

ADVANCED REGRESSION MODELS WITH SAS AND R

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Preface

This book presents the material that I had the privilege of teaching to Master's level students at California State University, Long Beach. The material was very well received by the students, and helped them a great deal in finding good jobs. Now this book will serve as a textbook for an introductory upper-division undergraduate course in linear regression models.

Chapters 1 through 7 present 22 regression models: for responses with normal, gamma, binary, multinomial, Poisson, negative binomial, and beta distributions. The last three chapters (Chapters 8 – 10) deal with models for repeated measures and clustered data. Such aspects of regression are covered in this book as model setting and definition, formula for fitted model, goodness of model fit, interpretation of estimated regression parameters, and use of the fitted model for prediction. One example with complete SAS and R codes and relevant outputs is shown for each regression. Results in each example are discussed for SAS outputs, while R scripts and outputs are given without discussion.

The topic that was deliberately left out (not an easy decision) is model building via variable selection procedures, which would require significantly larger data sets and longer codes.

The settings for examples came from consulting projects, which I had been involved in for the past three years as the Faculty Director of the Statistical Consulting Group at my university. To simplify the discussion and focus on the models and their applications, the data have been “smoothed out” in a sense that the issues of missing values, outliers, multi-collinearity, and transformations of predictor variables don't have to be addressed.

The website that accompanies this book <http://web.csulb.edu/~okoroste/regressions.html> contains complete SAS and R codes for all examples, and data sets for all exercises in .csv format. A complete solutions manual is also available to instructors upon request.

Respectfully,
The author.

Contents

Preface	3
1 Introduction: General and Generalized Linear Regression Models	13
1.1 Definition of General Linear Regression Model	13
1.2 Definition of Generalized Linear Regression Model	14
1.3 Parameter Estimation and Significance Test for Coefficients . .	15
1.4 Fitted Model	15
1.5 Interpretation of Estimated Regression Coefficients	16
1.6 Model Goodness-of-Fit Check	16
1.7 Predicted Response	18
1.8 SAS Implementation	18
1.9 R Implementation	20
1.10 Example	21
Exercises	27
2 Regression Models for Response with Right-skewed Distribution	35
2.1 Box-Cox Power Transformation	35
2.1.1 Model Definition	35
2.1.2 Fitted Model	36
2.1.3 Interpretation of Estimated Regression Coefficients . .	36
2.1.4 Predicted Response	37
2.1.5 SAS Implementation	37
2.1.6 R Implementation	38
2.1.7 Example	39
2.2 Gamma Regression Model	48
2.2.1 Model Definition	48
2.2.2 Fitted Model	49
2.2.3 Interpretation of Estimated Regression Coefficients . .	49
2.2.4 Predicted Response	50
2.2.5 SAS Implementation	50

2.2.6	R Implementation	50
2.2.7	Example	50
	Exercises	54
3	Regression Models for Binary Response	61
3.1	Binary Logistic Regression Model	61
3.1.1	Model Definition	61
3.1.2	Fitted Model	62
3.1.3	Interpretation of Estimated Regression Coefficients . .	63
3.1.4	Predicted Probability	64
3.1.5	SAS Implementation	64
3.1.6	R Implementation	64
3.1.7	Example	64
3.2	Probit Model	68
3.2.1	Model Definition	68
3.2.2	Fitted Model	69
3.2.3	Interpretation of Estimated Regression Coefficients . .	69
3.2.4	Predicted Probability	69
3.2.5	SAS Implementation	69
3.2.6	R Implementation	70
3.2.7	Example	70
3.3	Complementary Log-Log Model	73
3.3.1	Model Definition	73
3.3.2	Fitted Model	73
3.3.3	Interpretation of Estimated Regression Coefficients . .	73
3.3.4	Predicted Probability	74
3.3.5	SAS Implementation	74
3.3.6	R Implementation	74
3.3.7	Example	74
	Exercises	78
4	Regression Models for Categorical Response	83
4.1	Cumulative Logit Model	84
4.1.1	Model Definition	84
4.1.2	Fitted Model	85
4.1.3	Interpretation of Estimated Regression Coefficients . .	85
4.1.4	Predicted Probabilities	86
4.1.5	SAS Implementation	86
4.1.6	R Implementation	86
4.1.7	Example	87
4.2	Cumulative Probit Model	92
4.2.1	Model Definition	92

4.2.2	Fitted Model	92
4.2.3	Interpretation of Estimated Regression Coefficients . .	93
4.2.4	Predicted Probabilities	93
4.2.5	SAS Implementation	93
4.2.6	R Implementation	93
4.2.7	Example	94
4.3	Cumulative Complementary Log-Log Model	98
4.3.1	Model Definition	98
4.3.2	Fitted Model	98
4.3.3	Interpretation of Estimated Regression Coefficients . .	98
4.3.4	Predicted Probabilities	99
4.3.5	SAS Implementation	99
4.3.6	R Implementation	99
4.3.7	Example	99
4.4	Generalized Logit Model for Nominal Response	104
4.4.1	Model Definition	104
4.4.2	Fitted Model	104
4.4.3	Interpretation of Estimated Regression Coefficients . .	105
4.4.4	Predicted Probabilities	105
4.4.5	SAS Implementation	106
4.4.6	R Implementation	106
4.4.7	Example	106
	Exercises	110
5	Regression Models for Count Response	117
5.1	Poisson Regression Model	117
5.1.1	Model Definition	117
5.1.2	Fitted Model	118
5.1.3	Interpretation of Estimated Regression Coefficients . .	118
5.1.4	Predicted Response	119
5.1.5	SAS Implementation	119
5.1.6	R Implementation	119
5.1.7	Example	119
5.2	Zero-truncated Poisson Regression Model	122
5.2.1	Model Definition	122
5.2.2	Fitted Model	123
5.2.3	Interpretation of Estimated Regression Coefficients . .	123
5.2.4	Predicted Response	123
5.2.5	SAS Implementation	123
5.2.6	R Implementation	124
5.2.7	Example	124
5.3	Zero-inflated Poisson Regression Model	127

5.3.1	Model Definition	127
5.3.2	Fitted Model	128
5.3.3	Interpretation of Estimated Regression Coefficients . .	128
5.3.4	Predicted Response	129
5.3.5	SAS Implementation	129
5.3.6	R Implementation	129
5.3.7	Example	129
5.4	Hurdle Poisson Regression Model	133
5.4.1	Model Definition	133
5.4.2	Fitted Model	134
5.4.3	Interpretation of Estimated Regression Coefficients . .	134
5.4.4	Predicted Response	134
5.4.5	SAS Implementation	135
5.4.6	R Implementation	135
5.4.7	Example	135
	Exercises	139
6	Regression Models for Overdispersed Count Response	149
6.1	Negative Binomial Regression Model	149
6.1.1	Model Definition	149
6.1.2	Fitted Model	150
6.1.3	Interpretation of Estimated Regression Coefficients . .	150
6.1.4	Predicted Response	150
6.1.5	SAS Implementation	150
6.1.6	R Implementation	151
6.1.7	Example	151
6.2	Zero-truncated Negative Binomial Regression Model	154
6.2.1	Model Definition	154
6.2.2	Fitted Model	155
6.2.3	Interpretation of Estimated Regression Coefficients . .	155
6.2.4	Predicted Response	155
6.2.5	SAS Implementation	155
6.2.6	R Implementation	155
6.2.7	Example	156
6.3	Zero-inflated Negative Binomial Regression Model	159
6.3.1	Model Definition	159
6.3.2	Fitted Model	160
6.3.3	Interpretation of Estimated Regression Coefficients . .	160
6.3.4	Predicted Response	160
6.3.5	SAS Implementation	160
6.3.6	R Implementation	161
6.3.7	Example	161

6.4	Hurdle Negative Binomial Regression Model	165
6.4.1	Model Definition	165
6.4.2	Fitted Model	165
6.4.3	Interpretation of Estimated Regression Coefficients . .	165
6.4.4	Predicted Response	166
6.4.5	SAS Implementation	166
6.4.6	R Implementation	167
6.4.7	Example	167
	Exercises	171
7	Regression Models for Proportion Response	179
7.1	Beta Regression Model	179
7.1.1	Model Definition	179
7.1.2	Fitted Model	180
7.1.3	Interpretation of Estimated Regression Coefficients . .	180
7.1.4	Predicted Response	180
7.1.5	SAS Implementation	181
7.1.6	R Implementation	181
7.1.7	Example	181
7.2	Zero-inflated Beta Regression Model	185
7.2.1	Model Definition	185
7.2.2	Fitted Model	185
7.2.3	Interpretation of Estimated Regression Coefficients . .	186
7.2.4	Predicted Response	186
7.2.5	SAS Implementation	186
7.2.6	R Implementation	187
7.2.7	Example	188
7.3	One-inflated Beta Regression Model	193
7.3.1	Model Definition	193
7.3.2	Fitted Model	194
7.3.3	Interpretation of Estimated Regression Coefficients . .	194
7.3.4	Predicted Response	194
7.3.5	SAS Implementation	195
7.3.6	R Implementation	195
7.3.7	Example	195
7.4	Zero-one-inflated Beta Regression Model	200
7.4.1	Model Definition	200
7.4.2	Fitted Model	201
7.4.3	Interpretation of Estimated Regression Coefficients . .	201
7.4.4	Predicted Response	202
7.4.5	SAS Implementation	202
7.4.6	R Implementation	203

7.4.7	Example	204
	Exercises	209
8	General Linear Regression Models for Repeated Measures Data	219
8.1	Random Slope and Intercept Model	219
8.1.1	Model Definition	219
8.1.2	Fitted Model	220
8.1.3	Interpretation of Estimated Regression Coefficients . .	220
8.1.4	Model Goodness-of-Fit Check	221
8.1.5	Predicted Response	221
8.1.6	SAS Implementation	221
8.1.7	R Implementation	222
8.1.8	Example	224
8.2	Random Slope and Intercept Model with Covariance Structure for Error	230
8.2.1	Model Definition	230
8.2.2	Fitted Model, Interpretation of Estimated Regression Coefficients, and Predicted Response	232
8.2.3	Model Goodness-of-fit Check	232
8.2.4	SAS Implementation	233
8.2.5	R Implementation	233
8.2.6	Example	234
8.3	Generalized Estimating Equations Model	247
8.3.1	Model Definition	247
8.3.2	Fitted Model, Interpretation of Estimated Regression Coefficients, and Predicted Response	250
8.3.3	Model Goodness-of-Fit Check	250
8.3.4	SAS Implementation	250
8.3.5	R Implementation	251
8.3.6	Example	252
	Exercises	259
9	Generalized Linear Regression Models for Repeated Measures Data	267
9.1	Generalized Random Slope and Intercept Model	267
9.1.1	Model Definition	267
9.1.2	Fitted Model, Interpretation of Estimated Regression Coefficients, Model Goodness-of-Fit Check, and Pre- dicted Response	268
9.1.3	SAS Implementation	268
9.1.4	R Implementation	269

9.1.5	Example	270
9.2	Generalized Estimating Equations Model	275
9.2.1	Model Definition	275
9.2.2	SAS Implementation	275
9.2.3	R Implementation	275
9.2.4	Example	276
	Exercises	282
10	Hierarchical Regression Model	289
10.1	Hierarchical Regression Model for Normal Response	289
10.1.1	Model Definition	289
10.1.2	Fitted Model, Interpretation of Estimated Regression Coefficients, Model Goodness-of-Fit Check, Predicted Response	290
10.1.3	SAS Implementation	291
10.1.4	R Implementation	291
10.1.5	Example	292
10.2	Hierarchical Regression Model for Non-normal Response	298
10.2.1	Model Definition	298
10.2.2	Fitted Model	298
10.2.3	Interpretation of Estimated Regression Coefficients	298
10.2.4	Model Goodness-of-Fit Check	298
10.2.5	Predicted Response	299
10.2.6	SAS Implementation	299
10.2.7	R Implementation	299
10.2.8	Example	300
	Exercises	304
	Recommended Books	313
	List of Notation	315
	Subject Index	316

Chapter 1

Introduction: General and Generalized Linear Regression Models

1.1 Definition of General Linear Regression Model

Suppose a random sample of size n is drawn from a population, and measurements $(x_{i1}, x_{i2}, \dots, x_{ik}, y_i), i = 1, \dots, n$, are obtained on the n individuals. The random variables x_1, \dots, x_k (with the lower-case notation for simplicity) are commonly termed *predictor variables* (or, simply, *predictors*), but, depending on the field of application, they may also be called *independent variables*, *covariates*, *regressors*, or *explanatory variables*. The y variable is the *response variable* (or, simply, *response*). Other terms include *dependent variable*, *variate*, or *outcome variable*. The *general linear regression model*¹ represents a relation between the response variable y and the predictor variables x_1, \dots, x_k of the form:

$$y = \beta_0 + \beta_1 x_1 + \dots + \beta_k x_k + \varepsilon \quad (1.1)$$

where β_0, \dots, β_k are constant *regression coefficients*, and ε is a *random error* that has a normal distribution with the mean zero and a constant variance σ^2 . Also, the random errors are assumed independent for different individuals in the sample. The parameters of the model β_0, \dots, β_k , and the variance σ^2 are unknown and have to be estimated from the data. The relation between y and x_1, \dots, x_k is not necessarily linear in the x variables as polynomial or interaction terms may be included, but it is necessarily linear in the beta

¹The first rigorous treatment of linear regression was published in Pearson, Karl (1896). “Mathematical Contributions to the Theory of Evolution. III. Regression, Heredity, and Panmixia”. *Philosophical Transactions of Royal Society of London, Series A*, 187, 253 – 318.

coefficients.

Note that in the general linear regression model, the response variable y has a normal distribution with the mean

$$\mathbb{E}(y) = \beta_0 + \beta_1 x_1 + \cdots + \beta_k x_k, \quad (1.2)$$

and variance σ^2 . Moreover, the values of y for different individuals are assumed independent.

1.2 Definition of Generalized Linear Regression Model

In a *generalized linear regression model*², the response variable y is assumed to follow a probability distribution from the exponential family of distributions, that is, the probability density function (in a continuous case) or probability mass function (in a discrete case) of y has the form

$$f(y; \theta, \phi) = \exp \left\{ \frac{y\theta - c(\theta)}{\phi} + h(y, \phi) \right\} \quad (1.3)$$

where $c(\cdot)$ and $h(\cdot)$ are some functions, and θ and ϕ are constants. The parameter θ is called *location parameter*, whereas ϕ is termed *dispersion* or *scale* parameter. Further, in a generalized linear regression model, the mean response $\mathbb{E}(y)$ is related to the linear combination of predictors x_1, \dots, x_k through an invertible *link function* $g(\cdot)$, that is, for some regression coefficients β_0, \dots, β_k ,

$$g(\mathbb{E}(y)) = \beta_0 + \beta_1 x_1 + \cdots + \beta_k x_k, \quad (1.4)$$

or, alternatively,

$$\mathbb{E}(y) = g^{-1}(\beta_0 + \beta_1 x_1 + \cdots + \beta_k x_k). \quad (1.5)$$

Note that the general linear regression defined by (1.1) is a special case of a generalized linear regression, since the normal density with mean μ and variance σ^2 belongs to the exponential family of distributions with $\theta = \mu$ and $\phi = \sigma^2$ (see Exercise 1.1). In addition, $\mathbb{E}(y) = \beta_0 + \beta_1 x_1 + \cdots + \beta_k x_k$, which tells us that the link function $g(\cdot)$ is the identity.

²Introduced in Nelder, J. and R. Wedderburn (1972). “Generalized linear models”. *Journal of the Royal Statistical Society, Series A*, 135 (3): 370 – 384.

1.3 Parameter Estimation and Significance Test for Coefficients

In a generalized linear regression model, the regression coefficients β_0, \dots, β_k , and the other parameters of the distribution are estimated by the method of the maximum likelihood estimation. The estimates are computed numerically via an iterative process.

From the theory it is known that for a large number of observations, the maximum likelihood estimators have an approximately normal distribution. In particular, it means that a standard z -test is appropriate to use to test for equality to zero of each regression coefficient. For this test, the null hypothesis is that the coefficient is equal to zero, while the alternative is that it is not equal to zero. A p -value below 0.05 would imply that the regression coefficient is a significant predictor of the response variable at the 5% level of significance. Alternatively, this test may be conducted based on t -distribution or a chi-squared distribution.

1.4 Fitted Model

In accordance to (1.2), the *fitted* general linear regression model has the estimated (also called *fitted*) mean response

$$\widehat{\mathbb{E}}(y) = \widehat{\beta}_0 + \widehat{\beta}_1 x_1 + \dots + \widehat{\beta}_k x_k, \quad (1.6)$$

and the estimated standard deviation $\widehat{\sigma}$. As explained above, $\widehat{\beta}_0, \dots, \widehat{\beta}_k$ and $\widehat{\sigma}$ are the maximum likelihood estimates.

In view of (1.4) and (1.5), in the case of a generalized linear regression with the link function $g(\cdot)$, the fitted model has the estimated mean response $\widehat{\mathbb{E}}(y)$ that satisfies

$$g(\widehat{\mathbb{E}}(y)) = \widehat{\beta}_0 + \widehat{\beta}_1 x_1 + \dots + \widehat{\beta}_k x_k, \quad (1.7)$$

or, equivalently,

$$\widehat{\mathbb{E}}(y) = g^{-1}(\widehat{\beta}_0 + \widehat{\beta}_1 x_1 + \dots + \widehat{\beta}_k x_k) \quad (1.8)$$

where the estimates of the beta coefficients as well as the estimates for all the other parameters of the underlying distribution are obtained by the method of maximum likelihood.

1.5 Interpretation of Estimated Regression Coefficients

In a fitted general linear regression model with the estimated mean response defined by (1.6), the estimates of the regression coefficients $\hat{\beta}_1, \dots, \hat{\beta}_k$ yield the following interpretation:

- If a predictor variable x_1 is numeric, then the corresponding estimated regression coefficient $\hat{\beta}_1$ indicates by how much the estimated mean response $\mathbb{E}(y)$ changes for a unit increase in x_1 , provided all the other predictors are held fixed. To see that, we can write $\hat{\mathbb{E}}(y|x_1 + 1) - \hat{\mathbb{E}}(y|x_1) = \hat{\beta}_0 + \hat{\beta}_1(x_1 + 1) + \hat{\beta}_2 x_2 + \dots + \hat{\beta}_k x_k - (\hat{\beta}_0 + \hat{\beta}_1 x_1 + \hat{\beta}_2 x_2 + \dots + \hat{\beta}_k x_k) = \hat{\beta}_1$.
- If a predictor variable x_1 is an *indicator variable* (also termed *0-1 variable* or *dummy variable*), then $\hat{\beta}_1$ has the meaning of the difference between the estimated mean response $\hat{\mathbb{E}}(y)$ for $x_1 = 1$ and that for $x_1 = 0$, controlling for the other predictors. Indeed, $\hat{\mathbb{E}}(y|x_1 = 1) - \hat{\mathbb{E}}(y|x_1 = 0) = \hat{\beta}_0 + \hat{\beta}_1 \cdot 1 + \hat{\beta}_2 x_2 + \dots + \hat{\beta}_k x_k - (\hat{\beta}_0 + \hat{\beta}_1 \cdot 0 + \hat{\beta}_2 x_2 + \dots + \hat{\beta}_k x_k) = \hat{\beta}_1$.

If the link function in (1.7) is not the identity, the interpretation of regression coefficients is analogous to the above, but is done in terms of $g(\hat{\mathbb{E}}(y))$, the link function of the estimated mean response.

1.6 Model Goodness-of-Fit Check

According to the theory of generalized linear regression modeling, relative goodness-of-fit of several models may be compared based on a number of criteria, including the Akaike information criterion³, corrected Akaike information criterion⁴, and Schwarz Bayesian information criterion⁵. These three criteria are built upon the log-likelihood function $\ln L$ of the model since the larger its value, the better the fit of the model. However, it is known that a perfect fit may be achieved by introducing a large number of predictors into the model. Therefore, these criteria penalize for fitting too many predictors.

³Akaike, H. (1974). “A new look at the statistical model identification”. *IEEE Transactions on Automatic Control*, 19 (6): 716 – 723.

⁴Sugiura, N. (1978). “Further analysis of the data by Akaike’s information criterion and the finite corrections”. *Communications in Statistics – Theory and Methods*, A7: 13 – 26.

⁵Schwarz, G. (1978). “Estimating the dimension of a model”. *Annals of Statistics*, 6(2): 461 – 464.

Let p denote the number of unknown parameters in the regression model that have to be estimated from the data. For instance, in the case of the general linear regression (1.1), there are a total of $k + 2$ parameters (β_0 through β_k , and σ).

The *Akaike Information Criterion (AIC)* value is defined as

$$AIC = -2 \ln L + 2p. \quad (1.9)$$

The *Corrected Akaike Information Criterion (AICC)* value is given by the formula

$$AICC = -2 \ln L + 2p \frac{n}{n - p - 1}. \quad (1.10)$$

The AICC represents the AIC with a correction for a small sample size n .

The *Schwarz Bayesian Information Criterion (BIC)* (or, simply, *Bayesian Information Criterion*) value is computed as

$$BIC = -2 \ln L + p \ln(n). \quad (1.11)$$

For each of the three criteria, a model with the smallest value has the best fit. Note that these criteria don't provide goodness-of-fit measure in absolute terms, only relative to other models. When several regression models for the same response variable are developed that are based on different distributions and/or link functions, then the best fitted model may be chosen according to the above criteria.

In absolute terms, though, the goodness-of-fit of a given model is based on the *deviance test* (also known as the *asymptotic likelihood ratio test*).⁶ In this test, the null hypothesis is that the *null model* has a better fit, and the alternative hypothesis is that the fitted model is better. Unless stated otherwise, the null model is the *intercept-only model*, which contains no predictors x_1, \dots, x_k . The test statistic is called the *deviance*, and is defined as -2 multiplied by the difference in log-likelihoods of the null and fitted models, that is,

$$deviance = -2 \left(\ln L(\text{null model}) - \ln L(\text{fitted model}) \right).$$

Under H_0 , the test statistic has a chi-squared distribution with k degrees of freedom, and the p -value is calculated as the area under the density curve

⁶Introduced in Wilks, S. S. (1938). "The Large-sample distribution of the likelihood ratio for testing composite hypotheses". *The Annals of Mathematical Statistics*, 9(1): 60 – 62.

above the test statistic. The number of degrees of freedom is calculated as the difference between the number of parameters of the fitted and null models.

1.7 Predicted Response

For a general linear regression model, the formula for the fitted mean response (1.6) may be used to predict the value y^0 of the response variable for a fixed set of predictors x_1^0, \dots, x_k^0 . The prediction is carried out by calculating

$$y^0 = \hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \dots + \hat{\beta}_k x_k^0. \quad (1.12)$$

For a generalized linear regression model, in view of (1.8), the *predicted response* is computed as

$$y^0 = g^{-1}(\hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \dots + \hat{\beta}_k x_k^0). \quad (1.13)$$

1.8 SAS Implementation

Prior to fitting a general linear regression, it is wise to verify that the distribution of the response variable is indeed normal. To this end, we can plot a histogram for the measurements of y and overlay it with a normal probability density curve, which mean and standard deviation are estimated from the data. This can be done with the following syntax:

```
proc univariate data=data_name;
    var response_name;
    histogram /normal;
run;
```

The output contains the requested graph as well as test statistics and p -values for several normality tests, which are goodness-of-fit tests for normal distribution with the null hypothesis being that the distribution is normal and the alternative being that it is non-normal. SAS outputs the results of the three tests: Kolmogorov-Smirnov test, Cramer-von Mises test, and Anderson-Darling test. For these tests, p -values larger than 0.05 indicate normality of the distribution of the response variable at the 5% level of significance.

Once normality is established, the general linear regression model could be fitted to the data. We describe next how to do that.

A generalized linear regression model may be fitted using the procedure `genmod` with a specified distribution of the response variable and the type of link function. As a special case, the general linear regression model is fitted with the normal distribution of y and the identity link function. Both of these are, in fact, defaults in SAS. In what follows, however, we will always specify the distribution and link function as a reminder to ourselves.

To include computation of predicted response for fixed values of predictor variables, the incomplete data may be added as the last row of the data set with a dot in place of the missing response, and the following syntax can be run on this data set:

```
proc genmod data=data_name;
  class catpredictor1_name (ref="level_name") catpredictor2_name
    (ref="level_name") ...;
model response_name = <list of predictors>/dist=dist_name link=link_type;
  output out=outdata_name p=predicted_response_name;
run;

proc print data=outdata_name;
run;
```

- All categorical predictors *catpredictor1_name*, *catpredictor2_name*, ... must be listed in the `class` statement, and the reference level should be specified. If the appropriate reference level is not specified, then SAS chooses the last level in alphabetical order as a reference level for this variable. For ease of practical interpretation, it is recommended that the reference level for each categorical predictor be chosen so that the estimated regression coefficients for all the other levels of this variable have the same sign (typically, positive, sometimes negative, depending on what response variable is modeled).
- In the `model` statement, all predictors are listed, categorical or numeric, separated by a space.
- SAS automatically outputs the log-likelihood function of the fitted model, the values of the AIC, AICC, and BIC criteria, the estimated beta coefficients along with p -values for significance tests, and the estimated scale parameter. In SAS, the scale parameter is termed `Scale`. In the case of the normal distribution, SAS outputs the estimate of the standard deviation σ .
- To conduct the goodness-of-fit test for a particular model, first fit the null model by running the code:

```
proc genmod data=data_name;
  model response_name = / dist=dist_name link=link_type;
```

```
run;
```

The deviance and the corresponding p -value may then be computed on a calculator, or in SAS. In SAS, for a given value of *deviance* and degrees of freedom *df*, the expression for the p -value becomes `1-probchi(deviance,df)`.

- The predicted response for the specified values of x variables can be found in the last row of the printed data set *outdata_name*.

1.9 R Implementation

To plot a histogram for the response variable and to check for normality of its distribution, use the following syntax:

```
library(rcompanion)
plotNormalHistogram(data.name$response.name)
shapiro.test(data.name$response.name)
```

The bell-shaped curve will be plotted on the same graph with the histogram. In addition, the results of the Shapiro-Wilk test for normality of distribution will be displayed. As expected, for this test, the null hypothesis claims that the distribution is normal, while alternative asserts otherwise. A p -value larger than 0.05 will indicate normality at the 5% level of significance.

Further, the R function `glm()` can be used to fit a generalized linear regression model. The basic script is:

```
summary(fitted.model.name<- glm(response.name ~ x1.name + ...
+ xk.name, data=data.name, family=dist.name(link=link.type)))
```

- Actually, the above script will work only if all the listed predictors are numeric. Categorical predictors with numeric levels should be included as `as.factor(predictor.name)`.

- For categorical predictors with character levels, the lowest alphabetically level is chosen as the reference. If you wish to change the reference category, apply the function `relevel()` first in the following manner:

```
reveled.predictor.name<- relevel(data.name$predictor.name,
ref="level.name").
```

- The function `summary()` outputs regression coefficients, corresponding p -values for the tests of significance and the value for the AIC. The value of BIC can be requested by typing `BIC(fitted.model.name)`. The value of AICC is not computed automatically. It can be calculated as

$$\text{AICC} \leftarrow -2 * \log\text{Lik}(fitted.model.name) + 2 * p * n / (n - p - 1)$$

with the appropriate values of p and n . Here `logLik(fitted.model.name)` refers to the log-likelihood function of the fitted model.

- The estimate of sigma may be printed by specifying `sigma(fitted.model.name)`. The estimates of sigma produced by R and SAS are related as

$$\hat{\sigma}_R = \hat{\sigma}_{SAS} \sqrt{\frac{n}{n - k - 1}}.$$

- To carry out the deviance test, first fit the null model and then compute the deviance and the p -value by adding the following lines to the script:

```
null.model.name<- glm(response.name ~ 1, data=data.name,
family=dist.name(link=link.type))
print(deviance.name<- -2*(logLik(null.model.name)-logLik(fitted.model.name)))
print(p.value.name<- pchisq(deviance.name, df=value, lower.tail=FALSE))
```

- To use the fitted model for prediction, implement the function `predict()`. The values for categorical predictors are placed in double quotation marks, whereas for numeric predictors no quotation marks are needed. The syntax is:

```
predict(fitted.model.name, data.frame(catpredictor1.name="value", ...,
numpredictork.name=value)).
```

1.10 Example

EXAMPLE 1.1. A survey of 48 employees of a large company was conducted with the purpose of determining how satisfied they are with their jobs. Such demographic variables as gender, age, and education (Bachelor, Master, or Doctoral degree) were recorded. The total satisfaction score was calculated as a sum of scores on 20 questions on a 5-point Likert scale. We use these data to develop a regression model that relates the job satisfaction score to the other variables. First, we plot the histogram for the scores, and conduct the normality tests. We submit the following code:

```

data job_satisfaction;
    input gender$ age educ$ score @@;
cards;
M 53 doctoral 93 M 48 bachelor 66 M 47 master 82
M 34 bachelor 95 F 35 master 78 M 25 master 62
F 31 bachelor 87 F 25 master 76 M 26 master 71
M 58 bachelor 80 F 41 master 75 F 55 bachelor 75
M 40 bachelor 93 M 22 bachelor 96 F 49 master 63
F 39 bachelor 77 F 56 doctoral 73 F 49 master 56
M 45 master 77 M 23 bachelor 77 M 46 bachelor 79
M 25 master 94 F 62 bachelor 76 M 32 master 90
F 42 master 74 M 53 bachelor 92 F 29 master 91
F 47 bachelor 87 F 47 bachelor 55 M 27 bachelor 92
F 30 master 69 M 36 master 62 M 64 bachelor 77
F 40 bachelor 65 F 34 master 81 M 48 bachelor 64
M 46 bachelor 97 M 43 bachelor 80 F 37 bachelor 60
F 33 master 81 F 55 doctoral 68 M 22 bachelor 100
M 24 bachelor 68 M 54 bachelor 76 M 42 doctoral 81
F 63 bachelor 51 F 32 master 75 M 51 doctoral 81
;

proc univariate;
    var score;
    histogram/normal;
run;

```

The histogram and p -values for normality tests are given below.

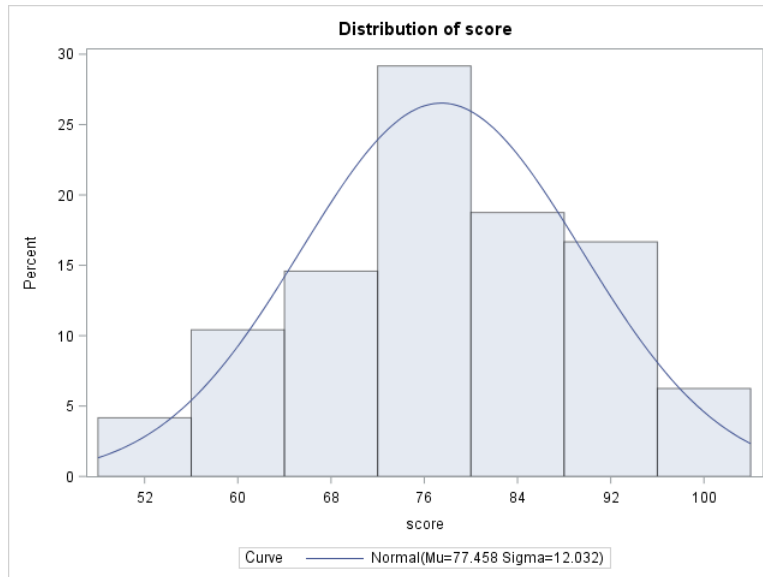


Figure 1.1: Histogram for Score in SAS

Test	p Value
Kolmogorov-Smirnov	>0.150
Cramer-von Mises	>0.250
Anderson-Darling	>0.250

Judging by the histogram and the large p -values, the distribution of the scores is normal. Now we are ready to fit a general linear model. We write

```
proc genmod;
  class gender(ref="F") educ(ref="master");
  model score=gender age educ/dist=normal link=identity;
run;
```

The following estimators of the regression coefficients with the corresponding p -values for the test of significance are outputted. The value of the log-likelihood function and the estimate $\hat{\sigma}$ of the standard deviation (termed Scale) are also given.

Log Likelihood -180.4720

Parameter	Estimate	Pr > ChiSq
Intercept	84.2229	<.0001
gender M	7.4876	0.0184
age	-0.3330	0.0216

educ bachelor	3.8754	0.2743
educ doctoral	7.5983	0.1938
Scale	10.3905	

From this output, the fitted regression model is $\hat{\mathbb{E}}(\text{score}) = 84.2229 + 7.4876 \cdot \text{male} - 0.3330 \cdot \text{age} + 3.8754 \cdot \text{bachelor} + 7.5983 \cdot \text{doctoral}$, and the estimated standard deviation of the error is $\hat{\sigma} = 10.3905$. Only gender and age, however, are statistically significant predictors of job satisfaction score at the 5% level of significance, since the corresponding p -values are less than 0.05. In this model, the estimated mean satisfaction score for men is 7.4876 points larger than that for women. In addition, with a one-year increase in age, the estimated average job satisfaction score is reduced by 0.333 points.

To address the question of whether this model fits the data well, we note from the output that the log-likelihood function for the fitted model is equal to -180.4720 . Next we fit the intercept-only model by submitting these statements:

```
proc genmod;
  model score=/dist=normal link=identity;
run;
```

```
Log Likelihood  -187.0063
```

Now we are ready to calculate the deviance statistic and carry out the goodness-of-fit test. The code and output are as follows:

```
data deviance_test;
  deviance=-2*(-187.0063-(-180.4720));
  pvalue=1-probchi(deviance,4);
run;
```

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

deviance	pvalue
13.0686	0.010945

The p -value is less than 0.05, thus we conclude that at the 5% level of significance, the fitted model has a better fit.

Lastly, suppose we would like to use the fitted model to predict the job satisfaction score for a new female employee of this company who is 40 years of age and has a bachelor degree. To this end, we compute $y^0 = 84.2229 - 0.3330 \cdot 40 + 3.8754 = 74.7783$. SAS outputs a very similar prediction, when the following statements are submitted. Here we first create a data set containing the values of the predictors, then turn it into the last row in the data set on which the model is run.

```
data prediction;
input gender$ age educ$;
cards;
F 40 bachelor
;

data job_satisfaction;
  set job_satisfaction prediction;
run;

proc genmod;
  class gender educ;
  model score=gender age educ/dist=normal link=identity;
  output out=outdata p=pred_score;
run;

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

pred_score
  74.7802
```

The annotated R script that is needed to conduct all of the above analyses is given below along with the informative output.

```
job.satisfaction.data<- read.csv(file="./Example1.1Data.csv",
header=TRUE, sep=",")

#plotting histogram with fitted normal density
library(rcompanion)
plotNormalHistogram(job.satisfaction.data$score)
```

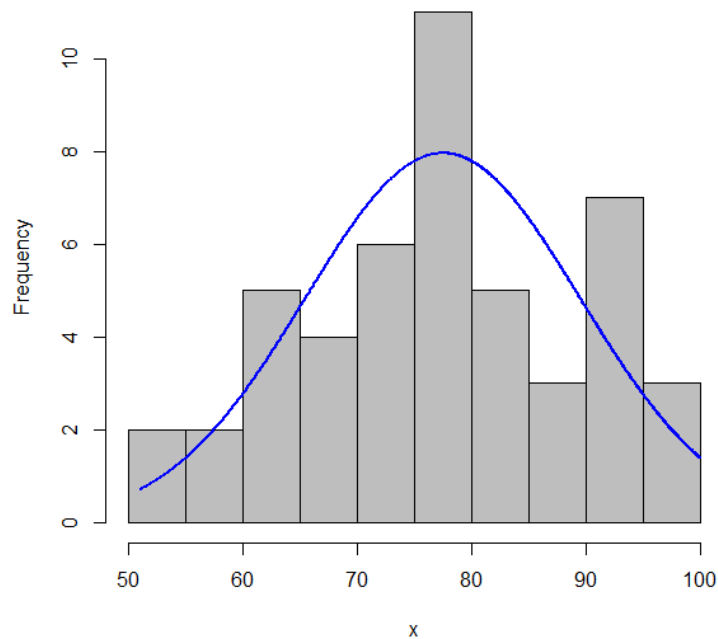


Figure 1.2: Histogram for Score in R

```
#testing normality of distribution
shapiro.test(job.satisfaction.data$score)

Shapiro-Wilk normality test
W = 0.97436, p-value = 0.3706

#specifying reference levels
educ.rel<- relevel(job.satisfaction.data$educ, ref="master")

#fitting general linear model
summary(fitted.model<- glm(score ~ gender + age + educ.rel,
data=job.satisfaction.data, family=gaussian(link=identity)))
```

Coefficients:

	Estimate	Pr(> t)
(Intercept)	84.2229	<2e-16
gender.relM	7.4876	0.0309
age	-0.3330	0.0352
educ.relbachelor	3.8754	0.3066
educ.reldoctoral	7.5983	0.2254

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

```
10.97801
```

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

```
13.06871
```

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

```
0.01094489
```

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(gender="F", age=40,
educ.rel="bachelor")))
```

```
74.78019
```

□

Exercises for Chapter 1

EXERCISE 1.1. Show that the general linear regression model (1.1) is a special case of the generalized linear regression, that is, show that the normal distribution of the response variable y belongs to the exponential family of distributions (1.3) with $\theta = \mu$ and $\phi = \sigma^2$.

EXERCISE 1.2. A small-scale clinical trial is conducted to compare the efficacy of two drugs (A and B) in reduction of excess body weight. Drug (A or B), age, and gender were recorded at the baseline. The percent excess body weight loss (EWL) was recorded 3 months into the study. The data are available on 32 subjects:

Drug	Age	Gender	EWL	Drug	Age	Gender	EWL
A	49	F	14.2	A	44	F	6.7
A	54	M	25.4	B	52	F	29.4
A	37	F	14.1	B	51	M	21.9
A	43	F	20.0	B	44	F	23.6
A	57	M	11.7	B	53	F	23.8
A	48	M	16.6	B	55	M	7.4
A	34	F	15.9	B	30	F	23.1
A	51	F	17.4	B	47	M	16.8
A	54	F	22.8	B	26	M	14.1
A	45	F	16.7	B	56	F	24.6
A	36	M	12.7	B	28	F	17.8
A	57	M	15.0	B	34	M	27.8
A	44	M	8.4	B	43	M	10.6
A	56	M	11.2	B	55	M	26.8
A	44	M	17.3	B	52	F	15.7
A	47	M	20.5	B	54	F	23.7

- Verify normality of the response variable, then fit the linear regression model to the data. State the fitted model. Give estimates for all parameters.
- Which regression coefficients turn out to be significant at the 5%? Discuss goodness-of-fit of the model.
- Is one of the drugs more efficient for weight loss than the other? Interpret all estimated significant coefficients.
- 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?

EXERCISE 1.3. A person is thinking of buying a new car. He conducts an online search and collects information on makes and models that he likes. He conjectures that the following car characteristics may potentially influence its price: body style (coupe, hatchback, or sedan), country of manufacture (USA, Germany, or Japan), highway mileage (in mpg), number of doors (2 or 4), and whether the interior is leather or not. The data for these variables and the price (in U.S. dollars) are given below for 27 cars.

Bodystyle	Country	Hwy	Doors	Leather	Price
coupe	USA	26	4	no	17,445
coupe	USA	40	4	no	23,500
coupe	USA	35	2	no	19,600
coupe	Germany	37	4	no	23,400
coupe	Germany	25	4	no	24,100
coupe	Germany	24	2	no	12,400
coupe	Japan	26	2	no	13,300
coupe	Japan	27	4	no	15,550
coupe	Japan	20	4	yes	29,345
hatchback	USA	30	2	no	12,540
hatchback	USA	39	4	no	17,595
hatchback	USA	38	2	no	17,300
hatchback	Germany	38	4	no	17,800
hatchback	Germany	32	4	no	22,500
hatchback	Germany	34	4	no	20,300
hatchback	Japan	38	4	yes	27,300
hatchback	Japan	38	2	yes	23,300
hatchback	Japan	38	2	yes	29,300
sedan	USA	29	4	no	32,000
sedan	USA	25	2	yes	34,200
sedan	USA	33	4	yes	33,395
sedan	Germany	40	4	no	22,850
sedan	Germany	23	2	yes	36,000
sedan	Germany	25	4	no	19,900
sedan	Japan	40	4	yes	36,700
sedan	Japan	35	4	yes	31,600
sedan	Japan	37	4	no	24,600

- 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.
- How good is the model fit? Discuss significance of the regression coefficients.
- Interpret the estimates of those regression coefficients that differ significantly from zero.
- What is the predicted price of a sedan made in USA that has 4 doors, leather seats, and runs 30 mpg on highway?

EXERCISE 1.4. Fifty people were surveyed randomly regarding the number of hours of quality sleep they normally get per night. Additional measurements on surveyed participants were age (in years), gender(M/F), number of minutes per day spent having personal quiet time, number of children under

5 years of age in the household, daily stress level (on a scale of 1 to 10), current job status(full/part/unemployed/student), number of physical activities per week, and number of months since last vacation or a weekend get-away. The data are as follows:

Age	Gender	Quiet time	N of children	Stress level	Job status	N of activities	Months since vacation	Sleep hours
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
26	F	80	0	7	student	9	8	8.3
48	M	180	0	5	full	0	6	6.4
55	M	40	0	8	full	8	23	7.0
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

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Age	Gender	Quiet time	N of children	Stress level	Job status	N of activities	Months since vacation	Sleep hours
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

- 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.
- How good is the model fit? What beta coefficients are significantly different from zero at the 5% level of significance?
- Interpret the estimated significant regression coefficients.
- Find 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.

EXERCISE 1.5. A 25-year-old student is training for a reverse triathlon (5-kilometer run, 13-mile bike, and 200-meter swim). He is interested in finding out what variables predict the total time spent on transitions. He obtains data for 420 people who participated in this triathlon the previous year, and chooses randomly 42 of them to do a regression analysis. The data presented below consist of age, gender, run time, time spent on transition 1 (T1), bike time, time spent on transition 2 (T2), and swim time. All times are in

minutes.

age	gender	run	t1	bike	t2	swim	age	gender	run	t1	bike	t2	swim
55	M	24.17	2.6	37.95	2.5	5.7	42	F	25.12	1.72	39.52	2.5	4.55
59	F	34.88	2.83	52.15	3.05	5.2	42	F	26.33	1.7	48.98	2.3	5.02
24	M	32.97	2.55	59.2	3.47	5.37	41	F	36.75	3.95	62.85	3.13	6.93
53	F	22.2	1.83	46.7	2.15	5.5	15	M	25.12	1.7	44.75	3.2	7.48
51	M	27.35	1.75	42.05	2.32	3.75	48	M	26.52	4.43	40.98	3.82	6.58
38	F	32.13	2.38	50.92	2.95	6	37	M	28.3	2.85	41.78	3.47	6.02
66	M	25.39	1.95	41.57	2.8	3.93	55	M	31.25	2.7	43.43	3.25	5.25
30	F	24.67	1.58	48.28	2.77	5.68	42	M	24.38	1.45	37.13	1.83	3.7
43	F	42.33	2.78	63.6	4.08	7.18	25	M	33.45	2.25	51.38	4.03	7.45
47	F	28.73	2.35	45.57	3.9	6.62	12	F	27.62	2.23	55.47	2.97	4.37
26	F	29.62	2.92	51.23	3.85	4.92	23	F	28.55	2.17	54.57	2.55	7.9
45	M	22.23	2.07	38.95	2.35	4.28	49	M	33.88	2.77	54.82	3.87	6.9
29	F	26.93	2.1	44.33	2.45	7.47	53	F	26.97	1.77	42.33	3.4	6.58
34	M	17.75	0.75	33.27	1.23	3.65	45	F	26.58	1.65	44.3	2.52	5.4
39	M	37.47	2.52	55.67	4.47	8.6	33	F	32.32	2.1	54.87	2.32	6.25
54	M	36.63	3.27	43.92	3.08	7.15	63	M	40.53	3.78	69.75	3.83	12.17
26	M	34.42	2.73	52.62	2.67	9.23	50	M	33.68	3.07	43.57	3.13	5.77
36	M	27.38	2.22	39.03	2.92	7.43	43	F	34.93	2.58	62.35	2.95	7.92
42	M	21.37	2.12	35.95	1.93	3.95	24	M	22.88	1.82	39.55	2.12	4.03
49	M	29.03	4.5	38.53	3.95	8.8	44	M	29.25	2.47	45.6	2.75	9.18
42	F	28.53	3.27	49.85	3.67	8.13	51	F	36.98	3.7	46.58	5.18	7.6

- 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.
- Discuss the model fit. Are all the predictors in that model significant at the 5% significance level?
- Interpret only the estimated significant regression coefficients of this model.
- What is the predicted total time at transitions for the student, if his best result at 5-kilometer run is 27:32, 13-mile bike is 56:17, and 200-meter swim is 8:46? Hint: Convert the times into minutes first.

EXERCISE 1.6. A cardiologist conducts a study to find out what factors are good predictors of elevated heart rate (HR) in her patients. She measures heart rate at rest in 30 patients on their next visit, and obtains from the medical charts additional information on their age, gender, ethnicity(Black, Hispanic, or White), body mass index (BMI), and the number of currently taken heart medications. She also obtains the air quality index (AQI) for area

of residence of her patients (unhealthy/moderate/good). The data follow.

Age	Gender	Ethnicity	BMI	Meds	AQI	HR
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

- Check that the measurements for the heart rate are coming from a normal distribution. Fit the regression model and specify all estimated parameters.
- Discuss the goodness-of-fit of the model. What variables are significant predictors of heart rate at the 5% level of significance?
- Give interpretation of the estimated statistically significant regression coefficients.
- 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.

Chapter 2

Regression Models for Response with Right-skewed Distribution

Suppose the response variable y is continuous, assumes only positive values, and its histogram doesn't appear to be roughly symmetrical and bell-shaped (that is, normal) but rather has a long right tail (skewed to the right). In this chapter, we talk about two possible approaches to modeling such a response: the Box-Cox transformation and gamma regression.

2.1 Box-Cox Power Transformation

2.1.1 Model Definition

If the density of the response variable y is right-skewed, a transformation may be applied to y to make its density look more normally shaped. This transformation is referred to as *Box-Cox power transformation*¹ (or, simply, *Box-Cox transformation*). The transformed response variable, denoted here by \tilde{y} , has the form:

$$\tilde{y} = \begin{cases} \frac{y^\lambda - 1}{\lambda}, & \text{if } \lambda \neq 0, \\ \ln y, & \text{if } \lambda = 0. \end{cases} \quad (2.1)$$

This is a well-defined transformation since values of y are assumed positive, which can always be achieved by adding an appropriate constant to all values of y . Note also that the way this transformation is defined makes it continuous in λ . Indeed, by the l'Hôpital's rule, $\lim_{\lambda \rightarrow 0} \frac{y^\lambda - 1}{\lambda} = \lim_{\lambda \rightarrow 0} y^\lambda \ln y = \ln y$.

¹Introduced in Box, G. E. P. and Cox, D. R. (1964). "An analysis of transformations". *Journal of the Royal Statistical Society, Series B*, 26(2), 211 – 252.

The optimal value of λ is found by means of the maximum likelihood estimation. For a set of discrete values of λ , a linear model is fitted, where the transformed response \tilde{y} is regressed on predictor variables x_1, \dots, x_k . The value of λ that corresponds to the maximum of the likelihood function is chosen as the optimal value. However, the described optimization is carried out under the assumption that \tilde{y} is normally distributed, which doesn't hold exactly, so, in practice, researchers “round off” the values of λ to result in several meaningful transformations. These recommended transformations are summarized in the table below.

Range for optimal λ	Recommended value of λ	Transformed \tilde{y}	Transformation name
$[-2.5, -1.5)$	-2	$\frac{1}{2}(1 - \frac{1}{y^2})$	<i>inverse square</i>
$[-1.5, -0.75)$	-1	$1 - \frac{1}{y}$	<i>inverse (or reciprocal)</i>
$[-0.75, -0.25)$	-0.5	$2(1 - \frac{1}{\sqrt{y}})$	<i>inverse square root</i>
$[-0.25, 0.25)$	0	$\ln y$	<i>natural logarithm</i>
$[0.25, 0.75)$	0.5	$2(\sqrt{y} - 1)$	<i>square root</i>
$[0.75, 1.5)$	1	$y - 1$	<i>linear</i>
$[1.5, 2.5]$	2	$\frac{1}{2}(y^2 - 1)$	<i>square</i>

2.1.2 Fitted Model

Let λ denote the recommended value from the table above. The fitted mean for the Box-Cox transformed response is

$$\widehat{\mathbb{E}}(\tilde{y}) = \widehat{\mathbb{E}}\left(\frac{y^\lambda - 1}{\lambda}\right) = \widehat{\beta}_0 + \widehat{\beta}_1 x_1 + \dots + \widehat{\beta}_k x_k. \quad (2.2)$$

2.1.3 Interpretation of Estimated Regression Coefficients

By (2.2), for a continuous predictor x_1 , the estimated regression coefficient $\widehat{\beta}_1$ represents the change in estimated mean of the transformed response $\widehat{\mathbb{E}}(\tilde{y})$ when x_1 is increased by one unit, given that the other predictors stay fixed. If x_1 is an indicator variable, then $\widehat{\beta}_1$ is interpreted as the difference between the estimated mean of the transformed response $\widehat{\mathbb{E}}(\tilde{y})$ for $x_1 = 1$ and that for $x_1 = 0$, when the other predictors are kept unchanged.

2.1.4 Predicted Response

By (2.2), the predicted response y^0 for some given values of predictors x_1^0, \dots, x_k^0 is

$$y^0 = \left(\lambda(\hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \dots + \hat{\beta}_k x_k^0) + 1 \right)^{1/\lambda}.$$

2.1.5 SAS Implementation

The Box-Cox transformation may be performed via procedure **transreg** with the following syntax:

```
proc transreg;  
    model BoxCox(response_name) = identity(<list of predictors>);  
run;
```

- **BoxCox**(\cdot) specifies the Box-Cox transformation.
- **identity**(\cdot) specifies the identity transformation, since we assume no transformations are applied to the predictor variables. Within this function, predictors should be listed separated by spaces.
- Since the **class** statement is not allowed in this procedure, all categorical predictors must be 0-1 variables. Suppose we have a variable *variable_name* with levels “A”, “B”, and “C”, and we want to include it into the model with the level “C” as the reference level. We proceed to creating two indicator variables by running the two lines of code in the **data** statement:

```
levelA_name=(variable_name="A");  
levelB_name=(variable_name="B");
```

The general rule is that if a categorical predictor has c levels, then one of them must be chosen as a reference level, and $c - 1$ indicator variables must be created and entered into the model.

- SAS produces a graph of the log-likelihood functions and displays the optimal value of λ on the same graph.

Further, the transformed response variable may be computed with the help of the table above, and the general linear regression may be run on that variable. Prior to running the model, however, it is advisable to plot a histogram for the transformed variable, and to conduct the formal testing for normality of its distribution.

2.1.6 R Implementation

In R, the library **MASS** (stands for “Modern Applied Statistics with S”) needs to be called to find the optimal λ for a Box-Cox transformation. First the Box-Cox transformation is applied, and a column of lambda values is created along with a column of corresponding values of the profile log-likelihood function (which is proportional to the full log-likelihood function up to an additive constant). To match SAS output, we can request that the lambda values range between -3 and 3 with a step of 1/4, and that no interpolation is applied. Note that all categorical predictors in the function `boxcox()` should be re-leveled first, using the function `relevel()`. The syntax for the Box-Cox transformation is:

```
library(MASS)
```

```
BoxCox.fit.name <- boxcox(response.name ~ x1.name + ...  
+ xk.name, data=data.name, lambda=seq(-3,3,1/4), interp=FALSE)
```

In order to extract the value of lambda that corresponds to the largest value of the profile log-likelihood function, first one has to create a data frame with lambda and profile log-likelihood function columns as follows.

```
BoxCox.data.name <- data.frame(BoxCox.fit.name$x, BoxCox.fit.name$y)
```

Next, the two columns should be sorted in descending order with respect to the profile log-likelihood function values, so that the optimal lambda appears in the top row. The script that does that is below.

```
ordered.data.name <- BoxCox.data.name[with(BoxCox.data.name,  
order(-BoxCox.fit.name.y)),]
```

The final step is to display the value of the optimal lambda in the top row.

```
ordered.data.name[1,]
```

Once the value of lambda is identified, the table above should be used to determine the recommended value of λ . Then the transformation (2.1) should be carried out, its normality checked, and the general linear regression model fitted to the transformed response.

2.1.7 Example

EXAMPLE 2.1. A real estate specialist is interested in modeling house prices in a certain U.S. region. He suspects that house prices depend on such characteristics as the number of bedrooms, number of bathrooms, square footage of the house, type of heating (central/electrical/none), presence of air conditioner (A/C) (yes/no), and lot size. He obtains the data on 30 houses currently on the market.

The SAS code below conducts the appropriate analysis. To avoid working with large numbers, we divide price by 10,000, and divide square footage and lot size by 1000. Also, since the variables that describe the type of heating and presence or absence of air conditioner are categorical, we create appropriate indicator variables. The levels "none" for heating and "no" for A/C are chosen as references. The data statement in SAS looks like this:

```
data real_estate;
input price beds baths sqft heating$ AC$ lot;
price10K=price/10000;
sqftK=sqft/1000;
central=(heating="central");
electric=(heating="electric");
ACyes=(AC="yes");
lotK=lot/1000;
cards;
669000 3 2 1733 central no 5641
715000 4 3.5 1812 none yes 4995
634900 5 3 2217 none no 8019
640000 3 2 1336 none no 7283
966000 5 3 4000 central no 7424
889000 3 2 2005 central no 7130
745000 4 3.5 2276 none no 7936
685000 2 1.5 1018 central yes 6141
549500 2 1 920 central no 5545
868999 5 2.5 1670 electric yes 5750
624900 3 2 1519 electric no 8267
549900 2 1 956 none no 4978
589900 3 2 1601 central no 5005
829000 5 3 2652 central yes 5601
599900 4 2 1802 none yes 5262
875000 6 2.5 3414 electric yes 6534
635000 3 2 1565 central no 5619
```

```

599999 2 1 832 none no 5601
734997 3 2.5 1780 central yes 5400
699999 3 2 1969 electric no 5488
759000 4 2 1530 central yes 6446
684900 3 2 1519 central no 8267
888000 5 2.75 2039 central yes 5976
599999 4 2 1513 electric no 5937
565000 2 2 1616 central no 5227
825000 3 2.5 1421 central yes 5871
659900 3 2 1547 electric yes 4791
746000 3 2 1130 central no 5301
1089000 5 2.5 3314 central yes 7129
1195499 5 3.5 3760 central yes 6000
;

```

Prior to fitting a linear model, we would want to plot a histogram of the re-scaled price to assess its deviation from normality. We run the code below to obtain the histogram with an overlaid normal density curve.

```

proc univariate;
  var price10K;
  histogram /normal;
run;

```

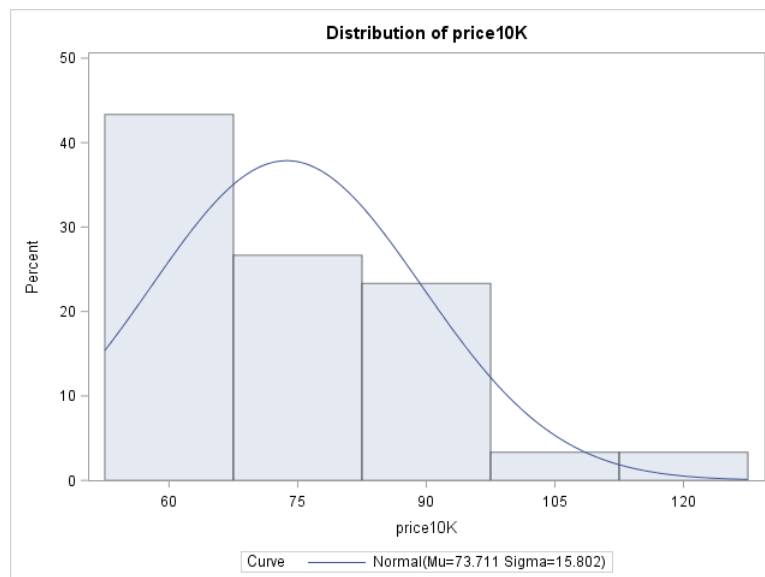


Figure 2.1: Histogram for Price10K in SAS

Goodness-of-Fit Tests for Normal Distribution

Test	p Value
Kolmogorov-Smirnov	>0.105
Cramer-von Mises	>0.024
Anderson-Darling	>0.018

The histogram exhibits a long right tail, suggesting that the distribution is right-skewed. Also, two out of the three tests refute normality of the response, since their p -values are below 0.05.

Our next step would be to transform the response variable by means of the Box-Cox transformation. We run procedure `transreg` as follows:

```
proc transreg data=real_estate;
model BoxCox(price10K) = identity(beds baths sqftK central
electric ACyes lotK);
run;
```

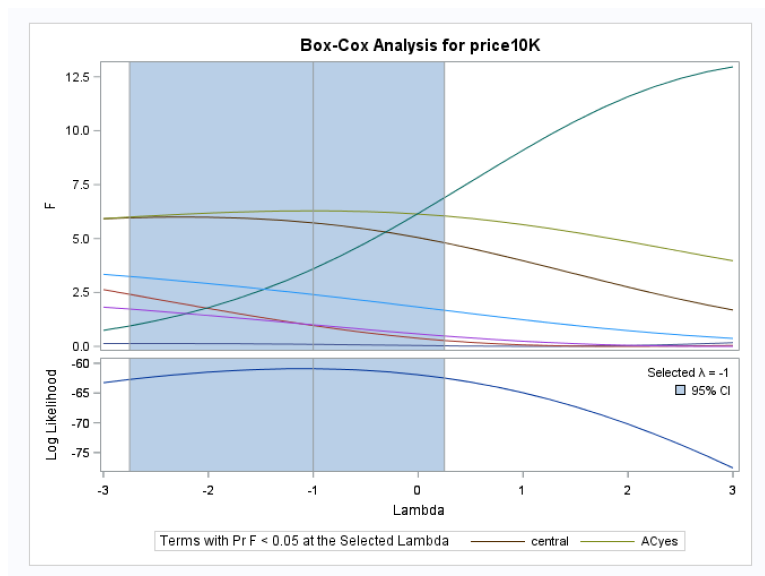


Figure 2.2: Graph of Log-Likelihood Functions

As seen from the graph, the optimal value of λ that corresponds to the largest value of the log-likelihood function is -1, which, according to Table 2.1, is a convenient value of λ . Thus, an inverse transformation is recommended.

Further, we perform the recommended transformation and plot the histogram of the transformed response. The code that accomplishes this is as follows:

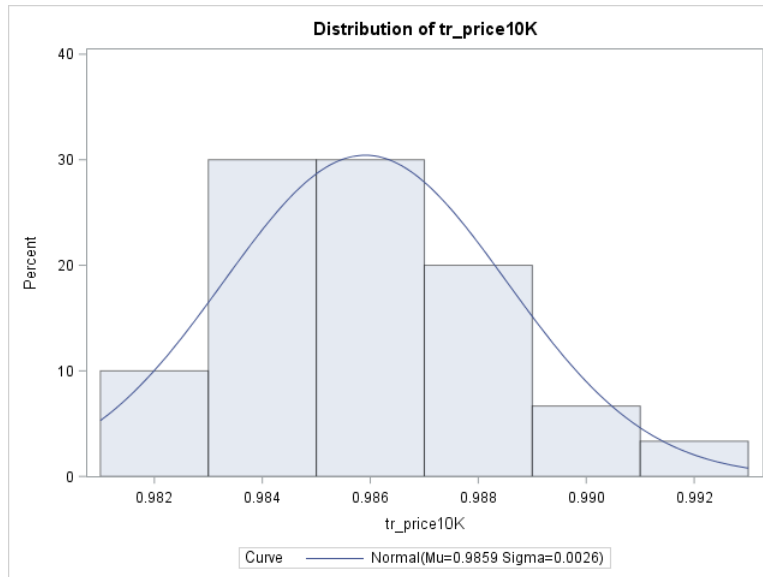


Figure 2.3: Histogram for Transformed Price10K in SAS

```
data real_estate;
  set real_estate;
  tr_price10K=1-(1/price10K);
run;

proc univariate;
  var tr_price10K;
  histogram /normal;
run;
```

As seen on the histogram and confirmed by the large p -values (larger than 0.05) for the normality tests, the transformed response is indeed normally distributed.

Goodness-of-Fit Tests for Normal Distribution

Test	p Value
Kolmogorov-Smirnov	>0.150
Cramer-von Mises	>0.250
Anderson-Darling	>0.250

Finally, we fit the general linear model to the transformed response, regressing it on all the predictors. Here we use the original predictors and the `class` statement rather than the calculated indicator variables `central`, `electric`, and `ACyes`, which would give us an alternative solution.

```
proc genmod;
class heating(ref="none") AC(ref="no");
model tr_price10K=beds baths sqftK heating AC lotK/dist=normal
      link=identity;
run;
```

The relevant output is

Log Likelihood 157.9841

Analysis Of Maximum Likelihood Parameter Estimates

Parameter	Estimate	Pr > ChiSq
Intercept	0.9768	<.0001
beds	0.0002	0.7175
baths	0.0007	0.2512
sqftK	0.0012	0.0269
heating central	0.0017	0.0052
heating electric	0.0009	0.2425
heating none	0.0000	.
AC yes	0.0018	0.0034
AC no	0.0000	.
lotK	0.0005	0.0704
Scale	0.0012	

Addressing the issue of goodness-of-fit of the fitted model, we can find in the output that log-likelihood for the fitted model is 157.9841. We obtain the log-likelihood function for the intercept-only model and conduct the deviance test. The code and appropriate output are:

```
proc genmod data=real_estate;
model tr_price10K=/dist=normal link=identity;
run;
```

Full Log Likelihood 136.2538

```
data deviance_test;
deviance=-2*(136.2538-(157.9841));
pvalue=1-probchi(deviance,7);
run;
```

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

deviance	pvalue
43.4606	0.000000272

The p -value is way below 0.05. This, the fitted model has a good fit.

In the fitted model, only the square footage of a house, presence of central heater, and presence of air conditioner turn out to be significant predictors of the house price at the 5% level. If the square footage of the house were one thousand square feet larger, the estimated average inverse-transformed price (in \$10,000) would be 0.0012 units larger. For houses with central heater, the estimated inverse-transformed price is, on average, 0.0017 units larger than that for house with no heater. The estimated mean inverse-transformed price for a house with an air conditioner is 0.0018 units larger than that for a house with no air conditioner.

Next, we might want to use the model to predict the price of a house that has four bedrooms, two bathrooms, area of 1680 square feet, central heater, no A/C, and lot size of 5000 square feet. The formula that should be used for prediction is (show it!):

$$price^0 = \$10,000 \cdot \left[1 - (0.9768 + 0.0002 \cdot beds^0 + 0.0007 \cdot baths^0 + 0.0012 \cdot \frac{sqft^0}{1000} + 0.0017 \cdot central + 0.0009 \cdot electric + 0.0018 \cdot ACyes + 0.0005 \cdot \frac{lot^0}{1000}) \right]^{-1}.$$

Plugging the appropriate values into the formula above, we get that the predicted price is equal to

$$price^0 = \$10,000 \cdot \left[1 - (0.9768 + 0.0002 \cdot 4 + 0.0007 \cdot 2 + 0.0012 \cdot \frac{1680}{1000} + 0.0017 + 0.0005 \cdot \frac{5000}{1000}) \right]^{-1} = \$676,406.93.$$

The prediction can also be requested in SAS via the following statements:

```
data prediction;
input beds baths sqftK heating$ AC$ lotK;
cards;
4 2 1.68 central no 5
;

data real_estate;
set real_estate prediction;
```

```

run;

proc genmod;
class heating AC;
model tr_price10K=beds baths sqftK heating AC lotK/dist=normal
      link=identity;
output out=outdata p=predicted;
run;

data outdata;
  set outdata;
  pred_price=10000/(1-predicted);
run;

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

```

The output is

```

pred_price
658569.23

```

Thus, the predicted price of the house in SAS is \$658,569.23. Note that the discrepancy between the predicted prices computed by hand and in SAS is due to the round-off error. For calculations, SAS uses more digits in the estimates of the regression coefficients than it displays.

The R script that does the same tasks as described in this example is given below. Recall that in R, the Shapiro-Wilk test is used to verify normality. Relevant outputs are also presented.

```

real.estate.data<- read.csv(file="./Example2.1Data.csv",
header=TRUE, sep=",")

#rescaling variables and specifying reference categories
price10K<- real.estate.data$price/10000
sqftK<- real.estate.data$sqft/1000
heating.rel<- relevel(real.estate.data$heating, ref="none")
AC.rel<- relevel(real.estate.data$AC, ref="no")
lotK<- real.estate.data$lot/1000

```

```
#plotting histogram with fitted normal density
library(rcompanion)

plotNormalHistogram(price10K)
```

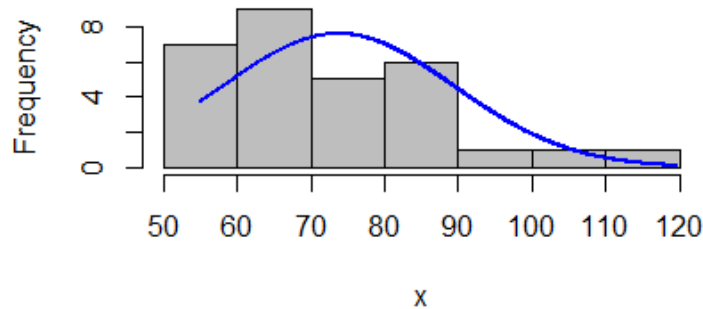


Figure 2.4: Histogram for Price10K in R

```
#testing for normality of distribution
shapiro.test(price10K)

Shapiro-Wilk normality test
W = 0.89581, p-value = 0.006642

#finding optimal lambda for Box-Cox transformation
library(MASS)
BoxCox.fit<- boxcox(price10K ~ beds + baths + sqftK + heating.rel
+ AC.rel + lotK, data=real.estate.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 21.13092

#applying Box-Cox transformation with lambda=-1
tr.price10K<- 1-(1/price10K)

#plotting histogram for tranformed response
plotNormalHistogram(tr.price10K)
```

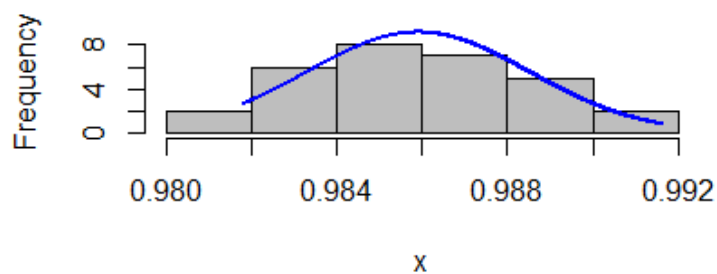


Figure 2.5: Histogram for Transformed Price10K in R

```
#testint or normality of distribution
shapiro.test(tr.price10K)
```

Shapiro-Wilk normality test
W = 0.96903, p-value = 0.5131

```
#fitting general linear model to transformed response
summary(fitted.model<- glm(tr.price10K ~ beds + baths + sqftK + heating.rel
+ AC.rel + lotK, data=real.estate.data, family=gaussian(link=identity)))
```

Coefficients:

	Estimate	Pr(> t)
(Intercept)	0.9767546	<2e-16
beds	0.0001599	0.7596
baths	0.0006527	0.3365
sqftK	0.0011973	0.0712
heating.relcentral	0.0017088	0.0257
heating.relelectric	0.0008685	0.3278
AC.relyes	0.0017836	0.0200
lotK	0.0004792	0.1355

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

0.001459009

```
#checking model fit
null.model<- glm(tr.price10K ~ 1, family=gaussian(link=identity))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

43.46061

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

2.717569e-07

```
#using fitted model for prediction
pred.tr.price10K<-predict(fitted.model, data.frame(beds=4, baths=2,
sqftK=1.68, heating.rel="central", AC.rel="no", lotK=5))
print(pred.price<- 10000/(1-pred.tr.price10K))
```

658569.2

Note that R outputs more digits in the estimates for beta coefficients. If we use these estimates when computing the predicted value, we would get a more accurate result. Indeed,

$$price^0 = \$10,000 \cdot \left[1 - (0.9767546 + 0.0001599 \cdot 4 + 0.0006527 \cdot 2 + 0.0011973 \cdot 1.68 + 0.0017088 + 0.0004792 \cdot 5) \right]^{-1} = \$658,582.09.$$

□

2.2 Gamma Regression Model

2.2.1 Model Definition

A *gamma regression*² may be fitted to a positive response y with a right-skewed distribution. In this model, y has a gamma distribution with the density

$$f_Y(y) = \frac{y^{\alpha-1}}{\Gamma(\alpha) \beta^\alpha} e^{-y/\beta}, \quad \alpha, \beta > 0, \quad y > 0. \quad (2.3)$$

REMARK. Note that in some settings, the response variable might have a shifted gamma distribution which support includes a zero and even negative values. The gamma regression is still applicable but all the response values must be made strictly positive, for example, by subtracting the smallest value and adding a one.

²Discussed for the first time in Nelder, J.A. and Wedderburn, R.W.M. (1972). "Generalized linear models". *Journal of the Royal Statistical Society, Series A*, 135 (3): 370 – 384.

The expected value of y is $\mathbb{E}(y) = \alpha\beta$. The relation between the mean response and the predictor variables is modeled via a log link function:

$$\ln \mathbb{E}(y) = \beta_0 + \beta_1 x_1 + \cdots + \beta_k x_k. \quad (2.4)$$

Here the parameters β_0, \dots, β_k , and α are unknown and are estimated from the data by the method of maximum likelihood.

It can be shown (see Exercise 2.5) that the gamma distribution belongs to the exponential family of distributions since its density can be written in the form (1.3) with the location parameter $\theta = -1/(\alpha\beta)$ and the dispersion parameter $\phi = 1/\alpha$. Hence, the gamma regression is a generalized linear regression model with the log link function.

2.2.2 Fitted Model

The fitted mean response has the form:

$$\widehat{\mathbb{E}}(y) = \widehat{\alpha}\widehat{\beta} = \exp\{\widehat{\beta}_0 + \widehat{\beta}_1 x_1 + \cdots + \widehat{\beta}_k x_k\}, \quad (2.5)$$

and the estimated dispersion parameter $\widehat{\phi} = 1/\widehat{\alpha}$. Thus, in the fitted model, the estimated parameters satisfy:

$$\widehat{\alpha} = 1/\widehat{\phi}, \text{ and } \widehat{\beta} = \widehat{\phi} \exp\{\widehat{\beta}_0 + \widehat{\beta}_1 x_1 + \cdots + \widehat{\beta}_k x_k\}.$$

2.2.3 Interpretation of Estimated Regression Coefficients

According to (2.5), estimated regression coefficients in a gamma regression yield the following interpretation:

- If a predictor variable x_1 is numeric, then the corresponding estimated beta coefficient $\widehat{\beta}_1$ indicates by how much the natural logarithm of the estimated mean response $\ln \widehat{\mathbb{E}}(y)$ changes for a unit increase in x_1 , provided all the other predictors stay unchanged. Or, equivalently, $(\exp\{\widehat{\beta}_1\} - 1) \cdot 100\%$ represents the percent change in estimated mean response for a unit increase in x_1 . To obtain that, we write

$$\begin{aligned} & \left(\widehat{\mathbb{E}}(y|x_1+1) - \widehat{\mathbb{E}}(y|x_1) \right) / \widehat{\mathbb{E}}(y|x_1) = \left(\exp\{\widehat{\beta}_0 + \widehat{\beta}_1(x_1+1) + \widehat{\beta}_2 x_2 + \cdots + \widehat{\beta}_k x_k\} \right. \\ & \left. - \exp\{\widehat{\beta}_0 + \widehat{\beta}_1 x_1 + \cdots + \widehat{\beta}_k x_k\} \right) / \exp\{\widehat{\beta}_0 + \widehat{\beta}_1 x_1 + \cdots + \widehat{\beta}_k x_k\} = \exp\{\widehat{\beta}_1\} - 1. \end{aligned}$$

- If a predictor variable x_1 is an indicator variable, then $\exp\{\widehat{\beta}_1\} \cdot 100\%$ has the meaning of the percent ratio of estimated mean response $\widehat{\mathbb{E}}(y)$ for $x_1 = 1$

and that for $x_1 = 0$, keeping the other predictors intact. Indeed,

$$\begin{aligned}\widehat{\mathbb{E}}(y|x_1 = 1)/\widehat{\mathbb{E}}(y|x_1 = 0) &= \exp\{\widehat{\beta}_0 + \widehat{\beta}_1 \cdot 1 + \widehat{\beta}_2 x_2 + \cdots + \widehat{\beta}_k x_k\} / \\ &\exp\{\widehat{\beta}_0 + \widehat{\beta}_1 \cdot 0 + \widehat{\beta}_2 x_2 + \cdots + \widehat{\beta}_k x_k\} = \exp\{\widehat{\beta}_1\}.\end{aligned}$$

2.2.4 Predicted Response

From (2.5), the predicted response y^0 for a concrete set of predictors x_1^0, \dots, x_k^0 can be found as $y^0 = \exp\{\widehat{\beta}_0 + \widehat{\beta}_1 x_1^0 + \cdots + \widehat{\beta}_k x_k^0\}$.

2.2.5 SAS Implementation

A gamma distribution may be fitted using `proc genmod` with `dist=gamma` and `link=log`. SAS outputs the estimate of `Scale` which is the reciprocal of $\widehat{\alpha}$. Thus, $\widehat{\alpha} = 1/\text{Scale}$.

2.2.6 R Implementation

The R function `glm()` will fit the gamma regression if `family=Gamma(link=log)` is specified. To obtain the predicted response, the option `type="response"` must appear in the function `predict()`. The `Dispersion` parameter that R outputs is the estimate of α .

2.2.7 Example

EXAMPLE 2.2. Consider the data `real_estate` in Example 2.1. We fit the gamma model and use it for prediction by running these lines of code:

```
proc genmod;
class heating(ref="none") AC(ref="no");
model price10K = beds baths sqftK heating AC lotK
      /dist=gamma link=log;
run;
```

The informative output is:

```
Log Likelihood   -100.0395
```

Analysis Of Maximum Likelihood Parameter Estimates

		Estimate	Pr > ChiSq
Intercept		3.6462	<.0001
beds		0.0091	0.7837
baths		0.0295	0.4887
sqftK		0.1165	0.0035
heating	central	0.1206	0.0084
heating	electric	0.0484	0.3879
heating	none	0.0000	.
AC	yes	0.1292	0.0052
AC	no	0.0000	.
lotK		0.0303	0.1326
Scale		113.4926	

Next, we check whether this model has a good fit. The code and relevant output are:

```
proc genmod;
  model price10K=/dist=gamma link=log;
run;
```

Full Log Likelihood -122.8174

```
data deviance_test;
  deviance=-2*(-122.8174-(-100.0395));
  pvalue=1-probchi(deviance,7);
run;
```

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

```
deviance      pvalue
45.5558      0.000000107
```

Since the p -value for the deviance test is very small, we conclude that the model with all the predictors fits the data well. The fitted model is

$$\hat{\mathbb{E}}(\text{price}) = \exp\{3.6462 + 0.0091 \cdot \text{beds} + 0.0295 \cdot \text{baths} + 0.1165 \cdot \text{sqftK} \\ + 0.1206 \cdot \text{central} + 0.0484 \cdot \text{electric} + 0.1292 \cdot \text{ACyes} + 0.0303 \cdot \text{lotK}\},$$

and $\hat{\alpha} = 1/113.4926 = 0.0088$. We see that the square footage of the house, central heater, and presence of A/C are significant predictors (the same as

in the model in Example 2.1). If the square footage of a house were larger by one thousand square feet, then the estimated average price would be larger by $(\exp\{0.1165\} - 1) \cdot 100\% = 12.36\%$. For a house with central heater, the estimated mean of the price is $\exp\{0.1206\} \cdot 100\% = 112.82\%$ of that for a house with no heater. Houses with air conditioner have estimated average price $\exp\{0.1292\} \cdot 100\% = 113.79\%$ of that for houses where air conditioner is not installed.

Further, to predict the price of a house with four bedrooms, two bathrooms, area of 1680 square feet, central heating, no A/C, and lot size of 5000 square feet, we compute:

$$\begin{aligned} price^0 &= \$10,000 \cdot \exp\{3.6462 + 0.0091 \cdot 4 + 0.0295 \cdot 2 + 0.1165 \cdot 1.68 + 0.1206 + 0.0303 \cdot 5\} \\ &= \$673,174.84. \end{aligned}$$

To reveal the predicted value in SAS, we run these statements:

```
data prediction;
input beds baths sqftK heating$ AC$ lotK;
cards;
4 2 1.68 central no 5
;

data real_estate;
set real_estate prediction;
run;

proc genmod;
class heating AC;
model price10K = beds baths sqftK heating AC lotK/dist=gamma
link=log;
output out=outdata p=pprice;
run;

data outdata;
set outdata;
pred_price=10000*pprice;
run;

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

The output is:

```
pred_price  
673237.87
```

The difference between the predicted values computed by hand and in SAS is due to the fact that SAS uses more digits in the estimated beta coefficients than are displayed in the output.

Finally, the R script below outputs the estimates that are close to those produced by SAS.

```
#fitting gamma regression  
summary(fitted.model<- glm(price10K ~ beds + baths + sqftK  
+ heating.rel + AC.rel + lotK, data=real.estate.data,  
family=Gamma(link=log)))
```

Coefficients:

	Estimate	Pr(> t)
(Intercept)	3.646245	<2e-16
beds	0.009136	0.8183
baths	0.029540	0.5650
sqftK	0.116481	0.0241
heating.relcentral	0.120590	0.0371
heating.relelectric	0.048372	0.4717
AC.relyes	0.129186	0.0261
lotK	0.030274	0.2117

Dispersion parameter for Gamma family taken to be 0.01233554

```
#checking model fit
null.model<- glm(price10K ~ 1, family=Gamma(link=log))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

45.55644

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

1.066286e-07

```
#using fitted model for prediction
print(10000*predict(fitted.model, data.frame(beds=4, baths=2,
sqftK=1.68, heating.rel="central", AC.rel="no", lotK=5), type="response"))
```

673237.9

□

Exercises for Chapter 2

EXERCISE 2.1. An intervention-control study on childhood obesity was conducted at a children's clinic. A cohort of 36 obese children, ages 6 through 16, were followed for 9 months. The intervention consisted of educational sessions for parents and vigorous exercise activities for kids. The control group participants were provided with resources regarding other active and healthy lifestyle programs offered in their community. Their gender(M/F), age (in years), group (intervention Tx or control Cx), and percentiles for pre-

and post-BMIs were recorded. The data are provided in the table below:

Gender	Age	Group	PreBMI	PostBMI	Gender	Age	Group	PreBMI	PostBMI
F	6	Cx	85.7	83.8	M	6	Cx	92.6	88.1
F	6	Cx	93.8	92.9	M	7	Cx	95.8	94.7
F	7	Cx	93.5	92.5	M	7	Cx	90.4	89.1
F	8	Cx	90.1	89.8	M	7	Cx	91.2	88.6
F	9	Tx	92.3	90.7	M	8	Tx	94.4	87.8
F	9	Tx	90.3	88.3	M	8	Tx	93.2	87.3
F	12	Cx	87.6	85.9	M	10	Cx	93.9	91.5
F	12	Cx	87.2	84.1	M	10	Tx	96.2	91.1
F	12	Tx	96.9	94.9	M	10	Tx	89.4	87.9
F	12	Tx	85.8	81.2	M	11	Tx	86.2	77.1
F	13	Cx	96.7	94.1	M	11	Tx	95.4	84.8
F	13	Cx	93.5	92.9	M	12	Cx	97.7	95.8
F	13	Tx	92.3	87.5	M	13	Tx	85.3	80.0
F	13	Tx	85.3	83.7	M	13	Tx	86.2	82.4
F	14	Tx	95.5	78.7	M	14	Cx	85.5	83.6
F	15	Cx	91.3	89.9	M	14	Cx	97.8	93.8
F	15	Tx	95.8	87.1	M	16	Cx	95.0	93.6
F	16	Tx	90.7	87.2	M	16	Tx	93.1	86.8

- Is the decrease in BMI percentile (preBMI-postBMI) normally distributed? Plot a histogram and test for normality of the distribution.
- 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.
- Fit the general regression model to the Box-Cox transformed change in BMI percentile. Does this model have a good fit?
- What predictors are significant at the 5% level? Write the interpretation of the estimated regression coefficients for the significant predictors only.
- Predict change in BMI percentile for a 9-year old girl in the control group.

EXERCISE 2.2. Investigators at a large medical center conducted a quality improvement (QI) study which consisted of a six-month-long series of seminars and practical instructional tools on how to improve quality assurance for future projects at this center. Data were collected on participants' designation (nurse/doctor/staff), years of work at the center, whether had a prior experience with QI projects, and the score on the knowledge and attitude test taken at the end of the study. The score was constructed as the sum of 20 questions on a 5-point Likert scale, thus potentially ranging between 20 and 100. The large value indicates better knowledge about QI and more confidence and desire to use it in upcoming projects. The data on 45 study

participants are summarized as follows:

Desgn	Wrkyrs	PriorQI	Score	Desgn	Wrkyrs	PriorQI	Score
nurse	16	yes	63	nurse	8	yes	62
nurse	9	yes	93	nurse	22	yes	68
nurse	8	yes	74	nurse	4	no	93
nurse	1	no	69	nurse	6	no	77
nurse	5	no	67	nurse	2	no	59
nurse	3	no	66	nurse	20	no	64
nurse	24	no	86	nurse	2	no	70
nurse	4	no	74	nurse	3	no	63
nurse	1	no	88	nurse	16	no	65
nurse	24	no	84	nurse	18	no	73
nurse	3	no	97	nurse	15	no	76
doctor	2	yes	88	doctor	2	yes	85
doctor	5	yes	78	doctor	7	yes	91
doctor	26	yes	82	doctor	2	yes	69
doctor	3	no	57	doctor	20	no	66
doctor	3	no	88	doctor	13	no	55
doctor	15	no	78	doctor	8	no	62
doctor	4	no	65	doctor	14	no	61
doctor	25	no	78	staff	9	yes	57
staff	3	yes	62	staff	11	yes	69
staff	21	no	55	staff	19	no	64
staff	8	no	62	staff	17	no	76
staff	11	no	67				

- Construct a histogram of the score. Does the distribution look normal? Perform the test for normality. Draw conclusion.
- 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.
- Run the general linear regression model on the transformed score. What predictors are significant at the 0.05 level?
- Interpret the estimates of the significant beta coefficients. Does the model fit the data well? Conduct the chi-squared deviance test.
- 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.

EXERCISE 2.3. A group of 24 beginner-level cycling enthusiasts met at the park for bicycling race that consists of biking for 30 minutes along a 1.3-mile loop. The winner is the one who bikes the longest distance. The information recorded for each participant is gender (M/F), whether had a prior experi-

ence in races like this (yes/no), self-evaluation of abilities to finish the race and do well (on a 10-point scale, with 10 being the highest confidence), and the distance biked (in miles). The data are presented below:

Gender	Prior Expr	Self Eval	Distance	Gender	Prior Expr	Self Eval	Distance
F	no	2	1.9	F	no	7	4.4
F	no	2	2.1	F	yes	3	3.1
F	yes	8	3.8	M	yes	10	6.4
F	yes	4	3.0	F	yes	4	3.2
M	no	5	4.2	F	no	6	5.1
F	yes	10	8.2	M	no	10	5.9
F	no	3	3.1	F	no	6	5.0
F	no	4	2.4	M	yes	3	3.6
F	no	5	4.6	F	no	7	4.4
M	yes	6	8.7	M	yes	10	11.2
F	no	6	4.7	F	yes	3	3.0
M	yes	7	4.2	M	yes	7	4.3

- Are the distances normally distributed? Plot the histogram, do the testing. Explain.
- 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.
- Fit the general linear regression model to the transformed distance. Show that the model has a good fit. Discuss significance of predictors.
- Give interpretation for the estimates of the statistically significant regression coefficients. Use $\alpha=0.05$.
- 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.

EXERCISE 2.4. A health insurance firm is doing an analysis of the aggregate insurance claims that were received in a particular fiscal year. Investigators randomly select 40 companies that are insured by this firm and, for each company, pull out the data on the number of policies, number of years insured with the firm, percent of open claims from last year, and the aggregate claim amount from this year (in millions of dollars). The data are:

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

- 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.
- Fit a linear regression model, relating the transformed claim amounts to all the other variables. Which variables are significant predictors at the 5% level?
- Assess the model fit. Interpret estimated significant regression coefficients.
- 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.

EXERCISE 2.5. Show that a gamma distribution with density defined by (2.3) belongs to the exponential family of distributions (1.3) with $\theta = -1/(\alpha\beta)$ and $\phi = 1/\alpha$. Conclude that the gamma regression is a generalized linear regression. Give its link function.

EXERCISE 2.6. For the data in Exercise 2.1,

- (a) Fit the gamma regression model with the log link function. Write down the fitted model. Check its goodness of fit.
- (b) What variables are significant predictors in this model? Use the 5% significance level.
- (c) Interpret estimated significant regression coefficients.
- (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.

EXERCISE 2.7. For the data in Exercise 2.2,

- (a) Fit the gamma regression model with the log link function. Present the fitted model and discuss its goodness-of-fit.
- (b) Discuss significance of the beta coefficients. Interpret the estimated significant coefficients.
- (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.

EXERCISE 2.8. Consider the data set in Exercise 2.3. Fit the gamma model and do the following:

- (a) Write out explicitly the estimated model. Check goodness of fit of this model.
- (b) Which predictors would really influence the response, if changed? Give interpretation of the estimated significant regression coefficients.
- (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.

EXERCISE 2.9. Refer to Exercise 2.4. Answer the questions below for the data in that exercise.

- (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.
- (b) Interpret estimates of the significant beta coefficients. How good is the model fit?
- (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.

Chapter 3

Regression Models for Binary Response

Suppose the response variable y is *binary* (or *dichotomous*) variable, that is, it assumes only two possible values. For simplicity, we will denote these values by 0 and 1. The relation between y and predictors cannot be modeled by a linear regression because the error terms would not be normally distributed. The way out of this predicament is to use the generalized linear regression approach and to model not y itself but the probability that y is equal to one. In this chapter, three models for the binary response are presented: logistic, probit, and complementary log-log models.

3.1 Binary Logistic Regression Model

3.1.1 Model Definition

Denote by π the probability that y is equal to one, that is, $\pi = \mathbb{P}(y = 1)$. Note that π is also the mean of y . Indeed, $\mathbb{E}(y) = (1)(\pi) + (0)(1 - \pi) = \pi$. The *binary* (or *dichotomous*) *logistic regression model*¹ with the predictors x_1, \dots, x_k has the form:

$$\pi = \mathbb{E}(y) = \frac{\exp\{\beta_0 + \beta_1 x_1 + \dots + \beta_k x_k\}}{1 + \exp\{\beta_0 + \beta_1 x_1 + \dots + \beta_k x_k\}}.$$

The name “logistic” comes from the fact that the distribution with the cumulative distribution function $F(x) = \frac{e^x}{1 + e^x}$, $-\infty < x < \infty$, is called the

¹Introduced in Cox, D.R. (1958). “The regression analysis of binary sequences”. *Journal of the Royal Statistical Society, Series B*, 20(2): 215 – 242.

logistic distribution.

An alternative form of the binary logistic regression model is derived via the use of the *logit link function* of π (“logit”=“logistic”+“unit”), defined as:

$$\text{logit } \pi = \ln \frac{\pi}{1 - \pi} .$$

The ratio $\frac{\pi}{1 - \pi} = \frac{\mathbb{P}(y = 1)}{\mathbb{P}(y = 0)}$ represents the *odds in favor of* the event $y = 1$.

Using the logit transformation, the binary logistic regression model may be written in the form (verify!)

$$\text{logit } \pi = \ln \frac{\pi}{1 - \pi} = \beta_0 + \beta_1 x_1 + \cdots + \beta_k x_k . \quad (3.1)$$

Thus, the binary logistic regression is a linear model for the natural logarithm of the odds and hence is sometimes called *log-odds model*.

It can be proven (see Exercise 3.1) that the logistic regression is an example of a generalized linear model with the logit link function.

3.1.2 Fitted Model

The only model parameters that are unknown and have to be estimated from the observations are the beta regression coefficients. The fitted binary logistic model has the form

$$\hat{\pi} = \hat{\mathbb{E}}(y) = \frac{\exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_k x_k\}}{1 + \exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_k x_k\}} . \quad (3.2)$$

Alternative ways to write the fitted model, which aid better in interpretation of the estimated beta coefficients, are:

$$\text{logit } \hat{\pi} = \ln \frac{\hat{\pi}}{1 - \hat{\pi}} = \hat{\beta}_0 + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_k x_k, \quad (3.3)$$

and

$$\frac{\hat{\pi}}{1 - \hat{\pi}} = \exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_k x_k\}. \quad (3.4)$$

3.1.3 Interpretation of Estimated Regression Coefficients

In view of (3.3) and (3.4), in the logistic regression model, the estimates of the regression coefficients yield the following interpretation.

- If a predictor variable x_1 is numeric, then the estimated regression parameter $\hat{\beta}_1$ can be interpreted as the estimated *change in the log-odds* for every unit increase in x_1 , holding all the other predictors fixed. Indeed, if x_1 is replaced by $x_1 + 1$, the difference in estimated log-odds is

$$\begin{aligned} & \ln \frac{\hat{\pi}|_{x_1+1}}{1 - \hat{\pi}|_{x_1+1}} - \ln \frac{\hat{\pi}|_{x_1}}{1 - \hat{\pi}|_{x_1}} \\ &= \hat{\beta}_0 + \hat{\beta}_1(x_1 + 1) + \hat{\beta}_2 x_2 + \cdots + \hat{\beta}_k x_k - (\hat{\beta}_0 + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_k x_k) = \hat{\beta}_1. \end{aligned}$$

Alternatively, the quantity $(\exp\{\hat{\beta}_1\} - 1) \cdot 100\%$ represents the estimated *percent change in odds* when x_1 is increased by one unit, and the other predictors are held fixed. This can be seen by writing:

$$\begin{aligned} & \frac{\frac{\hat{\pi}|_{x_1+1}}{1 - \hat{\pi}|_{x_1+1}} - \frac{\hat{\pi}|_{x_1}}{1 - \hat{\pi}|_{x_1}}}{\frac{\hat{\pi}|_{x_1}}{1 - \hat{\pi}|_{x_1}}} \cdot 100\% = \left(\frac{\frac{\hat{\pi}|_{x_1+1}}{1 - \hat{\pi}|_{x_1+1}}}{\frac{\hat{\pi}|_{x_1}}{1 - \hat{\pi}|_{x_1}}} - 1 \right) \cdot 100\% \\ &= \left(\frac{\exp\{\hat{\beta}_0 + \hat{\beta}_1(x_1 + 1) + \hat{\beta}_2 x_2 + \cdots + \hat{\beta}_k x_k\}}{\exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_k x_k\}} - 1 \right) \cdot 100\% = (\exp\{\hat{\beta}_1\} - 1) \cdot 100\%. \end{aligned}$$

- If a predictor variable x_1 is an indicator variable, then the estimated parameter $\hat{\beta}_1$ can be interpreted as the estimated *difference in log-odds* when $x_1 = 1$ and when $x_1 = 0$, controlling for all the other predictors. To see that, we write

$$\begin{aligned} & \ln \frac{\hat{\pi}|_{x_1=1}}{1 - \hat{\pi}|_{x_1=1}} - \ln \frac{\hat{\pi}|_{x_1=0}}{1 - \hat{\pi}|_{x_1=0}} \\ &= \hat{\beta}_0 + \hat{\beta}_1 \cdot 1 + \hat{\beta}_2 x_2 + \cdots + \hat{\beta}_k x_k - (\hat{\beta}_0 + \hat{\beta}_1 \cdot 0 + \hat{\beta}_2 x_2 + \cdots + \hat{\beta}_k x_k) = \hat{\beta}_1. \end{aligned}$$

Alternatively, the estimated ratio of odds for $x_1 = 1$ and that for $x_1 = 0$, expressed as percentage, is

$$\begin{aligned} & \frac{\frac{\hat{\pi}|_{x_1=1}}{1 - \hat{\pi}|_{x_1=1}}}{\frac{\hat{\pi}|_{x_1=0}}{1 - \hat{\pi}|_{x_1=0}}} \cdot 100\% = \frac{\exp\{\hat{\beta}_0 + \hat{\beta}_1 \cdot 1 + \hat{\beta}_2 x_2 + \cdots + \hat{\beta}_k x_k\}}{\exp\{\hat{\beta}_0 + \hat{\beta}_1 \cdot 0 + \hat{\beta}_2 x_2 + \cdots + \hat{\beta}_k x_k\}} \cdot 100\% \\ &= \exp\{\hat{\beta}_1\} \cdot 100\%, \end{aligned}$$

hence, the quantity $\exp\{\hat{\beta}_1\} \cdot 100\%$ represents the estimated *percent ratio in odds* when $x_1 = 1$ and when $x_1 = 0$, while the other predictors are held constant.

3.1.4 Predicted Probability

Taking into consideration (3.2), for particular values of predictor variables x_1^0, \dots, x_k^0 , the predicted probability π^0 can be found as

$$\pi^0 = \frac{\exp\{\widehat{\beta}_0 + \widehat{\beta}_1 x_1^0 + \dots + \widehat{\beta}_k x_k^0\}}{1 + \exp\{\widehat{\beta}_0 + \widehat{\beta}_1 x_1^0 + \dots + \widehat{\beta}_k x_k^0\}}.$$

3.1.5 SAS Implementation

The procedure `genmod` with `dist=binomial` and `link=logit` may be applied to fit the binary logistic regression. SAS orders the levels of the response variable in alphabetical order (if categorical) or in ascending order (if numeric) and models the probability of the lower level. To reverse that, one has to include `descending` after `proc genmod` statement. Or in the `model` statement, after `response_name` include `(event="level_name")`.

3.1.6 R Implementation

The function `glm()` with specifications `family=binomial(link=logit)` will fit a binary logistic regression model.

3.1.7 Example

EXAMPLE 3.1. A professor of organization and management is interested in studying the factors that influence the approach that company managers promote among their employees, competition or collaboration. The data on 50 companies are collected. The variables are the type of company ownership (sole ownership, partnership, or stock company), the number of employees, and the promoted approach (competition or collaboration). The SAS code given below models the probability of collaboration via logistic regression. In the output, we also included the values of AIC, AICC, and BIC criteria which will be utilized later, in Example 3.3, to compare fits of logistic, probit, and complementary log-log models.

```
data companies;
input ownership$ nemployees approach$ @@;
cards;
partner 88 comp sole 60 coll stock 24 comp
partner 108 coll stock 88 coll stock 119 comp
partner 25 comp partner 53 comp stock 82 comp
```



```

stock 69 coll stock 24 comp partner 94 coll
stock 86 coll stock 46 coll partner 106 coll
stock 92 coll stock 22 coll stock 94 coll
sole 20 coll stock 30 comp partner 92 coll
sole 90 coll stock 114 coll sole 66 coll
sole 26 coll stock 59 comp sole 54 coll
sole 69 comp partner 75 comp partner 62 coll
stock 26 comp sole 112 coll sole 87 comp
stock 104 comp partner 25 comp stock 63 comp
stock 21 comp sole 93 comp stock 91 coll
sole 33 comp sole 97 coll sole 93 coll
stock 41 comp partner 73 comp partner 32 comp
partner 56 comp partner 98 comp partner 97 comp
stock 117 coll stock 75 comp
;

proc genmod;
  class ownership(ref="partner");
  model approach(event="coll") = ownership nemployees /
    dist=binomial link=logit;
run;

```

The relevant output is as follows:

```

Log Likelihood    -29.9675
AIC      67.9350
AICC    68.8239
BIC     75.5831

```

Analysis Of Maximum Likelihood Parameter Estimates

Parameter	Estimate	Pr > ChiSq
Intercept	-2.5147	0.0148
ownership sole	1.7388	0.0455
ownership stock	0.6726	0.3629
nemployees	0.0241	0.0267

To check how good the fit of this model is, we run the statements below.

```

proc genmod;
  model approach = /dist=binomial link=logit;
run;

```

Full Log Likelihood -34.6173

```
data deviance_test;
  deviance=-2*(-34.6173-(-29.9675));
  pvalue=1-probchi(deviance,3);
run;

proc print noobs;
run;
```

```
deviance    pvalue
  9.2996    0.025562
```

Since the p -value is not in excess of 0.05, we conclude that the fitted model has a better fit than the intercept-only model. The fitted model for $\pi = \mathbb{P}(\text{collaboration})$ is

$$\text{logit } \hat{\pi} = -2.5146 + 1.7388 \cdot \text{sole} + 0.6726 \cdot \text{stock} + 0.0241 \cdot \text{nemployees},$$

with sole ownership and number of employees being significant predictors at the 5% level of significance. In this model, the estimated odds in favor of the collaborative approach in companies with a single owner are $\exp\{1.7388\} \cdot 100\% = 569.1\%$ of those in companies with multiple partners. For every additional employee, the estimated odds of collaborative strategy increase by $(\exp\{0.0241\} - 1) \cdot 100\% = 2.4\%$.

Finally, suppose the professor would like to estimate the probability of the collaborative approach in a solely owned company with 40 employees. To predict this probability we compute

$$\mathbb{P}^0(\text{collaboration}) = \frac{\exp\{-2.5146 + 1.7388 + 0.0241 \cdot 40\}}{1 + \exp\{-2.5146 + 1.7388 + 0.0241 \cdot 40\}} = 0.5469.$$

To get the same predicted probability in SAS, we run the following code:

```
data prediction;
input ownership$ nemployees;
cards;
sole 40
;

data companies;
  set companies prediction;
run;
```

```

proc genmod;
  class ownership;
model approach = ownership nemployees / dist=binomial link=logit;
  output out=outdata p=pred_probcoll;
run;

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

pred_probcoll
      0.54688

```

The R output presented below matches the output of the SAS code.

```

companies.data<- read.csv(file="./Example3.1Data.csv",
header=TRUE, sep=",")

#specifying reference categories
ownership.rel<- relevel(companies.data$ownership, ref="partner")
approach.rel<- relevel(companies.data$approach, ref="comp")

#fitting logistic model
summary(fitted.model<- glm(approach.rel ~ ownership.rel + nemployees,
data=companies.data, family=binomial(link=logit)))

```

Coefficients:

	Estimate	Pr(> z)
(Intercept)	-2.51469	0.0148
ownership.relsole	1.73882	0.0455
ownership.relstock	0.67256	0.3629
nemployees	0.02410	0.0267

AIC: 67.935

```

#extracting AICC and BIC for fitted model
p<- 4
n<- 50
print(AICC<- -2*logLik(fitted.model)+2*p*n/(n-p-1))

68.82389

```

```

BIC(fitted.model)

75.58309

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

9.2997

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

0.02556052

#using fitted model for prediction
print(predict(fitted.model, data.frame(ownership.rel="sole",
nemployees=40), type="response"))

0.5468756

□

```

3.2 Probit Model

3.2.1 Model Definition

Consider a binary response variable y and predictors x_1, \dots, x_k . Let $\pi = \mathbb{P}(y = 1) = \mathbb{E}(y)$. The *probit regression model*² (“probit”=“probability”+“unit”) is given by:

$$\pi = \mathbb{E}(y) = \Phi(\beta_0 + \beta_1 x_1 + \dots + \beta_k x_k)$$

where $\Phi(\cdot)$ is the cumulative distribution function of a $\mathcal{N}(0, 1)$ distribution.

Alternatively, the above relation may be written as

$$\Phi^{-1}(\pi) = \Phi^{-1}(\mathbb{E}(y)) = \beta_0 + \beta_1 x_1 + \dots + \beta_k x_k.$$

The function $\Phi^{-1}(\cdot)$ is called the *probit link function*.

It may be shown (see Exercise 3.1) that the probit regression model belongs to the class of generalized linear models.

²First appears in Bliss, C. I. (1935). “The calculation of the dosage-mortality curve”. *Annals of Applied Biology*, 22(1): 134 – 167.

3.2.2 Fitted Model

The fitted probit model looks like this:

$$\Phi^{-1}(\hat{\pi}) = \hat{\beta}_0 + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_k x_k, \quad (3.5)$$

or, equivalently,

$$\hat{\pi} = \Phi(\hat{\beta}_0 + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_k x_k). \quad (3.6)$$

3.2.3 Interpretation of Estimated Regression Coefficients

Taking into account (3.5), estimated regression coefficients in the probit model are interpreted in terms of *z-score* (or *probit index*), which is a percentile of the standard normal distribution.

- For a numeric predictor variable x_1 , the estimated coefficient $\hat{\beta}_1$ gives the change in the estimated *z-score* of the response variable for a unit increase in x_1 , keeping all the other predictors unchanged. Indeed, we have

$$\begin{aligned} \Phi^{-1}(\hat{\pi}|_{x_1+1}) - \Phi^{-1}(\hat{\pi}|_{x_1}) &= \hat{\beta}_0 + \hat{\beta}_1(x_1 + 1) + \hat{\beta}_2 x_2 + \cdots + \hat{\beta}_k x_k \\ &\quad - (\hat{\beta}_0 + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_k x_k) = \hat{\beta}_1. \end{aligned}$$

- For a 0-1 predictor x_1 , the estimated coefficient $\hat{\beta}_1$ is interpreted as a difference in the estimated *z-scores* of the response variable for the levels $x_1 = 1$ and $x_1 = 0$, controlling for the other predictors, since

$$\begin{aligned} \Phi^{-1}(\hat{\pi}|_{x_1=1}) - \Phi^{-1}(\hat{\pi}|_{x_1=0}) &= \hat{\beta}_0 + \hat{\beta}_1 \cdot 1 + \hat{\beta}_2 x_2 + \cdots + \hat{\beta}_k x_k \\ &\quad - (\hat{\beta}_0 + \hat{\beta}_1 \cdot 0 + \hat{\beta}_2 x_2 + \cdots + \hat{\beta}_k x_k) = \hat{\beta}_1. \end{aligned}$$

3.2.4 Predicted Probability

Suppose we are given certain values of the predictors x_1^0, \dots, x_k^0 . Then, in accordance with (3.6), we predict the probability π^0 by

$$\pi^0 = \Phi(\hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \cdots + \hat{\beta}_k x_k^0).$$

3.2.5 SAS Implementation

To fit a probit model, use the procedure `genmod` with the option `dist=binomial link=probit`.

3.2.6 R Implementation

The function `glm()` with `family=binomial(link=probit)` may be used to fit a probit model in R.

3.2.7 Example

EXAMPLE 3.2. We fit the probit model to the data in Example 3.1. The code and relevant output are given below.

```
proc genmod;
  class ownership(ref="partner");
model approach(event="coll") = ownership nemployees /
  dist=binomial link=probit;
run;
```

```
Log Likelihood  -29.9519
AIC    67.9038
AICC   68.7926
BIC    75.5518
```

Analysis Of Maximum Likelihood Parameter Estimates

Parameter	Estimate	Pr > ChiSq
Intercept	-1.5544	0.0099
ownership sole	1.0584	0.0404
ownership stock	0.4227	0.3449
nemployees	0.0148	0.0214

```
proc genmod;
  class ownership;
  model approach = / dist=binomial link=probit;
run;
```

```
Full Log Likelihood  -34.6173
```

```
data deviance_test;
  deviance=-2*(-34.6173 -(-29.9519));
  pvalue=1-probchi(deviance,3);
run;
```

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

deviance	pvalue
9.3308	0.025201

The p -value for the deviance test is less than 0.05, indicating a good fit of the model with all predictors. At the 5% significance level, sole ownership and the number of employees are significant predictors, as in the logistic model. The fitted probit model is

$$\Phi^{-1}(\hat{\pi}) = -1.5544 + 1.0584 \cdot \text{sole} + 0.4227 \cdot \text{stock} + 0.0148 \cdot \text{nemployees}.$$

The estimated z -score of the collaborative approach in companies with a single owner is larger by 1.0584 than that in companies with multiple partners. For every additional employee, the estimated z -score of the collaborative strategy increases by 0.0148.

To estimate the probability of the collaborative approach in a solely owned company with 40 employees, we calculate

$$\pi^0 = \Phi(-1.5544 + 1.0584 + 0.0148 \cdot 40) = 0.5382.$$

SAS gives a similar prediction. The code follows.

```
data prediction;
  input ownership$ nemployees;
cards;
sole 40
;

data companies;
  set companies prediction;
run;

proc genmod;
  class ownership;
  model approach = ownership nemployees / dist=binomial link=probit;
  output out=outdata p=pred_probcoll;
run;

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

pred_probcoll
  0.53774
```

The R script which output matches the output in SAS is as follows:

```
companies.data<-read.csv(file="./Example3.1Data.csv",
header=TRUE, sep=",")

# specifying reference categories
ownership.rel<- relevel(companies.data$ownership, ref="partner")
approach.rel<- relevel(companies.data$approach, ref = "comp")

# fitting probit model
summary(fitted.model <- glm(approach.rel ~ ownership.rel + nemployees,
data=companies.data, family=binomial(link=probit)))

Coefficients:
                Estimate Pr(>|z|)
(Intercept)      -1.554466  0.0099
ownership.relsole  1.058424  0.0404
ownership.relstock 0.422743  0.3449
nemployees         0.014770  0.0214

AIC: 67.904

#extracting AICC and BIC for fitted model
p<- 4
n<- 50
print(AICC<- -2*logLik(fitted.model)+2*p*n/(n-p-1))
68.79264

BIC(fitted.model)
75.55185

#checking model fit
null.model<- glm(approach.rel ~ 1, family=binomial(link=probit))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
9.330941

print(p.value<- pchisq(deviance, df=3, lower.tail=FALSE))
0.02519957

#using fitted model for prediction
print(predict(fitted.model, data.frame(ownership.rel="sole",
nemployees=40), type="response"))
0.5377392

□
```


3.3 Complementary Log-Log Model

3.3.1 Model Definition

Consider a binary response variable y and predictors x_1, \dots, x_k . Let $\pi = \mathbb{P}(y = 1)$. The *complementary log-log model*³ has the form

$$\pi = 1 - \exp \left\{ - \exp \left\{ \beta_0 + \beta_1 x_1 + \dots + \beta_k x_k \right\} \right\},$$

or, equivalently,

$$\ln \left(- \ln(1 - \pi) \right) = \beta_0 + \beta_1 x_1 + \dots + \beta_k x_k.$$

Here the function $\ln \left(- \ln(1 - \pi) \right)$ is referred to as *complementary log-log link function*, since the log-log function is applied to the complement of π . On a side note, the function $F(x) = \exp\{-\exp\{-x\}\}$, $-\infty < x < \infty$, that is used in this model, is the cumulative distribution function of the *Gumbel* or *extreme value* distribution.

Similar to the binary logistic and probit models, the complementary log-log regression represents the class of generalized linear models (see Exercise 3.1).

3.3.2 Fitted Model

To ease interpretation of the estimated regression coefficients (see below), it is convenient to write the fitted model in the form

$$1 - \hat{\pi} = \exp \left\{ - \exp \left\{ \hat{\beta}_0 + \hat{\beta}_1 x_1 + \dots + \hat{\beta}_k x_k \right\} \right\}. \quad (3.7)$$

3.3.3 Interpretation of Estimated Regression Coefficients

By (3.7), in the complementary log-log model, the estimated regression coefficients are interpreted as follows.

- For a numeric random predictor x_1 , the estimate of the coefficient $\hat{\beta}_1$ gives the estimated rate ratio for a unit increase in x_1 . To see that, we write

$$1 - \hat{\pi}|_{x_1+1} = \exp \left\{ - \exp \left\{ \hat{\beta}_0 + \hat{\beta}_1 (x_1 + 1) + \hat{\beta}_2 x_2 + \dots + \hat{\beta}_k x_k \right\} \right\}$$

³ First application of this model appeared in Draper, C. C., Voller, A., and R. G. Carpenter, (1972). "The Epidemiologic interpretation of serologic data in malaria". *American Journal of Tropical Medicine and Hygiene*, 21 (5 Suppl): 696 – 703.

$$= \exp \left\{ - \exp \left\{ \widehat{\beta}_0 + \widehat{\beta}_1 x_1 + \cdots + \widehat{\beta}_k x_k \right\} \exp \{ \widehat{\beta}_1 \} \right\} = \left(1 - \widehat{\pi}_{|x_1} \right)^{\exp \{ \widehat{\beta}_1 \}},$$

that is, the probability $1 - \widehat{\pi}_{|x_1+1}$ equals the probability $1 - \widehat{\pi}_{|x_1}$ raised to the power $\exp \{ \widehat{\beta}_1 \}$.

• If x_1 is an indicator variable, then the estimated regression coefficient $\widehat{\beta}_1$ is interpreted as the estimated rate ratio for $x_1 = 1$ and $x_1 = 0$. Indeed, we have

$$\begin{aligned} 1 - \widehat{\pi}_{|x_1=1} &= \exp \left\{ - \exp \left\{ \widehat{\beta}_0 + \widehat{\beta}_1 \cdot 1 + \widehat{\beta}_2 x_2 + \cdots + \widehat{\beta}_k x_k \right\} \right\} \\ &= \exp \left\{ - \exp \left\{ \widehat{\beta}_0 + \widehat{\beta}_1 \cdot 0 + \widehat{\beta}_2 x_2 + \cdots + \widehat{\beta}_k x_k \right\} \exp \{ \widehat{\beta}_1 \} \right\} = \left(1 - \widehat{\pi}_{|x_1=0} \right)^{\exp \{ \widehat{\beta}_1 \}}, \end{aligned}$$

that is, the probability $1 - \widehat{\pi}_{|x_1=1}$ equals to the probability $1 - \widehat{\pi}_{|x_1=0}$ raised to the power $\exp \{ \widehat{\beta}_1 \}$.

3.3.4 Predicted Probability

Using the expression (3.7), for a fixed set of predictors x_1^0, \dots, x_k^0 , the predicted probability π_0 is calculated as

$$\pi^0 = 1 - \exp \left\{ - \exp \left\{ \widehat{\beta}_0 + \widehat{\beta}_1 x_1^0 + \cdots + \widehat{\beta}_k x_k^0 \right\} \right\}.$$

3.3.5 SAS Implementation

To fit a complementary log-log model, use the procedure `genmod` with the option `dist=binomial link=cloglog` in the `model` statement.

3.3.6 R Implementation

The function `glm()` with `family=binomial(link=cloglog)` will fit a complementary log-log model.

3.3.7 Example

EXAMPLE 3.3. We fit the complementary log-log model to the data in Example 3.1. The SAS code and important output are as follows:

```
proc genmod;
  class ownership(ref="partner");
  model approach(event="coll") = ownership nemployees /
    dist=binomial link=cloglog;
run;
```

```
Log Likelihood  -30.3467
AIC    68.6934
AICC   69.5823
BIC    76.3415
```

Parameter		Estimate	Pr > ChiSq
Intercept		-2.0826	0.0058
ownership	sole	1.0631	0.0656
ownership	stock	0.4455	0.4249
nemployees		0.0161	0.0362

```
proc genmod;
  class ownership;
  model approach = / dist=binomial link=cloglog;
run;
```

```
Full Log Likelihood  -34.6173
```

```
data deviance_test;
  deviance=-2*(-34.6173-(-30.3467));
  pvalue=1-probchi(deviance,3);
run;
```

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

```
deviance    pvalue
  8.5412    0.036056
```

From the output, the estimated complement log-log model is $1 - \hat{\pi} = 1 - \hat{\mathbb{P}}(\text{collaboration}) = \hat{\mathbb{P}}(\text{competition}) = \exp \left\{ -\exp \left\{ -2.08025 + 1.0631 \cdot \text{sole} + 0.4455 \cdot \text{stock} + 0.0161 \cdot \text{nemployees} \right\} \right\}$. The p -value for the deviance test is less than 0.05, leading us to the conclusion that this model has a good fit. It is more convenient to interpret the estimated regression coefficients in terms of the probability of competition rather than collaboration. Unlike in the two previous models, sole ownership is significant here only at the 10% level, but not 5%. The number of employees is still a significant predictor at the 5%

level, since their p -values are smaller than 0.05. The estimated probability of competition for single owner companies equals to the estimated probability of competition for companies owned by partners raised to the power $\exp\{1.0631\} = 2.8953$. Also, if the number of employees of a company is increased by one, the new estimated probability of competition is the old one raised to the power $\exp\{0.0161\} = 1.0162$.

The model estimates the probability of the collaborative approach in a solely owned company with 40 employees as

$$\mathbb{P}^0(\text{collaboration}) = 1 - \exp \left\{ -\exp \left\{ -2.08025 + 1.0631 + 0.0161 \cdot 40 \right\} \right\} = 0.4977.$$

The following statements produce the output in SAS.

```
data prediction;
  input ownership$ nemployees;
cards;
sole 40
;

data companies;
  set companies prediction;
run;

proc genmod;
  class ownership;
model approach=ownership nemployees/dist=binomial link=cloglog;
  output out=outdata p=pred_probcoll;
run;

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

pred_probcoll
  0.49708
```

The corresponding R script is given below. Its output matches the one by SAS.

```
companies.data<- read.csv(file="./Example3.1Data.csv",
header=TRUE, sep=",")
```

```
#specifying reference categories
ownership.rel<- relevel(companies.data$ownership, ref="partner")
approach.rel<- relevel(companies.data$approach, ref = "comp")

#fitting complementary log-log model
summary(fitted.model <- glm(approach.rel ~ ownership.rel + nemployees,
data=companies.data, family=binomial(link=cloglog)))
```

Coefficients:

	Estimate	Pr(> z)
(Intercept)	-2.082608	0.00628
ownership.relsole	1.063128	0.06688
ownership.relstock	0.445539	0.41893
nemployees	0.016113	0.03474

AIC: 68.693

```
#extracting AICC and BIC for fitted model
p<- 4
n<- 50
print(AICC<- -2*logLik(fitted.model)+2*p*n/(n-p-1))
```

69.58228

BIC(fitted.model)

76.34148

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

8.54131

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

0.03605396

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(ownership.rel="sole",
nemployees=40), type="response"))
```

0.4970774

Finally, to compare the fitted logistic, probit, and complementary log-log models in terms of goodness-of-fit, we compare the values for the AIC, AICC, and BIC criteria. These were displayed in examples above. For convenience, we repeat the quantities here:

	logistic	probit	cloglog
AIC	67.9350	67.9038	68.6934
AICC	68.8239	68.7926	69.5823
BIC	75.5831	75.5518	76.3415

The probit model has the smallest values in all the three criteria. We conclude that the probit model should be accorded a preference over the other two models. \square

Exercises for Chapter 3

EXERCISE 3.1. Let y be a Bernoulli random variable with the probability of a success π . Show that the probability mass function belongs to the exponential family of distributions, that is, show that it can be written in the form (1.3) with the location parameter $\theta = \ln \frac{\pi}{1-\pi}$ and the dispersion parameter $\phi = 1$. Conclude that the logistic, probit, and complement log-log models are special cases of the generalized linear regression. Specify the respective link functions.

EXERCISE 3.2. Dermatologists in a hospital study patients with acute psoriasis, a skin disease. They would like to know whether medication A is more effective in relieving the symptoms of psoriasis than medication B. The data are retrospectively collected on 30 patients. The variables are gender (M/F), age (in years), medication(A/B), and response (1=relief, 0=no relief). The data are as follows.

Gender	Age	Medication	Response	Gender	Age	Medication	Response
M	37	A	1	M	16	A	1
F	24	A	1	F	33	A	1
F	15	A	1	F	28	A	0
M	31	B	1	M	51	B	1
F	39	B	1	F	35	B	0
M	31	B	1	M	16	B	0
M	20	A	1	F	25	A	0
M	32	A	1	M	18	A	1
M	30	A	1	F	19	A	1
F	24	B	0	M	39	B	1
M	17	B	0	M	38	B	1
F	33	B	1	M	37	B	1
M	24	A	1	F	24	B	0
M	32	A	1	F	39	B	0
F	27	A	1	F	33	B	0

- Fit a binary logistic model. Write down the fitted model. Discuss significance of predictor variables, and goodness of fit of the model. Use $\alpha = 0.05$.
- Give interpretation of the estimated significant regression coefficients.
- Find the predicted probability of relief from psoriasis for a 50-year old woman who is administered the medication A treatment.
- Repeat parts (a)-(c) but fit a probit model. Compare the results.
- 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?

EXERCISE 3.3. A study is conducted to reveal what factors underlie a financial success of a novel. A random sample of 44 published novels is drawn. It is recorded whether each novel is successful financially (yes/no), whether the book cover is catchy (yes/no), the number of publisher's promotional methods (none/one/many), author's popularity (first novel/several novels/many novels), and the number of years the publisher was in business before the novel was published. The observations are

Success	Cover	Methods	Novels	Years	Success	Cover	Methods	Novels	Years
yes	yes	one	many	18	no	no	one	several	9
no	no	one	first	7	yes	no	many	several	13
no	yes	none	several	10	yes	yes	none	first	6
yes	yes	many	many	6	no	no	none	many	2
no	yes	none	several	1	yes	yes	one	several	7
no	no	one	several	1	yes	yes	many	many	17
no	no	one	first	11	yes	yes	many	first	18
yes	no	one	several	19	yes	yes	one	several	17
yes	yes	none	first	5	no	yes	none	several	9
no	no	none	many	2	no	no	one	several	11
no	no	one	several	10	yes	yes	many	first	17
no	no	many	many	9	no	no	many	many	1
yes	no	many	several	6	no	no	many	many	6
yes	yes	many	many	8	no	yes	none	several	1
no	no	one	several	12	yes	yes	many	first	6
no	no	none	many	2	yes	yes	one	many	4
yes	no	none	several	17	no	yes	none	many	7
yes	yes	many	first	10	no	no	one	first	12
yes	no	none	several	7	no	no	one	several	7
no	no	one	first	12	yes	yes	one	several	9
no	yes	none	several	7	no	no	one	several	8
no	yes	none	many	4	no	no	one	several	2

- 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?
- Give interpretation of the estimated significant beta coefficients.
- 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.
- Redo parts (a) through (c), fitting a probit model.
- Redo parts (a) through (c) with the complementary log-log model. How good is the model fit compared to the logistic and probit models?

EXERCISE 3.4. A bank needs to estimate the default rate of customers' home equity loans. A random sample of 35 customers is drawn. The selected variables are loan-to-value (LTV) ratio defined as the ratio of a loan to the value of an asset purchased (in percent), age (in years), income (high/low), and response (yes=default, no=payoff). The data are

LTV	Age	Income	Default	LTV	Age	Income	Default
70	41	low	no	40	44	low	no
70	25	high	yes	80	36	high	no
65	48	low	no	90	47	high	no
65	48	high	no	80	29	high	no
60	32	high	yes	70	24	low	yes
50	48	high	no	30	42	high	no
55	53	low	no	50	33	low	no
85	38	high	yes	80	36	low	no
80	43	low	yes	75	54	low	no
50	33	low	no	75	29	high	yes
60	42	low	no	70	38	low	no
90	23	low	yes	60	35	low	no
80	31	high	no	95	30	low	yes
70	37	high	no	80	34	low	yes
40	39	high	no	75	43	low	yes
80	40	low	no	75	47	high	no
70	52	high	no	85	47	low	yes
80	29	low	yes				

- 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.
- Interpret the estimated significant beta coefficients. What is your suggestion in order for the bank to decrease the default rate of home equity loans?
- 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.
- Repeat the previous parts, fitting a probit model. How different are the results?
- 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?

EXERCISE 3.5. There are three basic dermatoglyphic patterns occurring in the population: loops, whorls, and arches. A cardiologist is interested in finding whether a significant difference exists in the count of the fingerprint patterns in cardiac patients and in the control group. He obtained a clear fingerprint pattern readings for 24 male cardiac patients, and those for 24 healthy males. The variables are group (1=cardiac, 0=control), the number of arches (A), and the number of whorls (W). Note that the number of loops (L) can be recovered by subtraction from 10, therefore, it is not included as a predictor. The data are presented below.

Group	A	W	Group	A	W	Group	A	W	Group	A	W
1	8	2	1	2	7	0	0	9	0	3	2
1	1	2	1	2	8	0	2	1	0	1	2
1	2	1	1	6	0	0	0	8	0	2	5
1	4	0	1	3	5	0	1	3	0	4	0
1	2	7	1	1	0	0	3	1	0	8	1
1	6	3	1	7	1	0	1	4	0	2	7
1	2	8	1	4	3	0	0	8	0	0	10
1	1	9	1	2	4	0	1	6	0	0	5
1	3	0	1	5	3	0	0	9	0	0	6
1	0	2	1	7	1	0	2	2	0	2	1
1	3	2	1	8	1	0	4	4	0	0	7
1	2	7	1	0	6	0	0	6	0	0	6

- (a) Model the probability of being a cardiac patient via the binary logistic regression. Write the fitted model explicitly. Discuss goodness-of-fit of the model and significance of regression coefficients. Assume $\alpha = 0.01$ for all tests.
- (b) Interpret the estimated significant regression coefficients. For which fingerprint pattern the fitted probability is the largest? For which, the lowest?
- (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-L-W. What is this predicted probability?
- (d) In parts (a)-(c), fit a probit model. Compare results.
- (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?

Chapter 4

Regression Models for Categorical Response

A natural extension of the binary (dichotomous) regression model introduced in Chapter 3 is when the categorical response variable assumes more than two values, e.g., 0, 1, or 2. This model is called a *multinomial* (or *polytomous*) regression model.

Two types of multinomial regression models are distinguished, depending on whether the response variable is measured on an ordinal or nominal scale. A categorical variable is measured on an *ordinal scale* (called an *ordinal variable*) if the categories have a natural ordering. For example, health status has ordered categories “poor,” “fair,” “good,” or “excellent”.

On the other hand, if the categories don’t have a natural ordering, the variable is called the *nominal variable*, and is measured on *nominal scale*. In this case the categories may be simply treated as names. For instance, race is a nominal variable with unordered categories “African American,” “Hispanic,” “Caucasian,” “Asian,” and “Other”.

In this chapter, we study three models for an ordinal response variable: cumulative logit, cumulative probit, and cumulative complementary log-log models; and one model for a nominal response, a generalized logit model.

4.1 Cumulative Logit Model

4.1.1 Model Definition

Let y denote an ordinal response variable with categories $1, \dots, c$. The probability $\mathbb{P}(y \leq j)$ is the probability of y falling in one of the categories $1, \dots, j$. This is called a *cumulative probability*. For example, if $c = 3$, the cumulative probabilities are

$$\mathbb{P}(y \leq 1) = \mathbb{P}(y = 1), \quad \mathbb{P}(y \leq 2) = \mathbb{P}(y = 1) + \mathbb{P}(y = 2),$$

and

$$\mathbb{P}(y \leq 3) = \mathbb{P}(y = 1) + \mathbb{P}(y = 2) + \mathbb{P}(y = 3) = 1.$$

The ratio $\frac{\mathbb{P}(y \leq j)}{\mathbb{P}(y > j)} = \frac{\mathbb{P}(y \leq j)}{1 - \mathbb{P}(y \leq j)}$ represents the odds of response y being in the category j or below. The *logits of the cumulative probabilities* (called *cumulative logits*) are the functions

$$\text{logit } \mathbb{P}(y \leq j) = \ln \frac{\mathbb{P}(y \leq j)}{\mathbb{P}(y > j)} = \ln \frac{\mathbb{P}(y \leq j)}{1 - \mathbb{P}(y \leq j)}, \quad j = 1, \dots, c - 1.$$

For example, with $c = 3$,

$$\begin{aligned} \text{logit } \mathbb{P}(y \leq 1) &= \ln \frac{\mathbb{P}(y \leq 1)}{\mathbb{P}(y > 1)} = \ln \frac{\mathbb{P}(y = 1)}{\mathbb{P}(y = 2) + \mathbb{P}(y = 3)}, \\ \text{logit } \mathbb{P}(y \leq 2) &= \ln \frac{\mathbb{P}(y \leq 2)}{\mathbb{P}(y > 2)} = \ln \frac{\mathbb{P}(y = 1) + \mathbb{P}(y = 2)}{\mathbb{P}(y = 3)}, \end{aligned}$$

and since $\mathbb{P}(y \leq 3) = 1$, $\text{logit } \mathbb{P}(y \leq 3)$ is not defined.

The *cumulative logit model*¹ for an ordinal response y and predictors x_1, \dots, x_k has the form

$$\text{logit } \mathbb{P}(y \leq j) = \alpha_j + \beta_1 x_1 + \dots + \beta_k x_k, \quad j = 1, \dots, c - 1. \quad (4.1)$$

Note that this model requires a separate intercept parameter α_j for each cumulative probability. Thus, there are a total of $c + k - 1$ unknown parameters in this model ($c - 1$ intercepts and k beta coefficients). Because the beta coefficients don't depend on j , this model is sometimes termed the *proportional odds model*.

¹Introduced in McCullagh, P. (1980). "Regression models for ordinal data". *Journal of the Royal Statistical Society, Series B*, 42 (2): 109 – 142.

To show that the cumulative logit model belongs to the class of generalized linear models, we notice that $\mathbb{P}(y \leq j)$ is the mean of the indicator random variable of the event $\{y \leq j\}$, which has a Bernoulli distribution. As shown in Exercise 3.1, Bernoulli distribution belongs to the exponential family. In addition, by (4.1), the link function in this model is logit.

4.1.2 Fitted Model

In view of (4.1), the fitted cumulative logit model is of the form:

$$\text{logit } \hat{\mathbb{P}}(y \leq j) = \ln \frac{\hat{\mathbb{P}}(y \leq j)}{1 - \hat{\mathbb{P}}(y \leq j)} = \hat{\alpha}_j + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_k x_k, \quad j = 1, \dots, c-1,$$

or, equivalently,

$$\hat{\mathbb{P}}(y \leq j) = \frac{\exp \{ \hat{\alpha}_j + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_k x_k \}}{1 + \exp \{ \hat{\alpha}_j + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_k x_k \}}, \quad j = 1, \dots, c-1. \quad (4.2)$$

4.1.3 Interpretation of Estimated Regression Coefficients

The estimates of the regression coefficients are interpreted as follows:

- If a predictor variable x_1 is numeric, then $(\exp\{\hat{\beta}_1\} - 1) \cdot 100\%$ represents the estimated percent change in odds of the event $\{y \leq j\}$ as opposed to the event $\{y > j\}$, for any $j = 1, \dots, c-1$, when x_1 is increased by one unit, and the other predictors are held fixed. This can be seen by writing

$$\begin{aligned} & \frac{\hat{\mathbb{P}}(y \leq j | x_1 + 1) / \hat{\mathbb{P}}(y > j | x_1 + 1) - \hat{\mathbb{P}}(y \leq j | x_1) / \hat{\mathbb{P}}(y > j | x_1)}{\hat{\mathbb{P}}(y \leq j | x_1) / \hat{\mathbb{P}}(y > j | x_1)} \cdot 100\% \\ &= \left(\frac{\exp\{\hat{\alpha}_j + \hat{\beta}_1(x_1 + 1) + \hat{\beta}_2 x_2 + \cdots + \hat{\beta}_k x_k\}}{\exp\{\hat{\alpha}_j + \hat{\beta}_1 x_1 + \hat{\beta}_2 x_2 + \cdots + \hat{\beta}_k x_k\}} - 1 \right) \cdot 100\% = (\exp\{\hat{\beta}_1\} - 1) \cdot 100\%. \end{aligned}$$

- If a predictor variable x_1 is an indicator variable, then the quantity $\exp\{\hat{\beta}_1\} \cdot 100\%$ is interpreted as the ratio of odds in favor of $\{y \leq j\}$ against $\{y > j\}$ when $x_1 = 1$ and when $x_1 = 0$, provided the other predictors are unchanged. This is obtained as follows:

$$\begin{aligned} & \frac{\hat{\mathbb{P}}(y \leq j | x_1 = 1) / \hat{\mathbb{P}}(y > j | x_1 = 1)}{\hat{\mathbb{P}}(y \leq j | x_1 = 0) / \hat{\mathbb{P}}(y > j | x_1 = 0)} \cdot 100\% \\ &= \frac{\exp\{\hat{\alpha}_j + \hat{\beta}_1 \cdot 1 + \hat{\beta}_2 x_2 + \cdots + \hat{\beta}_k x_k\}}{\exp\{\hat{\alpha}_j + \hat{\beta}_1 \cdot 0 + \hat{\beta}_2 x_2 + \cdots + \hat{\beta}_k x_k\}} \cdot 100\% = \exp\{\hat{\beta}_1\} \cdot 100\%. \end{aligned}$$

4.1.4 Predicted Probabilities

From (4.2), for given values of predictors x_1^0, \dots, x_k^0 , the predicted cumulative probabilities may be found as

$$\mathbb{P}^0(y \leq j) = \frac{\exp \{ \hat{\alpha}_j + \hat{\beta}_1 x_1^0 + \dots + \hat{\beta}_k x_k^0 \}}{1 + \exp \{ \hat{\alpha}_j + \hat{\beta}_1 x_1^0 + \dots + \hat{\beta}_k x_k^0 \}}, \quad j = 1, \dots, c-1.$$

Moreover, we can predict the probability of exact equality to a value as the difference of two consecutive predicted cumulative probabilities. Like this:

$$\begin{aligned} \mathbb{P}^0(y = j) &= \mathbb{P}^0(y \leq j) - \mathbb{P}^0(y \leq j-1), \quad j = 2, \dots, c-1, \\ \mathbb{P}^0(y = 1) &= \mathbb{P}^0(y \leq 1), \quad \text{and} \quad \mathbb{P}^0(y = c) = 1 - \mathbb{P}^0(y \leq c-1). \end{aligned} \quad (4.3)$$

4.1.5 SAS Implementation

The procedure `genmod` with `dist=multnomial link=cumlogit` may be used to run the cumulative logit model. Since the values of the response variable must be on ordinal scale, it is convenient to present them as numbers, for instance, $1, 2, \dots, c$, and possibly describe the levels in a `proc format` statement like this:

```
proc format;
  value response_namefmt 1="level1_name"
                        2="level2_name" ... c="levelc_name";
run;
```

Another possibility would be to enter level names as words but in `proc format` put digits 1 through c in front on the names. For example, "1poor", "2fair", "3good", "4excellent".

- By default, SAS orders the levels in alphabetical order and models the cumulative probabilities of the response variable having lower ordered values. If it is desired to reverse the order, the option `descending` may be used in the `proc genmod` statement.
- SAS predicts cumulative probability for each category, that is, the probability of being in a given category or in any category that precedes it.

4.1.6 R Implementation

Function `clm()` in the library `ordinal` may be utilized to fit the cumulative logit model. The name stands for “cumulative link models”. The syntax is

```
summary(fitted.model.name<- clm(response.name ~ x1.name + ...
+ xk.name, data = data.name, link="logit"))
```

- R outputs beta coefficients with reversed signs. The signs of the intercepts are not changed. This means that R outputs estimates for $\alpha_1, \dots, \alpha_{c-1}$, and β_0, \dots, β_k where

$$\text{logit } \mathbb{P}(y \leq j) = \alpha_j - \beta_1 x_1 - \dots - \beta_k x_k, \quad j = 1, \dots, c-1.$$

- The intercepts are termed **Threshold coefficients**.
- R outputs the individual (non-cumulative) predicted probability for each category. The argument `type="prob"` should be included in the `predict()` function.

4.1.7 Example

EXAMPLE 4.1. The California Health Interview Survey (CHIS) is a large-scale survey of the health of Californians. Among the variables measured are gender (M/F), age (in years), marital status (“yes”=married, “no”=not married), the highest educational degree obtained (<HS/HSgrad/HSgrad+), and the health status (poor/fair/good/excellent). The code below fits the cumulative logit model to the data on 32 respondents.

```
data health_survey;
  length health$ 10.;
  input gender$ age marital$ educ$ health$ @@;
cards;
M 46 yes <HS      good      M 72 yes <HS      poor
M 52 yes HSgrad   excellent  M 50 no  <HS      fair
F 44 no  HSgrad+  poor      F 68 no  HSgrad   fair
F 50 no  HSgrad+  fair      F 93 no  <HS      poor
M 50 yes HSgrad   excellent  M 88 no  HSgrad+  good
M 58 yes HSgrad   excellent  M 52 yes HSgrad   good
F 64 yes HSgrad+  good      F 49 yes HSgrad   good
F 41 yes HSgrad+  excellent  M 32 no  HSgrad+  good
F 88 no  HSgrad   poor      F 36 yes HSgrad+  excellent
M 35 no  HSgrad+  excellent  F 38 no  HSgrad+  fair
M 39 yes HSgrad+  excellent  F 43 no  <HS      good
M 61 yes HSgrad   good      F 41 yes HSgrad+  excellent
F 36 yes <HS      good      F 44 yes HSgrad+  excellent
M 41 no  HSgrad   good      M 55 yes <HS      good
```

```

M 57 no <HS      fair      M 28 yes HSgrad+ excellent
F 40 yes HSgrad  good      F 97 no  HSgrad  poor
;

proc format;
value $healthfmt "poor"="1poor" "fair"="2fair"
    "good"="3good" "excellent"="4excellent";
run;

proc genmod;
class gender(ref="M") marital(ref="yes") educ(ref="HSgrad+");
model health=gender age marital educ/dist=multinomial
    link=cumlogit;
format health $healthfmt.;
run;

Log Likelihood  -24.0727
AIC      64.1455
AICC     70.4064
BIC      75.8714

Analysis Of Maximum Likelihood Parameter Estimates
Parameter      Estimate    Pr > ChiSq
Intercept1     -11.7440    <.0001
Intercept2      -9.7021    <.0001
Intercept3      -5.9098     0.0014
gender F         2.0630     0.0281
age              0.0805     0.0145
marital no       3.3593     0.0021
educ <HS         3.2609     0.0093
educ HSgrad      1.1877     0.2420

proc genmod;
    model health=/dist=multinomial link=cumlogit;
run;

Log Likelihood  -41.9644

data deviance_test;
    deviance=-2*(-41.9644-(-24.0727));
    pvalue=1-probchi(deviance,5);
run;

proc print noobs;
run;

```


deviance	pvalue
35.7834	0.000001049

In view of the fact that the p -value is tiny, we conclude that the fitted model has a good fit. The fitted model is:

$$\frac{\widehat{\mathbb{P}}(poor)}{1 - \widehat{\mathbb{P}}(poor)} = \exp \left\{ -11.7440 + 2.0630 \cdot female \right. \\ \left. + 0.0805 \cdot age + 3.3593 \cdot not\ married + 3.2609 \cdot < HS + 1.1877 \cdot HSgrad \right\},$$

$$\frac{\widehat{\mathbb{P}}(poor, \text{ or } fair)}{1 - \widehat{\mathbb{P}}(poor, \text{ or } fair)} = \exp \left\{ -9.7021 + 2.0630 \cdot female \right. \\ \left. + 0.0805 \cdot age + 3.3593 \cdot not\ married + 3.2609 \cdot < HS + 1.1877 \cdot HSgrad \right\},$$

and

$$\frac{\widehat{\mathbb{P}}(poor, fair, \text{ or } good)}{\widehat{\mathbb{P}}(excellent)} = \exp \left\{ -5.9098 + 2.0630 \cdot female \right. \\ \left. + 0.0805 \cdot age + 3.3593 \cdot not\ married + 3.2609 \cdot < HS + 1.1877 \cdot HSgrad \right\}.$$

The significant predictors at the 5% level are gender, age, marital status, and less than high-school educational level. The corresponding estimated regression coefficients may be interpreted as follows. The estimated odds in favor of worse health rather than better health for females are $\exp\{2.0630\} \cdot 100\% = 786.95\%$ of the estimated odds for males. For a one-year increase in age, these estimated odds increase by $(\exp\{0.0805\} - 1) \cdot 100\% = 8.38\%$. These odds for not married people are estimated to be $\exp\{3.3593\} \cdot 100\% = 2,876.90\%$ of those for married people. For people with less than high school education, these odds are $\exp\{3.2609\} \cdot 100\% = 2,607.30\%$ of those for people with some college education.

Finally, suppose we would like to find the predicted probability for each of the health levels for a married 52-year-old male with a high school diploma. We calculate:

$$\mathbb{P}^0(poor) = \frac{\exp\{-11.7440 + 0.0805 \cdot 52 + 1.1877\}}{1 + \exp\{-11.7440 + 0.0805 \cdot 52 + 1.1877\}} = 0.0017,$$

$$\mathbb{P}^0(poor \text{ or } fair) = \frac{\exp\{-9.7021 + 0.0805 \cdot 52 + 1.1877\}}{1 + \exp\{-9.7021 + 0.0805 \cdot 52 + 1.1877\}} = 0.0130,$$

and

$$\mathbb{P}^0(poor, fair, \text{ or } good) = \frac{\exp\{-5.9098 + 0.0805 \cdot 52 + 1.1877\}}{1 + \exp\{-5.9098 + 0.0805 \cdot 52 + 1.1877\}} = 0.3691.$$

The predicted probabilities for individual categories are: $\mathbb{P}^0(\text{poor}) = 0.0017$, $\mathbb{P}^0(\text{fair}) = \mathbb{P}^0(\text{poor or fair}) - \mathbb{P}^0(\text{poor}) = 0.0130 - 0.0017 = 0.0113$, $\mathbb{P}^0(\text{good}) = \mathbb{P}^0(\text{poor, fair, or good}) - \mathbb{P}^0(\text{poor or fair}) = 0.3691 - 0.0130 = 0.3561$, and $\mathbb{P}^0(\text{excellent}) = 1 - \mathbb{P}^0(\text{poor, fair, or good}) = 1 - 0.3691 = 0.6309$.

The following lines of code produce predicted cumulative probabilities in SAS:

```
data prediction;
input gender$ age marital$ educ$;
cards;
M 52 yes HSgrad
;

data health_survey;
  set health_survey prediction;
run;

proc genmod;
class gender marital educ;
  model health=gender age marital educ/dist=multinomial
    link=cumlogit;
output out=outdata p=pred_prob;
format health $healthfmt.;
run;

proc print data=outdata (firstobs=97) noobs;
var _level_ pred_prob;
run;
```

LEVEL	pred_prob
1poor	0.00171
2fair	0.01303
3good	0.36934

Thus, the predicted probabilities for individual health categories predicted by SAS are: $\mathbb{P}^0(\text{poor}) = 0.00171$, $\mathbb{P}^0(\text{fair}) = 0.01303 - 0.00171 = 0.01132$, $\mathbb{P}^0(\text{good}) = 0.36934 - 0.01303 = 0.35631$, and $\mathbb{P}^0(\text{excellent}) = 1 - 0.36934 = 0.63066$.

The R script and relevant output for this example are below.

```
health.survey.data<-read.csv(file="./Example4.1Data.csv",
header=TRUE, sep=",")
```

```
#specifying reference categories
```

```
gender.rel<- relevel(health.survey.data$gender, ref="M")
marital.rel<- relevel(health.survey.data$marital, ref="yes")
educ.rel<- relevel(health.survey.data$educ, ref="HSgrad+")
```

```
#fitting cumulative logit model
```

```
library("ordinal")
summary(fitted.model<- clm(health ~ gender.rel + age
+ marital.rel + educ.rel, data=health.survey.data, link="logit"))
```

AIC

64.15

Coefficients:

	Estimate	Pr(> z)
gender.relF	-2.06296	0.02810
age	-0.08052	0.01450
marital.relno	-3.35931	0.00206
educ.rel<HS	-3.26088	0.00926
educ.relHSgrad	-1.18772	0.24200

Threshold coefficients:

	Estimate
1poor 2fair	-11.744
2fair 3good	-9.702
3good 4excellent	-5.910

```
#extracting AICC and BIC for fitted model
```

```
p<- 8
n<- 32
print(AICC<- -2*logLik(fitted.model)+2*p*n/(n-p-1))
```

70.40635

```
BIC(fitted.model)
```

75.87137

```
#checking model fit
```

```
null.model<- clm(health ~ 1, data=health.survey.data, link="logit")
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

35.78339

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

1.049431e-06

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(gender.rel="M", age=52,
marital.rel="yes", educ.rel="HSgrad"), type="prob"))
```

	1poor	2fair	3good	4excellent
	0.001710524	0.01132041	0.3563093	0.6306598

□

4.2 Cumulative Probit Model

4.2.1 Model Definition

The *cumulative probit model*² for an ordinal response y with values in categories $1, \dots, c$ and predictors x_1, \dots, x_k has the form

$$\mathbb{P}(y \leq j) = \Phi(\alpha_j + \beta_1 x_1 + \dots + \beta_k x_k), \quad j = 1, \dots, c-1,$$

where $\Phi(\cdot)$ denotes the cumulative distribution function of a standard normal random variable. Note that like the cumulative logistic regression, the cumulative probit model also belongs to the class of generalized linear regressions, with the probit link function.

4.2.2 Fitted Model

The fitted model may be written as

$$\Phi^{-1}(\hat{\mathbb{P}}(y \leq j)) = \hat{\alpha}_j + \hat{\beta}_1 x_1 + \dots + \hat{\beta}_k x_k, \quad j = 1, \dots, c-1, \quad (4.4)$$

or

$$\hat{\mathbb{P}}(y \leq j) = \Phi(\hat{\alpha}_j + \hat{\beta}_1 x_1 + \dots + \hat{\beta}_k x_k), \quad j = 1, \dots, c-1. \quad (4.5)$$

²First proposed in McKelvey, R.D. and W. Zavoina (1975). "A statistical model for the analysis of ordinal level dependent variables". *Journal of Mathematical Sociology*, 4: 103 – 120.

4.2.3 Interpretation of Estimated Regression Coefficients

In view of (4.4), the estimated cumulative probit regression coefficients are interpreted as described below.

- If a predictor variable x_1 is numeric, then $\hat{\beta}_1$ gives the change in the estimated z -score for a one-unit increase in x_1 , controlling for the other predictors. Indeed,

$$\begin{aligned} & \Phi^{-1}(\hat{\mathbb{P}}(y \leq j|x_1 + 1)) - \Phi^{-1}(\hat{\mathbb{P}}(y \leq j|x_1)) \\ &= \hat{\beta}_1(x_1+1) + \hat{\beta}_2 x_2 + \cdots + \hat{\beta}_k x_k - (\hat{\beta}_1 x_1 + \hat{\beta}_2 x_2 + \cdots + \hat{\beta}_k x_k) = \hat{\beta}_1, \quad j = 1, \dots, c-1. \end{aligned}$$

- If a predictor variable x_1 is an indicator variable, then $\hat{\beta}_1$ represents the difference in the estimated z -scores when $x_1 = 1$ and $x_1 = 0$, provided all the other predictor variables stay unchanged. We write

$$\begin{aligned} & \Phi^{-1}(\hat{\mathbb{P}}(y \leq j|x_1 = 1)) - \Phi^{-1}(\hat{\mathbb{P}}(y \leq j|x_1 = 0)) \\ &= \hat{\beta}_1 \cdot 1 + \hat{\beta}_2 x_2 + \cdots + \hat{\beta}_k x_k - (\hat{\beta}_1 \cdot 0 + \hat{\beta}_2 x_2 + \cdots + \hat{\beta}_k x_k) = \hat{\beta}_1, \quad j = 1, \dots, c-1. \end{aligned}$$

4.2.4 Predicted Probabilities

Taking into account (4.5), in the cumulative probit model, predicted cumulative probabilities are computed as

$$\mathbb{P}^0(y \leq j) = \Phi(\hat{\alpha}_j + \hat{\beta}_1 x_1^0 + \cdots + \hat{\beta}_k x_k^0), \quad j = 1, \dots, c-1,$$

for predetermined values x_1^0, \dots, x_k^0 . Predicted probabilities of exact equality to $j, j = 1, \dots, c$, are found via the same equations (4.3) as in the cumulative logit model.

4.2.5 SAS Implementation

The procedure `genmod` with `dist=multnomial link=cumprobit` may be used to run the cumulative probit model.

4.2.6 R Implementation

The cumulative probit model may be fit using function `clm()` with the option `link="probit"`.

4.2.7 Example

EXAMPLE 4.2. Consider the data `health_survey` in Example 4.1. We fit the cumulative probit model to the data set, check its goodness-of-fit, and use the fitted model for prediction. The code and important outputs are given below.

```
proc genmod;
class gender(ref="M") marital(ref="yes") educ(ref="HSgrad+");
model health=gender age marital educ/dist=multinomial
      link=cumprobit;
format health $healthfmt.;
run;
```

```
Log Likelihood  -24.1213
AIC      64.2426
AICC     70.5035
BIC      75.9685
```

Parameter	Estimate	Pr > ChiSq
Intercept1	-6.7442	<.0001
Intercept2	-5.6721	<.0001
Intercept3	-3.4867	0.0007
gender F	1.1447	0.0257
age	0.0499	0.0062
marital no	1.8788	0.0010
educ <HS	1.8103	0.0057
educ HSgrad	0.6060	0.2942

```
proc genmod;
      model health=/dist=multinomial link=cumprobit;
run;
```

```
Full Log Likelihood  -41.9644
```

```
data deviance_test;
      deviance=-2*(-41.9644-(-24.1213));
      pvalue=1-probchi(deviance,5);
run;
```

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

deviance	pvalue
35.6862	0.000001097

The fitted model has the form:

$$\begin{aligned}\widehat{\mathbb{P}}(\textit{poor}) &= \Phi(-6.7442 + 1.1447 \cdot \textit{female} + 0.0499 \cdot \textit{age} \\ &\quad + 1.8788 \cdot \textit{not married} + 1.8103 \cdot < HS + 0.6060 \cdot HSgrad), \\ \widehat{\mathbb{P}}(\textit{poor}, \textit{or fair}) &= \Phi(-5.6721 + 1.1447 \cdot \textit{female} + 0.0499 \cdot \textit{age} \\ &\quad + 1.8788 \cdot \textit{not married} + 1.8103 \cdot < HS + 0.6060 \cdot HSgrad),\end{aligned}$$

and

$$\begin{aligned}\widehat{\mathbb{P}}(\textit{poor}, \textit{fair}, \textit{or good}) &= \Phi(-3.4867 + 1.1447 \cdot \textit{female} + 0.0499 \cdot \textit{age} \\ &\quad + 1.8788 \cdot \textit{not married} + 1.8103 \cdot < HS + 0.6060 \cdot HSgrad).\end{aligned}$$

We can see that the fitted model has a good fit because the p -value in the deviance test is very small. Similar to the cumulative logistic model, in this case gender, age, marital status, and less than high school educational level are statistically significant predictors. Their estimated beta coefficients may be interpreted as follows. The estimated z -score for women is larger than that for men by 1.1447. As age increases by one year, the estimated z -score increases by 0.0499. People who are not married have estimated z -scores larger by 1.8788 compared to their married counterparts. Finally, estimated z -score for people with less than high school education exceeds that for people who studied in college by 1.8103.

Next, we will find predicted probabilities of each category of health status for a 52-year-old married man who has a high school diploma. To this end, we write:

$$\begin{aligned}\mathbb{P}^0(\textit{poor}) &= \Phi(-6.7442 + 0.0499 \cdot 52 + 0.6060) = 0.00020, \\ \mathbb{P}^0(\textit{poor}, \textit{or fair}) &= \Phi(-5.6721 + 0.0499 \cdot 52 + 0.6060) = 0.00673,\end{aligned}$$

and

$$\mathbb{P}(\textit{poor}, \textit{fair}, \textit{or good}) = \Phi(-3.4867 + 0.0499 \cdot 52 + 0.6060) = 0.38748.$$

From here, the individual predicted probabilities are $\mathbb{P}^0(\textit{poor}) = 0.00020$, $\mathbb{P}^0(\textit{fair}) = 0.00673 - 0.00020 = 0.00653$, $\mathbb{P}^0(\textit{good}) = 0.38748 - 0.00673 = 0.380746$, and $\mathbb{P}^0(\textit{excellent}) = 1 - 0.38748 = 0.61252$.

The cumulative probabilities can be requested in SAS by entering the following statements:

```

data prediction;
input gender$ age marital$ educ$;
cards;
M 52 yes HSgrad
;

data health_survey;
  set health_survey prediction;
run;

proc genmod;
class gender marital educ;
  model health=gender age marital educ/dist=multinomial
  link=cumprobit;
output out=outdata p=pred_prob;
format health $healthfmt.;
run;

proc print data=outdata (firstobs=97) noobs;
var _level_ pred_prob;
run;

```

LEVEL	pred_prob
1poor	0.00020
2fair	0.00669
3good	0.38658

We can obtain the non-cumulative probabilities by subtraction: $\mathbb{P}^0(\text{poor}) = 0.00020$, $\mathbb{P}^0(\text{fair}) = 0.00669 - 0.00020 = 0.00649$, $\mathbb{P}^0(\text{good}) = 0.38658 - 0.00669 = 0.37989$, and $\mathbb{P}^0(\text{excellent}) = 1 - 0.38658 = 0.61342$.

The R script below reproduces the results that were obtained in SAS.

```

health_survey.data<- read.csv(file="./Example4.1Data.csv",
header=TRUE, sep=",")

#specifying reference categories
gender.rel<- relevel(health_survey.data$gender, ref="M")
marital.rel<- relevel(health_survey.data$marital, ref="yes")
educ.rel<- relevel(health_survey.data$educ, ref="HSgrad+")

#fitting cumulative probit model

```



```

library("ordinal")
summary(fitted.model<- clm(health ~ gender.rel + age
+ marital.rel + educ.rel, data=health.survey.data, link="probit"))

AIC
64.24

Coefficients:
              Estimate   Pr(>|z|)
gender.relF    -1.14467  0.025685
age            -0.04986  0.006244
marital.relno  -1.87884  0.000952
educ.rel<HS    -1.81028  0.005683
educ.relHSgrad -0.60599  0.294219

Threshold coefficients:
              Estimate
1poor|2fair    -6.744
2fair|3good    -5.672
3good|4excellent -3.487

#extracting AICC and BIC for fitted model
p<- 8
n<- 32
print(AICC<- -2*logLik(fitted.model)+2*p*n/(n-p-1))
70.50345

BIC(fitted.model)
75.96847

#checking model fit
null.model<- clm(health ~ 1, data=health.survey.data, link="probit")
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
35.68629

print(p.value<- pchisq(deviance, df=5, lower.tail=FALSE))
1.0974e-06

#using fitted model for prediction
print(predict(fitted.model, data.frame(gender.rel="M", age=52,
marital.rel="yes", educ.rel="HSgrad"), type="prob"))

      1poor      2fair      3good      4excellent
0.0001957589 0.006491104 0.3798914 0.6134217

```

□

4.3 Cumulative Complementary Log-Log Model

4.3.1 Model Definition

The *cumulative complementary log-log model*³ for an ordinal response y and predictors x_1, \dots, x_k is defined by

$$\ln \left[-\ln (1 - \mathbb{P}(y \leq j)) \right] = \alpha_j + \beta_1 x_1 + \dots + \beta_k x_k, \quad j = 1, \dots, c-1,$$

or, equivalently,

$$\mathbb{P}(y \leq j) = 1 - \exp \left\{ -\exp \{ \alpha_j + \beta_1 x_1 + \dots + \beta_k x_k \} \right\}, \quad j = 1, \dots, c-1.$$

Similar to cumulative logit and probit models, the cumulative complementary log-log model falls into the class of generalized linear models with the complementary log-log link function.

4.3.2 Fitted Model

In the fitted cumulative complementary log-log model, the estimated cumulative probabilities satisfy

$$\widehat{\mathbb{P}}(y \leq j) = 1 - \exp \left\{ -\exp \{ \widehat{\alpha}_j + \widehat{\beta}_1 x_1 + \dots + \widehat{\beta}_k x_k \} \right\}, \quad j = 1, \dots, c-1. \quad (4.6)$$

4.3.3 Interpretation of Estimated Regression Coefficients

From (4.6), the estimated regression coefficients are interpreted as:

- If a predictor variable x_1 is numeric, then $\exp \{ \widehat{\beta}_1 \}$ gives the estimated *rate ratio* for a unit increase in x_1 , given that other predictors remain the same, since for any $j = 1, \dots, c-1$,

$$\begin{aligned} 1 - \widehat{\mathbb{P}}(y \leq j | x_1 + 1) &= \exp \left\{ -\exp \{ \widehat{\alpha}_j + \widehat{\beta}_1(x_1 + 1) + \widehat{\beta}_2 x_2 + \dots + \widehat{\beta}_k x_k \} \right\} \\ &= \exp \left\{ -\exp \{ \widehat{\alpha}_j + \widehat{\beta}_1 x_1 + \widehat{\beta}_2 x_2 + \dots + \widehat{\beta}_k x_k \} \exp \{ \widehat{\beta}_1 \} \right\} \\ &= \left[\exp \left\{ -\exp \{ \widehat{\alpha}_j + \widehat{\beta}_1 x_1 + \widehat{\beta}_2 x_2 + \dots + \widehat{\beta}_k x_k \} \right\} \right]^{\exp \{ \widehat{\beta}_1 \}} = \left[1 - \widehat{\mathbb{P}}(y \leq j | x_1) \right]^{\exp \{ \widehat{\beta}_1 \}}. \end{aligned}$$

³First appears in McCullagh, P. (1980). “Regression models for ordinal data”. *Journal of the Royal Statistical Society, Series B*, 42 (2): 109 – 142.

Thus, when x_1 increases by one unit, the estimated complement cumulative probability $1 - \widehat{\mathbb{P}}(y \leq j|x_1 + 1)$ equals to the complement cumulative probability $1 - \widehat{\mathbb{P}}(y \leq j|x_1)$ raised to the power $\exp\{\widehat{\beta}_1\}$.

- If a predictor variable x_1 is an indicator variable with two levels 0 and 1, then $\exp\{\widehat{\beta}_1\}$ gives the estimated *rate ratio* for the levels $x_1 = 1$ and $x_1 = 0$, provided the other predictors stay intact, which can be seen by writing

$$\begin{aligned} 1 - \widehat{\mathbb{P}}(y \leq j|x_1 = 1) &= \exp \left\{ - \exp \left\{ \widehat{\alpha}_j + \widehat{\beta}_1 \cdot 1 + \widehat{\beta}_2 x_2 + \cdots + \widehat{\beta}_k x_k \right\} \right\} \\ &= \left[\exp \left\{ - \exp \left\{ \widehat{\alpha}_j + \widehat{\beta}_1 \cdot 0 + \widehat{\beta}_2 x_2 + \cdots + \widehat{\beta}_k x_k \right\} \right\} \right]^{\exp\{\widehat{\beta}_1\}} \\ &= \left[1 - \widehat{\mathbb{P}}(y \leq j|x_1 = 0) \right]^{\exp\{\widehat{\beta}_1\}}, \quad j = 1, \dots, c - 1. \end{aligned}$$

4.3.4 Predicted Probabilities

Using (4.6), we can write the equations for the predicted cumulative probabilities for some defined values of predictors x_1^0, \dots, x_k^0 as

$$\mathbb{P}^0(y \leq j) = 1 - \exp \left\{ - \exp \left\{ \widehat{\alpha}_j + \widehat{\beta}_1 x_1^0 + \cdots + \widehat{\beta}_k x_k^0 \right\} \right\}, \quad j = 1, \dots, c - 1.$$

The individual probabilities may be obtained via the expressions in (4.3).

4.3.5 SAS Implementation

To fit the cumulative complementary log-log model, use `proc genmod` with the option `dist=multimonial link=cumcll`.

4.3.6 R Implementation

The `clm()` function with the option `link="cloglog"` would fit the cumulative complement log-log model.

4.3.7 Example

EXAMPLE 4.3. We will fit the cumulative complementary log-log model to the data in Example 4.1. Referring to the data set `health_survey`, we run the following statements. The relevant output is also presented.

```
proc genmod;
class gender(ref="M") marital(ref="yes") educ(ref="HSgrad+");
model health=gender age marital educ/dist=multinomial
      link=cumcll;
format health $healthfmt.;
run;
```

```
Full Log Likelihood  -23.6572
AIC    63.3144
AICC   69.5753
BIC    75.0403
```

Analysis Of Maximum Likelihood Parameter Estimates

Parameter	Estimate	Pr > ChiSq
Intercept1	-9.2186	<.0001
Intercept2	-7.7333	<.0001
Intercept3	-4.7078	0.0003
gender F	1.2741	0.0239
age	0.0624	0.0046
marital no	2.2980	0.0029
educ <HS	2.2481	0.0034
educ HSgrad	0.9700	0.1353

```
proc genmod;
      model health=/dist=multinomial link=cumcll;
run;
```

```
Log Likelihood  -41.9644
```

```
data deviance_test;
      deviance=-2*(-41.9644-(-23.6572));
      pvalue=1-probchi(deviance,5);
run;
```

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

```
deviance      pvalue
36.6144  0.000000716
```

The fitted model takes the form: $\hat{\mathbb{P}}(\text{poor}) = 1 - \exp \left\{ - \exp \left\{ -9.2186 + 1.2741 \cdot \text{female} + 0.0624 \cdot \text{age} + 2.2980 \cdot \text{not married} + 2.2481 \cdot < HS + 0.9700 \cdot HSgrad \right\} \right\}$, $\hat{\mathbb{P}}(\text{poor, or fair}) = 1 - \exp \left\{ - \exp \left\{ -7.7333 + 1.2741 \cdot \text{female} + \right. \right.$

$0.0624 \cdot age + 2.2980 \cdot not\ married + 2.2481 \cdot < HS + 0.9700 \cdot HSgrad \}$, and
 $\hat{\mathbb{P}}(poor, fair, or good) = 1 - \exp \left\{ - \exp \left\{ -4.7078 + 1.2741 \cdot female + 0.0624 \cdot \right. \right.$
 $\left. age + 2.2980 \cdot not\ married + 2.2481 \cdot < HS + 0.9700 \cdot HSgrad \right\} \right\}.$

Like in the cumulative logit and probit models, in this model gender, age, marital status, and less than high school educational level are significant at the 5% level. The estimated probability of better health for women is that for men raised to the power $\exp \{1.2741\} = 3.5755$. For a one-year increase in age, this estimated probability is the old one raised to the power $\exp\{0.0624\} = 1.0644$. For a not married person, the estimated probability is that for a married one raised to the power $\exp\{2.2980\} = 9.9543$. For those with less than high school education, the estimated probability is the one for individuals with some college raised to the power $\exp\{2.2481\} = 9.4697$.

For a 52-year-old men who is married and has graduated from a high school, the predicted cumulative probabilities can be found as

$$\begin{aligned}\hat{\mathbb{P}}(poor) &= 1 - \exp \left\{ - \exp \left\{ -9.2186 + 0.0624 \cdot 52 + 0.9700 \right\} \right\} = 0.00669, \\ \hat{\mathbb{P}}(poor, or fair) &= 1 - \exp \left\{ - \exp \left\{ -7.7333 + 0.0624 \cdot 52 + 0.9700 \right\} \right\} = 0.02921, \\ \text{and} \\ \hat{\mathbb{P}}(poor, fair, or good) &= 1 - \exp \left\{ - \exp \left\{ -4.7078 + 0.0624 \cdot 52 + 0.9700 \right\} \right\} = 0.45708.\end{aligned}$$

The predicted probabilities for individual categories are computed as $\hat{\mathbb{P}}(poor) = 0.00669$, $\hat{\mathbb{P}}(fair) = 0.02921 - 0.00669 = 0.02252$, $\hat{\mathbb{P}}(good) = 0.45708 - 0.02921 = 0.42787$, and $\hat{\mathbb{P}}(excellent) = 1 - 0.45708 = 0.54292$. The same predictions for cumulative probabilities are made by SAS via the following statements:

```
data prediction;
input gender$ age marital$ educ$;
cards;
M 52 yes HSgrad
;

data health_survey;
set health_survey prediction;
run;
```

```

proc genmod;
class gender marital educ;
model health=gender age marital educ/dist=multinomial
      link=cumc11;
output out=outdata p=pred_prob;
format health $healthfmt.;
run;

proc print data=outdata (firstobs=97) noobs;
var _level_ pred_prob;
run;

```

LEVEL	pred_prob
1poor	0.00669
2fair	0.02921
3good	0.45708

The R script and the output for this example follow.

```

health.survey.data<- read.csv(file="./Example4.1Data.csv",
header=TRUE, sep=",")

#specifying reference categories
gender.rel<- relevel(health.survey.data$gender, ref="M")
marital.rel<- relevel(health.survey.data$marital, ref="yes")
educ.rel<- relevel(health.survey.data$educ, ref="HSgrad+")

#fitting cumulative complementary log-log model
library("ordinal")
summary(fitted.model<- clm(health ~ gender.rel + age
+ marital.rel + educ.rel, data=health.survey.data,
link="cloglog"))

AIC
63.31

Coefficients:

```

	Estimate	Pr(> z)
gender.relF	-1.27412	0.02392
age	-0.06240	0.00458
marital.relno	-2.29800	0.00288
educ.rel<HS	-2.24809	0.00337
educ.relHSgrad	-0.97005	0.13527

Threshold coefficients:

	Estimate
1poor 2fair	-9.219
2fair 3good	-7.733
3good 4excellent	-4.708

```
#extracting AICC and BIC for the fitted probit model
```

```
p<- 8
```

```
n<- 32
```

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

```
69.57525
```

```
BIC(fitted.model)
```

```
75.04027
```

```
#checking model fit
```

```
null.model<- clm(health ~ 1, data=health.survey.data,link="cloglog")
```

```
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
36.6145
```

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

```
7.155456e-07
```

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

```
print(predict(fitted.model, data.frame(gender.rel="M", age=52,  
marital.rel="yes", educ.rel="HSgrad"), type="prob"))
```

	1poor	2fair	3good	4excellent
1	0.006689841	0.02251738	0.4278729	0.5429199

The last thing we do in this example is to select the best-fitted model among the cumulative logit, probit, and complementary log-log models. Here we summarize the values for the AIC, AICC, and BIC criteria that were given in the outputs for these models.

	cumlogit	cumprobit	cumcloglog
AIC	64.15	64.24	63.31
AICC	70.4064	70.5035	69.5753
BIC	75.8714	75.9685	75.0403

The values are the smallest for the cumulative complementary log-log model, thus it fits the data the best and should be preferred over the other two models. □

4.4 Generalized Logit Model for Nominal Response

4.4.1 Model Definition

Suppose the response y is a nominal variable with categories $j = 1, \dots, c$. Let the category c be the reference category. The *generalized logit functions* pair each category with the reference category, that is,

$$\text{logit } \mathbb{P}(y = j) = \ln \frac{\mathbb{P}(y = j)}{\mathbb{P}(y = c)}, \quad j = 1, \dots, c - 1.$$

If, for example, $c = 3$, then

$$\text{logit } \mathbb{P}(y = 1) = \ln \frac{\mathbb{P}(y = 1)}{\mathbb{P}(y = 3)}, \quad \text{and} \quad \text{logit } \mathbb{P}(y = 2) = \ln \frac{\mathbb{P}(y = 2)}{\mathbb{P}(y = 3)}.$$

The *generalized logit model*⁴ for a nominal response y and predictors x_1, \dots, x_k is given by

$$\text{logit } \mathbb{P}(y = j) = \alpha_j + \beta_{j1} x_1 + \dots + \beta_{jk} x_k, \quad j = 1, \dots, c - 1.$$

Note that in this model all regression coefficients are different. There are $c - 1$ intercepts and $(c - 1)k$ beta coefficients. This model doesn't belong to the class of generalized linear regressions.

4.4.2 Fitted Model

Once the regression coefficients are estimated, the fitted model may be written as

$$\ln \frac{\widehat{\mathbb{P}}(y = j)}{\widehat{\mathbb{P}}(y = c)} = \widehat{\alpha}_j + \widehat{\beta}_{j1} x_1 + \dots + \widehat{\beta}_{jk} x_k, \quad j = 1, \dots, c - 1,$$

or, equivalently,

$$\frac{\widehat{\mathbb{P}}(y = j)}{\widehat{\mathbb{P}}(y = c)} = \exp \left\{ \widehat{\alpha}_j + \widehat{\beta}_{j1} x_1 + \dots + \widehat{\beta}_{jk} x_k \right\} \quad j = 1, \dots, c - 1. \quad (4.7)$$

⁴A common reference to the primary source is Agresti, A. (1990). “*Categorical Data Analysis*,” Wiley, New York.

4.4.3 Interpretation of Estimated Regression Coefficients

The estimated regression coefficients are interpreted as follows.

- If a predictor variable x_1 is numeric, then the quantity $(\exp\{\widehat{\beta}_{j1}\} - 1) \cdot 100\%$ represents the percent change in estimated odds of the event $\{y = j\}$ as opposed to $\{y = c\}$ for a unit increase in x_1 , controlling for all the other predictors. Indeed,

$$\begin{aligned} & \left(\frac{\widehat{\mathbb{P}}(y = j|x_1 + 1)/\widehat{\mathbb{P}}(y = c|x_1 + 1) - \widehat{\mathbb{P}}(y = j|x_1)/\widehat{\mathbb{P}}(y = c|x_1)}{\widehat{\mathbb{P}}(y = j|x_1)/\widehat{\mathbb{P}}(y = c|x_1)} \right) \cdot 100\% \\ &= \left(\frac{\exp\{\widehat{\alpha}_j + \widehat{\beta}_{j1}(x_1 + 1) + \widehat{\beta}_{j2}x_2 + \cdots + \widehat{\beta}_{jk}x_k\}}{\exp\{\widehat{\alpha}_j + \widehat{\beta}_{j1}x_1 + \widehat{\beta}_{j2}x_2 + \cdots + \widehat{\beta}_{jk}x_k\}} - 1 \right) \cdot 100\% \\ &= \left(\exp\{\widehat{\beta}_{j1}\} - 1 \right) \cdot 100\%. \end{aligned}$$

- If a predictor x_1 is a 0-1 variable, then $\exp\{\widehat{\beta}_{j1}\} \cdot 100\%$ gives the ratio of the estimated odds of $\{y = j\}$ versus $\{y = c\}$ for the levels $x_1 = 1$ and $x_1 = 0$, provided the other predictors stay unchanged. We write

$$\begin{aligned} & \left(\frac{\widehat{\mathbb{P}}(y = j|x_1 = 1)/\widehat{\mathbb{P}}(y = c|x_1 = 1)}{\widehat{\mathbb{P}}(y = j|x_1 = 0)/\widehat{\mathbb{P}}(y = c|x_1 = 0)} \right) \cdot 100\% \\ &= \frac{\exp\{\widehat{\alpha}_j + \widehat{\beta}_{j1} \cdot 1 + \widehat{\beta}_{j2}x_2 + \cdots + \widehat{\beta}_{jk}x_k\}}{\exp\{\widehat{\alpha}_j + \widehat{\beta}_{j1} \cdot 0 + \widehat{\beta}_{j2}x_2 + \cdots + \widehat{\beta}_{jk}x_k\}} \cdot 100\% = \exp\{\widehat{\beta}_{j1}\} \cdot 100\%. \end{aligned}$$

4.4.4 Predicted Probabilities

In view of (4.7), for a fixed set of predictors x_1^0, \dots, x_k^0 , the predicted probability that $y = j$, where $j = 1, \dots, c - 1$, is

$$\mathbb{P}^0(y = j) = \mathbb{P}^0(y = c) \exp \left\{ \widehat{\alpha}_j + \widehat{\beta}_{j1}x_1^0 + \cdots + \widehat{\beta}_{jk}x_k^0 \right\}, \quad (4.8)$$

and, since the probabilities must add up to one,

$$\mathbb{P}^0(y = c) = \left(1 + \sum_{j=1}^{c-1} \exp \left\{ \widehat{\alpha}_j + \widehat{\beta}_{j1}x_1^0 + \cdots + \widehat{\beta}_{jk}x_k^0 \right\} \right)^{-1}. \quad (4.9)$$

4.4.5 SAS Implementation

The generalized logit model may be fitted by using the `logistic` procedure with the option `link=glogit`. The syntax is:

```
proc logistic data=data_name;
  class catpredictor1_name (ref="level_name") catpredictor2_name
    (ref="level_name") .../param=ref;
model response_name(ref="level_name") = <list of predictors>/link=glogit;
  output out=outdata_name p=predicted_response_name;
run;
```

- The option `param=ref` must be included in the `class` statement in order for proper indicator functions to be created. If this option is omitted, then SAS creates variables that assume values 1 and -1 instead of 1 and 0.
- The reference level for the response variable can be specified in the model statement, if needed.

4.4.6 R Implementation

The function `multinom()` from the package `nnet` (stands for “neural networks”) may be used to fit the generalized logit model. The syntax is

```
summary(fitted.model.name <- multinom(response.name ~ x1.name + ...
+ xk.name, data=data.name))
```

4.4.7 Example

EXAMPLE 4.4. In a dental clinic, an oral hygienist surveys new patients in order to find out what factors influence their choice of toothpaste. For each patient, she records gender, age, the number of problematic teeth (teeth with fillings, root canals, or extracted), and the type of toothpaste used (tartar control, cavity protection, or for sensitive teeth). The following SAS code fits a generalized logit model for the choice of toothpaste.

```
data oral_hygiene;
  length choice$ 9.;
input ID gender$ age nteeth choice$ @@;
cards;
1 F 48 7 sensitive 2 M 30 5 cavity
```

```

3  M 34 6  tartar      4  M 50 8 sensitive
5  M 68 4  tartar      6  F 22 1 cavity
7  M 53 8  sensitive   8  F 38 2 cavity
9  M 36 7  sensitive   10 F 25 1 cavity
11 F 32 7  sensitive   12 F 54 2 tartar
13 M 32 8  sensitive   14 M 26 3 cavity
15 F 35 2  cavity      16 F 33 8 cavity
17 F 52 4  tartar      18 F 43 9 sensitive
19 M 58 2  tartar      20 F 43 3 cavity
21 F 60 6  tartar      22 M 28 3 tartar
23 M 70 10 sensitive   24 M 41 2 tartar
25 F 43 5  cavity      26 M 18 1 cavity
27 M 66 12 sensitive   28 M 34 2 sensitive
;

proc logistic;
  class gender(ref="M")/param=ref;
  model choice(ref="tartar")=gender age nteeth/link=glogit;
run;

```

The output is

```

Testing Global Null Hypothesis: BETA=0
Test          Chi-Square   DF    Pr > ChiSq
Likelihood Ratio    35.8586    6      <.0001

```

The p -value is extremely small compared to 0.05. Thus, the model has a good fit.

Analysis of Maximum Likelihood Estimates

Parameter	choice	Estimate	Pr > ChiSq
Intercept	cavity	9.7152	0.0310
Intercept	sensitive	-1.3987	0.6361
gender	F cavity	5.0207	0.0369
gender	F sensitive	0.4061	0.8106
age	cavity	-0.3176	0.0143
age	sensitive	-0.0903	0.2323
nteeth	cavity	0.00143	0.9976
nteeth	sensitive	0.9806	0.0164

The fitted model is

$$\frac{\hat{\mathbb{P}}(\text{cavity})}{\hat{\mathbb{P}}(\text{tartar})} = \exp \{ 9.7152 + 5.0207 \cdot \text{female} - 0.3176 \cdot \text{age} + 0.00143 \cdot \text{nteeth} \},$$

and

$$\frac{\widehat{\mathbb{P}}(sensitive)}{\widehat{\mathbb{P}}(tartar)} = \exp \{ -1.3987 + 0.4061 \cdot female - 0.0903 \cdot age + 0.9806 \cdot nteeth \}.$$

Gender and age are significant predictors of odds in favor of cavity protection versus tartar control toothpaste, since both p -values are less than 0.05. The estimated odds in favor of cavity protection versus tartar control toothpaste for women is $\exp\{5.0207\} \cdot 100\% = 15,151.73\%$ of those for men. Also, as age increases by one year, the estimated odds change by $(\exp\{-0.3176\} - 1) \cdot 100\% = -27.21\%$, that is, decrease by 27.21%.

The number of problematic teeth is the only significant predictor of odds in favor of toothpaste for sensitive teeth versus tartar control toothpaste, since its p -value is less than 0.05. As the number of problematic teeth increases by one, the estimated odds grow by $(\exp\{0.9806\} - 1) \cdot 100\% = 166.61\%$.

To estimate the probabilities of choosing each type of toothpaste by a 49-year-old male patient with seven problematic teeth, we compute $\mathbb{P}^0(cavity) = \exp\{9.7152 - 0.3176 \cdot 49 + 0.00143 \cdot 7\} / (1 + \exp\{9.7152 - 0.3176 \cdot 49 + 0.00143 \cdot 7\} + \exp\{-1.3987 - 0.0903 \cdot 49 + 0.9806 \cdot 7\})^{-1} = 0.00076$, $\mathbb{P}^0(sensitive) = \exp\{-1.3987 - 0.0903 \cdot 49 + 0.9806 \cdot 7\} / (1 + \exp\{9.7152 - 0.3176 \cdot 49 + 0.00143 \cdot 7\} + \exp\{-1.3987 - 0.0903 \cdot 49 + 0.9806 \cdot 7\})^{-1} = 0.73844$, $\mathbb{P}^0(tartar) = (1 + \exp\{9.7152 - 0.3176 \cdot 49 + 0.00143 \cdot 7\} + \exp\{-1.3987 - 0.0903 \cdot 49 + 0.9806 \cdot 7\})^{-1} = 0.26080$.

SAS outputs similar predicted values, which can be checked by running the following lines of code.

```
data prediction;
input gender$ age nteeth;
cards;
M 49 7
;

data oral_hygiene;
set oral_hygiene prediction;
run;

proc logistic;
class gender;
model choice=gender age nteeth/link=glogit;
```

```

    output out=outdata p=pred_prob;
run;

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

```

The output is:

<code>_LEVEL_</code>	<code>pred_prob</code>
cavity	0.00076
sensitive	0.73839
tartar	0.26085

The statements in R that produce the same results as in SAS and the corresponding relevant outputs are located below.

```

oralhygiene.data<-read.csv(file="./Example4.4Data.csv",
header=TRUE, sep=",")

#specifying reference categories
gender.rel<- relevel(oralhygiene.data$gender, ref="M")
choice.rel<- relevel(oralhygiene.data$choice, ref="tartar")

#fitting generalized logits model
library(nnet)
summary(fitted.model<- multinom(choice.rel ~ gender.rel + age + nteeth,
data = oralhygiene.data))

Coefficients:
            (Intercept)  gender.relF      age      nteeth
cavity      9.715717   5.0209204 -0.3175656 0.001382412
sensitive  -1.398798   0.4061775 -0.0903070 0.980622823

#checking model fit
summary(intercept.model<- multinom(choice.rel ~ 1,data=oralhygiene.data))
print(deviance<- deviance(intercept.model)
-deviance(fitted.model))

35.85856

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

```

2.936716e-06

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(gender.rel="M",
age=49, nteeth=7), type="prob"))
```

```
          tartar          cavity          sensitive
0.2608508757 0.0007623345 0.7383867899
```

□

Exercises for Chapter 4

EXERCISE 4.1. Grade point average (GPA) and graduate management aptitude test (GMAT) scores are used by admission office of a business school to decide which applicant should be admitted to the school's graduate program. The data below are GPA and GMAT scores for 42 recent applicants who have been categorized as admitted, borderline, or not admitted.

GPA	GMAT	status	GPA	GMAT	status	GPA	GMAT	status
2.96	596	admit	3.47	552	admit	3.12	463	border
3.14	473	admit	3.35	520	admit	3.08	440	notadmit
3.22	482	admit	2.89	543	admit	3.01	453	notadmit
3.29	527	admit	2.28	523	admit	3.03	414	notadmit
3.69	505	admit	3.21	530	admit	3.04	446	notadmit
2.46	693	admit	3.58	564	admit	2.89	485	notadmit
3.03	626	admit	3.33	565	admit	2.79	490	notadmit
3.19	663	admit	2.8	444	border	2.54	446	notadmit
3.63	447	admit	3.13	416	border	2.43	425	notadmit
3.59	588	admit	2.89	431	border	2.2	474	notadmit
3.3	563	admit	3.01	471	border	3.36	531	notadmit
3.78	591	admit	2.91	446	border	2.57	542	notadmit
3.44	692	admit	2.75	546	border	2.36	482	notadmit
3.48	528	admit	2.73	467	border	3.66	420	notadmit

- 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.
- Redo part (a), fitting the cumulative probit model.
- Redo part (a), fitting the cumulative complementary log-log model.
- Which of the models obtained in parts (a)-(c) has the best fit?

EXERCISE 4.2. A satellite television provider is focusing on improving customer service. The company surveys subscribers who contact the call center and record how long the callers have been subscribed with the company (in months), whether they receive their monthly programming magazine (yes/no), whether the issue they called about was resolved (yes/no), and overall satisfaction with the customer service, measured on a five-point Likert scale (1=very dissatisfied, 2=dissatisfied, 3=neutral, 4=satisfied, 5=very satisfied). The data for 36 callers are recorded below.

Subscr	Magzn	Resolved	Satisf	Subscr	Magzn	Resolved	Satisf
5	yes	no	5	2	no	yes	4
49	yes	no	5	11	no	no	2
56	no	no	3	98	yes	yes	5
13	yes	yes	5	11	no	yes	5
27	no	yes	4	46	no	no	4
41	yes	yes	5	7	no	no	3
2	yes	yes	5	7	no	yes	5
64	yes	yes	4	9	yes	yes	5
88	yes	yes	4	17	no	no	2
43	yes	yes	4	8	no	yes	2
94	yes	no	4	9	no	yes	1
8	no	no	1	95	no	no	4
9	yes	no	2	60	no	yes	3
68	yes	no	4	80	no	yes	4
5	no	yes	2	2	yes	no	3
108	no	yes	3	33	yes	yes	4
21	yes	yes	4	5	yes	no	3
25	yes	no	3	7	no	no	1

- 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.
- Redo part (a), running the cumulative probit model.
- Redo part (a), running the cumulative complementary log-log model.
- Discuss the relative fit of the models obtained in parts (a)-(c).

EXERCISE 4.3. A large office supply corporation has collected data on purchasing habits of their customers (which are companies). The data for a sample of 34 companies that purchased products during one-month period are made available. The record is kept on how long the company has been

in business (<1 year, 1-5 years, or 5+ years), whether it is a first-time buyer (yes/no), what type of supply is bought (stationary, electronics, or furniture), and the amount of money spent (in U.S. dollars). The data are:

In business	1st time	Type	Amount	In business	1st time	Type	Amount
< 1 year	yes	stationary	\$5,690	1-5 years	no	electronics	\$24,336
1-5 years	yes	stationary	\$14,454	5+ years	yes	stationary	\$452
5+ years	yes	electronics	\$20,489	< 1 year	yes	stationary	\$3,600
5+ years	no	stationary	\$13,115	5+ years	yes	furniture	\$2,450
< 1 year	no	electronics	\$44,885	< 1 year	no	electronics	\$12,230
< 1 year	no	electronics	\$28,182	5+ years	yes	stationary	\$2,451
< 1 year	no	furniture	\$40,982	1-5 years	no	stationary	\$1,110
< 1 year	no	stationary	\$10,160	< 1 year	yes	electronics	\$69,280
1-5 years	no	furniture	\$51,363	< 1 year	yes	furniture	\$119,613
5+ years	yes	electronics	\$29,448	< 1 year	no	electronics	\$21,770
5+ years	no	stationary	\$2,093	< 1 year	yes	electronics	\$64,160
< 1 year	no	furniture	\$127,133	< 1 year	no	furniture	\$78,900
1-5 years	yes	furniture	\$21,593	< 1 year	no	electronics	\$75,095
< 1 year	no	furniture	\$220,909	5+ years	no	furniture	\$7,450
1-5 years	no	electronics	\$17,000	5+ years	no	furniture	\$5,200
1-5 years	yes	electronics	\$22,812	< 1 year	no	furniture	\$32,099
1-5 years	yes	electronics	\$13,090	5+ years	no	electronics	\$1,997

- Categorize the amount spent into the three categories: (1) "<\$10,000", (2) "\$10,000– <\$30,000", and (3) "\$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.
- Fit a cumulative probit model to the data, and answer the questions in part (a).
- Repeat part (a) with a cumulative complementary log-log model.
- Which of the three fitted models has the best fit?

EXERCISE 4.4. In aviation, the weather forecast often plays a decisive role. A data set for 30 large airports around the country was obtained. The independent variables are airport elevation (in feet above the sea level), its proximity to a large body of water (whether within 20 miles of lake, sea, or ocean), wind direction (in degrees, clockwise from north), and wind speed (in knots=1.15mph). The dependent variable is the outcome of the weather forecast: correct prediction, false alarm (when the actual conditions were better than predicted), or failure to detect (when the actual conditions were worse than predicted). The measurements are as follows:

Elev	Water	Wdir	Wspeed	Outcome	Elev	Water	Wdir	Wspeed	Outcome
146	yes	270	2	FA	1026	no	290	1	C
841	no	360	13	FA	17	yes	180	2	C
672	yes	360	4	FA	20	yes	270	6	C
312	no	250	5	FA	15	yes	0	3	C
126	yes	170	8	FA	1135	no	20	13	C
607	no	360	8	FA	21	yes	30	8	C
748	no	270	15	FA	98	no	140	8	C
620	yes	290	5	FA	36	yes	10	3	C
5431	no	200	2	FD	8	yes	270	10	C
2181	yes	310	8	FD	26	yes	0	3	C
645	yes	170	7	FD	13	yes	170	9	C
433	no	270	6	FD	9	yes	270	6	C
360	no	140	15	FD	18	yes	200	12	C
4227	yes	200	2	FD	96	no	200	8	C
14	yes	150	7	C	60	yes	240	9	C

- (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.
- (b) How good is the model fit? Which variables are significant predictors at the 10% level of significance?
- (c) Give interpretation of the estimated significant coefficients.
- (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.

EXERCISE 4.5. A group of 25 school-age patients in an orthopedic clinic are studied and their age, gender and ankle condition (sprained, torn ligament, or broken) are recorded. The data are

Age	Gender	Condition	Age	Gender	Condition
7	female	sprained	10	female	sprained
9	male	torn	9	female	torn
11	male	broken	8	male	sprained
12	male	broken	8	female	sprained
8	male	torn	7	female	torn
8	female	torn	15	male	broken
9	female	broken	17	male	broken
13	male	broken	18	male	broken
13	male	torn	18	female	sprained
15	female	sprained	18	female	torn
16	female	sprained	16	female	torn
11	male	torn	12	male	broken
12	male	broken			

- 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.
- Write down the estimated model. Discuss its goodness-of-fit.
- Interpret the estimates of the regression coefficients that significantly differ from zero.
- What are the predicted probabilities of each type of ankle injury for a 9-year-old girl?

EXERCISE 4.6. A sample of 40 female users who were matched with male candidates was obtained from a dating website. The following variables were computed: communication status (0 if neither sent messages, 1 if the user sent a message, 2 if the candidate sent a message, and 3 if they exchanged messages), age difference between the user and candidate (in years), their height difference (in inches), and an indicator of same drinking preferences (1=same, 0=different). The data are presented in the table below.

Status	Agediff	Heightdiff	Drinking	Status	Agediff	Heightdiff	Drinking
3	-3	-1	0	2	0	-7	1
3	3	-2	1	2	4	-3	0
3	2	-3	1	1	8	-7	1
3	0	1	1	1	1	0	1
3	-5	0	1	1	11	0	0
3	-6	-6	1	1	-4	-7	0
3	2	-5	1	1	7	-6	1
3	0	-4	1	1	14	-6	1
3	4	-7	1	1	-1	-8	0
3	-1	-8	1	1	-5	-4	0
3	-5	1	1	1	-1	-7	0
3	-2	2	1	1	-3	-8	1
3	-6	-4	1	1	8	-4	1
3	-7	-6	0	1	4	-5	1
2	-5	-1	0	0	4	-8	1
2	-18	0	1	0	-6	3	0
2	-8	3	0	0	-4	3	0
2	4	0	1	0	8	-2	0
2	-4	2	1	0	-5	3	1
2	1	-8	1	0	-6	3	0

- 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.
- Evaluate goodness-of-fit of the model. What predictors are significant at the 5% level of significance?
- Give interpretation of the estimated significant beta coefficients.
- Find the predicted probabilities for each communication status for the case of the same age, height, and drinking preference.

Chapter 5

Regression Models for Count Response

Suppose the response variable y assumes values $0, 1, 2, \dots$, but large values are very unlikely. In this chapter we consider four regressions that may be applied to model this response: Poisson regression, zero-truncated Poisson (if y is strictly positive), zero-inflated Poisson (if zero is an allowed value for y , and, moreover, there are too many zeros observed than can be accounted for by the Poisson distribution), and hurdle Poisson (where zeros are modeled separately from the positive values of y).

5.1 Poisson Regression Model

5.1.1 Model Definition

A variable that assumes only non-negative integer values ($0, 1, 2, \dots$) is called a *count variable*. When the response is a count variable which follows a Poisson distribution, the data may be modeled using a Poisson regression. The *Poisson regression model*¹ specifies that given predictors x_1, \dots, x_k , the response variable y follows a Poisson distribution with the probability mass function

$$\mathbb{P}(Y = y) = \frac{\lambda^y \exp\{-\lambda\}}{y!}, \quad y = 0, 1, 2, \dots,$$

¹The first application appears in Cochran, W.G. (1940). “The analysis of variance when experimental errors follow the Poisson or binomial law”. *Annals of Mathematical Statistics*, 11(3): 335 – 347.

where the rate

$$\lambda = \mathbb{E}(y) = \exp \{ \beta_0 + \beta_1 x_1 + \cdots + \beta_k x_k \}. \quad (5.1)$$

This model belongs to the class of generalized linear models with the log link function. It can be shown (do it!) that the above function can be written in the form (1.3) with $\theta = \ln \lambda$ and $\phi = 1$.

5.1.2 Fitted Model

By (5.1), in a fitted Poisson regression model, the estimated mean response has the form

$$\hat{\lambda} = \exp \{ \hat{\beta}_0 + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_k x_k \}. \quad (5.2)$$

5.1.3 Interpretation of Estimated Regression Coefficients

From (5.2), in the Poisson regression model, the estimates of the regression coefficients are interpreted as follows.

- If a predictor variable x_1 is numeric, then the exponentiated estimate of the respective regression coefficient $\exp\{\hat{\beta}_1\}$ represents an estimated *rate ratio* corresponding to a unit increase in the predictor. Indeed,

$$\frac{\hat{\lambda}|_{x_1+1}}{\hat{\lambda}|_{x_1}} = \frac{\exp \{ \hat{\beta}_0 + \hat{\beta}_1 (x_1 + 1) + \hat{\beta}_2 x_2 + \cdots + \hat{\beta}_k x_k \}}{\exp \{ \hat{\beta}_0 + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_k x_k \}} = \exp \{ \hat{\beta}_1 \}.$$

Equivalently, $(\exp\{\hat{\beta}_1\} - 1) \cdot 100\%$ may be interpreted as the estimated percent change in rate when x_1 increases by one unit, while all the other predictors are held fixed.

- If a predictor variable x_1 is an indicator variable, then the exponentiated estimated coefficient $\exp\{\hat{\beta}_1\}$ represents the ratio of the estimated rates when $x_1 = 1$ and when $x_1 = 0$. To see that, we write

$$\frac{\hat{\lambda}|_{x_1=1}}{\hat{\lambda}|_{x_1=0}} = \frac{\exp \{ \hat{\beta}_0 + \hat{\beta}_1 \cdot 1 + \hat{\beta}_2 x_2 + \cdots + \hat{\beta}_k x_k \}}{\exp \{ \hat{\beta}_0 + \hat{\beta}_1 \cdot 0 + \cdots + \hat{\beta}_k x_k \}} = \exp \{ \hat{\beta}_1 \}.$$

Equivalently, the quantity $\exp\{\hat{\beta}_1\} \cdot 100\%$ represents the estimated percent ratio of rates when $x_1 = 1$ and when $x_1 = 0$, while the other predictors are held constant.

5.1.4 Predicted Response

Taking into account (5.2), for a given set of predictors x_1^0, \dots, x_k^0 , the predicted response y^0 is computed as $y^0 = \exp \{ \hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \dots + \hat{\beta}_k x_k^0 \}$.

5.1.5 SAS Implementation

In SAS, the procedure `genmod` with the option `dist=poisson link=log` is used to fit a Poisson regression model.

5.1.6 R Implementation

In R, the function `glm()` with the option `family="poisson"(link=log)` fits a Poisson regression model.

5.1.7 Example

EXAMPLE 5.1. Number of days of hospital stay was recorded for 45 patients with chest pain, along with their gender, age, and history of chronic cardiac illness. We regress the number of days on the other variables via a Poisson regression model. To this end, we run the following SAS code:

```
data hospital_stay;
input days gender$ age illness$ @@;
cards;
1 F 31 yes 0 F 28 no 0 M 52 yes
1 M 72 yes 0 F 29 no 0 F 30 no
1 M 74 no 2 M 30 yes 2 F 72 no
1 M 58 no 2 F 28 no 2 F 65 no
2 M 65 no 1 M 52 no 4 M 51 no
2 F 63 no 0 F 31 no 1 F 47 yes
1 M 49 no 2 M 71 yes 2 M 48 no
2 F 47 no 0 F 31 no 3 M 44 yes
3 M 44 no 3 M 54 yes 4 F 72 yes
4 M 56 yes 3 F 73 yes 1 F 46 no
3 M 58 no 4 M 70 yes 2 M 36 no
1 M 50 no 1 M 59 no 0 M 52 no
6 M 68 yes 2 F 41 no 1 M 31 yes
1 M 69 no 3 M 73 no 3 F 77 yes
2 F 54 no 4 M 69 yes 5 M 68 yes
;
```

```
proc genmod;
class gender(ref="F") illness(ref="no");
  model days=gender age illness/dist=poisson link=log;
run;
```

The relevant output is:

Full Log Likelihood -68.2139

Analysis Of Maximum Likelihood Parameter Estimates

Parameter	Estimate	Pr > ChiSq
Intercept	-0.8263	0.0789
gender M	0.2264	0.3315
age	0.0205	0.0093
illness yes	0.4477	0.0440

```
proc genmod;
  model days=/dist=poisson link=log;
run;
```

Full Log Likelihood -77.0978

```
data deviance_test;
  deviance=-2*(-77.0978-(-68.2139));
  pvalue=1-probchi(deviance,3);
run;
```

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

deviance	pvalue
17.7678	0.000491110

In the fitted model, the estimated rate is $\hat{\lambda} = \exp \{ -0.8263 + 0.2264 \cdot \text{male} + 0.0205 \cdot \text{age} + 0.4477 \cdot \text{illness} \}$. The p -value in the deviance test is less than 0.05, and so the model has a good fit. Patient's age and indicator of a chronic cardiac illness are significant predictors of average length of stay at the 5% significance level. For a one-year increase in patient's age, the estimated average number of days of hospital stay increases by $(\exp\{0.0205\} - 1) \cdot 100\% = 2.07\%$. Also, the estimated average number of days of hospital stay for patients with a chronic cardiac illness is $\exp\{0.4477\} \cdot 100\% = 156.47\%$ of that

for patients without it.

The predicted length of stay for a 55-year old male with no chronic cardiac illness is computed as $y^0 = \exp \{ -0.8263 + 0.2264 + 0.0205 \cdot 55 \} = 1.6949$. This value can be verified in SAS by running the following statements:

```
data prediction;
input gender$ age illness$;
cards;
M 55 no
;

data hospital_stay;
set hospital_stay prediction;
run;

proc genmod;
class gender illness;
model days=gender age illness/dist=poissonlink=log;
output out=outdata p=pred_days;
run;

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

pred_days
1.69207
```

The R script and the relevant output are given below.

```
hospitalstay.data<-read.csv(file="./Example5.1Data.csv",
header=TRUE, sep=",")

#fitting Poisson model
summary(fitted.model<- glm(days ~ gender + age + illness,
data=hospitalstay.data, family=poisson(link=log)))
```

Coefficients:

	Estimate	Pr(> z)
(Intercept)	-0.826269	0.07888
genderM	0.226425	0.33145

```

age          0.020469  0.00931
illnessyes   0.447653  0.04404

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

17.76773

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

0.0004911253

#using fitted model for prediction
print(predict(fitted.model, data.frame(gender="M", age=55, illness="no"),
type="response"))

1.692066

□

```

5.2 Zero-truncated Poisson Regression Model

5.2.1 Model Definition

If the response variable y assumes only positive integer values (no zeros), then the data may be modeled by means of a *zero-truncated Poisson regression model*². Let x_1, \dots, x_k be the predictors in this model. Then the response variable y follows a zero-truncated Poisson distribution with the probability mass function

$$\mathbb{P}(Y = y) = \frac{\lambda^y \exp\{-\lambda\}}{y! (1 - \exp\{-\lambda\})}, \quad y = 1, 2, \dots,$$

where

$$\lambda = \exp \{ \beta_0 + \beta_1 x_1 + \dots + \beta_k x_k \}. \quad (5.3)$$

For a zero-truncated Poisson distribution, the expected value of y is (show it!)

$$\mathbb{E}(y) = \frac{\lambda}{1 - \exp\{-\lambda\}}, \quad (5.4)$$

and, even though, the probability mass function belongs to the exponential family of distributions, this regression is not a generalized linear model because the log link function in (5.3) relates linear regression to λ which is not the expected value of y .

²Introduced in Gurmu, S. (1991). "Tests for detecting overdispersion in the positive Poisson regression model". *Journal of Business and Economic Statistics*, 9(2): 215 – 222.

5.2.2 Fitted Model

In a fitted zero-truncated Poisson regression model, according to (5.3), the estimate of λ is written as

$$\widehat{\lambda} = \exp \{ \widehat{\beta}_0 + \widehat{\beta}_1 x_1 + \cdots + \widehat{\beta}_k x_k \}. \quad (5.5)$$

5.2.3 Interpretation of Estimated Regression Coefficients

The formula for the expected value of y (5.4) contains an exponentiated λ . Since by (5.3) λ itself is an exponential function, this expected value may be assumed negligibly different from λ for most values of λ . Hence, the way the estimated regression coefficients are interpreted in the fitted Poisson regression model (see Subsection 5.1.3) remains in effect.

5.2.4 Predicted Response

In view of (5.4) and (5.5), for some given values x_1^0, \dots, x_k^0 , the predicted response y^0 is found as

$$y^0 = \frac{\exp \{ \widehat{\beta}_0 + \widehat{\beta}_1 x_1^0 + \cdots + \widehat{\beta}_k x_k^0 \}}{1 - \exp \{ - \exp \{ \widehat{\beta}_0 + \widehat{\beta}_1 x_1^0 + \cdots + \widehat{\beta}_k x_k^0 \} \}}.$$

5.2.5 SAS Implementation

The procedure `fmm` (stands for “finite mixture models”) with the option `dist=truncpoisson` in the model statement may be used to fit a zero-truncated Poisson model. The following syntax invokes the procedure:

```
proc fmm data=data_name;
  class <list of categorical predictors>;
  model response_name=<list of predictors>/dist=truncpoisson;
  output out=outdata_name pred=predicted_response_name;
run;
```

For categorical predictors, the level that comes last in alphabetical order is used for reference. The `fmm` procedure doesn't allow specification of reference categories in the `class` statement. It can be done by changing the format of categorical variables in a `proc format` statement.

5.2.6 R Implementation

In R, the function `vglm()` (stands for “vector generalized linear models”) in the library `VGAM` (“Vector Generalized Linear and Additive Models”) is used to fit a zero-truncated Poisson model. The general form of this function is

```
summary(fitted.model.name<- vglm(response.name ~ x1.name + ...  
+ xk.name, data=data.name, family=pospoisson()))
```

- The function `pospoisson()` fits a positive Poisson distribution, that is, the zero-truncated Poisson.

5.2.7 Example

EXAMPLE 5.2. Consider the setting in Example 5.1. Suppose investigators are not concerned with outpatients, that is, those who were treated and dismissed the same day. Hence, the data are reduced to the 38 patients who spent at least one day in the hospital. We run a zero-truncated Poisson model with the three predictor variables along with the intercept-only model to check the fit. The SAS code and respective outputs are:

```
data hospital_days;  
  set hospital_stay;  
  if (days>0);  
run;
```

```
proc format;  
value $genderfmt "F"="ref_F";  
value $illnessfmt "yes"="illness" "no"="ref";  
run;
```

```
proc fmm;  
class gender illness;  
model days=gender age illness/dist=truncpoisson;  
format gender $genderfmt. illness $illnessfmt.;  
run;
```

-2 Log Likelihood 105.2

Parameter Estimates for Truncated Poisson Model

Effect	gender illness	Estimate	Pr > z
Intercept		-0.7041	0.2797

gender	M	0.2146	0.4559
gender	ref	0	.
age		0.01604	0.1056
illness	illness	0.5903	0.0296
illness	ref	0	.

```
proc fmm;
  model days=/dist=truncpoisson;
run;
```

-2 Log Likelihood 115.2

```
data deviance_test;
  deviance=115.2-105.2;
  pvalue=1-probchi(deviance,3);
run;
```

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

```
deviance    pvalue
      10 0.018566
```

In the fitted model, the estimated rate is $\hat{\lambda} = \exp \{ -0.7041 + 0.2146 \cdot \text{male} + 0.01604 \cdot \text{age} + 0.5903 \cdot \text{illness} \}$. The p -value in the goodness-of-fit test is smaller than 0.05, confirming that the model fits the data well. Only presence of chronic cardiac illness is significant at the 5% level. The estimated average number of days of hospital stay for patients with a chronic cardiac illness is $\exp\{0.5903\} \cdot 100\% = 180.45\%$ of that for patients without it.

To predict the number of days of hospital stay for a 55-year old male without a chronic cardiac illness, we calculate

$$y^0 = \frac{\exp \{ -0.7041 + 0.2146 + 0.01604 \cdot 55 \}}{1 - \exp \{ -\exp \{ -0.7041 + 0.2146 + 0.01604 \cdot 55 \} \}} = 1.9169.$$

A similar result may be obtained from SAS by running these lines of code:

```
data prediction;
input gender$ age illness$;
cards;
M 55 no
;
```

```

data hospital_days;
  set hospital_days prediction;
run;

proc fmm;
class gender illness;
  model days=gender age illness/dist=truncpoisson;
  output out=outdata pred=pred_days;
run;

proc print data=outdata(firstobs=39) noobs;
var pred_days;
run;

pred_days
  1.91706

```

R script and output for this example are presented below.

```

hospitalstay.data<- read.csv(file="./Example5.1Data.csv",
header=TRUE, sep=",")

#eliminating zeros from the original data set
hospitaldays.data<- hospitalstay.data[which(hospitalstay.data$days!=0),]

#fitting zero-truncated Poisson model
library(VGAM)
summary(fitted.model<- vglm(days ~ gender + age + illness,
data=hospitaldays.data, family=pospoisson()))

Coefficients:
              Estimate Pr(>|z|)
(Intercept) -0.704061  0.2797
genderM      0.214611  0.4558
age          0.016042  0.1056
illnessyes   0.590345  0.0296

#checking model fit
null.model<- vglm(days ~ 1, data=hospitaldays.data, family=pospoisson())
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))

```

9.993755

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

0.0186193

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(gender="M", age=55, illness="no"),
type="response"))
```

1.917057

□

5.3 Zero-inflated Poisson Regression Model

5.3.1 Model Definition

Suppose that one of the variables recorded during a health survey was the number of cigarettes the respondent smoked yesterday. Some respondents may have reported zero number of cigarettes smoked. There are two possible scenarios: either the respondents do not smoke at all, or they happened not to smoke a single cigarette that day. That is, the observed zero may be either a *structural zero*, when the respondent's behavior lies outside of the behavioral repertoire under study (for example, a person doesn't smoke), or a *chance zero*, when the respondent's typical behavior falls within the behavioral range under study, but just not during a particular time period (in this case, a person normally smokes at least one cigarette a day, but just happened not to smoke yesterday).

The presence of structural zeros inflates the number of zeros in the Poisson model, which makes the Poisson model invalid, and a *zero-inflated Poisson model* (often abbreviated as ZIP) should be used instead. The ZIP model attempts to separate the structural zeros from the chance zeros, by viewing the response variable y as assuming the value zero with probability π (the case of a structural zero), and otherwise, with probability $1 - \pi$, being a count variable with the Poisson distribution with rate λ .

To increase the rigor, in the *zero-inflated Poisson regression model*³ with the predictor variables x_1, \dots, x_k , the response variable y has a probability distribution defined as follows:

³Introduced in Lambert, D. (1992). "Zero-inflated Poisson regression, with an application to defects in manufacturing". *Technometrics*, 34(1): 1 – 14.

$$\mathbb{P}(Y = y) = \begin{cases} \pi + (1 - \pi) \exp\{-\lambda\}, & \text{if } y = 0, \\ (1 - \pi) \frac{\lambda^y \exp\{-\lambda\}}{y!}, & \text{if } y = 1, 2, \dots, \end{cases} \quad (5.6)$$

where

$$\pi = \frac{\exp\{\beta_0 + \beta_1 x_1 + \dots + \beta_m x_m\}}{1 + \exp\{\beta_0 + \beta_1 x_1 + \dots + \beta_m x_m\}}, \quad (5.7)$$

and

$$\lambda = \exp\{\gamma_0 + \gamma_1 x_{m+1} + \dots + \gamma_{k-m} x_k\}. \quad (5.8)$$

Here the first m of the predictor variables are being used to model the probability of a structural zero π , while the rest of the x variables are used as predictors for the Poisson rate λ . The β and γ coefficients are the parameters of this model.

The zero-inflated Poisson distribution defined in (5.6) is a mixture of two distributions: a Poisson and a point mass at zero. This type of distribution is not a representative of the exponential family of distributions. Consequently, the zero-inflated Poisson model is not a member of the class of generalized linear models.

5.3.2 Fitted Model

By (5.7) and (5.8), in the fitted zero-inflated Poisson regression model, the estimated parameters are

$$\hat{\pi} = \frac{\exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1 + \dots + \hat{\beta}_m x_m\}}{1 + \exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1 + \dots + \hat{\beta}_m x_m\}}, \quad (5.9)$$

and

$$\hat{\lambda} = \exp\{\hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1} + \dots + \hat{\gamma}_{k-m} x_k\}. \quad (5.10)$$

5.3.3 Interpretation of Estimated Regression Coefficients

Since in the zero-inflated Poisson model the probability π is modeled via a logistic link function, the interpretation of the estimated beta coefficients is identical to those in a binary logistic regression model (see Subsection 3.1.3). Also, the expected value of the response variable y is $\mathbb{E}(y) = (1 - \pi)\lambda$ (see Exercise 5.7), and the sets of x variables in the definitions of π and λ are chosen to be non-overlapping. This implies that when we are interpreting the estimated gamma coefficients, we may assume that π is fixed, and thus the interpretation is the same as in the Poisson regression model (see Subsection

5.1.3). Note that it is possible to use the same x variables in the regression parts of π and λ , but the estimates of the regression coefficients won't be easily interpretable.

5.3.4 Predicted Response

In view of the above expression for $\mathbb{E}(y)$ and formulas (5.9) and (5.10), when $x_1^0, x_2^0, \dots, x_k^0$ are fixed, the predicted response y^0 is computed as

$$y^0 = \left(1 - \frac{\exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \dots + \hat{\beta}_m x_m^0\}}{1 + \exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \dots + \hat{\beta}_m x_m^0\}}\right) \exp\{\hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1}^0 + \dots + \hat{\gamma}_{k-m} x_k^0\}. \quad (5.11)$$

5.3.5 SAS Implementation

The ZIP model may be requested in SAS by adding an option `dist=zip` to the `model` statement of the `genmod` procedure, and including the `zeromodel` statement. The general syntax is

```
proc genmod data=data_name;
  class <list of categorical predictors>;
  model response_name = <list of predictors>/dist=zip;
  zeromodel <list of predictors of structural zeros>;
run;
```

5.3.6 R Implementation

Function `zeroinfl()` in the library `pscl`, which stands for “Political Science Computational Laboratory”, is used to fit a zero-inflated Poisson model in R. The general form of this function is

```
summary(fitted.model.name<- zeroinfl(response.name ~ x{m+1}.name
+ ... + xk.name|x1.name + ... + xm.name, data = data.name))
```

5.3.7 Example

EXAMPLE 5.3. A health survey was been administered to a random sample of 40 people aged between 25 and 50. Their gender, self-reported health

condition (excellent or good), age, and the number of cigarettes they smoked yesterday were recorded. Since those respondents who don't smoke were included in the survey, it is expected that the number of cigarettes smoked would have a Poisson distribution with inflated number of zeros. Below we fit a ZIP model where health condition is used as the predictor of structural zero, while gender and age are the count model predictors. The SAS code and output are:

```
data smoking;
input gender$ health$ age cigarettes @@;
cards;
M good    34 3   F exclnt 48 1   M exclnt 26 0   M good    39 0
F good    27 1   M good    28 5   F good    44 1   M exclnt 30 0
F exclnt 26 0   F good    38 2   F good    40 1   F exclnt 31 0
M good    27 3   F exclnt 34 1   F good    36 2   F exclnt 34 2
F exclnt 39 0   F good    42 1   F good    48 4   M good    32 5
M good    47 2   M good    29 3   M exclnt 38 0   F good    50 4
M good    30 3   M good    38 2   M good    31 6   F exclnt 33 0
F good    28 0   F good    42 3   M exclnt 28 0   M good    31 2
F exclnt 31 0   F exclnt 42 0   F good    44 4   F good    39 1
M good    40 6   M good    39 3   M exclnt 25 0   F good    45 2
;
```

```
proc genmod;
class gender(ref="F") health(ref="good");
model cigarettes=gender age/dist=zip;
zeromodel health;
run;
```

Log Likelihood -57.0406

Analysis Of Maximum Likelihood Parameter Estimates

Parameter	Estimate	Pr > ChiSq
Intercept	-0.1381	0.8692
gender M	0.7268	0.0107
gender F	0.0000	.
age	0.0186	0.3509

Analysis Of Maximum Likelihood Zero Inflation Parameter Estimates

Parameter	Estimate	Pr > ChiSq
Intercept	-3.7950	0.0876
health exclnt	4.9195	0.0341
health good	0.0000	.

```

proc genmod;
  model cigarettes=/dist=zip;
  zeromodel;
run;

Full Log Likelihood  -71.3892

data deviance_test;
  deviance=-2*(-71.3892-(-57.0406));
  pvalue=1-probchi(deviance,3);
run;

proc print noobs;
run;

deviance      pvalue
28.6972  0.000002593

```

From this output, the fitted regression model has estimated parameters

$$\hat{\pi} = \frac{\exp\{-3.7950 + 4.9195 \cdot \text{excellent_health}\}}{1 + \exp\{-3.7950 + 4.9195 \cdot \text{excellent_health}\}},$$

and

$$\hat{\lambda} = \exp\{-0.1381 + 0.0186 \cdot \text{age} + 0.7268 \cdot \text{male}\}.$$

This model has a good fit, since the p -value in the deviance test is very small. At the 5% level, health status significantly predicts the odds of being a non-smoker, whereas gender has a significant effect on the average number of cigarettes smoked in a day. As follows from these estimates, the estimated odds of not smoking for people in excellent health is $\exp\{4.9195\} \cdot 100\% = 13,694.26\%$ of those for people in good health. Also, the estimated average number of cigarettes smoked in a day by men is $\exp\{0.7268\} \cdot 100\% = 206.85\%$ of the average number of cigarettes smoked by women.

Further, by (5.11), the predicted number of cigarettes smoked per day by a 50-year old male who is in good health is found as

$$y^0 = \left(1 - \frac{\exp\{-3.7950\}}{1 + \exp\{-3.7950\}}\right) \exp\{-0.1381 + 0.0186 \cdot 50 + 0.7268\} = 4.4659.$$

The SAS code for prediction is

```

data prediction;
input gender$ health$ age;
cards;
M good 50
;

data smoking;
  set smoking prediction;
run;

proc genmod;
class gender health;
  model cigarettes=gender age/dist=zip;
  zeromodel health;
  output out=outdata p=pred_cig;
run;

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

pred_cig
  4.47333

```

R script and output for this example follow.

```

smoking.data<-read.csv(file="./Example5.3Data.csv",
header=TRUE, sep=",")

#specifying reference category
health.rel<- relevel(smoking.data$health, ref="good")

#fitting zero-inflated Poisson model
library(pscl)
summary(fitted.model<- zeroinfl(cigarettes ~ gender + age|health.rel,
data=smoking.data))

```

Count model coefficients (poisson with log link):

	Estimate	Pr(> z)
(Intercept)	-0.13820	0.8690
genderM	0.72686	0.0107
age	0.01863	0.3506

Zero-inflation model coefficients (binomial with logit link):

	Estimate	Pr(> z)
(Intercept)	-3.795	0.0875
health.relexclnt	4.920	0.0341

```
#checking model fit
```

```
null.model<- zeroinfl(cigarettes ~ 1, data=smoking.data)
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

```
28.6972
```

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

```
2.592711e-06
```

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

```
print(predict(fitted.model, data.frame(gender="M", health.rel="good",
age=50)))
```

```
4.473475
```

□

5.4 Hurdle Poisson Regression Model

5.4.1 Model Definition

The hurdle Poisson regression is applied when the response variable y has a Poisson distribution with an inflated number of zeros, and, moreover, there is a reason to believe that the underlying characteristics of cases with zeros systematically differ from those with positive responses. Put differently, zeros are modeled separately from zero-truncated Poisson observations. Thus, for predictors x_1, \dots, x_k , the *hurdle Poisson regression model*⁴ assumes that the response variable y has a probability distribution function

$$\mathbb{P}(Y = y) = \begin{cases} \pi, & \text{if } y = 0, \\ (1 - \pi) \frac{\lambda^y \exp\{-\lambda\}}{y!(1 - \exp\{-\lambda\})}, & \text{if } y = 1, 2, \dots, \end{cases} \quad (5.12)$$

where

$$\pi = \frac{\exp\{\beta_0 + \beta_1 x_1 + \dots + \beta_m x_m\}}{1 + \exp\{\beta_0 + \beta_1 x_1 + \dots + \beta_m x_m\}}, \quad (5.13)$$

⁴Originally examined in Mullahy, J. (1986). "Specification and testing of some modified count data models". *Journal of Econometrics*, 33(3): 341 – 365.

and

$$\lambda = \exp \{ \gamma_0 + \gamma_1 x_{m+1} + \cdots + \gamma_{k-m} x_k \}. \quad (5.14)$$

The distribution of y is a mixture of a degenerate distribution at zero and a zero-truncated Poisson distribution. This type of distribution is not in the exponential family, and thus, the hurdle Poisson model is not a generalized linear model.

5.4.2 Fitted Model

By (5.13) and (5.14), in a fitted hurdle Poisson regression model, estimated parameters are

$$\hat{\pi} = \frac{\exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_m x_m\}}{1 + \exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_m x_m\}} \quad (5.15)$$

and

$$\hat{\lambda} = \exp \{ \hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1} + \cdots + \hat{\gamma}_{k-m} x_k \}. \quad (5.16)$$

5.4.3 Interpretation of Estimated Regression Coefficients

It can be shown (see Exercise 5.11) that the expected value of the response variable $\mathbb{E}(y) = (1 - \pi) \frac{\lambda}{1 - \exp\{-\lambda\}}$, and thus, estimated regression coefficients in π and λ are interpreted as in a binary logistic (see Subsection 3.1.3) and Poisson regressions (see Subsection 5.1.3), respectively, provided all the other predictors remain the same.

5.4.4 Predicted Response

Taking into account the above expression for the expected value of y and relations (5.15) and (5.16), we can write the predicted response as

$$\begin{aligned} y^0 &= \left(1 - \frac{\exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \cdots + \hat{\beta}_m x_m^0\}}{1 + \exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \cdots + \hat{\beta}_m x_m^0\}} \right) \times \\ &\times \frac{\exp \{ \hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1}^0 + \cdots + \hat{\gamma}_{k-m} x_k^0 \}}{1 - \exp \{ - \exp \{ \hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1}^0 + \cdots + \hat{\gamma}_{k-m} x_k^0 \} \}}. \end{aligned}$$

5.4.5 SAS Implementation

The hurdle Poisson model may be fit by means of the `fmm` procedure with the syntax below.

```
proc fmm data=data_name;
  class <list of categorical predictors>;
  model response_name = <list of predictors>/dist=truncpoisson;
  model + /dist=constant;
  probmodel <list of predictors of zeros>;
  output out=outdata_name pred=predicted_response_name;
run;
```

- The second `model` statement adds a degenerate distribution at point zero.
- The `probmodel` statement fits the probability of zero that, in our notation, is equal to $1 - \pi$. Applying (5.13), we obtain

$$\begin{aligned} 1 - \pi &= 1 - \frac{\exp\{\beta_0 + \beta_1 x_1 + \cdots + \beta_m x_m\}}{1 + \exp\{\beta_0 + \beta_1 x_1 + \cdots + \beta_m x_m\}} \\ &= \frac{\exp\{-(\beta_0 + \beta_1 x_1 + \cdots + \beta_m x_m)\}}{1 + \exp\{-(\beta_0 + \beta_1 x_1 + \cdots + \beta_m x_m)\}}. \end{aligned}$$

It means that when fitting the model using our notation, the signs of estimated beta regression coefficients have to be reversed.

5.4.6 R Implementation

In R, the function `hurdle()` in the library `pscl` may be used to fit a hurdle Poisson regression model. The general syntax is

```
summary(fitted.model.name<- hurdle(response.name ~ x{m+1}.name + ...
+ xk.name | x1.name + ... + xm.name, data = data.name,
dist="poisson", zero.dist="binomial", link="logit"))
```

Note that similar to SAS, R evaluates $1 - \pi$ and thus the estimated regression coefficients for π have to be taken with the opposite sign.

5.4.7 Example

EXAMPLE 5.4. A college bookstore wants to gain insight into the textbook purchasing habits of students. A random sample of 40 students was drawn, and it was recorded how many textbooks each student purchased through

the bookstore for the current term, whether the student is currently renting any textbooks, and whether a student has a financial aid. The manager at the bookstore conjectures that no textbook purchase might be attributed to students' renting textbooks, and that students with financial aid tend to purchase more textbooks. The data and the analysis follow.

```
data bookstore;
input ntextbooks renting aid$ @@;
cards;
0 3 no 0 2 no 3 0 yes 0 0 no 0 1 no 1 0 no
0 3 no 2 0 yes 4 0 no 0 2 no 4 1 no 7 0 yes
3 2 yes 0 4 no 1 2 no 0 0 no 0 5 no 1 0 no
0 2 no 3 0 no 0 3 no 6 1 yes 2 1 yes 1 0 no
6 0 yes 2 0 no 0 3 no 4 0 yes 0 1 no 0 2 no
3 0 no 3 2 no 3 0 yes 2 0 yes 0 3 no 2 1 no
3 0 yes 1 3 no 3 0 yes 0 2 no
```

```
proc format;
value $aidfmt "no"="ref_no" "yes"="aid";
run;
```

```
proc fmm;
class aid;
model ntextbooks=aid/dist=truncpoisson;
model+ /dist=constant;
probmodel renting;
run;
```

-2 Log Likelihood 115.7

Parameter Estimates for Truncated Poisson Model

Effect	aid	Estimate	Pr > z
Intercept		0.5951	0.0147
aid	aid	0.6754	0.0204
aid	ref	0	.

Parameter Estimates for Mixing Probabilities

Effect	Estimate	Pr > z
Intercept	2.0494	0.0016
renting	-1.2749	0.0009

```
proc fmm;
```



```

model ntextbooks=/dist=truncpoisson;
model + /dist=constant;
probmodel;
run;

```

-2 Log Likelihood 139.1

```

data deviance_test;
deviance=139.1-115.7;
pvalue=1-probchi(deviance,2);
run;

```

```

proc print noobs;
run;

```

```

deviance      pvalue
    23.4      0.000008294

```

Reversing the estimated beta coefficients, we obtain that in the fitted model, the parameter estimates are $\hat{\pi} = \frac{\exp\{-2.0494 + 1.2749 \cdot \text{renting}\}}{1 + \exp\{-2.0494 + 1.2749 \cdot \text{renting}\}}$, and $\hat{\lambda} = \exp\{0.5951 + 0.6754 \cdot \text{aid}\}$. The model fits the data well since the p -value in the deviance test is tiny. Whether a student rents textbooks significantly predicts the probability of not purchasing them, whereas presence of financial aid is significantly associated with the mean number of purchased textbooks. If the number of rented books increases by one, the estimated odds in favor of not buying textbooks increase by $(\exp\{1.2749\} - 1) \cdot 100\% = 257.83\%$. The estimated average number of purchased textbooks for a student with a financial aid is $\exp\{0.6754\} \cdot 100\% = 196.48\%$ of that for a student without it.

Prediction of the number of textbooks purchased by a student who has no rented books or financial aid is calculated as follows:

$$y^0 = \left(1 - \frac{\exp\{-2.0494\}}{1 + \exp\{-2.0494\}}\right) \cdot \frac{\exp\{0.5951\}}{1 - \exp\{-\exp\{0.5951\}\}} = 1.9194.$$

SAS produces similar prediction as can be seen by running the statements below.

```

data prediction;
input renting aid$;
cards;
0 no

```

```

;

data bookstore;
  set bookstore prediction;
run;

proc fmm;
class aid;
  model ntextbooks=aid/dist=truncpoisson;
  model+ /dist=constant;
probmodel renting;
  output out=outdata pred=p_ntextbooks;
run;

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

p_ntextbooks
      1.91942

```

The R script and output are:

```

bookstore.data<-read.csv(file="./Example5.4Data.csv",
header=TRUE, sep=",")

#fitting hurdle Poisson model
library(pscl)
summary(fitted.model<- hurdle(ntextbooks ~ aid|renting,
data=bookstore.data, dist="poisson", zero.dist="binomial",
link="logit"))

```

Count model coefficients (truncated poisson with log link):

	Estimate	Pr(> z)
(Intercept)	0.5951	0.0147
aidyes	0.6754	0.0204

Zero hurdle model coefficients (binomial with logit link):

	Estimate	Pr(> z)
(Intercept)	2.0494	0.001610
renting	-1.2749	0.000923

```
#checking model fit
null.model<- hurdle(n textbooks ~ 1, data=bookstore.data, dist="poisson",
zero.dist="binomial", link="logit")
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))

23.39548

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

8.312594e-06

#using fitted model for prediction
print(predict(fitted.model, data.frame(renting=0, aid="no")))

1.919422
```

□

Exercises for Chapter 5

EXERCISE 5.1. The number of defective items produced by a machine operator during one shift is modeled through a Poisson regression where independent variables are the length of work experience as a machine operator (in years), and whether it was a morning, day, evening, or night shift. The data were obtained for 36 randomly chosen shifts and operators.

NDefectives	Exprience	Shift	NDefectives	Exprience	Shift
2	3.1	morning	0	2.1	day
5	2.1	morning	2	3.0	day
3	8.0	morning	5	8.2	evening
3	7.6	morning	4	4.0	evening
2	5.9	morning	4	6.2	evening
2	4.0	morning	3	2.9	evening
1	1.7	morning	2	2.1	evening
0	1.8	morning	2	1.9	evening
0	8.2	morning	1	6.7	evening
1	8.1	morning	1	3.4	evening
3	3.0	day	1	7.6	evening
3	7.7	day	6	5.1	night
2	6.3	day	4	3.2	night
2	8.1	day	4	7.6	night
2	7.7	day	4	2.5	night
1	2.4	day	3	6.2	night
1	3.0	day	3	2.0	night
1	4.6	day	5	4.0	night

- (a) Run the Poisson regression model. Discuss the significance of predictors at the 5% level of significance.
- (b) Write down the estimated model. How good is the fit of the model?
- (c) Give interpretation of the estimated significant coefficients.
- (d) Predict the number of defective items produced during a night shift by an operator with six months of experience.

EXERCISE 5.2. A large automobile insurance company is studying the relation between the total number of auto accidents (including minor) that a policyholder had caused, and the policyholder's gender, age, and total number of miles driven (in thousands). The data for 48 randomly chosen policyholders are given in the table below.

NAccidents	Gender	Age	Miles	NAccidents	Gender	Age	Miles
1	M	27	90	0	F	36	190
1	M	60	70	0	F	57	140
1	M	36	160	1	F	47	160
2	M	32	80	1	F	59	70
2	M	27	150	1	F	55	180
2	M	58	150	2	F	44	170
2	M	38	105	2	F	36	100
3	M	42	75	2	F	40	170
3	M	55	170	2	F	58	60
3	M	42	70	3	F	53	200
3	M	30	110	3	F	29	180
3	M	54	170	3	F	51	150
4	M	36	120	3	F	49	150
4	M	47	145	4	F	32	180
5	M	20	25	4	F	51	90
5	M	67	160	4	F	43	90
5	M	33	140	4	F	43	20
5	M	41	50	4	F	31	120
5	M	43	150	4	F	50	130
6	M	59	130	4	F	36	50
7	M	65	90	5	F	40	100
9	M	68	180	6	F	48	170
0	F	33	110	6	F	57	180
0	F	40	190	8	F	66	130

- (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 $\alpha = 0.05$.
- (b) Check goodness-of-fit of the model.

- (c) Interpret the estimated significant regression coefficients.
- (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.

EXERCISE 5.3. A howling survey is a productive method for estimating the minimum number of wolves within a pack. Thirty two surveys have been conducted at one site per 100 acres of land. The count of individual wolves that called back, time of howling session (dusk or night) and wind speed (in mph) were recorded. Also, presence of source of drinking water was noted. The data are summarized in the table below.

NCalls	Time	Wind	Water	NCalls	Time	Wind	Water
2	dusk	0	yes	3	dusk	0	yes
2	dusk	1	yes	0	dusk	3	no
3	dusk	0	no	1	dusk	3	yes
2	night	6	no	2	dusk	3	yes
3	dusk	2	no	7	night	2	yes
4	night	3	yes	5	dusk	0	yes
5	dusk	1	yes	2	night	0	yes
3	night	5	yes	4	night	2	no
4	night	5	yes	6	night	1	yes
7	night	0	yes	3	night	3	yes
1	dusk	6	yes	0	dusk	1	no
2	night	1	no	1	dusk	3	no
4	dusk	2	yes	4	night	3	yes
6	night	2	yes	1	dusk	0	yes
5	dusk	3	yes	4	dusk	2	yes
2	night	3	yes	1	dusk	2	yes

- (a) Fit a Poisson regression model for the number of calls. Discuss the model fit.
- (b) Specify the fitted model. Give estimates of all parameters. Which variables are significant at the 5%?
- (c) Give interpretation of estimated significant regression coefficients.
- (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?

EXERCISE 5.4. Reduce the data in Exercise 5.1 to only those operators who produced defective items.

- (a) Model the number of defective items via the zero-truncated Poisson regression model. Display the fitted model. List the significant predictors.
- (b) Discuss the model fit.
- (c) Interpret estimated significant coefficients.

- (d) Predict the number of defective items produced during a night shift by an operator with six months of experience.

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?
- (b) Discuss the fit of the model.
- (c) Interpret the estimated significant beta coefficients.
- (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.

EXERCISE 5.6. Trim the data in Exercise 5.3, leaving the records of the howling sessions when wolves were present in the area and responded.

- (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?
- (b) Test the goodness-of-fit of the model.
- (c) Give interpretation of the estimated significant regression coefficients.
- (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.

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 $\mathbb{E}(y) = (1 - \pi)\lambda$.
- (b) Prove that the estimated gamma coefficients in the expression for $\hat{\lambda}$ yield the same interpretation as in the Poisson regression model (see Subsection 5.1.3). Hint: Use the fact that the predictors in the definitions of λ and π are different.

EXERCISE 5.8. On the day of a race, runners were asked how many races they participated in during the past four months. The runners' bib numbers were also noted, and after the race the data were obtained on the runners' gender, age, type of run on that day (5K/10K/full marathon). In addition, the average pace was calculated for each runner (in minutes per mile) from the distance and time of the runs. The data on 36 runners are

NRaces	Gender	Age	Run	Pace	NRaces	Gender	Age	Run	Pace
0	F	33	10K	10.04	1	F	51	5K	12.28
5	M	26	Full	7.17	4	F	35	10K	6.98
0	M	32	10K	11.14	2	M	25	10K	12.01
3	F	27	5K	9.18	3	M	34	5K	6.78
0	M	48	5K	7.52	0	M	28	5K	11.66
4	F	47	10K	11.59	0	F	39	10K	12.31
1	M	51	5K	9.44	2	M	32	Full	6.58
2	F	49	5K	9.53	5	F	44	Full	7.46
0	M	54	10K	8.48	0	F	49	10K	11.11
3	F	27	5K	11.71	2	M	52	Full	9.20
2	M	24	10K	7.56	1	M	30	5K	6.41
0	F	14	5K	13.78	1	M	43	10K	7.70
3	M	35	Full	7.34	1	M	30	10K	10.01
0	M	50	5K	7.51	0	M	53	5K	7.56
0	M	44	5K	8.92	2	F	46	Full	8.34
6	F	37	5K	10.71	0	F	28	5K	9.67
0	M	54	5K	8.72	2	F	50	Full	10.07
2	F	51	10K	7.41	2	F	54	5K	7.58

- Fit the zero-inflated Poisson regression to model the number of races in the previous four months. Check if pace is significantly associated with inflation of zeros. Write down the fitted model.
- Discuss the model fit.
- Interpret the estimated significant coefficients.
- 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.

EXERCISE 5.9. In an elementary school, children participate in a home reading club. They are asked to read at least 15 minutes every day and submit at the end of each month a list of books read. Some teachers make this assignment a part of the homework, others leave it as optional. A random sample of 50 students is drawn and the following variables recorded: grade level, whether reading assignment was a part of homework (yes/no), gender, and the number of books read at the proper grade level or above. The books below the grade level were not counted. If a student didn't turn in the list of books, then a zero was recorded for the number of books. The data are given below.

Grade	HW	Gender	NBooks	Grade	HW	Gender	NBooks
3	no	M	3	2	yes	F	0
3	yes	M	3	2	yes	M	3
2	no	F	4	2	no	M	3
2	yes	M	3	3	yes	F	4
3	no	F	2	3	yes	M	3
1	yes	F	0	3	yes	F	1
1	yes	F	4	1	no	M	0
2	no	F	0	2	no	M	0
1	no	M	0	1	yes	M	0
3	no	M	1	2	yes	F	6
3	yes	F	3	2	yes	F	2
2	no	F	4	2	no	F	3
3	no	M	0	2	no	F	0
2	no	M	0	3	no	F	5
1	yes	F	5	3	yes	M	2
3	yes	M	2	1	no	M	0
1	no	F	1	3	no	F	2
3	no	F	4	2	yes	F	0
1	no	F	0	2	no	M	2
2	yes	F	2	2	no	M	0
3	no	F	4	3	no	F	3
1	no	M	2	1	yes	F	1
2	no	M	0	2	no	F	0
2	no	F	4	1	yes	M	1
3	no	F	5	2	yes	M	2

- (a) Model these data using a zero-inflated Poisson regression with grade (considered as a continuous variable) 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?
- (b) Is it a reliable model? Present the quantitative argument for the goodness-of-fit of the model.
- (c) How are the estimated significant coefficients interpreted?
- (d) What is the predicted number of books read by a second-grade girl for whom the reading is part of the homework?

EXERCISE 5.10. Forty patients in a large hospital were randomly chosen for a survey. The variables recorded were patient's BMI, age, gender, indicator of current smoking, and the number of mild to severe asthma attacks in the past three months. The data are summarized in the table below.

BMI	Age	Gender	Smoking	NAttacks	BMI	Age	Gender	Smoking	NAttacks
25.1	61	F	no	2	28.6	50	F	no	0
27.1	33	F	yes	0	20.0	65	F	yes	3
26.8	61	F	no	1	31.5	58	F	no	2
23.9	53	F	yes	1	25.8	64	M	yes	5
26.9	59	M	yes	2	38.3	56	F	no	1
18.8	45	F	no	0	41.4	45	F	no	0
25.2	54	M	yes	2	31.2	26	F	no	0
23.5	75	M	yes	5	18.5	42	M	yes	0
29.7	64	F	no	3	32.2	26	F	no	0
24.5	55	F	no	1	23.9	65	F	no	3
21.5	63	M	yes	2	31.3	52	M	no	2
37.9	52	M	no	0	25.6	32	F	no	0
22.6	43	M	no	0	33.2	31	M	no	0
23.0	56	F	no	1	23.8	60	M	no	2
28.1	50	F	no	0	31.4	55	M	no	1
24.8	86	M	yes	6	34.0	53	F	no	1
30.6	74	M	yes	4	27.4	42	M	no	3
33.7	71	F	yes	3	20.6	61	F	yes	2
26.4	66	F	yes	1	28.3	64	M	no	3
27.4	25	F	no	0	30.1	52	M	yes	3

- Run a ZIP model with age and smoking predicting the probability of excess zeros. Fit the model, estimate the parameters. Discuss significance of predictors.
- How good is the model fit?
- Interpret the estimates of the significant regression coefficients.
- 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.

EXERCISE 5.11. Consider the hurdle Poisson regression model defined by (5.12) – (5.14).

- Show that the expected value of the response variable has the form

$$\mathbb{E}(y|x_1, \dots, x_k) = (1 - \pi) \frac{\lambda}{1 - \exp(-\lambda)}.$$

- Argue that the estimated regression coefficients in π and λ have the same interpretation as in a binary logistic and Poisson regression models, respectively.

EXERCISE 5.12. A coordinator of librarianship program within a school district is concerned with the negative effect of budget cuts on libraries. She

randomly chooses 34 schools within the district and collects information on the number of computers, number of books (in thousands), number of journals during the current academic year, and the budget size (expenditure per student, in dollars). The data are:

NComps	NBooks	NJrnls	Budget	NComps	NBooks	NJrnls	Budget
0	8.2	0	0.00	22	9.0	16	0.00
19	11.7	10	16.45	32	18.3	23	22.22
0	2.0	0	5.29	0	12.0	5	0.17
13	8.2	8	23.50	6	8.8	12	7.14
5	30.0	2	6.33	1	14.0	60	1.83
16	14.1	15	7.20	5	12.5	32	24.66
12	9.5	0	3.07	7	3.0	5	7.07
6	21.8	0	4.00	3	16.3	40	12.00
12	9.0	11	4.39	1	6.5	40	13.85
22	5.0	20	17.07	3	8.5	4	18.22
0	15.7	4	1.82	4	10.0	20	30.49
7	19.3	66	9.09	7	18.0	100	0.81
6	20.8	2	10.49	0	11.5	2	0.61
28	11.0	30	0.47	3	9.1	0	9.19
0	9.3	0	0.06	13	10.4	36	25.67
11	12.7	14	0.00	36	7.5	55	7.89
17	15.6	14	22.22	0	19.7	8	1.00

- 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.
- Discuss the model fit.
- Interpret estimated significant parameters. State the practical conclusion.
- What is the predicted number of computers in a library with 10,000 books, 25 periodicals, and annual budget of \$15 per student?

EXERCISE 5.13. Health care professionals conduct a study on medication adherence among senior citizens. They obtain medical and pharmaceutical records for a random sample of 30 patients (15 men, 15 women) who were prescribed the same once-daily heart medication. The variables that the investigators use for the analysis are: the number of days a patient forgot to take the prescribed medication (according to the pharmaceutical record), gender, age, and the number of other medications prescribed. The investigators suspect that patients with more medications are more likely to account for zeros in the response variable, and that women and older patients have larger average positive responses. The collected data are given in the follow-

ing table.

N of Days no meds	Gender	Age	N of Other meds	N of Days no meds	Gender	Age	N of Other meds
0	F	87	12	1	F	71	2
2	M	65	3	2	M	65	1
0	M	85	3	5	F	68	7
1	F	68	3	4	M	73	4
5	F	76	18	4	F	72	3
1	F	72	9	0	M	86	13
4	F	73	5	3	F	66	4
1	M	64	0	5	F	70	5
2	M	71	1	1	M	70	5
7	F	81	5	3	M	62	3
0	M	89	7	0	M	93	15
4	F	87	8	5	F	70	1
2	M	78	9	3	F	68	11
0	F	87	9	3	M	75	2
1	M	77	4	2	M	88	11

- Fit the hurdle Poisson model to verify the hypotheses. Identify all parameters in the predicted model. Is the conclusion supportive of the research hypotheses?
- How good is the model fit?
- Give interpretation of estimated significant regression coefficients.
- 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.

Chapter 6

Regression Models for Overdispersed Count Response

Suppose the response y is a count variable assuming non-negative integer values but unlike in the Poisson model, y may assume large values. In this chapter we consider four models that are reasonable alternatives to their Poisson-based models considered in the previous chapter: negative binomial, zero-truncated negative binomial, zero-inflated negative binomial, and hurdle negative binomial models.

6.1 Negative Binomial Regression Model

6.1.1 Model Definition

Recall that for a Poisson random variable, the mean is equal to the variance. A count variable for which the variance is larger than the mean is termed *overdispersed*. In this case a negative binomial regression would be a more appropriate model.

In a *negative binomial regression model*¹ with predictors x_1, \dots, x_k , the response y follows a negative binomial distribution with the probability mass function given as:

$$\mathbb{P}(Y = y) = \left(\frac{r}{r + \lambda}\right)^r \frac{\Gamma(r + y)}{y! \Gamma(r)} \left(\frac{\lambda}{r + \lambda}\right)^y, \quad y = 0, 1, 2, \dots, \quad (6.1)$$

¹First rigorous treatment can be found in Hausman, J., Hall, B.H., and Z. Griliches (1984). “Econometric models for count data with an application to the patents – R & D relationship”. *Econometrica*, 52(4): 909 – 938.

where

$$\lambda = \exp \{ \beta_0 + \beta_1 x_1 + \cdots + \beta_k x_k \}, \text{ and } r \text{ is a positive integer.} \quad (6.2)$$

It can be proven (see Exercise 6.1) that $\mathbb{E}(y) = \lambda$ and $\mathbb{V}ar(y) = \lambda + \lambda^2/r$. Thus, if the response y has a large variance compared to its mean, the value of the parameter r is small. For this reason, r is called the *dispersion parameter*. If we let r go to infinity, the second term in the variance tends to zero, and, in fact, the limiting distribution is Poisson with rate λ .

Further, one can show (see Exercise 6.1) that the negative binomial distribution belongs to the exponential family of distributions, and thus the negative binomial model is an example of a generalized linear model with the log link function.

6.1.2 Fitted Model

From (6.2), in a fitted negative binomial regression model, the estimated parameters are $\hat{\lambda} = \exp \{ \hat{\beta}_0 + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_k x_k \}$, and \hat{r} .

6.1.3 Interpretation of Estimated Regression Coefficients

Since the mean of y is λ , the interpretation of estimated regression coefficients is identical to that in Poisson model (see Subsection 5.1.3).

6.1.4 Predicted Response

Considering the above expression for $\hat{\lambda}$, for a given set of predictors $x_1^0, x_2^0, \dots, x_k^0$, the predicted response y^0 is computed as $y^0 = \exp \{ \hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \cdots + \hat{\beta}_k x_k^0 \}$.

6.1.5 SAS Implementation

The `genmod` procedure invoked with the option `dist=negbin` fits a negative binomial regression.

- SAS outputs the quantity $1/r$ and terms it **dispersion parameter**. If the dispersion parameter is zero or close to zero, then the Poisson model is more appropriate. If it is much larger than zero, then negative binomial regression is valid.

6.1.6 R Implementation

In R, the function `glm.nb()` in the library **MASS** may be used to fit a negative binomial regression model. The general script looks like this:

```
summary(fitted.model.name<- glm.nb(response.name ~ x1.name + ...  
+ xk.name, data = data.name))
```

- R outputs the estimate of the dispersion parameter r and calls it **Theta**.

6.1.7 Example

EXAMPLE 6.1. A college offers a 20-mile swim challenge program to all students, faculty, and staff. People who within 12 weeks complete a 20-mile swim in the pool on the college campus are awarded T-shirts. Number of laps swam is recorded in sets of 20 after every swim. The organizers have the data for 30 program participants for the first week of the program. They are interested in regressing the distance swam (in sets of 20 laps) on swimmer's gender, age, and whether it is their first time in this program. Since it is a self-paced program, it is expected to see a great variability in the number of sets swam during one week. The SAS code and relevant output are below.

```
data swim;  
input gender$ age firsttime$ sets @@;  
cards;  
M 38 yes 20 M 26 no 0 M 21 yes 8  
M 19 yes 13 M 18 yes 28 M 20 yes 2  
F 26 yes 8 M 21 no 14 F 20 no 0  
F 18 yes 3 M 25 yes 6 F 42 yes 1  
F 24 yes 7 M 58 yes 27 M 19 yes 10  
F 32 no 17 F 46 no 12 M 21 yes 4  
F 26 no 3 M 22 no 35 F 19 yes 2  
F 56 yes 11 F 41 no 15 M 25 no 1  
M 25 yes 9 M 21 no 8 M 19 yes 11  
M 37 no 34 F 22 yes 8 F 23 yes 5  
;  
  
proc genmod;  
class gender(ref="F") firsttime(ref="yes");  
model sets=gender age firsttime/dist=negbin;  
run;
```

Full Log Likelihood -97.8206

Analysis Of Maximum Likelihood Parameter Estimates

Parameter	Estimate	Pr > ChiSq
Intercept	0.9316	0.0603
gender M	0.8250	0.0082
age	0.0278	0.0474
firsttime no	0.2596	0.4021
Dispersion	0.5446	

```
proc genmod;  
model sets=/dist=negbin;  
run;
```

Full Log Likelihood -102.1982

```
data deviance_test;  
  deviance=-2*(-102.1982-(-97.8206));  
  pvalue=1-probchi(deviance,3);  
run;
```

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

deviance	pvalue
8.7552	0.032729

The estimates of the parameters in the model are $\hat{\lambda} = \exp\{0.9316 + 0.8250 \cdot \text{male} + 0.0278 \cdot \text{age} + 0.2596 \cdot \text{notfirsttime}\}$ and $\hat{r} = 1/0.5446 = 1.8362$. The model fits the data well since the p -value of the deviance test is below 0.05. The significant predictors are gender and age. The estimated average number of sets of laps swam by a male is $\exp\{0.8250\} \cdot 100\% = 228.19\%$ of that for female. For every one-year increase in age, the estimated average number of sets increases by $(\exp\{0.0278\} - 1) \cdot 100\% = 2.82\%$.

Suppose that we would like to predict the number of lap sets that a 20-year old female student who has never participated in the 20-mile swim challenge would swim during the first week. Calculated by hand, the predicted number of lap sets is $\exp\{0.9316 + 0.0278 \cdot 20\} = 4.4264$. The same prediction is produced by SAS when running the following statements:


```

data prediction;
input gender$ age firsttime$;
cards;
F 20 yes
;

data swim;
  set swim prediction;
run;

proc genmod;
class gender firsttime;
  model sets=gender age firsttime/dist=negbin;
  output out=outdata p=pred_sets;
run;

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

pred_sets
  4.42282

```

The R script and output for this example are below.

```

swim.data<-read.csv(file="./Example6.1Data.csv",
header=TRUE, sep=",")

#specifying reference category
firsttime.rel<- relevel(swim.data$firsttime, ref="yes")

#fitting negative binomial model
library(MASS)
summary(fitted.model <- glm.nb(sets ~ gender + age + firsttime.rel,
data=swim.data))

```

Coefficients:

	Estimate	Pr(> z)
(Intercept)	0.93159	0.06034
genderM	0.82503	0.00784
age	0.02776	0.04222
firsttime.reln	0.25961	0.39579

Theta: 1.836

```
#checking model fit
null.model<- glm.nb(sets ~ 1, data=swim.data)
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))

8.755082

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

0.03273083

#using fitted model for prediction
print(predict(fitted.model, data.frame(gender="F", age=20,
firsttime.rel="yes"), type="response"))

4.422816
```

□

6.2 Zero-truncated Negative Binomial Regression Model

6.2.1 Model Definition

When a response variable y is a count variable that assumes only positive values and is overly dispersed, then a *zero-truncated negative binomial regression model*² maybe be appropriate. For predictors x_1, \dots, x_k , the probability distribution function of the response variable y is modeled as a negative binomial truncated at zero:

$$\mathbb{P}(Y = y) = \frac{\left(\frac{r}{r+\lambda}\right)^r \frac{\Gamma(r+y)}{y! \Gamma(r)} \left(\frac{\lambda}{r+\lambda}\right)^y}{1 - \left(\frac{r}{r+\lambda}\right)^r}, \quad y = 1, 2, \dots,$$

where $\lambda = \exp\{\beta_0 + \beta_1 x_1 + \dots + \beta_k x_k\}$, and r is a positive integer. This model is not a generalized linear regression. Even though the distribution is a representative of the exponential family of distributions, the expected value of y is

$$\mathbb{E}(y) = \frac{\lambda}{1 - \left(\frac{r}{r+\lambda}\right)^r}, \quad (6.3)$$

thus, the log link function relates lambda but not the expected value of y to the linear regression.

²First considered in Gurmu, S. (1991). "Tests for detecting overdispersion in the positive Poisson regression model". *Journal of Business and Economic Statistics*, 9(2): 215 – 222.

6.2.2 Fitted Model

In a fitted zero-truncated negative binomial regression model, the parameter estimates are $\hat{\lambda} = \exp \{ \hat{\beta}_0 + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_k x_k \}$, and \hat{r} .

6.2.3 Interpretation of Estimated Regression Coefficients

Since the mean of y , given in (6.3), describes a relatively complex relation between the response and predictors, in this model there is no easy interpretation of the estimated regression coefficients. Traditionally, interpretation is omitted.

6.2.4 Predicted Response

Taking into account (6.3) and the above expression for the estimate of λ , for a given set of predictors $x_1^0, x_2^0, \dots, x_k^0$, the predicted response is computed as

$$\begin{aligned} y^0 &= \frac{\hat{\lambda}}{1 - \left(\frac{\hat{r}}{\hat{r} + \hat{\lambda}} \right)^{\hat{r}}} = \frac{\hat{\lambda}}{1 - (1 + \hat{\lambda}/\hat{r})^{-\hat{r}}} \\ &= \frac{\exp \{ \hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \cdots + \hat{\beta}_k x_k^0 \}}{1 - (1 + \exp \{ \hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \cdots + \hat{\beta}_k x_k^0 \} / \hat{r})^{-\hat{r}}}. \end{aligned}$$

6.2.5 SAS Implementation

A zero-truncated negative binomial model may be fitted by applying the `fm` procedure with the option `dist=truncnegbin` in the model statement.

- SAS produces the estimate $1/\hat{r}$, the reciprocal of the estimated dispersion parameter. The term that SAS uses for its estimate is **Scale Parameter**.

6.2.6 R Implementation

The function `vglm()` in the library `VGAM` may be used to fit a zero-truncated negative binomial regression model in R. The script is

```
summary(fitted.model.name<- vglm(response.name ~ x1.name + ...  
+ xk.name, data = data.name, family = posnegbinomial()))
```

As part of the output, two intercepts are fitted, called `(Intercept):1` and `(Intercept):2`. The first one is the regression intercept $\hat{\beta}_0$, whereas the second one is $\ln(\hat{\tau})$, the natural logarithm of the estimated dispersion parameter.

6.2.7 Example

EXAMPLE 6.2. An assistant general manager of a luxury hotel is put in charge of implementing a budget-friendly new ideas to help reduce the number of complaints by hotel guests. She collects data on a random sample of 28 guests who made at least one complaint, recording the number of complaints made by the guest, room floor, whether the guest is an elite member, and the duration of the stay (in days). SAS code and output are given below.

```
data hotel;
input  ncomplaints floor member$ days@@;
cards;
2  6 no  3  1 7 no  12  3 6 no  7  3 7 yes 3
3  8 yes 2  9 3 no  4  1 8 no  4  2 6 yes 5
6  5 no  8  2 8 no  11  1 2 yes 5  2 3 no  3
2  4 no  8  2 3 no  6  7 4 yes 4  4 5 yes 5
8  2 yes 3  3 5 no  8  4 5 yes 4  4 2 no  3
1  2 yes 4  1 7 no  3  6 3 no  2  3 3 no  2
12 2 yes 4  2 6 no  1  1 6 no  3  5 3 no  8
;

proc format;
value $memberfmt "no"="ref" "yes"="member";
run;

proc fmm;
class member;
model ncomplaints=floor member days/dist=truncnegbin;
format member $memberfmt.;
run;
```

-2 Log Likelihood 108.6

Parameter Estimates for Truncated Negative Binomial Model

Effect	Estimate	Pr > z
Intercept	1.9919	<.0001
floor	-0.2400	0.0076

member member	0.3712	0.2560
member ref	0	.
days	0.006069	0.9319
Scale Parameter	0.2446	

```
proc fmm;
  model ncomplaints=/dist=truncnegbin;
run;
```

-2 Log Likelihood 118.1

```
data deviance_test;
  deviance=118.1-108.6;
  pvalue=1-probchi(deviance,3);
run;
```

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

deviance	pvalue
9.5	0.023331

The fitted model has parameter estimates $\hat{\lambda} = \exp \{1.9919 - 0.2400 \cdot \text{floor} + 0.3712 \cdot \text{member} + 0.006069 \cdot \text{days}\}$, and $\hat{r} = 1/0.2446 = 4.0883$. The model has a decent fit since the p -value in the deviance test is smaller than 0.05. In this model, the room floor is the only significant predictor at the 5% level. As mentioned above, the estimated coefficients do not yield a straightforward interpretation.

To predict the number of complaints made by an elite member who stays for two nights and whose room is on the forth floor, we compute:

$$y^0 = \frac{\exp\{1.9919 - 0.2400 \cdot 4 + 0.3712 + 0.006069 \cdot 2\}}{1 - (1 + \exp\{1.9919 - 0.2400 \cdot 4 + 0.3712 + 0.006069 \cdot 2\}/4.0883)^{-4.0883}} = 4.3707.$$

This is the same prediction as in SAS, which can be seen by running this code:

```
data prediction;
input floor member$ days;
cards;
4 yes 2
;
```

```

data hotel;
  set hotel prediction;
run;

proc fmm;
class member;
  model ncomplaints=floor member days/dist=truncnegbin;
  output out=outdata pred=p_ncomplaints;
run;

proc print data=outdata(firstobs=29) noobs;
var p_ncomplaints;
run;

p_ncomplaints
      4.37130

```

The R code that reproduces the output in SAS is as follows:

```

hotel.data<-read.csv(file="./Example6.2Data.csv", header=TRUE, sep=",")

#fitting truncated negative binomial model
library(VGAM)
summary(fitted.model<- vglm(ncomplaints ~ floor + member + days,
data=hotel.data, family=posnegbinomial()))

Coefficients:
                Estimate Pr(>|z|)
(Intercept):1    1.991913 6.79e-05
(Intercept):2    1.408035 0.08584
floor            -0.239965 0.00523
memberyes         0.371197 0.24786
days             0.006074 0.93034

#checking model fit
null.model<- vglm(ncomplaints ~ 1, data=hotel.data, family=posnegbinomial())
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))

9.489394

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

```

0.02344446

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(floor=4, member="yes", days=2),
type="response"))
```

4.371325

Note that since (Intercept):2 1.408035, the estimated dispersion parameter is $\hat{r} = \exp\{1.408035\} = 4.0879$. \square

6.3 Zero-inflated Negative Binomial Regression Model

6.3.1 Model Definition

A *zero-inflated negative binomial (ZINB) regression model*³ is used when the response is a count variable that exhibits overdispersion and has a large number of zeros which cannot be explained through a chance alone. The ZINB model better accounts for overdispersed characteristics than the zero-inflated Poisson regression. In the ZINB regression model, the response variable has the probability mass function defined by:

$$\mathbb{P}(Y = y) = \begin{cases} \pi + (1 - \pi) \left(\frac{r}{r + \lambda} \right)^r, & \text{if } y = 0, \\ (1 - \pi) \left(\frac{r}{r + \lambda} \right)^r \frac{\Gamma(r + y)}{y! \Gamma(r)} \left(\frac{\lambda}{r + \lambda} \right)^y, & \text{if } y = 1, 2, \dots, \end{cases}$$

where

$$\pi = \frac{\exp\{\beta_0 + \beta_1 x_1 + \dots + \beta_m x_m\}}{1 + \exp\{\beta_0 + \beta_1 x_1 + \dots + \beta_m x_m\}}, \quad (6.4)$$

$$\lambda = \exp\{\gamma_0 + \gamma_1 x_{m+1} + \dots + \gamma_{k-m} x_k\}, \text{ and } r \text{ is a positive integer.} \quad (6.5)$$

The zero-inflated negative binomial distribution is a mixture of two distributions and, thus, is not a member of the exponential family of distributions. Consequently, the model doesn't belong to the class of generalized linear models.

³Originally considered in Greene, W. H. (1994). "Some Accounting for Excess Zeros and Sample Selection in Poisson and Negative Binomial Regression Models". *Working Paper EC-94-10: Department of Economics, New York University*.

6.3.2 Fitted Model

By (6.4) and (6.5), the fitted zero-inflated negative binomial model has the estimated parameters of the form:

$$\hat{\pi} = \frac{\exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_m x_m\}}{1 + \exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_m x_m\}}, \quad (6.6)$$

$$\hat{\lambda} = \exp\{\hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1} + \cdots + \hat{\gamma}_{k-m} x_k\}, \text{ and } \hat{r}. \quad (6.7)$$

6.3.3 Interpretation of Estimated Regression Coefficients

The mean of the response is (show it!) $\mathbb{E}(y) = (1 - \pi)\lambda$, thus the interpretation of the estimated regression coefficients coincides with that in the ZIP model (see Subsection 5.3.3), that is, the estimated beta coefficients are interpreted as in a binary logistic model, whereas the estimated gamma coefficients are interpreted as in the Poisson model.

6.3.4 Predicted Response

Making use of the formula for the mean response $\mathbb{E}(y) = (1 - \pi)\lambda$, and expressions (6.6) and (6.7), we see that for some concrete values of predictors x_1^0, \dots, x_k^0 , the predicted response is calculated as:

$$\begin{aligned} y^0 &= \left(1 - \frac{\exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \cdots + \hat{\beta}_m x_m^0\}}{1 + \exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \cdots + \hat{\beta}_m x_m^0\}}\right) \exp\{\hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1}^0 + \cdots + \hat{\gamma}_{k-m} x_k^0\} \\ &= \frac{\exp\{\hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1}^0 + \cdots + \hat{\gamma}_{k-m} x_k^0\}}{1 + \exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \cdots + \hat{\beta}_m x_m^0\}}. \end{aligned}$$

6.3.5 SAS Implementation

The `genmod` procedure with the option `dist=zinb` and `zeromodel` statement fits a zero-inflated negative binomial regression. The syntax is:

```
proc genmod data=data_name;
  class <list of categorical predictors>F;
  model response_name=<list of predictors>/dist=zinb;
  zeromodel <list of predictors of structural zeros>;
run;
```


- SAS outputs the estimate of the dispersion parameter (called **Dispersion**) that is equal to $1/\hat{r}$.

6.3.6 R Implementation

The function `zeroinfl()` in the library `pscl` may be used to fit a zero-inflated negative binomial regression in R. The syntax for this function is

```
summary(fitted.model.name<- zeroinfl(response.name ~ x{m+1}.name
+ ... + xk.name|x1.name + ... + xm.name, data = data.name,
dist = "negbin")
```

- R prints the estimate of the dispersion parameter r and terms it **Theta**.

6.3.7 Example

EXAMPLE 6.3. Sixty Californian weather stations with continuous records between 1965 and 2014 were randomly chosen for the analysis. For each station, its elevation (in meters), average annual temperature (in Fahrenheit), and the number of years when it snowed were considered. The number of snowy years ranged between 0 and 50, with 26 stations having zero years of snow. We fit the zero-inflated negative binomial regression with the elevation as the predictor of π , and the average annual temperature as the predictor of λ . The SAS code is presented below.

```
data weather;
  input elevation avgtemp snowyears @@;
cards;
131.1 72.6 0 81.7 68.7 0 602 65.4 2
1338.1 58.8 50 18.3 67.0 2 310.3 64.6 1
18.3 67.5 2 182.9 67.9 0 1444.4 54.5 44
1278.6 57.0 27 1389.9 57.7 49 1295.4 59.9 21
712.6 62.2 7 256.0 69.2 0 27.4 65.4 0
974.8 56.3 44 271.3 70.7 0 381.9 63.9 26
71.0 68.9 0 1088.1 66.8 12 3.7 70.9 0
28.0 73.1 0 520.6 65.4 6 2139.7 60.1 24
974.8 59.1 44 18.3 67.6 0 18.0 67.7 0
101.5 70.3 2 44.2 68.2 0 327.7 68.0 6
125.0 68.0 0 999.7 62.1 50 146.3 67.4 0
77.4 66.6 1 146.3 68.7 0 240.8 69.9 0
391.7 65.4 0 222.5 66.9 0 1165.9 63.1 22
132.6 65.8 0 483.4 65.0 1 712.6 64.7 7
847.6 61.7 45 725.4 66.5 16 36.6 65.9 0
```

```

81.7    68.6 0    6.1      69.1 0    73.8    67.4 0
1516.4 55.5 50 1160.7    61.5 50 111.3    67.9 1
21.0    67.6 1    12.2     66.2 0    83.8    66.2 0
1160.7 62.5 50 576.4    67.2 0    398.4    64.2 4
1431.0 59.6 41 41.5     67.9 7    1179.6    64.0 49
;

```

```

proc genmod;
  model snowyears=avgtemp/dist=zinb;
  zeromodel elevation;
run;

```

Log Likelihood -151.5915

Analysis Of Maximum Likelihood Parameter Estimates

Parameter	Estimate	Pr > ChiSq
Intercept	19.0986	<.0001
avgtemp	-0.2593	<.0001
Dispersion	0.7447	

Analysis Of Maximum Likelihood Zero Inflation Parameter Estimates

Parameter	Estimate	Pr > ChiSq
Intercept	1.2623	0.0228
elevation	-0.0056	0.0054

```

proc genmod;
  model snowyears=/dist=zinb;
  zeromodel;
run;

```

Full Log Likelihood -178.2204

```

data deviance_test;
  deviance=-2*(-178.2204-(-151.5915));
  pvalue=1-probchi(deviance,2);
run;

```

```

proc print noobs;
run;

```

deviance	pvalue
53.2578	2.724E-12

The fitted model has parameter estimates $\hat{\pi} = \exp\{1.2623 - 0.0056 \cdot \text{elevation}\} / (1 + \exp\{1.2623 - 0.0056 \cdot \text{elevation}\})$, $\hat{\lambda} = \exp\{19.0986 - 0.2593 \cdot \text{avgtemp}\}$, and $\hat{r} = 1/0.7447 = 1.3428$. The model has a good fit as judged by the tiny p -value for the goodness-of-fit test. Both average annual temperature and elevation are significant predictors in this model. For a one-meter increase in elevation, the estimated odds in favor of zero years with snow change by $(\exp\{-0.0056\} - 1) \cdot 100\% = -0.56\%$, that is, decrease by 0.56%. For a one-degree increase in average annual temperature, the estimated average number of snowy years changes by $(\exp\{-0.2593\} - 1) \cdot 100\% = -22.84\%$, or decreases by 22.84%.

Consider the station at the elevation of 1,165.9 meters where the average annual temperature is 63.1 degrees Fahrenheit. The observed number of years when it snowed is 22. The value predicted by the model is found as

$$y^0 = \frac{\exp\{19.0986 - 0.2593 \cdot 63.1\}}{1 + \exp\{1.2623 - 0.0056 \cdot 1165.9\}} = 15.3578.$$

The same predicted value is outputted by SAS if we run these statements:

```
data prediction;
input elevation avgtemp;
cards;
1165.9 63.1
;

data weather;
  set weather prediction;
run;

proc genmod;
  model snowyears=avgtemp/dist=zinb;
  zeromodel elevation;
  output out=outdata p=p_snowyears;
run;

proc print data=outdata(firstobs=61) noobs;
var p_snowyears;
run;

p_snowyears
  15.3545
```

The R code that produces matching output is below.

```
weather.data<-read.csv(file="./Example6.3Data.csv",
header=TRUE, sep=",")

#fitting zero-inflated negative binomial model
library(pscl)
summary(fitted.model<- zeroinfl(snowyears ~ avgtemp|elevation,
data = weather.data, dist = "negbin"))
```

Count model coefficients (negbin with log link):

	Estimate	Pr(> z)
(Intercept)	19.09858	4.04e-09
avgtemp	-0.25931	5.23e-07

Zero-inflation model coefficients (binomial with logit link):

	Estimate	Pr(> z)
(Intercept)	1.262349	0.02124
elevation	-0.005642	0.00349

Theta = 1.3428

```
#checking model fit
null.model<- zeroinfl(snowyears ~ 1, data=weather.data, dist="negbin")
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

53.25778

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

2.724081e-12

```
#using fitted model for prediction
print(predict(fitted.model,
data.frame(elevation=1165.9, avgtemp=63.1)))
```

15.35455

□

6.4 Hurdle Negative Binomial Regression Model

6.4.1 Model Definition

For a count response variable with overdispersion, zeros may be modeled independently of positive responses. The *hurdle negative binomial regression model*⁴ accomplishes just that. In this model, assuming x_1, \dots, x_k are the predictors, the response variable y has the probability distribution function

$$\mathbb{P}(Y = y) = \begin{cases} \pi, & \text{if } y = 0, \\ (1 - \pi) \frac{\left(\frac{r}{r+\lambda}\right)^r \frac{\Gamma(r+y)}{y! \Gamma(r)} \left(\frac{\lambda}{r+\lambda}\right)^y}{1 - \left(\frac{r}{r+\lambda}\right)^r}, & \text{if } y = 1, 2, \dots, \end{cases}$$

where

$$\pi = \frac{\exp\{\beta_0 + \beta_1 x_1 + \dots + \beta_m x_m\}}{1 + \exp\{\beta_0 + \beta_1 x_1 + \dots + \beta_m x_m\}}, \quad (6.8)$$

$$\lambda = \exp\{\gamma_0 + \gamma_1 x_{m+1} + \dots + \gamma_{k-m} x_k\}, \text{ and } r \text{ is a positive integer.} \quad (6.9)$$

This model is not a generalized linear model, since the distribution is a mixture distribution.

6.4.2 Fitted Model

From (6.8) and (6.9), in the fitted hurdle negative binomial regression model, the estimated parameters take the form

$$\hat{\pi} = \frac{\exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1 + \dots + \hat{\beta}_m x_m\}}{1 + \exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1 + \dots + \hat{\beta}_m x_m\}}, \quad (6.10)$$

$$\hat{\lambda} = \exp\{\hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1} + \dots + \hat{\gamma}_{k-m} x_k\}, \text{ and } \hat{r}. \quad (6.11)$$

6.4.3 Interpretation of Estimated Regression Coefficients

The estimated beta coefficients are interpreted as in the logistic regression, in terms of the odds in favor of zero. Also, it can be shown (do it!) that the expected response depends on the parameters via the relation

$$\mathbb{E}(y) = (1 - \pi) \frac{\lambda}{1 - \left(\frac{r}{r+\lambda}\right)^r} = (1 - \pi) \frac{\lambda}{1 - \left(1 + \lambda/r\right)^{-r}}.$$

⁴First studied in Mullahy, J. (1986). "Specification and testing of some modified count data models". *Journal of Econometrics*, 33(3): 341 – 365.

This relation is too complex to yield an easy interpretation of the estimated gamma regression coefficients.

6.4.4 Predicted Response

In view of the above expression for the expected value of y , and also (6.10) and (6.11), the predicted value y^0 , when predictor variables assume certain fixed values x_1^0, \dots, x_k^0 , can be found as

$$\begin{aligned}
 y^0 &= \left(1 - \frac{\exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \dots + \hat{\beta}_m x_m^0\}}{1 + \exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \dots + \hat{\beta}_m x_m^0\}} \right) \times \\
 &\times \frac{\exp\{\hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1}^0 + \dots + \hat{\gamma}_{k-m} x_k^0\}}{1 - \left(1 + \exp\{\hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1}^0 + \dots + \hat{\gamma}_{k-m} x_k^0\} / \hat{r} \right)^{-\hat{r}}} \\
 &= \frac{\left(1 + \exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \dots + \hat{\beta}_m x_m^0\} \right)^{-1} \exp\{\hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1}^0 + \dots + \hat{\gamma}_{k-m} x_k^0\}}{1 - \left(1 + \exp\{\hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1}^0 + \dots + \hat{\gamma}_{k-m} x_k^0\} / \hat{r} \right)^{-\hat{r}}}.
 \end{aligned}$$

6.4.5 SAS Implementation

Invoking the `fmm` procedure with the `dist=truncnegbin` option in the `model` statement fits the hurdle negative binomial model. The complete syntax follows.

```

proc fmm data=data_name;
  class <list of categorical predictors>;
  model response_name=<list of predictors>/dist=truncnegbin;
  model + /dist=constant;
  probmodel <list of predictors of zeros>;
  output out=outdata_name pred=predicted_response_name;
run;

```

- As explained in Subsection 5.4.5, when writing down the fitted model, the estimated regression coefficients in $\hat{\pi}$ have to be taken with the opposite sign.
- SAS estimates the inverse of the dispersion parameter r , and terms it **Scale Parameter**.

6.4.6 R Implementation

The function `hurdle()` in the library `pscl` may be used to fit a hurdle negative binomial model in R. The syntax in this case is

```
summary(fitted.model.name<- hurdle(response.name ~ x{m+1}.name + ...
+ xk.name | x1.name + ... + xm.name, data=data.name, dist="negbin",
zero.dist= "binomial", link="logit"))
```

- R prints the estimate of the dispersion parameter. The name for the quantity is `Theta`.
- Similar to SAS, R evaluates $1 - \pi$, and therefore, the estimated regression coefficients for π have to be taken with the opposite sign.

6.4.7 Example

EXAMPLE 6.4. A bank wants to estimate the risk of delinquent credit card accounts for new applicants. A random sample of 35 applicants is drawn. The selected variables are the number of previously delinquent credit card accounts, age, gender, current income (high/low), and the total number of years ever unemployed. The conjecture is that age could account for zero delinquent accounts, whereas gender, income, and the number of unemployed years might be associated with positive responses. The code that fits a hurdle negative binomial model is as follows:

```
data creditcards;
input ndelinqaccounts age gender$ income$ nunemployyears @@;
cards;
12 53 M Low 8 0 26 F Low 4 16 49 M Low 8 0 23 M Low 5
7 28 F High 6 2 44 M Low 2 11 49 F Low 7 4 43 M Low 4
0 25 M Low 0 0 28 M High 5 4 25 M High 1 5 40 M High 6
1 37 M Low 3 0 48 M High 1 7 36 F Low 5 0 48 M Low 4
13 56 M Low 10 0 22 M Low 0 7 36 F High 4 3 35 M Low 1
7 35 F High 0 0 42 F Low 0 1 56 M Low 4 5 22 M Low 0
0 38 F Low 7 4 52 M High 5 1 30 F Low 6 0 27 M High 1
0 32 F High 3 4 46 F Low 1 2 32 M Low 2 7 26 F Low 6
0 23 M Low 5 3 30 M High 2 0 25 M Low 3
;

proc fmm;
class gender income;
```

```

model ndelinqaccounts=gender income
  nunemployyears/dist=truncnegbin;
model+/dist=constant;
probmodel age;
run;

```

-2 Log Likelihood 144.5

Parameter Estimates for Truncated Negative Binomial Model

Effect	gender	income	Estimate	Pr > z
Intercept			0.7462	0.0153
gender	F		0.2343	0.3352
gender	M		0	.
income		High	0.1526	0.5687
income		Low	0	.
nunemployyears			0.1740	<.0001
Scale Parameter			0.09103	

Parameter Estimates for Mixing Probabilities

Effect	Estimate	Pr > z
Intercept	-2.3203	0.1006
age	0.08147	0.0442

```

proc fmm;
model ndelinqaccounts=/dist=truncnegbin;
model+/dist=constant;
probmodel;
run;

```

-2 Log Likelihood 161.4

```

data deviance_test;
deviance=161.4-144.5;
pvalue=1-probchi(deviance,4);
run;

```

```

proc print noobs;
run;

```

deviance	pvalue
16.9	0.002021359

In the fitted model, the estimated parameters are $\hat{\pi} = \frac{\exp\{2.3203 - 0.08147 \cdot \text{age}\}}{1 + \exp\{2.3203 - 0.08147 \cdot \text{age}\}}$, $\hat{\lambda} = \exp\{0.7462 + 0.2343 \cdot \text{female} + 0.1526 \cdot \text{highincome} + 0.1740 \cdot \text{nunemployyears}\}$, and $\hat{r} = 1/0.09103 = 10.9854$. This model fits the data well, as demonstrated by a small p -value in the deviance test. Age is a significant predictor of π , whereas the number of unemployed years is the only significant predictor of λ . For a one-year increase in age, the estimated odds in favor of zero delinquent accounts change by $(\exp\{-0.08147\} - 1) \cdot 100\% = -7.82\%$, or is reduced by 7.82%. Further, due to complexity of the model, we will not attempt to interpret the estimated gamma regression coefficients.

To predict the number of delinquent accounts for a 45-year old male with high income and zero years of unemployment, we compute

$$y^0 = \frac{\exp\{0.7462 + 0.1526\} (1 + \exp\{2.3203 - 0.08147 \cdot 45\})^{-1}}{1 - \left(1 + \exp\{0.7462 + 0.1526\}/10.9854\right)^{-10.9854}} = 2.1878.$$

The same value is outputted in SAS:

```
data prediction;
input age gender$ income$ nunemployyears;
cards;
45 M High 0
;

data creditcards;
set creditcards prediction;
run;

proc fmm;
class gender income;
model ndelinqaccounts=gender income
nunemployyears/dist=truncnegbin;
model +/dist=constant;
probmodel age;
output out=outdata pred=p_ndelinqaccounts;
run;

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

```
p_ndelinqaccounts
2.18752
```

The script and output in R are given below.

```
creditcards.data<-read.csv(file="./Example6.4Data.csv",
header=TRUE, sep=",")

#specifying reference categories
gender.rel<- relevel(creditcards.data$gender, ref="M")
income.rel<- relevel(creditcards.data$income, ref="Low")

#fitting hurdle negative binomial model
library(pscl)
summary(fitted.model<- hurdle(ndelinqaccounts ~ gender.rel
+ income.rel + nunemployyears|age, data=creditcards.data,
dist="negbin", zero.dist="binomial", link="logit"))

Count model coefficients (truncated negbin with log link):
              Estimate Pr(>|z|)
(Intercept)   0.74619   0.0153
gender.relF    0.23427   0.3352
income.relHigh 0.15257   0.5687
nunemployyears 0.17401  7.51e-05

Zero hurdle model coefficients (binomial with logit link):
              Estimate Pr(>|z|)
(Intercept) -2.32034   0.1006
age          0.08147   0.0442

Theta: count = 10.9851

#checking model fit
null.model<- hurdle(ndelinqaccounts ~ 1, data=creditcards.data,
dist="negbin", zero.dist="binomial", link="logit")
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))

16.80772

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

0.002106471
```

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(age=45, gender.rel="M",
income.rel="High", nunemployyears=0)))
```

2.187517

□

Exercises for 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) Argue that X , the number of successes observed until the r th failure, is a negative binomial random variable with the probability mass function

$$P(X = x) = \binom{x+r-1}{x} p^x (1-p)^r, \quad x = 0, 1, 2, \dots$$

Show that for a fixed r , this distribution is a special case of the exponential family of distributions, that is, it can be written in the form (1.3) where $\theta = \ln p$ and $\phi = 1$.

(b) Using the substitution $p = \frac{\lambda}{r + \lambda}$, rewrite the probability mass function in part (a) as

$$P(X = x) = \left(\frac{r}{r + \lambda}\right)^r \frac{\Gamma(r+x)}{x! \Gamma(r)} \left(\frac{\lambda}{r + \lambda}\right)^x, \quad x = 0, 1, 2, \dots$$

Derive that $\mathbb{E}(X) = \lambda$ and $\text{Var}(X) = \lambda + \lambda^2/r$. Hint: Use the fact that for a negative binomial random variable with a mass function defined in part (a), the mean is $\frac{pr}{1-p}$, and variance is $\frac{pr}{(1-p)^2}$.

(c) Suppose the parameter r goes to infinity, but the mean λ is constant. Show that the limiting probability mass function is that of a Poisson distribution, that is, prove that

$$\begin{aligned} & \lim_{r \rightarrow \infty} \left(\frac{r}{r + \lambda}\right)^r \frac{\Gamma(r+x)}{x! \Gamma(r)} \left(\frac{\lambda}{r + \lambda}\right)^x \\ &= \frac{\lambda^x}{x!} \lim_{r \rightarrow \infty} \frac{\Gamma(r+x)}{\Gamma(r)} \left(1 + \frac{\lambda}{r}\right)^{-r} = \frac{\lambda^x}{x!} e^{-\lambda}, \quad x = 0, 1, 2, \dots \end{aligned}$$

EXERCISE 6.2. Graduate students in marine biology conducted an experiment on mussel *Mytilus californicus* survival. They prepared 24 cages with 50 mussels each, and placed them in various plots in tidal areas along the shoreline. The food was supplied daily at high, medium, or low levels. Maximum and minimum daily temperatures were logged by an automatic data recorder positioned in each cage. The number of mussels that died in each cage was recorded two weeks later. The data are:

Max temp	Min temp	Feeding level	N dead mussels	Max temp	Min temp	Feeding level	N dead mussels
77	60	high	0	83	62	med	8
88	59	high	1	75	63	med	3
78	62	high	1	76	61	med	2
85	60	high	2	86	62	med	1
78	61	high	0	92	62	low	2
89	63	high	0	89	64	low	3
92	62	high	2	96	68	low	19
75	58	high	0	86	62	low	7
80	59	med	1	74	61	low	3
90	61	med	2	88	62	low	12
74	63	med	4	97	63	low	9
92	62	med	6	91	61	low	7

- Model mussel mortality via the negative binomial regression. Present the fitted model. What predictors turn out to be significant at the 5% level?
- How good is the model fit?
- How would you interpret the estimated significant coefficients?
- 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.

EXERCISE 6.3. Researchers in K-12 education are conducting a study on daily allowance that high-school students receive from their parents. They randomly select 30 students and record their age, gender, whether they have had a job during the past summer, and an approximate weekly allowance (in units of \$5). The data are:

Age	Gender	Job	Allowance	Age	Gender	Job	Allowance
15	M	yes	0	15	M	no	0
18	F	yes	3	15	M	no	12
18	M	yes	3	18	M	no	3
14	F	no	6	15	M	no	4
16	F	yes	2	18	M	yes	0
17	F	yes	1	15	F	no	8
18	F	yes	1	15	M	no	5
15	F	no	4	15	M	no	5
16	M	yes	1	14	M	no	4
16	F	no	9	16	F	yes	3
16	M	no	3	17	M	no	2
16	M	no	10	18	M	yes	2
16	F	yes	0	17	F	yes	11
14	M	no	9	15	M	no	6
17	M	yes	1	16	M	no	12

- Is the negative binomial regression appropriate in modeling the amount of weekly allowance? Fit the model and discuss significance of the predictor variables.
- How good is the model fit?
- Interpret the estimated significant regression coefficients.
- Predict the amount of weekly allowance for a male student, age 16, who hasn't held a summer job.

EXERCISE 6.4. A state park is interested in proper allocation of recreational resources. As part of the analysis, data were collected on 30 randomly chosen kayak rentals. The number of kayaks rented, party size, length of route (in hours), and whether the party camped overnight (and returned kayaks the next day). Note that some parties owned some number of kayaks and rented just a few, so party size is not necessarily linearly proportional to the number of rented kayaks. In addition, rented kayaks could be two- or three-seaters. The data are given below.

N rented kayaks	Party size	Route length	Camped overnight	N rented kayaks	Party size	Route length	Camped overnight
6	12	1	yes	7	14	3	no
2	4	3	yes	2	7	12	no
3	7	12	no	2	6	12	yes
2	6	3	no	3	18	6	yes
1	3	2	no	2	4	1	yes
2	7	6	yes	2	4	4	yes
2	4	2	no	4	9	12	yes
1	3	6	yes	3	10	2	no
3	9	12	yes	1	2	3	no
5	10	4	no	12	12	4	no
1	2	1	no	10	12	12	yes
2	6	12	no	2	7	6	yes
4	9	4	no	3	8	12	no
1	3	2	no	7	14	3	no
3	7	2	no	1	3	6	yes

- 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.
- Discuss model fit.
- Interpret the estimated significant regression coefficients, whatever are possible to interpret.
- Predict the number of rented kayaks for a party of 5 people who plan to take a 6-hour route and to camp overnight.

EXERCISE 6.5. A sociologist is studying popularity of YouTube vlogs. He selects a random sample of 40 video channels and records the number of new videos posted in the past month, total number of videos posted by the vlogger, number of subscribers (in thousands), number of views (in thousands), and type of videos (comedy, fashion, life advice, news, popular science, or new products and brands). The data are summarized in the following table.

N new videos	Num videos	Num subscr	Num views	Video type	N new videos	Num videos	Num subscr	Num views	Video type
3	81	3.9	205.8	life advice	3	212	1.3	121.1	products
4	188	27.0	213.6	fashion	4	86	4.2	160.2	fashion
1	55	10.1	176.8	products	12	517	85.4	163.7	life advice
4	123	14.4	59.7	science	7	100	8.0	91.5	news
1	65	5.0	508.7	life advice	9	130	2.8	38.9	life advice
2	118	3.5	280.6	comedy	2	34	2.4	151.9	fashion
3	119	4.7	25.7	fashion	30	396	7.6	118.4	comedy
1	47	4.4	135.8	products	12	52	0.9	617.2	life advice
2	405	58.0	423.6	comedy	9	43	7.7	542.6	comedy
4	160	10.9	212.8	science	22	304	2.6	150.5	news
4	123	1.3	204.1	fashion	10	430	1.4	242.1	comedy
1	96	1.1	449.0	comedy	2	76	15.2	106.7	fashion
2	44	2.7	217.7	fashion	2	53	3.6	121.1	fashion
1	71	8.0	12.3	life advice	9	98	1.0	160.2	news
4	190	6.7	433.3	life advice	19	56	4.7	163.7	news
1	59	9.5	90.4	science	4	102	0.9	91.5	fashion
1	36	9.2	423.9	products	2	43	0.5	38.9	fashion
3	511	92.5	158.4	products	14	81	3.2	151.9	products
2	112	4.2	225.7	products	4	86	3.2	118.4	products
4	156	32.4	140.8	comedy	10	90	2.6	617.2	products

- 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?
- Does the model have a good fit?
- Interpret estimated significant regression coefficients, if possible.
- 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.

EXERCISE 6.6. A large insurance company that offers a range of insurance policies would like to model the number of insurance claims submitted within a five-year period. The data are retrieved for a random sample of 40 policyholders who have been with the company for at least ten years. The data include the number of claims made in the past five years, the number of claims made during the previous five years, current age, and gender of each policyholder. The data are given in the table below.

N claims past 5 years	N claims previous 5 years	Age	Gender	N claims past 5 years	N claims previous 5 years	Age	Gender
1	1	39	M	8	3	69	F
1	2	66	M	0	2	70	M
7	0	56	M	7	2	70	M
3	4	43	F	3	1	54	F
4	1	42	F	2	1	38	M
4	2	52	M	3	1	50	F
0	0	39	F	0	1	62	M
4	6	68	M	8	2	54	M
6	1	41	F	0	0	59	M
0	1	54	F	0	1	61	F
4	2	50	F	0	0	69	F
6	4	57	M	8	3	57	F
5	4	47	F	0	0	57	M
1	2	43	M	12	5	72	F
1	1	36	M	0	2	42	M
1	2	55	F	6	2	42	F
5	5	57	F	7	2	66	M
8	5	53	M	7	4	53	M
0	1	72	M	6	0	52	M
0	1	67	F	3	3	57	F

- 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?
- Interpret the estimated significant coefficients.
- How good is the model fit? Give a quantitative answer.
- 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?

EXERCISE 6.7. The aim of the study conducted by dental researchers is to model decayed, missing, and filled teeth (DMFT) index data. They considered dental records for 38 randomly selected patients and picked age, gender, and oral hygiene as predictors. The data are presented in the table below.

DMFT index	Age	Gender	Oral hygiene	DMFT index	Age	Gender	Oral hygiene
0	28	F	high	11	29	M	low
2	30	F	med	0	20	F	high
0	26	F	high	0	25	F	high
15	55	M	high	1	22	F	high
8	40	F	med	7	37	M	med
2	19	M	med	2	56	F	med
0	24	F	med	15	63	M	high
8	77	F	low	0	21	M	med
5	48	F	high	5	55	F	high
3	21	F	med	0	25	F	high
11	59	M	med	2	68	M	low
9	50	M	high	4	25	M	med
1	24	F	med	6	59	F	low
0	26	M	med	9	58	F	med
1	23	F	high	0	37	M	med
2	24	F	med	0	18	M	high
1	21	M	low	16	73	M	med
2	40	M	med	3	23	M	med
0	31	F	med	8	65	M	med

- 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.
- Analyze the fit of the model.
- Give interpretation of the estimated significant coefficients.
- Find the predicted value of the DMFT index for a man, aged 28, with a high level of oral hygiene.

EXERCISE 6.8. Consider the data in Exercise 6.6.

- 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?
- Discuss goodness-of-fit of the model.
- Interpret the estimated significant coefficients. What is the direction of the relationships?
- 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.

EXERCISE 6.9. Researchers in sports medicine are interested in modeling the number of sport related injuries a collegiate athlete has during games throughout her/his career. They select 30 records that contain the total number of injuries (major or minor), athlete's gender, how many sports the athlete has participated in, and the number of injuries during practice. The researchers hypothesize that a lower number of injuries during practice might help explain zero injuries during games, while a larger number of sports might account for a larger number of injuries. They also hypothesize that female athletes have fewer injuries than males. The data are:

N game injuries	Gender	N sports	N practice injuries	N game injuries	Gender	N sports	N practice injuries
0	M	2	2	2	F	2	0
0	M	1	1	0	F	2	0
1	F	2	3	1	F	2	2
1	F	1	0	2	M	2	3
2	F	1	1	0	M	1	0
0	F	2	1	3	M	2	4
0	M	1	0	5	F	1	4
6	M	2	3	0	M	2	0
7	M	1	5	7	M	3	4
2	M	2	4	7	F	2	3
8	M	3	1	3	F	3	4
10	M	2	2	8	M	1	2
4	M	1	7	3	F	3	5
0	F	1	1	7	M	3	6
2	M	2	2	12	M	2	5

- 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.
- Analyze the model fit.
- Give interpretation of the estimated significant coefficients.
- 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.

Chapter 7

Regression Models for Proportion Response

Suppose the response variable y assumes continuous values in an interval $(0,1)$, where the endpoints may or may not be included. In this chapter we discuss four models that might be applied in this case: beta regression, zero-inflated beta regression (if zero is included in the range), one-inflated beta regression (if one is a possible observation), and zero-one-inflated beta regression (where both zero and one may be observed).

7.1 Beta Regression Model

7.1.1 Model Definition

Consider a response variable y that represents a proportion of events of interest (for instance, the proportion of books returned on-time in a library per week). We will suppose that y assumes values that range continuously between zero and one, not including the endpoints. The *beta regression model*¹ with predictors x_1, \dots, x_k prescribes that y follows a beta distribution with the probability density function

$$f(y) = \frac{y^{\mu\phi-1} (1-y)^{(1-\mu)\phi-1}}{B(\mu\phi, (1-\mu)\phi)}, \quad 0 < y < 1, \quad (7.1)$$

where the *location parameter*

$$\mu = \frac{\exp\{\beta_0 + \beta_1 x_1 + \dots + \beta_k x_k\}}{1 + \exp\{\beta_0 + \beta_1 x_1 + \dots + \beta_k x_k\}}, \quad (7.2)$$

¹Originally proposed in Ferrari, S.L.P. and F. Cribari-Neto (2004). “Beta regression for modelling rates and proportions”. *Journal of Applied Statistics*, 31(7): 799 – 815.

and the *dispersion* (or *scale*) *parameter* ϕ is a positive real number. It can be shown (see Exercise 7.1) that y has mean $\mathbb{E}(y) = \mu$ and variance $\mathbb{V}ar(y) = \frac{\mu(1-\mu)}{1+\phi}$.

7.1.2 Fitted Model

According to (7.2), the estimated parameters of the fitted model are

$$\hat{\mu} = \frac{\exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_k x_k\}}{1 + \exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_k x_k\}} \quad \text{and} \quad \hat{\phi}. \quad (7.3)$$

Technically speaking, the beta regression belongs to the class of generalized linear models. After a proper re-parametrization, it can be shown that the beta distribution belongs to the exponential family of distributions, and the mean response μ is related to the predictors through the logit link function.

7.1.3 Interpretation of Estimated Regression Coefficients

From (7.3), $\frac{\mu}{1-\mu} = \exp\{\beta_0 + \beta_1 x_1 + \cdots + \beta_k x_k\}$. Thus,

- for a unit increase in a numerical predictor x_1 , the percent change in the estimated ratio $\frac{\hat{\mu}}{1-\hat{\mu}} = \frac{\hat{\mathbb{E}}(y)}{1-\hat{\mathbb{E}}(y)}$ is $(\exp\{\hat{\beta}_1\} - 1) \cdot 100\%$, controlling for the other predictors.
- If x_1 is an indicator variable, then $\exp\{\hat{\beta}_1\} \cdot 100\%$ represents the percent ratio of $\frac{\hat{\mu}}{1-\hat{\mu}}$ for $x_1 = 1$ and that for $x_1 = 0$, keeping all the other predictors fixed.

7.1.4 Predicted Response

Since the mean of the response y is μ and using (7.3), we see that for some given predictors x_1^0, \dots, x_k^0 , the predicted response satisfies

$$y^0 = \frac{\exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \cdots + \hat{\beta}_k x_k^0\}}{1 + \exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \cdots + \hat{\beta}_k x_k^0\}}. \quad (7.4)$$

7.1.5 SAS Implementation

In SAS, a beta regression is estimated via the `glimmix` procedure (which stands for “generalized linear mixed” modeling). The syntax is:

```
proc glimmix data=data_name;
  class catpredictor1_name (ref="level_name") catpredictor2_name
    (ref="level_name") ...;
model response_name=<list of predictors>/dist=beta link=logit solution;
  output out=outdata pred(ilink)=predicted_name;
run;
```

- The option `solution` requests the estimates of the regression coefficients.
- SAS outputs the value of $\hat{\phi}$, which is termed `Scale`.
- By default, SAS outputs the linear predictor $\hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \cdots + \hat{\beta}_k x_k^0$. The option `(ilink)` (stands for “inverse link”) computes the predicted value of the response according to the formula (7.4).

7.1.6 R Implementation

The function `betareg()` in the library `betareg` fits the beta regression model. The syntax is

```
summary(fitted.model.name<- betareg(response.name~x1.name+...
+ xk.name, data=data.name, link="logit"))
```

- In the output, the estimate of the dispersion parameter is termed `(phi)`.

7.1.7 Example

EXAMPLE 7.1. A professor of Library and Information Science has collected a random sample of 28 libraries and recorded total number of books each library has (in thousands), number of card holders (in thousands), library location (urban or rural), number of books checked out during a one-month period, and number of the books that were returned on-time, that is, on or prior to the due date. The professor has calculated the proportion of books returned on-time as the ratio between the number of books returned on-time and number of books checked out, and is interested in studying associations between this proportion and the three predictor variables. The code below fits the beta regression model.

```

data libraries;
input nbooks ncardholders location$ propontime @@;
cards;
9.8 0.7 rural 0.39 25.4 7.8 urban 0.81
14.7 1.7 urban 0.71 38.2 9.5 urban 0.85
35.5 5.8 urban 0.74 14.1 2.6 rural 0.47
16.3 2.9 rural 0.72 33.3 7.7 urban 0.83
19.9 3.1 rural 0.69 38.0 4.6 urban 0.76
44.1 8.3 urban 0.85 34.2 5.4 urban 0.86
12.7 2.7 rural 0.53 28.7 3.4 urban 0.78
9.5 1.0 rural 0.55 31.8 8.7 urban 0.78
21.1 6.2 urban 0.82 12.1 2.3 rural 0.42
26.3 0.9 rural 0.88 16.4 8.4 urban 0.88
11.8 1.6 rural 0.45 31.6 8.8 rural 0.64
24.6 4.5 rural 0.81 25.3 1.8 urban 0.73
12.4 1.9 rural 0.38 16.2 7.3 rural 0.66
13.7 6.2 urban 0.84 29.4 6.3 urban 0.72
;

```

```

proc glimmix;
  class location(ref="rural");
  model propontime=nbooks ncardholders location/
    dist=beta link=logit solution;
run;

```

-2 Log Likelihood -53.40

Parameter Estimates			
Effect	location	Estimate	Pr > t
Intercept		-0.2058	0.3896
nbooks		0.02624	0.0480
ncardholders		0.04494	0.2999
location	urban	0.5236	0.0316
location	rural	0	.
Scale		20.6478	

```

proc glimmix;
  model propontime=/dist=beta link=logit;
run;

```

-2 Log Likelihood -30.66

```

data deviance_test;

```

```

deviance=-30.66-(-53.40);
pvalue=1-probchi(deviance,3);
run;

proc print noobs;
run;

deviance      pvalue
22.74  0.000045749

```

In the fitted model, the estimated mean has the form

$$\hat{\mu} = \frac{\exp\{-0.2058 + 0.02624 \cdot nbooks + 0.04494 \cdot ncardholders + 0.5236 \cdot urban\}}{1 + \exp\{-0.2058 + 0.02624 \cdot nbooks + 0.04494 \cdot ncardholders + 0.5236 \cdot urban\}},$$

and the estimated dispersion parameter is $\hat{\phi} = 20.6478$. The model fits the data well since the p -value of the corresponding test is tiny. The number of books and library location are significant predictors of the proportion of books returned on time at the 5% level. As the number of books increases by one thousand, the estimated ratio of the mean proportion of books returned on-time and the mean proportion of books not returned on-time, $\frac{\hat{\mu}}{1 - \hat{\mu}}$, increases by $(\exp\{0.02624\} - 1) \cdot 100\% = 2.66\%$. This ratio for urban libraries is $\exp\{0.5236\} \cdot 100\% = 168.81\%$ of that for rural libraries.

To illustrate the calculations required for prediction, suppose we would like to predict proportion of books that are returned on time for a library in a rural area with 15,000 books and 2,500 card holders. We have

$$\begin{aligned}
y^0 &= \frac{\exp\{-0.2058 + 0.02624 \cdot 15 + 0.04494 \cdot 2.5\}}{1 + \exp\{-0.2058 + 0.02624 \cdot 15 + 0.04494 \cdot 2.5\}} \\
&= \frac{\exp\{0.30015\}}{1 + \exp\{0.30015\}} = 0.57448.
\end{aligned}$$

The same prediction can be computed in SAS by typing:

```

data prediction;
input nbooks ncardholders location$;
cards;
15 2.5 rural
;

data libraries;

```

```

set libraries prediction;
run;

proc glimmix;
  class location;
model propontime=nbooks ncardholders location/dist=beta
  link=logit solution;
  output out=outdata pred(ilink)=p_propontime;
run;

proc print data=outdata (firstobs=29) noobs;
var p_propontime;
run;

p__propontime
      0.57447

```

The R code and output for this example are:

```

libraries.data<-read.csv(file="./Example7.1Data.csv",
header=TRUE, sep=",")

#specifying reference category
location.rel<- relevel(libraries.data$location, ref="rural")

#fitting beta regression model
library(betareg)
summary(fitted.model<- betareg(propontime ~ nbooks + ncardholders
+ location.rel, data=libraries.data, link="logit"))

```

	Estimate	Pr(> z)
(Intercept)	-0.20579	0.3729
nbooks	0.02624	0.0447
ncardholders	0.04494	0.2960
location.relurban	0.52357	0.0239
(phi)	20.648	

```

#checking model fit
null.model<- betareg(propontime ~ 1, data=libraries.data, link="logit")
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))

22.73631

```



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

4.582989e-05

#using fitted model for prediction
print(predict(fitted.model, data.frame(nbooks=15, ncardholders=2.5,
location.rel="rural")))

0.5744721

□
```

7.2 Zero-inflated Beta Regression Model

7.2.1 Model Definition

When zero is a regular observation for the modeled proportion, a *zero-inflated beta regression* may be used. In this model, the response variable y has a mixture of a beta distribution and a point mass at zero. That is, the distribution function is modeled as

$$f(y) = \begin{cases} \pi_0, & \text{if } y = 0, \\ (1 - \pi_0) \frac{y^{\mu\phi-1} (1-y)^{(1-\mu)\phi-1}}{B(\mu\phi, (1-\mu)\phi)}, & \text{if } 0 < y < 1, \end{cases} \quad (7.5)$$

where the probability of zero

$$\pi_0 = \frac{\exp\{\beta_0 + \beta_1 x_1 + \cdots + \beta_m x_m\}}{1 + \exp\{\beta_0 + \beta_1 x_1 + \cdots + \beta_m x_m\}}, \quad (7.6)$$

the location parameter

$$\mu = \frac{\exp\{\gamma_0 + \gamma_1 x_{m+1} + \cdots + \gamma_{k-m} x_k\}}{1 + \exp\{\gamma_0 + \gamma_1 x_{m+1} + \cdots + \gamma_{k-m} x_k\}}, \quad (7.7)$$

and the dispersion parameter ϕ is a positive real number. Being a mixture of beta distribution and a degenerate distribution at zero, this distribution doesn't belong to the exponential family, and thus the model is not a generalized linear model.

7.2.2 Fitted Model

By (7.6) and (7.7), the fitted model has the estimated parameters of the form:

$$\hat{\pi}_0 = \frac{\exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_m x_m\}}{1 + \exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_m x_m\}}, \quad (7.8)$$

$$\hat{\mu} = \frac{\exp\{\hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1} + \cdots + \hat{\gamma}_{k-m} x_k\}}{1 + \exp\{\hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1} + \cdots + \hat{\gamma}_{k-m} x_k\}}, \text{ and } \hat{\phi}. \quad (7.9)$$

7.2.3 Interpretation of Estimated Regression Coefficients

If the two sets of predictor variables are different, the estimated beta and gamma coefficients yield the following interpretation. Estimated beta coefficients are interpreted as in the binary logistic regression in terms of odds in favor of observing a zero proportion (see Subsection 3.1.3). As for estimated gamma coefficients, for fixed values of x_1, \dots, x_k , we can assume that π_0 is a constant, and, so μ can be viewed as the conditional mean response given that an observation is strictly above zero, that is, $\mu = \mathbb{E}(y|y > 0)$ (prove it!). Thus, assuming all the other x variables are unchanged,

- for a unit increase in a continuous x_{m+1} , the quantity $(\exp\{\hat{\gamma}_1\} - 1) \cdot 100\%$ represents percent change in the estimated ratio $\frac{\hat{\mu}}{1 - \hat{\mu}} = \frac{\hat{\mathbb{E}}(y|y > 0)}{1 - \hat{\mathbb{E}}(y|y > 0)}$.
- If x_{m+1} is an indicator variable, then $\exp\{\hat{\gamma}_1\} \cdot 100\%$ is interpreted as the estimated percent ratio of $\frac{\hat{\mu}}{1 - \hat{\mu}}$ for $x_{m+1} = 1$ and that for $x_{m+1} = 0$.

7.2.4 Predicted Response

Since $\mathbb{E}(y) = (1 - \pi_0)\mu$ (show it!), and using (7.8) and (7.9), we see that for a fixed set x_1^0, \dots, x_k^0 , the predicted response y^0 is found according to the formula:

$$\begin{aligned} y^0 &= \left(1 - \frac{\exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \cdots + \hat{\beta}_m x_m^0\}}{1 + \exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \cdots + \hat{\beta}_m x_m^0\}}\right) \frac{\exp\{\hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1}^0 + \cdots + \hat{\gamma}_{k-m} x_k^0\}}{1 + \exp\{\hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1}^0 + \cdots + \hat{\gamma}_{k-m} x_k^0\}} \\ &= \left(1 + \exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \cdots + \hat{\beta}_m x_m^0\}\right)^{-1} \frac{\exp\{\hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1}^0 + \cdots + \hat{\gamma}_{k-m} x_k^0\}}{1 + \exp\{\hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1}^0 + \cdots + \hat{\gamma}_{k-m} x_k^0\}}. \end{aligned} \quad (7.10)$$

7.2.5 SAS Implementation

There is currently no ready procedure that would fit a zero-inflated beta regression in SAS. One would need to use the `nlmixed` procedure (“non-linear mixed”) that allows to specify any log-likelihood function of the response variable. In this procedure, all predictors must be either numeric or 0-1 variables. We express the log-likelihood function in terms of the natural logarithm of

the gamma function `lgamma`, that is, we write the log-likelihood function as: for $y = 0$, log-likelihood = $\ln \pi_0$, and, for $0 < y < 1$, log-likelihood = $\ln \left[(1-\pi_0) \frac{y^{\mu\phi-1} (1-y)^{(1-\mu)\phi-1}}{B(\mu\phi, (1-\mu)\phi)} \right] = \ln \left[(1-\pi_0) \frac{\Gamma(\phi)}{\Gamma(\mu\phi)\Gamma((1-\mu)\phi)} y^{\mu\phi-1} (1-y)^{(1-\mu)\phi-1} \right] = \ln(1-\pi_0) + \ln \Gamma(\phi) - \ln \Gamma(\mu\phi) - \ln \Gamma((1-\mu)\phi) + (\mu\phi-1) \ln y + ((1-\mu)\phi-1) \ln(1-y)$.

The syntax for fitting the zero-inflated beta regression and predicting response is below. It is assumed that the last row in the data set contains the values for prediction.

```
proc nlmixed data=data_name;
  parms b0=init_value ... bm=init_value g0=init_value ...
        g{k-m}=init_value phi=init_value;
  pi0 = exp(b0+b1*x1_name+...+bm*xm_name)/
        (1+exp(b0+b1*x1_name+...+bm*xm_name));
  mu = exp(g0+g1*x{m+1}_name+...+g{k-m}*xk_name)/
        (1+exp(g0+g1*x{m+1}_name+...+g{k-m}*xk_name));
  if (response_name=0) then loglikelihood_name=log(pi0);
  else loglikelihood_name=log(1-pi0)+lgamma(phi)-lgamma(mu*phi)
    -lgamma((1-mu)*phi)+(mu*phi-1)*log(response_name)
    +((1-mu)*phi-1)*log(1-response_name);
  model response_name ~ general(loglikelihood_name);
  predict (1-pi0)*mu out=outdata_name;
run;
```

- In the `parms` statement, the initial values for the variables `b0`, ..., `bm`, `g0`, ..., `g{k-m}`, and `phi` can be chosen arbitrarily.
- The predicted response can be found in the last row of the data set `outdata_name`.

7.2.6 R Implementation

In R, the function `gamlss()` in the library `gamlss` can be applied to fit a zero-inflated beta regression. Here “gamlss” stands for “generalized additive models for location, scale, and shape”. R uses the term `mu` for the location parameter μ , `nu` for the probability of zero π_0 , and `sigma` for the log of the dispersion parameter ϕ , that is, `sigma` = $\ln \phi$. The syntax is

```
summary(fitted.model.name<- gamlss(response.name ~ x{m+1}.name + ...
+ xk.name, mu.link="logit", nu.formula=~ x1.name + ... + xm.name,
```

```
nu.link="logit", data=data.name, family=BEZI))
```

If one wishes to predict response for a new data point, the quickest way to do that is to use function `predictAll()` as shown below:

```
parampred.name<- predictAll(fitted.model, newdata  
=data.frame(catpredictor1.name="value", ...,  
numpredictork.name=value), type="response")
```

The *parampred.name* contains predicted values for parameters *mu* and *nu*, thus the predicted response can be retrieved by specifying the expression

```
print(pred.name<- (1-parampred.name$nu)*parampred.name$mu)
```

- It is important to know that the variables in *newdata* must match the variables in the original data *data_name*. It means that prior to running the function `gamlss()`, all the predictor variables that are computed or modified, must be added to the data set *data.name*. This can be accomplished by giving them names that reference the data set, *data.name\$variable.name*.

7.2.7 Example

EXAMPLE 7.2. A college Parking and Transportation Services conducted a survey regarding the mode of transportation to campus in the past four weeks. For this analysis, a stratified sample of 60 respondents was drawn for the purpose of oversampling people who sometimes bike to campus. The variables recorded are the number of trips to campus in the past four weeks, the number of times the respondent biked to campus, respondent's status (student/faculty/staff), respondent's gender (F/M), duration of parking permit (6, 9, or 12-month, modeled as a continuous variable), and distance to campus. The code below fits a zero-inflated beta regression to the proportion of time a respondent biked to campus. Gender and distance to campus were used as predictors of π_0 , whereas status and parking permit were used to model μ .

```
data transport;  
input ntrips nbiked status$ gender$ parking distance @@;  
propbiked=nbiked/ntrips;  
faculty=(status="faculty");  
staff=(status="staff");  
male=(gender="M");
```

```

cards;
26 6 student F 6 7 13 0 faculty M 9 15 17 0 faculty M 9 31
15 0 faculty M 9 9 17 0 student M 6 34 20 13 staff F 6 3
17 0 student F 9 17 14 0 faculty F 9 10 26 7 student M 6 3
8 5 faculty F 12 3 17 0 student F 12 22 18 0 student M 12 8
15 0 staff F 12 4 17 7 faculty F 12 5 20 15 staff M 9 6
8 0 student F 6 5 26 9 student M 9 3 12 11 faculty F 6 12
13 5 student M 9 7 8 6 faculty M 9 5 9 0 student M 9 7
12 2 faculty F 9 8 11 0 student F 6 13 8 1 staff F 9 16
14 0 faculty M 12 35 9 2 staff F 12 8 19 12 student M 6 5
20 0 faculty M 12 60 28 11 staff M 9 1 10 0 faculty F 6 30
14 4 staff M 12 4 8 5 student F 6 2 9 0 staff F 12 16
12 0 faculty M 12 15 12 0 student F 9 25 21 19 faculty M 9 3
23 22 faculty F 6 14 27 22 faculty M 9 6 14 3 student F 6 12
15 9 faculty M 12 3 8 2 student F 9 6 15 5 faculty F 12 6
12 10 student F 6 3 8 5 faculty M 9 4 14 4 student F 6 2
15 0 student M 6 10 12 7 student F 6 6 23 7 staff M 12 2
18 13 student F 6 2 9 0 student M 6 16 10 9 faculty M 9 6
8 1 staff M 12 7 12 2 student F 6 12 14 0 staff M 12 7
8 7 student F 12 12 16 14 student M 6 2 11 4 faculty F 12 5
10 0 faculty F 12 22 16 0 staff M 12 4 10 0 faculty M 12 11
;

```

```

proc nlmixed;
  parms b0=0.1 b1=0.1 b2=0.1 g0=0.1 g1=0.1 g2=0.1 g3=0.1 phi=0.1;
  pi0 = exp(b0+b1*male+b2*distance)/(1+exp(b0+b1*male+b2*distance));
  mu = exp(g0+g1*faculty+g2*staff+g3*parking)/(1+
    exp(g0+g1*faculty+g2*staff+g3*parking));
  if (propbiked=0) then loglikelihood=log(pi0);
  else loglikelihood=log(1-pi0)+lgamma(phi)-lgamma(mu*phi)
    -lgamma((1-mu)*phi)+(mu*phi-1)*log(propbiked)
    +((1-mu)*phi-1)*log(1-propbiked);
  model propbiked~general(loglikelihood);
run;

```

-2 Log Likelihood 33.3

Parameter Estimates

Parameter	Estimate	Pr > t
b0	-4.4897	0.0006
b1	1.7728	0.0484
b2	0.3396	0.0009
g0	1.1040	0.0665

```

g1      1.0635      0.0127
g2      0.03280     0.9455
g3      -0.1638     0.0475
phi      3.9871

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 (propbiked=0) then loglikelihood=log(pi0);
  else loglikelihood =log(1-pi0)+lgamma(phi)-lgamma(mu*phi)
    -lgamma((1-mu)*phi)+(mu*phi-1)*log(propbiked)
    +((1-mu)*phi-1)*log(1-propbiked);
  model propbiked~general(loglikelihood);
run;

-2 Log Likelihood 77.5

data deviance_test;
  deviance=77.5-33.3;
  pvalue=1-probchi(deviance,5);
run;

proc print noobs;
run;

deviance    pvalue
  44.2    2.1095E-8

```

In the fitted model, the estimates of the parameters are

$$\hat{\pi}_0 = \frac{\exp\{-4.4897 + 1.7728 \cdot \text{male} + 0.3396 \cdot \text{distance}\}}{1 + \exp\{-4.4897 + 1.7728 \cdot \text{male} + 0.3396 \cdot \text{distance}\}},$$

$$\hat{\mu} = \frac{\exp\{1.1040 + 1.0635 \cdot \text{faculty} + 0.03280 \cdot \text{staff} - 0.1638 \cdot \text{parking}\}}{1 + \exp\{1.1040 + 1.0635 \cdot \text{faculty} + 0.03280 \cdot \text{staff} - 0.1638 \cdot \text{parking}\}},$$

and $\hat{\phi} = 3.9871$. The model fits the data well as evidenced by a tiny p -value in the deviance test. At the 5% significance level, male and distance are significant predictors of π_0 , whereas faculty and parking significantly predict μ . The estimated odds in favor of not biking to campus for males are $\exp\{1.7728\} \cdot 100\% = 588.73\%$ of those for females, and for a one-mile increase in distance, these estimated odds increase by $(\exp\{0.3396\} - 1) \cdot 100\% = 40.44\%$. The estimated ratio $\frac{\hat{\mu}}{1 - \hat{\mu}}$ for faculty is $\exp\{1.0635\} \cdot 100\% = 289.65\%$ of that

for students. For a one-month increase in duration of parking permit, the estimated ratio changes by $(\exp\{-0.1638\} - 1) \cdot 100\% = -15.11\%$, that is, it decreases by 15.11%.

To predict the response for a female student who lives 3 miles away from campus and who purchases parking permit for 6 months during a year. Utilizing (7.10), we have

$$y^0 = \left(1 + \exp\{-4.4897 + 0.3396 \cdot 3\}\right)^{-1} \frac{\exp\{1.1040 - 0.1638 \cdot 6\}}{1 + \exp\{1.1040 - 0.1638 \cdot 6\}} = 0.5143.$$

In SAS, the following lines of code produce the same predicted value. We present only the relevant quantities in the output.

```
data prediction;
input parking distance faculty staff male;
cards;
6 3 0 0 0
;

data transport;
  set transport prediction;
run;

proc nlmixed;
  parms b0=0.1 b1=0.1 b2=0.1 g0=0.1 g1=0.1 g2=0.1
        g3=0.1 phi=0.1;
  pi0 = exp(b0+b1*male+b2*distance)/(1+
    exp(b0+b1*male+b2*distance));
  mu = exp(g0+g1*faculty+g2*staff+g3*parking)/(1+
    exp(g0+g1*faculty+g2*staff+g3*parking));
  if (propbiked=0) then loglikelihood=log(pi0);
  else loglikelihood =log(1-pi0)+lgamma(phi)-lgamma(mu*phi)
    -lgamma((1-mu)*phi)+(mu*phi-1)*log(propbiked)
    +((1-mu)*phi-1)*log(1-propbiked);
  model propbiked~general(loglikelihood);
  predict (1-pi0)*mu out=outdata;
run;

proc print data=outdata (firstobs=61) noobs;
var Pred;
run;
```

Pred
0.51433

Finally, the script and relevant output in R are given below.

```
transport.data<-read.csv(file="./Example7.2Data.csv", header=TRUE,  
sep=",")
```

```
#computing new variables and making them part of the original data set  
transport.data$propbiked<- transport.data$nbiked/transport.data$ntrips  
transport.data$faculty<-ifelse(transport.data$status=="faculty",1,0)  
transport.data$staff<-ifelse(transport.data$status=="staff",1,0)  
transport.data$male<-ifelse(transport.data$gender=="M",1,0)
```

```
#fitting zero-inflated beta regression model  
library(gamlss)  
summary(fitted.model<- gamlss(propbiked ~ faculty + staff + parking,  
mu.link="logit", nu.formula= ~ male + distance, nu.link="logit",  
data=transport.data, family=BEZI))
```

Mu link function: logit

Mu Coefficients:

	Estimate	Pr(> t)
(Intercept)	1.10390	0.0673
faculty	1.06338	0.0131
staff	0.03265	0.9458
parking	-0.16374	0.0482

Sigma link function: log

Sigma Coefficients:

	Estimate
(Intercept)	1.3831

Nu link function: logit

Nu Coefficients:

	Estimate	Pr(> t)
(Intercept)	-4.48970	0.000699
male	1.77277	0.049067
distance	0.33957	0.000960

```
#checking model fit
```

```
null.model<- gamlss(propbiked ~ 1, mu.link="logit", nu.formula= ~ 1,  
nu.link="logit", data=transport.data, family=BEZI)  
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```


44.18192

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

2.127389e-08

```
#using fitted model for prediction
param.pred<- predictAll(fitted.model, newdata
=data.frame(parking=6, distance=3, faculty=0, staff=0,
male=0), type="response")
print((1-param.pred$nu)*param.pred$mu)
```

0.5143409

□

7.3 One-inflated Beta Regression Model

7.3.1 Model Definition

Suppose y variable assumes values in the interval $(0,1]$, that is, 1 is a possible observation. Then the data may be modeled by a *one-inflated beta regression*. In this model, the response variable y has a mixture beta distribution with a point mass at one. That is, the distribution function of y is

$$f(y) = \begin{cases} (1 - \pi_1) \frac{y^{\mu\phi-1} (1-y)^{(1-\mu)\phi-1}}{B(\mu\phi, (1-\mu)\phi)}, & \text{if } 0 < y < 1, \\ \pi_1, & \text{if } y = 1. \end{cases}$$

Here the probability of one

$$\pi_1 = \frac{\exp\{\beta_0 + \beta_1 x_1 + \cdots + \beta_m x_m\}}{1 + \exp\{\beta_0 + \beta_1 x_1 + \cdots + \beta_m x_m\}}, \quad (7.11)$$

the location parameter

$$\mu = \frac{\exp\{\gamma_0 + \gamma_1 x_{m+1} + \cdots + \gamma_{k-m} x_k\}}{1 + \exp\{\gamma_0 + \gamma_1 x_{m+1} + \cdots + \gamma_{k-m} x_k\}}, \quad (7.12)$$

and the dispersion parameter ϕ is a positive real number.

Analogously to zero-inflated beta regression, since the underlying distribution is a mixture distribution, this model is not a generalized linear regression model.

7.3.2 Fitted Model

In view of expressions (7.11) and (7.12), the fitted model has the estimated parameters

$$\hat{\pi}_1 = \frac{\exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_m x_m\}}{1 + \exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_m x_m\}}, \quad (7.13)$$

$$\hat{\mu} = \frac{\exp\{\hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1} + \cdots + \hat{\gamma}_{k-m} x_k\}}{1 + \exp\{\hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1} + \cdots + \hat{\gamma}_{k-m} x_k\}}, \quad \text{and } \hat{\phi}. \quad (7.14)$$

7.3.3 Interpretation of Estimated Regression Coefficients

The estimated beta coefficients are interpreted as in the logistic regression in terms of odds in favor of observing a one (see Subsection 3.1.3). As concerns the estimated gamma coefficients, for fixed values of x_1, \dots, x_m , we can assume π_1 is a constant, and so, μ represents the conditional mean response given that an observation is below one; that is, $\mu = \mathbb{E}(y|y < 1)$ (show it!). Therefore, under the assumption that all the other predictors stay fixed,

- when a continuous x_{m+1} increases by one unit, the percent change in the estimated ratio $\frac{\hat{\mu}}{1 - \hat{\mu}} = \frac{\mathbb{E}(y|y < 1)}{1 - \mathbb{E}(y|y < 1)}$ is $(\exp\{\hat{\gamma}_1\} - 1) \cdot 100\%$.
- For an indicator variable x_{m+1} , the quantity $\exp\{\hat{\gamma}_1\} \cdot 100\%$ represents the percent ratio of $\frac{\hat{\mu}}{1 - \hat{\mu}}$ for $x_1 = 1$ and that for $x_1 = 0$.

7.3.4 Predicted Response

It can be proven (do it!) that $\mathbb{E}(y) = \pi_1 + (1 - \pi_1)\mu$. Thus, utilizing (7.13) and (7.14), we find that for given x_1^0, \dots, x_k^0 , the predicted response y^0 satisfies:

$$\begin{aligned} y^0 &= \frac{\exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \cdots + \hat{\beta}_m x_m^0\}}{1 + \exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \cdots + \hat{\beta}_m x_m^0\}} + \left(1 - \frac{\exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \cdots + \hat{\beta}_m x_m^0\}}{1 + \exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \cdots + \hat{\beta}_m x_m^0\}}\right) \times \\ &\times \frac{\exp\{\hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1}^0 + \cdots + \hat{\gamma}_{k-m} x_k^0\}}{1 + \exp\{\hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1}^0 + \cdots + \hat{\gamma}_{k-m} x_k^0\}} = \left(1 + \exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \cdots + \hat{\beta}_m x_m^0\}\right)^{-1} \times \\ &\times \left(\exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \cdots + \hat{\beta}_m x_m^0\} + \frac{\exp\{\hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1}^0 + \cdots + \hat{\gamma}_{k-m} x_k^0\}}{1 + \exp\{\hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1}^0 + \cdots + \hat{\gamma}_{k-m} x_k^0\}}\right). \end{aligned} \quad (7.15)$$

7.3.5 SAS Implementation

The procedure `nlmixed` is used to fit a one-inflated beta regression. The syntax is:

```
proc nlmixed data=data_name;
  parms b0=init_value ... bm=init_value g0=init_value ...
        g{k-m}=init_value phi=init_value;
  pi1 = exp(b0+b1*x1_name+...+bm*xm_name)/
        (1+exp(b0+b1*x1_name+...+bm*xm_name));
  mu = exp(g0+g1*x{m+1}_name+...+g{k-m}*xk_name)/
        (1+exp(g0+g1*x{m+1}_name+...+g{k-m}*xk_name));
  if (response_name=1) then loglikelihood_name=log(pi1);
  else loglikelihood_name=log(1-pi1)+lgamma(phi)-lgamma(mu*phi)
    -lgamma((1-mu)*phi)+(mu*phi-1)*log(response_name)
    +((1-mu)*phi-1)*log(1-response_name);
  model response_name ~ general(loglikelihood_name);
  predict pi1+(1-pi1)*mu out=outdata_name;
run;
```

7.3.6 R Implementation

In R, the function `gamlss()` in the library `gamlss` fits a one-inflated beta regression. In the output, `mu` is the location parameter μ , `nu` is the probability of one π_1 , and `sigma` = $\ln \phi$. The syntax is

```
summary(fitted.model.name<- gamlss(response.name ~ x{m+1}.name + ...
+ xk.name, mu.link="logit", nu.formula=~x1.name+...+xm.name,
nu.link="logit", data =data.name, family=BE0I))
```

```
parampred.name<- predictAll(fitted.model, newdata
=data.frame(catpredictor1.name="value", ...,
numpredictork.name=value), type="response")
```

```
print(parampred.name$nu+(1-parampred.name$nu)*parampred.name$mu)
```

- Variables listed in `newdata` must be contained in the original data set `data_name`.

7.3.7 Example

EXAMPLE 7.3. A medical student is studying medication adherence in patients with high cholesterol. He collects data on patients' age (in years),

gender (M/F), depression (1=yes/0=no), diabetes (1=yes/0=no), and total number of medications taken daily. In addition, he obtains pharmaceutical records and calculates proportion of days covered (pdc) for cholesterol-lowering medication, that is, the proportion of days that the patient has taken the medication. For patients who consistently adhere to their medication regimen, proportion of days covered is equal to one, and therefore fitting one-inflated regression would be appropriate. Below are the statements and outputs in SAS. In what follows π_1 is regressed on diabetes and number of medications, whereas μ is modeled as a function of age, gender, and depression.

```
data medadherence;
input age gender$ depression diabetes nmeds pdc@@;
female=(gender="F");
cards;
62 M 0 1 2 1.00 73 M 1 0 5 0.96 56 M 0 0 5 0.08
58 M 0 0 4 0.32 56 F 0 0 3 1.00 62 F 0 0 4 0.86
31 F 0 1 5 0.62 59 M 0 0 5 0.23 64 M 0 1 3 0.56
67 F 0 0 4 0.91 59 F 0 0 3 0.39 90 M 1 0 4 0.86
83 M 0 1 2 1.00 70 F 0 0 2 0.41 58 M 1 0 6 0.36
61 F 0 0 2 0.85 70 F 1 1 4 0.87 56 M 0 0 3 0.28
67 F 0 0 3 0.80 60 F 0 0 3 0.16 67 M 0 1 3 1.00
67 M 1 0 3 0.24 71 M 1 0 2 0.64 67 F 1 1 2 1.00
46 M 0 0 3 0.48 62 F 0 0 6 0.32 63 M 0 1 1 0.27
67 F 0 1 4 0.92 83 M 0 0 2 0.83 62 M 0 1 4 0.47
71 F 0 1 3 1.00 49 F 1 0 5 0.26 66 M 0 0 1 1.00
61 M 0 0 4 0.51 66 F 0 0 4 0.66 71 M 0 0 5 0.82
58 F 0 0 3 0.40 70 F 0 1 4 0.88 83 M 0 1 2 1.00
64 M 0 0 5 0.39
;

proc nlmixed;
parms b0=0.1 b1=0.1 b2=0.1 g0=0.1 g1=0.1 g2=0.1 g3=0.1 phi=0.1;
pi1 = exp(b0+b1*diabetes+b2*nmeds)/(1+exp(b0+b1*diabetes+b2*nmeds));
mu = exp(g0+g1*age+g2*female+g3*depression)/(1+
exp(g0+g1*age+g2*female+g3*depression));
if (pdc=1) then loglikelihood=log(pi1);
else loglikelihood =log(1-pi1)+lgamma(phi)-lgamma(mu*phi)
-lgamma((1-mu)*phi)+ (mu*phi-1)*log(pdc)
+((1-mu)*phi-1)*log(1-pdc);
model pdc ~ general(loglikelihood);
run;
```

-2 Log Likelihood 6.4

Parameter Estimates

Parameter	Estimate	Pr > t
b0	1.5679	0.3348
b1	2.4896	0.0327
b2	-1.4320	0.0214
g0	-3.9846	0.0041
g1	0.06073	0.0045
g2	0.7162	0.0281
g3	0.1210	0.7489
phi	4.5022	

```
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 (pdc=1) then loglikelihood=log(pi1);
    else loglikelihood =log(1-pi1)+lgamma(phi)-lgamma(mu*phi)
      -lgamma((1-mu)*phi)+(mu*phi-1)*log(pdc)+((1-mu)*phi-1)*log(1-pdc);
    model pdc~general(loglikelihood);
run;
```

-2 Log Likelihood 36.4

```
data deviance_test;
  deviance=36.4-6.4;
  pvalue=1-probchi(deviance,5);
run;
```

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

deviance	pvalue
30	0.000014749

The parameters of the fitted model are

$$\hat{\pi}_1 = \frac{\exp\{1.5679 + 2.4896 \cdot \text{diabetes} - 1.4320 \cdot \text{nmeds}\}}{1 + \exp\{1.5679 + 2.4896 \cdot \text{diabetes} - 1.4320 \cdot \text{nmeds}\}},$$
$$\hat{\mu} = \frac{\exp\{-3.9846 + 0.06073 \cdot \text{age} + 0.1210 \cdot \text{depression} + 0.7162 \cdot \text{female}\}}{1 + \exp\{-3.9846 + 0.06073 \cdot \text{age} + 0.7162 \cdot \text{female} + 0.1210 \cdot \text{depression}\}},$$

and $\hat{\phi} = 4.5022$. This model has a good fit due to a low p -value in the goodness-of-fit test. Diabetes and number of medications are significant predictors of probability of one, whereas age and female are significant predictors of μ , at the 0.05 level of significance. For patients with diabetes, the estimated odds in favor of perfect medication adherence are $(\exp\{2.4896\}) \cdot 100\% = 1,205.65\%$ of those without diabetes. If the number of medications increases by one, the estimated odds in favor of 100%-adherence change by $(\exp\{-1.4320\} - 1) \cdot 100\% = -76.12\%$, that is, decreases by 76.12%. When age increases by one year, the estimated ratio $\frac{\hat{\mu}}{1 - \hat{\mu}} = \frac{\hat{\mathbb{E}}(y|y < 1)}{1 - \hat{\mathbb{E}}(y|y < 1)}$ increases by $(\exp\{0.06073\} - 1) \cdot 100\% = 6.26\%$. For females, this estimated ratio is $\exp\{0.7162\} \cdot 100\% = 204.66\%$ of that for males.

Further, according to (7.15), the predicted proportion of days covered for a 77-year old female patient who has no depression but has diabetes and who takes a total of three medications is computed as

$$y^0 = \left(1 + \exp\{1.5679 + 2.4896 - 1.4320 \cdot 3\}\right)^{-1} \times \\ \times \left(\exp\{1.5679 + 2.4896 - 1.4320 \cdot 3\} + \frac{\exp\{-3.9846 + 0.06073 \cdot 77 + 0.7162\}}{1 + \exp\{-3.9846 + 0.06073 \cdot 77 + 0.7162\}}\right) \\ = 0.8900.$$

SAS calculates the same predicted value by running the following statements.

```
data prediction;
input age female depression diabetes nmeds;
cards;
77 1 0 1 3
;

data medadherence;
set medadherence prediction;
run;

proc nlmixed;
parms b0=0.1 b1=0.1 b2=0.1 g0=0.1 g1=0.1
      g2=0.1 g3=0.1 phi=0.1;
pi1 = exp(b0+b1*diabetes+b2*nmeds)/(1+
exp(b0+b1*diabetes+b2*nmeds));
mu = exp(g0+g1*age+g2*female+g3*depression)/(1+
exp(g0+g1*age+g2*female+g3*depression));
```

```

        if (pdc=1) then loglikelihood=log(pi1);
    else loglikelihood =log(1-pi1)+lgamma(phi)-lgamma(mu*phi)
        -lgamma((1-mu)*phi)+(mu*phi-1)*log(pdc)+((1-mu)*phi-1)*log(1-pdc);
    model pdc ~ general(loglikelihood);
        predict pi1+(1-pi1)*mu out=outdata;
run;

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

    Pred
0.89003

```

The R script and output for this example are presented below.

```

medadherence.data<-read.csv(file="./Example7.3Data.csv",
header=TRUE, sep=",")

#computing new variable and making it part of the original data set
medadherence.data$female<- ifelse(medadherence.data$gender=="F",1,0)

#fitting one-inflated beta regression model
library(gamlss)
summary(fitted.model<- gamlss(pdc ~ age + female + depression,
mu.link="logit", nu.formula= ~ diabetes + nmeds, nu.link="logit",
data=medadherence.data, family=BE01))

Mu link function: logit
Mu Coefficients:
            Estimate Pr(>|t|)
(Intercept) -3.97514  0.00469
age          0.06058  0.00511
female       0.71620  0.02951
depression   0.12123  0.74883

Sigma link function: log
Sigma Coefficients:
            Estimate
(Intercept)  1.504

Nu link function: logit

```

Nu Coefficients:

	Estimate	Pr(> t)
(Intercept)	1.5679	0.3362
diabetes	2.4896	0.0342
nmeds	-1.4320	0.0227

```
#checking model fit
null.model<- gamlss(pdc ~ 1, mu.link="logit", nu.formula= ~ 1,
nu.link="logit", data=medadherence.data, family=BE0I)
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

29.97312

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

1.492935e-05

```
#using fitted model for prediction
param.pred<- predictAll(fitted.model, newdata=data.frame(age=77,
female=1, depression=0, diabetes=1, nmeds=3), type="response")
print(param.pred$nu+(1-param.pred$nu)*param.pred$mu)
```

0.889879

□

7.4 Zero-one-inflated Beta Regression Model

7.4.1 Model Definition

In the *zero-one-inflated beta regression model*, the response variable y changes according to a distribution with the density:

$$f(y) = \begin{cases} \pi_0, & \text{if } y = 0, \\ (1 - \pi_0 - \pi_1) \frac{y^{\mu\phi-1} (1-y)^{(1-\mu)\phi-1}}{B(\mu\phi, (1-\mu)\phi)}, & \text{if } 0 < y < 1, \\ \pi_1, & \text{if } y = 1. \end{cases}$$

Here the parameters depend on predictors x_1, \dots, x_k via the following relations:

$$\mu = \frac{\exp\{\beta_0 + \beta_1 x_1 + \dots + \beta_m x_m\}}{1 + \exp\{\beta_0 + \beta_1 x_1 + \dots + \beta_m x_m\}}, \quad (7.16)$$

$$\pi_0 = \frac{\nu}{1 + \nu + \tau}, \quad \text{and} \quad \pi_1 = \frac{\tau}{1 + \nu + \tau}, \quad (7.17)$$

where

$$\nu = \exp\{\gamma_0 + \gamma_1 x_{m+1} + \cdots + \gamma_{l-m} x_l\} \quad \text{and} \quad \tau = \exp\{\zeta_0 + \zeta_1 x_{l+1} + \cdots + \zeta_{k-l} x_k\}, \quad (7.18)$$

and the dispersion parameter ϕ is a positive constant. Note that the probabilities of zero and one cannot be modeled completely independently of each other, and the given parametrization makes the regression parameters estimable.

Also, similarly to zero- and one-inflated beta regressions, in this situation the distribution of the response is a mixture distribution, and thus, the regression doesn't belong to the class of generalized linear models.

7.4.2 Fitted Model

Taking into account (7.16)-(7.18), the estimated parameters in the fitted model can be written as:

$$\hat{\mu} = \frac{\exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_m x_m\}}{1 + \exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_m x_m\}}, \quad (7.19)$$

$$\hat{\pi}_0 = \frac{\hat{\nu}}{1 + \hat{\nu} + \hat{\tau}}, \quad \text{and} \quad \hat{\pi}_1 = \frac{\hat{\tau}}{1 + \hat{\nu} + \hat{\tau}}, \quad (7.20)$$

where

$$\hat{\nu} = \exp\{\hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1} + \cdots + \hat{\gamma}_{l-m} x_l\}, \quad \hat{\tau} = \exp\{\hat{\zeta}_0 + \hat{\zeta}_1 x_{l+1} + \cdots + \hat{\zeta}_{k-l} x_k\}, \quad (7.21)$$

and the estimated dispersion parameter is $\hat{\phi}$.

7.4.3 Interpretation of Estimated Regression Coefficients

It can be shown (do it!) that if π_0 and π_1 are fixed, then μ is the conditional expectation of y given $0 < y < 1$, i.e., $\mu = \mathbb{E}(y|0 < y < 1)$. Therefore,

- if x_1 is a continuous predictor, then $(\exp\{\hat{\beta}_1\} - 1) \cdot 100\%$ gives the percent

change in the estimated ratio $\frac{\hat{\mu}}{1 - \hat{\mu}} = \frac{\hat{\mathbb{E}}(y|0 < y < 1)}{1 - \hat{\mathbb{E}}(y|0 < y < 1)}$ for a one-unit increase in x_1 , provided all the other predictors stay unchanged.

- If x_1 is an indicator variable, then $\exp\{\hat{\beta}_1\} \cdot 100\%$ represents the percent ratio of $\frac{\hat{\mu}}{1 - \hat{\mu}}$ for $x_1 = 1$ and that for $x_1 = 0$.

Further, the parameters for this model are chosen in such a way (prove it!) that $\nu = \frac{\pi_0}{1 - \pi_0 - \pi_1} = \frac{\mathbb{P}(y = 0)}{\mathbb{P}(0 < y < 1)}$ and $\tau = \frac{\pi_1}{1 - \pi_0 - \pi_1} = \frac{\mathbb{P}(y = 1)}{\mathbb{P}(0 < y < 1)}$. That means that ν represents the odds in favor of $y = 0$ versus $0 < y < 1$, and τ represents the odds of $y = 1$ against $0 < y < 1$. Consequently, estimated gamma coefficients are interpreted as in the logistic regression (see Subsection 3.1.3) in terms of odds of observing $y = 0$ versus $0 < y < 1$, and estimated zeta coefficients are interpreted as in the logistic regression in terms of odds of observing $y = 1$ against $0 < y < 1$.

7.4.4 Predicted Response

The mean of y in this model is equal to (show it!)

$$\mathbb{E}(y) = \pi_1 + (1 - \pi_0 - \pi_1) \mu = \frac{\tau + \mu}{1 + \nu + \tau},$$

and thus, in view of (7.19)-(7.21), the predicted response for given values of x variables, $x_1^0, x_2^0, \dots, x_k^0$, may be found through the formula

$$y^0 = \left(\exp\{\hat{\zeta}_0 + \hat{\zeta}_1 x_{l+1}^0 + \dots + \hat{\zeta}_{k-l} x_k^0\} + \frac{\exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \dots + \hat{\beta}_m x_m^0\}}{1 + \exp\{\hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \dots + \hat{\beta}_m x_m^0\}} \right) \times \left(1 + \exp\{\hat{\gamma}_0 + \hat{\gamma}_1 x_{m+1}^0 + \dots + \hat{\gamma}_{l-m} x_l^0\} + \exp\{\hat{\zeta}_0 + \hat{\zeta}_1 x_{l+1}^0 + \dots + \hat{\zeta}_{k-l} x_k^0\} \right)^{-1}.$$

7.4.5 SAS Implementation

Zero-one-inflated beta regression model can be programmed into SAS, using the `nlmixed` procedure. The general syntax is:

```
proc nlmixed data=data_name;
  parms b0=init_value <...> bm=init_value g0=init_value <...>
    g{1-m}=init_value z0=init_value <...> z{k-l}=init_value phi=init_value;
mu = exp(b0+b1*x1_name+...+bm*xm_name)/(1+exp(b0+b1*x1_name
  +...+bm*xm_name));
nu = exp(g0+g1*x{m+1}_name+...+g{1-m}*xl_name);
tau = exp(z0+z1*x{l+1}_name+z2*...+z{k-l}*xk_name);
pi0=nu/(1+nu+tau);
pi1=tau/(1+nu+tau);
if (response_name=0) then loglikelihood_name=log(pi0);
  if (response_name=1) then loglikelihood_name=log(pi1);
if (response_name >0 and response_name <1) then
```

```

loglikelihood_name=log(1-pi0-pi1)+lgamma(phi)-lgamma(mu*phi)
-lgamma((1-mu)*phi)+(mu*phi-1)*log(response_name)
+((1-mu)*phi-1)*log(1-response_name);
model response_name~ general(loglikelihood_name);
predict pi1+(1-pi0-pi1)*mu out=outdat_name;
run;

proc print data=outdata;
run;

```

7.4.6 R Implementation

In R, zero-one-inflated beta regression is fitted via function `gamlss()` in the library `gamlss`. The syntax is

```

fitted.model.name<- gamlss(response.name~x1.name+...+xm.name, mu.link="logit",
nu.formula=~x{l+1}.name+...+xl.name, nu.link="log", tau.formula=~x{l+1}.name+...
+xk.name, tau.link="log", data =data.name, family=BEINF)

parampred.name<- predictAll(fitted.model, newdata=data.frame(catpredictor1.name
="value", ..., numpredictork.name=value), type="response")

print((parampred.name$tau+parampred.name$mu)/(1+parampred.name$nu
+parampred.name$tau))

```

- In this model, the parameter **Sigma** is related to ϕ as $\text{Sigma}^2 = \frac{1}{1 + \phi}$. Moreover, R outputs the value of **(Intercept)** that relates to **Sigma** via a logit link function. Thus, to recover the estimate of ϕ from **(Intercept)**, we use the formula

$$\hat{\phi} = \frac{1 - \text{Sigma}^2}{\text{Sigma}^2} = \frac{1 - \left(\exp\{(\text{Intercept})\} / (1 + \exp\{(\text{Intercept})\}) \right)^2}{\left(\exp\{(\text{Intercept})\} / (1 + \exp\{(\text{Intercept})\}) \right)^2}.$$

- Variables listed in `newdata` must be contained in the original data set `data_name`.

7.4.7 Example

EXAMPLE 7.4. As an experiment, a school district has implemented an online math coaching program in a single K-8 school. Administrators are interested in finding out what factors predict completion of weekly assignments. The data are collected on students' grade level (5, 6, 7, or 8, fitted as a continuous variable), gender (M/F), score in math class (in percent, can exceed 100 due to extra credit), and proportion of solved exercises in a certain weekly online assignment. Since some students may not have completed any exercises, a zero is a possible response. On the other hand, some students might have completed all of the exercises, so a one is also a plausible response. A proportion of completed exercises for all other students would be between zero and one. The setting calls for a zero-one-inflated beta regression, which is fitted below. Here, the parameter μ is regressed on gender, ν on mathscore, and τ on grade.

```
data assignment;
input grade gender$ mathscore propassign @@;
female=(gender="F");
cards;
5 M 87.5 0.62 7 F 68.4 0.00 8 F 100.0 0.95 6 M 84.5 0.50
7 F 76.1 1.00 5 M 87.3 0.32 6 M 66.9 0.80 5 F 91.5 1.00
7 M 90.6 0.45 6 M 85.9 0.27 7 M 97.1 0.55 6 F 104.9 0.85
8 F 98.2 1.00 5 F 103.8 0.95 5 F 80.2 0.97 8 M 56.1 0.00
7 M 68.1 0.00 7 M 76.3 0.70 6 M 97.3 0.30 8 F 66.3 1.00
7 M 79.0 0.00 6 M 73.9 0.46 8 M 77.3 0.22 7 M 80.2 0.72
7 M 77.1 1.00 8 F 103.1 1.00 7 M 104.8 1.00 7 F 55.7 0.00
7 M 69.4 0.67 5 F 83.6 0.68 8 F 81.4 1.00 7 M 84.7 0.59
6 F 92.1 0.51 5 M 97.8 0.65 7 M 88.2 0.00 8 F 69.5 0.96
6 M 94.8 0.21 7 M 84.7 0.35 5 M 67.7 0.00 7 F 100.3 1.00
8 M 104.2 0.92 7 F 77.2 0.20 7 M 70.9 0.73 6 M 96.7 0.62
;

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*female)/(1+exp(b0+b1*female));
nu = exp(g0+g1*mathscore);
tau = exp(z0+z1*grade);
pi0=nu/(1+nu+tau);
pi1=tau/(1+nu+tau);
if (propassign=0) then loglikelihood=log(pi0);
if (propassign=1) then loglikelihood=log(pi1);
```

```

        if (propassign >0 and propassign <1) then
loglikelihood =log(1-pi0-pi1)+lgamma(phi)-lgamma(mu*phi)
               -lgamma((1-mu)*phi)+(mu*phi-1)*log(propassign)
               +((1-mu)*phi-1)*log(1-propassign);
model propassign~general(loglikelihood);
run;

```

2 Log Likelihood 47.8

Parameter Estimates

Parameter	Estimate	Pr > t
b0	0.1299	0.5070
b1	1.1173	0.0064
g0	10.4743	0.0159
g1	-0.1532	0.0098
z0	-7.8921	0.0280
z1	0.9879	0.0491
phi	4.1694	

```

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 (propassign=0) then loglikelihood=log(pi0);
  if (propassign=1) then loglikelihood=log(pi1);
  if (propassign >0 and propassign <1) then
    loglikelihood =log(1-pi0-pi1)+lgamma(phi)-lgamma(mu*phi)
                  -lgamma((1-mu)*phi)+(mu*phi-1)*log(propassign)
                  +((1-mu)*phi-1)*log(1-propassign);
model propassign~general(loglikelihood);
run;

```

2 Log Likelihood 73.3

```

data deviance_test;
  deviance=73.3-47.8;
  pvalue=1-probchi(deviance,3);
run;

proc print noobs;
run;

```

deviance	pvalue
25.5	0.000012136

The estimated parameters of the fitted model are

$$\hat{\mu} = \frac{\exp\{0.1299 + 1.1173 \cdot \text{female}\}}{1 + \exp\{0.1299 + 1.1173 \cdot \text{female}\}}, \quad \hat{\pi}_0 = \frac{\hat{\nu}}{1 + \hat{\nu} + \hat{\tau}}, \quad \text{and} \quad \hat{\pi}_1 = \frac{\hat{\tau}}{1 + \hat{\nu} + \hat{\tau}},$$

where

$$\hat{\nu} = \frac{\hat{\mathbb{P}}(y = 0)}{\hat{\mathbb{P}}(0 < y < 1)} = \exp\{10.4743 - 0.1532 \cdot \text{mathscore}\},$$

and

$$\hat{\tau} = \frac{\hat{\mathbb{P}}(y = 1)}{\hat{\mathbb{P}}(0 < y < 1)} = \exp\{-7.8921 + 0.9879 \cdot \text{grade}\},$$

and $\hat{\phi} = 4.1694$. This model fits the data well since the p -value in the goodness-of-fit test is way below 0.05. All the three predictors are significant at the 5% level.

For females, the estimated ratio $\frac{\hat{\mu}}{1 - \hat{\mu}} = \frac{\hat{\mathbb{E}}(y|0 < y < 1)}{1 - \hat{\mathbb{E}}(y|0 < y < 1)}$ is $\exp\{1.1173\} \cdot 100\% = 305.66\%$ of that for males. For a one-point increase in math score, the estimated odds in favor of $y = 0$ against $0 < y < 1$ change by $(\exp\{-0.1532\} - 1) \cdot 100\% = -14.20\%$, that is, decrease by 14.20%. As grade increases by one, the estimated odds in favor of $y = 1$ against $0 < y < 1$ increase by $(\exp\{0.9879\} - 1) \cdot 100\% = 168.56\%$.

Now we estimate the proportion of completed exercises for an 8th grade boy with 101% in math class. To this end, we compute

$$y^0 = \left(\exp\{-7.8921 + 0.9879 \cdot 8\} + \frac{\exp\{0.1299\}}{1 + \exp\{0.1299\}} \right) \times \\ \times \left(1 + \exp\{10.4743 - 0.1532 \cdot 101\} + \exp\{-7.8921 + 0.9879 \cdot 8\} \right)^{-1} = 0.7649.$$

The SAS code for the prediction follows.

```
data prediction;
input grade mathscore female;
cards;
8 101 0
;
```

```

data assignment;
  set assignment prediction;
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*female)/(1+exp(b0+b1*female));
  nu = exp(g0+g1*mathscore);
  tau = exp(z0+z1*grade);
  pi0=nu/(1+nu+tau);
  pi1=tau/(1+nu+tau);
  if (propassign=0) then loglikelihood=log(pi0);
  if (propassign=1) then loglikelihood=log(pi1);
  if (propassign >0 and propassign <1) then
    loglikelihood=log(1-pi0-pi1)+lgamma(phi)-lgamma(mu*phi)-lgamma((1-mu)*phi)+
      (mu*phi-1)*log(propassign)+((1-mu)*phi-1)*log(1-propassign);
  model propassign~general(loglikelihood);
  predict (tau+mu)/(1+nu+tau) out=outdata;
run;

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

```

```

    Pred
0.76493

```

The R script and output are below.

```

assignment.data<-read.csv(file="./Example7.4Data.csv",
header=TRUE, sep=",")

#computing new variable and making it part of the original data set
assignment.data$female<- ifelse(assignment.data$gender=="F",1,0)

#fitting zero-one-inflated beta regression model
library(gamlss)
summary(fitted.model<- gamlss(propassign~ female, mu.link="logit",
nu.formula=~ mathscore, nu.link="log", tau.formula=~ grade,
tau.link="log", data=assignment.data, family=BEINF))

```

Mu link function: logit

Mu Coefficients:

	Estimate	Pr(> t)
(Intercept)	1.2467	0.000782
female	1.1169	0.006916

Sigma link function: logit

Sigma Coefficients:

	Estimate
(Intercept)	-0.2418

Note that $\hat{\phi} = \frac{1 - \left(\exp\{-0.2418\} / (1 + \exp\{-0.2418\}) \right)^2}{\left(\exp\{-0.2418\} / (1 + \exp\{-0.2418\}) \right)^2} = 4.168981674$.

Nu link function: log

Nu Coefficients:

	Estimate	Pr(> t)
(Intercept)	10.47368	0.0163
mathscore	-0.15321	0.0101

Tau link function: log

Tau Coefficients:

	Estimate	Pr(> t)
(Intercept)	-7.8920	0.0290
grade	0.9879	0.0502

#checking model fit

```
null.model<- gamlss(propassign ~ 1, mu.link="logit", nu.formula=~ 1,
nu.link="log", tau.formula=~ 1, tau.link="log",
data=assignment.data, family=BEINF)
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
```

25.51013

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

1.207707e-05

#using fitted model for prediction

```
param.pred<- predictAll(fitted.model, newdata
=data.frame(grade=8, mathscore=101, female=0), type="response")
print((param.pred$tau+param.pred$mu)/(1+param.pred$nu+param.pred$tau))
```

0.7649165

□

Exercises for Chapter 7

EXERCISE 7.1. Prove that for the beta regression defined by (7.1) and (7.2), the mean of y is $\mathbb{E}(y) = \mu$, and the variance of y is $\text{Var}(y) = \frac{\mu(1-\mu)}{1+\phi}$.

EXERCISE 7.2. Ornithologists have collected data on migration of birds. They ringed 20 flocks of migratory birds prior to migration, and recorded for each flock the number of ringed birds, average mass (in grams), and average wingspan (in cm). The ringed flocks were observed later at the wintering grounds and the number of successfully migrated birds were counted. The distances traveled (in km) were also observed. The data are presented below.

Mass	Wingspan	Distance	N birds ringed	N birds migrated
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

- 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?
- Analyze the model fit.
- Give interpretation of the estimated significant parameters.
- 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.

EXERCISE 7.3. The department of Health Care Administration is analyzing utilization of hospital resources. They retrieve data on 30 randomly chosen U.S. hospitals, and are looking at percent of emergency room (ER) patients who were hospitalized, hospital location (urban or rural), hospital type (public or private), and hospital size by number of beds. The data are:

Percent hospzd	Hosp loc	Hosp type	N beds	Percent hospzd	Hosp loc	Hosp type	N beds
17	rural	private	56	4	urban	public	91
39	rural	public	144	6	urban	public	77
38	urban	public	61	39	urban	private	237
48	rural	public	186	41	urban	private	56
30	rural	private	132	45	rural	public	43
25	urban	private	589	13	urban	public	64
5	urban	public	53	42	rural	public	193
4	rural	private	73	28	urban	private	363
48	rural	private	154	31	urban	public	600
4	urban	public	38	48	rural	public	468
26	rural	private	318	41	rural	public	311
15	urban	public	35	9	urban	public	65
28	urban	private	184	13	urban	private	44
34	urban	private	173	44	urban	public	479
31	urban	public	63	16	rural	public	72

- Model the proportion of hospitalized ER patients. Write down the fitted model. What factors are significant predictors? Use $\alpha = 0.05$.
- How good is the model fit?
- Interpret estimated significant regression coefficients.
- Give the predicted proportion of hospitalized ER patients for a rural public hospital with 50 beds.

EXERCISE 7.4. In commercial fishing, an issue of concern is large percent of by-catch, an unwanted marine life caught along with intended fish. An analyst at a tuna fishery collected data on a randomly chosen sample of catches made by 20 fishing vessels. The variables are the distance to shore (in nautical miles), method of fishing (trawling, purse seining, or longline fishing), fishing depth (in meters), and the percentage of by-catch. The data are:

Distance to shore	Fishing method	Fishing depth	Percent by-catch	Distance to shore	Fishing method	Fishing depth	Percent by-catch
120	trawl	250	14	115	trawl	300	8
115	trawl	150	6	160	trawl	200	10
70	trawl	300	24	160	trawl	200	10
130	trawl	150	6	50	trawl	150	15
90	seine	200	56	10	seine	150	16
15	seine	350	32	25	seine	200	22
15	seine	150	13	15	seine	300	21
20	seine	350	23	40	longline	100	21
15	longline	200	10	60	longline	200	4
40	longline	150	7	50	longline	150	17

- Use the beta regression to model proportion of by-catch. Convert depth to kilometers. Write down the fitted model.
- Discuss significance of predictor variables and model fit.
- Give interpretation of the estimates of the regression coefficients for the significant predictors.
- Find the predicted percent of by-catch for a trawler that fishes 80 nautical miles off shore at the depth of 250 meters.

EXERCISE 7.5. A real estate intern is interested in modeling the proportion of houses that were sold in one month as having beta distribution with predictor variables: an average house price in subdivision (in thousands of dollars), the number of houses in subdivision, and age of subdivision (in years). The data for the past year on 30 randomly chosen subdivisions were available. They are:

Percent sold	Average price	N houses	Age	Percent sold	Average price	N houses	Age
0	455	69	21	80	308	223	15
0	316	244	24	75	159	84	13
36.4	210	236	31	0	147	54	37
50	557	183	16	44.4	704	199	18
33.3	232	73	6	0	593	119	38
50	626	230	20	20	738	156	8
27.3	343	60	14	55.6	256	206	34
80	246	201	17	85.7	345	38	22
42.9	631	217	11	50	450	158	7
0	630	222	42	0	491	239	27
71.4	356	85	22	28.6	441	103	15
25	481	240	16	88.9	212	222	18
50	181	197	42	50	574	56	35
20	264	235	19	33.3	647	138	35
87.5	297	88	17	0	630	18	60

- 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.
- Present the fitted model. Does this model have a decent fit?
- Interpret parameter estimates for statistically significant predictors.
- 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?

EXERCISE 7.6. Head instructors at a chain of traditional martial arts studios want to see if there is an association between the proportion of first-place trophies a studio wins during a tournament and such predictors as the number of years a studio has been in existence, the number of pupils, and the number of black-belt instructors. For each studio, the proportion of first-place trophies is defined as the ratio of the number of first-place trophies to the total number of trophies a studio wins. Data are collected on 26 studios.

Trophies	Firstplaces	Years	Blackbelts	Pupils
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	77
6	0	1	1	45
19	12	7	5	42
21	7	4	3	86
32	24	11	6	151
5	0	3	1	58
23	9	5	2	81
8	0	3	2	45
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	2	2	2	42
19	2	3	1	39
14	2	2	3	105

- 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.
- Discuss the model fit. Present the fitted model.
- Interpret the estimates of significant regression coefficients.
- 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.

EXERCISE 7.7. Parks and Recreation Department is conducting a study on mortality of young trees planted in parks. Investigators have collected data on the number of planted trees, number of trees that survived for two years, frequencies of pest control and soil fertilization, average annual precipitation (in inches), and average annual wind speed (in miles per hour). The data are as follows:

N planted trees	N survived trees	Freq of pest control	Freq of fertilization	Precip	Wind speed
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	10.0
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

- 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.
- Present the fitted model and discuss its fit.
- Interpret the estimated significant parameters.
- 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?

EXERCISE 7.8. A manager of a store that specializes in selling name-brand travel luggage is interested in finding out what characteristics of a salesperson best predict the proportion of initiated sales that are successfully completed. He looks up records of the sales team members and collects the data on gender, years of experience, amount of bonus received the previous year (in units of \$1,000) and the proportion of completed sales. The data are given in the table below.

Gender	Expyr	Bonus	Propsales	Gender	Expyr	Bonus	Propsales
F	1	1.1	0.67	F	2	1.2	0.65
M	11	0.5	1.00	F	13	0.6	1.00
M	4	1.1	0.90	F	8	0.9	0.54
M	2	1.6	0.93	M	4	0.6	0.63
F	2	0.7	0.49	F	17	2.4	1.00
F	4	1.05	0.88	F	3	1.6	1.00
M	1	1.6	0.96	F	2	1.4	0.88
F	2	1.2	0.67	F	4	1.05	0.85
M	2	1.6	0.94	F	8	1.4	1.00
M	7	1.4	0.77	M	4	1.35	0.95
F	4	1.55	1.00	F	3	1	0.83
F	4	0.9	0.51	F	18	1.25	1.00
F	8	0.95	0.59	M	4	0.4	0.66

- 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.
- How good is the model fit?
- Interpret the estimated significant regression coefficients.
- 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.

EXERCISE 7.9. An agricultural laboratory is testing germination of corn seeds at various locations. The variables of interest are soil electrical conductivity (EC, in millisiemens per centimeter squared), mean soil temperature (in degrees Fahrenheit), plot altitude (in feet), and rate of seed germination. At some locations seeds didn't germinate at all, whereas in some other locations they germinated at 100% rate. The data are provided below.

EC	Soiltemp	Altitude	Germrate	EC	Soiltemp	Altitude	Germrate
2.7	67	4368	0.00	2.5	64	4229	0.17
1.1	67	1689	1.00	1.8	69	2933	0.47
1.8	69	3156	0.87	1.8	63	6110	0.32
1.6	67	4884	0.58	1.5	67	461	1.00
2.4	66	4926	0.00	2.5	67	5269	0.00
1.6	63	3854	0.23	1.7	74	197	1.00
2.3	67	5146	0.00	1.6	65	607	1.00
1.2	64	2202	0.48	2.6	67	5263	0.16
1.1	62	2759	0.82	1.2	69	651	1.00
1.9	62	2774	0.61	1.7	65	863	0.80
1.5	71	5927	0.19	1.5	62	4386	0.23
1.7	61	827	0.93	1.7	68	165	1.00
2.8	62	3631	0.00	1.7	62	234	0.73

- (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.
- (b) Discuss the model fit.
- (c) Give interpretation of the estimated significant regression coefficients.
- (d) Use the fitted model to predict the germination rate for a plot with EC of 1.5 mS/cm², soil temperature of 68°F, and altitude of 950 feet.

EXERCISE 7.10. A college football analytic team is trying to determine what attributes of a player predict the proportion of games played in a season by that player. They collect data retrospectively on BMI, forty-yard dash (in seconds), vertical jump (in inches), broad jump (in inches), number of bench press repetitions at 225 pounds, and proportion of games played. Some players went through the training but never played in big games, while some others were very successful and played in every game. The data are given below.

BMI	Fortyyd	Vertical	Broad	Bench	Propgames
31.1	4.58	35.0	108	20	0.00
28.5	4.70	30.5	115	21	1.00
32.4	4.39	36.0	116	18	0.00
30.8	4.67	33.0	121	15	0.87
29.6	4.41	33.0	116	26	0.47
30.0	4.56	38.0	122	21	0.80
31.3	4.50	35.0	119	29	0.80
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	1.00
29.5	4.60	32.0	121	15	0.47
30.7	4.40	34.5	113	22	0.47
29.4	4.73	34.0	114	15	0.60
29.1	4.57	35.0	111	19	0.87
30.6	4.60	30.5	114	24	0.47
29.3	4.55	36.0	115	17	0.87
28.1	4.59	35.5	109	14	0.87
31.7	4.62	37.0	121	19	0.80
29.7	4.73	34.0	118	21	1.00
30.7	4.80	34.0	114	15	0.33
28.8	4.37	36.0	121	19	0.73
30.7	4.68	34.0	105	14	0.00
30.7	4.64	33.0	116	21	0.47
30.3	4.50	35.5	115	25	0.60
30.0	4.48	34.0	119	20	0.67
28.6	4.59	36.0	123	17	1.00
30.8	4.43	34.0	117	18	0.53
27.7	4.51	33.0	117	20	0.73
30.7	4.50	38.0	114	18	1.00
28.1	4.59	36.0	115	17	0.93
29.3	4.61	32.0	113	20	0.00
27.9	4.64	33.0	118	23	1.00
29.7	4.67	41.0	124	21	1.00
29.9	4.48	35.0	111	18	0.00
32.0	4.51	33.5	116	25	0.67
29.6	4.37	37.0	115	24	0.93
32.9	4.55	33.0	122	27	0.47
27.6	4.67	33.5	118	26	1.00
30.4	4.55	32.0	109	17	0.73
31.4	4.50	38.0	121	18	0.67

- (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?
- (b) Analyze the fit of the model.
- (c) Give interpretation of the estimated significant coefficients.
- (d) Predict the proportion of games that a new player will play, if his BMI is 27.8 kg/m², forty-dash run is 4.67 seconds, vertical jump is 32 inches, broad jump is 117 inches, and bench press is 16 repetitions.

Chapter 8

General Linear Regression Models for Repeated Measures Data

In the previous chapters, observations for different individuals were assumed independent. In this chapter, we will consider cases when multiple observations are collected on the same individuals repeatedly over time, or space, or under different treatment conditions. Such observations are referred to as *repeated measures*. In these models, observations for different individuals are assumed uncorrelated. However, observations for each individual are modeled as correlated. This potential correlation is included into the model by introducing additive random terms. Thus, along with usual predictors (termed *fixed-effects predictors*), the model also contains random variables (called *random-effects terms*). Such a model is generally referred to as a *mixed-effects linear regression model*¹ (or, simply, a *mixed* model).

A special case of repeated measures is *longitudinal data*, which are data collected at several time points. Below we will give the theoretical framework referring to longitudinal data and using variable *time* to index repeated observations. The specificity of longitudinal data is that times between the repeated measures are not necessarily equally distant.

8.1 Random Slope and Intercept Model

8.1.1 Model Definition

Suppose data are collected longitudinally at times t_1, \dots, t_a . For each individual i , $i = 1, \dots, n$, at time t_j , $j = 1, \dots, a$, the observations are

¹Mixed-effect modeling was introduced in Laird, Nan M. and James H. Ware (1982). “Random-Effects Models for Longitudinal Data”. *Biometrics*, 38(4): 963 – 974.

$x_{1ij}, \dots, x_{kij}, y_{ij}$. The *random slope and intercept model* is defined as

$$y_{ij} = \beta_0 + \beta_1 x_{1ij} + \dots + \beta_k x_{kij} + \beta_{k+1} t_j + u_{1i} + u_{2i} t_j + \varepsilon_{ij} \quad (8.1)$$

where u_{1i} 's are independent $\mathcal{N}(0, \sigma_{u_1}^2)$ *random intercepts*, u_{2i} 's are independent $\mathcal{N}(0, \sigma_{u_2}^2)$ *random slopes*, and ε_{ij} 's are independent $\mathcal{N}(0, \sigma^2)$ *errors* that are also independent of u_{1i} 's and u_{2i} 's. It is assumed that $\text{Cov}(u_{1i}, u_{2i}) = \sigma_{u_1 u_2}$, and $\text{Cov}(u_{1i}, u_{2i'}) = 0$ for $i \neq i'$.

In this model, the predictor variables x_1, \dots, x_k have fixed effects, whereas the random intercept u_1 and slope u_2 have random effects. It is also noteworthy that the predictors x_1, \dots, x_k may vary with time.

It can be shown (see Exercise 8.1) that $\text{Cov}(y_{ij}, y_{i'j'}) = 0$, $i \neq i'$, meaning that the responses for different individuals are uncorrelated for any time points. It can also be shown that responses between different time points for the same individual may be correlated, since $\text{Cov}(y_{ij}, y_{ij'}) = \sigma_{u_1}^2 + \sigma_{u_1 u_2} (t_j + t_{j'}) + \sigma_{u_2}^2 t_j t_{j'}$, for $j \neq j'$. In addition, it can be verified that the response variable y_{ij} is normally distributed with the mean

$$\mathbb{E}(y) = \beta_0 + \beta_1 x_1 + \dots + \beta_k x_k + \beta_{k+1} t \quad (8.2)$$

and variance $\text{Var}(y_{ij}) = \sigma_{u_1}^2 + 2\sigma_{u_1 u_2} t_j + \sigma_{u_2}^2 t_j^2 + \sigma^2$. Note that if there is no random slope in the model (called the *random intercept-only model*), the variance of the response variable is constant and doesn't vary with time.

8.1.2 Fitted Model

By (8.2), in the random slope and intercept model, the fitted mean response can be expressed as

$$\widehat{\mathbb{E}}(y) = \widehat{\beta}_0 + \widehat{\beta}_1 x_1 + \dots + \widehat{\beta}_k x_k + \widehat{\beta}_{k+1} t. \quad (8.3)$$

All beta parameters along with $\sigma_{u_1}^2$, $\sigma_{u_1 u_2}$, $\sigma_{u_2}^2$, and σ^2 are estimated by maximizing the likelihood function, or, alternatively, by maximizing the restricted likelihood function. The *restricted maximum likelihood* (REML) method utilizes a certain linear transformation of y , chosen in such a way that the resulting likelihood function doesn't depend on β 's. It is known that the maximum likelihood estimators of the variances and covariance are biased, whereas the REML method produces unbiased estimators.

8.1.3 Interpretation of Estimated Regression Coefficients

In view of (8.3), the fitted beta coefficients are interpreted as in the general linear regression model (see Subsection 1.5), in terms of an average change

in the mean response for a unit-increase in a continuous predictor, or as the difference between mean responses for level 1 and level 0 for a 0-1 predictor, provided all the other predictors stay unchanged.

8.1.4 Model Goodness-of-Fit Check

To compare the fit of several models, the AIC, AICC, and BIC criteria may be used.

To check goodness-of-fit of a particular model, a chi-squared deviance test is used (see Subsection 1.6). In this case, the null model has only fixed-effects predictor variables. Since the random-effects terms bring three parameters into the model (two variances and a covariance), this test has three degrees of freedom.

8.1.5 Predicted Response

By (8.3), for a deterministic set of values x_1^0, \dots, x_k^0, t^0 , the predicted response is $y^0 = \hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \dots + \hat{\beta}_k x_k^0 + \hat{\beta}_{k+1} t^0$.

8.1.6 SAS Implementation

Suppose the data set is given in the *short-and-wide form*, that is, it contains n rows for the n individuals: one column for individual's id, k columns for the variables x_1, \dots, x_k , and a columns for the responses at the a time points y_1, \dots, y_a . Prior to fitting a mixed-effects model, a *long-form data set* must be created, a data set that contains p rows for each individual, one row for each time point. This can be done via the following data statement:

```
data longform_data_name;
  set data_name;
  array time_array_name[a] (time1_name...timea_name);
  array response_array_name[a] y1_name...ya_name;
  do count_variable_name=1 to a;
    time_name=time_array_name[count_variable_name];
    response_name=response_array_name[count_variable_name];
    output;
  end;
  keep id_name x1_name...xk_name time_name response_name;
```

```
run;
```

The procedure `mixed` fits mixed-effects models on long-form data sets that contain one row per individual per time point. The general statements are:

```
proc mixed data=longform_data_name covtest maxiter=number;
  class <list of categorical predictors>;
  model response_name=<list of x predictors> time_name/solution
        outpm=outdata_name;
  random intercept time_name/subject=id_name type=un;
run;
```

- The option `covtest` requests p -values in the tests for significance of the variance-covariance parameters.
- SAS outputs estimates of the beta coefficients only if the option `solution` is specified.
- The `outpm=` produces prediction of the response y for each row in the data set. If a new prediction is desired, the case must be added to the data set.
- Specification of `type=un`, an unstructured type of variance-covariance matrix, requests an estimate of the covariance $\sigma_{u_1u_2}$.
- In the output, the estimators of $\sigma_{u_1}^2$, $\sigma_{u_1u_2}$, $\sigma_{u_2}^2$, and σ^2 are termed `UN(1,1)`, `UN(2,1)`, `UN(2,2)` and `Residual`, respectively.
- As part of the output, SAS shows the results of the deviance test, calling it `Null Model Likelihood Ratio Test`. The number of degrees of freedom, chi-squared test statistic, and the p -value are displayed.

8.1.7 R Implementation

To create a long-form data set from a short-and-wide form `data.name` with columns `id.name`, `x1.name`, ..., `xk.name`, `y1.name`, ..., `ya.name`, the function `melt()` in the library `reshape2` may be used. The script is as follows:

```
library(reshape2)

longform.data.name<- melt(data.name, id.vars=c("id.name", "x1.name",
..., "xk.name"), variable.name = "response.variables.name",
value.name="response.name")
```

Here the categorical variable `response.variables.name` contains the names of the variables `y1.name`, ..., `ya.name`, whereas the variable `response.name` contains the actual numeric responses.

In a more general case, the short-and-wide data set might contain one predictor variable that varies with time, that is, the columns could be *id.name*, *x1.name*, ..., *x{k-1}.name*, *xk1.name*, ..., *xka.name*, *y1.name*, ..., *ya.name*. A long-form data set then can be created by separating the response columns from the rest of the data, turning the two files into long form, and then merging them. The syntax is:

```
longform.data1.name<- melt(data.name[,c("id.name", "x1.name",
..., "x{k-1}.name", "xk1.name",..., "xka.name")], id.vars=c("id.name",
"x1.name", ..., "x{k-1}.name"), variable.name="xk.variables.name",
value.name="xk.name")
```

```
longform.data2.name<- melt(data.name[,c("y1.name", ..., "ya.name")],
variable.name="response.variables.name", value.name="response.name")
```

```
longform.data.name<- cbind(longform.data1.name, longform.data2.name)
```

If more than one predictor depends on time, then it would be necessary to split the original data set into several data sets, transform them into long form, and then merge together.

Next, the variable *response.variables.name* has to be recoded into a numeric variable that contains time values. This can be done as follows:

```
time.name<- ifelse(longform.data.name$response.variables.name=="y1.name",
time1.value, ifelse(longform.data.name$response.variables.name=="y2.name",
time2.value,..., ifelse(longform.data.name$response.variables.name=="y{a-
1}.name", time{a-1}.value, timea.value)))
```

Next, for the long-form data set, the function `lme()` in the library `nlme` fits the random slope and intercept model. The statements are as follows:

```
summary(fitted.model.name<- lme(response.name~x1.name+...+xk.name+time.name,
random=~ 1+time.name|id.name, control=lmeControl(opt="optim"),
data=longform.data.name))
intervals(fitted.model.name)
```

- The optional function `lmeControl()` aids in model convergence.
- R outputs estimated standard deviations and correlation coefficient for the random terms as opposed to SAS that outputs estimated variances and co-variance.
- R doesn't conduct tests of significance for the variance-covariance param-

eters. The 95% confidence intervals based on a normal approximation may be requested by including the `intervals()` function.

- R outputs AIC and BIC values automatically. The AICC value has to be computed as

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

where n is the number of individuals and p is the total number of parameters of the model.

- To check the goodness of fit of a model, the following syntax should be used:

```
null.model.name<- glm(response.name~x1.name+... +xk.name+time.name,
data=longform.data.name)
print(deviance.name<- -2*(logLik(null.model.name)-logLik(fitted.model.name)))
print(p.value.name<- pchisq(deviance.name, df=value, lower.tail = FALSE))
```

- To obtain a predicted response value, use the function `predict()` with the added argument `level=0`.

8.1.8 Example

EXAMPLE 8.1. In a clinic, doctors are testing a certain cholesterol lowering medication. Patients' gender and age at the beginning of the study are recorded for 27 patients. The low-density lipoprotein (LDL) cholesterol levels are measured in all the patients at the baseline, and then at 6-, 9-, and 24-month visits. The SAS code below creates a long-form data set.

```
data cholesterol;
input id gender$ age LDL0 LDL6 LDL9 LDL24 @@;
cards;
1 M 50 73 71 80 85 2 F 72 174 164 139 112
3 M 46 85 86 82 90 4 F 71 172 150 139 127
5 F 75 186 177 153 145 6 F 68 184 169 153 138
7 F 63 196 188 163 155 8 M 73 137 137 132 104
9 M 59 135 120 106 106 10 M 60 111 110 100 76
11 F 59 127 126 106 99 12 M 46 88 87 84 80
13 F 67 176 150 156 153 14 F 52 155 135 128 120
15 M 65 142 117 114 97 16 F 75 158 143 145 135
17 F 57 148 131 138 102 18 M 58 125 111 118 124
19 M 48 76 65 94 98 20 M 47 116 108 94 107
21 F 53 191 185 162 113 22 F 73 167 165 162 140
23 M 62 109 104 93 94 24 F 77 167 164 155 155
```



```

25 M 55 103 94 75 78 26 F 74 122 126 105 111
27 F 79 203 204 178 145
;

```

```

data longform;
  set cholesterol;
  array m[4] (0 6 9 24);
  array c[4] LDL0 LDL6 LDL9 LDL24;
  do i=1 to 4;
    month=m[i];
    LDL=c[i];
  output;
  end;
keep id gender age month LDL;
run;

```

Next, we show that the variable LDL, which contains all the cholesterol measurements, has a normal distribution. To this end, we construct a histogram with fitted bell-shaped curve and conduct normality testing.

```

proc univariate data=longform;
  var LDL;
  histogram LDL/normal;
run;

```

The output follows. Since the histogram resembles a normal density and all the p -values exceed 0.05, we conclude that the response variable is normally distributed.

Goodness-of-Fit Tests for Normal Distribution

Test	p Value
Kolmogorov-Smirnov	>0.150
Cramer-von Mises	0.126
Anderson-Darling	0.106

Our next step is to fit a random slope and intercept model, regressing LDL on the other variables. The code and relevant output are given below.

```

proc mixed data=longform covtest;
  class gender;
  model LDL=gender age month/solution;
  random intercept month/subject=id type=un;
run;

```

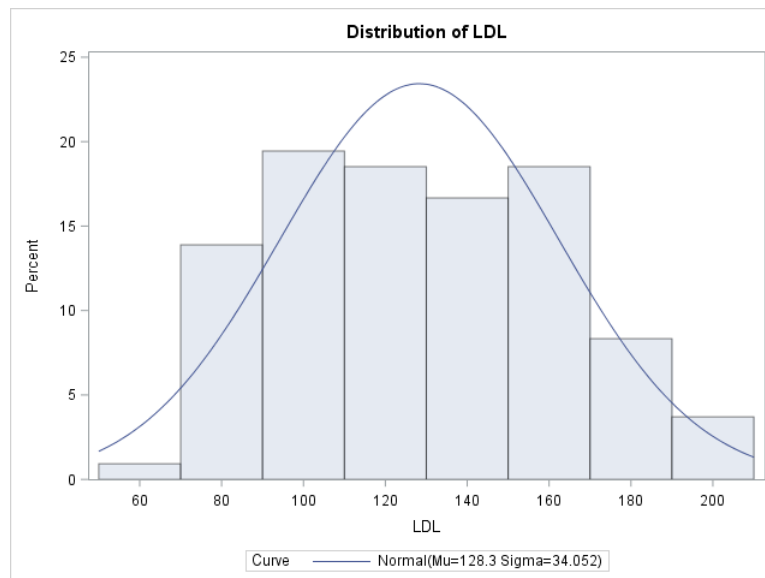


Figure 8.1: Histogram for LDL in SAS

Covariance Parameter Estimates

Cov Parm	Estimate	Pr Z
UN(1,1)	520.17	0.0013
UN(2,1)	-16.3953	0.0087
UN(2,2)	0.7846	0.0028
Residual	69.8556	<.0001

Fit Statistics

AIC	870.3
AICC	870.7
BIC	875.5

Null Model Likelihood Ratio Test

DF	Chi-Square	Pr > ChiSq
3	72.86	<.0001

Solution for Fixed Effects

Effect	gender	Estimate	Pr > t
Intercept		65.0163	0.0029
gender	F	29.8105	<.0001
gender	M	0	.
age		0.9203	0.0085
month		-1.0957	<.0001

From the output, the variances of the random slope, intercept, and error, as well as the covariance term are all statistically significant, which validates

the use of all the random terms in the model. The null-model likelihood test gives a small p -value, indicating a good fit. The fitted model can be written as $\hat{E}(LDL) = 65.0163 + 29.8105 \cdot female + 0.9203 \cdot age - 1.0957 \cdot month$, with all predictors being significant. For female patients, the estimated average cholesterol is 29.8105 points higher than that for males. With a one-year increase in age, the cholesterol level goes up, on average, by estimated 0.9203 points. As time increases by one month, the estimated average LDL measurement decreases by 1.0957 points.

The values for the AIC, AICC, and BIC criteria that are included in the above output will be used in Example 8.2.

To predict the LDL level at 3 months for a 48-year-old female patient, we compute $LDL^0 = 65.0163 + 29.8105 + 0.9203 \cdot 48 - 1.0957 \cdot 3 = 135.7141$.

To produce the same result in SAS, we run the following statements:

```
data prediction;
input id gender$ age month;
cards;
28 F 48 3
;

data longform;
  set longform prediction;
run;

proc mixed covtest;
class gender;
model LDL=gender age month/outpm=outdata;
random intercept month/subject=id type=un;
run;

proc print data=outdata (firstobs=109) noobs;
var Pred;
run;

      Pred
135.716
```

The R script for this example is presented below.

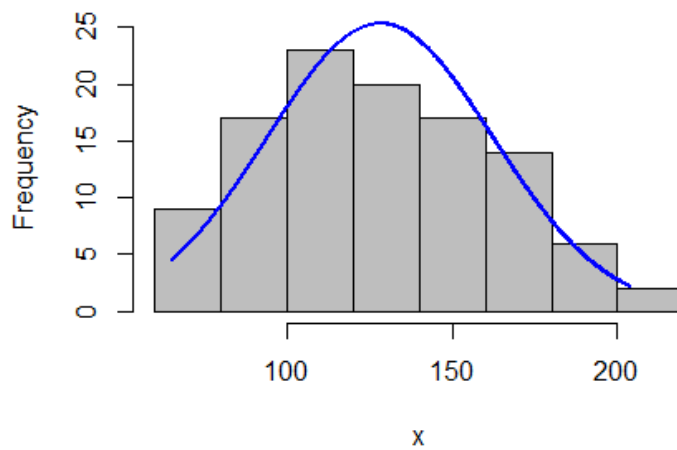


Figure 8.2: Histogram for LDL in R

```
cholesterol.data<-read.csv(file="./Example8.1Data.csv",
header=TRUE, sep=",")

#creating long-form data set
library(reshape2)
longform.data<- melt(cholesterol.data, id.vars=c("id",
"gender", "age"), variable.name="LDLmonth", value.name="LDL")

#creating variable for time
month<- ifelse(longform.data$LDLmonth=="LDL0", 0,
ifelse(longform.data$LDLmonth=="LDL6", 6,
ifelse(longform.data$LDLmonth=="LDL9",9,24)))

#plotting histogram with fitted normal density
library(rcompanion)
plotNormalHistogram(longform.data$LDL)

#testing for normality of distribution
shapiro.test(longform.data$LDL)

Shapiro-Wilk normality test
W = 0.97668, p-value = 0.05449

#specifying reference categories
```

```
gender.rel<- relevel(longform.data$gender, ref="M")

#fitting random slope and intercept model
library(nlme)
summary(fitted.model<- lme(LDL ~ gender.rel + age + month,
random=~ 1 + month|id, data=longform.data))
```

```
Linear mixed-effects model fit
      AIC      BIC    logLik
878.3294 899.4845 -431.1647
```

```
Random effects:
              StdDev   Corr
(Intercept) 22.8072879 (Intr)
month       0.8857844 -0.812
Residual    8.3579458
```

```
Fixed effects:
              Value    p-value
(Intercept) 65.01614 0.0014
gender.relF 29.81056 0.0003
age         0.92033 0.0116
month      -1.09566 0.0000
```

```
intervals(fitted.model)
```

```
Random Effects:
              lower    est.    upper
sd((Intercept)) 16.4912656 22.8072879 31.542296
sd(month)       0.6229652 0.8857844 1.259483
cor((Intercept),month) -0.9325355 -0.8115565 -0.526760
```

```
Within-group standard error:
      lower    est.    upper
6.921510 8.357946 10.092488
```

```
#computing AICC
n<- 108
p<- 8
print(AICC<- -2*logLik(fitted.model)+2*p*n/(n-p-1))
```

```
879.784
```

```
#checking model fit
null.model<- glm(LDL ~ gender.rel + age + month, data=longform.data)
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))

77.80585

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

9.069804e-17

#using fitted model for prediction
print(predict(fitted.model, data.frame(gender.rel="F",age=48, month=3),
level=0))

135.7156
```

□

8.2 Random Slope and Intercept Model with Covariance Structure for Error

8.2.1 Model Definition

In the random slope and intercept model introduced in (8.1), the variance-covariance matrix for the error terms has a diagonal structure. It is of the form $\sigma^2 \mathbb{I}$, where \mathbb{I} denotes a $na \times na$ identity matrix, with ones on the main diagonal and zeros everywhere else. This structure assumes that the errors are independent, and thus is termed an *independent structure*.

The random slope and intercept models with other structures for the variance-covariance matrix of the error terms can be considered. The most general is an *unstructured* one with an $na \times na$ block-diagonal matrix with n identical blocks of size $a \times a$ of the form:

$$\begin{bmatrix} \sigma_1^2 & \sigma_{12} & \sigma_{13} & \dots & \sigma_{1a} \\ \sigma_{12} & \sigma_2^2 & \sigma_{23} & \dots & \sigma_{2a} \\ \sigma_{13} & \sigma_{23} & \sigma_3^2 & \dots & \sigma_{3a} \\ \dots & \dots & \dots & \dots & \dots \\ \sigma_{1a} & \sigma_{2a} & \sigma_{3a} & \dots & \sigma_a^2 \end{bmatrix}.$$

This matrix has a symmetric structure with a variances and $a(a-1)/2$ covariances, for a total of $a(a+1)/2$ parameters that have to be estimated from the data. If the size of the data set permits, the model with unstructured

variance-covariance matrix of the error terms should be fitted. This model doesn't make any assumptions regarding the structure and allows the estimate of each parameter to take on its own value.

If the size of the data set is too small to fit a general unstructured variance-covariance matrix, there are several sparse but meaningful structures that may be tried. Here we present four most commonly used models.

- The first model has the blocks in the variance-covariance matrix that have constant values on each of the descending diagonals, that is, the matrix has the form:

$$\begin{bmatrix} \sigma^2 & \sigma_1 & \sigma_2 & \dots & \sigma_{a-1} \\ \sigma_1 & \sigma^2 & \sigma_1 & \dots & \sigma_{a-2} \\ \sigma_2 & \sigma_1 & \sigma^2 & \dots & \sigma_{a-3} \\ \dots & \dots & \dots & \dots & \dots \\ \sigma_{a-1} & \sigma_{a-2} & \sigma_{a-3} & \dots & \sigma^2 \end{bmatrix}.$$

Using this structure implies that observations that are the same number of time points apart are equally correlated. There are a total of a unknown parameters $\sigma^2, \sigma_1, \dots, \sigma_{a-1}$. This model is said to have the *Toeplitz* covariance structure, which is sometimes referred to as an autoregressive-moving average ARMA(1,1) structure.

- Another model with useful structure of the variance-covariance matrix relies on the fact that typically as time goes on, observations become less correlated with the earlier ones. In this model, each block in the variance-covariance matrix has $\sigma^2 \rho^{|t_i - t_j|}$ in the ij -th cell, $i, j = 1, \dots, a$, that is, it looks like this:

$$\sigma^2 \begin{bmatrix} 1 & \rho^{|t_1 - t_2|} & \rho^{|t_1 - t_3|} & \dots & \rho^{|t_1 - t_a|} \\ \rho^{|t_1 - t_2|} & 1 & \rho^{|t_2 - t_3|} & \dots & \rho^{|t_2 - t_a|} \\ \rho^{|t_1 - t_3|} & \rho^{|t_2 - t_3|} & 1 & \dots & \rho^{|t_3 - t_a|} \\ \dots & \dots & \dots & \dots & \dots \\ \rho^{|t_1 - t_a|} & \rho^{|t_2 - t_a|} & \rho^{|t_3 - t_a|} & \dots & 1 \end{bmatrix}.$$

Here σ^2 and ρ are the unknown constants, $|\rho| < 1$. Note that in this matrix the entries decrease as the distance between times t_i and t_j increases. The matrix of this form is termed a *spatial power matrix*, and hence the model is said to have a *spatial power* variance-covariance structure of the error terms.

- A special case of this model is when the times are equal to $1, 2, 3, \dots, a$. Then the $a \times a$ blocks of the variance-covariance matrix become:

$$\sigma^2 \begin{bmatrix} 1 & \rho & \rho^2 & \dots & \rho^{a-1} \\ \rho & 1 & \rho & \dots & \rho^{a-2} \\ \rho^2 & \rho & 1 & \dots & \rho^{a-3} \\ \dots & \dots & \dots & \dots & \dots \\ \rho^{a-1} & \rho^{a-2} & \rho^{a-3} & \dots & 1 \end{bmatrix}.$$

This model is said to have an *autoregressive* variance-covariance structure of the error terms, referring to an AR(1) model, an autoregressive time series model with lag one that has the same covariance structure. Note that the autoregressive matrix is a special case of both Toeplitz and spatial power matrices.

- The last model that we introduce here is the model with *compound symmetric* (or *exchangeable*) variance-covariance matrix of the error terms. In this matrix, all variances are assumed to be equal to σ^2 , and all correlations are assumed to be equal to ρ . That is, the matrix has the form:

$$\sigma^2 \begin{bmatrix} 1 & \rho & \rho & \dots & \rho \\ \rho & 1 & \rho & \dots & \rho \\ \rho & \rho & 1 & \dots & \rho \\ \dots & \dots & \dots & \dots & \dots \\ \rho & \rho & \rho & \dots & 1 \end{bmatrix}.$$

This variance-covariance structure better suits situations when repeated measurements are taken under various treatment conditions rather than longitudinally since all observations are assumed equally correlated.

8.2.2 Fitted Model, Interpretation of Estimated Regression Coefficients, and Predicted Response

The fitted model has the same form as the fitted slope and intercept model with independent covariance structure for errors (8.3). Estimated regression coefficients are interpreted the same way, and predicted responses for fixed sets of predictors are computed similarly (see Subsections 8.1.2, 8.1.3, and 8.1.5).

8.2.3 Model Goodness-of-fit Check

Goodness-of-fit of several models are compared based on AIC, AICC, and BIC criteria.

For a given model, the goodness of fit may be verified by carrying out the chi-squared deviance test. In this case, there are no random-effects terms in the null model, thus it has $k + 3$ parameters: $\beta_0, \dots, \beta_{k+1}$, and σ . The fitted model has $k + 2$ beta parameters, 3 random-effects parameters $\sigma_{u_1}^2, \sigma_{u_1 u_2}$, and $\sigma_{u_2}^2$, plus the number of parameters in the variance-covariance matrix of error terms. Since the number of degrees of freedom is calculated as the difference between the number of parameters in the fitted and null models, the number of degrees of freedom is: for unstructured covariance matrix, $df = k + 5 + \frac{a(a+1)}{2} - (k + 3) = \frac{a(a+1)}{2} + 2$, for Toeplitz matrix, $df = k + 5 + a - (k + 3) = a + 2$, and for spatial power, autoregressive, and compound symmetric matrices, $df = k + 5 + 2 - (k + 3) = 4$.

8.2.4 SAS Implementation

The random slope and intercept model with a certain covariance structure for the error terms is fitted in SAS by running `proc mixed` described in Subsection 8.1.6 with the `repeated` statement added as follows:

```
repeated / subject=id_name type=covtype_name r;
```

- Covariance structures in the option `type=` are `un` (unstructured), `toep` (Toeplitz), `sp(pow)(time_name)` (spatial power), `ar(1)` (autoregressive), or `cs` (compound symmetric).
- By specifying the option `r` we request that SAS outputs an estimated individual block of the variance-covariance matrix of the error terms, labeling it `Estimated R Matrix for Subject 1`.
- Estimated correlation coefficient ρ in the output is labeled `SP(POW)` (spatial power) and `AR(1)` (autoregressive).
- In the case of the compound symmetric covariance structure, SAS outputs two quantities: `CS` and `Residual`. The estimated individual block of the variance-covariance matrix of the errors has the sum `CS+Residual` on the main diagonal and `CS` off the main diagonal. Thus, the estimate of σ^2 is `CS+Residual`, and the estimated correlation coefficient is $\hat{\rho} = \text{CS}/(\text{CS} + \text{Residual})$.

8.2.5 R Implementation

The syntax for the random slope and intercept model with the independent structure for errors (see Subsection 8.1.7) is valid for all the other structures.

- A structure can be specified by adding `correlation=` to the syntax within

the `lme()` function. The choices are:

```
corSymm() (unstructured),
corARMA(form=~ 1|id.name, p=1, q=1) (Toeplitz),
corCAR1(form=~1|id.name) (spatial power),
corAR1(form=~1|id.name) (autoregressive),
and
corCompSymm(form=~1|id.name) (compound symmetric).
```

- In the model with an unstructured variance-covariance matrix, by default, R produces identical estimates of the variances. To lift this restriction, one should add to the function `lme()` the argument `weights=varIdent(form=~id.name|time.name)`.
- A fitted individual block of the variance-covariance matrix can be viewed by typing on a separate line `getVarCov(fitted.model.name, type="conditional")`.
- In the models with spatial power and autoregressive variance-covariance structures, the parameter ρ is termed “Phi” in the output.

8.2.6 Example

EXAMPLE 8.2. In Example 8.1, we fitted random slope and intercept model with the independent structure of the error terms. The outputted goodness-of-fit statistics were AIC=870.3, AICC=870.7, and BIC=875.5. Below we run models with the unstructured, Toeplitz, spatial power, autoregressive, and compound symmetric structures, and compare their fit statistics.

```
/*fitting random slope and intercept model with
unstructured covariance matrix of error terms*/
proc mixed data=longform covtest;
  class gender;
  model LDL=gender age month/solution;
  random intercept month/subject=id type=un;
  repeated/subject=id type=un r;
run;
```

In this model, the estimated matrix entries are all different:

Estimated R Matrix for Subject 1				
Row	Col1	Col2	Col3	Col4
1	398.30	339.18	189.07	101.14
2	339.18	355.61	190.89	90.9265

3	189.07	190.89	222.62	141.82
4	101.14	90.9265	141.82	320.07

The variances and covariance of the random terms are given below. Note that they are not statistically significant at the 5% level.

Covariance Parameter Estimates		
Cov Parm	Estimate	Pr > Z
UN(1,1)	185.94	0.1593
UN(2,1)	-5.2666	0.4776
UN(2,2)	0.02170	0.4757

The goodness-of-fit criteria values and the results for the asymptotic likelihood ratio test are:

Fit Statistics	
AIC	874.7
AICC	878.7
BIC	891.5

Null Model Likelihood Ratio Test		
DF	Chi-Square	Pr > ChiSq
12	86.49	<.0001

The estimated coefficients for the fixed-effects terms are:

Solution for Fixed Effects			
Effect	gender	Estimate	Pr > t
Intercept		60.6156	0.0039
gender	F	28.5591	<.0001
gender	M	0	.
age		0.9601	0.0049
month		-1.0250	<.0001

```

/*fitting random slope and intercept model with
Toeplitz covariance matrix of error terms*/
proc mixed data=longform covtest;
  class gender;
  model LDL=gender age month/solution;
  random intercept month/subject=id type=un;
  repeated / subject=id type=toep r;
run;

```

For each individual, the fitted variance-covariance block is:

Estimated R Matrix for Subject 1				
Row	Col1	Col2	Col3	Col4
1	89.3298	26.1821	-11.1480	38.7476
2	26.1821	89.3298	26.1821	-11.1480
3	-11.1480	26.1821	89.3298	26.1821
4	38.7476	-11.1480	26.1821	89.3298

Note that in this matrix the values on each descending diagonal are the same.

Further, the parameters for the random terms are statistically significant since the respective p -values are less than 0.05, as seen in the following output:

Covariance Parameter Estimates		
Cov Parm	Estimate	Pr > Z
UN(1,1)	466.45	0.0016
UN(2,1)	-13.9159	0.0206
UN(2,2)	0.6376	0.0239

The model fit results are given as:

Fit Statistics	
AIC	871.2
AICC	872.3
BIC	880.2

Null Model Likelihood Ratio Test		
DF	Chi-Square	Pr > ChiSq
6	78.03	<.0001

The estimated beta coefficients for the fixed-effects terms are:

Solution for Fixed Effects			
Effect	gender	Estimate	Pr > t
Intercept		61.1870	0.0041
gender	F	29.5657	<.0001
gender	M	0	.
age		0.9662	0.0053
month		-0.9946	<.0001

```

/*fitting random slope and intercept model with
spatial power covariance matrix of error terms*/
proc mixed data=longform covtest;
  class gender;
  model LDL=gender age month/solution;
  random intercept month/subject=id type=un;
  repeated / subject=id type=sp(pow)(month) r;
run;

```

Each estimated block in the variance-covariance matrix is:

Estimated R Matrix for Subject 1

Row	Col1	Col2	Col3	Col4
1	69.8556	3.14E-12	0	0
2	3.14E-12	69.8556	0.000015	0
3	0	0.000015	69.8556	0
4	0	0	0	69.8556

The random-effects parameters are estimated as:

Covariance Parameter Estimates

Cov Parm	Estimate	Pr Z
UN(1,1)	520.17	0.0013
UN(2,1)	-16.3953	0.0087
UN(2,2)	0.7846	0.0028
SP(POW)	0.005962	0.9985
Residual	69.8556	<.0001

In this model, the correlation coefficient ρ is statistically indistinguishable from zero, since $\hat{\rho} = \text{SP(POW)} = 0.005962$ with the p -value = 0.9985 > 0.05. The times of measurements are $t_1 = 0$, $t_2 = 6$, $t_3 = 9$, and $t_4 = 24$. The differences between these times assume values 3, 6, 9, 15, 18, and 24, and thus the off-diagonal entries in the matrix are: $\hat{\sigma}^2 \hat{\rho}^3$, $\hat{\sigma}^2 \hat{\rho}^6$, $\hat{\sigma}^2 \hat{\rho}^9$, $\hat{\sigma}^2 \hat{\rho}^{15}$, $\hat{\sigma}^2 \hat{\rho}^{18}$, $\hat{\sigma}^2 \hat{\rho}^{24}$, which are all estimated to be very close to zero. The quantity on the main diagonal is the estimated σ^2 , that is, $\hat{\sigma}^2 = \text{Residual} = 69.8556$.

The summary of the model fit is given below.

Fit Statistics
AIC 872.3
AICC 872.9
BIC 878.8

Null Model Likelihood Ratio Test

DF	Chi-Square	Pr > ChiSq
4	72.86	<.0001

The estimated regression coefficients for the fixed-effects terms are:

Solution for Fixed Effects			
Effect	gender	Estimate	Pr > t
Intercept		65.0163	0.0029
gender	F	29.8105	<.0001
gender	M	0	.
age		0.9203	0.0085
month		-1.0957	<.0001

```
/*fitting random slope and intercept model with
autoregressive covariance matrix of error terms*/
proc mixed data=longform covtest;
  class gender;
  model LDL=gender age month/solution;
  random intercept month/subject=id type=un;
  repeated / subject=id type=ar(1) r;
run;
```

Each estimated block in the variance-covariance matrix is:

Estimated R Matrix for Subject 1				
Row	Col1	Col2	Col3	Col4
1	157.02	87.6923	48.9756	27.3526
2	87.6923	157.02	87.6923	48.9756
3	48.9756	87.6923	157.02	87.6923
4	27.3526	48.9756	87.6923	157.02

The random-effects parameters are estimated as:

Covariance Parameter Estimates		
Cov Parm	Estimate	Pr Z
UN(1,1)	388.12	0.0365
UN(2,1)	-11.7246	0.0610
UN(2,2)	0.4812	0.0527
AR(1)	0.5585	0.0816
Residual	157.02	0.1019

The estimates $\hat{\sigma}^2 = \text{Residual} = 157.02$ and $\hat{\rho} = \text{AR}(1) = 0.5585$. The entries in the estimated matrix are $\hat{\sigma}^2 = 157.02$, $\hat{\sigma}^2\hat{\rho} = (157.02)(0.5585) = 87.69$, $\hat{\sigma}^2\hat{\rho}^2 = (157.02)(0.5585^2) = 48.97$, and $\hat{\sigma}^2\hat{\rho}^3 = (157.02)(0.5585^3) = 27.35$.

The model fit statistics are given below.

Fit Statistics

AIC 869.6
AICC 870.2
BIC 876.0

Null Model Likelihood Ratio Test

DF Chi-Square Pr > ChiSq
4 75.63 <.0001

The estimated beta coefficients for the fixed-effects terms are:

Solution for Fixed Effects			
Effect	gender	Estimate	Pr > t
Intercept		62.9465	0.0044
gender	F	30.6095	<.0001
gender	M	0	.
age		0.9378	0.0088
month		-0.9640	<.0001

```
/*fitting random slope and intercept model with
compound symmetric covariance matrix of error terms*/
proc mixed data=longform covtest;
  class gender;
  model LDL=gender age month/solution;
  random intercept month/subject=id type=un;
  repeated / subject=id type=cs r;
run;
```

For each individual, the fitted block is:

Estimated R Matrix for Subject 1				
Row	Col1	Col2	Col3	Col4
1	102.03	32.1771	32.1771	32.1771
2	32.1771	102.03	32.1771	32.1771
3	32.1771	32.1771	102.03	32.1771
4	32.1771	32.1771	32.1771	102.03

The estimates of the variance-covariance parameters for the random terms are as follows:

Covariance Parameter Estimates		
Cov Parm	Estimate	Pr > Z
UN(1,1)	487.99	0.0024
UN(2,1)	-16.3952	0.0087
UN(2,2)	0.7846	0.0028
CS	32.1771	<.0001
Residual	69.8558	<.0001

In the estimated R matrix, on the main diagonal we see the estimated σ^2 which is $\hat{\sigma}^2 = \text{CS} + \text{Residual} = 32.1771 + 69.8558 = 102.0329$. Off the main diagonal, the entries are identical and equal to $\text{CS} = 32.1771$. The estimate of the correlation coefficient is calculated as $\hat{\rho} = \text{CS} / (\text{CS} + \text{Residual}) = 32.1771 / 102.0329 = 0.31536$.

The goodness-of-fit related output is:

Fit Statistics
AIC 872.3
AICC 872.9
BIC 878.8

Null Model Likelihood Ratio Test
DF Chi-Square Pr > ChiSq
4 72.86 <.0001

The estimated regression coefficients for the fixed-effects terms are:

Solution for Fixed Effects			
Effect	gender	Estimate	Pr > t
Intercept		65.0161	0.0029
gender	F	29.8106	<.0001
gender	M	0	.
age		0.9203	0.0085
month		-1.0957	<.0001

To identify the best-fitted model, we compare the values for AIC, AICC, and BIC criteria and identify the smallest ones. We summarize them here:

	Ind	Un	Toep	SpPow	AR	Exch
AIC	870.3	874.7	871.2	872.3	869.6	872.3
AICC	870.7	878.7	872.3	872.9	870.2	872.9
BIC	875.5	891.5	880.2	878.8	876.0	878.8

According to AIC and AICC criteria, the model with autoregressive structure is optimal, whereas the BIC criterion dictates that the model with the independent structure is better.

The fitted model with the autoregressive structure is $\hat{E}(LDL) = 62.9465 + 30.6095 \cdot female + 0.9378 \cdot age - 0.9640 \cdot month$. On average, the estimated cholesterol level is 30.6095 points higher for female than for male patients. As age increases by one year, the estimated mean LDL increases by 0.9378 points, and it decreases by 0.9640 points for every additional month in the study.

To compute the predicted LDL level for a 48-year-old female patient three months into the study, we write $LDL^0 = 62.9465 + 30.6095 + 0.9378 \cdot 48 - 0.9640 \cdot 3 = 135.6784$. SAS outputs the same result:

```
data prediction;
input id gender$ age month;
cards;
28 F 48 3
;

data longform;
  set longform prediction;
run;

proc mixed covtest;
  class gender;
  model LDL=gender age month/outpm=outdata;
  random intercept month/subject=id type=un;
  repeated/subject=id type=ar(1);
run;

proc print data=outdata (firstobs=109) noobs;
var Pred;
run;

    Pred
135.678
```

The R codes and outputs for the long-form data set in this example follow.

```
#fitting random slope and intercept model with unstructured covariance
```

```

#matrix of error terms
library(nlme)
summary(un.fitted.model<-lme(LDL ~ gender.rel + age + month,
random = ~ 1 + month|id, data=longform.data,
correlation=corSymm(), weights=varIdent(form = ~ id|month)))
getVarCov(un.fitted.model, type="conditional")

      AIC      BIC    logLik
882.703  927.6576  -424.3515

Random effects:
              StdDev      Corr
(Intercept) 22.1065205  (Intr)
month       0.8202094  -0.767

Fixed effects:
              Value    p-value
(Intercept) 60.61574    0.0020
gender.relF 28.55931    0.0003
age         0.96009    0.0072
month      -1.02503    0.0000

Conditional variance covariance matrix
      1      2      3      4
1 95.5290 57.655 -35.968  8.6119
2 57.6550 56.814 -11.431 -46.5200
3 -35.9680 -11.431 22.571 -25.3850
4  8.6119 -46.520 -25.385 133.0400

# computing AICC
n<- 108
p<- 17
print(AICC<- -2*logLik(un.fitted.model)+2*p*n/(n-p-1))

889.503

#checking model fit
summary(null.model<- glm(LDL ~ gender.rel + age + month,
data=longform.data))
print(deviance<- -2*(logLik(null.model)-logLik(un.fitted.model)))

91.43229

print(p.value<- pchisq(deviance, df=12, lower.tail=FALSE))

```

2.605906e-14

```
#fitting random slope and intercept model with Toeplitz covariance
#matrix of error terms
summary(toep.fitted.model<- lme(LDL ~ gender.rel + age + month,
random = ~ 1 + month|id, data=longform.data,
correlation=corARMA(form = ~ 1|id, p=1, q=1)))
getVarCov(toep.fitted.model, type="conditional")
```

	AIC	BIC	logLik
	877.5213	903.9653	-428.7607

Random effects:

	StdDev	Corr
(Intercept)	21.0541831	(Intr)
month	0.7154187	-0.813

Fixed effects:

	Value	p-value
(Intercept)	61.41936	0.0024
gender.relF	30.11579	0.0002
age	0.95896	0.0091
month	-0.95868	0.0000

Conditional variance covariance matrix

	1	2	3	4
1	101.4400	35.200	-10.762	3.2906
2	35.2000	101.440	35.200	-10.7620
3	-10.7620	35.200	101.440	35.2000
4	3.2906	-10.762	35.200	101.4400

```
#computing AICC
```

```
p<- 11
```

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

882.2713

```
#checking model fit
```

```
print(deviance<- -2*(logLik(null.model)-logLik(toep.fitted.model)))
```

82.61391

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

1.029563e-15

```
#fitting random slope and intercept model with spatial power
#covariance matrix of error terms
summary(sppow.fitted.model<- lme( LDL ~ gender.rel + age + month,
random = ~ 1 + month|id, data=longform.data,
correlation=corCAR1(form = ~ month|id)))
getVarCov(sppow.fitted.model, type="conditional")
```

	AIC	BIC	logLik
	880.3294	904.1289	-431.1647

Random effects:

	StdDev	Corr
(Intercept)	22.8068074	(Intr)
month	0.8857947	-0.812
Residual	8.3578134	

Parameter estimate:

Phi
0.005521199

Fixed effects:

	Value	p-value
(Intercept)	65.01447	0.0014
gender.relF	29.81150	0.0003
age	0.92035	0.0116
month	-1.09566	0.0000

Conditional variance covariance matrix

	1	2	3	4
1	6.9853e+01	1.9787e-12	3.3303e-19	4.4977e-53
2	1.9787e-12	6.9853e+01	1.1757e-05	1.5878e-39
3	3.3303e-19	1.1757e-05	6.9853e+01	9.4338e-33
4	4.4977e-53	1.5878e-39	9.4338e-33	6.9853e+01

```
#computing AICC
```

```
p<- 9
print(AICC<- -2*logLik(sppow.fitted.model)+2*p*n/(n-p-1))
```

882.1661

```
#checking model fit
```

```
print(deviance<- -2*(logLik(null.model)-logLik(sppow.fitted.model)))
```

77.80585

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

5.077837e-16

```
#fitting random slope and intercept model with autoregressive
#covariance matrix of error terms
summary(ar1.fitted.model<- lme(LDL ~ gender.rel + age + month,
random = ~ 1 + month|id, data=longform.data,
correlation=corAR1(form = ~ 1|id)))
getVarCov(ar1.fitted.model, type="conditional")
```

AIC	BIC	logLik
877.5555	901.355	-429.7777

Random effects:

	StdDev	Corr
(Intercept)	19.7010538	(Intr)
month	0.6936938	-0.858
Residual	12.5304689	

Parameter estimate:

Phi
0.5584911

Fixed effects:

	Value	p-value
(Intercept)	62.94677	0.0023
gender.relF	30.60932	0.0003
age	0.93779	0.0120
month	-0.96402	0.0000

Conditional variance covariance matrix

	1	2	3	4
1	157.010	87.690	48.974	27.352
2	87.690	157.010	87.690	48.974
3	48.974	87.690	157.010	87.690
4	27.352	48.974	87.690	157.010

```
#computing AICC
```

```
p<- 9
```

```
print(AICC<- -2*logLik(ar1.fitted.model)+2*p*n/(n-p-1))
```

879.3922

```
#checking model fit
print(deviance<- -2*(logLik(null.model)-logLik(ar1.fitted.model)))
```

80.57979

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

1.312697e-16

```
#fitting random slope and intercept model with compound symmetric
#covariance matrix of error terms
summary(cs.fitted.model<- lme(LDL ~ gender.rel + age + month,
random = ~ 1 + month|id, data=longform.data,
correlation=corCompSymm(form = ~ 1|id)))
```

```
getVarCov(cs.fitted.model, type="conditional")
```

	AIC	BIC	logLik
	880.3294	904.1289	-431.1647

Parameter estimate:

Rho
0

Random effects:

	StdDev	Corr
(Intercept)	22.8072879	(Intr)
month	0.8857844	-0.812
Residual	8.3579458	

Fixed effects:

	Value	p-value
(Intercept)	65.01614	0.0014
gender.relF	29.81056	0.0003
age	0.92033	0.0116
month	-1.09566	0.0000

Conditional variance covariance matrix

	1	2	3	4
1	69.855	0.000	0.000	0.000
2	0.000	69.855	0.000	0.000
3	0.000	0.000	69.855	0.000
4	0.000	0.000	0.000	69.855

```
#computing AICC
p<- 9
print(AICC<- -2*logLik(cs.fitted.model)+2*p*n/(n-p-1))

882.1661

#checking model fit
print(deviance<- -2*(logLik(null.model)-logLik(cs.fitted.model)))

77.80585

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

5.077834e-16
```

Next, we summarize the fit statistics to decide which model is optimal.

	Ind	Un	Toep	SpPow	AR	Exch
AIC	878.3	882.7	877.5	880.3	877.6	880.3
AICC	879.8	889.5	882.3	882.2	879.4	882.2
BIC	899.5	927.7	904.0	904.1	901.4	904.1

Here we make the same conclusion as in SAS: AIC and AICC criteria choose the autoregressive structure, while the independent structure is better with respect to the BIC criterion.

Finally, similar to the analysis done in SAS, we use the model with the autoregressive covariance structure for prediction. The script and output follow.

```
#using AR fitted model for prediction
print(predict(ar1.fitted.model, data.frame(gender.rel="F",
age=48, month=3), level=0))
```

```
135.6782
```

□

8.3 Generalized Estimating Equations Model

8.3.1 Model Definition

So far in this chapter we considered modeling data with repeated measures by a random slope and intercept model with a specified structure of the

variance-covariance matrix of the error terms. Another way to model repeated measures data is to use a *Generalized Estimating Equations*² (GEE) approach. In the GEE model, there are no random-effects terms. Instead, the response variable relates to the predictors via the generalized linear regression model with only fixed-effects terms, and the variance-covariance structure of the response variable itself is specified, rather than that for the error terms.

Suppose that for each individual i , $i = 1, \dots, n$, at time t_j , $j = 1, \dots, a$, the observations are $x_{1ij}, \dots, x_{kij}, y_{ij}$. Denote by $\mu_{ij} = \mathbb{E}(y_{ij})$, the *mean response*, and assume that $g(\mu_{ij}) = \beta_0 + \beta_1 x_{1ij} + \dots + \beta_k x_{kij} + \beta_{k+1} t_j$ where $g(\cdot)$ is the link function.

Next, we write the variance of y_{ij} as a function of μ_{ij} , $\text{Var}(y_{ij}) = V(\mu_{ij})$. The function $V(\cdot)$ is termed the *variance function*.

Further, we model the covariance structure of correlated responses for a given individual i , $i = 1, \dots, n$. Observations between individuals are assumed independent. Let \mathbf{A}_i denote a $a \times a$ diagonal matrix

$$\mathbf{A}_i = \begin{bmatrix} V(\mu_{i1}) & 0 & \dots & 0 \\ 0 & V(\mu_{i2}) & \dots & 0 \\ \dots & \dots & \dots & \dots \\ 0 & 0 & \dots & V(\mu_{ia}) \end{bmatrix}.$$

Also, let $\mathbf{R}_i(\boldsymbol{\alpha})$ be the *working correlation matrix* of the repeated responses for the i -th individual, where $\boldsymbol{\alpha}$ denotes a vector of unknown parameters which are the same for all individuals. The working covariance matrix for $\mathbf{y}_i = (y_{i1}, y_{i2}, \dots, y_{ia})'$ is then

$$\mathbf{V}_i(\boldsymbol{\alpha}) = \mathbf{A}_i^{1/2} \mathbf{R}_i(\boldsymbol{\alpha}) \mathbf{A}_i^{1/2}.$$

The regression coefficients β 's and the vector of parameters $\boldsymbol{\alpha}$ are the only unknowns of the GEE model and must be estimated from the data. Five structures are commonly used for the working correlation matrix $\mathbf{R}_i(\boldsymbol{\alpha})$. They are:

- unstructured (with all different off-diagonal entries, a total of $a(a-1)/2$ unknown parameters)

²Originally discussed in Liang, K.-Y. and S.L. Zeger (1986). "Longitudinal Data Analysis Using Generalized Linear Models". *Biometrika*, 73(1): 13 – 22, and in Zeger, S.L. and K.-Y. Liang (1986). "Longitudinal Data Analysis for Discrete and Continuous Outcomes". *Biometrics*, 42(1): 121 – 130.

$$\mathbf{R}_i(\boldsymbol{\alpha}) = \begin{bmatrix} 1 & \alpha_{12} & \alpha_{13} & \dots & \alpha_{1a} \\ \alpha_{12} & 1 & \alpha_{23} & \dots & \alpha_{2a} \\ \alpha_{13} & \alpha_{23} & 1 & \dots & \alpha_{3a} \\ \dots & \dots & \dots & \dots & \dots \\ \alpha_{1a} & \alpha_{2a} & \alpha_{3a} & \dots & 1 \end{bmatrix},$$

- Toeplitz (with identical entries on each descending diagonal, a total of $a-1$ unknown parameters)

$$\mathbf{R}_i(\boldsymbol{\alpha}) = \begin{bmatrix} 1 & \alpha_1 & \alpha_2 & \dots & \alpha_{a-1} \\ \alpha_1 & 1 & \alpha_1 & \dots & \alpha_{a-2} \\ \alpha_2 & \alpha_1 & 1 & \dots & \alpha_{a-3} \\ \dots & \dots & \dots & \dots & \dots \\ \alpha_{a-1} & \alpha_{a-2} & \alpha_{a-3} & \dots & 1 \end{bmatrix},$$

- autoregressive (with $\alpha^{|i-j|}$ in the ij -th position, a total of one unknown parameter)

$$\mathbf{R}_i(\boldsymbol{\alpha}) = \begin{bmatrix} 1 & \alpha & \alpha^2 & \dots & \alpha^{a-1} \\ \alpha & 1 & \alpha & \dots & \alpha^{a-2} \\ \alpha^2 & \alpha & 1 & \dots & \alpha^{a-3} \\ \dots & \dots & \dots & \dots & \dots \\ \alpha^{a-1} & \alpha^{a-2} & \alpha^{a-3} & \dots & 1 \end{bmatrix},$$

- compound symmetric or exchangeable (with all identical off-diagonal elements, a total of one unknown parameter)

$$\mathbf{R}_i(\boldsymbol{\alpha}) = \begin{bmatrix} 1 & \alpha & \alpha & \dots & \alpha \\ \alpha & 1 & \alpha & \dots & \alpha \\ \alpha & \alpha & 1 & \dots & \alpha \\ \dots & \dots & \dots & \dots & \dots \\ \alpha & \alpha & \alpha & \alpha & 1 \end{bmatrix},$$

- independent (identity matrix, no unknown parameters)

$$\mathbf{R}_i(\boldsymbol{\alpha}) = \begin{bmatrix} 1 & 0 & 0 & \dots & 0 \\ 0 & 1 & 0 & \dots & 0 \\ 0 & 0 & 1 & \dots & 0 \\ \dots & \dots & \dots & \dots & \dots \\ 0 & 0 & 0 & \dots & 1 \end{bmatrix}.$$

The GEE estimate of $\boldsymbol{\beta} = (\beta_0, \beta_1, \dots, \beta_{k+1})'$ is the solution of the *generalized estimating equations*:

$$\sum_{i=1}^n \left(\frac{\partial \boldsymbol{\mu}_i}{\partial \boldsymbol{\beta}} \right)_{(k+2) \times a} [\mathbf{V}_i(\hat{\boldsymbol{\alpha}})]_{a \times a}^{-1} (\mathbf{y}_i - \boldsymbol{\mu}_i)_{a \times 1} = \mathbf{0}_{(k+2) \times 1}$$

where $\boldsymbol{\mu}_i = (\mu_{i1}, \dots, \mu_{ia})'$ is the vector of mean responses, and the estimator $\hat{\boldsymbol{\alpha}}$ is the method of moments estimator of the vector of parameters.

8.3.2 Fitted Model, Interpretation of Estimated Regression Coefficients, and Predicted Response

In this chapter we consider the GEE model with a normally distributed response, hence, the link function is the identity function, $\mathbb{E}(y_{ij}) = \beta_0 + \beta_1 x_{1ij} + \dots + \beta_k x_{kij} + \beta_{k+1} t_j$. The fitted model, interpretation of beta estimates, and prediction are the same as in the random slope and intercept model (see Subsections 8.1.2, 8.1.3, and 8.1.5).

8.3.3 Model Goodness-of-Fit Check

The *quasi-likelihood under the independence* (QIC) model criterion statistic³ is used as the goodness-of-fit measure. It is based on the *quasi-likelihood function* Q defined as follows:

$$Q = \sum_{i=1}^n \sum_{j=1}^a \int_{y_{ij}}^{\mu_{ij}} \frac{y_{ij} - u}{V(u)} du.$$

The QIC is used to select the best-fitted working correlation structure. The one with the smallest value wins.

8.3.4 SAS Implementation

To fit a GEE model, one can use the `genmod` procedure with the `repeated` statement. The syntax is below.

```
proc genmod data=longform_data_name;
  class <list of categorical predictors>;
  model response_name=<list of x predictors> time_name/
    dist=normal link=identity;
  output out=outdata_name p=predicted_response_name;
  repeated subject=id_name/type=corrtype_name corrw;
```

³Introduced in Pan, W. (2001). "Akaike's Information Criterion in Generalized Estimating Equations". *Biometrics*, 57(1): 120 – 125.

`run;`

- The option `dist=normal link=identity` is a default in this procedure and may be omitted.
- The types of the working correlation matrix are `un` for unstructured, `ar` for autoregressive, `cs` or `exch` for compound symmetric (or exchangeable), and `ind` for independent.
- For a Toeplitz working correlation matrix, specify `mdep(m)` with $m \leq a - 1$ where a is the number of time points or repeated observations. This will correspond to an *m-dependent Toeplitz matrix*, for which correlations that are more than m units apart are assumed equal to zero. One can try to run the model with $m = a - 1$ first, and if it doesn't converge, decrease the value of m , so that the peripheral descending diagonals are set to contain all zeros.
 - Specifying the option `corrw` produces the estimated working correlation matrix for a single individual.

8.3.5 R Implementation

Function `geeglm()` in package `geepack` may be employed to fit a GEE model with the specified underlying distribution. In this chapter we model only the normally distributed response. Other distributions will be considered in the next chapter. This function should be run on a long-form data set that is sorted by individuals' id. The syntax for sorting is:

```
longform.data.name <- longform.data.name[order(longform.data.name$id.name),]
```

The syntax for fitting GEE models is as follows:

```
summary(fitted.model.name <- geeglm(response.name ~ x1.name + ...  
+ xk.name + time.name, data=longform.data.name, id=id.name,  
family=gaussian(link="identity"), corstr="corr.structure.name"))
```

- R doesn't automatically fit models with the Toeplitz correlation matrix. The choices for the correlation structures are `unstructured`, `ar1`, `exchangeable`, and `independence`.
- To request the value of QIC, one should type `QIC(fitted.model.name)`, preliminary installing the package `MuMIn`, which performs multi-model inference.

8.3.6 Example

EXAMPLE 8.3. We will use the data in Example 8.1 to fit GEE models with various working correlation matrices, and select the best-fitted one. The SAS code and relevant outputs follow.

```
/*fitting GEE model with unstructured working correlation matrix */
proc genmod data=longform;
class id gender;
model ldl=gender age month/dist=normal link=identity;
repeated subject=id/type=un corrw;
run;
```

WARNING: Iteration limit exceeded.

Working Correlation Matrix

	Col1	Col2	Col3	Col4
Row1	1.0000	0.9810	0.9810	0.8160
Row2	0.9810	1.0000	0.9810	0.7583
Row3	0.9810	0.9810	1.0000	0.6895
Row4	0.8160	0.7583	0.6895	1.0000

GEE Fit Criteria
QIC 144.1917

Analysis Of GEE Parameter Estimates

Parameter		Estimate	Pr > Z
Intercept		403.9145	0.0763
gender	F	-163.042	0.0354
gender	M	0.0000	.
age		-2.7167	0.4942
month		-1.5905	<.0001

Note that the algorithm doesn't converge, and therefore we eliminate this model from the list of candidates.

```
/*fitting GEE model with Toeplitz working correlation matrix */
proc genmod data=longform;
class id gender;
model ldl=gender age month/dist=normal link=identity;
repeated subject=id /type=mdep(3) corrw;
run;
```

Working Correlation Matrix

	Col1	Col2	Col3	Col4
Row1	1.0000	0.7536	0.4798	0.3084
Row2	0.7536	1.0000	0.7536	0.4798
Row3	0.4798	0.7536	1.0000	0.7536
Row4	0.3084	0.4798	0.7536	1.0000

GEE Fit Criteria

QIC 119.1042

Analysis Of GEE Parameter Estimates

Parameter		Estimate	Pr > Z
Intercept		54.1516	0.0028
gender	F	36.0994	<.0001
gender	M	0.0000	.
age		1.0174	0.0010
month		-0.8347	<.0001

```
/*fitting GEE model with autoregressive working correlation matrix*/
proc genmod data=longform;
class id gender;
model ldl=gender age month/dist=normal link=identity;
repeated subject=id /type=ar corrw;
run;
```

Working Correlation Matrix

	Col1	Col2	Col3	Col4
Row1	1.0000	0.7523	0.5659	0.4257
Row2	0.7523	1.0000	0.7523	0.5659
Row3	0.5659	0.7523	1.0000	0.7523
Row4	0.4257	0.5659	0.7523	1.0000

GEE Fit Criteria

QIC 119.4599

Analysis Of GEE Parameter Estimates

Parameter		Estimate	Pr > Z
Intercept		54.0026	0.0036
gender	F	36.3525	<.0001
gender	M	0.0000	.
age		1.0274	0.0012
month		-0.9119	<.0001

```

/*fitting GEE model with compound symmetric working correlation matrix*/
proc genmod data=longform;
class id gender;
model ldl=gender age month/dist=normal link=identity;
repeated subject=id /type=cs corrw;
run;

```

Working Correlation Matrix

	Col1	Col2	Col3	Col4
Row1	1.0000	0.5743	0.5743	0.5743
Row2	0.5743	1.0000	0.5743	0.5743
Row3	0.5743	0.5743	1.0000	0.5743
Row4	0.5743	0.5743	0.5743	1.0000

GEE Fit Criteria
QIC 120.8579

Analysis Of GEE Parameter Estimates

Parameter		Estimate	Pr > Z
Intercept		51.5122	0.0122
gender	F	37.4045	<.0001
gender	M	0.0000	.
age		1.0692	0.0024
month		-1.0957	<.0001

```

/*fitting GEE model with independent working correlation matrix*/
proc genmod data=longform;
class id gender;
model ldl=gender age month/dist=normal link=identity;
repeated subject=id /type=ind corrw;
run;

```

Working Correlation Matrix

	Col1	Col2	Col3	Col4
Row1	1.0000	0.0000	0.0000	0.0000
Row2	0.0000	1.0000	0.0000	0.0000
Row3	0.0000	0.0000	1.0000	0.0000
Row4	0.0000	0.0000	0.0000	1.0000

GEE Fit Criteria
QIC 120.8579

Analysis Of GEE Parameter Estimates

Parameter		Estimate	Pr > Z
Intercept		51.5122	0.0122
gender	F	37.4045	<.0001
gender	M	0.0000	.
age		1.0692	0.0024
month		-1.0957	<.0001

The model with the Toeplitz correlation structure has the smallest QIC value and thus it is the optimal according to this criterion. All the predictors are significant, and the predicted model has the form $\hat{E}(LDL) = 54.1516 + 36.0994 \cdot \text{female} + 1.0174 \cdot \text{age} - 0.8347 \cdot \text{month}$. The estimated mean LDL level for females exceeds that for males by 37.5045 points. When age increases by one year, the estimated average cholesterol level increases by 1.0174 points. As estimated, the mean LDL level decreases by 0.8347 points for every one-month increase in time.

Predicted response at 3 months for a 48-year-old female patient is calculated as $LDL^0 = 54.1516 + 36.0994 + 1.0174 \cdot 48 - 0.8347 \cdot 3 = 136.5821$. SAS outputs the same predicted value:

```
data prediction;
input id gender$ age month;
cards;
28 F 48 3
;

data longform;
  set longform prediction;
run;

proc genmod;
class id gender;
  model ldl=gender age month/dist=normal link=identity;
  output out=outdata p=pred_ldl;
repeated subject=id/type=mdep(3);
run;

proc print data=outdata (firstobs=109) noobs;
var pred_ldl;
run;

pred_ldl
```

136.580

The R script that fits the GEE models to the long-form dataset and the related output are given below.

```
cholesterol.data<- read.csv(file="C:/./Example8.1Data.csv",
header=TRUE, sep=",")

#creating longform data set
library(reshape2)
longform.data<- melt(cholesterol.data, id.vars=c("id", "gender", "age"),
variable.name = "LDLmonth", value.name="LDL")

#sorting data by id
longform.data<- longform.data[order(longform.data$id),]

#creating numeric variable for time
month<- ifelse(longform.data$LDLmonth=="LDL0", 0,
ifelse(longform.data$LDLmonth=="LDL6", 6,
ifelse(longform.data$LDLmonth=="LDL9",9,24)))

#fitting GEE model with unstructured working correlation matrix
library(geepack)
library(MuMIn)
summary(un.fitted.model<- geeglm(LDL ~ gender.rel + age + month,
data=longform.data, id=id, family=gaussian(link="identity"),
corstr="unstructured"))
```

Coefficients:

	Estimate	Pr(> W)
(Intercept)	49.487	0.0061
gender.relF	34.315	1.3e-07
age	1.008	0.0006
month	-0.479	0.2396

Estimated Correlation Parameters:

	Estimate
alpha.1:2	1.138
alpha.1:3	0.644
alpha.1:4	0.142
alpha.2:3	0.608
alpha.2:4	0.153
alpha.3:4	0.427


```
QIC(un.fitted.model)
```

```
QIC  
656.1
```

Note that the estimated correlation matrix is not reliable because one of the estimates is larger than one. Therefore, we will omit this model from further consideration.

```
#fitting GEE model with autoregressive working correlation matrix  
summary(ar.fitted.model<- geeglm(LDL ~ gender.rel + age + month,  
data=longform.data, id=id, family=gaussian(link="identity"),  
corstr="ar1"))
```

Coefficients:

	Estimate	Pr(> W)
(Intercept)	53.708	0.0042
gender.relF	36.463	1.5e-07
age	1.032	0.0012
month	-0.926	9.3e-08

Estimated Correlation Parameters:

	Estimate
alpha	0.701

```
QIC(ar.fitted.model)
```

```
QIC  
650
```

```
#fitting GEE model with compound symmetric (exchangeable)  
#working correlation matrix  
summary(cs.fitted.model<- geeglm(LDL ~ gender.rel + age+ month,  
data=longform.data, id=id, family=gaussian(link="identity"),  
corstr="exchangeable"))
```

Coefficients:

	Estimate	Pr(> W)
(Intercept)	51.512	0.0122
gender.relF	37.405	3.0e-07
age	1.069	0.0024
month	-1.096	7.5e-09

Estimated Correlation Parameters:

	Estimate
alpha	0.582

```
QIC(cs.fitted.model)
```

QIC
651

```
#fitting GEE model with independent working correlation matrix  
summary(ind.fitted.model<- geeglm(LDL ~ gender.rel + age + month,  
data=longform.data, id=id, family=gaussian(link="identity"),  
corstr="independence"))
```

Coefficients:

	Estimate	Pr(> W)
(Intercept)	51.512	0.0122
gender.relF	37.405	3.0e-07
age	1.069	0.0024
month	-1.096	7.5e-09

```
QIC(ind.fitted.model)
```

QIC
651

The QIC-optimal model is the one with autoregressive working correlation matrix. The statement below computes the predicted response based on this model.

```
#using autoregressive fitted model for prediction  
print(predict(ar.fitted.model, data.frame(gender.rel="F", age=48,  
month=3)))
```

136.9

□

Exercises for Chapter 8

EXERCISE 8.1. Show that in the random slope and intercept model defined in (8.1),

- (a) For any $i \neq i'$, $\text{Cov}(y_{ij}, y_{i'j'}) = 0$. Note: j may be equal to j' .
- (b) For any given i and $j \neq j'$, $\text{Cov}(y_{ij}, y_{ij'}) = \sigma_{u_1}^2 + \sigma_{u_1 u_2} (t_j + t_{j'}) + \sigma_{u_2}^2 t_j t_{j'}$.
- (c) The response variable y_{ij} has a normal distribution with the mean $\mathbb{E}(y_{ij}) = \beta_0 + \beta_1 x_{1ij} + \cdots + \beta_k x_{kij} + \beta_{k+1} t_j$ and variance $\text{Var}(y_{ij}) = \sigma_{u_1}^2 + 2\sigma_{u_1 u_2} t_j + \sigma_{u_2}^2 t_j^2 + \sigma^2$.

EXERCISE 8.2. A new manager in a department store wants to introduce a new incentive compensation program for the floor employees. She looks at the historical data on the yearly bonuses in the past three years, and such characteristics of each employee as the number of years with the company and the current employment status (full- or part-time). The data for 15 employees are:

ID	Total Years	Status	Bonus 2018	Bonus 2019	Bonus 2020
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

- (a) Carry out tests for normality of the bonus and plot the histogram. Is this variable normally distributed?
- (b) 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?
- (c) Write down the fitted model, specifying all estimated parameters. What predictors are significant at the 5% significance level?
- (d) Give interpretation of the estimated significant regression coefficients.
- (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?

EXERCISE 8.3. In order to improve the quality of medical service, an orthopedic clinic conducts a survey of their patients. After each visit, patients fill out a questionnaire, scoring the quality of service on the 0 to 10 continuous scale (larger values indicate better quality). The data for two doctors (referred to as A and B) are available. The variables are patient ID, gender, age (in years), doctor visited (A or B), length of the visit (in minutes) for three visits, and scores patients gave to these visits. The data on 35 patients are:

ID	Gender	Age	Doctor	Length1	Length2	Length3	Score1	Score2	Score3
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

- Create a long-form data set.
- Confirm that the quality of service is normally distributed by plotting a histogram and conducting normality tests.
- Fit a random slope and intercept model to regress the quality of service scores on all the predictor variables. Discuss the model fit.
- What parameters of the random terms are significant at the 5% level? Are the scores for each patient correlated?
- What fixed-effects variables are significant predictors at the 5% signifi-

cance level? Write down the fitted model.

(f) Interpret the estimates of the significant regression coefficients.

(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.

EXERCISE 8.4. Measurements were taken on 20 people involved in a physical fitness course. The data below contain participants' gender, age, oxygen intake (in ml per kg body weight per minute), run time (time to run 1 mile, in minutes), and pulse (average heart rate while running). The running was done under three different conditions: the first one on a treadmill, the second one on an indoor running track, and the third one on an outdoor running track. The data are summarized in the table below.

ID	Gender	Age	Oxgn1	Rtime1	Pulse1	Oxgn2	Rtime2	Pulse2	Oxgn3	Rtime3	Pulse3
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	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

(a) Check that pulse has a normal distribution. Construct a histogram and conduct normality tests.

(b) Run a random slope and intercept regression model for pulse. Discuss the model fit.

(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?

(d) Interpret the estimated regression coefficients for the significant fixed-effects terms.

(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.

EXERCISE 8.5. A health center conducted a study on efficacy of an intervention on weight loss. The intervention consisted of a lecture on proper nutrition and importance of exercising, followed by a cooking class. The study had a wait list control group. For each of the 34 study participants, the investigators recorded the group (intervention or control), gender (F/M), the typical length of daily exercise in the past week (in minutes), and BMI (in kg/m^2) at the beginning of the study, and at 1 and 3 months afterwards. The data are as follows:

ID	Group	Gender	aExercise	aBMI	bExercise	bBMI	cExercise	cBMI
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

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ID	Group	Gender	aExercise	aBMI	bExercise	bBMI	cExercise	cBMI
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

- Verify normality of the response variable BMI by plotting the histogram and carrying out normality tests.
- Fit the random slope and intercept model. How good is the model fit?
- Present the fitted model and specify all estimated parameters. Discuss significance of the parameters at the 5% significance level.
- Give interpretation of the estimated significant beta coefficients. Is the intervention efficient?
- Compute the predicted BMI at 3 months for an intervention group female participant, if she exercises for 1 hour every day.

EXERCISE 8.6. Consider the data in Exercise 8.2. Answer the questions below.

- 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.
- 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.

EXERCISE 8.7. For the data in Exercise 8.3,

- 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.
- Which of the fitted models has the best fit according to the AIC, AICC, and BIC criteria?
- Answer parts (e)-(g) in Exercise 8.3 as applied to the best fitted model.

EXERCISE 8.8. Use the data in Exercise 8.4 to do the following analysis:

- 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.

(b) Find the best-fitted model according to the AIC, AICC, and BIC criteria.

(c) Answer questions (c)-(e) in Exercise 8.4 for the model that fits the data the best.

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.

(b) Which of the models has the best fit according to AIC, AICC, and BIC criteria?

(c) For the best-fitted model, do the analysis for questions (c) through (e) in Exercise 8.5.

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.

(b) Find the best model using the QIC criterion.

(c) For the model that fits the data the best, answer questions (c)-(e) in Exercise 8.2.

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.

(b) Which of the fitted models has the best fit according to the QIC criterion?

(c) Answer parts (e)-(g) in Exercise 8.3 in relation to the best-fitted model.

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.

(b) Compare the QIC values for the fitted models and choose the optimal

one.

- (c) For the optimal model, do questions (c)-(e) in Exercise 8.4.

EXERCISE 8.13. For the data given in Exercise 8.5, do the following questions:

- (a) Fit the GEE models with unstructured, Toeplitz (only in SAS), autoregressive, compound symmetric, and independent working correlation matrices of the response variable BMI.
- (b) Choose the best-fitted model with respect to the QIC criterion.
- (c) For the best-fitted model, do parts (c)-(e) in Exercise 8.5.

Chapter 9

Generalized Linear Regression Models for Repeated Measures Data

Generalized linear mixed-effects and GEE models are regression models that extend the classes of random slope and intercept (Section 8.1) and GEE (Section 8.3) models for normally distributed response variables, respectively. Generalized models can be used to model repeated measures data with skewed, categorical, or count response.

Random slope and intercept models with covariance structure for errors that we considered in Section 8.2 are not applicable in this case, because the models for data with non-normally distributed response don't contain error terms.

9.1 Generalized Random Slope and Intercept Model

9.1.1 Model Definition

A *generalized random slope and intercept model* (also termed the *generalized linear mixed model*) is a generalization of the linear mixed-effects model introduced in (8.1) to any distribution of the response variable in the exponential family of distributions, and the corresponding link function. In this chapter we talk about the models considered earlier: gamma (in Section 2.2), binary logistic (in Section 3.1), Poisson (in Section 5.1), negative binomial (in Section 6.1), and beta (in Section 7.1). In the setting of each regression, we assume that the data were collected longitudinally at times

t_1, \dots, t_a , and that for the i -th individual at time t_j the observations are x_{1ij}, \dots, x_{kij} , and y_{ij} where $i = 1, \dots, n$, and $j = 1, \dots, a$, and y_{ij} 's have one of the aforementioned distributions. The generalized mixed-effects model in each case has two random additive terms in the linear regression expression: $\beta_0 + \beta_1 x_{1ij} + \dots + \beta_k x_{kij} + \beta_{k+1} t_j + u_{1i} + u_{2i} t_j$ where u_{1i} 's are independent $\mathcal{N}(0, \sigma_{u_1}^2)$ random intercepts, u_{2i} 's are independent $\mathcal{N}(0, \sigma_{u_2}^2)$ random slopes, $\text{Cov}(u_{1i}, u_{2i}) = \sigma_{u_1 u_2}$, and $\text{Cov}(u_{1i}, u_{2i'}) = 0$ for $i \neq i'$.

A simpler model that contains only the random intercept may be considered if the model with random slope and intercept is not estimable.

Remark. Fitting a negative binomial regression might not be necessary as the random-effects terms in a Poisson model will take care for overdispersion in the count data.

9.1.2 Fitted Model, Interpretation of Estimated Regression Coefficients, Model Goodness-of-Fit Check, and Predicted Response

Fitted generalized random slope and intercept model has the form

$$g(\hat{\mathbb{E}}(y)) = \hat{\beta}_0 + \hat{\beta}_1 x_1 + \dots + \hat{\beta}_k x_k + \hat{\beta}_{k+1} t$$

where $g(\cdot)$ is the link function that corresponds to the underlying distribution.

Interpretation of the estimated beta coefficients and computation of predicted response for a fixed set of predictors are done the same way as in the appropriate regression model (gamma, binary logistic, Poisson, or beta).

The goodness-of-fit test is the standard deviance test where the null model contains only fixed-effects terms.

9.1.3 SAS Implementation

The procedure `glimmix`, employed in Section 7.1 for fitting a beta regression, can handle generalized linear mixed-effects models if the `random` statement is added. The general statements should be:

```
proc glimmix data=data_name method=Laplace;
class catpredictor1_name (ref="level_name") catpredictor2_name
      (ref="level_name") ...;
```

```

model response_name=<list of predictors>/dist=dist_name link=link_type
solution;
  output out=outdata pred(ilink)=predicted_name;
  random intercept time_name/subject=id_name type=un;
  covtest/wald;
run;

```

- The option `method=Laplace` specifies the method of parameter estimation, in which the output contains the values of $-2 \times \log$ -likelihood. This value is needed for computation of model deviance and carrying out the test of model fit.
- The choices for the distributions and corresponding links are: `dist=gamma link=log`, `dist=binomial link=logit`, `dist=poisson link=log`, `dist=nb link=log`, and `dist=beta link=logit`.
- Along with specific values for all predictors, the row for prediction must contain a hypothesized value for *id_name*.
- The statement `covtest/wald` should be added to request the Wald z-test results for the parameters of the random-effects terms.
- In the output for gamma regression, the estimate of parameter α is called **Residual**.
- In the output for negative binomial regression, the estimate of r is called **Scale**.

9.1.4 R Implementation

To fit a generalized random slope and intercept gamma, logistic, or Poisson model in R, the function `glmer()` in the library `lme4` is used. The data set must be in the long form. The general script is:

```

summary(fitted.model.name<- glmer(response.name ~ x1.name + ...
+ xk.name + time.name + (1+ time.name|id.name), control=glmerControl(),
data=longform.data.name, family=dist.name(link="link.type")))

```

- The distribution names and the link types can be specified as `Gamma(link="log")`, `binomial(link="logit")`, or `poisson(link="log")`.
- In the output for gamma regression, the estimate of parameter α is called **Residual**.
- The optional function `glmerControl()` aids in model convergence.
- Currently there is no built-in procedure to carry out tests of significance for the variance-covariance parameters, but R outputs the estimates and their standard errors. Thus, the two-sided z-test may be conducted by hand.

- To output the predicted value of the response variable for a fixed set of predictors, the function `predict()` should be used with the following syntax:

```
predict(fitted.model.name, data.frame(catpredictor1.name="value", ...,
numpredictork.name=value, time.name=value), re.form=NA, type="response")
```

The argument `re.form=NA` requests predicted response not conditioned on any values of the random-effects terms.

To fit a negative binomial model with random-effects terms, one can use the function `glmer.nb()` in the library `lme4`, with the distribution and link function specified as `family=negative.binomial(link="log")`. The output contains the exponentiated dispersion parameter $\exp\{r\}$.

To fit a beta regression model with random-effects terms, the function `glmmTMB()` can be employed in the library `glmmTMB` which stands for “generalized linear mixed models using Template Model Builder”. The distribution and link function should be specified as `family=beta_family(link="logit")`. Also, in this case, when predicting a value, one has to use options `allow.new.levels=TRUE` and `type="response"` in the function `predict()`.

9.1.5 Example

EXAMPLE 9.1. A dermatologist tests a new ointment treatment for psoriasis. He administers the ointment to five patients, and keeps five patients as control. The control patients take a medication that is commonly prescribed against the disease. The doctor sees the patients next day, then after one week, two weeks, five weeks, and finally, after three months. He records the number of psoriatic patches that are visible on patients’ bodies. The code below fits the random slope and intercept Poisson model to the data.

```
data psoriasis;
input patid group$ day1 week1 week2 week5 month3 @@;
cards;
1 Tx 15 12 9 3 0 2 Tx 24 17 9 8 8
3 Cx 14 14 15 15 14 4 Cx 23 20 19 19 15
5 Tx 11 10 3 2 0 6 Cx 11 10 8 7 5
7 Tx 7 6 5 3 0 8 Tx 9 6 2 0 0
9 Cx 9 9 9 9 9 10 Cx 21 16 16 15 15
;

data longform;
```

```

set psoriasis;
array w{5}(0.14 1 2 5 13);
array x{5} day1 week1 week2 week5 month3;
do i=1 to 5;
    weeks=w{i};
    npatches=x{i};
    output;
end;
keep patid group weeks npatches;
run;

proc glimmix method=Laplace;
class group;
model npatches=group weeks/solution dist=poisson
link=log;
random intercept weeks/subject=patid type=un;
covtest/wald;
run;

```

Covariance Parameter Estimates

Cov Parm	Estimate	Pr Z
UN(1,1)	0.1139	0.1292
UN(2,1)	0.04259	0.2046
UN(2,2)	0.02408	0.0749

Solutions for Fixed Effects

Effect	group	Estimate	Pr > t
Intercept		2.6503	<.0001
group	Cx	-0.1916	0.5762
group	Tx	0	.
weeks		-0.1570	0.0229

The output shows that the variances and covariance of the random-effects terms are not significant at the 5% level. A reasonable simpler model to run in this case would be a random intercept-only model, where the random slope is omitted.

```

proc glimmix method=Laplace;
class group;
model npatches=group weeks/solution dist=poisson
link=log;
random intercept/subject=patid type=un;

```

```

covtest/wald;
run;

-2 Log Likelihood 289.31

Covariance Parameter Estimates
Cov Parm    Estimate    Pr > Z
UN(1,1)      0.1492    0.0281

```

```

Solutions for Fixed Effects
Effect      group    Estimate    Pr > |t|
Intercept                2.0222    <.0001
group        Cx         0.7391    0.0080
group        Tx          0         .
weeks                -0.05778    <.0001

```

In the fitted random intercept-only Poisson model, the estimated rate $\hat{\lambda} = \hat{E}(y) = \exp\{2.0222 + 0.7391 \cdot Cx - 0.05778 \cdot weeks\}$. Both group and weeks are significant predictors at the 0.05 level. The estimated average number of psoriatic patches for patients in the control group is $\exp\{0.7391\} \cdot 100\% = 209.41\%$ of that for the patients in the treatment group. Each week, the estimated average number of patches changes by $(\exp\{-0.05778\} - 1) \cdot 100\% = -5.61\%$, that is, decreases by 5.61%.

Next, we fit the null model, which in this case is the model with only the fixed effects, and conduct the deviance test of model fit.

```

proc glimmix;
class group;
model npatches=group weeks/solution dist=poisson
link=log;
run;

data deviance_test;
deviance=336.27-289.31;
pvalue=1-probchi(deviance,1);
run;

proc print;
run;

deviance    pvalue
46.96      7.245E-12

```


The p -value is tiny which indicates a good model fit. Finally, we would like to use the estimated model to predict the number of psoriatic patches for a patient in the treatment group at five weeks. We compute $y^0 = \exp\{2.0222 - 0.05778 \cdot 5\} = 5.66$. To produce the prediction in SAS, we write:

```
data prediction;
input patid group$ weeks;
cards;
11 Tx 5
;

data longform;
  set longform prediction;
run;

proc glimmix method=Laplace;
  class group;
  model npatches=group weeks/dist=poisson link=log;
  random intercept/subject=patid type=un;
  output out=outdata pred(ilink)=p_npatches;
run;

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

p_npatches
    5.65951
```

Note that the row for prediction must contain a (hypothesized) value of the id variable.

Further, the R script and appropriate output for this example are as follows:

```
psoriasis.data<-read.csv(file="./Example9.1Data.csv", header=TRUE, sep=",")

#creating long-form data set
library(reshape2)
longform.data<- melt(psoriasis.data, id.vars=c("patid", "group"),
variable.name = "visits", value.name="npatches")
```

```

#creating numeric variable for time
weeks<- ifelse(longform.data$visits=="day1", 0.14,
ifelse(longform.data$visits=="week1", 1,
ifelse(longform.data$visits=="week2",
2,ifelse(longform.data$visits=="week5", 5, 13)))

#specifying reference category
group.rel<- relevel(longform.data$group, ref="Tx")

#fitting random slope and intercept Poisson model
library(lme4)
summary(glmer(npatches ~ group.rel + weeks + (1 + weeks|patid),
data=longform.data, family=poisson(link="log")))

Random effects:
Groups Name      Variance Corr
patid (Intercept) 0.11393
      weeks      0.02403 0.81

Fixed effects:
      Estimate Pr(>|z|)
(Intercept) 2.65008 < 2e-16
group.relCx -0.19148 0.57023
weeks      -0.15681 0.00565

#fitting random intercept-only Poisson model
summary(fitted.model<- glmer(npatches ~ group.rel + weeks + (1|patid),
data=longform.data, family=poisson(link="log")))

Random effects:
Groups Name      Variance
patid (Intercept) 0.1492

Fixed effects:
      Estimate Pr(>|z|)
(Intercept) 2.02224 < 2e-16
group.relCx 0.73904 0.00515
weeks      -0.05778 2.74e-07

#checking model fit
null.model<- glm(npatches ~ group.rel + weeks, data=longform.data,
family=poisson(link=log))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))

```

46.96343

```
print(p.value<- pchisq(deviance, df=1, lower.tail=FALSE))
```

7.232377e-12

```
#using the model for prediction
print(predict(fitted.model, data.frame(patid=11, group.rel="Tx",
weeks=5), re.form=NA, type="response"))
```

5.659691

□

9.2 Generalized Estimating Equations Model

9.2.1 Model Definition

The Generalized Estimating Equations model described in Section 8.3 translates directly to the gamma, logistic, Poisson, and negative binomial models. Neither SAS nor R can handle GEE for a beta distribution, so this model will be omitted from consideration.

9.2.2 SAS Implementation

In SAS, `proc genmod` is used to fit GEEs with the syntax given in Subsection 8.3.4. Allowable distributions and link types are: `dist=gamma link=log`, `dist=bin link=logit`, `dist=poisson link=log`, and `dist=nb link=log`. When the distribution is logistic, include `descending` in the *proc* statement to model the probability of level “1”.

9.2.3 R Implementation

In R, the function `geeglm()` is employed for fitting a Generalized Estimating Equations model. The general form of the script was presented in Subsection 8.3.5.

- The underlying response distributions and the corresponding links are given as: `gamma(link="log")`, `binomial(link="logit")`, `poisson(link="log")`, and `nb(link="log")`.
- To request predicted response, the argument `type="response"` should be added to the function `predict()`.

9.2.4 Example

EXAMPLE 9.2. We fit GEE models to the data in Example 9.1. In SAS, the model with unstructured working correlation matrix doesn't converge. Therefore, we present results for the Toeplitz, autoregressive, exchangeable, and independent structures.

```
/*fitting GEE with Toeplitz working correlation matrix*/
proc genmod;
  class patid group;
  model npatches=group weeks/dist=poisson link=log;
  repeated subject=patid/type=mdep(3) corrw;
run;
```

Working Correlation Matrix					
	Col1	Col2	Col3	Col4	Col5
Row1	1.0000	0.7495	0.4228	0.2298	0.0000
Row2	0.7495	1.0000	0.7495	0.4228	0.2298
Row3	0.4228	0.7495	1.0000	0.7495	0.4228
Row4	0.2298	0.4228	0.7495	1.0000	0.7495
Row5	0.0000	0.2298	0.4228	0.7495	1.0000

GEE Fit Criteria
QIC -483.3303

Analysis Of GEE Parameter Estimates			
Parameter		Estimate	Pr > Z
Intercept		2.1455	<.0001
group	Cx	0.6625	0.0303
group	Tx	0.0000	.
weeks		-0.0362	0.0019

```
/*fitting GEE with autoregressive working correlation matrix*/
proc genmod;
  class patid group;
  model npatches=group weeks/dist=poisson link=log;
  repeated subject=patid/type=ar corrw;
run;
```

Working Correlation Matrix					
	Col1	Col2	Col3	Col4	Col5
Row1	1.0000	0.7504	0.5631	0.4225	0.3171

Row2	0.7504	1.0000	0.7504	0.5631	0.4225
Row3	0.5631	0.7504	1.0000	0.7504	0.5631
Row4	0.4225	0.5631	0.7504	1.0000	0.7504
Row5	0.3171	0.4225	0.5631	0.7504	1.0000

GEE Fit Criteria
QIC -494.0739

Analysis Of GEE Parameter Estimates

Parameter	Estimate	Pr > Z
Intercept	2.2059	<.0001
group Cx	0.5637	0.0379
group Tx	0.0000	.
weeks	-0.0424	0.0016

```
/*fitting GEE with exchangeable working correlation matrix*/
proc genmod;
  class patid group;
  model npatches=group weeks/dist=poisson link=log;
  repeated subject=patid/type=cs corrw;
run;
```

Working Correlation Matrix

	Col1	Col2	Col3	Col4	Col5
Row1	1.0000	0.5775	0.5775	0.5775	0.5775
Row2	0.5775	1.0000	0.5775	0.5775	0.5775
Row3	0.5775	0.5775	1.0000	0.5775	0.5775
Row4	0.5775	0.5775	0.5775	1.0000	0.5775
Row5	0.5775	0.5775	0.5775	0.5775	1.0000

GEE Fit Criteria
QIC -438.9074

Analysis Of GEE Parameter Estimates

Parameter	Estimate	Pr > Z
Intercept	2.3502	<.0001
group Cx	0.3174	0.1689
group Tx	0.0000	.
weeks	-0.0579	0.0054

```
/*fitting GEE with independent working correlation matrix*/
proc genmod;
```

```

class patid group;
  model npatches=group weeks/dist=poisson link=log;
  repeated subject=patid/type=ind corrw;
run;

```

```

Working Correlation Matrix
      Col1   Col2   Col3   Col4   Col5
Row1 1.0000  0.0000  0.0000  0.0000  0.0000
Row2 0.0000  1.0000  0.0000  0.0000  0.0000
Row3 0.0000  0.0000  1.0000  0.0000  0.0000
Row4 0.0000  0.0000  0.0000  1.0000  0.0000
Row5 0.0000  0.0000  0.0000  0.0000  1.0000

```

```

GEE Fit Criteria
QIC -459.7895

```

```

Analysis Of GEE Parameter Estimates
Parameter      Estimate    Pr > |Z|
Intercept           2.1223    <.0001
group      Cx         0.6902    0.0118
group      Tx         0.0000      .
weeks           -0.0578    0.0052

```

The model with the autoregressive working correlation structure has the smallest QIC value, thus, this model has the best fit. In this case, the estimated rate $\hat{\lambda} = \hat{E}(y) = \exp\{2.2059 + 0.5637 \cdot Cx - 0.0424 \cdot weeks\}$, where both predictors are significant at the 5% significance level. The estimated average number of psoriatic patches for patients in the control group is $\exp\{0.6902\} \cdot 100\% = 199.41\%$ of that for the patients in the treatment group. Each week, the estimated average number of patches changes by $(\exp\{-0.0578\} - 1) \cdot 100\% = -5.62\%$, that is, decreases by 5.62%.

To predict the number of psoriatic patches for a patient in the treatment group five weeks into the study, we calculate $y^0 = \exp\{2.2059 - 0.0424 \cdot 5\} = 7.34$. In SAS, the following statements produce the prediction:

```

data prediction;
input patid group$ weeks;
cards;
11 Tx 5
;

```

```

data longform;
  set longform prediction;
run;

proc genmod;
  class patid group;
  model npatches=group weeks/dist=poisson link=log;
  output out=outdata p=p_npatches;
  repeated subject=patid/type=ar;
run;

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

```

```

p_npatches
  7.34378

```

Below we give the R statements for this example and corresponding outputs. We use the long-form data set already created in Example 9.1 but we need to sort it by ID.

```

#sorting data by id
longform.data<- longform.data[order(longform.data$patid),]

#specifying reference category
group.rel<- relevel(as.factor(longform.data$group), ref="Tx")

library(geepack)
library(MuMIn)

#fitting GEE model with unstructured working correlation matrix
summary(un.fitted.model<- geeglm(npatches ~ group.rel + weeks,
data=longform.data, id=patid, family=poisson(link="log"),
corstr="unstructured"))

```

Coefficients:

```

      Estimate Pr(>|W|)
(Intercept)  1.8166 2e-12
group.relCx  0.8773 0.0019
weeks       -0.0212 0.3846

```

Estimated Correlation Parameters:

	Estimate	Std.err
alpha.1:2	1.4478	0.2470
alpha.1:3	0.4449	0.2001
alpha.1:4	0.0376	0.2068
alpha.1:5	-0.2015	0.3470
alpha.2:3	0.3136	0.1478
alpha.2:4	0.0762	0.1557
alpha.2:5	-0.0721	0.2616
alpha.3:4	0.3201	0.1263
alpha.3:5	0.3052	0.1493
alpha.4:5	0.6064	0.0983

```

\begin{verbatim}
\begin{verbatim}
QIC(un.fitted.model)
\end{verbatim}
\begin{verbatim}
QIC
-1378

```

```

#fitting GEE model with autoregressive working correlation matrix
summary(ar.fitted.model<- geeglm(npatches ~ group.rel + weeks,
data=longform.data, id=patid, family=poisson(link="log"), corstr="ar1"))

```

Coefficients:

	Estimate	Pr(> W)
(Intercept)	1.9935	4.4e-16
group.relCx	0.7336	0.0064
weeks	-0.0218	0.3960

Estimated Correlation Parameters:

	Estimate
alpha	0.544

```

QIC(ar.fitted.model)

```

```

QIC
-1379

```

```

#fitting GEE model with exchangeable working correlation matrix
summary(exch.fitted.model<- geeglm(npatches ~ group.rel + weeks,
data=longform.data, id=patid, family=poisson(link="log"),
corstr="exchangeable"))

```


Coefficients:

	Estimate	Pr(> W)
(Intercept)	1.9666	<2e-16
group.relCx	0.7649	0.0032
weeks	-0.0231	0.3497

Estimated Correlation Parameters:

	Estimate
alpha	0.328

QIC(exch.fitted.model)

QIC
-1380

```
#fitting GEE model with independent working correlation matrix
summary(ind.fitted.model<- geeglm(npatches ~ group.rel + weeks,
data=longform.data, id=patid, family=poisson(link="log"),
corstr="independence"))
QIC(ind.fitted.model)
```

Coefficients:

	Estimate	Pr(> W)
(Intercept)	1.9666	<2e-16
group.relCx	0.7649	0.0032
weeks	-0.0231	0.3497

QIC
-1380

The models with exchangeable and independent working correlation matrices have the smallest QIC value. The one with the independent structure is simpler and will be used for prediction.

```
#using autoregressive fitted model for prediction
print(predict(ind.fitted.model, data.frame(patid=11,
group.rel="Tx", weeks=5), type="response"))
```

6.37

□

Exercises for Chapter 9

EXERCISE 9.1. A center for medical weight loss is considering buying a shipment of a new medication that was recently marketed. Prior to the purchase, the doctors decide to conduct a trial with their patients to test superiority of this new medication as compared to the one that they have been prescribing on the regular basis. They administer this medication to 8 patients while keeping another 8 patients as a control group. For each subject in the trial, the doctors record group (Tx/Cx), gender (M/F), and excess body weight loss (EWL, in percent) between measurement sessions: from the baseline to 1 month (EWL1), 1 month to 2 months (EWL2), 2 months to 3 months (EWL3), and 3 months to 6 months (EWL4). The data are:

PatID	Group	Gender	EWL1	EWL2	EWL3	EWL4
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
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

- Plot the histogram of the EWL to see that this variable has a right-skewed distribution.
- 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.
- What parameters are significant at the 5% level? Give the fitted model, specifying all parameter estimates.
- Give interpretation of the estimates of significant fixed-effects parameters. Is the new medication superior to the regularly used one?
- 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?

EXERCISE 9.2. A pharmaceutical company conducted a dosage trial for a painkiller medication. Five dosages were tested and two were picked as the winners (dosages A and B). Further investigation was launched into a long-run safety of these dosages. An experiment was set up with 7 subjects in each of the two groups, taking dosages A and B, respectively. The goal of the experiment was to identify which dosage is less likely to cause side effects. The data set below contains participants' ID, dosage (A or B), gender, age, and presence or absence of side effects (1=present, or 0=absent) at 1, 3, 7, and 16 weeks.

PatID	Dosage	Gender	Age	Week1	Week3	Week7	Week16
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

(Continues on the next page)

(Continued from the previous page)

PatID	Dosage	Gender	Age	Week1	Week3	Week7	Week16
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

- 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.
- Specify the fitted model, giving the estimates of all parameters. Which parameters are significant at the 5% significance level? At the 10% level?
- Interpret the estimates of the significant beta coefficients. What dosage should be preferred?
- Predict the probability of side effects occurring at week 7 for a 40-year-old woman taking dosage A.

EXERCISE 9.3. A new general manager of a hotel chain is interested in measuring and improving hotel performance. He obtains a year worth of data on 18 hotels in the same tier, and records seasonal values for such hotel performance metrics as the average daily rate (ADR) defined as the average rental income per paid occupied room (in U.S. dollars), and the number of days the hotel occupancy rate (OCR) was below 65%. He also notes if the hotels are situated in rural or urban areas. The data for the four seasons (summer, fall, winter, and spring) are:

Hotel	Area	ADR1	OCR1	ADR2	OCR2	ADR3	OCR3	ADR4	OCR4
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

- 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.
- State the fitted model. Identify all significant parameters. Use $\alpha = 0.05$. Are responses over seasons correlated within each hotel?
- Interpret the estimates of all significant beta coefficients.
- Predict the number of days with occupancy rate below 65% for the winter season in a rural hotel with average daily rate of \$75.

EXERCISE 9.4. As part of her dissertation, a Ph.D. student in the School of Pharmacy set up a study to evaluate effectiveness of medication adherence educational classes. Twenty seven patients diagnosed with diabetes took part in the study. They were referred to the study by their doctors because their medication adherence for the initial refill was relatively poor. The student conducted an educational class, and throughout the study collected data on participants' gender, age, level of education, and proportion of days that they took diabetes medication for 60-day refills (called proportion days covered or PDC). The data are:

ID	Gender	Age	Educ	PDC1	PDC2	PDC3	PDC4
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

- 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.
- Specify the fitted model and interpret all estimated significant fixed-effects parameters. Use the significance level of 0.10.
- What is the predicted PDC value for the second refill of medication for a 50-year-old man with a Bachelor's degree?

EXERCISE 9.5. Use the data in Exercise 9.1 to do the following:

- 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.
- Compare model fits. Use the QIC criterion.

(c) For the model that has the best fit, do questions (c)-(e) from Exercise 9.1.

EXERCISE 9.6. Use the data in Exercise 9.2 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.
- (b) Choose the best model according to the QIC value.
- (c) For the best-fitted model, answer questions (b)-(d) from Exercise 9.2.

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.
- (b) Choose the QIC-optimal model.
- (c) Answer parts (b)-(d) in Exercise 9.3 for the optimal model.

Chapter 10

Hierarchical Regression Model

In this chapter, we introduce models in which observations may be collected once or repeatedly for each individual, but individuals are logically aggregated in some way, possibly at multiple levels (for example, students are clustered within classrooms, which are clustered within schools). These models incorporate potential correlation among observations at each hierarchical level.

10.1 Hierarchical Regression Model for Normal Response

10.1.1 Model Definition

We assume that data are collected at three levels, and, for ease of presentation, will formulate a three-level hierarchical regression model for a special case when data are collected longitudinally for individuals who are clustered in some way. Suppose data are recorded at times t_1, \dots, t_a on each of n individuals, who are grouped into c clusters. For each individual, there are k predictor variables and one normally distributed response. An observation at time j for individual i in cluster m is $(x_{1ijm}, \dots, x_{kijm}, y_{ijm})$, where $i = 1, \dots, n$, $j = 1, \dots, a$, and $m = 1, \dots, c$. Some of the x variables may be characteristics of times (level 1), or of individuals (level 2), or of clusters (level 3). A general form of the *three-level hierarchical model* (also termed *three-stage hierarchical regression model*¹ or *multilevel model* or *model for clustered data*) for a normal response is:

¹The model was introduced in Goldstein, H. (1986). "Multilevel mixed linear model analysis using iterative generalized least squares". *Biometrika*, 73(1): 43 – 56.

$$y_{ijm} = \beta_0 + \beta_1 x_{1ijm} + \cdots + \beta_k x_{kijm} + \beta_{k+1} t_j + u_{1im} + u_{2im} t_j + \tau_{1m} + \tau_{2m} t_j + \varepsilon_{ijm} \quad (10.1)$$

where $u_{1im} \stackrel{iid}{\sim} \mathcal{N}(0, \sigma_{u_1}^2)$, $u_{2im} \stackrel{iid}{\sim} \mathcal{N}(0, \sigma_{u_2}^2)$, $\text{Cov}(u_{1im}, u_{2im}) = \sigma_{u_1 u_2}$, and $\text{Cov}(u_{1im}, u_{2i'm'}) = 0$ for $i \neq i'$. These two random variables are the *level-2 random slope and intercept*, respectively. Also, $\tau_{1m} \stackrel{iid}{\sim} \mathcal{N}(0, \sigma_{\tau_1}^2)$, $\tau_{2m} \stackrel{iid}{\sim} \mathcal{N}(0, \sigma_{\tau_2}^2)$, and $\text{Cov}(\tau_{1m}, \tau_{2m}) = \sigma_{\tau_1 \tau_2}$. These variables are, respectively, the *level-3 random slope and intercept*. The random errors ε_{ijm} 's are independent with $\mathcal{N}(0, \sigma^2)$ distribution. In addition, all u 's are independent of τ 's, and both are independent of ε 's.

As defined in the above formula, the index i for individuals (or, more generally, level-2 variable) ranges between 1 and n . It is also possible to enumerate individuals only within each cluster: $i = 1, \dots, n_m$ where $\sum_{m=1}^c n_m = n$.

It can be shown (see Exercise 10.1) that

- Observations within each individual i in cluster m for different times j and j' have covariance $\text{Cov}(y_{ijm}, y_{ij'm}) = \sigma_{u_1}^2 + \sigma_{\tau_1}^2 + (\sigma_{u_1 u_2} + \sigma_{\tau_1 \tau_2})(t_j + t_{j'}) + (\sigma_{u_2}^2 + \sigma_{\tau_2}^2) t_j t_{j'}$. It means that if at least one of these parameters statistically differs from zero, the observations over time within one individual are correlated.
- 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 $\text{Cov}(y_{ijm}, y_{i'j'm}) = \sigma_{\tau_1}^2 + \sigma_{\tau_1 \tau_2}(t_j + t_{j'}) + \sigma_{\tau_2}^2 t_j t_{j'}$. If any of the sigma's are statistically distinguishable from zero, the observations are correlated for different individuals within the same cluster.
- Observations for two individuals in different clusters are always uncorrelated, that is, $\text{Cov}(y_{ijm}, y_{i'j'm'}) = 0$ where $i \neq i'$ and $m \neq m'$.

10.1.2 Fitted Model, Interpretation of Estimated Regression Coefficients, Model Goodness-of-Fit Check, Predicted Response

A fitted hierarchical model has the estimated mean response of the form $\hat{\mathbb{E}}(y) = \hat{\beta}_0 + \hat{\beta}_1 x_1 + \cdots + \hat{\beta}_k x_k + \hat{\beta}_{k+1} t$. Estimated regression coefficients are interpreted identically to how they are interpreted in a general linear regression model (see Section 1.5). The log-likelihood deviance test is used to check the model fit. The null model in this case has only fixed-effects terms. As expected, the predicted response for a given set of predictors x_1^0, \dots, x_k^0 , and t^0 can be calculated as $y^0 = \hat{\beta}_0 + \hat{\beta}_1 x_1^0 + \cdots + \hat{\beta}_k x_k^0 + \hat{\beta}_{k+1} t^0$.

10.1.3 SAS Implementation

The procedure `mixed` fits hierarchical regression with a normally distributed response. To accommodate the hierarchical structure, `random` statements should be included for variables defining levels 2 and 3 of the model. The full syntax is presented below.

```
proc mixed data=longform_data_name covtest;
  class cluster_name individual_name <list of categorical predictors>;
  model response_name=<list of predictors> time_name/solution
    outpm=outdata_name;
  random intercept time_name/subject=cluster_name type=un;
  random intercept time_name/subject=individual_name(cluster_name)
    type=un;
run;
```

- For prediction, the long-form data set must contain a row with specified values of all the x variables and the time variable. And in addition, one has to specify some (sometimes hypothesized) values for a cluster and an individual within this cluster, possibly defining a new cluster with individual number 1.

10.1.4 R Implementation

Hierarchical model for normally distributed response variable may be fitted to a long-form data set with function `lmer()` in the library `lme4`. The syntax is:

```
summary(fitted.model.name<- lmer(response.name ~ x1.name + ...
+ xk.name + time.name + (1 + time.name| cluster.name)
+ (1 + time.name| cluster.name:individual.name), data = data.name)).
```

- As usually, prediction can be carried out using the function `predict()`. In the `data.frame` argument, however, some values for a cluster and an individual must be specified. Since a new cluster and individual are added, the argument `allow.new.levels=TRUE` must be included. The syntax looks like this:

```
predict(fitted.model.name, data.frame(cluster.name=new.value, individual.name=1, catpredictor1.name="value", ..., numpredictork.name=value, time.name=value), allow.new.levels=TRUE, re.form=NA)
```

10.1.5 Example

EXAMPLE 10.1. Mothers and daughters from 24 families with signs of depression were invited for a study of efficacy of a new method of intensive psychotherapy. At the baseline, one- and three-month visits, the quality of life (QOL) questionnaire was filled out by each of the participant, and a QOL score was computed. Higher values of this score indicate better quality of life. Whether signs of depression were present was also recorded (1=present, or 0=absent). The study was done on mother-daughter dyads. This type of study is called *familial* or *dyadic*. The scores are logically expected to be correlated over time for each individual, and also members of the same family might have correlated responses. For some families, more than one daughter participated. Below we develop a three-stage hierarchical model for the data.

```
data dyads;
input family individual relation$ depression1
depression2 depression3 qol1 qol2 qol3 @@;
cards;
1 1 M 1 1 1 4.0 4.1 4.9 1 2 D 1 1 0 2.5 3.2 4.2
2 1 M 1 1 1 2.6 2.8 4.1 2 2 D 1 1 1 2.8 3.1 4.2
3 1 M 1 1 1 2.5 3.8 4.0 3 2 D 1 1 1 2.4 5.1 3.3
4 1 M 1 0 0 2.1 3.3 4.6 4 2 D 1 0 0 3.7 3.1 4.4
5 1 M 1 0 0 2.9 4.2 3.4 5 2 D 1 0 0 2.4 2.6 2.7
6 1 M 1 1 0 3.3 4.2 4.7 6 2 D 1 1 0 2.7 4.0 4.1
7 1 M 1 1 0 3.7 4.3 3.8 7 2 D 1 1 0 2.8 3.2 3.6
8 1 M 1 0 0 3.5 4.1 4.3 8 2 D 1 1 0 1.6 2.6 3.5
9 1 M 1 0 0 4.0 4.4 3.6 9 2 D 1 0 1 1.8 2.5 3.1
10 1 M 1 1 1 3.0 3.7 4.3 10 2 D 1 1 1 2.2 2.0 3.3
11 1 M 1 1 1 4.3 5.0 3.7 11 2 D 1 1 1 3.3 2.5 3.2
12 1 M 1 1 1 3.5 5.4 4.7 12 2 D 1 1 1 3.5 3.6 4.2
13 1 M 1 0 0 4.1 4.5 3.2 13 2 D 1 0 0 3.7 4.2 3.5
14 1 M 1 1 0 5.0 4.2 3.6 14 2 D 1 0 0 3.3 4.6 3.0
15 1 M 1 1 0 1.8 2.2 2.3 15 2 D 1 0 0 2.4 3.5 3.6
16 1 M 1 0 0 3.1 2.5 3.9 16 2 D 1 1 0 2.0 2.9 2.4
17 1 M 1 1 0 3.4 5.5 4.7 17 2 D 1 0 1 3.2 4.3 3.7
18 1 M 1 0 0 3.4 5.3 4.1 18 2 D 1 1 0 1.8 3.4 3.1
19 1 M 1 0 0 3.5 3.3 5.1 19 2 D 1 0 0 2.8 4.3 3.4
```

```

20 1 M 1 0 0 3.5 3.3 5.1 20 2 D 1 0 0 3.2 4.9 3.6
21 1 M 1 0 0 2.9 2.7 3.5 21 2 D 1 0 0 4.3 3.7 2.5
22 1 M 1 0 0 4.8 4.3 4.3 22 2 D 1 0 0 4.5 3.8 3.3
23 1 M 1 1 0 3.6 3.9 3.7 23 2 D 1 0 0 3.7 3.7 3.5
23 3 D 1 1 0 2.5 1.8 2.3 24 1 M 1 1 0 5.0 4.4 4.2
24 2 D 1 1 0 4.9 3.2 2.5 24 3 D 1 0 0 2.7 3.1 4.1
24 4 D 1 0 1 3.0 3.5 3.6
;

```

```

data longform;
  set dyads;
array d[3] depression1-depression3;
array q[3] qol1-qol3;
  do visit=1 to 3;
    depression=d[visit];
    qol_score=q[visit];
    output;
  end;
keep family individual relation depression visit qol_score;
run;

```

```

proc univariate;
  var qol_score;
  histogram/normal;
run;

```

Goodness-of-Fit Tests for Normal Distribution

Test	p Value
Kolmogorov-Smirnov	0.150
Cramer-von Mises	>0.250
Anderson-Darling	>0.250

The tests support normality, and the histogram shows a roughly bell-shaped curve. Therefore, we will fit a hierarchical model based on normal distribution.

```

proc mixed covtest;
  class family individual relation(ref="D") depression;
  model qol_score=relation depression visit/solution;
  random intercept visit/subject=family type=un;
random intercept visit/subject=individual(family) type=un;
run;

```

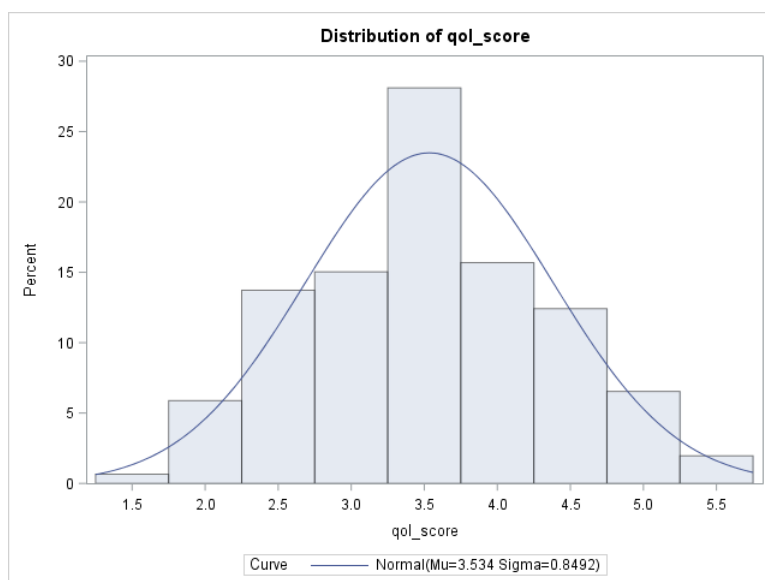


Figure 10.1: Histogram for QOL_score in SAS

Covariance Parameter Estimates

Cov Parm	Subject	Estimate	Pr > Z
UN(1,1)	family	0.2827	0.1694
UN(2,1)	family	-0.1238	0.2730
UN(2,2)	family	0.06723	0.0840
UN(1,1)	individual(family)	0.4795	0.0111
UN(2,1)	individual(family)	-0.09011	0.0342
UN(2,2)	individual(family)	0	.
Residual		0.3882	<.0001

Null Model Likelihood Ratio Test

DF	Chi-Square	Pr > ChiSq
5	17.83	0.0032

Solution for Fixed Effects

Effect	mother depression	Estimate	Pr > t
Intercept		2.7180	<.0001
relation	M	0.6060	<.0001
relation	D	0	.
depression	0	0.04226	0.7777
depression	1	0	.
visit		0.2569	0.0150

This model has a reasonable fit since the p -value in the likelihood ratio test is smaller than 0.05. At the individual level, the variance of the random

intercept, and covariance between the intercept and the slope are significant at the 5% level. At the family level, variance of the random slope is significant at the 10% level. Thus, at the 5% significance level, observations are correlated for each individual, but not between family members. At the 10% level, however, correlation between family members also exists. The estimated mean QOL score may be written as $\widehat{E}(QOL) = 2.7180 + 0.6060 \cdot mother + 0.04226 \cdot no_depression + 0.2569 \cdot visit$. At the 5% level, depression is not a significant predictor of quality of life, whereas both mother and visit are significant predictors. Estimated average QOL score for mothers is larger than that for daughters by 0.6060, and the estimated score increases, on average, by 0.2569 between visits.

Suppose now that we would like to predict the QOL score for a mother at visit 3 who doesn't show any symptoms of depression. We calculate $QOL^0 = 2.7180 + 0.6060 + 0.04226 + 0.2569 \cdot 3 = 4.13696$. SAS outputs similar value as seen below.

```
data prediction;
input family individual relation$ depression visit;
cards;
25 1 M 0 3
run;

data longform;
  set longform prediction;
run;

proc mixed covtest;
  class family individual relation(ref="D") depression;
  model qol_score=relation depression visit/solution outpm=outdata;
  random intercept visit/subject=family type=un;
  random intercept visit/subject=individual(family) type=un;
run;

proc print data=outdata (firstobs=154 obs=154);
var Pred;
run;

      Pred
4.13688
```

The R script and output for fitting the hierarchical model are:

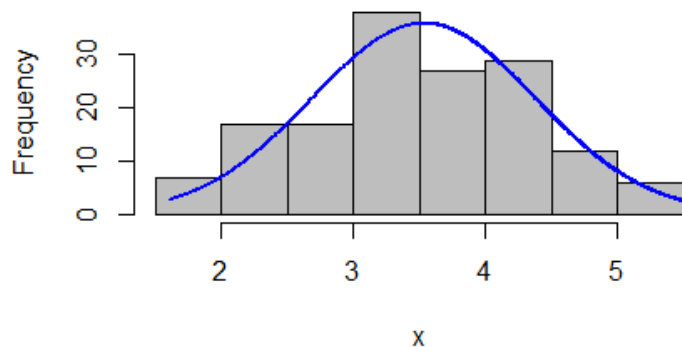


Figure 10.2: Histogram for QOL in R

```
dyads.data<-read.csv(file="./Example10.1Data.csv",
header=TRUE, sep=",")

#creating long-form data set
install.packages("reshape2")
library(reshape2)

data.depr<- melt(dyads.data[,c("family", "individual", "relation",
"depression1","depression2", "depression3")], id.vars=c("family",
"individual", "relation"), variable.name="depr.visits",
value.name="depression")
data.qol<- melt(dyads.data[,c("qol1","qol2", "qol3")],
variable.name="qol.visits", value.name="qol")
longform.data<- cbind(data.depr, data.qol)

#creating numeric variable for time
visit<- ifelse(longform.data$depr.visits=="depression1", 1,
ifelse(longform.data$depr.visits=="depression2", 2, 3))

#plotting histogram with fitted normal density
install.packages("rcompanion")
library(rcompanion)

plotNormalHistogram(longform.data$qol)

#testing for normality of distribution
```



```

shapiro.test(longform.data$qol)

Shapiro-Wilk normality test
W = 0.98955, p-value = 0.3147

#specifying reference category
depression.rel<- relevel(as.factor(longform.data$depression), ref="1"))

#fitting hierarchical model
install.packages("lme4")
library(lme4)

summary(fitted.model<- lmer(qol ~ relation + depression.rel + visit
+ (1 + visit|family)+ (1 + visit|family:individual),
data=longform.data))

Random effects:

```

Groups	Name	Variance	Corr
family:individual	(Intercept)	0.54480	
	visit	0.03518	-1.00
family	(Intercept)	0.28400	
	visit	0.05722	-0.90
Residual		0.35886	

```

Fixed effects:

```

	Estimate	t value
(Intercept)	2.71793	12.731
relationM	0.60277	4.458
depression.rel0	0.03476	0.235
visit	0.25838	2.651

```

#checking model fit
null.model<- glm(qol ~ relation + depression.rel + visit,
data=longform.data)
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))
5.332274

print(p.value<- pchisq(deviance, df=6, lower.tail=FALSE))
0.5019591

#using fitted model for prediction
print(predict(fitted.model, data.frame(family=25, individual=1,
relation="M", depression.rel="0", visit=3), allow.new.levels=TRUE))
4.130584

□

```

10.2 Hierarchical Regression Model for Non-normal Response

10.2.1 Model Definition

A hierarchical regression model for the response variable y_{ijm} that has a gamma, or logistic, or Poisson, or negative binomial, or beta distribution is defined similarly to a normally distributed response but the expression (10.1) takes the form

$$g(\mathbb{E}(y_{ijm})) = \beta_0 + \beta_1 x_{1ijm} + \cdots + \beta_k x_{kijm} + \beta_{k+1} t_j + u_{1im} + u_{2im} t_j + \tau_{1m} + \tau_{2m} t_j$$

where $g(\cdot)$ is the link function that corresponds to the underlying distribution.

10.2.2 Fitted Model

A fitted hierarchical model with the link function $g(\cdot)$ is

$$g(\widehat{\mathbb{E}}(y)) = \widehat{\beta}_0 + \widehat{\beta}_1 x_1 + \cdots + \widehat{\beta}_k x_k + \widehat{\beta}_{k+1} t. \quad (10.2)$$

10.2.3 Interpretation of Estimated Regression Coefficients

In view of (10.2), in the hierarchical regression model with non-normal response, estimated regression coefficients are interpreted identically to how they are interpreted in a generalized linear regression model, in terms of a change or difference in the link function of the estimated mean response. Or, more specifically, the same way as estimated regression coefficients are interpreted for each of the appropriate regressions models: gamma (Subsection 2.2.3), logistic (Subsection 3.1.3), Poisson (Subsection 5.1.3), negative binomial (Subsection 6.1.3), and beta (Subsection 7.1.3).

10.2.4 Model Goodness-of-Fit Check

The model fit can be verified via the standard log-likelihood deviance test, where the null model has no random-effects terms.

10.2.5 Predicted Response

By (10.2), the predicted response for a given set of predictors x_1^0, \dots, x_k^2 , and t^0 is found as $y^0 = g^{-1}(\widehat{\beta}_0 + \widehat{\beta}_1 x_1^0 + \dots + \widehat{\beta}_k x_k^0 + \widehat{\beta}_{k+1} t^0)$ for the appropriate link function $g(\cdot)$.

10.2.6 SAS Implementation

The syntax for procedure `glimmix` presented in Subsection 9.1.3 applies directly to fitting hierarchical regression models. Two `random` statements should be included for variables defining levels 2 and 3 of the model. The general syntax is:

```
proc glimmix data=data_name method=Laplace;
class cluster_name individual_name catpredictor1_name (ref="level_name")
catpredictor2_name (ref="level_name") ...;
model response_name=<list of predictors> time_name/solution dist=dist_name
link=link_type;
    output out=outdata pred(ilink)=predicted_name;
random intercept time_name/subject=cluster_name type=un;
random intercept time_name/subject=individual_name(cluster_name) type=un;
    covtest/wald;
run;
```

- For prediction purposes, one has to add to the long-form data set a row containing a value for cluster, a value for individual, and values for all predictor and time variables.

10.2.7 R Implementation

Function `glmer()` in the library `lme4` may be used to fit a hierarchical model for a response variable with a gamma, logistic, and poisson distributions. The statements are:

```
summary(fitted.model.name<- glmer(response.name ~ x1.name + ...
+ xk.name + time.name + (1 + time.name| cluster.name)
+ (1 + time.name| cluster.name/individual.name), data=data.name,
family=dist.name("link.type")))
```

- The choices for distribution names and link types are `Gamma("log")`, `binomial("logit")`, and `poisson("log")`.

To fit a hierarchical model for a response variable with a negative binomial distribution, one can use the function `glmer.nb()` in the library `lme4`. The syntax is the same as above with `family=negative.binomial("log")`.

A hierarchical model with a beta distributed response can be fitted using the function `glmmTMB` in the library `glmmTMB`, where the syntax above is valid with `family=beta_family(link="logit")`.

- The syntax for prediction is:

```
predict(fitted.model.name, data.frame(cluster.name=new.value, individual.name=1, catpredictor1.name="value", ..., numpredictork.name=value, time.name=value), allow.new.levels=TRUE, re.form=NA, type="response")
```

10.2.8 Example

EXAMPLE 10.2. For the long-form data set created in the previous example, we fit a hierarchical model based on logistic distribution to model presence of symptoms of depression. First we try a complete three-stage model. The code is given below. This model, however, doesn't converge.

```
proc glimmix method=Laplace;
  class family individual relation(ref="D");
  model depression=relation qol_score visit/solution dist=binomial
    link=logit;
  random intercept visit/subject=family type=un;
  random intercept visit/subject=individual(family) type=un;
  covtest/wald;
run;
```

The most complex model that converges is the one with the intercept at the family level only.

```
proc glimmix method=Laplace;
  class family individual relation(ref="D");
  model depression=relation qol_score visit/solution dist=binomial
    link=logit;
  random intercept/subject=family type=un;
  covtest/wald;
run;
```

-2 Log Likelihood 123.46

Covariance Parameter Estimates

Cov Parm	Subject	Estimate	Pr > Z
UN(1,1)	family	5.9549	0.0491

Solutions for Fixed Effects

Effect		Estimate	Pr > t
Intercept		9.3445	0.0009
relation	M	0.2761	0.6400
relation	D	0	.
qol_score		-0.5214	0.2576
visit		-3.2363	<.0001

The variance of the random intercept at the family level is statistically significant at the 5% level. Next, we conduct the goodness-of-fit test.

```
proc glimmix;
  class family individual relation;
  model depression=relation qol_score visit/dist=binomial link=logit;
run;
```

-2 Log Likelihood 143.50

```
data deviance_test;
  deviance=143.50-123.46;
  pvalue=1-probchi(deviance,1);
run;
```

```
proc print;
run;
```

deviance	pvalue
20.04	.000007584

The p -value is below 0.05, indicating a good fit. The fitted model has the form

$$\hat{\mathbb{P}}(depr = 1) = \frac{\exp\{9.3445 + 0.2761 \cdot mother - 0.5214 \cdot qol_score - 3.2363 \cdot visit\}}{1 + \exp\{9.3445 + 0.2761 \cdot mother - 0.5214 \cdot qol_score - 3.2363 \cdot visit\}}.$$

Significant predictor is only the visit number. The estimated odds in favor of presence of symptoms of depression change by $(\exp\{-3.2363\} - 1) \cdot 100\% =$

−96.07%, that is, decrease by 96.07% from visit to visit.

The predicted probability that a mother with the quality of life score of 3.5 shows symptoms of depression during the third visit is

$$\mathbb{P}^0(depr) = \frac{\exp\{9.3445 + 0.2761 - 0.5214 \cdot 3.5 - 3.2363 \cdot 3\}}{1 + \exp\{9.3445 + 0.2761 - 0.5214 \cdot 3.5 - 3.2363 \cdot 3\}} = 0.12862.$$

The prediction in SAS is carried out via the following statements.

```
data prediction;
input family individual relation$ qol_score visit;
cards;
25 1 M 3.5 3
;

data longform;
  set longform prediction;
run;

proc glimmix method=Laplace;
  class family individual relation;
  model depression=relation qol_score visit/dist=binomial link=logit;
  random intercept/subject=family type=un;
  output out=outdata pred(ilink)=p_probdepr;
run;

proc print data=outdata (firstobs=154) noobs;
var p_probdepr;
run;

p_probdepr
  0.12862
```

R script and relevant output for this example follow.

```
dyads.data<- read.csv(file="./Example10.1Data.csv", header=TRUE,
sep=",")

#creating long-form data set
library(reshape2)
data.depr<- melt(dyads.data[,c("family", "individual", "relation",
```

```

"depression1", "depression2", "depression3")], id.vars=c("family",
"individual", "relation"), variable.name="depr.visits",
value.name="depression")
data.qol<- melt(dyads.data[,c("qol1","qol2", "qol3")],
variable.name="qol.visits", value.name="qol")
longform.data<- cbind(data.depr, data.qol)

#creating numeric variable for time
visit<- ifelse(longform.data$depr.visits=="depression1", 1,
ifelse(longform.data$depr.visits=="depression2", 2, 3))

#fitting hierarchical model (fails to converge)
library(lme4)
summary(glmer(depression ~ relation + qol + visit + (1 + visit|family)
+ (1 + visit|family:individual), data=longform.data,
family=binomial(link="logit")))

#fitting simpler hierarchical model (converges)
summary(fitted.model<- glmer(depression ~ relation + qol + visit
+ (1|family), data=longform.data, family=binomial(link="logit")))

```

Random effects:

Groups	Name	Variance
family	(Intercept)	5.955

Fixed effects:

	Estimate	Pr(> z)
(Intercept)	9.3444	0.000138
mother	0.2761	0.639248
qol	-0.5214	0.255404
visit	-3.2363	2.24e-07

#checking model fit

```

null.model<- glm(depression ~ relation + qol + visit,
data=longform.data, family=binomial(link=logit))
print(deviance<- -2*(logLik(null.model)-logLik(fitted.model)))

```

20.03607

```
print(p.value<- pchisq(deviance, df=1, lower.tail=FALSE))
```

7.599509e-06

```
#using fitted model for prediction
print(predict(fitted.model, data.frame(family=25, individual=1,
relation="M", qol=3.5, visit=3), allow.new.levels=TRUE,
re.form=NA, type="response"))
```

0.1286211

□

Exercises for 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 $\text{Cov}(y_{ijm}, y_{ij'm}) = \sigma_{u_1}^2 + \sigma_{\tau_1}^2 + (\sigma_{u_1 u_2} + \sigma_{\tau_1 \tau_2})(t_j + t_{j'}) + (\sigma_{u_2}^2 + \sigma_{\tau_2}^2) t_j t_{j'}$.
- (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 $\text{Cov}(y_{ijm}, y_{i'j'm}) = \sigma_{\tau_1}^2 + \sigma_{\tau_1 \tau_2}(t_j + t_{j'}) + \sigma_{\tau_2}^2 t_j t_{j'}$.
- (c) Observations for two individuals in different clusters are not correlated, that is, $\text{Cov}(y_{ijm}, y_{i'j'm'}) = 0$ where $i \neq i'$ and $m \neq m'$.
- (d) The response variable y_{ijm} has a normal distribution with the mean $\mathbb{E}(y_{ijm}) = \beta_0 + \beta_1 x_{1ijm} + \cdots + \beta_k x_{kijm} + \beta_{k+1} t_j$ and variance $\text{Var}(y_{ijm}) = \sigma_{u_1}^2 + \sigma_{\tau_1}^2 + 2(\sigma_{u_1 u_2} + \sigma_{\tau_1 \tau_2}) t_j + (\sigma_{u_2}^2 + \sigma_{\tau_2}^2) t_j^2 + \sigma^2$.

EXERCISE 10.2. A team of school inspectors is studying scores on tests in English Language Arts (ELA), Mathematics, and Science and their relation to schools' Academic Performance Index (API) and classroom size. Data on average classroom scores for five consecutive years at two schools are available.

School	API	Subject	Class size	Year	Score
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	84.9
1	917	Math	24	17	86.12
1	917	Math	23	18	88.99
1	919	Math	23	19	88.4
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	70.3
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

- (a) Plot a histogram for test scores and conduct normality testing. Verify that the underlying distribution may be modeled as normal.
- (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.
- (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?

- (d) Give interpretation for all estimated significant fixed-effects coefficients. Use $\alpha = 0.10$.
- (e) Use the fitted model to predict average score on a math test for a class of 36 students in 2019 in a school with an API of 753.

EXERCISE 10.3. An environmental health scientist studies levels of pollution. For the study he randomly chooses three states and two counties within each state. In each county he randomly samples eight townships, and measures levels of an atmospheric particulate matter that have a diameter of less than 2.5 micrometers (PM2.5). For each township, he also records population size (in thousands of people) and whether pesticides are applied on a large scale in farming. The collected data are summarized in the following table.

state	county	township	popl	pest	pm2_5	state	county	township	popl	pest	pm2_5
S1	A	1	4.1	no	22.97	S2	D	1	6.6	no	9.13
S1	A	2	22.0	no	23.05	S2	D	2	7.2	no	11.04
S1	A	3	6.3	no	24.97	S2	D	3	8.3	no	8.98
S1	A	4	3.2	no	23.77	S2	D	4	5.2	yes	5.75
S1	A	5	13.4	no	23.09	S2	D	5	9.1	yes	11.28
S1	A	6	3.9	yes	24.75	S2	D	6	4.3	no	6.88
S1	A	7	3.8	yes	36.93	S2	D	7	6.9	yes	9.21
S1	A	8	25.6	yes	45.83	S2	D	8	8.5	yes	11.23
S1	B	1	12.7	no	13.19	S3	E	1	6.1	no	5.44
S1	B	2	17.8	no	22.90	S3	E	2	3.9	no	4.33
S1	B	3	23.7	no	31.45	S3	E	3	3.5	no	5.04
S1	B	4	11.8	yes	25.40	S3	E	4	2.4	no	3.31
S1	B	5	12.9	yes	44.15	S3	E	5	4.3	no	5.24
S1	B	6	13.0	yes	25.16	S3	E	6	2.8	yes	14.34
S1	B	7	12.0	yes	54.36	S3	E	7	3.4	no	4.90
S1	B	8	13.0	no	24.38	S3	E	8	3.6	no	3.59
S2	C	1	9.9	no	7.25	S3	F	1	5.3	no	5.01
S2	C	2	5.6	yes	28.46	S3	F	2	4.5	no	5.73
S2	C	3	3.9	no	7.06	S3	F	3	2.5	no	4.28
S2	C	4	7.3	no	9.33	S3	F	4	3.1	yes	15.42
S2	C	5	4.7	no	5.59	S3	F	5	3.5	no	3.59
S2	C	6	8.9	yes	9.94	S3	F	6	5.7	no	4.69
S2	C	7	6.7	yes	8.49	S3	F	7	7.1	no	4.06
S2	C	8	6.5	yes	6.97	S3	F	8	4.6	no	3.98

- (a) Plot a histogram of the particulate matter (PM2.5). Describe its shape. Argue that a gamma distribution is appropriate.
- (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.

(c) Write down the fitted model. Specify all estimates. Are PM2.5 readings correlated within each county? Between different counties within each state? Use $\alpha = 0.10$.

(d) What fixed-effects predictors are significant at the 5% level? Interpret them.

(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.

EXERCISE 10.4. A financial analyst is studying behavior of certain portfolios with stocks, bonds, and currency. He records whether the prices of the assets went up at the closure of the stock exchange at the end of five consecutive business days (1=went up, 0=went down or stayed the same). The data follow.

Portfolio	Asset	Type	Day1	Day2	Day3	Day4	Day5
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

- (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?
- (b) What predictors are significant at the 5% level? Interpret the estimated

significant regression coefficients.

(c) According to the fitted model, what is the predicted probability of an increase in value of a currency on the third day?

EXERCISE 10.5. A team of child psychologists conducted a study with third graders. They administered a test to high performing students at all third-grade classes at three schools. The computer-based test consisted of four tasks. The researchers were interested in how many additional attempts beyond one it would take each student to complete each task. The measurements are summarized in the following table.

School	Class	Student	Gender	Task1	Task2	Task3	Task4
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

- (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?
- (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.
- (c) Use the fitted model to predict the number of extra attempts it would take a girl to complete the fourth task.

EXERCISE 10.6. An undergraduate advisor in Mathematics at a Master's degree granting university is interested in finding out how many students who graduate with a Bachelor's degree stay on at the same department to get a Master's degree. She records the data for her university and also sends out a brief survey to Biology, Chemistry, and Mathematics departments at seven comparable universities. The data she obtains are for the most recent three years.

Univ	Dept	Year1	Year2	Year3	Univ	Dept	Year1	Year2	Year3
1	bio	6	13	17	5	bio	7	16	15
1	chem	8	7	12	5	chem	4	4	4
1	math	10	14	13	5	math	8	1	6
2	bio	0	8	8	6	bio	5	3	3
2	chem	0	9	9	6	chem	5	3	4
2	math	0	5	8	6	math	23	32	45
3	bio	2	8	5	7	bio	7	2	8
3	chem	3	3	5	7	chem	9	12	9
3	math	18	19	26	7	math	7	15	16
4	bio	1	11	12	8	bio	3	6	8
4	chem	1	5	4	8	chem	32	11	20
4	math	5	16	17	8	math	8	4	13

- (a) Argue that the data may be modeled as having a negative binomial distribution. What quantities support your argument?
- (b) Run a multilevel model, using department and year as predictors. Does the model fit the data well?
- (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.
- (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 $\alpha = 0.10$. (e) What is the predicted number of students who would stay on for a Master's program in a math department in year 4?

EXERCISE 10.7. A multi-center clinical trial in pharmacology studies the response for different medications. Same subjects test four medications with proper washout periods observed in-between. The response to medications is measured on a continuous scale. The data are as follows.

Center	Subject	Gender	Med A	Med B	Med C	Med D
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

- (a) Run the multilevel regression to model the response to medication, assuming that it follows a beta distribution.
- (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.
- (c) Interpret the results. Are responses correlated for each subject? For each center? Interpret estimated significant fixed-effects terms.
- (d) Use the fitted model to predict the response to medication A for a female subject.

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List of Notation

Q , 250	π^0 , 64, 69, 74
$V(\cdot)$, 248	π_0 , 185, 201
$\Phi(\cdot)$, 68, 92	π_1 , 193, 201
$\Phi^{-1}(\cdot)$, 68	ρ , 231, 232
α , 48, 249	σ^2 , 13, 220, 231, 232, 290
$\alpha_1, \dots, \alpha_{c-1}$, 84, 92, 98, 104	$\sigma_{\tau_1}^2$, 290, 304
β , 48	$\sigma_{\tau_1}^2$, 290
β_0, \dots, β_k , 13, 14, 48, 61, 68, 73, 117, 122, 150, 154, 180	$\sigma_{\tau_2}^2$, 290, 304
β_0, \dots, β_m , 128, 134, 159, 165, 185, 193, 201	$\sigma_{u_1}^2$, 220, 259, 268, 290, 304
$\beta_0, \dots, \beta_{k+1}$, 220, 248, 268, 290, 298, 304	$\sigma_{u_2}^2$, 220, 259, 268, 290, 304
β_1, \dots, β_k , 84, 92, 98	$\sigma_1, \dots, \sigma_{a-1}$, 231
$\beta_{j1}, \dots, \beta_{jk}$, 104	$\sigma_{\tau_1 \tau_2}$, 290, 304
$\gamma_0, \dots, \gamma_{k-m}$, 128, 134, 159, 165, 185, 193	$\sigma_{u_1 u_2}$, 220, 259, 268, 290, 304
$\gamma_0, \dots, \gamma_{l-m}$, 201	τ , 201
λ , 35, 117, 122, 128, 134, 150, 154, 159, 165, 180, 185, 193	τ_{1m} , 290, 298
$\ln L$, 16	τ_{2m} , 290, 298
$\mathbb{E}(y)$, 14, 48, 61, 68, 117, 122, 123, 128, 129, 134, 142, 150, 154, 160, 166, 180, 186, 194, 202, 209, 220	θ , 14
\mathbf{A}_i , 248	\tilde{y} , 35
$\mathbf{R}_i(\boldsymbol{\alpha})$, 248	ε , 13
\mathbf{y}_i , 248	ε_{1jm} , 290
μ , 180, 185, 193, 201, 209	ε_{ij} , 220
μ_{ij} , 248	\hat{r} , 150, 155, 160, 165
ν , 201	$\hat{\alpha}$, 49
ϕ , 14, 49, 180, 185, 193, 201, 209	$\hat{\alpha}_1, \dots, \hat{\alpha}_{c-1}$, 85, 92, 98, 104
π , 61, 68, 73, 128, 134, 159, 165	$\hat{\beta}$, 49
	$\hat{\beta}_0, \dots, \hat{\beta}_k$, 15, 36, 49, 62, 69, 73, 118, 123, 150, 155, 180
	$\hat{\beta}_0, \dots, \hat{\beta}_m$, 128, 134, 160, 165, 186, 194, 201
	$\hat{\beta}_0, \dots, \hat{\beta}_{k+1}$, 220, 298
	$\hat{\beta}_1, \dots, \hat{\beta}_k$, 85, 92, 98
	$\hat{\beta}_{j1}, \dots, \hat{\beta}_{jk}$, 104
	$\hat{\gamma}_0, \dots, \hat{\gamma}_{k-m}$, 128, 134, 160, 165,

$186, 194$
 $\widehat{\gamma}_0, \dots, \widehat{\gamma}_{l-m}, 201$
 $\widehat{\lambda}, 118, 123, 128, 134, 150, 155,$
 $160, 165$
 $\widehat{\mu}, 180, 186, 194, 201$
 $\widehat{\nu}, 201$
 $\widehat{\phi}, 49, 186, 194$
 $\widehat{\pi}, 62, 69, 73, 128, 134, 160, 165$
 $\widehat{\pi}_0, 186, 201$
 $\widehat{\pi}_1, 194, 201$
 $\widehat{\sigma}, 15$
 $\widehat{\tau}, 201$
 $\widehat{\zeta}_0, \dots, \widehat{\zeta}_{k-l}, 201$
 $\widehat{\mathbb{E}}(\tilde{y}), 36$
 $\widehat{\mathbb{E}}(y), 15, 16, 49, 62, 290, 298$
 $\zeta_0, \dots, \zeta_{k-l}, 201$
 $a, 219, 248, 268, 289, 298$
 $c(\cdot), 14$
 $g(\cdot), 14, 248, 298$
 $h(\cdot), 14$
 $r, 150, 154, 159, 165, 171$
 $t_1, \dots, t_a, 219, 248, 268, 289, 298$
 $t_1, \dots, t_p, 290$
 $u_{1im}, 290, 298$

$u_{1i}, 220, 268$
 $u_{2im}, 290, 298$
 $u_{2i}, 220, 268$
 $x_1, \dots, x_k, 13, 14, 36, 48, 61, 68,$
 $73, 84, 92, 98, 104, 117,$
 $122, 128, 134, 150, 154,$
 $159, 165, 180, 185, 193,$
 201
 $x_1^0, \dots, x_k^0, 18, 37, 50, 64, 69, 74,$
 $86, 93, 99, 105, 119, 123,$
 $129, 134, 150, 155, 160,$
 $166, 180, 186, 194, 202$
 $x_1^0, \dots, x_k^0, t^0, 221, 291, 299$
 $x_{1ijm}, \dots, x_{kijm}, y_{ijm}, 290, 298$
 $x_{1ij}, \dots, x_{kij}, y_{ij}, 220, 248, 268$
 $x_{i1}, x_{i2}, \dots, x_{ik}, y_i, 13$
 $y, 13, 14, 48, 61, 68, 73, 84, 92,$
 $98, 104, 117, 122, 128,$
 $134, 150, 154, 159, 165,$
 $180, 185, 193, 201$
 $y^0, 18, 37, 50, 119, 123, 129, 134,$
 $150, 155, 160, 166, 180,$
 $186, 194, 202, 221, 291,$
 299
 $\text{logit } \pi, 62$

Subject Index

- z*-score, 69, 93
- AIC, *see* Akaike Information Criterion, 17
- AICC, *see* Corrected Akaike Information Criterion, 17
- Akaike Information Criterion (AIC), 17
- asymptotic likelihood ratio test, *see* deviance test, 17
- autoregressive covariance structure of errors, 232
- autoregressive working correlation matrix, 249
- Bayesian Information Criterion (BIC), 17
- beta regression model, 179
- BIC, *see* Bayesian Information Criterion, 17
- binary logistic regression model, 61
- binary variable, 61
- Box-Cox transformation, 35
- chance zero, 127
- change in log-odds, 63
- complementary log-log link function, 73
- complementary log-log model, 73
- compound symmetric covariance structure of errors, 232
- Corrected Akaike Information Criterion (AICC), 17
- count variable, 117
 - overdispersed, 149
- covariance structure of errors
 - autoregressive, 232
 - compound symmetric, 232
 - exchangeable, 232
 - independent, 230
 - spatial power, 231
 - Toeplitz, 231
 - unstructured, 230
- covariate, *see* predictor variable, 13
- cumulative complementary log-log model, 98
- cumulative logit, 84
- cumulative logit model, 84
- cumulative probability, 84
- cumulative probit model, 92
- dependent variable, *see* response variable, 13
- deviance, 17
- deviance test, 17
- dichotomous logistic regression model, *see* binary logistic regression model, 61
- dichotomous variable, *see* binary variable, 61
- difference in log-odds, 63
- dummy variable, *see* indicator variable, 16
- estimated mean response, 15, 16
- estimated rate ratio, 99

- exchangeable working correlation matrix, 249
- exchangeable, *see* compound symmetric covariance structure of errors, 232
- explanatory variable, *see* predictor variable, 13
- exponential family of distributions, 14
- extreme value distribution, *see* Gumbel distribution, 73
- fitted mean response, *see* estimated mean response, 15
- fixed-effects predictor, 219
- gamma regression, 48
- GEE, *see* Generalized Estimating Equations, 248, 275
- general linear regression model, 13
- Generalized Estimating Equations (GEE), 248, 275
- generalized linear mixed model, *see* generalized random slope and intercept model, 267
- generalized linear regression model, 14
- generalized logit function, 104
- generalized logit model, 104
- generalized random slope and intercept model, 267
- Gumbel distribution, 73
- hierarchical regression model, 289, 298
- hurdle negative binomial regression model, 165
- hurdle Poisson regression model, 133
- independent covariance structure of errors, 230
- independent variable, *see* predictor variable, 13
- independent working correlation matrix, 249
- indicator variable, 16, 63, 69, 74, 85, 93, 99, 118
- link function, 14
 - complementary log-log, 73
 - logit, 62
 - probit, 68
- log-odds model, *see* binary logistic regression model, 62
- logistic distribution, 62
- logit link function, 62
- logit of cumulative probability, *see* cumulative logit, 84
- longitudinal data, 219
- mean response, 14
 - estimated, 15
- mixed-effects linear regression model, 219
- model for clustered data, *see* hierarchical regression model, 289
- multilevel, *see* hierarchical regression model, 289
- multinomial regression, 83
- negative binomial regression, 149
- nominal variable, 83
- odds in favor of event, 62
- one-inflated beta regression model, 193
- ordinal variable, 83
- outcome variable, *see* response variable, 13
- overdispersed count variable, 149
- percent change in odds, 63, 85
- percent ratio in odds, 63
- Poisson regression model, 117
- polytomous regression, 83

- polytomous regression, *see*
 - multinomial regression, 83
- predicted response, 18, 37, 50
- predictor variable, 13
- probit index, *see* *z*-score, 69
- probit link function, 68
- probit regression model, 68
- R fuction
 - glm, 119
- R function
 - betareg, 181
 - boxcox, 38
 - clm, 86, 93
 - gamlss, 187, 195, 203
 - geeglm, 251, 275
 - glm, 20, 21, 50, 64, 70, 74
 - glm.nb, 151
 - glmer, 269, 299
 - hurdle, 135, 167
 - lme, 223, 234
 - lmer, 291
 - logLik, 21
 - multinom, 106
 - pchisq, 21
 - plotNormalHistogram, 20
 - predict, 21
 - print, 21
 - relevel, 20
 - shapiro.test, 20
 - summary, 20
 - vglm, 124, 155
 - zeroinfl, 129, 161
- R library
 - geepack, 251, 275
 - betareg, 181
 - gamlss, 187, 195, 203
 - lme4, 269, 291, 299
 - MASS, 38, 151
 - nlme, 223, 234
 - nnet, 106
 - ordinal, 86
 - pscl, 129, 135, 161, 167
 - rcompanion, 20
 - VGAM, 124, 155
- random error, 13
- random intercept, 220
- random intercept-only model, 220
- random slope, 220
- random slope and intercept
 - model, 220
- random-effects term, 219
- rate ratio, 98
- regression
 - beta, 179
 - binary logistic, 61
 - complementary log-log model, 73
 - cumulative complementary
 - log-log, 98
 - cumulative logit, 84
 - cumulative probit, 92
 - dichotomous logistic, 61
 - gamma, 48
 - general linear, 13
 - Generalized Estimating
 - Equations, 248, 275
 - generalized linear, 14
 - generalized linear mixed, 267
 - generalized logit model, 104
 - generalized random slope and
 - intercept, 267
 - hierarchical, 289, 298
 - hurdle negative binomial, 165
 - hurdle Poisson, 133
 - mixed-effects linear, 219
 - multinomial, 83
 - negative binomial, 149
 - one-inflated beta, 193
 - Poisson, 117
 - probit, 68
 - random slope and intercept, 220
 - zero-inflated beta, 185
 - zero-inflated negative

- binomial, 159
 - zero-inflated Poisson, 127
 - zero-one-inflated beta, 200
 - zero-truncated negative binomial, 154
 - zero-truncated Poisson, 122
- regression coefficient, 13
- regressor, *see* predictor variable, 13
- repeated measures, 219
- response variable, 13
- response, *see* response variable, 13
- SAS procedure
 - fmm, 123, 135, 166
 - genmod, 19, 50, 64, 69, 74, 86, 93, 99, 129, 160, 250, 275
 - glimmix, 181, 268, 299
 - logistic, 106
 - mixed, 222, 233, 291
 - nlmixed, 186, 195, 202
 - transreg, 37
 - univariate, 18
- Schwartz Bayesian Information Criterion (BIC), 17
- spatial power covariance structure of errors, 231
- structural zero, 127
- Toeplitz covariance structure of errors, 231
- Toeplitz working correlation matrix, 249
- m*-dependent, 251
- unstructured covariance matrix of errors, 230
- unstructured working correlation matrix, 249
- variance function, 248
- variate, *see* response variable, 13
- working correlation matrix, 248
 - autoregressive, 249
 - exchangeable, 249
 - independent, 249
 - Toeplitz, 249
 - unstructured, 249
- zero-inflated beta regression model, 185
- zero-inflated negative binomial regression model, 159
- zero-inflated Poisson regression model (ZIP), 127
- zero-one-inflated beta regression model, 200
- zero-truncated negative binomial regression model, 154
- zero-truncated Poisson regression model, 122
- ZINB, *see* zero-inflated negative binomial regression model, 159
- ZIP, *see* zero-inflated Poisson regression model, 127