  9.1  9.3  126 M 64 A 25 30 30 5.6 6.3 6.3
127 M 51 A 35 40 30 5.1  4.6  3.9  128 F 70 B 35 25 15 6.8 7.1 7.6
129 M 61 A 35 40 50 5.5  5.2  4.8  130 M 62 B 60 40 65 3.7 3.4 2.4
131 F 68 A 20 35 35 5.3  5.6  4.9  132 F 68 B 35 30 15 7.2 6.2 5.6
133 M 64 B 40 20 30 5.4  4.9  4.5  134 F 76 B 30 45 25 5.5 4.7 4.6
135 F 78 B 25 20 15 7.6  8.3  9.2
;

/*creating longform dataset*/
data longform;
set orthoclinic;
 array l[3] length1-length3;
 array s[3] score1-score3;
  do visit=1 to 3;
  length=l[visit];
  score=s[visit];
   output;
    end;
keep id gender age doctor visit length score;
run;

/*fitting GEE model with unstructured working correlation matrix*/
proc genmod;
 class id gender doctor;
  model score = gender age doctor length visit;
   repeated subject = id / type=un;
run;
```

```
WARNING: Iteration limit exceeded.
```

```
/*fitting GEE model with Toeplitz working correlation matrix*/
proc genmod;
 class id gender doctor;
  model score = gender age doctor length visit;
   repeated subject = id / type=mdep(2);
run;
```

```
QIC 121.5327
```

```
/*fitting GEE model with autoregressive working correlation matrix*/
proc genmod;
 class id gender doctor;
  model score = gender age doctor length visit;
   repeated subject = id / type=ar;
run;
```

```
QIC 120.1484
```

```
/*fitting GEE model with compound symmetric working correlation matrix*/
proc genmod;
 class id gender doctor;
  model score = gender age doctor length visit;
   repeated subject = id / type=cs;
run;
```

```
QIC 120.1274
```

```
/*fitting GEE model with independent working correlation matrix*/
```

```
proc genmod;
 class id gender doctor;
  model score = gender age doctor length visit;
   repeated subject = id / type=ind;
run;
```

QIC 117.0717

In R:

```
orthoclinic.data<- read.csv(file='C:/<insert path>/Exercise8.3Data.csv',
header=TRUE, sep=',')

#creating longform dataset
library(reshape2)
data1<-
melt(orthoclinic.data[,c('id','gender','age','doctor','length1','length2',
'length3')],id.vars=c('id','gender','age','doctor'),variable.name='length.visit',
value.name='length')
data2<- melt(orthoclinic.data[,c('score1','score2','score3')],
variable.name='score.visit', value.name='score')
longform.data<- cbind(data1,data2)
visit<- ifelse(longform.data$score.visit=='score1',1,
ifelse(longform.data$score.visit=='score2',2,3))

#specifying reference levels
gender.rel<- relevel(longform.data$gender, ref="M")
doctor.rel<- relevel(longform.data$doctor, ref="B")

library(geepack)
library(MuMIn)
#fitting GEE model with unstructured working correlation matrix
summary(un.fitted.model<- geeglm(score ~ gender.rel + age + doctor.rel
+ length + visit, data=longform.data, id=id, family=gaussian(link='identity'),
corstr = 'unstrectured'))
QIC(un.fitted.model)
```

The model doesn’t converge.

```
#fitting GEE model with autoregressive working correlation matrix
summary(ar.fitted.model<- geeglm(score ~ gender.rel + age + doctor.rel
+ length + visit, data=longform.data, id=id, family=gaussian(link='identity'),
corstr = 'ar1'))
QIC(ar.fitted.model)
```

```
QIC
117
```

```
#fitting GEE model with compound symmetric working correlation matrix
summary(cs.fitted.model<- geeglm(score ~ gender.rel + age + doctor.rel
+ length + visit, data=longform.data, id=id, family=gaussian(link='identity'),
corstr = 'exchangeable'))
QIC(cs.fitted.model)
```

```
QIC
117
```

```
#fitting GEE model with independent working correlation matrix
summary(ind.fitted.model<- geeglm(score ~ gender.rel + age + doctor.rel
+ length + visit, data=longform.data, id=id, family=gaussian(link='identity'),
corstr = 'independence'))
QIC(ind.fitted.model)

QIC
117
```

(b) Which of the fitted models has the best fit according to the QIC criterion?

The QIC values outputted by SAS are summarized here:

	Toep	AR	CS	Ind
QIC	121.533	120.148	120.127	117.072

The optimal model is the one with the independent working correlation matrix. R outputs the same QIC value for autoregressive, compound symmetric, and independent, and the estimated parameters are the same in all three models. Thus, the optimal model is the one with independent working correlation matrix.

(c) Answer parts (e)-(g) in Exercise 8.3 in relation to the best-fitted model.

In SAS:

```
/*fitting GEE model with independent working correlation matrix*/
proc genmod;
 class id gender doctor;
  model score = gender age doctor length visit;
   repeated subject = id / type=ind corrw;
run;
```

```
Working Correlation Matrix
        Col1    Col2    Col3
Row1  1.0000  0.0000  0.0000
Row2  0.0000  1.0000  0.0000
Row3  0.0000  0.0000  1.0000
```

```
                 Analysis Of GEE Parameter Estimates
                  Empirical Standard Error Estimates
Parameter    Estimate Standard 95% Confidence Limits      Z Pr > |Z|
                         Error
Intercept      7.9262   1.3954    5.1913    10.6612  5.68   <.0001
gender     F   1.0438   0.4448    0.1720     1.9156  2.35   0.0189
gender     M   0.0000   0.0000    0.0000     0.0000     .        .
age            0.0067   0.0198   -0.0322     0.0456  0.34   0.7358
doctor     A   0.0797   0.3108   -0.5295     0.6889  0.26   0.7977
doctor     B   0.0000   0.0000    0.0000     0.0000     .        .
length        -0.0933   0.0140   -0.1207    -0.0659 -6.68   <.0001
visit          0.0071   0.1139   -0.2160     0.2303  0.06   0.9501
```

The fitted model is $\hat{E}(score) = 7.9262 + 1.0438 \cdot female + 0.0067 \cdot age + 0.0797 \cdot doctor\ A - 0.0933 \cdot visit\ length + 0.0071 \cdot visit\ number$. The working correlation matrix is $\begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix}$.

Gender and visit length are significant predictors of score. It is estimated that scores given by female patients are, on average, 1.0438 points larger than that given by male patients. As the length of a visit increases by one minute, the estimated average score decreases by 0.0933 points.

The predicted score that would be given by a 55-year-old male patient on his fourth visit to Dr. A with a 30-minute appointment is computed as follows: is $\widehat{score}^0 = 7.9262 + 0.0067 \cdot 55 + 0.0797 - 0.0933 \cdot 30 + 0.0071 \cdot 4 = 5.6038$.

In SAS:

```
data predict;
input id gender$ age doctor$ length visit;
cards;
136 M 55 A 30 4
;

data longform;
set longform predict;
run;

proc genmod;
 class id gender doctor;
  model score = gender age doctor length visit;
   repeated subject = id / type=ind;
      output out=outdata p=pscore;

run;

proc print data=outdata (firstobs=106) noobs;
 var pscore;
run;
```

```
 pscore
5.60333
```

In R:

```
#fitting GEE model with independent working correlation matrix
summary(ind.fitted.model<- geeglm(score ~ gender.rel + age + doctor.rel
+ length + visit, data=longform.data, id=id, family=gaussian(link='identity'),
corstr = 'independence'))

Coefficients:
            Estimate  Std.err  Wald Pr(>|W|)
(Intercept)  7.92624  1.08787 53.09  3.2e-13
gender.relF  1.04380  0.30192 11.95  0.00055
age          0.00670  0.01513  0.20  0.65804
doctor.relA  0.07969  0.22584  0.12  0.72421
length      -0.09331  0.00968 92.97  < 2e-16
visit        0.00713  0.13883  0.00  0.95905

print(predict(ind.fitted.model, data.frame(id=136, gender.rel='M', age=55,
doctor.rel='A',length=30, visit=4)))

5.6
```

EXERCISE 8.12. Consider the data in Exercise 8.4.
(a) Run the generalized estimating equations models with unstructured, Toeplitz (only in SAS), autoregressive, compound symmetric, and independent working correlation matrices for the pulse.

In SAS:

```
data fitness;
input id gender$ age oxygen1 runtime1 pulse1 oxygen2 runtime2 pulse2
oxygen3 runtime3 pulse3;
cards;
1  F 39 37.4 11.4 151 36.6 17.8 158 36.1 15.4 152
2  M 42 60.1 11.5 121 59.0 9.6  131 58.2 9.0  143
3  F 34 44.6 9.6  138 39.8 9.3  148 38.8 9.1  144
4  M 36 51.9 10.5 125 53.4 9.8  135 50.4 9.6  163
5  F 45 40.8 13.1 142 39.5 12.4 151 38.5 12.7 133
6  M 37 45.4 10.3 133 40.6 11.9 145 40.2 11.2 141
7  F 49 45.3 13.1 135 40.6 12.1 148 39.7 11.5 157
8  F 47 44.8 12.1 135 40.1 12.3 148 39.0 11.9 151
9  M 50 48.7 12.6 131 42.3 11.0 143 44.3 10.5 150
10 M 34 45.8 10.8 132 40.9 11.8 144 41.1 11.1 160
11 M 35 50.4 9.6  129 45.9 10.4 137 44.8 10.4 138
12 M 48 50.5 12.9 125 48.6 10.3 135 49.0 9.8  132
13 F 50 44.8 14.0 135 40.3 13.1 148 39.5 12.6 163
14 F 53 39.4 12.7 145 39.3 14.1 154 37.0 12.8 148
15 M 44 46.1 11.0 132 40.9 11.3 144 41.1 10.8 148
16 F 32 39.2 9.1  146 38.7 9.7  158 36.7 10.2 170
17 M 39 54.3 9.4  123 55.1 9.7  132 57.4 9.4  162
18 F 33 39.4 11.6 144 39.4 12.7 154 37.4 12.7 155
19 M 33 47.9 10.1 132 42.2 11.2 143 42.6 10.6 140
20 M 46 49.2 11.2 130 43.9 10.8 141 44.7 10.5 142
;

/*creating longform dataset*/
data longform;
set fitness;
 array o[3] oxygen1-oxygen3;
 array r[3] runtime1-runtime3;
 array p[3] pulse1-pulse3;
  do condition=1 to 3;
  oxygen=o[condition];
  runtime=r[condition];
  pulse=p[condition];
  output;
   end;
keep id gender age oxygen runtime pulse condition;
run;

/*fitting GEE model with unstructured working correlation matrix*/
proc genmod;
 class id gender;
  model pulse = gender age oxygen runtime condition;
   repeated subject = id / type=un;
run;
```

QIC 66.0288

```
/*fitting GEE model with Toeplitz working correlation matrix*/
proc genmod;
 class id gender;
  model pulse = gender age oxygen runtime condition;
   repeated subject = id / type=mdep(2);
run;
```

QIC 66.3730

```
/*fitting GEE model with autoregressive working correlation matrix*/
proc genmod;
 class id gender;
  model pulse = gender age oxygen runtime condition;
   repeated subject = id / type=ar;
run;
```

QIC 65.0370

```
/*fitting GEE model with compound symmetric working correlation matrix*/
proc genmod;
 class id gender;
  model pulse = gender age oxygen runtime condition;
  repeated subject = id / type=cs;
run;
```

QIC 64.9567

```
/*fitting GEE model with independent working correlation matrix*/
proc genmod data=longform;
 class id gender;
  model pulse = gender age oxygen runtime condition;
   repeated subject = id /type=ind;
run;
```

QIC 64.9492

In R:

```
fitness.data<- read.csv(file='C:/<insert path>/Exercise8.4Data.csv',
header=TRUE, sep=',')

#creating longform dataset
library(reshape2)
data1<- melt(fitness.data[,c('id','gender','age','oxygen1','oxygen2','oxygen3')],
id.vars=c('id','gender','age'),variable.name='oxygen.cond',value.name='oxygen')
data2<- melt(fitness.data[,c('runtime1','runtime2','runtime3')],variable.name=
'runtime.cond',value.name='runtime')
data3<- melt(fitness.data[,c('pulse1','pulse2','pulse3')],variable.name=
'pulse.cond',value.name='pulse')
longform.data<- cbind(data1,data2,data3)
condition<- ifelse(longform.data$pulse.cond=='pulse1',1,
ifelse(longform.data$pulse.cond=='pulse2',2,3))

#specifying reference level
gender.rel<- relevel(longform.data$gender, ref="M")

library(geepack)
library(MuMIn)
#fitting GEE model with unstructured working correlation matrix
summary(un.fitted.model<- geeglm(pulse ~ gender.rel + age + oxygen + runtime
+ condition,data=longform.data,id=id, family = gaussian(link='identity'),
corstr = 'unstructured'))
QIC(un.fitted.model)
```

The model doesn’t converge.

```
#fitting GEE model with autoregressive working correlation matrix
summary(ar.fitted.model<- geeglm(pulse ~ gender.rel + age + oxygen + runtime
+ condition,data=longform.data,id=id, family = gaussian(link='identity'),
corstr = 'ar1'))
QIC(ar.fitted.model)

 QIC
73.2

#fitting GEE model with compound symmetric working correlation matrix
summary(cs.fitted.model<- geeglm(pulse ~ gender.rel + age + oxygen + runtime
+ condition,data=longform.data,id=id, family = gaussian(link='identity'),
corstr = 'exchangeable'))
QIC(cs.fitted.model)

 QIC
73.2

#fitting GEE model with independent working correlation matrix
summary(ind.fitted.model<- geeglm(pulse ~ gender.rel + age + oxygen + runtime
+ condition,data=longform.data,id=id, family = gaussian(link='identity'),
corstr = 'independence'))
QIC(ind.fitted.model)

 QIC
73.2
```

(b) Compare the QIC values for the fitted models and choose the optimal one.

In SAS, the model with the independent working correlation matrix is optimal. The QIC values are summarized below:

	UN	Toep	AR	CS	Ind
QIC	66.0288	66.373	65.037	64.9567	64.9492

In R, the three models (autoregressive, compound symmetric, and independent) have the same parameter estimates.

(c) For the optimal model, do questions (c)-(e) in Exercise 8.4.

In SAS:

```
/*fitting GEE model with independent working correlation matrix*/
proc genmod;
 class id gender;
  model pulse = gender age oxygen runtime condition;
   repeated subject=id / type=ind corrw;
run;
```

```
Working Correlation Matrix
        Col1   Col2   Col3
Row1  1.0000 0.0000 0.0000
Row2  0.0000 1.0000 0.0000
Row3  0.0000 0.0000 1.0000
```

```
                 Analysis Of GEE Parameter Estimates
                  Empirical Standard Error Estimates
Parameter   Estimate Standard 95% Confidence Limits     Z Pr > |Z|
                        Error
Intercept   152.8172  15.2280   122.9708   182.6636 10.04   <.0001
gender    F   7.0418   2.4289     2.2812    11.8023  2.90   0.0037
gender    M   0.0000   0.0000     0.0000     0.0000   .       .
age          -0.2128   0.1217    -0.4513     0.0257 -1.75   0.0803
oxygen       -0.4401   0.2151    -0.8617    -0.0185 -2.05   0.0407
runtime       0.1080   0.5751    -1.0192     1.2352  0.19   0.8510
condition     6.9483   1.5668     3.8774    10.0192  4.43   <.0001
```

The fitted model is $\hat{E}(pulse) = 152.8172 + 7.0418 \cdot female - 0.2128 \cdot age - 0.4401 \cdot oxygen + 0.1080 \cdot runtime + 6.9483 \cdot condition$. The working correlation matrix is $\begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix}$. Gender, oxygen intake, and condition are significant predictors of pulse. It is estimated that the pulse for female runners is, on average, 7.0418 points larger than that for male runners. As oxygen intake increases by one unit, the estimated mean pulse decreases by 0.4401 units. As the condition number increases by one, the estimated mean pulse increases by 9.9483.

Next, we predict an average heart rate for a 36-year-old woman who is running on a treadmill, if her oxygen intake is 40.2 units, and her run time is 10.3 minutes per mile. We compute $pulse^0 = 152.8172 + 7.0418 - 0.2128 \cdot 36 - 0.4401 \cdot 40.2 + 0.1080 \cdot 10.3 + 6.9483 = 142.567.$

In SAS:

```
data predict;
input id gender$ age oxygen runtime condition;
cards;
21 F 36 40.2 10.3 1
;

data longform;
set longform predict;
run;

proc genmod;
 class id gender;
  model pulse = gender age oxygen runtime condition;
   repeated subject = id / type=ind;
    output out=outdata p=ppulse;
run;

proc print data=outdata (firstobs=61) noobs;
 var ppulse;
run;
```

```
 ppulse
142.568
```

In R:

```
#fitting GEE model with independent working correlation matrix
```

```
summary(ind.fitted.model<- geeglm(pulse ~ gender.rel + age + oxygen + runtime
+ condition,data=longform.data,id=id,family = gaussian(link='identity'),
corstr = 'independence'))
```

```
Coefficients:
            Estimate Std.err  Wald Pr(>|W|)
(Intercept)  152.817  15.895 92.43  < 2e-16
gender.relF    7.042   2.258  9.73   0.0018
age           -0.213   0.129  2.70   0.1001
oxygen        -0.440   0.266  2.74   0.0982
runtime        0.108   0.663  0.03   0.8706
condition      6.948   1.508 21.23  4.1e-06
```

```
print(predict(ind.fitted.model, data.frame(gender.rel='F', age=36,
oxygen=40.2, runtime=10.3, condition=1)))
```

```
143
```

EXERCISE 8.13. For the data given in Exercise 8.5, do the following questions:
(a) Fit the GEE models with unstructured, Toeplitz, autoregressive, compound symmetric, and independent working correlation matrices of the response variable BMI.

In SAS:

```
data weightloss;
input id group$ gender$ aexercise aBMI bexercise bBMI cexercise cBMI @@;
cards;
1  Int F 0  42.4 50 40.0 120 36.8  2  Int F 15 32.9 20 30.6 25  28.6
3  Int M 10 32.0 30 30.8 30  26.1  4  Int M 20 26.1 80 25.5 80  21.1
5  Int F 0  27.5 20 26.4 20  22.5  6  Int F 30 40.4 75 38.3 180 32.1
7  Int M 15 33.5 50 28.2 50  25.8  8  Int F 15 35.2 35 34.8 90  30.6
9  Int F 0  39.5 55 37.1 50  35.3  10 Int M 20 27.3 30 26.3 30  22.6
11 Int M 0  46.9 50 43.5 50  40.3  12 Int M 20 34.4 80 32.2 85  28.1
13 Int F 0  34.2 60 31.0 65  26.8  14 Int F 45 26.5 30 24.6 30  20.8
15 Int F 0  29.6 20 28.2 20  24.9  16 Int F 10 31.2 80 29.3 50  28.6
17 Cnt F 0  29.3 25 28.9 30  26.3  18 Cnt M 20 45.9 10 43.1 15  42.9
19 Cnt M 0  41.5 20 38.8 30  39.9  20 Cnt F 30 33.3 25 33.4 35  33.2
21 Cnt M 15 31.1 35 30.9 0   30.9  22 Cnt F 10 43.3 35 43.6 30  44.5
23 Cnt M 15 35.5 0  36.5 5   35.3  24 Cnt F 10 42.4 15 43.4 50  42.3
25 Cnt F 20 37.0 30 36.6 45  35.5  26 Cnt M 0  37.8 30 35.7 45  34.3
27 Cnt F 20 23.7 10 23.1 0   23.7  28 Cnt F 10 38.7 15 20.4 25  20.1
29 Cnt F 0  41.2 15 41.2 55  39.7  30 Cnt F 30 30.2 35 29.9 5   29.4
31 Cnt M 10 38.4 20 38.1 30  37.0  32 Cnt F 10 37.5 15 37.4 5   36.8
33 Cnt M 30 34.5 10 34.4 20  33.9  34 Cnt M 15 37.6 35 36.2 25  36.0
;

/*creating longform dataset*/
data longform;
set weightloss;
 array m[3] (0 1 3);
 array e[3] aexercise bexercise cexercise;
 array b[3] aBMI bBMI cBMI;
  do i=1 to 3;
  month=m[i];
  exercise=e[i];
  BMI=b[i];
  output;
  end;
keep id group gender exercise BMI month;
run;

/*fitting GEE model with unstructured working correlation matrix*/
proc genmod;
 class id group gender(ref='F');
  model BMI = group gender exercise month;
   repeated subject = id / type=un;
run;
```

```
WARNING: Iteration limit exceeded.
```

```
/*fitting GEE model with Toeplitz working correlation matrix*/
proc genmod;
 class id group gender(ref='F');
  model BMI = group gender exercise month;
   repeated subject = id / type=mdep(2);
run;
```

```
QIC 113.0602
```

```
/*fitting GEE model with autoregressive working correlation matrix*/
proc genmod;
 class id group gender(ref='F');
  model BMI = group gender exercise month;
   repeated subject = id / type=ar;
run;
```

```
QIC 112.7227
```

```
/*fitting GEE model with compound symmetric working correlation matrix*/
proc genmod;
 class id group gender(ref='F');
  model BMI = group gender exercise month;
   repeated subject = id / type=cs;
run;
```

```
QIC 113.0680
```

```
/*fitting GEE model with independent working correlation matrix*/
proc genmod;
 class id group gender(ref='F');
  model BMI = group gender exercise month;
   repeated subject = id / type=ind;
run;
```

```
QIC 113.7968
```

In R:

```
weightloss.data<- read.csv(file='C:/<insert path>/Exercise8.5Data.csv',
header=TRUE, sep=',')

#creating longform dataset
library(reshape2)
data1<- melt(weightloss.data[,c('id','group','gender','aexercise','bexercise',
'cexercise')], id.vars=c('id','group','gender'),variable.name='exercise.visit',
value.name='exercise')
```

```
data2<- melt(weightloss.data[,c('aBMI','bBMI','cBMI')],variable.name='BMI.visit',
value.name='BMI')
longform.data<- cbind(data1,data2)
month<- ifelse(longform.data$BMI.visit=='aBMI',0,ifelse(longform.data$BMI.visit
=='bBMI',1,3))

#specifying reference levels
group.rel<- relevel(longform.data$group, ref="Int")
gender.rel<- relevel(longform.data$gender, ref="F")

library(geepack)
library(MuMIn)
#fitting GEE model with unstructured working correlation matrix
summary(un.fitted.model<- geeglm(BMI ~ group.rel + gender.rel + exercise
+ month, data=longform.data, id=id, family=gaussian(link='identity'),
corstr = 'unstructured'))
QIC(un.fitted.model)
```

```
The model doesn't converge.
```

```
#fitting GEE model with autoregressive working correlation matrix
summary(ar.fitted.model<- geeglm(BMI ~ group.rel + gender.rel + exercise
+ month, data=longform.data, id=id, family=gaussian(link='identity'),
corstr = 'ar1'))
QIC(ar.fitted.model)
```

```
  QIC
111.4
```

```
#fitting GEE model with compound symmetric working correlation matrix
summary(cs.fitted.model<- geeglm(BMI ~ group.rel + gender.rel + exercise
+ month, data=longform.data, id=id, family=gaussian(link='identity'),
corstr = 'exchangeable'))
QIC(cs.fitted.model)
```

```
QIC
111
```

```
#fitting GEE model with independent working correlation matrix
summary(ind.fitted.model<- geeglm(BMI ~ group.rel + gender.rel + exercise
+ month, data=longform.data, id=id, family=gaussian(link='identity'),
corstr = 'independence'))
QIC(ind.fitted.model)
```

```
QIC
111
```

(b) Choose the best-fitted model with respect to the QIC criterion.

SAS selects the model with autoregressive working correlation matrix as the optimal one, according to the QIC criterion. The values are summarized in the table below.

	Toep	**AR**	**CS**	**Ind**
QIC	113.06	112.723	113.068	113.797

In R, the best-fitted model is the one with the compound symmetric working correlation matrix (which has the same parameter estimates as the model with the independent working correlation matrix). The QIC values are summed up here:

	AR	CS	Ind
QIC	111.4	111	111

(c) For the best-fitted model, do parts (c)-(e) in Exercise 8.5.

In SAS:

```
/*fitting GEE model with autoregressive working correlation matrix*/
proc genmod;
 class id group gender(ref='F');
  model BMI = group gender exercise month;
   repeated subject = id / type=ar corrw;
run;
```

```
Working Correlation Matrix
        Col1   Col2   Col3
Row1  1.0000 0.9373 0.8785
Row2  0.9373 1.0000 0.9373
Row3  0.8785 0.9373 1.0000
```

```
                Analysis Of GEE Parameter Estimates
                 Empirical Standard Error Estimates
Parameter     Estimate Standard 95% Confidence Limits     Z Pr > |Z|
                          Error
Intercept      32.9479   1.5936    29.8244    36.0713 20.67   <.0001
group     Cnt   4.0902   2.0527     0.0670     8.1133  1.99   0.0463
group     Int   0.0000   0.0000     0.0000     0.0000     .        .
gender    M     0.8958   1.9807    -2.9863     4.7779  0.45   0.6511
gender    F     0.0000   0.0000     0.0000     0.0000     .        .
exercise       -0.0241   0.0050    -0.0339    -0.0144 -4.87   <.0001
month          -0.9506   0.1629    -1.2699    -0.6312 -5.83   <.0001
```

The fitted model is $\hat{E}(BMI) = 32.9479 + 4.0902 \cdot control + 0.8958 \cdot male - 0.0241 \cdot exercise - 0.9506 \cdot month$. The working correlation matrix is $\begin{pmatrix} 1 & 0.9373 & 0.8785 \\ 0.9373 & 1 & 0.9373 \\ 0.8785 & 0.9373 & 1 \end{pmatrix}$.

Group, exercise, and month are significant predictors of BMI. It is estimated that the BMI for study participants in the control group is, on average, 4.0902 points larger than that for the intervention group participants. For an additional minute of daily exercise, the estimated average BMI decreases by 0.0241 points. For an additional month in the study, the estimated average BMI decreases by 0.9506 points.

Computing the predicted BMI at 3 months for an intervention group female participant, if she exercises for 1 hour every day, we get $BMI^0 = 32.9479 - 0.0241 \cdot 60 - 0.9506 \cdot 3 = 28.6501$.
In SAS:

```
data predict;
input id group$ gender$ exercise month;
cards;
35 Int F 60 3
;
```

```
data longform;
set longform predict;
run;

proc genmod;
 class id group gender(ref='F');
  model BMI = group gender exercise month;
   repeated subject = id / type=ar;
    output out=outdata p=pBMI;
run;

proc print data=outdata (firstobs=103) noobs;
 var pBMI;
run;
```

```
   pBMI
28.6482
```

In R:

```
#fitting GEE model with independent working correlation matrix
summary(ind.fitted.model<- geeglm(BMI ~ group.rel + gender.rel + exercise
+ month, data=longform.data, id=id, family=gaussian(link='identity'),
corstr = 'independence'))
```

```
Coefficients:
             Estimate Std.err   Wald Pr(>|W|)
(Intercept)   31.6674  1.2787 613.37  < 2e-16
group.relCnt   4.6539  1.2829  13.16  0.00029
gender.relM    1.0787  1.1845   0.83  0.36250
exercise       0.0250  0.0206   1.48  0.22412
month         -1.4161  0.5016   7.97  0.00476
```

The fitted model is $\hat{E}(BMI) = 31.6674 + 4.6539 \cdot control + 1.0787 \cdot male + 0.025 \cdot exercise - 1.4161 \cdot month$. The working correlation matrix is $\begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix}$. Group and month are significant predictors of BMI. It is estimated that the BMI for study participants in the control group is, on average, 4.6539 points larger than that for the intervention group participants. For an additional month in the study, the estimated average BMI decreases by 1.4161 points.

Next, we compute the predicted value of BMI at 3 months for an intervention group female participant, if she exercises for 1 hour every day. We write $BMI^0 = 31.6674 + 0.025 \cdot 60 - 1.4161 \cdot 3 = 28.9191$.

In R:

```
print(predict(ind.fitted.model, data.frame(group.rel='Int', gender.rel='F',
exercise=60, month=3)))
```

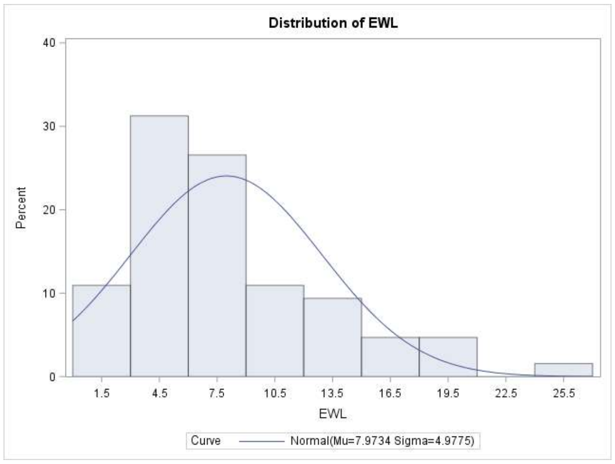
```
28.9
```

CHAPTER 9

EXERCISE 9.1. (a) Plot the histogram of the EWL to see that this variable has a distribution with a long right tail.

In SAS:

```
data weightloss;
input patid group$ gender$ EWL1 EWL2 EWL3 EWL4 @@;
cards;
1  Tx M 11.8 16.4 7.1  4.5  2  Tx F 18.3 7.7  10.7 4.1
3  Tx F 20.1 8.2  7.2  6.3  4  Tx F 15.6 7.8  7.2  2.7
5  Tx M 12.5 8.6  9.7  5.4  6  Tx F 24.4 8.7  6.6  4.7
7  Tx F 18.8 12.3 6.7  4.5  8  Tx M 11.2 9.1  5.6  3.1
9  Cx F 13.9 14.3 4.1  5.0  10 Cx F 6.8  5.2  4.5  1.4
11 Cx M 8.1  12.7 12.3 4.9  12 Cx F 5.6  16.5 4.8  1.8
13 Cx M 9.6  9.9  3.6  3.5  14 Cx M 6.8  7.5  5.1  1.7
15 Cx F 4.7  8.3  3.2  2.4  16 Cx F 6.7  4.1  2.4  1.3
;

/*creating longform dataset*/
data longform;
set weightloss;
  array e[4] EWL1 EWL2 EWL3 EWL4;
   do visit=1 to 4;
     EWL=e[visit];
      output;
       end;
keep patid group gender visit EWL;
run;

/*plotting histogram*/
proc univariate;
 var EWL;
 histogram / normal;
run;
```

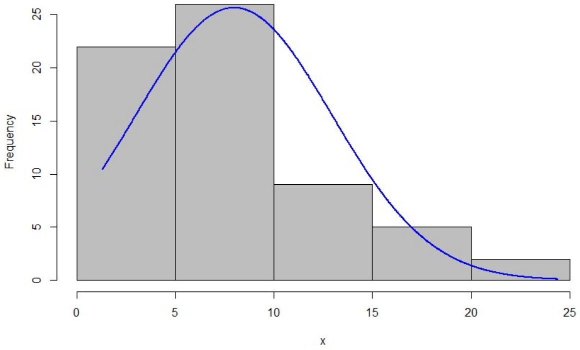


The histogram shows a right-skewed distribution of excess body weight loss amount. In the normality tests, the p-values are below 0.05, confirming that the distribution is not normal.

```
  Goodness-of-Fit Tests for Normal Distribution
Test                 Statistic        p Value
Kolmogorov-Smirnov D    0.13009496 Pr > D    <0.010
Cramer-von Mises   W-Sq 0.29506648 Pr > W-Sq <0.005
Anderson-Darling   A-Sq 1.72390544 Pr > A-Sq <0.005
```

In R:

```
weightloss.data<- read.csv(file='C:/<insert path>/Exercise9.1Data.csv',
header=TRUE, sep=',')

#creating longform dataset
library(reshape2)
longform.data<- melt(weightloss.data, id.vars=c('patid', 'group','gender'),
variable.name='EWLn',value.name='EWL')
visit<- ifelse(longform.data$EWLn=='EWL1',1,ifelse(longform.data$EWLn
=='EWL2',2,ifelse(longform.data$EWLn=='EWL3',3,4)))

#plotting histogram
library(rcompanion)
plotNormalHistogram(longform.data$EWL)
```



```
shapiro.test(longform.data$EWL)
```

```
Shapiro-Wilk normality test

W = 0.91034, p-value = 0.000201
```

(b) Try to run a generalized random slope and intercept model for the EWL based on a gamma distribution. If it doesn't run, fit an intercept-only model. Discuss the fit of this model. Hint: as time variable, use visits with values 1, 2, 3, or 4.

In SAS:

```
/*fitting gamma regression model with random slope and intercept*/
proc glimmix method=Laplace;
 class group(ref='Cx') gender(ref='F');
  model EWL = group gender visit / solution dist=gamma link=log;
  random intercept visit / subject=patid type=un;
  covtest/wald;
run;
```

```
The model doesn’t converge.
```

```
/*fitting gamma regression model with random intercept only*/
proc glimmix method=Laplace;
 class group(ref='Cx') gender(ref='F');
  model EWL = group gender visit / solution dist=gamma link=log;
  random intercept / subject=patid type=un;
  covtest/wald;
run;
```

```
-2 Log Likelihood 299.97

         Covariance Parameter Estimates
Cov Parm Subject Estimate Standard Z Value Pr > Z
                             Error
UN(1,1)  patid    0.04284  0.02584    1.66 0.0487
Residual           0.1131  0.02255    5.01 <.0001

                Solutions for Fixed Effects
Effect    group gender Estimate Standard DF t Value Pr > |t|
                                   Error
Intercept                2.7307   0.1452 13   18.80   <.0001
group     Tx             0.4356   0.1338 47    3.26   0.0021
group     Cx                  0        .  .       .        .
gender          M        0.1008   0.1381 47    0.73   0.4692
gender          F             0        .  .       .        .
visit                   -0.4192  0.03950 47  -10.61   <.0001
```

```
/*checking model fit*/
proc glimmix;
 class group gender;
  model EWL = group gender visit / dist=gamma link=log;
run;
```

```
-2 Log Likelihood 305.82
```

```
data deviance;
 deviance = 305.82 - 299.97;
 pvalue = 1 - probchi(deviance,1);
run;

proc print noobs;
run;
```

```
deviance   pvalue
    5.85 0.015577
```

Fitted in SAS, the gamma regression model with random intercept only has a good fit as supported by the p-value below 0.05.

In R:

```
#specifying reference levels
group.rel<- relevel(longform.data$group, ref="Cx")
gender.rel<- relevel(longform.data$gender, ref="F")
```

```
#fitting gamma regression model with random slope and intercept
library(lme4)
summary(fitted.model<- glmer(EWL ~ group.rel + gender.rel
+ visit + (1 + visit | patid), data=longform.data, family=Gamma(link='log')))
```

```
Random effects:
 Groups   Name        Variance Std.Dev. Corr
 patid    (Intercept) 0.010594 0.10293
          time        0.002103 0.04585  1.00
 Residual             0.124364 0.35265

Fixed effects:
            Estimate Std. Error t value Pr(>|z|)
(Intercept)  2.75279    0.15307  17.983   <2e-16
group.relTx  0.46247    0.16694   2.770   0.0056
gender.relM -0.01279    0.19227  -0.067   0.9470
visit       -0.42625    0.04005 -10.644   <2e-16
```

```
#checking model fit
null.model<- glm(EWL ~ group.rel + gender.rel + visit, data=longform.data,
family=Gamma(link='log'))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
14.65092
```

```
print(pvalue<- pchisq(deviance, df=3, lower.tail = FALSE))
```

```
0.002140621
```

Fitted in R, the gamma regression model with random slope and intercept fits the data well, as suggested by a small p-value in the deviance test.

(c) What parameters are significant at the 5% level? Give the fitted model, specifying all parameter estimates.

The gamma model fitted in SAS has the form $\hat{E}(EWL) = \exp(2.7307 + 0.4356 \cdot Tx + 0.1008 \cdot male - 0.4192 \cdot visit)$, and $\hat{\alpha} =$ `Residual` $= 0.1131$. The random intercept has the estimated variance $\hat{\sigma}^2_{u_1} = 0.04284$.

The model fitted in R has the estimated parameters $\hat{E}(EWL) = \exp(2.75279 + 0.46247 \cdot Tx - 0.01279 \cdot male - 0.42625 \cdot visit)$, and $\hat{\alpha} =$ `Residual` $= 0.124364$. The estimated random-effect parameters are $\hat{\sigma}^2_{u_1} = 0.010594, \hat{\sigma}^2_{u_2} = 0.002103$, and $\hat{\rho}_{u_1 u_2} = 1$.

The variance of the random intercept is significant at the 5% level, indicating that the fitted mixed-effects regression is appropriate. Group and time are significant predictors of EWL.

(d) Give interpretation of the estimates of significant fixed-effects parameters. Is the new medication superior to the regularly used one?

The estimated average percent excess body weight loss for patients in the treatment group is 0.4356 (0.46247) units larger than that for patients in the control group, suggesting that the new medication is superior to the regularly used one. The estimated average percent excess body weight loss decreases by 0.4192 (0.42625) units with each additional visit.

(e) What percent excess body weight loss can the doctors expect to see between 3 and 6 months in male patients who will be taking this new medication?

Using the model fitted in SAS, we compute the predicted percent excess body weight loss as $EWL^0 = \exp(2.7307 + 0.4356 + 0.1008 - 0.4192 \cdot 4) = 4.9052$.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input patid group$ gender$ visit;
cards;
17 Tx M 4
;

data longform;
set longform predict;
run;

proc glimmix method=Laplace;
 class group(ref='Cx') gender(ref='F');
  model EWL = group gender visit / dist=gamma link=log;
  random intercept / subject=patid type=un;
  output out=outdata pred(ilink)=pEWL;
run;

proc print data=outdata (firstobs=65) noobs;
 var pEWL;
run;
```

```
   pEWL
4.90585
```

For the model fitted in R, the predicted value is $EWL^0 = \exp(2.75279 + 0.46247 - 0.01279 - 0.42625 \cdot 4) = 4.4704$.

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(patid=17, group.rel='Tx', gender.rel='M',
visit=4), re.form=NA, type='response'))
```

```
4.470331
```

EXERCISE 9.2. (a) Model the logistically distributed presence of side effects via a generalized random slope and intercept model. In SAS, to obtain better estimates, scale age by a factor of 100. Discuss the model fit.

In SAS:

```
data pharma;
input patid dosage$ gender$ age week1 week3 week7 week16 @@;
cards;
```

```
1  A F 56 1 1 0 0  2  A F 53 1 1 1 0  3  A F 32 0 1 0 1
4  A F 22 0 0 0 0  5  A F 38 0 0 1 1  6  A F 42 0 1 1 1
7  A F 46 0 1 1 0  8  A M 33 1 1 1 1  9  A M 44 0 0 1 1
10 A M 34 0 1 0 0  11 A M 38 0 0 1 1  12 A M 40 0 0 1 1
13 A M 43 0 0 0 0  14 A M 44 0 0 1 0  15 A F 48 0 0 0 0
16 A F 29 0 1 0 0  17 A F 30 0 0 0 0  18 B F 30 0 0 0 0
19 B F 31 0 0 0 0  20 B F 32 1 1 0 0  21 B F 31 0 0 1 0
22 B F 50 0 0 0 1  23 B F 38 0 0 0 0  24 B M 51 0 0 1 1
25 B M 32 0 0 1 1  26 B M 25 0 0 0 0  27 B M 24 0 0 0 0
28 B M 34 0 0 0 0  29 B M 36 0 0 0 1  30 B M 44 0 0 1 1
31 B M 40 1 1 0 0  32 B M 29 0 1 0 0  33 B M 33 1 1 0 0
34 B M 38 0 0 1 0
;

/*creating longform dataset*/
data longform;
set pharma;
 array w[4] (1 3 7 16);
 array s[4] week1 week3 week7 week16;
  do i=1 to 4;
   week=w[i];
   sideeffects=s[i];
    age=age/100;
   output;
   end;
keep patid dosage gender age week sideeffects;
run;

/*fitting logistic regression model with random slope and intercept*/
proc glimmix method=Laplace;
 class dosage(ref='B') gender(ref='F');
  model sideeffects = dosage gender age week / solution dist=binomial link=logit;
  random intercept week / subject=patid type=un;
  covtest/wald;
run;
```

```
-2 Log Likelihood 147.31

         Covariance Parameter Estimates
Cov Parm Subject Estimate Standard Z Value   Pr Z
                             Error
UN(1,1)  patid    17.8005  11.6113    1.53 0.0626
UN(2,1)  patid    -3.1901   2.0170   -1.58 0.1137
UN(2,2)  patid     0.6761   0.4185    1.62 0.0531

                 Solutions for Fixed Effects
Effect    dosage gender Estimate Standard DF t Value Pr > |t|
                                    Error
Intercept                -1.5838   1.2540 31   -1.26   0.2160
dosage    A               2.1726   1.0608 67    2.05   0.0445
dosage    B                    0        .  .       .        .
gender           M        0.6921   0.9485 67    0.73   0.4681
gender           F             0        .  .       .        .
age                      -7.9672   2.9241 67   -2.72   0.0082
week                     -0.2236   0.1787 33   -1.25   0.2194
```

```
/*checking model fit*/
```

```
proc glimmix;
 class dosage gender;
  model sideeffects = dosage gender age week / dist=binomial link=logit;
run;
```

```
-2 Log Likelihood 162.82
```

```
data deviance;
 deviance = 162.82 - 147.31;
 pvalue = 1 - probchi(deviance, 3);
run;

proc print noobs;
run;
```

```
deviance     pvalue
   15.51 .001428836
```

The model has a very good fit as evidenced by the tiny p-value in the deviance test.

In R:

```
pharma.data<- read.csv(file='C:/<insert path>/Exercise9.3Data.csv', header=TRUE,
sep=',')

#creating longform dataset
library(reshape2)
longform.data<- melt(pharma.data, id.vars=c('patid', 'dosage','gender','age'),
variable.name='weekn', value.name='sideeffects')
week<- ifelse(longform.data$weekn=='week1',1, ifelse(longform.data$weekn
=='week3',3,ifelse(longform.data$weekn=='week7',7,16)))

#fitting logistic model with random slope and intercept
library(lme4)
summary(fitted.model<- glmer(sideeffects ~ dosage + gender + age + week
+ (1 + week | patid), data=longform.data, family=binomial(link='logit')))
```

```
Random effects:
 Groups Name        Variance Std.Dev. Corr
 patid  (Intercept) 5.5846   2.3632
        week        0.2157   0.4644   -0.91

Fixed effects:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -4.24086    1.95170  -2.173   0.0298
dosageB     -0.97776    0.70953  -1.378   0.1682
genderM      0.59956    0.68388   0.877   0.3807
age          0.08335    0.04429   1.882   0.0598
week        -0.01254    0.10554  -0.119   0.9054
```

```
#checking model fit
null.model<- glm(sideeffects ~ dosage + gender + age + week,
data=longform.data, family=binomial(link='logit'))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
6.901126
```

```
print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))
```

```
0.07511689
```

(b) Specify the fitted model, giving the estimates of all parameters. Which parameters are significant at the 5% significance level? At the 10% level?

In SAS, the estimated parameters in the fitted logistic model are:

$$\frac{\hat{P}(side\ effects)}{1-\hat{P}(side\ effects)} = \exp(-1.5838 + 2.1726 \cdot dosage\ A + 0.6921 \cdot male$$
$$-7.9672 \cdot age/100 - 0.2236 \cdot week), \hat{\sigma}_{u_1}^2 = 17.8005, \hat{\sigma}_{u_2}^2 = 0.6761, \text{ and } \hat{\sigma}_{u_1 u_2} = -3.1901.$$

Variances of random slope and intercept are significant at the 10% level. Dosage and age are significant predictors of the probability of side effects at the 5% level.

In R, the estimated parameters in the fitted model are:

$$\frac{\hat{P}(side\ effects)}{1-\hat{P}(side\ effects)} = \exp(-4.24086 - 0.97776 \cdot dosage\ B + 0.59956 \cdot male$$
$$+0.08335 \cdot age - 0.01254 \cdot week), \hat{\sigma}_{u_1}^2 = 5.5846, \hat{\sigma}_{u_2}^2 = 0.2157, \text{ and } \hat{\rho}_{u_1 u_2} = -0.91.$$

The variance of random intercept is significantly different from zero since p-value $= P(Z > 5.5846/2.3632) = P(Z > 2.363152) = 0.00906 < 0.01$. Also, age is marginally significant at the 5% level.

(c) Interpret the estimates of the significant beta coefficients. What dosage should be preferred?

For the model fitted in SAS, for the subjects taking dosage A, the estimated odds in favor of side effects are $\exp(2.1726) \cdot 100\% = 878.1085\%$ of those for subjects taking dosage B. Thus, dosage B should be preferred. Also, as age increases by one year, the estimated odds in favor of side effects change by $(\exp(-0.079272) - 1) \cdot 100\% = -7.62114\%$, that is, decrease by 7.62114%.

For the model fitted in R, as age increases by one year, the estimated odds in favor of side effects change by $(\exp(-0.08335) - 1) \cdot 100\% = -7.99709\%$, that is, decrease by 7.99709%.

(d) Predict the probability of side effects occurring at week 7 for a 40-year-old woman taking dosage A.

Using the model fitted in SAS, we obtain

$$P^0(side\ effects = 1) = \frac{\exp(-1.5838+\ .1726-7.9672\cdot\frac{40}{100}-0.2236\cdot 7)}{1+\exp(-1.5838+2.1726-7.9672\cdot\frac{40}{100}-0.2236\cdot 7)} = 0.015318.$$

For the model fitted in R, we predict

$$P^0(side\ effects = 1) = \frac{\exp(-4.24086+0.08335\cdot 40-0.01254\cdot 7)}{1+\exp(-4.24086+0.08335\cdot 40-0.01254\cdot 7)} = 0.269997.$$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input patid dosage$ gender$ age week;
age=age/100;
cards;
35 A F 40 7
;

data longform;
set longform predict;
run;

proc glimmix method=Laplace;
 class dosage gender;
  model sideeffects = dosage gender age week / dist=binomial link=logit;
  random intercept week / subject=patid type=un;
   output out=outdata pred(ilink)=psideeffects;
run;

proc print data=outdata (firstobs=137) noobs;
 var psideeffects;
run;
```

```
psideeffects
    0.015315
```

In R:

```
#using model for prediction
print(predict(fitted.model, data.frame(patid=35,dosage='A',gender='F',age=40,
week=7),re.form=NA,type='response'))
```

```
0.2699819
```

EXERCISE 9.3. (a) Fit a random slope and intercept model (or random intercept-only model, if appropriate) for the days with occupancy below 65%. Use the Poisson distribution. Discuss the model fit.

In SAS:

```
data hotels;
input hotel region$ ADR1 OCR1 ADR2 OCR2 ADR3 OCR3 ADR4 OCR4 @@;
cards;
1 rural  88  3 76  8  74  11 78  17  2  rural 79  5 98  9  72  7  54  14
3 rural  84  2 67  4  64  9  98  13  4  rural 79  3 88  4  77  80 66  15
5 rural  68  1 75  8  58  16 80  21  6  rural 82  0 95  4  85  9  90  16
7 rural  92  4 93  8  87  13 92  20  8  rural 58  0 54  9  67  19 84  25
9 rural  84  1 87  9  94  6  92  19  10 rural 98  3 92  0  88  3  80  7
11 urban 112 1 137 11 114 5  137 23  12 urban 104 1 176 8  97  6  146 18
13 urban 195 3 171 5  175 6  137 11  14 urban 128 1 113 10 125 3  126 9
15 urban 96  2 152 10 145 5  153 10  16 urban 98  0 170 9  129 3  148 16
17 urban 119 2 121 8  128 6  147 18  18 urban 120 0 130 0  114 2  108 13
;
```

```
data longform;
set hotels;
 array a[4] ADR1 ADR2 ADR3 ADR4;
 array o[4] OCR1 OCR2 OCR3 OCR4;
  do season=1 to 4;
   ADR=a[season];
    OCR=o[season];
  output;
 end;
keep hotel region season ADR OCR;
run;

/*fitting Poisson model with random slope and intercept*/
 proc glimmix method=Laplace;
 class region;
  model OCR = region ADR season / solution dist=poisson link=log;
   random intercept season / subject=hotel type=un;
    covtest/wald;
run;
```

The model doesn’t converge.

```
/*fitting Poisson model with random intercept only*/
proc glimmix method=Laplace;
 class region;
  model OCR = region ADR season/ solution dist=poisson link=log;
   random intercept / subject=hotel type=un;
    covtest/wald;
run;
```

```
-2 Log Likelihood 503.98

         Covariance Parameter Estimates
Cov Parm Subject Estimate Standard Z Value Pr > Z
                             Error
UN(1,1)  hotel     0.1581  0.06353    2.49 0.0064

             Solutions for Fixed Effects
Effect    region Estimate Standard DF t Value Pr > |t|
                             Error
Intercept         -1.0197   0.4744 16   -2.15   0.0473
region    rural    0.9002   0.2721 52    3.31   0.0017
region    urban         0        .  .       .        .
ADR              0.009809 0.003106 52    3.16   0.0026
season             0.5615  0.03986 52   14.09   <.0001
```

```
/*checking model fit*/
proc glimmix;
 class region;
  model OCR = region ADR season / dist=poisson link=log;
run;
```

```
2 Log Likelihood 583.13
```

```
data deviance;
 deviance = 583.13 - 503.98;
 pvalue = 1 - probchi(deviance, 1);
```

```
run;

proc print noobs;
run;
```

```
deviance pvalue
   79.15      0
```

The model fits the data very well since the value of the deviance test statistic is very large and so the p-value is very small.

In R:

```
hotels.data<- read.csv(file='C:/<insert path>/Exercise9.3Data.csv', header=TRUE,
sep=',')

#creating longform dataset
library(reshape2)
data1<- melt(hotels.data[,c('hotel','region','ADR1','ADR2','ADR3','ADR4')],
id.vars=c('hotel','region'), variable.name='ADRn',value.name='ADR')
data2<- melt(hotels.data[,c('OCR1','OCR2','OCR3','OCR4')],variable.name
='OCRn',value.name='OCR')
longform.data<- cbind(data1,data2)
season<- ifelse(longform.data$ADRn=='ADR1',1,ifelse(longform.data$ADRn=='ADR2',
2,ifelse(longform.data$ADRn=='ADR3',3,4)))

#specifying reference level
region.rel<- relevel(longform.data$region, ref="urban")

#fitting Poisson model with random slope and intercept
library(lme4)
summary(fitted.model<- glmer( OCR ~ region.rel + ADR + season + (1 + season|
hotel), data=longform.data, family=poisson(link='log')))
```

```
Random effects:
 Groups Name        Variance Std.Dev. Corr
 hotel  (Intercept) 0.215785 0.4645
        season      0.000462 0.0215   -1.00

Fixed effects:
                 Estimate Std. Error z value Pr(>|z|)
(Intercept)     -1.027042   0.476134  -2.157 0.031002
region.relrural  0.893183   0.271415   3.291 0.000999
ADR              0.009643   0.003114   3.096 0.001959
season           0.570542   0.043169  13.216  < 2e-16
```

```
#checking model fit
null.model<- glm(OCR ~ region.rel + ADR + season, data=longform.data,
family=poisson(link='log'))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
79.46935
```

```
print(p.value<- pchisq(deviance, df=3, lower.tail = FALSE))
```

```
3.988909e-17
```

(b) State the fitted model. Identify all significant parameters. Use $\alpha = 0.05$. Are responses over seasons correlated within each hotel?

The Poisson model fitted in SAS has the estimated parameters $\hat{E}(OCR) = \exp(-1.0197 + 0.9002 \cdot rural + 0.009809 \cdot ADR + 0.5615 \cdot season)$, and the random intercept has the estimated variance $\hat{\sigma}^2_{u_1} = 0.1581$.

All predictors (region, ADR, and season) are statistically significant, and so is the random intercept.

The model fitted in R has the estimated parameters $\hat{E}(OCR) = \exp(-1.027042 + 0.893183 \cdot rural + 0.009643 \cdot ADR + 0.570542 \cdot season)$, $\hat{\sigma}^2_{u_1} = 0.215785, \hat{\sigma}^2_{u_2} = 0.000462,$ and $\hat{\rho}_{u_1 u_2} = -1.$

(c) Interpret the estimates of all significant beta coefficients.

For the model fitted in SAS, we interpret the estimated regression coefficients as follows. For rural hotels, the estimated average number of days the hotel occupancy rate is below 65% is $\exp(0.9002) \cdot 100\% = 246.0095\%$ of that for urban hotels. As the daily average rate increases by one dollar, the estimated average number of days the hotel occupancy rate is below 65% increases by $(\exp(0.009809) - 1) \cdot 100\% = 0.985727\%$. Every next season (summer to fall to winter to spring), the estimated average number of days the hotel occupancy rate is below 65% increases by $(\exp(0.5615) - 1) \cdot 100\% = 75.33005\%$.

For the model fitted in R, the interpretation goes as follows. For rural hotels, the estimated average number of days the hotel occupancy rate is below 65% is $\exp(0.893183) \cdot 100\% = 244.2893\%$ of that for urban hotels. As the daily average rate increases by one dollar, the estimated average number of days the hotel occupancy rate is below 65% increases by $(\exp(0.009643) - 1) \cdot 100\% = 0.968964\%$. Every next season (summer to fall to winter to spring), the estimated average number of days the hotel occupancy rate is below 65% increases by $(\exp(0.570542) - 1) \cdot 100\% = 76.92257\%$.

(d) Predict the number of days with occupancy rate below 65% for the winter season in a rural hotel with average daily rate of $75.

For the model fitted in SAS, the predicted value is $OCR^0 = \exp(-1.0197 + 0.9002 + 0.009809 \cdot 75 + 0.5615 \cdot 3)$=9.98092.

In SAS:

```
/*using the fitted model for prediction*/
data predict;
input hotel region$ ADR season;
cards;
19 rural 75 3
;

data longform;
set longform predict;
run;

proc glimmix method=Laplace;
 class region;
  model OCR = region ADR season / dist=poisson link=log;
   random intercept / subject=hotel type=un;
    output out=outdata pred(ilink)=pOCR;
```

```
run;

proc print data=outdata (firstobs=73) noobs;
var pOCR;
run;
```

```
   pOCR
9.97988
```

For the model fitted in R, the predicted value is $OCR^0 = \exp(-1.027042 + 0.893183 + 0.009643 \cdot 75 + 0.570542 \cdot 3) = 9.98408$.

In R:

```
#using the fitted model for prediction
print(predict(fitted.model, data.frame(hotel=19, region.rel='rural', ADR=75,
season=3), re.form=NA, type='response'))
```

```
9.984353
```

EXERCISE 9.4. (a) Run the random slope and intercept (possibly random intercept-only) model for the PDC, using a beta distribution. Does the model fit the data well? Use the 10% level of significance.

In SAS:

```
data adherence;
input id gender$ age edu$ pdc1 pdc2 pdc3 pdc4 @@;
cards;
1  F 38 >HS    0.05 0.25 0.62 0.87  2  M 57 >HS    0.10 0.60 0.77 0.25
3  M 46 <HS    0.05 0.10 0.15 0.15  4  M 57 <HS    0.02 0.20 0.37 0.37
5  F 39 <HS    0.23 0.90 0.93 0.95  6  F 40 <HS    0.12 0.13 0.57 0.90
7  F 66 HSgrad 0.02 0.28 0.12 0.57  8  F 50 HSgrad 0.20 0.23 0.38 0.10
9  F 43 >HS    0.08 0.72 0.87 0.97  10 F 69 HSgrad 0.18 0.50 0.75 0.63
11 F 45 <HS    0.03 0.10 0.40 0.98  12 F 41 >HS    0.13 0.82 0.93 0.65
13 F 43 HSgrad 0.05 0.75 0.98 0.38  14 M 49 HSgrad 0.17 0.37 0.20 0.58
15 F 39 >HS    0.05 0.20 0.92 0.30  16 M 47 >HS    0.03 0.57 0.67 0.60
17 M 65 >HS    0.02 0.18 0.15 0.33  18 F 59 <HS    0.03 0.07 0.18 0.37
19 F 41 >HS    0.02 0.88 0.92 0.85  20 F 49 >HS    0.05 0.13 0.05 0.03
21 F 36 HSgrad 0.08 0.20 0.32 0.13  22 M 42 HSgrad 0.13 0.33 0.22 0.37
23 M 45 HSgrad 0.03 0.15 0.33 0.70  24 M 49 <HS    0.03 0.03 0.18 0.85
25 M 56 <HS    0.03 0.67 0.48 0.50  26 M 49 HSgrad 0.07 0.15 0.20 0.12
27 M 41 HSgrad 0.12 0.23 0.53 0.32
;

/*creating longform dataset*/
data longform;
set adherence;
 array p[4] pdc1 pdc2 pdc3 pdc4;
  do refill=1 to 4;
   pdc=p[refill];
  output;
 end;
keep id gender age edu refill pdc;
```

```
run;

/*fitting beta model with random slope and intercept*/
proc glimmix method=Laplace;
 class gender(ref='M') edu(ref='<HS');
  model pdc = gender age edu refill / solution dist=beta link=logit;
   random intercept refill / subject=id type=un;
   covtest/wald;
run;
```

The model doesn't converge.

```
/*fitting beta model with random intercept only*/
proc glimmix method=Laplace;
 class gender(ref='M') edu(ref='HSgrad');
  model pdc = gender age edu refill / solution dist=beta link=logit;
   random intercept / subject=id type=un;
   covtest/wald;
run;
```

-2 Log Likelihood -69.56

```
         Covariance Parameter Estimates
Cov Parm Subject Estimate Standard Z Value   Pr Z
                             Error
UN(1,1)  id        0.1638   0.1253    1.31 0.0955
Scale              3.4024   0.5544    6.14 <.0001
```

```
                  Solutions for Fixed Effects
Effect    gender edu    Estimate Standard DF t Value Pr > |t|
                                    Error
Intercept                -1.4351   0.7980 22   -1.80   0.0859
gender    F               0.4345   0.2561 80    1.70   0.0936
gender    M                    0        .  .       .        .
age                     -0.02129  0.01427 80   -1.49   0.1397
edu              <HS      0.1276   0.2999 80    0.43   0.6715
edu              >HS      0.2823   0.2982 80    0.95   0.3467
edu              HSgrad        0        .  .       .        .
refill                    0.6161  0.08994 80    6.85   <.0001
```

```
/*checking model fit*/
proc glimmix;
 class gender edu;
  model pdc = gender age edu refill / dist=beta link=logit;
run;
```

-2 Log Likelihood -66.83

```
data deviance;
 deviance = -66.83 - (-69.56);
 pvalue = 1 - probchi(deviance, 1);
run;

proc print noobs;
run;
```

```
deviance   pvalue
    2.73 0.098479
```

In R:

```
adherence.data<- read.csv(file='C:/<insert path>/Exercise9.4Data.csv',
header=TRUE, sep=',')

#creating longform dataset and time variable
library(reshape2)
longform.data<- melt(adherence.data, id.vars=c('id','gender','age','edu'),
variable.name='pdcn',value.name='pdc')
refill<- ifelse(longform.data$pdcn=='pdc1',1,ifelse(longform.data$pdcn=='pdc2',
2,ifelse(longform.data$pdcn=='pdc3',3,4)))

#specifying reference levels
gender.rel<- relevel(longform.data$gender, ref="M")
edu.rel<- relevel(longform.data$edu, ref="HSgrad")

#fitting beta model with random slope and intercept
library(glmmTMB)
summary(glmmTMB(pdc ~ gender.rel + age + edu.rel + refill + (1 + refill | id),
data=longform.data, family=beta_family(link="logit")))
```

```
The model doesn't converge.
```

```
#fitting beta model with random intercept only
summary(fitted.model<- glmmTMB(pdc ~ gender.rel + age + edu.rel + refill + (1 |
id), data=longform.data, family=beta_family(link="logit")))
```

```
Random effects:

Groups Name        Variance Std.Dev.
 id    (Intercept) 0.1638   0.4048

Overdispersion parameter for beta family ():  3.4

Conditional model:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -1.43507    0.79810  -1.798   0.0722
gender.relF  0.43451    0.25607   1.697   0.0897
age         -0.02129    0.01427  -1.491   0.1358
edu.rel<HS   0.12764    0.29991   0.426   0.6704
edu.rel>HS   0.28231    0.29822   0.947   0.3438
refill       0.61606    0.08994   6.850  7.4e-12
```

```
#checking model fit
library(betareg)
null.model<- betareg(pdc ~ gender.rel + age + edu.rel + refill,
data=longform.data, link='logit')
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
2.728118
```

```
print(p.value<- pchisq(deviance, df=1, lower.tail = FALSE))
```

```
0.0985954
```

(b) Specify the fitted model and interpret all estimated significant fixed-effects parameters. Use the significance level of 0.10.

The fitted beta model has the estimated parameters

$\hat{\mu} = \frac{\exp(-1.4351+0.4345\cdot female-0.02129\cdot age+0.1276\cdot <HS + 0.2823\cdot >HS + 0.6161\cdot refill)}{1+\mathrm{e} \quad (-1.4351+ \ .4345\cdot female-0.02129\cdot age+0.1276\cdot <HS + 0.2823\cdot >HS + 0.6161\cdot refill)}$, $\hat{\sigma}^2_{u_1} = 0.1638,$ and $\hat{\phi} = 3.4$.

Gender and refill are significant predictors of μ, and the variance of the random intercept is significant.

For females, the ratio of estimated proportion of days that a patient took a diabetes medication and the estimated proportion of days that the medication wasn't taken is $\exp(0.4345)\cdot 100\% = 154.4191\%$ of that for males. With every additional refill, the estimated ratio increases by $(\exp(0.6161) - 1)\cdot 100\% = 85.16923\%$.

(c) What is the predicted PDC value for the second refill of medication for a 50-year-old man with a Bachelor's degree?

The predicted value is $PDC^0 = \frac{\exp(-1.4351-0.02129\cdot 50 + 0.2823 + 0.6161\cdot 2)}{1+\exp(-1.4351-0.02129\cdot 50 + 0.2823 + 0.6161\cdot 2)} = 0.271881.$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input id gender$ age edu$ refill;
cards;
28 M 50 >HS 2
;

data longform;
set longform predict;
run;

proc glimmix method=Laplace;
 class gender edu;
  model pdc = gender age edu refill / dist=beta link=logit;
   random intercept / subject=id type=un;
    output out=outdata pred(ilink)=ppdc;
run;

proc print data=outdata(firstobs=109) noobs;
 var ppdc;
run;
```

```
   ppdc
0.27191
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(id=28, gender.rel='M', age=50,
edu.rel='>HS', refill=2), allow.new.levels=TRUE, type='response'))
```

```
0.2719147
```

EXERCISE 9.5. Use the data in Exercise 9.1 to do the following:
(a) Fit the GEE models for the EWL with the gamma underlying distribution and with unstructured, Toeplitz (only in SAS), autoregressive, compound symmetric, and independent working correlation matrices.

In SAS:

```
data weightloss;
input patid group$ gender$ EWL1 EWL2 EWL3 EWL4 @@;
cards;
1  Tx M 11.8 16.4 7.1  4.5  2  Tx F 18.3 7.7  10.7 4.1
3  Tx F 20.1 8.2  7.2  6.3  4  Tx F 15.6 7.8  7.2  2.7
5  Tx M 12.5 8.6  9.7  5.4  6  Tx F 24.4 8.7  6.6  4.7
7  Tx F 18.8 12.3 6.7  4.5  8  Tx M 11.2 9.1  5.6  3.1
9  Cx F 13.9 14.3 4.1  5.0  10 Cx F 6.8  5.2  4.5  1.4
11 Cx M 8.1  12.7 12.3 4.9  12 Cx F 5.6  16.5 4.8  1.8
13 Cx M 9.6  9.9  3.6  3.5  14 Cx M 6.8  7.5  5.1  1.7
15 Cx F 4.7  8.3  3.2  2.4  16 Cx F 6.7  4.1  2.4  1.3
;

/*creating longform dataset*/
data longform;
set weightloss;
  array e[4] EWL1 EWL2 EWL3 EWL4;
   do visit=1 to 4;
       EWL=e[visit];
       output;
       end;
keep patid group gender visit EWL;
run;

/*fitting GEE gamma model with unstructured working correlation matrix*/
proc genmod;
 class patid group(ref='Cx') gender(ref='F');
  model EWL = group gender visit / dist=gamma link=log;
   repeated subject = patid / type=un;
run;
```

```
QIC 2000.1740
```

```
/*fitting GEE gamma model with Toeplitz working correlation matrix*/
proc genmod;
 class patid group(ref='Cx') gender(ref='F');
  model EWL = group gender visit / dist=gamma link=log;
   repeated subject = patid / type=mdep(3);
run;
```

```
QIC 2114.9666
```

```
/*fitting GEE gamma model with autoregressive working correlation matrix*/
proc genmod;
 class patid group(ref='Cx') gender(ref='F');
  model EWL = group gender visit / dist=gamma link=log;
   repeated subject = patid / type=ar;
run;
```

```
QIC 1926.1829
```

```
/*fitting GEE gamma model with compound symmetric working correlation matrix*/
proc genmod;
 class patid group(ref='Cx') gender(ref='F');
  model EWL = group gender visit / dist=gamma link=log;
   repeated subject = patid / type=cs;
run;
```

```
QIC 1980.8110
```

```
/*fitting GEE gamma model with independent working correlation matrix*/
proc genmod;
 class patid group(ref='Cx') gender(ref='F');
  model EWL = group gender visit / dist=gamma link=log;
   repeated subject = patid / type=ind;
run;
```

```
QIC 1980.8110
```

In R:

```
weightloss.data<- read.csv(file='C:/<insert path>/Exercise9.1Data.csv',
header=TRUE, sep=',')

#creating longform dataset
library(reshape2)
longform.data<- melt(weightloss.data, id.vars=c('patid', 'group', 'gender'),
variable.name='EWLn',value.name='EWL')
visit<- ifelse(longform.data$EWLn=='EWL1',1,ifelse(longform.data$EWLn=='EWL2',
2,ifelse(longform.data$EWLn=='EWL3',3,4)))

#specifying reference levels
group.rel<- relevel(longform.data$group, ref="Cx")
gender.rel<- relevel(longform.data$gender, ref="F")

#fitting GEE gamma model with unstructured working correlation matrix
library(geepack)
library(MuMIn)
summary(un.fitted.model<- geeglm(EWL ~ group.rel + gender.rel + visit,
data=longform.data, id=patid, family=Gamma(link='log'), corstr = 'unstructured'))
QIC(un.fitted.model)
```

The model doesn’t converge.

```
#fitting GEE gamma model with autoregressive working correlation matrix
summary(ar.fitted.model<- geeglm(EWL ~ group.rel + gender.rel + visit,
data=longform.data, id=patid, family=Gamma(link='log'), corstr = 'ar1'))
QIC(ar.fitted.model)
```

```
 QIC
2110
```

```
#fitting GEE gamma model with compound symmetric working correlation matrix
summary(cs.fitted.model<- geeglm(EWL ~ group.rel
+ gender.rel + visit, data=longform.data, id=patid,
family=Gamma(link='log'), corstr = 'exchangeable'))
QIC(cs.fitted.model)
```

```
 QIC
2110
```

```
#fitting GEE gamma model with independent working correlation matrix
summary(ind.fitted.model<- geeglm(EWL ~ group.rel
+ gender.rel + visit, data=longform.data, id=patid,
family=Gamma(link='log'), corstr = 'independence'))
QIC(ind.fitted.model)

 QIC
2110
```

(b) Compare model fits. Use the QIC criterion.

For the models fitted in SAS, the autoregressive has a better fit since the QIC value for this model is the smallest. The values are summarized in the table below.

	UN	Toep	AR	CS	Ind
QIC	2000.17	2114.97	1926.18	1980.81	1980.81

R fits the same model for autoregressive, compound symmetric, and independent working correlation matrices.

(c) For the model that has the best fit, do questions (c)-(e) from Exercise 9.1.

In SAS:

```
/*fitting GEE gamma model with autoregressive working correlation matrix*/
proc genmod;
 class patid group(ref='Cx') gender(ref='F');
  model EWL = group gender visit / dist=gamma link=log;
   repeated subject = patid / type=ar corrw;
run;
```

```
   Working Correlation Matrix
         Col1   Col2   Col3   Col4
Row1 1.0000 0.1504 0.0226 0.0034
Row2 0.1504 1.0000 0.1504 0.0226
Row3 0.0226 0.1504 1.0000 0.1504
Row4 0.0034 0.0226 0.1504 1.0000
```

```
                 Analysis Of GEE Parameter Estimates
                  Empirical Standard Error Estimates
Parameter    Estimate Standard 95% Confidence Limits      Z Pr > |Z|
                         Error
Intercept      2.7371   0.1329     2.4766     2.9976  20.59   <.0001
group     Tx   0.4107   0.1334     0.1493     0.6721   3.08   0.0021
group     Cx   0.0000   0.0000     0.0000     0.0000      .        .
gender    M    0.0893   0.1396    -0.1843     0.3629   0.64   0.5225
gender    F    0.0000   0.0000     0.0000     0.0000      .        .
visit         -0.4099   0.0264    -0.4616    -0.3582 -15.54   <.0001
```

In the fitted GEE gamma model, the percent excess body weight loss has estimated mean $\hat{E}(EWL) = \exp(2.7371 + 0.4107 \cdot Tx + 0.0893 \cdot male - 0.4099 \cdot visit)$, and the estimated correlation matrix for each individual $\begin{pmatrix} 1.000 & 0.1504 & 0.0226 & 0.0034 \\ 0.1504 & 1.000 & 0.1504 & 0.0226 \\ 0.0226 & 0.1504 & 1.000 & 0.1504 \\ 0.0034 & 0.0226 & 0.1504 & 1.000 \end{pmatrix}$. Group and visit are significant predictors of EWL. It is estimated that the EWL for participants in the treatment group is, on average, 0.4107 points larger than that for the control group participants (i.e., the new medication is efficient). From visit to visit, the estimated average EWL decreases by 0.4099 points.

Next, we compute the percent excess body weight loss that the doctors can expect to see between 3 and 6 months in male patients who will be taking this new medication. We obtain

$$EWL^0 = \exp(2.7371 + 0.4107 + 0.0893 - 0.4099 \cdot 4) = 4.940665.$$

In SAS:

```
data predict;
input patid group$ gender$ visit;
cards;
17 Tx M 4
;

data longform;
set longform predict;
run;

proc genmod;
 class patid group gender
  model EWL = group gender visit / dist=gamma link=log;
   repeated subject = patid / type=ar;
        output out=outdata p=pEWL;
run;

proc print data=outdata (firstobs=65) noobs;
 var pEWL;
run;
```

```
   pEWL
4.93989
```

In R:

```
#fitting GEE gamma model with autoregressive working correlation matrix
summary(ar.fitted.model<- geeglm(EWL ~ group.rel + gender.rel + visit,
data=longform.data, id=patid, family=Gamma(link='log'), corstr = 'ar1'))
```

```
Coefficients:
            Estimate Std.err  Wald Pr(>|W|)
(Intercept)   2.7572  0.1512 332.3   <2e-16
group.relTx   0.3947  0.1061  13.8   0.0002
gender.relM   0.0980  0.1096   0.8   0.3715
visit        -0.4127  0.0418  97.6   <2e-16

Estimated Correlation Parameters:
      Estimate
alpha        0
```

In the fitted model, the percent excess body weight loss has a gamma distribution with the estimated mean $\hat{E}(EWL) = \exp(2.7572 + 0.3947 \cdot Tx + 0.098 \cdot male - 0.4127 \cdot visit)$, and the estimated correlation matrix for each individual $\begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix}$. Group and visit are significant predictors of EWL. It is estimated that the EWL for participants in the treatment group is, on average, 0.3947 points larger than that for the control group participants (i.e., the new medication is efficient). From visit to visit, the estimated average EWL decreases by 0.4127 points.

To find the percent excess body weight loss that the doctors can expect to see between 3 and 6 months in male patients who will be taking this new medication, we write

$$EWL^0 = \exp(2.7572 + 0.3947 + 0.098 - 0.4127 \cdot 4) = 4.9486.$$

In R:

```
print(predict(ar.fitted.model, type='response', data.frame(patid=17,
group.rel='Tx', gender.rel='M', visit=4)))
```

```
4.95
```

EXERCISE 9.6 Use the data in Exercise 9.3 to carry out the following analysis:
(a) Fit the generalized estimating equations models for logistically distributed presence or absence of side effects, with unstructured, Toeplitz, autoregressive, compound symmetric, and independent working correlation matrices.

In SAS:

```
data pharma;
input patid dosage$ gender$ age week1 week3 week7 week16 @@;
cards;
1  A F 56 1 1 0 0  2  A F 53 1 1 1 0  3  A F 32 0 1 0 1
4  A F 22 0 0 0 0  5  A F 38 0 0 1 1  6  A F 42 0 1 1 1
7  A F 46 0 1 1 0  8  A M 33 1 1 1 1  9  A M 44 0 0 1 1
10 A M 34 0 1 0 0  11 A M 38 0 0 1 1  12 A M 40 0 0 1 1
13 A M 43 0 0 0 0  14 A M 44 0 0 1 0  15 A F 48 0 0 0 0
16 A F 29 0 1 0 0  17 A F 30 0 0 0 0  18 B F 30 0 0 0 0
19 B F 31 0 0 0 0  20 B F 32 1 1 0 0  21 B F 31 0 0 1 0
22 B F 50 0 0 0 1  23 B F 38 0 0 0 0  24 B M 51 0 0 1 1
25 B M 32 0 0 1 1  26 B M 25 0 0 0 0  27 B M 24 0 0 0 0
28 B M 34 0 0 0 0  29 B M 36 0 0 0 1  30 B M 44 0 0 1 1
31 B M 40 1 1 0 0  32 B M 29 0 1 0 0  33 B M 33 1 1 0 0
34 B M 38 0 0 1 0
;

/*creating longform dataset*/
data longform;
set pharma;
 array w[4] (1 3 7 16);
 array s[4] week1 week3 week7 week16;
  do i=1 to 4;
   week=w[i];
   sideeffects=s[i];
  age=age/100;
   output;
   end;
keep patid dosage gender age week sideeffects;
run;

/*fitting GEE logistic model with unstructured working correlation matrix*/
proc genmod;
 class patid dosage gender(ref='F');
  model sideeffects = dosage gender age week / dist=binomial link=logit;
   repeated subject = patid / type=un;
run;
```

QIC 173.0832

```
/*fitting GEE logistic model with Toeplitz working correlation matrix*/
proc genmod;
 class patid dosage gender(ref='F');
  model sideeffects = dosage gender age week / dist=binomial link=logit;
   repeated subject = patid / type=mdep(3);
run;
```

QIC 173.5626

```
/*fitting GEE logistic model with autoregressive working correlation matrix*/
proc genmod;
 class patid dosage gender(ref='F');
  model sideeffects = dosage gender age week / dist=binomial link=logit;
   repeated subject = patid / type=ar;
run;
```

QIC 173.6008

```
/*fitting GEE logistic model with compound symmetric working correlation matrix*/
proc genmod;
 class patid dosage gender(ref='F');
  model sideeffects = dosage gender age week / dist=binomial link=logit;
   repeated subject = patid / type=cs;
run;
```

QIC 174.0362

```
/*fitting GEE logistic model with independent working correlation matrix*/
proc genmod;
 class patid dosage gender(ref='F');
  model sideeffects = dosage gender age week / dist=binomial link=logit;
   repeated subject = patid / type=ind;
run;
```

QIC 174.0450

In R:

```
pharma.data<- read.csv(file='C:/<insert path>/Exercise9.3Data.csv',
header=TRUE, sep=',')

#creating longform dataset
```

```
library(reshape2)
longform.data<- melt(pharma.data, id.vars=c('patid', 'dosage','gender','age'),
variable.name='weekn', value.name='sideeffects')
week<- ifelse(longform.data$weekn=='week1',1,ifelse(longform.data$weekn
=='week3',3,ifelse(longform.data$weekn=='week7',7,16)))

#specifying reference level
dosage.rel<- relevel(longform.data$dosage, ref="B")

#fitting GEE logistic model with unstructured working correlation matrix
library(geepack)
library(MuMIn)
summary(un.fitted.model<- geeglm(sideeffects ~ dosage.rel + gender + age + week,
data=longform.data, id=patid, family=binomial(link='logit'),
corstr='unstructured'))
QIC(un.fitted.model)
```

```
The model doesn’t converge.
```

```
#fitting GEE logistic model with autoregressive working correlation matrix
summary(ar.fitted.model<- geeglm(sideeffects ~ dosage.rel + gender + age + week,
data=longform.data, id=patid, family=binomial(link='logit'), corstr='ar1'))
QIC(ar.fitted.model)
```

```
QIC
170
```

```
#fitting GEE logistic model with compound symmetric working correlation matrix
summary(cs.fitted.model<- geeglm(sideeffects ~ dosage.rel + gender + age + week,
data=longform.data, id=patid, family=binomial(link='logit'),
corstr='exchangeable'))
QIC(cs.fitted.model)
```

```
QIC
170
```

```
#fitting GEE logistic model with independent working correlation matrix
summary(ind.fitted.model<- geeglm(sideeffects ~ dosage.rel + gender + age + week,
data=longform.data, id=patid, family=binomial(link='logit'),
corstr = 'independence'))
QIC(ind.fitted.model)
```

```
QIC
170
```

(b) Choose the best model according to the QIC value.

Among the models fitted in SAS, the QIC-optimal model is the one with the Toeplitz working correlation matrix. QIC values are summarized in the table below.

	UN	Toep	AR	CS	Ind
QIC	173.0832	173.5626	173.6008	174.0362	174.0450

R fits the models with autoregressive, compound symmetric, and independent working correlations matrices as the same model.

(c) For the best-fitted model, answer questions (b)-(d) from Exercise 9.3.

In SAS:

```
/*fitting GEE logistic model with Toeplitz working correlation matrix*/
proc genmod;
 class patid dosage gender(ref='F');
  model sideeffects = dosage gender age week / dist=binomial link=logit;
   repeated subject = patid / type=mdep(3) corrw;
run;
```

```
     Working Correlation Matrix
        Col1    Col2    Col3    Col4
Row1  1.0000  0.3058 -0.1657 -0.2276
Row2  0.3058  1.0000  0.3058 -0.1657
Row3 -0.1657  0.3058  1.0000  0.3058
Row4 -0.2276 -0.1657  0.3058  1.0000
```

```
                Analysis Of GEE Parameter Estimates
                 Empirical Standard Error Estimates
Parameter    Estimate Standard 95% Confidence Limits      Z Pr > |Z|
                         Error
Intercept     -1.2620   0.5368   -2.3141    -0.2098 -2.35    0.0187
dosage     A   0.7311   0.4391   -0.1295     1.5918  1.66    0.0959
dosage     B   0.0000   0.0000    0.0000     0.0000   .         .
gender     M   0.4443   0.4475   -0.4327     1.3213  0.99    0.3208
gender     F   0.0000   0.0000    0.0000     0.0000   .         .
age           -1.7792   0.9669   -3.6743     0.1159 -1.84    0.0658
week           0.0013   0.0343   -0.0660     0.0686  0.04    0.9689
```

In the fitted GEE logistic model, the response has estimated mean $\hat{E}(side\ effects) = \hat{P}(side\ effects = 1) =$

$= \frac{\exp(-1.262+0.7311\cdot dosage\ A+0.4443\cdot male-1.7792\cdot age/100+0.0013\cdot week)}{1+\exp(-1.262+0.7311\cdot dosage\ A+0.4443\cdot male-1.7792\cdot age/100+0.0013\cdot week)}$, and the estimated

correlation matrix for each individual $\begin{pmatrix} 1.000 & 0.3058 & -0.1657 & -0.2276 \\ 0.3058 & 1.000 & 0.3058 & -0.1657 \\ -0.1657 & 0.3058 & 1.000 & 0.3058 \\ -0.2276 & -0.1657 & 0.3058 & 1.000 \end{pmatrix}$.

Dosage and age are significant predictors at the 10% level. For the subjects taking dosage A, the estimated odds in favor of side effects are $\exp(0.7311)\cdot 100\% = 207.7364\%$ of those for subjects taking dosage B. Thus, dosage B should be preferred. Also, as age increases by one year, the estimated odds in favor of side effects change by $(\exp(-1.7792)-1)\cdot 100\% = -83.12269\%$, that is, decrease by 83.12269%.

Further, we predict the probability of side effects occurring at week 7 for a 40-year-old woman taking dosage A. The prediction is

$P^0(side\ effects = 1) = = \frac{\exp(-1.262+0.7311-1.7792\cdot 40/100+0.0013\cdot 7)}{1+\exp(-1.262+0.7311-1.7792\cdot 40/100+0.0013\cdot 7)} = 0.22557.$

In SAS:

```
data predict;
input patid dosage$ gender$ age week;
```

```
age=age/100;
cards;
35 A F 40 7
;

data longform;
set longform predict;
run;

proc genmod;
 class patid dosage gender;
  model sideeffects = dosage gender age week / dist=binomial link=logit;
   repeated subject = patid / type=mdep(3);
        output out=outdata p=psideeffects;
run;

proc print data=outdata (firstobs=137) noobs;
 var psideeffects;
run;
```

```
psideeffects
     0.22563
```

In R:

```
#fitting GEE logistic model with autoregressive working correlation matrix
summary(ar.fitted.model<- geeglm(sideeffects ~ dosage.rel + gender + age + week,
data=longform.data, id=patid, family=binomial(link='logit'), corstr='ar1'))
```

```
             Estimate Std.err  Wald Pr(>|W|)
(Intercept)  -3.5341  0.9785 13.04   0.0003
dosage.relA   0.5888  0.4019  2.15   0.1429
genderM       0.4682  0.3963  1.40   0.2375
age           0.0518  0.0222  5.44   0.0197
week          0.0374  0.0320  1.37   0.2422

Estimated Correlation Parameters:
      Estimate
alpha        0
```

In the fitted model, the response has estimated mean $\hat{E}(side\ effects) = \hat{P}(side\ effects = 1) =$

$= \frac{\exp(-3.5341+0.5888\cdot dosage\ B+0.4682\cdot male+0.0518\cdot age+0.0374\cdot week)}{1+\exp(-3.5341+0.5888\cdot dosage\ B+0.4682\cdot male+0.0518\cdot age+0.0374\cdot week)}$, and the estimated

correlation matrix for each individual $\begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix}$. Age is the only6 significant predictor at the 5% level. In this model, the coefficient corresponding to dosage A is positive, suggesting that dosage A might be the winner. Dosage, however, is not a statistically significant predictor.

As age increases by one year, the estimated odds in favor of side effects increase by $(\exp(0.0518) - 1) \cdot 100\% = 5.3165\%$.

Finally, we predict the probability of side effects occurring at week 7 for a 40-year-old woman taking dosage A. The predicted value is

$$P^0(side\ effects = 1) = = \frac{\exp(-3.5341+0.0518\cdot 40+0.0374\cdot 7)}{1+\exp(-3.5341+0.0518\cdot 40+0.0374\cdot 7)} = 0.2314.$$

In R:

```
print(predict(ar.fitted.model,type='response',data.frame(patid=35,dosage.rel='A',
gender='F',age=40,week=7)))
```

```
0.352
```

EXERCISE 9.7. Consider the data given in Exercise 9.3. Answer the questions below.
(a) Fit a generalized estimating equations model for the days with occupancy below 65% based on a Poisson distribution. Try different working correlation matrices: unstructured, Toeplitz, autoregressive, compound symmetric, and independent.

In SAS:

```
data hotels;
input hotel region$ ADR1 OCR1 ADR2 OCR2 ADR3 OCR3 ADR4 OCR4 @@;
cards;
1 rural  88  3 76  8  74  11 78  17  2  rural 79  5 98  9  72  7  54  14
3 rural  84  2 67  4  64  9  98  13  4  rural 79  3 88  4  77  80 66  15
5 rural  68  1 75  8  58  16 80  21  6  rural 82  0 95  4  85  9  90  16
7 rural  92  4 93  8  87  13 92  20  8  rural 58  0 54  9  67  19 84  25
9 rural  84  1 87  9  94  6  92  19  10 rural 98  3 92  0  88  3  80  7
11 urban 112 1 137 11 114 5  137 23  12 urban 104 1 176 8  97  6  146 18
13 urban 195 3 171 5  175 6  137 11  14 urban 128 1 113 10 125 3  126 9
15 urban 96  2 152 10 145 5  153 10  16 urban 98  0 170 9  129 3  148 16
17 urban 119 2 121 8  128 6  147 18  18 urban 120 0 130 0  114 2  108 13
;

data longform;
set hotels;
 array a[4] ADR1 ADR2 ADR3 ADR4;
 array o[4] OCR1 OCR2 OCR3 OCR4;
  do season=1 to 4;
   ADR=a[season];
   OCR=o[season];
  output;
 end;
keep hotel region season ADR OCR;
run;

/*fitting GEE Poisson model with unstructured working correlation matrix*/
proc genmod;
 class hotel region;
  model OCR = region ADR season / dist=poisson link=log;
   repeated subject = hotel / type=un;
run;
```

```
QIC -231.0202
```

```
/*fitting GEE Poisson model with Toeplitz working correlation matrix*/
proc genmod;
 class hotel region;
```

```
  model OCR = region ADR season / dist=poisson link=log;
   repeated subject = hotel / type=mdep(3);
run;
```

QIC -227.9801

```
/*fitting GEE Poisson model with autoregressive working correlation matrix*/
proc genmod;
 class hotel region;
  model OCR = region ADR season / dist=poisson link=log;
   repeated subject = hotel / type=ar;
run;
```

QIC -227.1029

```
/*fitting GEE Poisson model with compound symmetric working correlation matrix*/
proc genmod;
 class hotel region;
  model OCR = region ADR season / dist=poisson link=log;
   repeated subject = hotel / type=cs;
run;
```

QIC -224.0231

```
/*fitting GEE Poisson model with independent working correlation matrix*/
proc genmod;
 class hotel region;
  model OCR = region ADR season / dist=poisson link=log;
   repeated subject = hotel / type=ind;
run;
```

QIC -223.9375

In R:

```
hotels.data<- read.csv(file='C:/<insert path>/Exercise9.3Data.csv', header=TRUE,
sep=',')

#creating longform dataset
library(reshape2)
data1<-
melt(hotels.data[,c('hotel','region','ADR1','ADR2','ADR3','ADR4')],id.vars=c('hot
el','region'), variable.name='ADRn',value.name='ADR')
data2<-
melt(hotels.data[,c('OCR1','OCR2','OCR3','OCR4')],variable.name='OCRn',value.name
='OCR')
longform.data<- cbind(data1,data2)
longform.data$season<-ifelse(longform.data$ADRn=='ADR1',1,
ifelse(longform.data$ADRn=='ADR2',2,ifelse(longform.data$ADRn=='ADR3',3,4)))

#specifying reference level
longform.data$region.rel<- relevel(longform.data$region, ref="urban")

#fitting GEE Poisson model with unstructured working correlation matrix
library(geepack)
library(MuMIn)
```

```
summary(un.fitted.model<- geeglm(OCR ~ region.rel + ADR + season,
data=longform.data, id=hotel,family=poisson(link='log'), corstr =
'unstructured'))
```

The model doesn't converge.

```
#fitting GEE Poisson model with autoregressive working correlation matrix
summary(ar.fitted.model<- geeglm(OCR ~ region.rel + ADR + season,
data=longform.data, id=hotel,family=poisson(link='log'), corstr = 'ar1'))
QIC(ar.fitted.model)

  QIC
-1811

#fitting GEE negative Poisson with compound symmetric working correlation matrix
summary(cs.fitted.model<- geeglm(OCR ~ region.rel + ADR + season,
data=longform.data, id=hotel,family=poisson(link='log'),corstr = 'exchangeable'))
QIC(cs.fitted.model)

  QIC
-1811

#fitting GEE negative Poisson with independent working correlation matrix
summary(ind.fitted.model<- geeglm(OCR ~ region.rel + ADR + season,
data=longform.data,id=hotel,family=poisson(link='log'), corstr = 'independence'))
QIC(ind.fitted.model)

  QIC
-1811
```

(b) Choose the QIC-optimal model.

For the GEE models fitted in SAS, the one with the unstructured working correlation fit has the best fit as judged by the QIC criterion.

	UN	**Toeplitz**	**AR**	**CS**	**Ind**
QIC	-231.0202	-227.9801	-227.1029	-224.0231	-223.9375

In R, all models have identical parameter estimates.

(c) Answer parts (b)-(d) in Exercise 9.4 for the optimal model.

In SAS:

```
/*fitting GEE Poisson model with unstructured working correlation matrix*/
proc genmod;
 class hotel region;
  model OCR = region ADR season / dist=poisson link=log;
   repeated subject = hotel / type=un corrw;
run;
```

```
     Working Correlation Matrix
         Col1    Col2    Col3    Col4
Row1  1.0000 -0.0519 -0.0137  0.0070
Row2 -0.0519  1.0000 -0.2281  0.1984
Row3 -0.0137 -0.2281  1.0000 -0.0944
Row4  0.0070  0.1984 -0.0944  1.0000
```

```
                      Analysis Of GEE Parameter Estimates
                       Empirical Standard Error Estimates
Parameter            Estimate Standard 95% Confidence Limits      Z Pr > |Z|
                                 Error
Intercept              0.1871   0.4643    -0.7229    1.0971  0.40   0.6869
region    rural        0.5636   0.2679     0.0384    1.0888  2.10   0.0354
region    urban        0.0000   0.0000     0.0000    0.0000     .        .
ADR                    0.0015   0.0032    -0.0047    0.0078  0.48   0.6288
season                 0.5399   0.0391     0.4632    0.6165 13.80   <.0001
```

The fitted GEE Poisson model has the estimated average number of days the hotel occupancy rate was below 65% $\hat{\lambda} = \exp(0.1871 + 0.5636 \cdot rural + 0.0015 \cdot ADR + 0.5399 \cdot season)$. Region and season are significant predictors. The estimated working correlation matrix is $\begin{pmatrix} 1.0000 & -0.0519 & -0.0137 & 0.0070 \\ -0.0519 & 1.0000 & -0.2281 & 0.1984 \\ -0.0137 & -0.2281 & 1.0000 & -0.0944 \\ 0.0070 & 0.1984 & -0.0944 & 1.0000 \end{pmatrix}$. For rural hotels, the estimated average number of days that the hotel occupancy rate is below 65% is $\exp(0.5636) \cdot 100\% = 175.6986\%$ of that for urban hotels. Every season (summer to fall to winter to spring), this estimated average increases by $(\exp(0.5399) - 1) \cdot 100\%$ =71.58353%.

To predict the number of days with occupancy rate below 65% for the winter season in a rural hotel with average daily rate of $75 we compute $OCR^0 = \exp(0.1871 + 0.5636 + 0.0015 \cdot 75 + 0.5399 \cdot 3) = 11.9759$.

In SAS:

```
data predict;
input hotel region$ ADR season;
cards;
19 rural 75 3
;

data longform;
set longform predict;
run;

proc genmod;
 class hotel region;
  model OCR = region ADR season / dist=poisson link=log;
   repeated subject = hotel / type=un corrw;
       output out=outdata p=pOCR;
run;

proc print data=outdata (firstobs=73) noobs;
 var pOCR;
run;
```

```
   pOCR
12.0168
```

In R:

```
#fitting GEE Poisson model with autoregressive working correlation matrix
summary(ar.fitted.model<- geeglm(OCR ~ region.rel + ADR + season,
data=longform.data, id=hotel,family=poisson(link='log'), corstr = 'ar1'))
```

```
Coefficients:
                Estimate Std.err   Wald Pr(>|W|)
(Intercept)      0.20987 0.53016   0.16    0.692
region.relrural  0.45808 0.22856   4.02    0.045
ADR              0.00189 0.00338   0.31    0.576
season           0.54573 0.05170 111.41   <2e-16

Estimated Correlation Parameters:
      Estimate
alpha        0
```

The fitted model has the estimated average number of days the hotel occupancy rate was below 65% $\hat{\lambda} = \exp(0.20987 + 0.45808 \cdot rural + 0.00189 \cdot ADR + 0.54573 \cdot season)$. Region and season are significant predictors. The estimated working correlation matrix is $\begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix}$. For rural hotels, the estimated average number of days that the hotel occupancy rate is below 65% is $\exp(0.45808) \cdot 100\% = 158.1035\%$ of that for urban hotels. Every season (summer to fall to winter to spring), this estimated average increases by $(\exp(0.54573) - 1) \cdot 100\%$ =72.58678%.

To predict the number of days with occupancy rate below 65% for the winter season in a rural hotel with average daily rate of $75 we compute $OCR^0 = \exp(0.20987 + 0.45808 + 0.00189 \cdot 75 + 0.54573 \cdot 3) = 11.5524$.

In R:

```
print(predict(ar.fitted.model, type="response", data.frame(hotel=19,
region.rel='rural', ADR=75, season=3)))
```

```
11.4
```

CHAPTER 10

EXERCISE 10.1. For the hierarchical model with normal response defined in (10.1), show that

(a) Observations within each individual i in cluster m for different times j and j' have covariance

$$Cov\left(y_{ijm}, y_{ij'm}\right) = Cov\left(\beta_0 + \beta_1 x_{1ijm} + \cdots + \beta_k x_{kijm} + \beta_{k+1} t_j + u_{1im} + u_{2i} \ \ t_j + \tau_{1m} + \tau_{2m} t_j + \varepsilon_{ijm} ,\ \beta_0 + \beta_1 x_{1ij'm} + \cdots + \beta_k x_{kij} \ \ \ + \beta_{k+1} t_{j'} + u_{1i} \ \ \ + u_{2im} t_{j'} + \tau_{1m} + \tau_{2m} t_{j'} + \varepsilon_{ij'm}\right) = Cov\left(u_{1im} + u_{2im} t_j + \tau_{1m} + \tau_{2m} t_j + \varepsilon_{ijm} ,\ u_{1im} + u_{2im} t_{j'} + \tau_{1m} + \tau_{2m} t_{j'} + \varepsilon_{ij'm}\right) = Cov(u_{1im} ,\ u_{1im}) + Cov(u_{1im} , u_{2im}) t_{j'} + Cov(u_{1im} ,\ \tau_{1m}) + Cov(u_{1i} \ \ \ ,\ \tau_{2m}) t_{j'} + Cov\left(u_{1im} , \varepsilon_{ij'm}\right) + Cov(u_{2im} , u_{1i} \ \ ) t_j + Cov(u_{2im} , u_{2i} \ \ ) t_j t_{j'} + Cov(u_{2im} , \tau_{1m}) t_j + Cov(u_{2im} , \tau_{2m}) t_j t_{j'} + \ Cov\left(u_{2im} , \varepsilon_{ij'm}\right) t_j + Cov(\tau_{1m} , u_{1im}) + Cov(\tau_{1m} , u_{2im}) t_{j'} + Cov(\tau_{1m} , \tau_{1m}) + Cov(\tau_{1m} , \tau_{2m}) t_{j'} + Cov\left(\tau_{1m} , \varepsilon_{ij'm}\right) + Cov(\tau_{2m} , u_{1im}) t_j + Cov(\ \tau_{2m} , u_{2im}) t_j t_{j'} + Cov(\tau_{2m} , \tau_{1m}) t_j + Cov(\tau_{2m} , \tau_{2m}) t_j t_{j'} + Cov\left(\tau_{2m} , \varepsilon_{ij'm}\right) + Cov\left(\varepsilon_{ijm},\ u_{1im}\right) + Cov(\varepsilon_{ijm} , u_{2im}) t_{j'} + Cov(\varepsilon_{ijm} , \tau_{1m}) + Cov(\varepsilon_{ijm} , \tau_{2m}) t_{j'} + Cov(\varepsilon_{ijm} , \varepsilon_{ij'm}) = Var(u_{1im}) + Cov(u_{1im} , u_{2im}) t_{j'} \ + Cov(u_{2im} , u_{1im}) t_j + Var(u_{2im}) t_j t_{j'} + Var(\tau_{1m}) + Cov(\tau_{1m} , \tau_{2m}) t_{j'} + Cov(\tau_{2m} , \tau_{1m}) t_j + Var(\tau_{2m}) t_j t_{j'} = \sigma_{u_1}^2 + \sigma_{\tau_1}^2 + (\sigma_{u_1 u_2} + \sigma_{\tau_1 \tau_2})(t_j + t_{j'}) + (\sigma_{u_2}^2 + \sigma_{\tau_2}^2) t_j t_{j'}.$$

(b) Observations for two individuals i and i' within the same cluster m at any two times t_j and $t_{j'}$, equal or not, have covariance $Cov\left(y_{ijm}, y_{i'j'm}\right) = Cov\left(\beta_0 + \beta_1 x_{1ijm} + \cdots + \beta_k x_{kijm} + \beta_{k+1} t_j + u_{1im} + u_{2im} t_j \ + \tau_{1m} + \tau_{2m} t_j \ + \varepsilon_{ijm} ,\ \beta_0 + \beta_1 x_{1i'j'm} + \cdots + \beta_k x_{ki'j'} \ \ + \beta_{k+1} t_{j'} + u_{1i'm} + u_{2i'm} t_{j'} + \tau_{1m} + \tau_{2m} t_{j'} + \varepsilon_{i'j'm}\right) = Cov\left(u_{1im} + u_{2im} t_j + \tau_{1m} + \tau_{2m} t_j + \varepsilon_{ijm} ,\ u_{1i'm} + u_{2i'm} t_{j'} + \tau_{1m} + \tau_{2m} t_{j'} + \varepsilon_{i'j'm}\right) = Cov(u_{1im} ,\ u_{1i'm}) + Cov(u_{1im} , u_{2i'm}) t_{j'} + Cov(u_{1im} ,\ \tau_{1m}) + Cov(u_{1im} ,\ \tau_{2m}) t_{j'} + Cov\left(u_{1im} , \varepsilon_{i'j'm}\right) + Cov(u_{2im} , u_{1i'm}) t_j + Cov(u_{2im} , u_{2i'm}) t_j t_{j'} + Cov(u_{2im} , \tau_{1m}) t_j + Cov(u_{2im} , \tau_{2m}) t_j t_{j'} + \ Cov\left(u_{2im} , \varepsilon_{i'j'm}\right) t_j + Cov(\tau_{1m} , u_{1i'm}) + Cov(\tau_{1m} , u_{2i'm}) t_{j'} + Cov(\tau_{1m} , \tau_{1m}) + Cov(\tau_{1m} , \tau_{2m}) t_{j'} + Cov\left(\tau_{1m} , \varepsilon_{i'j'm}\right) + Cov(\tau_{2m} , u_{1i'm}) t_j + Cov(\ \tau_{2m} , u_{2i'm}) t_j t_{j'} + Cov(\tau_{2m} , \tau_{1m}) t_j + Cov(\tau_{2m} , \tau_{2m}) t_j t_{j'} + Cov\left(\tau_{2m} , \varepsilon_{i'j'm}\right) t_j + Cov\left(\varepsilon_{ijm},\ u_{1i'm}\right) + Cov(\varepsilon_{ijm} , u_{2i'm}) t_{j'} + Cov(\varepsilon_{ijm} , \tau_{1m}) + Cov(\varepsilon_{ijm} , \tau_{2m}) t_{j'} + Cov(\varepsilon_{ijm} , \varepsilon_{i'j'm}) = Var(\tau_{1m}) + Cov(\tau_{1m} , \tau_{2m}) t_{j'} + Cov(\tau_{2m} , \tau_{1m}) t_j + Var(\tau_{2m}) t_j t_{j'} = \sigma_{\tau_1}^2 + \sigma_{\tau_1 \tau_2}(t_j + t_{j'}) + \sigma_{\tau_2}^2 t_j t_{j'}.$

(c) Observations for two individuals in different clusters are not correlated, that is, for $i \neq i'$ and $m \neq m'$, $Cov\left(y_{ijm}, y_{i'j'm'}\right) = Cov\left(\beta_0 + \beta_1 x_{1ijm} + \cdots + \beta_k x_{kijm} + \beta_{k+1} t_j + u_{1im} + u_{2im} t_j \ + \tau_{1m} + \tau_{2m} t_j \ + \varepsilon_{ijm} ,\ \beta_0 + \beta_1 x_{1i'j'm'} + \cdots + \beta_k x_{ki'j'm} \ + \beta_{k+1} t_{j'} + u_{1i'm'} + u_{2i'm'} t_{j'} + \tau_{1m'} + \tau_{2m'} t_{j'} + \varepsilon_{i'j'm'}\right) = Cov\left(u_{1im} + u_{2im} t_j + \tau_{1m} + \tau_{2m} t_j + \varepsilon_{ijm} ,\ u_{1i'm'} + u_{2i'm'} t_{j'} + \tau_{1m'} + \tau_{2m'} t_{j'} + \varepsilon_{i'j'm'}\right) = Cov(u_{1im} ,\ u_{1i'm'}) + Cov(u_{1im} , u_{2i'm'}) t_{j'} + Cov(u_{1im} ,\ \tau_{1m'}) + Cov(u_{1im} ,\ \tau_{2m'}) t_{j'} + Cov\left(u_{1im} , \varepsilon_{i'j'm'}\right) + Cov(u_{2im} , u_{1i'm'}) t_j + Cov(u_{2im} , u_{2i'm'}) t_j t_{j'} + Cov(u_{2im} , \tau_{1m'}) t_j + Cov(u_{2im} , \tau_{2m'}) t_j t_{j'} + \ Cov\left(u_{2im} , \varepsilon_{i'j'm'}\right) t_j + Cov(\tau_{1m} , u_{1i'm'}) + Cov(\tau_{1m} , u_{2i'm'}) t_{j'} + Cov(\tau_{1m} , \tau_{1m'}) + Cov(\tau_{1m} , \tau_{2m'}) t_{j'} + Cov\left(\tau_{1m} , \varepsilon_{i'j'm'}\right) + Cov(\tau_{2m} , u_{1i'm'}) t_j + Cov(\ \tau_{2m} , u_{2i'm'}) t_j t_{j'} + Cov(\tau_{2m} , \tau_{1m'}) t_j + Cov(\tau_{2m} , \tau_{2m'}) t_j t_{j'} +$

$Cov(\tau_{2m}, \varepsilon_{i'j'm'})t_j + Cov(\varepsilon_{ijm}, u_{1i'm'}) + Cov(\varepsilon_{ijm}, u_{2i'm'})t_{j'} + Cov(\varepsilon_{ijm}, \tau_{1m'}) + Cov(\varepsilon_{ijm}, \tau_{2m'})t_{j'} + Cov(\varepsilon_{ijm}, \varepsilon_{i'j'm'}) = 0.$

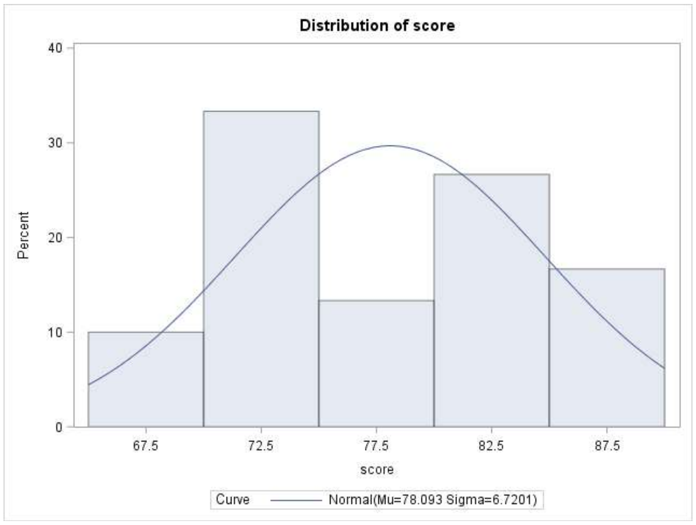
(d) The response variable $y_{ijm} = \beta_0 + \beta_1 x_{1ijm} + \cdots + \beta_k x_{kijm} + \beta_{k+1} t_j + u_{1i} \quad + u_{2im} t_j + \tau_{1m} + \tau_{2m} t_j + \varepsilon_{ijm}$ has a normal distribution being a linear combination of independent normally distributed random variables, has mean $E(y_{ijm}) = E(\beta_0 + \beta_1 x_{1ijm} + \cdots + \beta_k x_{kijm} + \beta_{k+1} t_j + u_{1im} + u_{2im} t_j + \tau_{1m} + \tau_{2m} t_j + \varepsilon_{ijm}) = \beta_0 + \beta_1 x_{1ijm} + \cdots + \beta_k x_{kijm} + \beta_{k+1} t_j + E(u_{1im}) + E(u_{2im}) t_j + E(\tau_{1m}) + E(\tau_{2m}) t_j + E(\varepsilon_{ijm}) = \beta_0 + \beta_1 x_{1i} \quad + \cdots + \beta_k x_{kijm} + \beta_{k+1} t_j$, and variance $Var(y_{ijm}) = Var(\beta_0 + \beta_1 x_{1ijm} + \cdots + \beta_k x_{kijm} + \beta_{k+1} t_j + u_{1im} + u_{2im} t_j + \tau_{1m} + \tau_{2m} t_j + \varepsilon_{ijm}) = Var(u_{1im} + u_{2im} t_j + \tau_{1m} + \tau_{2m} t_j + \varepsilon_{ijm}) = Cov(u_{1im} + u_{2im} t_j + \tau_{1m} + \tau_{2m} t_j + \varepsilon_{ijm}, u_{1im} + u_{2i} \quad t_j + \tau_{1m} + \tau_{2m} t_j + \varepsilon_{ijm}) = Cov(u_{1i} \quad, u_{1im}) + Cov(u_{1im}, u_{2im}) t_j + Cov(u_{1i} \quad, \tau_{1m}) + Cov(u_{1im}, \tau_{2m}) t_j + Cov(u_{1im}, \varepsilon_{ijm}) + Cov(u_{2im}, u_{1im}) t_j + Cov(u_{2im}, u_{2im}) t_j^2 + Cov(u_{2im}, \tau_{1m}) t_j + Cov(u_{2im}, \tau_{2m}) t_j^2 + Cov(u_{2i} \quad, \varepsilon_{ijm}) t_j + Cov(\tau_{1m}, u_{1i} \quad) + Cov(\tau_{1m}, u_{2im}) t_j + Cov(\tau_{1m}, \tau_{1m}) + Cov(\tau_{1m}, \tau_{2m}) t_j + Cov(\tau_{1m}, \varepsilon_{ijm}) + Cov(\tau_{2m}, u_{1im}) t_j + Cov(\tau_{2m}, u_{2im}) t_j^2 + Cov(\tau_{2m}, \tau_{1m}) t_j + Cov(\tau_{2m}, \tau_{2m}) t_j^2 + Cov(\tau_{2m}, \varepsilon_{ijm}) t_j + Cov(\varepsilon_{ijm}, u_{1im}) + Cov(\varepsilon_{ijm}, u_{2im}) t_j + Cov(\varepsilon_{ijm}, \tau_{1m}) + Cov(\varepsilon_{ijm}, \tau_{2m}) t_j + Cov(\varepsilon_{ijm}, \varepsilon_{ijm}) = Var(u_{1i} \quad) + Cov(u_{1im}, u_{2im}) t_j + Cov(u_{2im}, u_{1im}) t_j + Var(u_{2im}) t_j^2 + Var(\tau_{1m}) + Cov(\tau_{1m}, \tau_{2m}) t_j + Cov(\tau_{2m}, \tau_{1m}) t_j + Var(\tau_{2m}) t_j^2 + Var(\varepsilon_{ijm}) = \sigma_{u_1}^2 + \sigma_{\tau_1}^2 + 2(\sigma_{u_1 u_2} + \sigma_{\tau_1 \tau_2}) t_j + (\sigma_{u_2}^2 + \sigma_{\tau_2}^2) t_j^2 + \sigma^2.$

EXERCISE 10.2. (a) Plot a histogram for test scores and conduct normality testing. Verify that the underlying distribution may be modeled as normal.

In SAS:

```
data schools;
input school API subject$ classsize year score @@;
cards;
1 911 ELA     20 15 78.39  1 912 ELA     22 16 79.85
1 917 ELA     23 17 81.34  1 917 ELA     22 18 82.56
1 919 ELA     24 19 83.12  1 911 Math    21 15 83.77
1 912 Math    22 16 84.90  1 917 Math    24 17 86.12
1 917 Math    23 18 88.99  1 919 Math    23 19 88.40
1 911 Science 21 15 80.19  1 912 Science 22 16 83.15
1 917 Science 24 17 84.45  1 917 Science 23 18 86.66
1 919 Science 23 19 88.43  2 732 ELA     34 15 68.03
2 745 ELA     36 16 70.67  2 751 ELA     36 17 74.17
2 753 ELA     37 18 72.78  2 753 ELA     38 19 73.18
2 732 Math    34 15 67.88  2 745 Math    34 16 68.34
2 751 Math    35 17 70.30  2 753 Math    37 18 71.22
2 753 Math    36 19 72.12  2 732 Science 34 15 72.96
2 745 Science 34 16 73.65  2 751 Science 36 17 74.58
2 753 Science 35 18 76.36  2 753 Science 35 19 76.23
;

/*plotting histogram*/
proc univariate;
 var score;
```

```
  histogram/normal;
run;
```

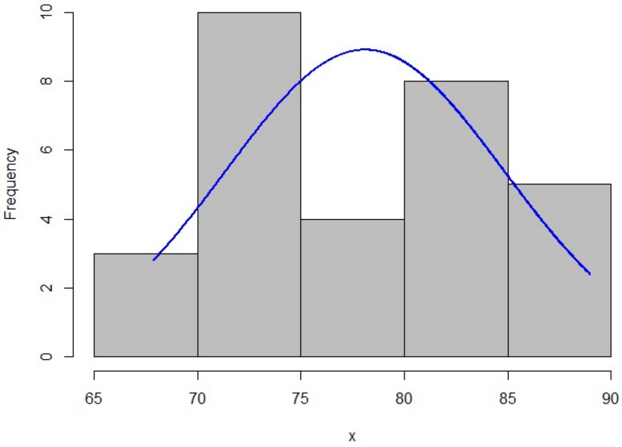


```
   Goodness-of-Fit Tests for Normal Distribution
Test                  Statistic        p Value
Kolmogorov-Smirnov D    0.13276200 Pr > D    >0.150
Cramer-von Mises   W-Sq 0.10207261 Pr > W-Sq  0.101
Anderson-Darling   A-Sq 0.60597790 Pr > A-Sq  0.106
```

The underflying distribution is normal as confirmed by the histogram and the large p-values in the normality tests.

In R:

```
schools.data<- read.csv(file='C:/<insert path>/Exercise10.2Data.csv', 
header=TRUE, sep=',')

#plotting histogram
library(rcompanion)
plotNormalHistogram(schools.data$score)
```



```
shapiro.test(schools.data$score)
```

```
Shapiro-Wilk normality test

W = 0.93668, p-value = 0.07407
```

(b) Run the hierarchical model with random slopes and intercepts at the school and subject-within-school levels. If there is a problem with convergence, gradually remove the random slopes and simplify the model to random intercepts only, if necessary. Discuss the overall model fit.

In SAS:

```
/*fitting hierarchical normal model with random slopes and intercepts*/
proc mixed covtest;
 class subject school;
  model score = API classsize year / solution;
   random intercept year / subject=school type=un;
   random intercept year / subject=subject(school) type=un;
run;
```

The model doesn’t converge.

```
/*fitting hierarchical normal model with random slope and intercept at
level 2, and intercept only at level 1*/
proc mixed covtest;
 class subject school;
  model score = API classsize year / solution;
   random intercept year / subject=school type=un;
   random intercept / subject=subject(school) type=un;
run;
```

The model doesn’t converge.

```
/*fitting hierarchical normal model with random slope and intercept at
level 1, and intercept only at level 2*/
proc mixed covtest;
 class subject school;
  model score = API classsize year / solution;
   random intercept / subject=school type=un;
   random intercept year / subject=subject(school) type=un;
run;
```

```
             Covariance Parameter Estimates
Cov Parm Subject         Estimate Standard Z Value   Pr Z
                                     Error
UN(1,1)  school                 0        .       .      .
UN(1,1)  subject(school)  43.5813  47.0828    0.93 0.1773
UN(2,1)  subject(school)  -2.1932   2.3457   -0.93 0.3498
UN(2,2)  subject(school)   0.1296   0.1267    1.02 0.1531
Residual                   0.6425   0.2203    2.92 0.0018
```

In this model, the parameters of the random-effects terms are either non-estimable or non-significant.

```
/*fitting hierarchical normal model with random intercepts only*/
proc mixed covtest;
 class subject school;
  model score = API classsize year / solution;
```

```
   random intercept / subject=school type=un;
   random intercept / subject=subject(school) type=un;
run;
```

```
             Covariance Parameter Estimates
Cov Parm Subject         Estimate Standard Z Value Pr > Z
                                     Error
UN(1,1)  school            8.5624  92.3691    0.09 0.4631
UN(1,1)  subject(school)   6.4797   4.7123    1.38 0.0846
Residual                   0.9194   0.2837    3.24 0.0006

Null Model Likelihood Ratio Test
 DF    Chi-Square    Pr > ChiSq
  2         34.04        <.0001

          Solution for Fixed Effects
Effect    Estimate Standard DF t Value Pr > |t|
                     Error
Intercept  18.6896  22.7718  1    0.82   0.5625
API        0.05080  0.02668 21    1.90   0.0707
classsize  -0.1082   0.2235 21   -0.48   0.6334
year        1.1952   0.2322 21    5.15   <.0001
```

The model fits the data well as indicated by a tiny p-value in the deviance test (null model likelihood ratio test).

In R:

```
#fitting hierarchical normal model with random slopes and intercepts
library(lme4)
summary(fitted.model<- lmer(score ~ API + classsize + year + (1 + year | school)
+ (1 + year |school:subject),data=schools.data))
```

```
Random effects:
 Groups         Name        Variance  Std.Dev. Corr
 school:subject (Intercept)  18.14986  4.2603
                year          0.04059  0.2015  -0.80
 school         (Intercept) 122.41231 11.0640
                year          0.19597  0.4427  -1.00
 Residual                     0.63146  0.7946


Fixed effects:
             Estimate Std. Error t value
(Intercept) -12.99487   21.09944  -0.616
API           0.09119    0.02231   4.087
classsize    -0.07799    0.18800  -0.415
year          1.03320    0.38184   2.706
```

```
#checking model fit
null.model<- glm(score ~ API + classsize + year, data=schools.data)
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
29.55178
```

```
print(p.value<- pchisq(deviance, df=6, lower.tail = FALSE))
```

```
4.782027e-05
```

(c) Write down the fitted model. Include all estimated parameters. Use $\alpha = 0.10$ to draw conclusion about significant parameters of the random effects. Are the scores for each subject correlated? Are the scores for different subjects within the same school correlated?

In SAS, the fitted hierarchical normal model has the estimated parameters $\hat{E}(score) = 18.6896 + 0.0508 \cdot API - 0.1082 \cdot class\ size + 1.1952 \cdot year$, $\hat{\sigma}_{u_1}^2 = 6.4797, \hat{\sigma}_{\tau_1}^2 = 8.5624$, and $\hat{\sigma}^2 = 0.9194$. At $\alpha = 0.10$, the variance of the random intercept at the subject-within-school level is significant, thus scores within each subject are correlated (see Exercise 10.1(a)). However, since $\sigma_{\tau_1}^2$ is not significant, scores for different subjects within the same school are not correlated (see Exercise 10.1(b)).

In R, the fitted hierarchical normal model has the estimated parameters $\hat{E}(score) = -12.99487 + 0.09119 \cdot API - 0.07799 \cdot class\ size + 1.0332 \cdot year$, $\hat{\sigma}_{u_1}^2 = 18.14986$, $\hat{\sigma}_{u_1 u_2} = -0.8$, $\hat{\sigma}_{u_2}^2 = 0.04059, \hat{\sigma}_{\tau_1}^2 = 122.41231, \hat{\sigma}_{\tau_1 \tau_2} = -1$, $\hat{\sigma}_{\tau_2}^2 = 0.19597$ and $\hat{\sigma}^2 = 0.63146$. The variances for both intercepts seem to be significantly different from zero (the ratios of estimate/stdev are large), thus in the model, scores for each subject as well as scores between different subjects within the same school are correlated.

(d) Give interpretation for all estimated significant fixed-effects coefficients. Use $\alpha = 0.10$.

API and year are significant predictors of mean score. For the model fitted in SAS, the API increases by one, the estimated average score increases by 0.0508. Each year, the estimated average score increases by 1.91952. For the model fitted in R, the API increases by one, the estimated average score increases by 0.09119. Each year, the estimated average score increases by 1.0332.

(e) Use the fitted model to predict an average score on a math test for a class of 36 students in 2019 in a school with an API of 753.

For the model fitted in SAS, the predicted score is $score^0 = 18.6896 + 0.0508 \cdot 753 - 0.1082 \cdot 36 + 1.1952 \cdot 19 = 75.7556$.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input school API subject$ classsize year;
cards;
2 753 Math 36 19
;

data schools;
set schools predict;
run;

proc mixed;
 class subject school;
  model score = API classsize year / outpm=outdata;
   random intercept / subject=school type=un;
     random intercept / subject=subject(school) type=un;
run;
proc print data=outdata (firstobs=31) noobs;
 var Pred;
run;
```

```
   Pred
 75.7565
```

For the model fitted in R, the predicted score is $score^0 = -12.99487 + 0.09119 \cdot 753 - 0.07799 \cdot 36 + 1.0332 \cdot 19 = 72.49436$.

In R:

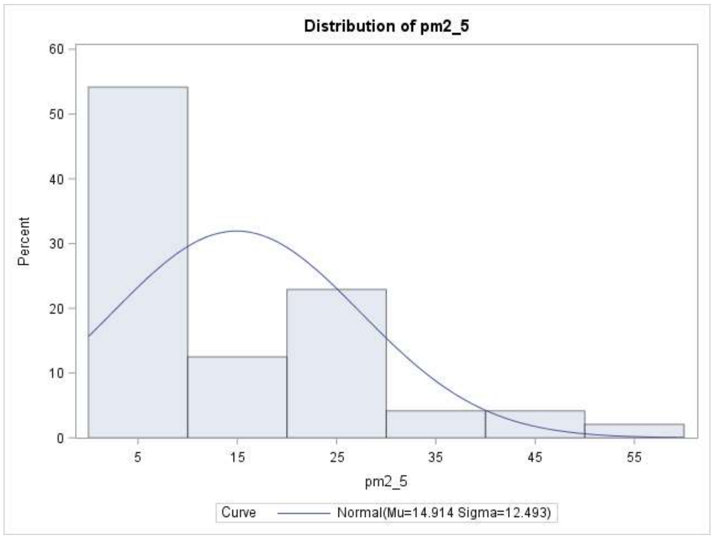
```
#using fitted model for prediction
print(predict(fitted.model, data.frame(school=2, API=753, subject='Math',
classsize=36, year=19), allow.new.levels=TRUE, re.form=NA))
```

```
72.49533
```

EXERCISE 10.3. (a) Plot a histogram of the particulate matter (PM2.5). Describe its shape. Argue that a gamma distribution is appropriate.

In SAS:

```
data pollution;
input state$ county$ township popl pest$ pm2_5 @@;
cards;
S1 A 1 4.1  no  22.97  S1 A 2 22.0 no  23.05  S1 A 3 6.3  no  24.97
S1 A 4 3.2  no  23.77  S1 A 5 13.4 no  23.09  S1 A 6 3.9  yes 24.75
S1 A 7 3.8  yes 36.93  S1 A 8 25.6 yes 45.83  S1 B 1 12.7 no  13.19
S1 B 2 17.8 no  22.9   S1 B 3 23.7 no  31.45  S1 B 4 11.8 yes 25.40
S1 B 5 12.9 yes 44.15  S1 B 6 13.0 yes 25.16  S1 B 7 12.0 yes 54.36
S1 B 8 13.0 no  24.38  S2 C 1 9.9  no  7.25   S2 C 2 5.6  yes 28.46
S2 C 3 3.9  no  7.06   S2 C 4 7.3  no  9.33   S2 C 5 4.7  no  5.59
S2 C 6 8.9  yes 9.94   S2 C 7 6.7  yes 8.49   S2 C 8 6.5  yes 6.97
S2 D 1 6.6  no  9.13   S2 D 2 7.2  no  11.04  S2 D 3 8.3  no  8.98
S2 D 4 5.2  yes 5.75   S2 D 5 9.1  yes 11.28  S2 D 6 4.3  no  6.88
S2 D 7 6.9  yes 9.21   S2 D 8 8.5  yes 11.23  S3 E 1 6.1  no  5.44
S3 E 2 3.9  no  4.33   S3 E 3 3.5  no  5.04   S3 E 4 2.4  no  3.31
S3 E 5 4.3  no  5.24   S3 E 6 2.8  yes 14.34  S3 E 7 3.4  no  4.90
S3 E 8 3.6  no  3.59   S3 F 1 5.3  no  5.01   S3 F 2 4.5  no  5.73
S3 F 3 2.5  no  4.28   S3 F 4 3.1  yes 15.42  S3 F 5 3.5  no  3.59
S3 F 6 5.7  no  4.69   S3 F 7 7.1  no  4.06   S3 F 8 4.6  no  3.98
;

/*plotting histogram*/
proc univariate;
 var pm2_5;
  histogram/normal;
run;
```

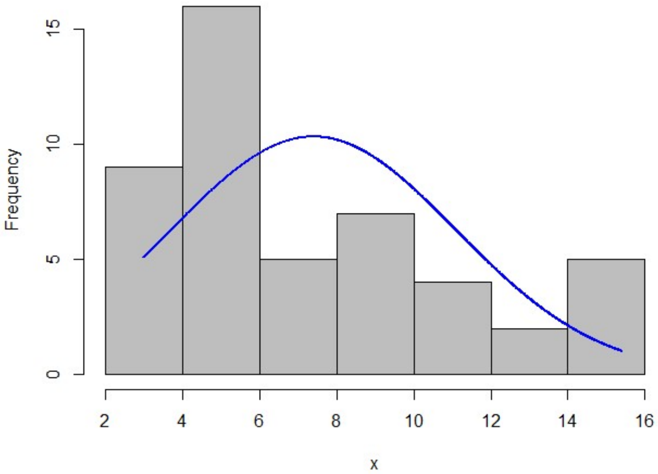


```
  Goodness-of-Fit Tests for Normal Distribution
Test                  Statistic        p Value
Kolmogorov-Smirnov D    0.21861080 Pr > D    <0.010
Cramer-von Mises   W-Sq 0.52542458 Pr > W-Sq <0.005
Anderson-Darling   A-Sq 2.98507256 Pr > A-Sq <0.005
```

The histrogram shows a right-skewed distribution and the normality tests all conclude that the distribution is not normal. Therefore, a gamma distribution would be a better choice.

In R:

```
pollution.data<- read.csv(file='C:/<insert path>/Exercise10.3Data.csv',
header=TRUE, sep=',')

#plotting histogram
library(rcompanion)
plotNormalHistogram(pollution.data$pm2_5)
```



```
shapiro.test(pollution.data$pm2_5)
```

```
Shapiro-Wilk normality test

W = 0.89215, p-value = 0.0003543
```

(b) Run the multilevel regression model for PM2.5, based on the gamma distribution. How well does the model fit the data? Hint: Townships variable indexes repeated measures within each county.

In SAS:

```
/*fitting hierarchical gamma model with random slopes and intercepts*/
proc glimmix method=Laplace;
 class state county pest;
  model pm2_5 = popl pest township / solution dist=gamma link=log;
   random intercept township / subject=state type=un;
    random intercept township / subject=county(state) type=un;
    covtest/wald;
run;
```

The model converges, but the estimates of the parameters of the random-effects terms are not statistically distinguishable from zero. The model that has significant parameters is given below.

```
/*fitting hierarchical gamma model with random intercept only for county level*/
proc glimmix method=Laplace;
 class state county pest(ref="no");
  model pm2_5 = popl pest township / solution dist=gamma link=log;
    random intercept / subject=county(state) type=un;
    covtest/wald;
run;
```

```
-2 Log Likelihood 273.79

            Covariance Parameter Estimates
Cov Parm Subject       Estimate Standard Z Value Pr > Z
                                  Error
UN(1,1)  county(state)   0.3178   0.1955    1.63 0.0521
Residual                0.09517  0.02048    4.65 <.0001

            Solutions for Fixed Effects
Effect    pest Estimate Standard DF t Value Pr > |t|
                          Error
Intercept        2.2944   0.2657  5    8.64   0.0003
popl            0.01628  0.01134 39    1.44   0.1590
pest      yes    0.6889   0.1059 39    6.51   <.0001
pest      no          0        .  .       .        .
township       -0.05147  0.02173 39   -2.37   0.0229
```

```
/*checking model fit*/
proc glimmix method=Laplace;
 class state county pest;
  model pm2_5 = popl pest township / dist=gamma link=log;
run;
```

```
2 Log Likelihood 315.24
```

```
data deviance;
 deviance = 315.24 - 273.79;
 pvalue = 1 - probchi(deviance, 1);
```

```
run;

proc print noobs;
run;
```

```
deviance     pvalue
   41.45 1.2092E-10
```

The model has an excellent fit as judged by a negligibly small p-value in the deviance test.

In R:

```
#fitting hierarchical gamma model with random slopes and intercepts
library(lme4)
summary(glmer(pm2_5 ~ popl + pest + township + (1+township | state)
+ (1+township| state:county), data=pollution.data, family=Gamma('log')))
```

```
The model doesn't converge.
```

```
#fitting hierarchical gamma model with random intercept only for county level
summary(fitted.model<- glmer(pm2_5 ~ popl + pest + township
+ (1 | state:county), data=pollution.data, family=Gamma('log')))
```

```
Random effects:
 Groups       Name        Variance Std.Dev.
 state:county (Intercept) 0.1222   0.3496  
 Residual                 0.1243   0.3526  

Fixed effects:
            Estimate Std. Error t value Pr(>|z|)
(Intercept)  2.28777    0.31448   7.275 3.47e-13
popl         0.01448    0.01078   1.344   0.1790
pestyes      0.68518    0.10150   6.751 1.47e-11
township    -0.05139    0.02083  -2.468   0.0136
```

```
#checking model fit
null.model<- glm(pm2_5 ~ popl + pest + township, data=pollution.data,
family=Gamma('log'))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
48.87942
```

```
print(p.value<- pchisq(deviance, df=1, lower.tail = FALSE))
```

```
2.72192e-12
```

(c) Write down the fitted model. Specify all estimates. Are PM2.5 readings correlated within each county? Between different counties within each state? Use $\alpha = 0.10$.

The fitted hierarchical gamma regression fitted in SAS has the estimated parameters $\hat{E}(PM2.5) = \exp(2.2944 + 0.01628 \cdot population\ size/1000\ + 0.6889 \cdot pesticides\ used - 0.05147 \cdot township)$, $\hat{\alpha} = 0.09517$, and $\hat{\sigma}^2_{county} = 0.3178$. Since this variance is statistically significant at the 10% level, it means that the responses are correlated for townships within the same county. There is no correlation between readings for different counties within the same state because the corresponding random-effects are not present in the fitted model.

For the model fitted in R, the parameters have estimates $\hat{E}(PM2.5) = \exp(2.28777 + 0.01448 \cdot population\ size/1000\ + 0.68518 \cdot pesticides\ used - 0.05139 \cdot township)$, $\hat{\alpha} = 0.1243$, and $\hat{\sigma}^2_{county} = 0.1222$.

(d) What fixed-effects predictors are significant at the 5% level? Interpret them.

Use of pesticides and township are significant predictors. In the townships where pesticides are used, the estimated average reading of PM2.5 is $\exp(0.6889) \cdot 100\% = 199.1524\%$ (for the model fitted in R, $\exp(0.68518) \cdot 100\% = 197.6999\%$) of that in townships where pesticides are not used. As the number of township increases by one, the estimated average PM2.5 reading changes by $(\exp(-0.05147) - 1) \cdot 100\% = -5.01679\%$, that is, decreases by 5.01679% (for the model fitted in R, $(\exp(-0.0519) - 1) \cdot 100\% = -5.00919\%$).

(e) Use the fitted model to predict the level of particulate matter in a town with population of 2,500 people if it is known that no pesticides are used in the fields that surround this town.

Using the model fitted in SAS, we compute the predicted value as follows (use township=1):

$PM2.5^0 = \exp(2.2944 + 0.01628 \cdot 2.5 - 0.05147) = 9.812234.$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input state$ county$ township popl pest$;
cards;
S4 G 1 2.5 no
;

data pollution;
set pollution predict;
run;

proc glimmix method=Laplace;
 class state county pest;
  model pm2_5 = popl pest township / dist=gamma link=log;
   random intercept /subject=county(state) type=un;
       output out=outdata pred(ilink)=ppm2_5;
run;

proc print data=outdata (firstobs=49) noobs;
 var ppm2_5;
run;
```

```
 ppm2_5
9.81257
```

Using the model fitted in R, the predicted value is $PM2.5^0 = \exp(2.28777 + 0.01448 \cdot 2.5 - 0.05139) = 9.704406$.
In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(state='S4', county='G', township=1,
popl=2.5, pest='no'), allow.new.levels=TRUE, re.form=NA, type='response'))
```

```
9.704524
```

EXERCISE 10.4. (a) Run a three-level hierarchical model for the binary response variable. Write down the fitted model. Are the measurements correlated within each asset over time? Are the measurements for different assets within the same portfolio correlated? Use the 10% significance level. How good is the model fit?

In SAS:

```
data portfolios;
input portfolio asset type$ day1 day2 day3 day4 day5 @@;
cards;
1 1  stock    0 0 0 0 1  1 2  stock    0 1 1 0 0  1 3  bond     0 0 0 0 0
1 4  bond     1 0 0 0 0  1 5  stock    1 1 1 0 1  1 6  stock    1 0 1 1 1
1 7  stock    1 1 1 1 1  2 8  currency 0 1 1 1 1  2 9  stock    0 1 1 1 1
2 10 bond     0 1 0 0 1  2 11 stock    1 0 1 1 1  3 12 currency 1 0 1 0 1
3 13 stock    0 0 1 0 1  3 14 stock    0 0 1 1 1  4 15 stock    1 0 1 0 0
4 16 bond     1 1 1 1 0  4 17 currency 0 0 0 0 1  4 18 stock    1 1 1 1 1
4 19 currency 0 0 0 0 1  5 20 stock    0 0 1 1 1  5 21 currency 1 0 0 1 1
5 22 stock    0 0 1 1 1  5 23 bond     1 1 0 0 0  5 24 stock    1 1 1 1 1
6 25 bond     1 0 0 1 1  6 26 stock    1 1 1 1 1  6 27 stock    1 1 1 1 1
6 28 stock    1 1 1 1 1  7 29 currency 0 1 1 1 1  7 30 currency 0 0 1 1 1
7 31 bond     1 1 1 1 0  7 32 currency 1 0 1 1 1  7 33 bond     0 0 0 1 1
7 34 bond     1 0 1 0 1  7 35 stock    1 1 1 1 1  7 36 stock    1 1 1 1 1
;

/*creating longform dataset*/
data longform;
set portfolios;
 array i[5] day1-day5;
  do day=1 to 5;
   increase=i[day];
    output;
  end;
keep portfolio asset type day increase;
run;

/*fitting hierarchical logistic model with random slopes and intercepts*/
proc glimmix method=Laplace;
 class portfolio asset type;
  model increase = type day / solution dist=binomial link=logit;
   random intercept day / subject=portfolio type=un;
   random intercept day / subject=asset(portfolio) type=un;
    covtest/wald;
run;
```

```
The model doesn't converge.
```

The model that does converge and has non-degenerate estimate of the parameters of the random-effects terms is as follows.

```
/*fitting hierarchical logistic model with random intercept only at asset level*/
proc glimmix method=Laplace;
 class portfolio asset type(ref="bond");
```

```
  model increase = type day / solution dist=binomial link=logit;
      random intercept / subject=asset(portfolio) type=un;
    covtest/wald;
run;
```

```
-2 Log Likelihood 211.02


             Covariance Parameter Estimates
Cov Parm Subject          Estimate Standard Z Value Pr > Z
                                   Error
UN(1,1)  asset(portfolio)   0.7504   0.5360    1.40 0.0808

              Solutions for Fixed Effects
Effect    type     Estimate Standard  DF t Value Pr > |t|
                            Error
Intercept           -1.1794   0.5912  33   -1.99   0.0544
type      currency   0.5227   0.6403 143    0.82   0.4157
type      stock      1.5515   0.5690 143    2.73   0.0072
type      bond            0        .   .       .        .
day                  0.3384   0.1299 143    2.60   0.0102
```

The fitted hierarchical logistic model has the estimated odds

$\frac{\hat{P}(increase=\ )}{1-\hat{P}(increase=1)} = \exp(-1.1794 + 0.5227 \cdot currency + 1.5515 \cdot stock + 0.3384 \cdot day)$ and $\hat{\sigma}^2_{asset} = 0.7504$. This variance is significant at the 10% level, therefore we can conclude that the measurements are correlated within each asset over time. However, the measurements for different assets are not correlated within each portfolio since the portfolio level random-effects terms are not present in the model.

```
/*checking model fit*/
proc glimmix method=Laplace;
 class portfolio asset type;
  model increase = day type / dist=binomial link=logit;
run;
```

```
-2 Log Likelihood 215.51
```

```
data deviance;
 deviance = 215.51 - 211.02;
 pvalue = 1 - probchi(deviance, 1);
run;

proc print noobs;
run;
```

```
deviance   pvalue
    4.49 0.034094
```

The model has a decent fit, significant at the 5% level, since the p-value is less than 0.05.

In R:

```
portfolios.data<- read.csv(file='C:/<insert path>/Exercise10.4Data.csv',
header=TRUE, sep=',')

#creating longform dataset
library(reshape2)
longform.data<- melt(portfolios.data, id.vars=c('portfolio','asset','type'),
variable.name='dayn',value.name='increase')
day<- ifelse(longform.data$dayn=='day1',1,ifelse(longform.data$dayn=='day2',
2,ifelse(longform.data$dayn=='day3',3, ifelse(longform.data$dayn=='day4',4,5))))

#fitting hierarchical logistic model with random slopes and intercepts
library(lme4)
summary(glmer(increase ~ type + day + (1 + day | portfolio)
+ (1 + day | portfolio:asset), data=longform.data, family=binomial('logit')))
```

The model converges but the only significant parameter of the random-effects terms is the intercept at the asset level, so a simpler model is run (the same as in SAS).

```
#fitting hierarchical logistic model with random intercept only at asset level
summary(fitted.model<- glmer(increase ~ type + day + (1 | portfolio:asset),
data=longform.data, family=binomial('logit')))
```

```
Random effects:
 Groups          Name        Variance Std.Dev.
 portfolio:asset (Intercept) 0.7504   0.8663

Fixed effects:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)   -1.1794     0.5912  -1.995  0.04606
typecurrency   0.5227     0.6403   0.816  0.41431
typestock      1.5514     0.5690   2.727  0.00640
day            0.3383     0.1299   2.605  0.00919
```

```
#checking model fit
null.model<- glm(increase ~ type + day, data=longform.data,
family=binomial('logit'))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
4.49183
```

```
print(p.value<- pchisq(deviance, df=1, lower.tail = FALSE))
```

```
0.03405719
```

(b) What predictors are significant at the 5% level? Interpret the estimated significant regression coefficients.

Stock and day are significant predictors. The estimated odds in favor of a stock going up at the closure of the stock exchange at the end of a day are $\exp(1.5515)\cdot 100\% = 471.8543\%$ of those for a bond. Each day, the estimated odds increase by $(\exp(0.3384)-1)\cdot 100\% = 40.27015\%$.

(c) According to the fitted model, what is the predicted probability of an increase in value of a currency on the third day?

The predicted probability is $P^0(increase = 1) = \frac{\exp(-1.1794+0.5227+0.3384\cdot 3)}{1+\exp(-1.1794+\ .5227+0.3384\cdot 3)} = 0.588677.$

In SAS:

```
/*using fitted model for prediction*/
```

```
data predict;
input portfolio asset type$ day;
cards;
8 37 currency 3
;

data longform;
set longform predict;
run;

proc glimmix method=Laplace;
 class portfolio asset type;
  model increase = type day/ dist=binomial link=logit;
     random intercept / subject=asset(portfolio) type=un;
  output out=outdata pred(ilink)=pincrease;
run;

proc print data=outdata (firstobs=181) noobs;
 var pincrease;
run;
```

```
pincrease
  0.58865
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(portfolio=8, asset=37,
type='currency', day=3), allow.new.levels=TRUE, re.form=NA, type='response'))
```

```
0.5886426
```

EXERCISE 10.5. (a) Fit a four-level hierarchical regression to model the number of additional attempts: level 1 are tasks, level 2 are students, level 3 are classrooms, and level 4 are schools. Assume that the underlying distribution is Poisson. What is the fit of this model?

In SAS:

```
data test;
input school class student gender$ task1 task2 task3 task4 @@;
cards;
1 1 1 boy  1  3  4  5  1 1  2 boy  0 0 3 4   1 1 3 boy  1  2  4 5
1 1 4 girl 3  3  5  5  1 1  5 boy  1 1 4 13  1 1 6 girl 2  4  3 4
1 1 7 girl 1  2  3  7  1 2  1 boy  1 2 3 5   1 2 2 boy  10 11 7 6
1 2 3 girl 3  14 8  7  1 2  4 boy  2 2 5 6   1 2 5 girl 3  3  5 8
2 1 1 boy  11 3  4  8  2 1  2 boy  0 5 5 3   2 1 3 girl 2  6  7 9
2 1 4 boy  0  2  4  6  2 1  5 boy  2 3 3 5   2 1 6 girl 3  5  4 9
2 1 7 boy  1  3  7  3  2 2  1 girl 0 2 6 5   2 2 2 boy  0  10 4 13
2 2 3 girl 3  4  7  6  2 2  4 boy  1 2 5 3   2 2 5 boy  3  4  2 12
2 2 6 girl 1  10 6  8  2 2  7 girl 4 3 8 7   2 2 8 girl 12 5  4 5
2 3 1 girl 1  0  12 1  2 3  2 girl 0 1 2 4   2 3 3 boy  0  1  1 3
2 3 4 boy  0  1  0  2  2 3  5 girl 1 1 1 2   2 3 6 boy  0  0  0 1
;
```

```
/*creating longform dataset*/
data longform;
set test;
 array a[4] task1-task4;
  do task=1 to 4;
   nattempts=a[task];
   output;
  end;
 keep school class student gender task nattempts;
 run;

/*fitting hierarchical Poisson model with random slopes and intercepts*/
proc glimmix method=Laplace;
  class school class student gender;
   model nattempts = gender task / solution dist=poisson link=log;
    random intercept task / subject=school type=un;
      random intercept task / subject=class(school) type=un;
      random intercept task / subject=student(class) type=un;
       covtest/wald;
run;
```

The model doesn't converge.

The model that does converge and gives nontrivial estimates of the parameters for the random-effects terms is the following model.

```
/*fitting hierarchical Poisson model with random intercepts only for class
and student levels*/
proc glimmix method=Laplace;
  class school class student gender(ref="boy");
   model nattempts = gender task / solution dist=poisson link=log;
     random intercept / subject=class(school) type=un;
      random intercept / subject=student(class) type=un;
 covtest/wald;
run;
```

```
-2 Log Likelihood 592.37

             Covariance Parameter Estimates
Cov Parm Subject        Estimate Standard Z Value Pr > Z
                                  Error
UN(1,1)  class(school)    0.2072   0.1523    1.36 0.0868
UN(1,1)  student(class) 0.06298  0.03682    1.71 0.0436

              Solutions for Fixed Effects
Effect    gender Estimate Standard  DF t Value Pr > |t|
                            Error
Intercept           0.3361   0.2542   4    1.32   0.2566
gender    girl      0.2879   0.1204 107    2.39   0.0185
gender    boy            0        .   .       .        .
task                0.2947  0.04040 107    7.29   <.0001
```

```
/*checking model fit*/
proc glimmix method=Laplace;
  class gender;
   model nattempts = gender task / dist=poisson link=log;
run;
```

```
2 Log Likelihood 661.07
```

```
data deviance;
 deviance = 661.07 - 592.37;
 pvalue  = 1 - probchi(deviance, 2);
run;

proc print noobs;
run;
```

```
deviance     pvalue
    68.7 1.2212E-15
```

The model has an excellent fit due to a very small p-value in the deviance test.

In R:

```
test.data<- read.csv(file='C:/<insert path>/Exercise10.5Data.csv', header=TRUE,
sep=',')

#creating longform dataset and numeric time variable
library(reshape2)
longform.data<- melt(test.data, id.vars=c('school','class','student', 'gender'),
variable.name='taskn',value.name='nattempts')
task<- ifelse(longform.data$taskn=='task1',1,ifelse(longform.data$taskn=='task2',
2,ifelse(longform.data$taskn=='task3',3,4)))

#fitting hierarchical Poisson model with random slopes
#and intercepts
library(lme4)
summary(glmer(nattempts ~ gender + task + (1 + task | school) + (1 + task |
school:class) + (1 + task | class:student), data=longform.data,
family=poisson('log')))
```

```
The model doesn’t converge.
```

```
#fitting hierarchical Poisson model with random intercepts only at class and
#student levels
summary(fitted.model<- glmer(nattempts ~ gender + task + (1 | school:class)
+ (1 | class:student), data=longform.data, family=poisson('log')))
```

```
Random effects:
 Groups        Name        Variance Std.Dev.
 class:student (Intercept) 0.06297  0.2509
 school:class  (Intercept) 0.20720  0.4552

Fixed effects:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.33609    0.25361   1.325   0.1851
gendergirl   0.28790    0.11972   2.405   0.0162
task         0.29469    0.04013   7.342  2.1e-13
```

```
#checking model fit
null.model<- glm(nattempts ~ gender + task, data=longform.data, family =
poisson('log'))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
68.70889
```

```
print(p.value<- pchisq(deviance, df=2, lower.tail = FALSE))
```

```
1.202414e-15
```

(b) Present the fitted model. What can you say about the correlation of the repeated measures for each student? Among the students in each classroom? Among the students in each school? Interpret estimated significant fixed-effects coefficients. Use the 10% level of significance.

The fitted hieirarchical Poisson model has the estimated parameters $\widehat{E}(nattempts) = \exp(0.3361 + 0.2879 \cdot girl + 0.2947 \cdot task)$, $\hat{\sigma}^2_{student} = 0.06298$, and $\hat{\sigma}^2_{class} = 0.2072$. Since both variances are significantly larger than zero, the repeated measure for each student are correlated, and the responses for students within each classroom are correlated as well. Responses for students within the same school are not correlated.

Both gender and task are significant fixed-effects predictors. The estimated average number of extra attempts for girls is $\exp(0.2879) \cdot 100\% = 133.3624\%$ of that for boys. As the task number increases by one, the estimated average number of extra attempts increases by $\exp(0.2947) \cdot 100\% = 134.2723\%$.

(c) Use the fitted model to predict the number of extra attempts it would take a girl to complete the fourth task.

The predicted value is $nattempts^0 = \exp(0.3361 + 0.2879 + 0.2947 \cdot 4) = 6.06661$.

In SAS:

```
/*using fitted model for prediction*/
data predict;
input school class student gender$ task;
cards;
4 4 9 girl 4
;

data longform;
set longform predict;
run;

proc glimmix method=Laplace;
  class school class student gender;
   model nattempts = gender task / dist=poisson link=log;
       random intercept / subject=class(school) type=un;
        random intercept / subject=student(class) type=un;
        output out=outdata pred(ilink)=pnattempts;
run;
proc print data=outdata (firstobs=133) noobs;
 var pnattempts;
run;
```

```
pnattempts
   6.06606
```

In R:

```
#using fitted model for prediction
```

```
print(predict(fitted.model, data.frame(school=4, class=4, student=9,
gender='girl', task=4), allow.new.levels=TRUE, re.form=NA, type='response'))
```

```
6.066223
```

EXERCISE 10.6. (a) Argue that the data may be modeled as having a negative binomial distribution. What quantities support your argument?

The number of students who stay for Masters degrees is an overly dispersed count data thus may be modeled as a negative binomial random variable.

(b) Run a multilevel model, using department and year as predictors. Does the model fit the data well?

In SAS:

```
data masters;
input univ dept$ year1 year2 year3 @@;
cards;
1 bio  6  13 17  1 chem 8  7  12  1 math 10 14 13  2 bio  0 8  8
2 chem 0  9  9   2 math 0  5  8   3 bio  2  8  5   3 chem 3 3  5
3 math 18 19 26  4 bio  1 11 12   4 chem 1  5  4   4 math 5 16 17
5 bio  7  16 15  5 chem 4  4  4   5 math 8  1  6   6 bio  5 3  3
6 chem 5  3  4   6 math 23 32 45  7 bio  7  2  8   7 chem 9 12 9
7 math 7  15 16  8 bio  3 6  8    8 chem 32 11 20  8 math 8  4  13
;

/*creating longform dataset*/
data longform;
set masters;
 array s[3] year1-year3;
  do year=1 to 3;
    nstay=s[year];
   output;
  end;
 keep univ dept year nstay;
run;

/*fitting hierarchical negative binomial model with random slopes and
intercepts*/
proc glimmix method=Laplace;
 class univ dept(ref='chem');
  model nstay = dept year / solution dist=negbin link=log;
   random intercept year / subject=univ type=un;
   random intercept year / subject=dept(univ) type=un;
    covtest/wald;
run;
```

```
The model doesn’t converge.
```

The model that converges and gives positive estimates for the parameters of the random-effects terms is the following:

```
/*fitting hierarchical negative binomial model with random intercept
only at the department level*/
```

```
proc glimmix method=Laplace;
 class univ dept(ref='chem');
  model nstay = dept year / solution dist=negbin link=log;
     random intercept / subject=dept(univ) type=un;
    covtest/wald;
run;
```

```
-2 Log Likelihood 427.95

          Covariance Parameter Estimates
Cov Parm Subject    Estimate Standard Z Value Pr > Z
                             Error
UN(1,1)  dept(univ)   0.2658  0.09659    2.75 0.0030
Scale                0.07351  0.04450    1.65 0.0493

           Solutions for Fixed Effects
Effect    dept Estimate Standard DF t Value Pr > |t|
                        Error
Intercept        1.3133   0.2489 21    5.28   <.0001
dept      bio   0.02657   0.2942 21    0.09   0.9289
dept      math   0.5766   0.2899 21    1.99   0.0599
dept      chem        0        .  .       .        .
year             0.2680  0.06508 47    4.12   0.0002
```

```
/*checking model fit*/
proc glimmix;
 class dept;
  model nstay = dept year / dist=negbin link=log;
run;
```

```
-2 Log Likelihood 450.08
```

```
data deviance;
 deviance = 450.08 - 427.95;
 pvalue = 1 - probchi(deviance, 1);
run;

proc print noobs;
run;
```

```
deviance     pvalue
   22.13 .000002548
```

The model has a very good fit as indicated by the tiny p-value in the deviance test.

In R:

```
masters.data<- read.csv(file='C:/<insert path>/Exercise10.6Data.csv',
header=TRUE, sep=',')

#creating longform dataset
library(reshape2)
longform.data<- melt(masters.data, id.vars=c('univ','dept'),
variable.name='yearn', value.name='nstay')
year<- ifelse(longform.data$yearn=='year1',1,
ifelse(longform.data$yearn=='year2',2,3))

#specifying reference level
dept.rel<- relevel(longform.data$dept, ref="chem")

#fitting hierarchical negative binomial model with random slopes and intercepts
library(lme4)
summary(glmer.nb(nstay ~ dept.rel + year + (1 + year | univ) + (1 + year |
univ:dept.rel), data=longform.data, family=negative.binomial('log')))
```

The model doesn't converge.

```
#fitting hierarchical negative binomial model with random
#intercept only at department level
summary(fitted.model<- glmer.nb(nstay ~ dept.rel + year + (1 | univ:dept.rel),
data=longform.data, family=negative.binomial('log')))
```

```
Family: Negative Binomial(13.5539)  ( log )

Random effects:
 Groups        Name        Variance Std.Dev.
 univ:dept.rel (Intercept) 0.2651   0.5149

Fixed effects:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)   1.30677    0.24837   5.261 1.43e-07
dept.relbio   0.02647    0.29368   0.090   0.9282
dept.relmath  0.57593    0.28943   1.990   0.0466
year          0.26652    0.06459   4.127 3.68e-05
```

```
#checking model fit
library(MASS)
null.model<- glm.nb(nstay ~ year, data=longform.data)
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
22.18095
```

```
print(p.value<- pchisq(deviance, df=1, lower.tail = FALSE))
```

```
2.481229e-06
```

(c) Are the observations correlated for each department over time? For the departments within the same university? State the fitted model, specifying all parameter estimates.

In SAS, the fitted hierarchical negative binomial model has the estimated parameters $\hat{E}(nstay) = \exp(1.3133 + 0.02657 \cdot biology\ dept + 0.5766 \cdot math\ dept + 0.268 \cdot year)$, $\hat{r} = 0.07351$, and $\hat{\sigma}^2_{u_1} = 0.2658$.
Since the variance of u_1 is statistically significant, we can conclude that observations over time within each department are correlated. Observations for each department within the same university are not correlated since τ_1 and τ_2 are not present in the fitted model.

In R, the fitted model has parameters $\hat{E}(nstay) = \exp(1.30677 + 0.02647 \cdot biology\ dept + 0.57593 \cdot math\ dept + 0.26652 \cdot year)$, $\hat{r} = \ln(13.5539) = 2.606674$, and $\hat{\sigma}^2_{u_1} = 0.2651$.

(d) Does the response change significantly over the years? Is there a difference in responses between departments? Give interpretation of the significant regression coefficients. Use $\alpha = 0.10$.

Math department and year are significant predictors, thus there is a difference in the response between departments, and the response changes significantly over the years.

In a math department, the estimated average number of students who stay on for a Master's degree is $\exp(0.5766) \cdot 100\% = 177.9976\%$ of that in a chemistry department (for the model fitted in R, $\exp(0.57593) \cdot 100\% = 177.8784\%$). As the year increases by one, the estimated average number of students who stay on for a Master's degree increases by $(\exp(0.268) - 1) \cdot 100\% = 30.73471\%$ (for the model fitted in R, $(\exp(0.26652) - 1) \cdot 100\% = 30.54137\%$).

(e) What is the predicted number of students who would stay on for a Master's program in a math department in year 4?

For the model fitted in SAS, the predicted value is $nstay^0 = \exp(1.3133 + 0.5766 + 0.268 \cdot 4) = 19.33467$.

In SAS:

```
/*using model for prediction*/
data predict;
input univ dept$ year;
cards;
9 math 4
;

data longform;
set longform predict;
run;

proc glimmix method=Laplace;
 class univ dept;
  model nstay = dept year / dist=negbin link=log;
     random intercept / subject=dept(univ) type=un;
       output out=outdata pred(ilink)=pnstay;
run;

proc print data=outdata (firstobs=73) noobs;
 var pnstay;
run;
```

```
 pnstay
19.3329
```

For the model fitted in R, the predicted value is $nstay^0 = \exp(1.30677 + 0.57593 + 0.26652 \cdot 4) = 19.08266$.

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(univ=9, dept.rel='math', year=4),
allow.new.levels=TRUE, re.form=NA, type='response'))
```

```
19.08261
```

EXERCISE 10.7. (a) Run the multilevel regression to model the response to medication, assuming that it follows a beta distribution.

In SAS:

```
data trial;
input center subject gender$ medA medB medC medD @@;
cards;
1 101 M 0.32 0.27 0.23 0.90  1 102 M 0.17 0.16 0.35 0.40
1 103 F 0.39 0.44 0.45 0.64  1 104 M 0.14 0.47 0.63 0.76
1 105 F 0.08 0.36 0.40 0.72  1 106 F 0.61 0.53 0.64 0.79
1 107 F 0.55 0.73 0.63 0.61  1 108 M 0.40 0.47 0.46 0.99
1 109 F 0.25 0.40 0.31 0.62  1 110 M 0.34 0.48 0.29 0.63
1 111 M 0.33 0.42 0.43 0.75  1 112 F 0.21 0.39 0.74 0.98
1 113 F 0.39 0.22 0.50 0.88  1 114 M 0.33 0.30 0.26 0.19
1 115 F 0.03 0.49 0.36 0.73  2 201 M 0.31 0.46 0.53 0.81
2 202 F 0.27 0.57 0.28 0.84  2 203 M 0.26 0.42 0.38 0.90
2 204 M 0.33 0.34 0.56 0.75  2 205 F 0.29 0.45 0.57 0.81
2 206 F 0.30 0.42 0.64 0.95  2 207 F 0.34 0.42 0.55 0.77
2 208 M 0.09 0.35 0.42 0.67  2 209 M 0.25 0.44 0.62 0.73
2 210 F 0.21 0.41 0.58 0.75  3 301 F 0.23 0.41 0.50 0.86
3 302 F 0.21 0.35 0.52 0.84  3 303 M 0.21 0.43 0.68 0.72
3 304 M 0.07 0.23 0.47 0.59  3 305 M 0.11 0.28 0.50 0.78
3 306 F 0.19 0.24 0.55 0.73  3 307 M 0.15 0.23 0.39 0.82
3 308 F 0.18 0.19 0.53 0.92
;

/*creating longform dataset*/
data longform;
set trial;
 array r[4] medA medB medC medD;
  do med=1 to 4;
   response=r[med];
   output;
  end;
 keep center subject gender med response;
run;

/*fitting hierarchical beta model with random slopes and intercepts*/
proc glimmix method=Laplace;
 class center subject gender;
  model response = gender med / solution dist=beta link=logit;
   random intercept med / subject=center type=un;
   random intercept med / subject=subject(center) type=un;
    covtest/wald;
run;
```

The model doesn’t converge.

The model that converges and gives positive estimates for the parameters of the random-effects terms is the following:

```
/*fitting hierarchical beta model with random intercept only at subject level*/
proc glimmix method=Laplace;
 class center subject gender;
  model response = gender med / solution dist=beta link=logit;
     random intercept / subject=subject(center) type=un;
   covtest/wald;
run;
```

```
-2 Log Likelihood -153.06

             Covariance Parameter Estimates
Cov Parm Subject         Estimate Standard Z Value   Pr Z
                                  Error
UN(1,1)  subject(center)  0.06449  0.04224    1.53 0.0634
Scale                     11.2305   1.5764    7.12 <.0001

             Solutions for Fixed Effects
Effect    gender Estimate Standard DF t Value Pr > |t|
                          Error
Intercept         -2.0131   0.1656 31  -12.16   <.0001
gender    F        0.2497   0.1386 98    1.80   0.0746
gender    M             0        .  .       .        .
med                0.7078  0.04973 98   14.23   <.0001
```

In R:

```
trial.data<- read.csv(file='C:/<insert path>/Exercise10.7Data.csv',
header=TRUE, sep=',')

#creating longform dataset
library(reshape2)
longform.data<- melt(trial.data, id.vars=c('center','subject','gender'),
variable.name='medn', value.name='response')
med<- ifelse(longform.data$medn=='medA',1,ifelse(longform.data$medn=='medB',
2,ifelse(longform.data$medn=='medC',3,4)))

#specifying reference level
gender.rel<- relevel(longform.data$gender, ref="M")

#fitting hierarchical beta model with random slopes and intercepts
library(glmmTMB)
summary(glmmTMB(response ~ gender.rel + med + (1 + med | center) + (1 + med |
center:subject), data=longform.data, family=beta_family(link='logit')))
```

```
The model converges but all estimates of random-effects terms are degrenerate.
```

```
#fitting hierarchical beta model with random intercept only at subject level
summary(fitted.model<- glmmTMB(response ~ gender.rel + med
+ (1 | center:subject), data=longform.data, family=beta_family(link='logit')))
```

```
Random effects:

Groups          Name        Variance Std.Dev.
 center:subject (Intercept) 0.06449  0.2539

Overdispersion parameter for beta family (): 11.2

Conditional model:
             Estimate Std. Error z value Pr(>|z|)
(Intercept) -2.01310    0.16555 -12.160   <2e-16
gender.relF  0.24967    0.13855   1.802   0.0715
med          0.70779    0.04973  14.233   <2e-16
```

(b) State the model and estimate the parameters. What random-effects terms are present? Discuss the model fit. For all significance use the 10% level.

The fitted hierarchical beta model has the estimated parameters

$\hat{E}(response) = \frac{\exp(-2.0131+\ .2497 \cdot female + 0.7078 \cdot medication)}{1+\exp(-2.0131+\ .2497 \cdot female + 0.7078 \cdot medication)}$ and $\hat{\alpha} = 11.2305.$

At the 10% significance level, the variance of the random intercept at the subject level is positive, and both gender and medication are significant predictors of the mean response.

The model fits the data well at the 10% significance level, since the p-value of the deviance test is below 0.10.

In SAS:

```
/*checking model fit*/
proc glimmix;
 class gender;
  model response = gender med / dist=beta link=logit;
run;
```

```
-2 Log Likelihood -149.36
```

```
data deviance;
 deviance = -149.36 - (-153.06);
 pvalue = 1 - probchi(deviance, 1);
run;

proc print noobs;
run;
```

```
deviance   pvalue
     3.7 0.054412
```

In R:

```
#checking model fit
library(betareg)
summary(null.model<- betareg(response ~ gender.rel + med,
data=longform.data,link='logit'))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
3.69739
```

```
print(p.value<- pchisq(deviance, df=1, lower.tail = FALSE))
```

```
0.05449765
```

(c) Interpret the results. Are responses correlated for each subject? For each center? Interpret estimated significant fixed-effects terms.

Since the variance of u_1 is positive, and the other random-effects terms are not present in the model, we conclude that responses to medications are correlated within each subject but uncorrelated between the subjects.

For female subjects, the ratio $\frac{\hat{\mu}}{1-\hat{\mu}}$ is $\exp(0.2497) \cdot 100\% = 128.364\%$ of that for male subjects. As the number of medication increases by one (A=1, B=2, C=3. D=4), the ratio $\frac{\hat{\mu}}{1-\hat{\mu}}$ increases by $(\exp(0.7078) - 1) \cdot 100\% = 102.9521\%$.

(d) Use the fitted model to predict the response to medication A in a female subject.

The predicted value is $response^0 = \frac{\exp(-2.0131+0.2497+0.7078)}{1+\mathrm{ex}\ \ (-2.0131+0.2497+\ \ .7078)} = 0.258151.$

In SAS:

```
/*using fitted model for prediction*/
data predict;
input center subject gender$ med;
cards;
4 309 F 1
;

data longform;
set longform predict;
run;

proc glimmix method=Laplace;
 class center subject gender;
  model response = gender med / dist=beta link=logit;
   random intercept / subject=subject(center) type=un;
       output out=outdata pred(ilink)=presponse;
run;

proc print data=outdata (firstobs=133) noobs;
 var presponse;
run;
```

```
presponse
  0.25815
```

In R:

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(center=4, subject=309, gender.rel='F',
med=1), allow.new.levels=TRUE, re.form=NA, type='response'))
```

```
0.2581452
```