A CASE STUDY IN HANDLING OVER-DISPERSION IN NEMATODE COUNT DATA

by

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Abstract

Traditionally the Poisson process is used to model count response variables. However, a problem arises when the particular response variable contains an inordinate number of both zeros and large observations, relative to the mean, for a typical Poisson process. In cases such as these, the variance of the data is greater than the mean and as such the data are over-dispersed with respect to the Poisson distribution due to the fact that the mean equals the variance for the Poisson distribution. This case study looks at several common and uncommon ways to attempt to properly account for this over-dispersion in a specific set of nematode count data using various procedures in SAS 9.2. These methods include but are not limited to a basic linear regression model, a generalized linear (log-linear) model, a zero-inflated Poisson model, a generalized Poisson model, and a Poisson hurdle model.

Based on the AIC statistics the generalized log-linear models with the Pearson-scale and deviance-scale corrections perform the best. However, based on residual plots, none of the models appear to fit the data adequately. Further work with non-parametric methods or the negative binomial distribution may yield more ideal results.

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Acknowledgements

Thanks to Dr. Murray for all her help and guidance on this paper.

Dedication

This paper is dedicated to Grandpa Bathurst. May he rest in peace.

CHAPTER 1 - Introduction and Motivation

Traditionally the Poisson process is used to model count response variables. However, a problem arises when the particular response variable contains an inordinate number of both zeros and large observations, relative to the mean, for a typical Poisson process. In cases such as these, the variance of the data is greater than the mean and as such the data are over-dispersed with respect to the Poisson distribution due to the fact that the mean equals the variance for the Poisson distribution. This case study looks at several common and uncommon ways to attempt to properly account for this over-dispersion in a specific set of nematode count data.

The data and motivation for this experiment come from a previous study by Ou et al. (2008) on the relationship between the southern root-knot nematode (*Meloidogyne incognita*, hereafter referred to as 'RKN'), yellow nutsedge (*Cyperus esculentus* L., hereafter referred to as 'YNS'), and purple nutsedge (*Cyperus rotundus* L., hereafter referred to as 'PNS'). The objective of the study was to attempt to create a quadratic regression equation that relates YNS and PNS counts to counts of RKN.

Data was collected during May, July, and September in 2005 and 2006. Each data set consists of RKN, YNS, and PNS counts taken from 80 randomly selected quadrats throughout the field in question. The original study focused on a generalized log-linear quadratic regression model to model the RKN counts using the Poisson distribution and the DSCALE correction for over-dispersion (explained in more detail in Ou et al., 2008). This study builds on this work by studying several newer methods that have been implemented in SAS version 9.2 (SAS Institute, Inc., 2010) for attempting to deal with the over-dispersion in the data while also considering methods used in the original paper.

CHAPTER 2 - Theoretical Background

2.1 Distributions

A quick and easy way to model any data is to assume that the data can be modeled by a normal distribution. Simple regression theory assumes that the data are distributed normally. However, while this is the simplest and easiest method, the assumption of normality does not always hold.

A common method for dealing with non-normal and over-dispersed data is to transform the response variable of interest. The stability of variance and the symmetry of a probability distribution can often be obtained by a transformation of the form *log(x + c)* on an observed data *x*, where *c* is a constant (Proctor and Marks, 1975). The transformation *ln(count + 1)* is commonly used in nematode count data to attempt to account for the non-normality of the data (Ou et al., 2008).

The *Poisson distribution* can be utilized for outcomes that are counts ($Y = 0, 1, 2, \ldots$), with a large count or frequency, in relation to the mean λ, being a rare event. The Poisson probability distribution function (hereafter referred to as 'PDF') is as follows:

$$Y \sim Poisson(\lambda)$$

if

$$\Pr(Y = j) = \frac{\lambda^j \exp(-\lambda)}{j!} \qquad j = 0, 1, 2, \ldots \tag{1}$$

where $\Pr(Y = j)$ denotes the probability that the outcome Y is equal to j, $j! = j \cdot (j-1) \ldots 3 \cdot 2 \cdot 1$, and $\lambda > 0$. The mean and variance of the Poisson distribution are

$$E[Y] = \lambda \ , \tag{2}$$

$$Var[Y] = \lambda \tag{3}$$

(Kutner et al., 2005; p. 618).

Over-dispersion sometimes occurs in measures of count data that might be modeled by the Poisson distribution. Over-dispersion with respect to the Poisson distribution happens when the variance of the data is greater than the mean of the data (equality being required for the data to follow a typical Poisson process). Over-dispersion causes problems during model inference in the estimation of model parameters. The coefficients are the same as the basic log-linear model; however, not accounting for over-dispersion leads to misleading inference since the estimated variance of the estimated coefficients is too small, leading to narrower confidence intervals and more liberal significance tests (Simonoff, 2003; p. 148-149).

If the data are over-dispersed with respect to the Poisson distribution, then a simple way to model this situation is to allow the variance function of the basic Poisson distribution to have a multiplicative over-dispersion factor ϕ so that:

$$Var[Y] = \phi\lambda \, . \tag{4}$$

There are several ways to estimate/model this over-dispersion factor. Two common ways are referred to as the *Pearson-scale* (PSCALE) and the *deviance-scale* (DSCALE) methods. The Pearson-scale method estimates ϕ as the model's Pearson's Chi-square divided by its degrees of freedom. For a random sample of size n, y_1, y_2, …, y_n, a model's Pearson's Chi-square is given by Agresti (2007; p. 212):

$$X^2 = \sum_{i=1}^{n} \frac{(y_i - \hat{\lambda})^2}{\hat{\lambda}} \tag{5}$$

where y_i is the observed count and $\hat{\lambda}$ is the expected count. The deviance-scale method estimates ϕ with the deviance of the model divided by its degrees of freedom. The deviance of a model is given by Agresti (2007 p. 212):

$$D = 2\sum_{i=1}^{n} y_i \ln\left(\frac{y_i}{\hat{\lambda}}\right) \tag{6}$$

where y_i is the observed count and $\hat{\lambda}$ is the expected count. In both of these cases the degrees of freedom are determined by:

$$df = n - \#\ of\ parameters\ being\ estimated. \tag{7}$$

All of the mean estimates for the regression parameters will be the same as with the basic log-linear model based on the basic Poisson distribution; however, the standard errors of the estimates will differ, based on which over-dispersion parameter estimation method is used. These methods are based on quasi-likelihood methods discussed in Simonoff (2003; p. 149-151).

A *zero-inflated Poisson (ZIP)* distribution is a Poisson distribution where an extra proportion of zeros is added to the zeros of a Poisson process. The ZIP distribution has a PDF of the form (Simonoff, 2003; p. 84):

$$Y \sim ZIP(\lambda, \pi)$$

if

$$Z \sim Poisson(\lambda)$$

and

$$\Pr(Y = j) = \begin{cases} \pi + (1-\pi) * \Pr(Z = 0) & j = 0 \\ \\ (1-\pi) * \Pr(Z = j) & j = 1,2,3,\ldots \end{cases} \tag{8}$$

where $\Pr(Y = j)$ is the probability that Y is equal to j, $0 < \pi < 1$ is the probability of a zero from a Bernoulli process, $\lambda > 0$ is the mean of the Poisson distribution, and $\Pr(Z = 0)$ is the probability of a zero contributing from the Poisson distribution from equation (1). Note that

$$\pi + (1-\pi) * \Pr(Z = 0) > \Pr(Z = 0) . \tag{9}$$

Also note that for π = 0, $Y \sim Poisson(\lambda)$. The mean and variance of this distribution are as follows:

$$E[Y] = \mu = (1-\pi)\lambda \ , \tag{10}$$

$$Var[Y] = \mu + \frac{\pi}{1-\pi}\mu^2 \ . \tag{11}$$

A *generalized Poisson* distribution is a Poisson distribution that allows for the modeling of both a mean and a variance term. A generalized Poisson distribution has the PDF given by Consul (1989):

$$\Pr(Y = j) = \frac{\lambda}{j!}(\lambda + \xi j)^{j-1} \exp(-\lambda - \xi j) \tag{12}$$

where $\lambda > 0$, $0 \le \xi < 1$, and $j = 0,1,2,\ldots$.

The mean and variance for a generalized Poisson distribution are as follows:

$$E[Y] = \mu = \frac{\lambda}{1-\xi} \tag{13}$$

$$Var[Y] = \frac{\mu}{(1-\xi)^2} \tag{14}$$

We can rearrange this PDF as follows to notice the similarities between this PDF and the PDF of the basic Poisson distribution in equation (1):

$$\Pr(Y = j) = \frac{\mu(1-\xi)}{j!}[\mu - \xi(\mu - j)]^{j-1} \exp[\mu - \xi(\mu - j)] \tag{15}$$

Note that for $\xi = 0$, $Y \sim Poisson(\lambda)$.

A *Poisson hurdle* distribution is a conditional model where one process generates zeros and one process generates non-zeros. We model the response as either (1) no counts present, or (2) counts greater than or equal to 1 are present. We model (1) as a logistic model and (2) as a truncated Poisson distribution as given by Grogger and Carson (1991). The Poisson hurdle PDF is given as follows. Suppose

$$\Pr(Y = 0) = \pi_0$$

and

$$\Pr\{Y \sim truncatedPoisson(\lambda)\} = 1 - \pi_0 .$$

Then

$$\Pr(Y = j) = \begin{cases} \pi_0 & j = 0 \\ \dfrac{(1-\pi_0)(\lambda^j)\exp(-\lambda)}{j![1-\exp(-\lambda)]} & j = 1,2,3,... \end{cases} \tag{16}$$

where $\Pr(Y = j)$ is the probability Y is equal to j, $0 < \pi_0 < 1$ is the probability of observing at least one count given that there is at least one count, and $\lambda > 0$ is the parameter of the truncated Poisson distribution which describes how many counts are observed (Welsh et al., 1996). The mean and variance of this distribution are given by (Appendix F):

$$E[Y] = \mu = \frac{\lambda(1-\pi_0)}{1-\exp(-\lambda)} \tag{17}$$

$$Var[Y] = \mu(1+\lambda) - \mu^2 . \tag{18}$$

Note that if $\pi_0 = \exp(-\lambda)$, then $Y \sim Poisson(\lambda)$. Also note that the zero-inflated Poisson distribution and the Poisson hurdle distribution are simply different forms of the same distribution.

2.2 Regression Models for the RKN count data

The first method used to model the RKN data is the basic multiple linear regression model with normally distributed random errors. With RKN as the response variable of interest, the regression model is:

$$RKN = \beta_0 + \beta_1 YNS + \beta_2 PNS + \beta_3 YNS^2 + \beta_4 PNS^2 + \beta_5 YNS * PNS + \varepsilon \tag{19}$$

In this model it is assumed that $E[\varepsilon] = 0$ and that $\varepsilon \sim Normal(0, \sigma_e^2)$. As a result, the expected value of the function for the regression model is:

$$E[RKN] = \beta_0 + \beta_1 YNS + \beta_2 PNS + \beta_3 YNS^2 + \beta_4 PNS^2 + \beta_5 YNS * PNS . \tag{20}$$

In this particular study, two different models are discussed that assume that the data are normally distributed: a simple linear regression model with the default count data as the response variable (in PROC MIXED; hereafter referred to as Model 1) and a simple linear regression model with the *log(RKN + 1)* as the response variable (in PROC MIXED; hereafter referred to as Model 2).

When the assumption of normality fails to hold, the next logical step is to delve into the realm of generalized linear models (hereafter referred to as 'GLMs'). These are models which do not necessarily rely on the assumption of normality and often involve theoretically correct ways to deal with non-normal data. A generalized linear model has three components. First, the *random component* identifies the response variable Y and specifies a probability distribution for it. Second, the *systematic component* specifies the explanatory variables for the model. These enter linearly as predictors in the right-hand side of the model equation. That is, the systematic component specifies the variables that are the $\{x_j\}$ in the formula

$$\beta_0 + \beta_1 x_1 + \beta_2 x_2 + ... + \beta_k x_k \tag{21}$$

Finally, the *link function* specifies a function $g(\bullet)$ of the expected value of Y, $E[Y] = \mu$, which the GLM relates to the explanatory variables through a linear prediction equation

$$g(\mu) = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + ... + \beta_k x_k \tag{22}$$

This link function connects the random and the systematic components of the model (Agresti, 2007).

The family of Poisson distributions fits into the log-linear group of GLMs. A log-linear model is a GLM that assumes a Poisson distribution for Y and uses the natural log link function (Agresti, 2007). The random component in this case assumes that the response variable Y is a count variable that is modeled by a Poisson distribution, and the link function in this case is the natural log of the mean λ of the Poisson distribution. This allows us to set up the general form of the log-linear GLM that we will be using straightforwardly and as a foundation for other models henceforth:

$$\ln(\lambda) = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + ... + \beta_k x_k \,. \tag{23}$$

The first generalized linear model that was used was the basic log-linear model which is a GLM with a Poisson random component and natural log link function (in PROC GENMOD; hereafter referred to as Model 3). The equation for the log-linear model is:

$$\ln(\lambda) = \beta_0 + \beta_1 YNS + \beta_2 PNS + \beta_3 YNS^2 + \beta_4 PNS^2 + \beta_5 YNS * PNS \tag{24}$$

where

$$RKN \sim Poisson(\lambda) \,.$$

The expected value of this model is:

$$\ln(\lambda) = \beta_0 + \beta_1 YNS + \beta_2 PNS + \beta_3 YNS^2 + \beta_4 PNS^2 + \beta_5 YNS * PNS \qquad (25)$$

which allows for an estimate of the mean parameter λ to be:

$$\hat{\lambda} = \exp(\hat{\beta}_0 + \hat{\beta}_1 YNS + \hat{\beta}_2 PNS + \hat{\beta}_3 YNS^2 + \hat{\beta}_4 PNS^2 + \hat{\beta}_5 YNS * PNS) \qquad (26)$$

The rest of the models that were studied fit under the theory of the generalized log-linear models. However, instead of *RKN* simply following the basic Poisson distribution, *RKN* follows each of the distributions mentioned above in the ***Distributions*** section: a Poisson distribution with the scale parameter estimated using the deviance-scale method (in PROC GENMOD; hereafter referred to as Model 4), a Poisson distribution with the scale parameter estimated using the Pearson-scale method (in PROC GENMOD; hereafter referred to as Model 5), a zero-inflated Poisson distribution (a built in ZIP model in PROC GENMOD and a custom-coded ZIP model in PROC NLMIXED; hereafter referred to as Models 6 and 8 respectively), a generalized Poisson distribution (in PROC GLIMMIX; hereafter referred to as Model 7), and a Poisson hurdle distribution (in PROC NLMIXED; hereafter referred to as Model 9).

2.3 Methods of Estimation

Both of the models based on normal-theory (Models 1 and 2) were implemented in PROC MIXED in SAS Version 9.2 (SAS Institute, Inc., 2008). The default estimation method was used in PROC MIXED which fits the selected model structure and estimates the model parameters with the restricted maximum likelihood (REML) estimation (SAS Institute, Inc., 2008). Note that PROC MIXED was used instead of PROC GLM due to the fact that PROC MIXED outputs the AIC for the given model while PROC GLM does not.

Models 4, 5, and 6 were implemented using PROC GENMOD. PROC GENMOD fits a generalized linear model to the data by maximum likelihood estimation of the model parameters (SAS Institute, Inc., 2008). Maximum likelihood estimation chooses estimates of model parameters that are most consistent with the sample data (Kutner et al., 2005).

Models 3 and 7 were implemented in PROC GLIMMIX. Model 3 was fit using maximum likelihood estimation for the model parameters. Model 7 was fit using quasi-likelihood estimation due to the fact that Model 7 contained a user-defined variance/covariance structure (SAS Institute, Inc., 2008).

Finally, PROC NLMIXED was used in the implementation of Models 8 and 9. PROC NLMIXED fits nonlinear mixed models by maximizing an approximation to the likelihood integrated over the random effects. Successful convergence of the optimization problem yields parameter estimates based on the second derivative matrix of the likelihood function (SAS Institute, Inc., 2008).

SAS code for all models is given in Appendix D.

2.4 Model Evaluation

The primary methods used to compare and select models are the Akaike Information Criterion (hereafter referred to as "AIC") and various residuals from the fitted model. The *AIC* is the primary characteristic used to compare the models (smaller is better). The various residuals for each model were graphed to check whether or not they appeared to be normally distributed. In addition, the parameter estimates for the intercept as well as the YNS, PNS, YNS2, PNS2, and YNSPNS terms, the standard errors for each of these estimates, and the p-values for testing whether or not the estimates were significant were summarized. The predicted values were also summarized to see how well the fitted model predicted the actual value from the data set and to examine differences in prediction between models.

2.3.1 Akaike Information Criterion (AIC)

The AIC is a model selection criterion that penalizes models for having a large number of predictor variables. We wish to find models with small values of the AIC relative to the other models in question. The AIC criterion is given by:

$$AIC = -2LL + 2p \tag{27}$$

where p is the number of parameters being estimated in the model and LL is the log of the likelihood function given by Simonoff (2003; p. 85). According to Burnham and Anderson (1998), models with AICs within 2 of the minimum AIC are considered equivalent, while models with AICs further apart than 7 are not equivalent.

2.3.2 Residuals

Also considered in comparing models and testing model fit are histograms and normal quantile plots of residuals from the fitted model. Ideally, if the model fits the data closely, then the residuals would have close to a normal distribution with a mean of 0 and a variance σ^2_e

(Kutner et al., 2005; p. 102). Histograms and normal quantile plots of the raw residuals, Pearson residuals, standardized Pearson residuals, Studentized residuals, deviance residuals, standardized deviance residuals, and the likelihood residuals were considered in this analysis.

The *raw residuals* e_i are merely the difference between the observed values and the fitted values based on the given model.

$$e_i = Y_i - \hat{Y}_i \tag{28}$$

where Y_i is the value that we actually observed and $\hat{Y}_i$ is the estimated count based on the given model (Kutner et al. 2005: p. 203). Raw residuals should have a mean of zero and a variance of σ^2_e, given that the model is appropriate. Note that raw residuals should only be normally distributed in the case of Models 1 and 2 where we assume that the errors are normally distributed. Raw residuals have limited usefulness for GLMs. For Poisson sampling, for instance, the standard deviation of a count is $\sqrt{\hat{Y}_i}$, so more variability tends to occur when $\hat{Y}_i$ is larger (Agresti, 2007: p. 86).

Calculation of raw residuals assumes that the variance for each residual is constant. This is not always the case. One way to account for unequal variances amongst the residuals is to compute the *Studentized residuals* r_i. Studentizing the residuals considers the magnitude of each e_i relative to its estimated standard deviation:

$$r_i = \frac{e_i}{s\{e_i\}} \ , \tag{29}$$

where e_i is the raw residual and $s\{e_i\}$ is the estimated standard deviation of that specific residual. Studentized residuals will have constant variance and a mean of zero, as long as the model is appropriate (Kutner et al., 2005: p. 394).

An alternative to the Studentized residual is the *Pearson residual* (Simonoff, 2003; p. 132). For Poisson sampling, the standard deviation of a count is $\sqrt{\lambda}$, so more variability tends to occur when λ is larger. The Pearson residual is a standardized residual:

$$e_{pi} = \frac{e_i}{\sqrt{\hat{Y}_i}} \tag{30}$$

where $\sqrt{\hat{Y}_i}$ is the estimated standard deviation of the estimated mean count. Pearson residuals fluctuate around zero and they follow an approximate normal distribution when λ is large

(Agresti, 2007: p. 86-87). Note, however, this is not necessarily the case in the data sets in question. Note that the standardized Pearson residual is simply each individual Pearson residual divided by its estimated standard deviation.

Likelihood residuals are simply another name for deleted residuals (Kutner et al., 2005; p. 395). A likelihood residual d_i is obtained by removing the ith observation from the data set and then fitting the model to the data set with the ith observation now removed. The likelihood residual is:

$$d_i = Y_i - \hat{Y}_{i(i)} \tag{31}$$

where $\hat{Y}_{i(i)}$ is the estimated expected value of the data with the ith observation removed. Likelihood residuals may then, at times, be able to identify outlying observation when other types of residuals may not be able to. Likelihood residuals should have a mean of zero and should follow an approximate normal distribution. If there are outliers in the likelihood residuals then there is a chance that one or more of the data points are outliers (Kutner et al., 2005: p. 395).

Finally, *deviance residuals* were also observed for several of the models. A deviance residual $r^D{}_i$ is given by Simonoff (2003; p. 132):

$$r_i^D = sign(y_i - \hat{y}_i) \cdot \sqrt{d_i} \tag{32}$$

where y_i is the observed count, $\hat{y}_i$ is the estimated mean count, and d_i is the component of the deviance accounted for by the specific observation y_i defined in Simonoff (2003; p. 129). Similar to Pearson residuals, deviance residuals should be centered on zero and follow a relatively normal distributional form. Note that a standardized deviance residual is simply a deviance residual divided by its estimated standard deviation.

CHAPTER 3 - Results

3.1 Preliminary Comments

The data gathered in May 2006 caused some problems in the analysis. Due to the fact the data only had one observation that had any PNS measurement and that measurement happened to be simply a 1, this made it impossible to look at the PNS^2 term in the model due to the fact that the column of PNS measurements were no longer linearly independent of the PNS^2 column. This caused the X’X matrix to be non-invertible and thus the estimate of the YNS^2 term was unable to be obtained. Due to the sparsity of the PNS measurements, the YNS*PNS interaction term which was created by multiplying the YNS measurements by the PNS measurements simply created a column of zeros for the YNS*PNS column and as such added in a linearly dependent column into X which once again caused the X'X matrix to be non-invertible and thus the estimates for the YNS*PNS term was unable to be obtained.

The *ln(rkn + 1)* models were simply looked at due to the fact that this transformation is a common transformation for count data. Due to the fact that this transformation is not based on any sound theory, it was analyzed and the residuals were observed but this model was not considered a valid option in the model selection process. Also, this transformation changes the scale of the measurement for the response variable in a non-invertible way. For example, the second author of Ou et al., (2008) has seen cases where means of logged data and the corresponding means of the original data are in a different order.

3.2 Analysis

In the given nematode data, there were three different distributional shapes that models were fitted to. The three sets were picked based on the physical appearance of the raw data histograms for each of the six data sets that were looked at. The three different sets are 1) the May 2005 data, 2) the July 2005 data, and 3) the September 2005, May 2006, July 2006, and September 2006 data sets.

3.2.1 Data sets with relatively equal low counts

The first group in which the models were compared was the May 2005 data set. This data set has the least number of zeros in the RKN counts compared to the other data sets and has relatively equal counts in the lower numbers (in this case the counts 0, 1, and 2; See Figure 3.1). This analysis will be primarily for data that is more spread out and that have relatively equal low counts.

Based on the AIC (Table 3.1), Model 5 (the GLM with the PSCALE option) performs the best (AIC = 153.427); however, Model 4 (the GLM with the DSCALE option) does not seem to provide significantly "worse" results (AIC = 157.8958). The rest of the observed models have AIC statistics much higher than these two. Based on the AIC, the normal-based regression model with the original count data performs the worst (AIC = 339) but surprisingly not very much worse than the rest of the models (Table 3.1).

Based on the residual plots, none of the models appear to be an ideal fit to the data (Appendix E.1). Most of the residual plots are centered on zero, but there is consistently a slight right skew to the residual histograms which hints that the models may not fit the data adequately. Figure 3.2 is the raw residual histogram for Model 5, which performs the best according to the AIC. As can be seen, the data is centered on zero but there is an over-arching right skew to the residuals.

Most of the parameter estimates for the May 2005 share the same sign excluding a few instances with Models 6 and 8 (both ZIP models). Also, the significance of each estimated parameter is consistent across all models ($\alpha = 0.05$) for this data set (Appendix C.1). In this case, none of the parameter estimates are significant. This shows that, based on comparison of parameter significance, none of the models are behaving better/worse than any of the others. The standard errors for the parameter estimates (Appendix C.1) are rather inconsistent across all models so it is difficult to make any conclusions based on this information.

While the AIC statistics and parameter estimates differ somewhat substantially between the different models, the predicted counts for all nine models are actually rather similar (Appendix G.1). However, none of the predicted values are considerably similar, point wise, to the actual RKN counts, which hints at the fact that none of the models perform very well. All of the models tend to overestimate the RKN counts that are 0 and 1. All of the models, aside from Model 2, seem to do a decent, at best, job at predicting RKN counts of 2, but for all of the other counts none of the models perform well. Large counts are continually underestimated by all models. Model 2 seems to perform the worst overall.

In conclusion it appears that Model 5 and Model 6 fit the best (according to the AIC), but based on the residuals and the predicted counts it does not appear that the models fit as adequately as one would hope.

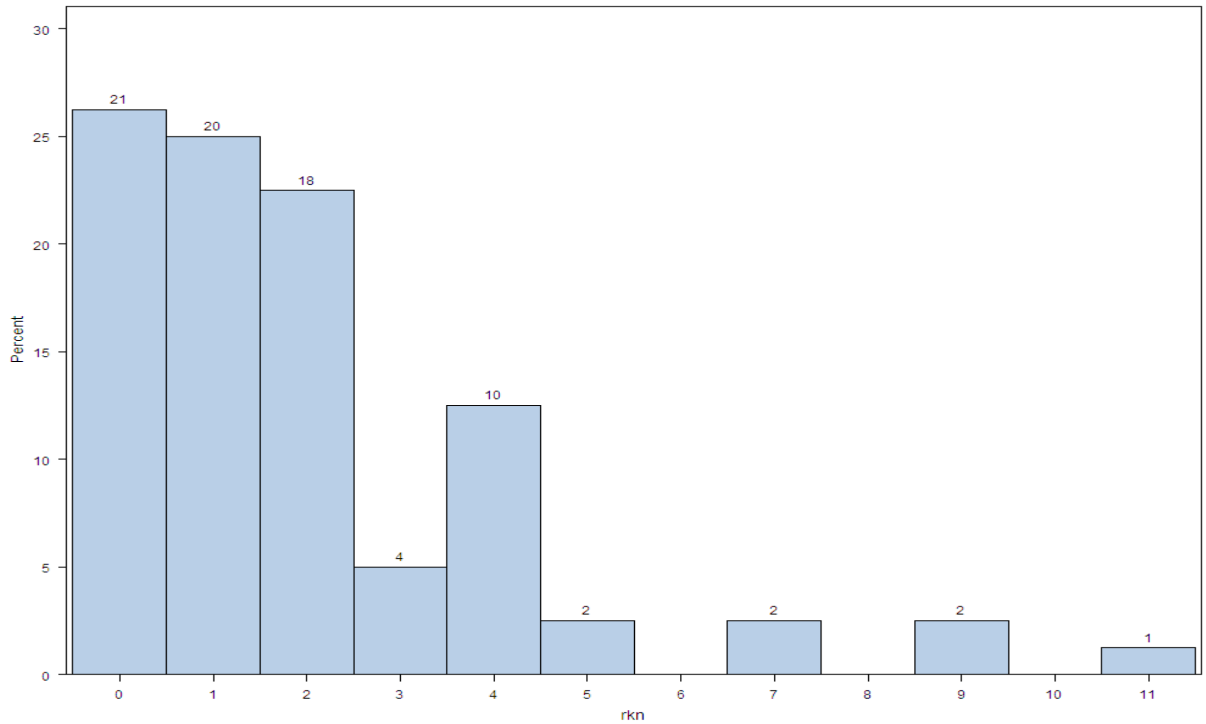


Figure 3.1 - Histogram of the May 2005 data

Model	Name	AIC
Model 1	Normal	339
Model 2	Normal with ln(count+1)	163
Model 3	Poisson	333.94
Model 4	Poisson DSCALE	157.86
Model 5	Poisson PSCALE	153.43
Model 6	ZIP – GENMOD	328.92
Model 7	Gen. Poisson	310.24
Model 8	ZIP – NLMIXED	324.4
Model 9	Poisson hurdle	326.9

Table 3.1 – AIC statistics for the May 2005 data

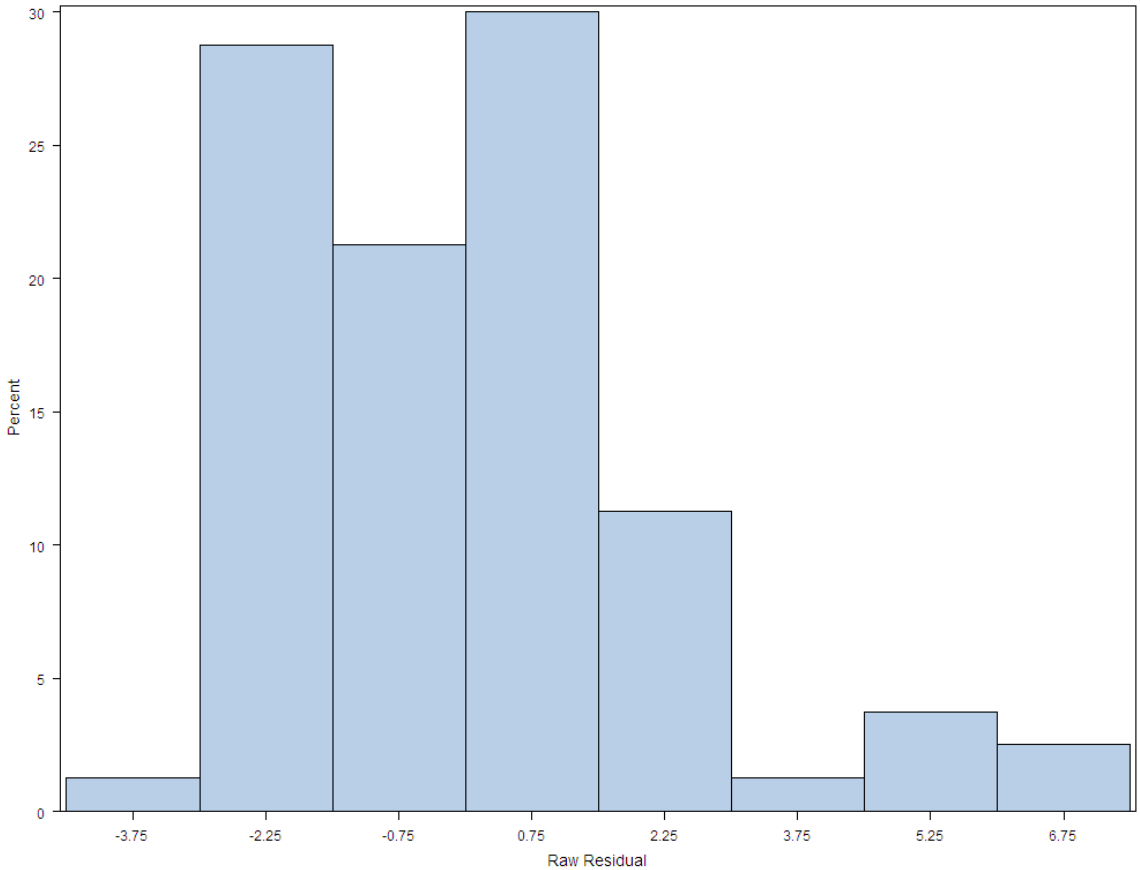


Figure 3.2 – Raw residual histogram for Model 5 and the May 2005 data

3.2.2 Data sets with gradual decline in counts as counts increase

The second group in which the models were compared was the July 2005 data set. This data set has the most gradual decline in counts of all of the data sets and has no spotty outliers (Figure 3.3). This analysis will be primarily for data that exhibits a gradual decline in number of counts.

Based on the AIC (Table 3.2), Model 4 (the GLM with the DSCALE option) performs the best (AIC = 153.266); however Model 5 (the GLM with the PSCALE option) does not seem to provide significantly "worse" results (AIC = 161.534). The rest of the observed models have AIC statistics much higher than these two. Based on the AIC, the normal-based regression model with the original count data performs the worst (AIC = 281) but surprisingly not very much worse than the rest of the models.

Based on the AIC, Model 4 performs the best. However, similar to the May 2005 data, nearly all of the residual plots continue to exhibit a slight right skew (Figure 3.4 and Appendix E.2). All residual plots for the July 2005 data can be found in Appendix E.2. Based on residuals alone, Model 2 (the *log(count+1)* data) performs the best (Figure 3.5); however, Model 2 cannot be compared to the other models based on the AIC due to the fact that the responses from Model 2 are on a different scale than the responses from the different models (discussed in Chapter 3.1 above).

The signs of the parameter estimates for all of the log-linear models (Models 3 – 9) are consistent across all models except for the PNS2 parameter estimates for both of the ZIP models (Appendix C.2). The actual estimated parameters and the standard errors of the parameter estimates are extremely consistent across all of the log-linear models. Both of the normal-based models (Models 1 and 2) have comparable parameter estimates as well as standard errors for those estimates. Based on this information alone it does not appear that a best model can be determined.

The AIC statistics for the models in question have some definite discrepancies but the predicted RKN counts for all of the models are relatively equal (Appendix G.2). However, none of the predicted values are considerably similar, point wise, to the actual RKN counts which once again hints at the fact that none of the models perform all that well. All of the models tend to overestimate the RKN counts that are 0. All of the models, aside from Model 2, seem to do a decent, at best, job at predicting RKN counts of 1, but for all of the other counts none of the models perform well. Large counts are continually underestimated by all models. Model 2 seems to perform the worst overall.

In conclusion, while Model 4 and Model 5 continue to have the lowest AIC values the residual plots from all of the models, except Model 2, continue to have a right skew to them. Once again this is indicative that the observed models are more than likely not adequate for fitting the data.

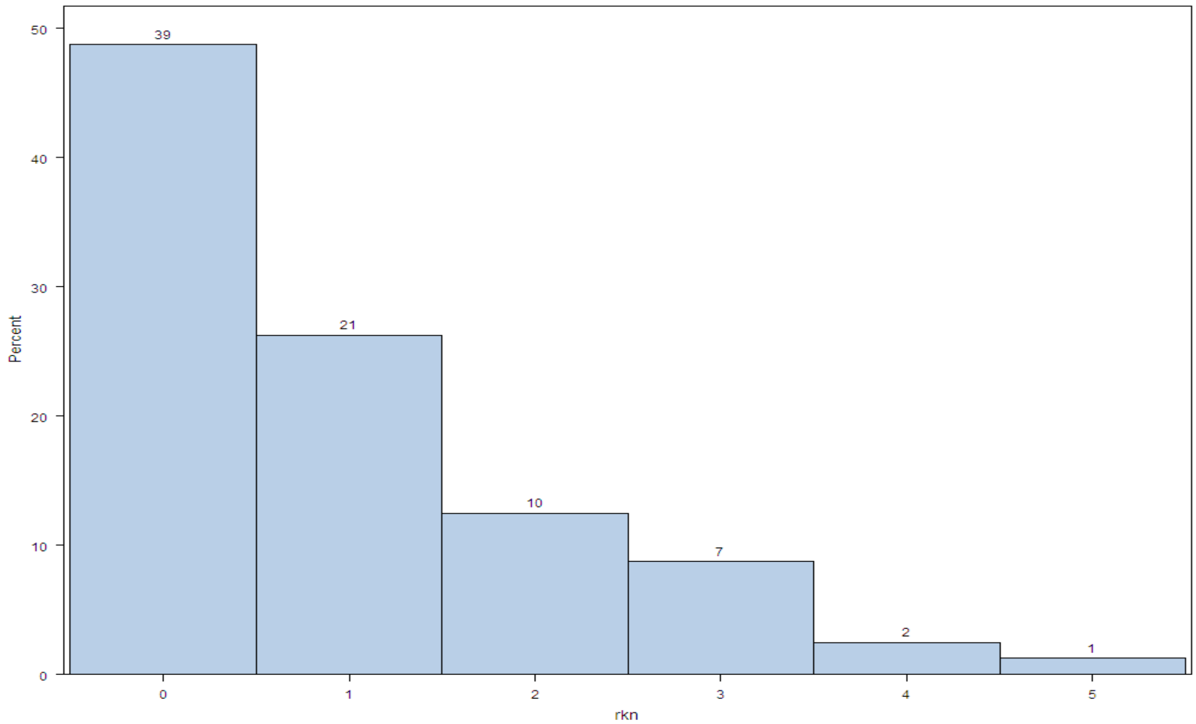


Figure 3.3 - Histogram of the July 2005 data

Model	Name	AIC
Model 1	Normal	281
Model 2	Normal with ln(count+1)	167.5
Model 3	Poisson	220.1
Model 4	Poisson DSCALE	153.266
Model 5	Poisson PSCALE	161.534
Model 6	ZIP – GENMOD	221.8935
Model 7	Gen. Poisson	219.01
Model 8	ZIP – NLMIXED	217
Model 9	Poisson hurdle	226

Table 3.2 - AIC statistics for the July 2005 data

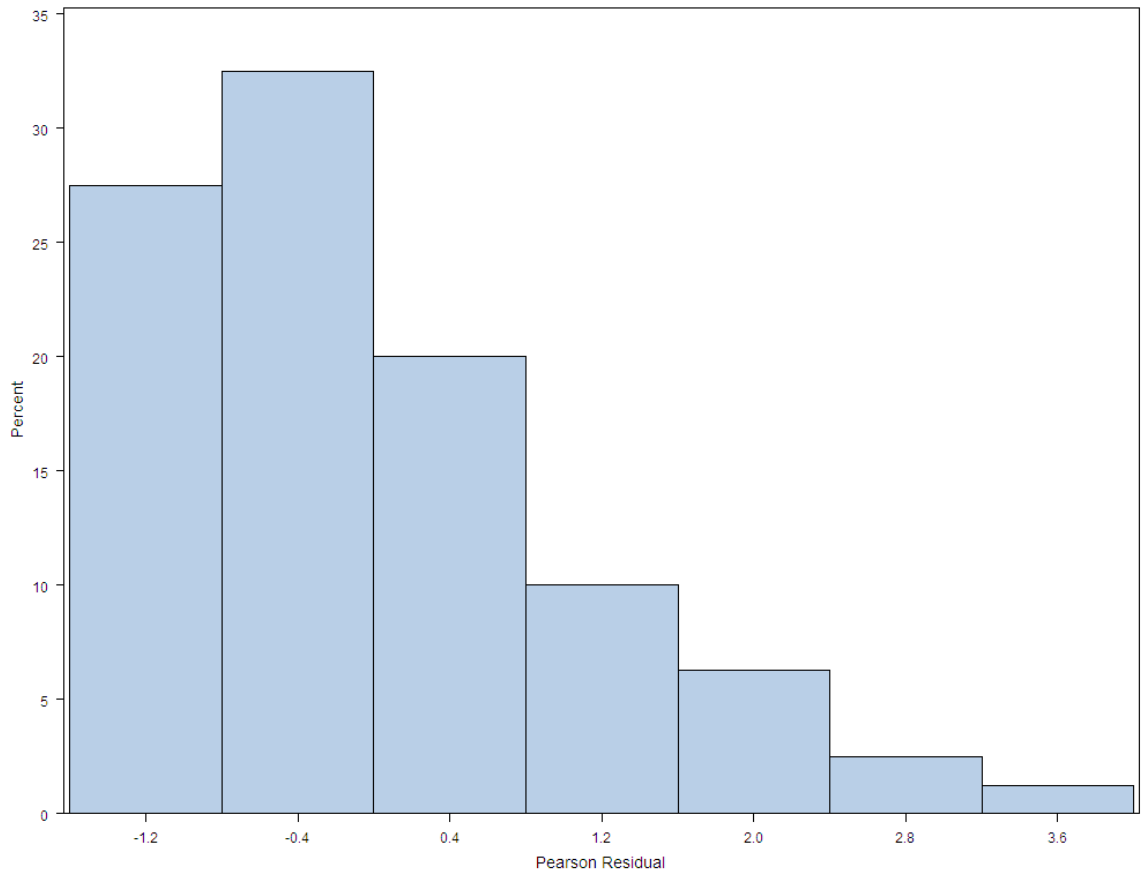


Figure 3.4 - Pearson residual histogram for Model 4 and the July 2005 data

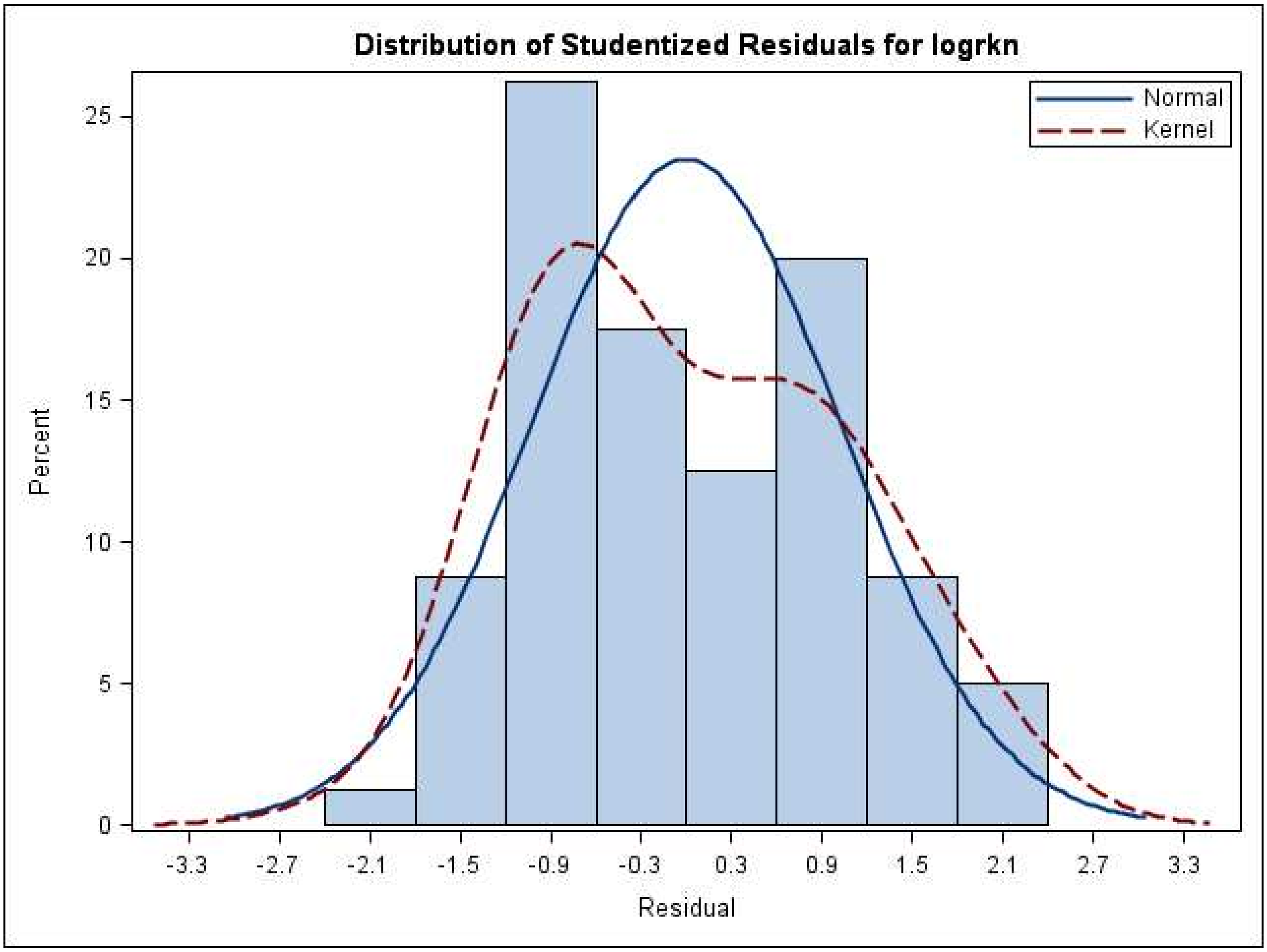


Figure 3.5 - Studentized residual histogram for Model 2 and the July 2005 data

3.2.3 Data sets with many zeros and several large observations (relative to the mean)

The final group in which the models were compared was the group consisting of the September 2005, May 2006, July 2006, and September 2006 data sets. These data sets have the most zeros and many large outliers relative to the mean of the data (Figure 3.6). This analysis will be primarily for data that exhibits many zeros as well as quite a few extreme observations.

According to the AIC (Table 3.3), Model 5 (the GLM with the PSCALE option) performs substantially better in all of these cases. Model 4 arguably performs the second best in all of these data sets and Models 3, 4, 5, 6, and 7 all perform relatively equally based on the AIC while Model 1 performs the worst overall.

Based on the residual plots none of the models perform well. All of the residual plots exhibit a significant right skew and clear non-normality (Figure 3.7 and Appendices E.3 – E.6). This non-normality is a clear indication that the models in question are not sufficient to model the given data.

The standard errors of the parameter estimates are fairly consistent across all the log-linear models and all four of the data sets (excluding the May 2005 data which is discussed in Chapter 3.1). However, parameter significance and the parameters themselves vary quite a bit between the different models, which make it nearly impossible to compare models based on this information (Appendices C.3 – C.6).

Nearly all of the predicted counts are the relatively similar across all models (Appendices G.3 – G.6). Model 2 and Model 8 tend to yield similar results yet different results from the rest of the models (whether or not it is a significant difference remains to be seen). While almost all of the predicted counts are similar across models, none of the predicted counts do an adequate job of actually predicting the actual RKN count. Point wise, all of the models tend to over-predict 0s while under-predicting all other RKN counts. This discrepancy goes to show that none of the models are adequate in modeling the data.

In conclusion, data with many zeros and quite a few spotty outliers are the hardest to model. All of the residual plots exhibit a drastic right skew as well as clear non-normality. Almost all of the estimated counts are similar to each other yet none of them do a good job of predicting the actual count. As such it can be said that none of the models do an adequate job of modeling the data.

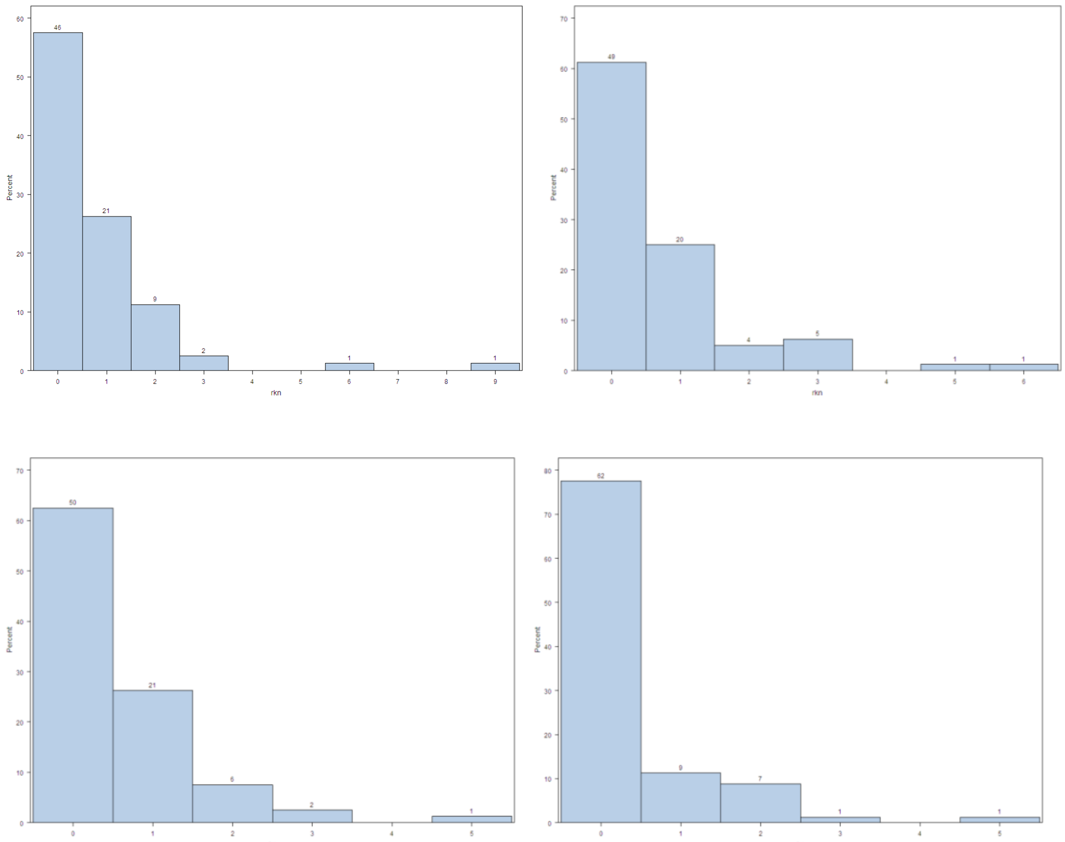


Figure 3.6 - Histograms of the Sept. 2005, May 2006, July 2006, and Sept. 2006 data

		Sept 2005	May 2006	July 2006	Sept 2006
Model	**Name**	**AIC**	**AIC**	**AIC**	**AIC**
Model 1	Normal	290.2	246.4	238.8	219.7
Model 2	Normal with ln(count+1)	151.1	120.5	136	114.3
Model 3	Poisson	214.25	198.37	176.09	148.98
Model 4	Poisson DSCALE	133.6489	130.802	137.2566	119.5923
Model 5	Poisson PSCALE	128.5639	102.8648	113.4259	86.2
Model 6	ZIP – GENMOD	190.4103	195.0774	180.1912	140.8276
Model 7	Gen. Poisson	202.41	184.94	172.53	138.38
Model 8	ZIP – NLMIXED	189.8	196.6	176	137.9
Model 9	Poisson hurdle	185.3	200	178.9	141.1

Table 3.3 - AIC statistics for the Sept. 2005, May 2006, July 2006, and Sept. 2006 data

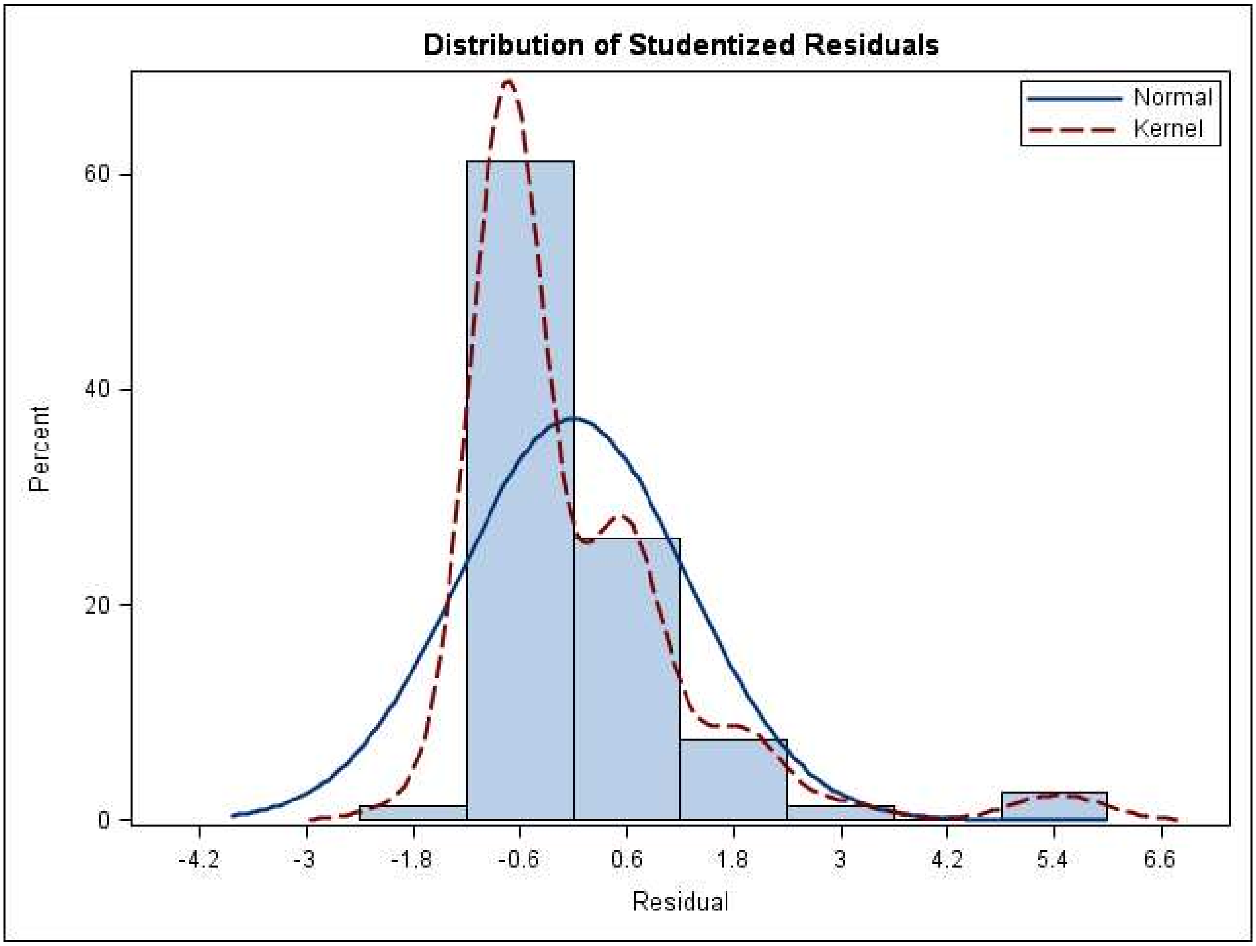


Figure 3.7 – Histogram of Studentized residuals for Model 3 and the July 2006 data

CHAPTER 4 - Future Work

In the future I hope to spend some more time working on this issue. I would like to look into using the Negative Binomial distribution to model the data instead of the Poisson distribution. The Negative Binomial is often used to model count data but already has a variance/dispersion parameter included in the model which the Poisson does not.

Sometime I hope to use the methods I have discussed on a wider range of data sets. My analysis was simply done on six data sets from the same experiment so while I have found that none of the methods seems to work all that well for this specific data it would be interesting to see how well they work with other data sets.

Being that the data that I am dealing with is highly non-normal and skewed I would be interesting to looking into some sort of nonparametric regression approach to the analysis. Nonparametric methods would not need any assumptions about the distribution of the data which has been the biggest problem in this study. It would be interesting to see if there exist any nonparametric methods that would effectively handle this over-dispersed data.

Finally, in the future I would like to spend some time collaborating with some biologists or nematologists on this issue. This paper is primarily focused solely on ad hoc procedures to handle the given data. Model comparisons are based on fairly simple statistical methods (AIC, residual plots, estimated parameters and related standard errors, etc…); however, a truly physical and real-world understanding of nematological and/or biological models may shed some light on the validity and applicability of the models in question.

CHAPTER 5 - Conclusion

Based on the AIC statistics the generalized log-linear models with the deviance-scale and Pearson-scale corrections perform the best (Models 4 and 5 respectively). However, nearly all of the residuals for the observed models exhibit a definite right skew and appear highly non-normal which may indicate that none of the models are adequate in modeling the specific set of given data. In each individual set of data the estimated mean counts are relatively equal however none of them come anywhere close to predicting the actual RKN count. In nearly all of the data sets the two normal-based models (Models 1 and 2) perform relatively equally and generally they perform the worst. The rest of the models perform about the same; better than the normal-theory models but not quite as good as the scale-corrected Poisson models.

Bibliography

Agresti, A. (2007). An Introduction to Categorical Data Analysis 2nd edition. Hoboken, NJ: John Wiley & Sons, Inc.

Burnham, K. P. and Anderson, D. R. (1998). Model Selection and Inference – A Practical Information-Theoretic Approach. New York City, NY: Springer-Verlag New York, Inc.

Consul, P. C. (1989). Generalized Poisson Distributions – Properties and Applications. New York City, NY: Marcel Dekker, Inc.

Grogger, J.T. and Carson, R.T., (1991). Models for truncated counts. Journal of Applied Econometrics, 6(2): 225-238.

Kutner, M. H., Nachtsheim, C. J., Neter, J., and Li, W. (2005). Applied Linear Statistical Models 5th edition. New York, NY: McGraw-Hill/Irwin.

Littell, R. C., Milliken, G. A., Stroup, W. W., Wolfinger, R. D., and Schabenberger, O. (2006). SAS for Mixed Models 2nd edition. Cary, NC: SAS Institute, Inc.

McCullagh, P. and Nelder, J. A. (1983). Generalized Linear Models 1st edition. New York City, NY: Chapman and Hall.

Ou, Z., Murray, L., Thomas, S. H., Schroeder, J., and Libbin, J. (2008). Nutsedge counts predict *Meloidogyne incognita* juvenile counts in an integrated management system. Journal of Nematology, 40(2): 99-108.

Proctor, J.R. and Marks, C.F. (1975). The determination of normalizing transformations for nematode count data from soil samples and of efficient schemes. Nematologica, 20: 395-406.

SAS Institute, Inc. (2010). SAS (Version 9.2) [computer software]. Cary, NC: SAS Institute, Inc.

SAS Institute, Inc. (2008). SAS OnlineDoc® 9.1.3. Cary, NC: SAS Institute Inc.

Schabenberger, O. and Stroup, W. W. (2008). Generalized Linear Mixed Models: Theory and Applications [PowerPoint slides]. Joint Statistical Meetings – Continuing Education Two-Day Course CE 01 C, Denver, CO, 2-3rd August 2008.

Simonoff, J. S. (2003). Analyzing Categorical Data. New York City, NY: Springer-Verlag New York, Inc.

Welsh, A. H., Cunningham, R.B., Donnelly, C.F., and Lindenmayer, D.B., (1996). Modelling the abundance of rare species: statistical models for counts with extra zeros. Ecological Modelling, 88(1): 298-308.

Appendix A - Raw Data

Table A.1 May 2005 Raw Data

sample	xcoord	ycoord	yns	pns	rkn
1	2	14	0	0	1
1	2	31	0	0	3
1	2	32	0	0	7
1	2	38	0	0	3
1	4	3	0	0	0
1	4	26	0	0	1
1	5	12	0	0	0
1	6	18	0	2	11
1	6	21	0	2	4
1	7	13	0	0	4
1	8	31	0	0	2
1	9	7	1	0	9
1	9	22	0	0	2
1	9	27	0	0	0
1	10	11	0	0	0
1	11	2	0	0	1
1	11	17	0	0	7
1	11	31	0	0	0
1	12	0	0	0	1
1	12	1	0	0	1
1	12	18	0	0	2
1	12	23	0	0	2
1	12	24	0	0	2
1	12	26	0	0	4
1	12	28	0	0	1
1	12	29	0	0	0
1	12	35	0	1	2
1	13	11	0	0	4
1	13	31	0	0	0
1	14	0	0	0	0
1	14	2	0	0	0
1	14	10	2	0	0
1	14	22	1	0	1
1	14	25	0	0	4
1	14	34	0	0	0
1	14	38	0	0	2
1	15	24	0	0	2
1	15	28	0	0	3
1	15	36	1	0	1
1	16	33	0	0	2
1	17	0	0	0	0
1	17	3	0	0	9
1	17	7	0	0	1
1	17	16	0	0	3
1	17	17	0	0	2

1	17	18	0	0	2
1	17	21	0	0	0
1	17	33	2	1	5
1	17	36	0	0	2
1	19	25	0	0	5
1	20	10	0	0	4
1	20	30	0	0	1
1	21	12	0	0	1
1	21	24	1	0	0
1	22	0	0	0	2
1	22	12	0	0	2
1	22	38	0	1	2
1	23	28	0	0	4
1	24	1	0	0	0
1	24	25	0	1	4
1	24	34	1	1	1
1	25	2	0	0	0
1	25	16	0	1	0
1	25	21	0	0	1
1	25	22	0	0	0
1	25	26	0	0	1
1	25	33	0	0	4
1	26	1	0	0	1
1	26	29	0	0	1
1	26	35	0	0	4
1	26	38	0	0	1
1	27	0	0	0	0
1	27	5	0	0	1
1	27	8	0	0	2
1	27	12	0	0	0
1	27	20	0	0	1
1	27	21	0	0	0
1	27	27	0	0	1
1	27	30	0	0	2
1	12	8	0	2	2

Table A.2 July 2005 Raw Data

sample	xcoord	ycoord	yns	pns	rkn
2	X-0	Y-17	0	2	0
2	X-0	Y-23	1	0	0
2	X-0	Y-35	1	0	1
2	X-1	Y-29	1	0	0
2	X-10	Y-10	0	2	1
2	X-10	Y-12	10	0	3
2	X-10	Y-14	4	4	0
2	X-10	Y-2	3	2	0
2	X-10	Y-24	6	0	0
2	X-10	Y-29	7	0	1
2	X-11	Y-10	7	5	0

2	X-11	Y-20	4	0	0
2	X-11	Y-3	3	5	1
2	X-11	Y-36	0	0	0
2	X-12	Y-10	5	1	1
2	X-12	Y-11	6	0	1
2	X-12	Y-16	16	1	1
2	X-12	Y-2	15	2	0
2	X-12	Y-21	11	7	2
2	X-12	Y-27	3	0	4
2	X-14	Y-23	0	2	0
2	X-14	Y-36	8	7	0
2	X-15	Y-22	2	1	0
2	X-16	Y-27	0	1	0
2	X-16	Y-32	2	4	0
2	X-17	Y-20	11	0	0
2	X-17	Y-27	1	2	0
2	X-18	Y-17	1	2	1
2	X-18	Y-29	4	6	0
2	X-2	Y-22	2	5	1
2	X-20	Y-13	6	2	0
2	X-20	Y-33	6	0	1
2	X-20	Y-8	2	6	2
2	X-21	Y-10	3	2	0
2	X-21	Y-17	9	3	0
2	X-21	Y-20	2	2	0
2	X-21	Y-22	0	1	2
2	X-21	Y-3	1	3	1
2	X-21	Y-33	6	7	3
2	X-22	Y-22	2	0	3
2	X-22	Y-28	5	1	0
2	X-22	Y-37	4	8	3
2	X-24	Y-20	0	2	0
2	X-25	Y-27	1	3	0
2	X-25	Y-30	7	13	2
2	X-25	Y-34	3	2	1
2	X-25	Y-9	0	3	2
2	X-26	Y-18	0	1	0
2	X-26	Y-26	2	0	0
2	X-26	Y-27	0	0	1
2	X-26	Y-32	0	1	0
2	X-26	Y-34	1	0	0
2	X-26	Y-37	2	0	1
2	X-27	Y-11	2	12	0
2	X-27	Y-37	21	7	0
2	X-3	Y-18	14	0	1
2	X-3	Y-34	5	3	2
2	X-4	Y-15	0	0	0
2	X-4	Y-4	0	2	1
2	X-5	Y-10	13	0	3
2	X-5	Y-21	7	6	5
2	X-5	Y-31	16	0	4
2	X-5	Y-36	9	0	0

2	X-6	Y-13	5	0	3
2	X-6	Y-16	8	0	0
2	X-6	Y-19	7	0	2
2	X-6	Y-3	9	0	1
2	X-6	Y-32	7	3	2
2	X-7	Y-1	3	2	1
2	X-7	Y-11	3	1	0
2	X-7	Y-18	0	2	1
2	X-7	Y-2	0	0	0
2	X-7	Y-22	8	0	2
2	X-7	Y-25	2	0	0
2	X-7	Y-5	1	0	1
2	X-8	Y-25	4	1	2
2	X-8	Y-28	3	2	3
2	X-8	Y-37	4	3	0
2	X-9	Y-17	0	1	0
2	X-9	Y-30	9	0	1

Table A.3 September 2005 Raw Data

sample	xcoord	ycoord	yns	pns	rkn
3	X-0	Y-10	1	1	0
3	X-0	Y-19	0	0	0
3	X-0	Y-2	0	1	1
3	X-0	Y-20	0	0	0
3	X-0	Y-32	0	0	0
3	X-0	Y-4	2	1	0
3	X-1	Y-0	0	0	0
3	X-1	Y-12	1	1	0
3	X-1	Y-31	0	3	1
3	X-1	Y-36	0	4	0
3	X-1	Y-7	0	0	0
3	X-1	Y-9	1	1	0
3	X-10	Y-22	0	1	0
3	X-10	Y-31	0	2	0
3	X-10	Y-5	0	0	1
3	X-11	Y-4	0	1	2
3	X-12	Y-14	2	0	9
3	X-12	Y-31	2	2	1
3	X-12	Y-4	1	2	0
3	X-13	Y-19	0	2	0
3	X-13	Y-20	2	6	0
3	X-13	Y-27	0	3	0
3	X-13	Y-33	1	7	0
3	X-14	Y-15	0	0	1
3	X-14	Y-19	1	5	1
3	X-14	Y-24	2	8	1
3	X-14	Y-3	0	2	0
3	X-16	Y-2	0	1	0
3	X-16	Y-24	3	3	2

3	X-17	Y-29	4	3	0
3	X-17	Y-38	0	2	2
3	X-19	Y-17	0	2	1
3	X-19	Y-37	2	1	0
3	X-19	Y-38	1	0	2
3	X-2	Y-13	0	3	2
3	X-2	Y-3	0	6	1
3	X-2	Y-34	0	2	2
3	X-20	Y-12	0	4	1
3	X-20	Y-32	0	1	0
3	X-21	Y-13	1	4	0
3	X-21	Y-25	3	1	0
3	X-21	Y-4	0	3	0
3	X-22	Y-24	4	0	0
3	X-22	Y-30	0	0	0
3	X-22	Y-33	1	1	1
3	X-23	Y-17	1	0	0
3	X-23	Y-24	0	0	2
3	X-23	Y-32	0	3	1
3	X-23	Y-34	1	2	0
3	X-23	Y-38	0	1	0
3	X-24	Y-3	0	2	0
3	X-25	Y-11	0	0	0
3	X-25	Y-35	1	1	0
3	X-26	Y-20	1	2	0
3	X-26	Y-4	0	3	0
3	X-26	Y-6	1	0	0
3	X-27	Y-1	0	1	1
3	X-27	Y-18	1	3	0
3	X-27	Y-33	1	1	0
3	X-3	Y-14	0	1	1
3	X-3	Y-32	0	5	2
3	X-3	Y-36	2	4	1
3	X-4	Y-20	0	1	1
3	X-4	Y-23	0	7	0
3	X-4	Y-34	0	0	3
3	X-4	Y-38	0	6	0
3	X-5	Y-14	3	2	3
3	X-5	Y-26	2	3	2
3	X-5	Y-37	0	7	6
3	X-6	Y-14	2	4	1
3	X-6	Y-4	0	1	0
3	X-7	Y-27	0	0	0
3	X-7	Y-30	0	0	1
3	X-7	Y-31	0	1	1
3	X-7	Y-33	0	0	0
3	X-7	Y-36	1	0	0
3	X-8	Y-24	0	2	0
3	X-8	Y-27	0	1	0
3	X-8	Y-33	3	5	1
3	X-9	Y-32	0	1	1

Table A.4 May 2006 Raw Data

sample	xcoord	ycoord	yns	pns	rkn
1	0	27	1	0	0
1	0	34	0	0	0
1	1	33	0	0	0
1	1	37	0	0	0
1	2	23	0	0	0
1	2	25	0	0	0
1	2	26	0	0	0
1	3	27	0	1	1
1	3	37	0	0	2
1	4	22	0	0	0
1	5	17	0	0	0
1	5	37	0	0	6
1	6	35	0	0	0
1	7	22	0	0	0
1	7	25	0	0	0
1	8	8	0	0	5
1	8	11	0	0	0
1	8	26	0	0	0
1	8	32	0	0	0
1	9	2	0	0	0
1	9	3	0	0	3
1	9	5	0	0	3
1	9	9	0	0	0
1	10	15	0	0	1
1	10	20	0	0	1
1	10	25	0	0	0
1	11	10	0	0	0
1	12	23	0	0	0
1	13	4	0	0	0
1	13	12	0	0	0
1	13	18	0	0	0
1	13	36	0	0	0
1	14	13	0	0	0
1	14	19	0	0	1
1	14	20	0	0	1
1	14	27	0	0	3
1	14	33	0	0	1
1	15	31	0	0	0
1	16	2	0	0	0
1	16	11	0	0	0
1	16	19	0	0	0
1	16	23	0	0	1
1	16	24	0	0	0
1	16	25	0	0	0
1	16	28	1	0	0
1	16	30	0	0	1
1	17	13	0	0	1
1	17	21	0	0	2
1	17	29	0	0	0

1	18	23	0	0	0
1	18	25	0	0	0
1	19	18	0	0	1
1	19	33	0	0	0
1	19	34	0	0	0
1	20	3	0	0	0
1	20	18	0	0	2
1	20	19	0	0	0
1	20	26	0	0	1
1	21	6	0	0	0
1	21	16	0	0	1
1	21	24	0	0	0
1	21	35	0	0	1
1	21	36	0	0	0
1	21	38	0	0	0
1	22	3	0	0	0
1	22	10	0	0	1
1	22	11	0	0	0
1	22	18	0	0	0
1	22	29	0	0	1
1	22	33	0	0	1
1	22	36	0	0	1
1	24	25	0	0	1
1	24	27	0	0	3
1	24	30	0	0	0
1	26	24	0	0	1
1	26	32	0	0	0
1	26	38	2	0	1
1	27	2	0	0	0
1	27	14	0	0	2
1	27	24	2	0	3

Table A.5 July 2006 Raw Data

sample	xcoord	ycoord	yns	pns	rkn
2	0	11	1	0	0
2	0	16	0	0	0
2	0	22	1	0	1
2	0	22	0	0	0
2	1	15	1	1	0
2	1	19	2	0	0
2	2	27	2	1	0
2	2	28	0	0	5
2	2	32	2	0	0
2	3	13	4	0	1
2	3	19	2	8	0
2	3	34	3	0	0
2	4	3	0	1	1
2	4	8	0	4	1
2	4	12	1	0	0

2	4	23	0	1	0
2	5	4	0	5	0
2	6	22	4	0	0
2	6	34	2	3	0
2	7	9	0	0	1
2	7	30	0	0	0
2	8	24	1	2	1
2	8	29	0	0	0
2	8	31	0	0	1
2	9	14	1	1	0
2	9	26	2	2	0
2	9	31	0	0	1
2	10	4	1	0	1
2	10	14	1	2	1
2	10	16	0	0	2
2	10	29	2	0	0
2	11	8	0	0	0
2	12	5	0	0	1
2	12	10	2	1	0
2	12	25	2	3	2
2	12	34	0	3	0
2	13	7	0	1	0
2	13	9	1	2	2
2	14	28	4	1	0
2	14	30	1	1	0
2	14	31	1	0	0
2	15	10	3	0	0
2	16	6	0	0	0
2	16	27	1	0	0
2	16	35	6	2	1
2	17	9	2	0	0
2	17	33	0	0	1
2	19	38	0	0	0
2	20	4	1	0	2
2	20	5	1	1	0
2	20	17	1	0	1
2	20	21	0	0	0
2	20	36	0	0	0
2	21	12	0	1	1
2	21	14	2	2	0
2	21	28	3	6	1
2	21	37	3	1	0
2	22	5	5	0	3
2	22	15	2	0	2
2	22	35	1	1	1
2	23	0	2	0	0
2	23	3	1	0	0
2	23	18	1	0	0
2	23	29	1	0	0
2	23	32	2	1	0
2	23	33	0	0	0
2	24	24	6	0	0

2	24	26	5	1	0
2	24	31	10	4	0
2	24	32	0	5	1
2	26	10	3	2	1
2	26	16	0	0	3
2	26	20	1	0	0
2	26	22	0	2	0
2	26	23	3	0	0
2	26	36	7	0	0
2	27	10	1	0	1
2	27	23	1	1	0
2	27	26	3	4	2
2	27	36	5	12	1

Table A.6 September 2006 Raw Data

sample	xcoord	ycoord	yns	pns	rkn
3	0	8	0	0	0
3	0	25	0	1	0
3	1	6	0	0	0
3	1	10	1	0	0
3	1	31	1	1	0
3	1	35	0	0	0
3	2	16	3	1	0
3	2	37	2	2	1
3	3	1	0	0	0
3	3	9	0	0	0
3	4	4	1	0	0
3	5	26	0	2	0
3	5	31	1	0	0
3	5	34	1	3	5
3	6	9	1	0	0
3	6	23	3	2	1
3	6	28	0	0	0
3	6	38	1	2	0
3	7	4	2	3	0
3	7	17	0	3	1
3	7	23	2	1	0
3	7	26	0	1	1
3	7	36	0	0	0
3	8	0	0	2	0
3	8	15	1	1	0
3	8	25	1	4	1
3	9	8	0	2	0
3	9	20	0	0	0
3	10	2	0	3	0
3	10	5	0	0	0
3	10	27	1	0	0
3	10	36	0	0	0
3	11	26	0	2	2

3	11	27	0	0	0
3	11	36	1	1	0
3	12	6	0	0	1
3	12	12	3	7	2
3	12	30	1	0	0
3	13	0	0	0	0
3	13	10	2	1	0
3	13	14	2	0	0
3	13	28	3	0	1
3	14	17	2	2	0
3	14	34	1	1	2
3	15	15	1	0	0
3	15	18	0	0	1
3	15	23	1	0	2
3	15	26	0	0	0
3	16	9	0	0	0
3	16	22	0	1	0
3	16	38	1	1	0
3	17	32	0	0	0
3	19	9	0	0	0
3	19	23	1	1	0
3	20	1	2	0	0
3	20	2	1	0	0
3	20	15	0	0	0
3	20	35	1	5	0
3	20	37	2	1	0
3	21	11	1	0	0
3	22	7	2	2	0
3	22	37	0	0	3
3	23	6	0	1	0
3	23	17	1	1	2
3	23	26	1	1	0
3	24	0	2	3	0
3	24	8	4	0	0
3	24	17	1	0	0
3	24	20	2	1	0
3	24	28	1	0	2
3	24	36	0	0	0
3	24	37	3	0	0
3	25	19	2	0	0
3	25	33	1	3	0
3	25	3	2	0	1
3	25	26	2	0	2
3	26	33	2	3	0
3	27	18	1	0	0
3	27	28	0	1	0
3	27	30	1	0	0

Appendix B - Raw Data Histograms

Figure B.1 May 2005 Raw Data Histogram

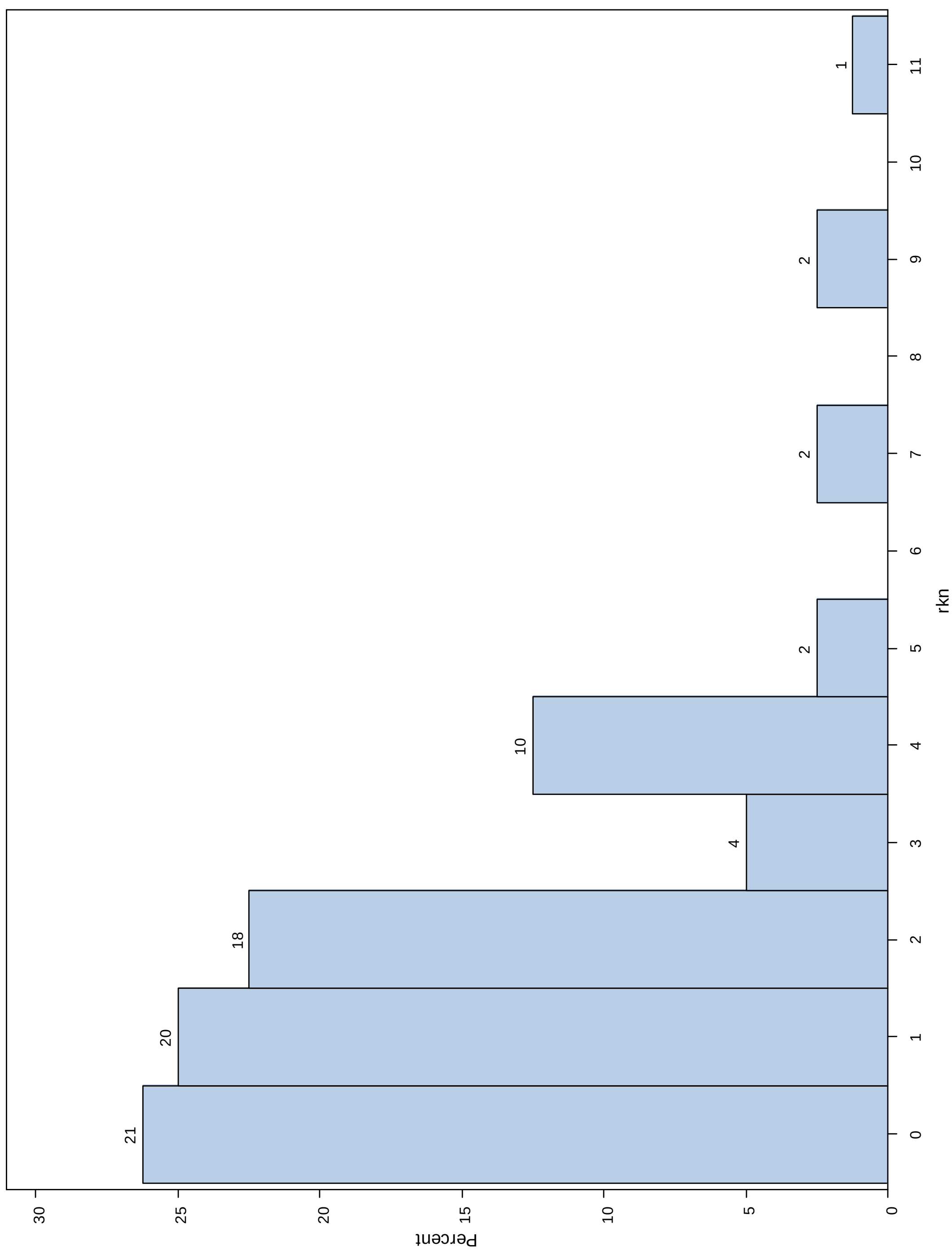


Figure B.2 July 2005 Raw Data Histogram

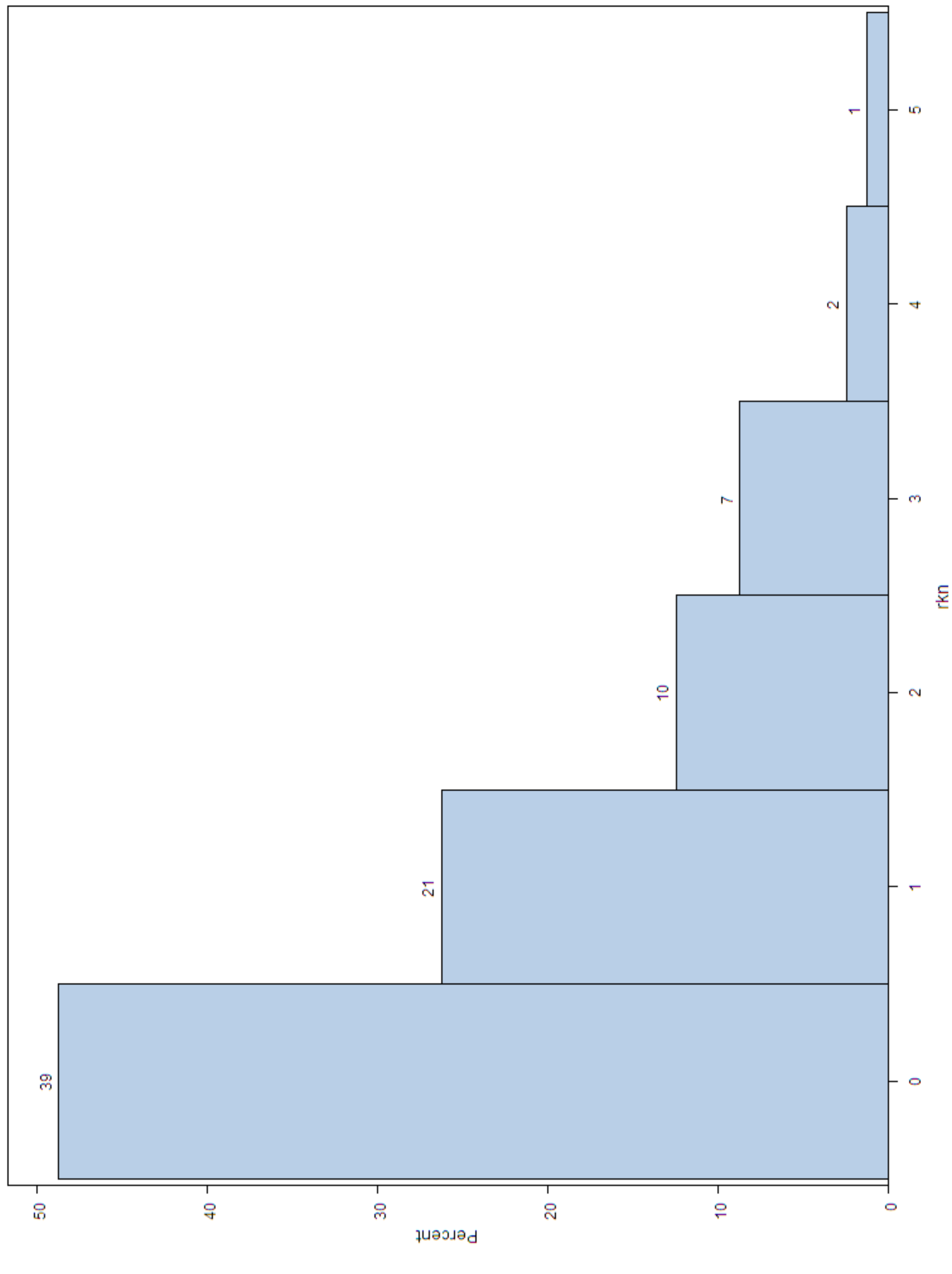


Figure B.3 September 2005 Raw Data Histogram

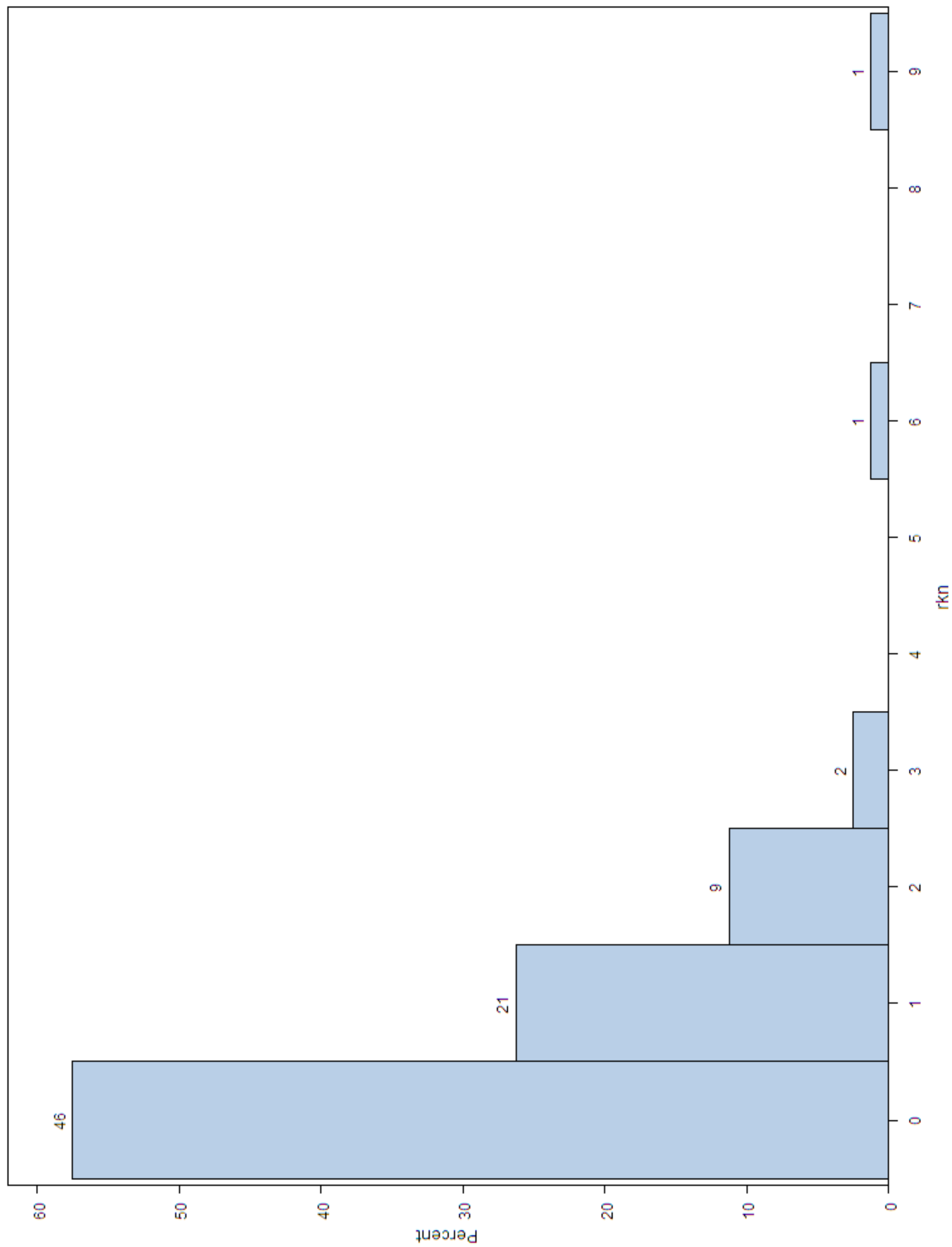


Figure B.4 May 2006 Raw Data Histogram

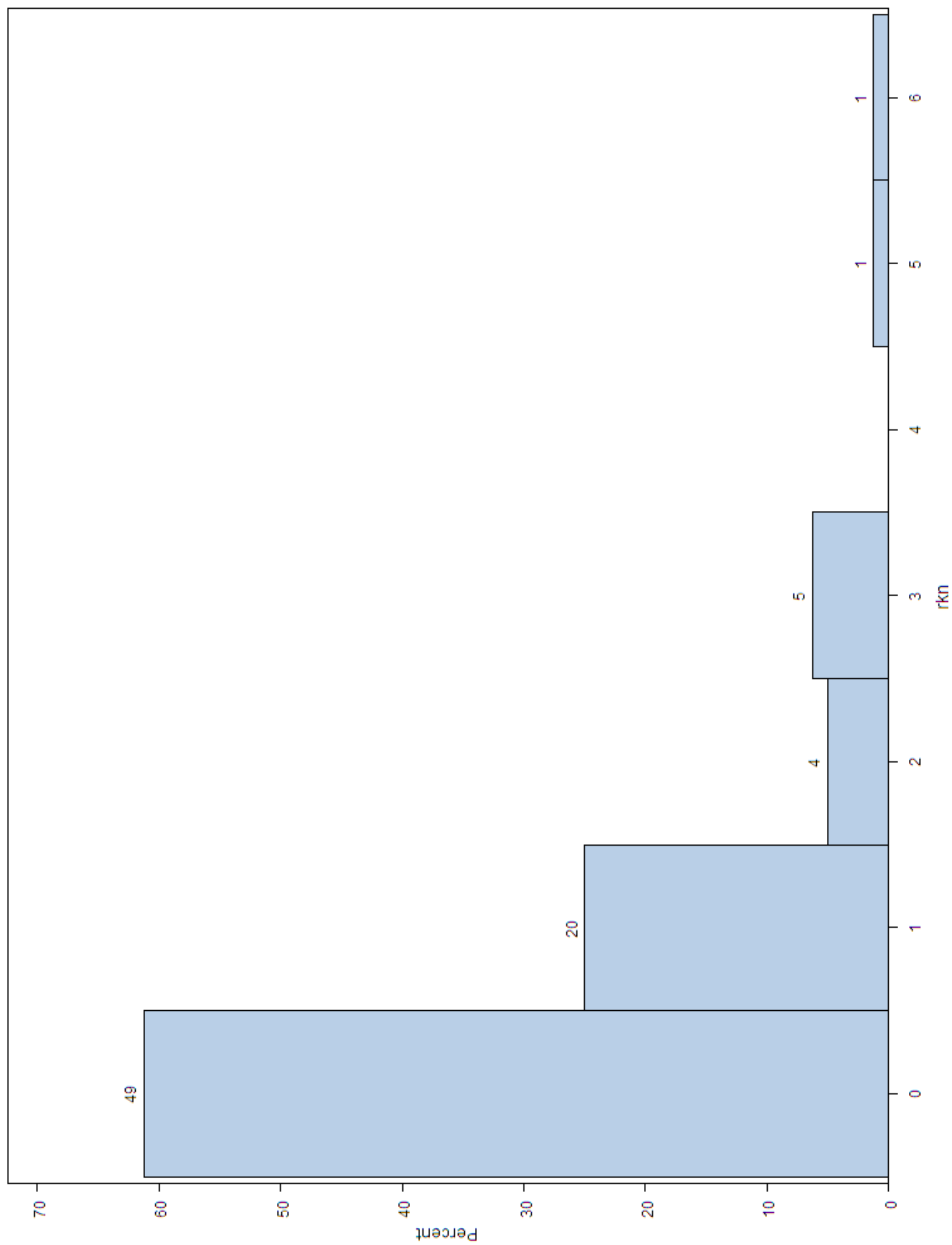


Figure B.5 July 2006 Raw Data Histogram

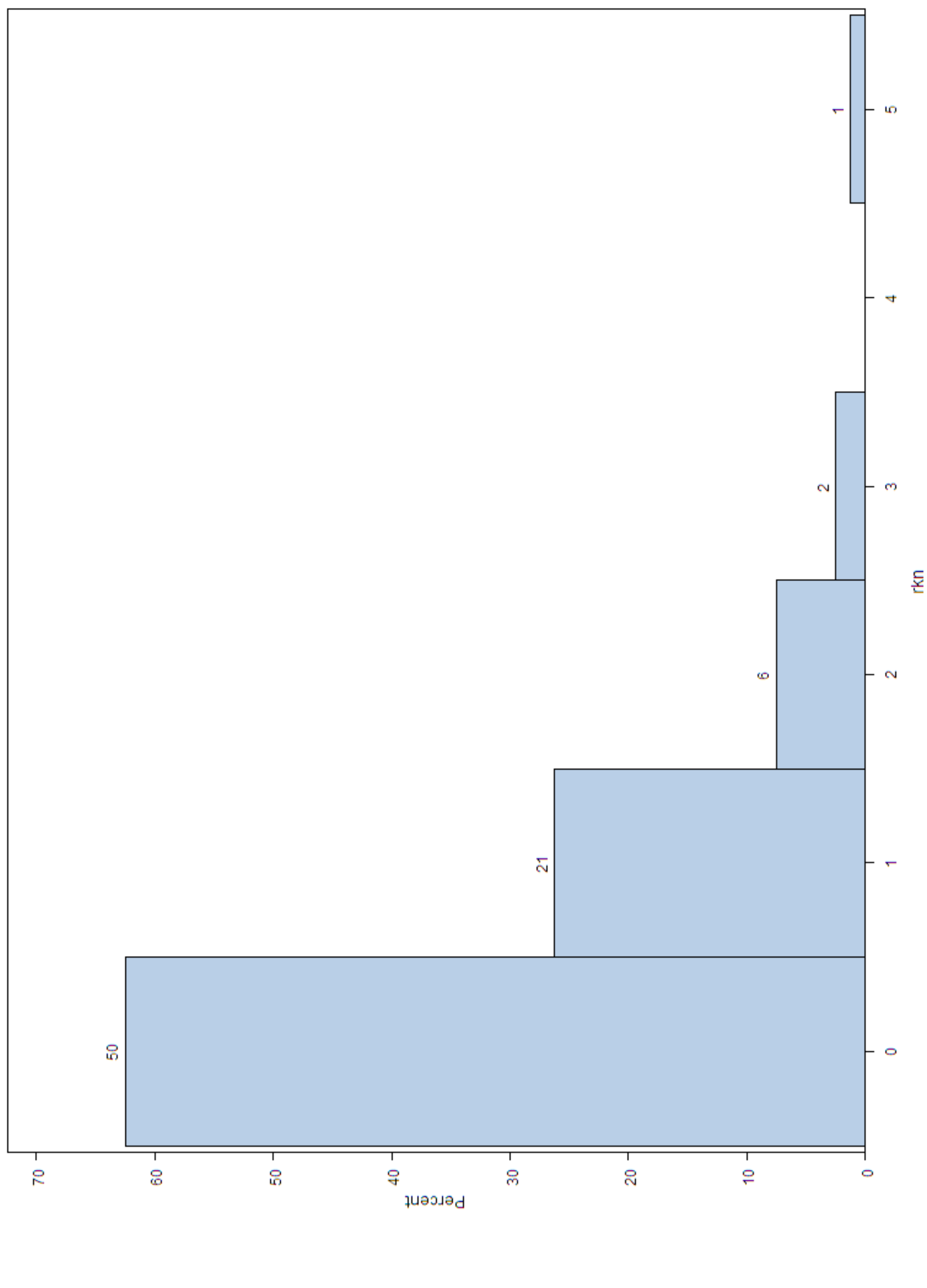
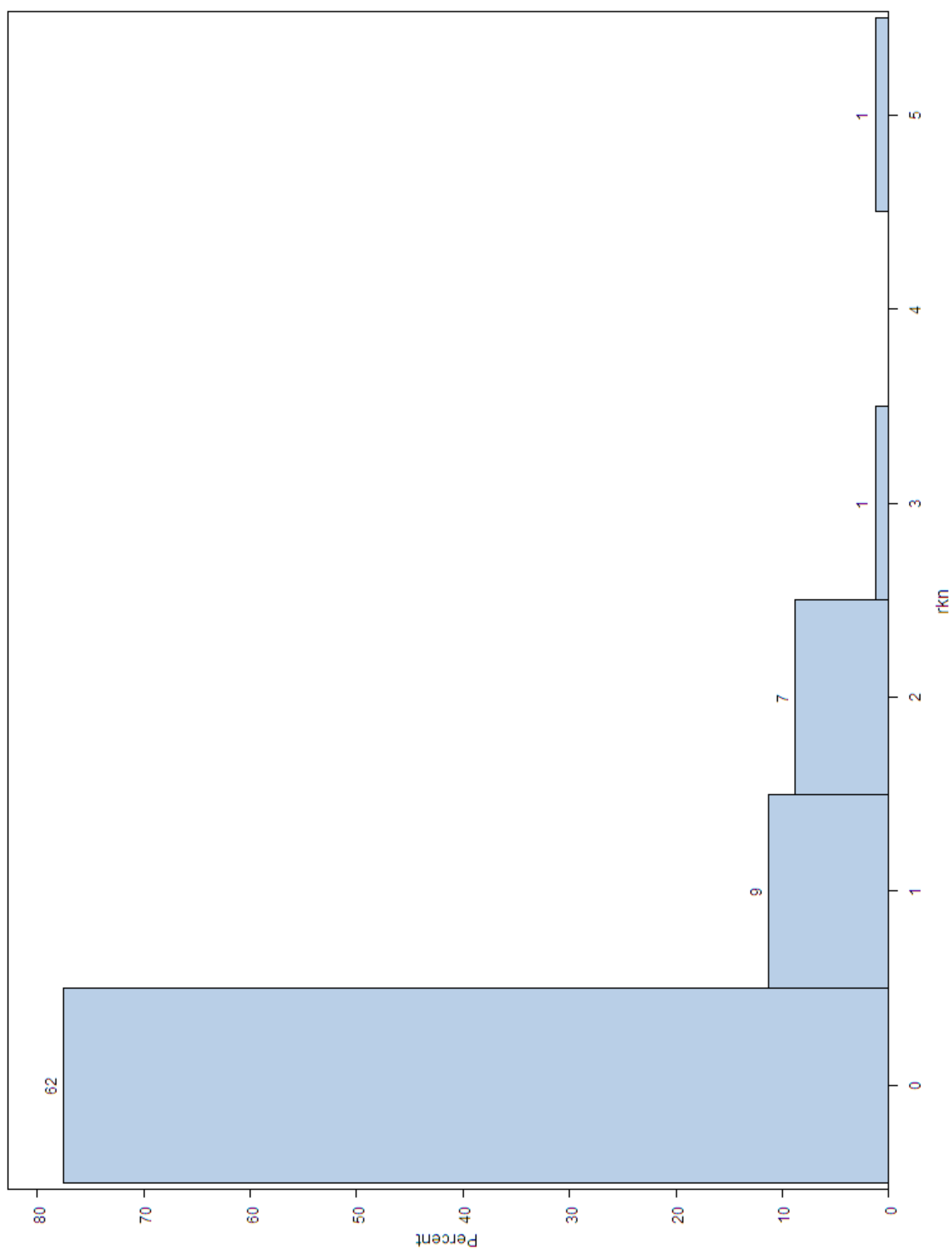


Figure B.6 September 2006 Raw Data Histogram



Appendix C - Parameter Estimates

Table C.1 May 2005 Parameter Estimates

Model	**AIC**	**Intercept**	**SE**	**P-value**	**YNS**	**SE**	**P-value**
Normal	339	1.8212	0.266	<.0001	0.9726	2.1249	0.6485
Normal with ln(count+1)	163	0.8373	0.081	<.0001	0.09931	0.6471	0.8784
Poisson	333.94	0.6	0.09105	<.0001	0.4886	0.6436	0.4501
Poisson DSCALE	157.86	0.6	0.1353	<.0001	0.4886	0.9561	0.6093
Poisson PSCALE	153.43	0.6	0.1374	<.0001	0.4886	0.971	0.6148
ZIP – GENMOD	328.92	0.7912	0.1075	<.0001	-0.7699	1.0972	0.4829
Gen. Poisson	310.24	0.6196	0.1303	<.0001	-0.1959	1.0286	0.8495
ZIP – NLMIXED	324.4	0.7918	0.1056	<.0001	-0.7808	1.0957	0.4782
Poisson hurdle	326.9						
(Non-zero model)		0.2618	0.1547	0.0944	10.1536	0.3218	<.0001
(Zeros model)		0.7913	0.1075	<.0001	-14.846	NA	NA

Model	**PNS**	**SE**	**P-value**	**YNS2**	**SE**	**P-value**
Normal	-2.1636	2.2478	0.3389	-0.6423	1.3052	0.6241
Normal with ln(count+1)	-0.3812	0.6845	0.5793	-0.1775	0.3975	0.6566
Poisson	-0.7233	0.77	0.3506	-0.3368	0.4183	0.4233
Poisson DSCALE	-0.7233	1.144	0.5272	-0.3368	0.6215	0.5878
Poisson PSCALE	-0.7233	1.1618	0.5336	-0.3368	0.6312	0.5936
ZIP – GENMOD	-0.2763	0.8328	0.74	1.2492	1.0444	0.2317
Gen. Poisson	-0.4631	0.9985	0.6442	-0.091	0.6036	0.8806
ZIP – NLMIXED	-0.2714	0.7908	0.7324	1.2506	1.0426	0.2338
Poisson hurdle						
(Non-zero model)	-5.7384	0.3218	<.0001	-10.089	0.3218	<.0001
(Zeros model)	-0.2746	0.833	0.7425	15.3254	NA	NA

Model	**PNS2**	**SE**	**P-value**	**YNS*PNS**	**SE**	**P-value**
Normal	2.0432	1.2389	0.1033	1.3631	1.4715	0.3573
Normal with ln(count+1)	0.414	0.3773	0.276	0.5534	0.4481	0.2208
Poisson	0.6453	0.3961	0.1075	0.5838	0.4818	0.2295
Poisson DSCALE	0.6453	0.5885	0.2728	0.5838	0.7159	0.4148
Poisson PSCALE	0.6453	0.5976	0.2802	0.5838	0.727	0.422
ZIP – GENMOD	0.374	0.4252	0.3791	-1.3682	1.1297	0.2259
Gen. Poisson	0.5033	0.518	0.3344	0.7929	0.6724	0.2421
ZIP – NLMIXED	0.3714	0.4054	0.3624	-1.3616	1.1224	0.2287
Poisson hurdle						
(Non-zero model)	5.8031	0.3218	<.0001	20.8284	0	<.0001
(Zeros model)	0.3723	0.4256	0.3843	-15.448	NA	NA

Table C.2 July 2005 Parameter Estimates

Model	AIC	Intercept	SE	P-value	YNS	SE	P-value
Normal	281	0.3563	0.2729	0.1957	0.1714	0.07717	0.0294
Normal with ln(count+1)	167.5	0.2481	0.1268	0.0542	0.07826	0.03586	0.0322
Poisson	220.1	-0.8472	0.3087	0.0076	0.2091	0.07796	0.009
Poisson DSCALE	153.266	-0.8472	0.3747	0.0238	0.2091	0.0946	0.0271
Poisson PSCALE	161.534	-0.8472	0.3642	0.02	0.2091	0.092	0.023
ZIP – GENMOD	221.8935	-0.7325	0.4783	0.1257	0.2082	0.1147	0.0694
Gen. Poisson	219.01	-0.8199	0.3532	0.023	0.2013	0.08755	0.0243
ZIP – NLMIXED	217	-0.6476	0.358	0.0742	0.2184	0.09003	0.0175
Poisson hurdle	226						
(Non-zero model)		-0.8521	0.3787	0.0272	0.1679	0.104	0.1101
(Zeros model)		-0.6563	0.5715	0.2542	0.2023	0.1402	0.1527

Model	PNS	SE	P-value	YNS2	SE	P-value
Normal	0.06348	0.1398	0.651	-0.0062	0.00532	0.2471
Normal with ln(count+1)	0.02506	0.06494	0.7006	-0.0029	0.00247	0.2493
Poisson	0.09688	0.1241	0.4375	-0.0083	0.00487	0.094
Poisson DSCALE	0.0969	0.1506	0.5201	-0.0083	0.0059	0.1622
Poisson PSCALE	0.0969	0.1464	0.5082	-0.0083	0.0057	0.1504
ZIP – GENMOD	0.1775	0.1508	0.2393	-0.0079	0.0067	0.2393
Gen. Poisson	0.09546	0.1432	0.507	-0.0078	0.00557	0.1647
ZIP – NLMIXED	0.1489	0.1322	0.2634	-0.0088	0.00564	0.1225
Poisson hurdle						
(Non-zero model)	0.05299	0.1904	0.7814	-0.0057	0.00711	0.4233
(Zeros model)	0.1586	0.1703	0.3546	-0.0081	0.00797	0.3132

Model	PNS2	SE	P-value	YNS*PNS	SE	P-value
Normal	0.002736	0.01176	0.8167	-0.0094	0.01212	0.441
Normal with ln(count+1)	0.001734	0.005464	0.7519	-0.0049	0.00563	0.3873
Poisson	0.000162	0.009191	0.986	-0.0109	0.01062	0.3097
Poisson DSCALE	0.0002	0.0112	0.9884	-0.0109	0.0129	0.3994
Poisson PSCALE	0.0002	0.0108	0.9881	-0.0109	0.0125	0.3859
ZIP – GENMOD	-0.012	0.0107	0.2604	-0.0015	0.013	0.9098
Gen. Poisson	0.000566	0.01052	0.9572	-0.0115	0.01208	0.3425
ZIP – NLMIXED	-0.00152	0.01187	0.8984	-0.0143	0.01709	0.4043
Poisson hurdle						
(Non-zero model)	0.003325	0.0144	0.818	-0.016	0.01655	0.3358
(Zeros model)	-0.00675	0.01182	0.5697	-0.0058	0.01817	0.7525

Table C.3 September 2005 Parameter Estimates

Model	AIC	Intercept	SE	P-value	YNS	SE	P-value
Normal	290.2	0.5748	0.2966	0.0564	0.5542	0.4667	0.2388
Normal with ln(count+1)	151.1	0.323	0.1159	0.0068	0.03076	0.1824	0.8665
Poisson	214.25	-0.5875	0.282	0.0407	0.7427	0.3922	0.0622
Poisson DSCALE	133.6489	-0.5875	0.3636	0.1061	0.7427	0.5057	0.1419
Poisson PSCALE	128.5639	-0.5875	0.3714	0.1137	0.7427	0.5166	0.1505
ZIP – GENMOD	190.4103	0.0835	0.3833	0.8276	0.0826	0.5685	0.8844
Gen. Poisson	202.41	-0.5064	0.3519	0.1543	-0.1184	0.5513	0.8305
ZIP – NLMIXED	189.8	0.03282	0.3353	0.9223	0.2096	0.5219	0.6891
Poisson hurdle	185.3						
(Non-zero model)		-0.7782	0.3602	0.0337	-0.4775	0.5505	0.3883
(Zeros model)		-0.1058	0.4971	0.832	0.2224	0.8212	0.7873

Model	PNS	SE	P-value	YNS2	SE	P-value
Normal	-0.1375	0.228	0.5483	-0.049	0.1311	0.7099
Normal with ln(count+1)	0.007339	0.08912	0.9346	0.00607	0.05123	0.906
Poisson	-0.1314	0.1948	0.5021	-0.1036	0.1033	0.3189
Poisson DSCALE	-0.1314	0.2511	0.6009	-0.1036	0.1332	0.4364
Poisson PSCALE	-0.1314	0.2565	0.6086	-0.1036	0.1361	0.4462
ZIP – GENMOD	-0.5419	0.2469	0.0282	0.4053	0.2024	0.0452
Gen. Poisson	0.1064	0.2442	0.6643	0.04522	0.1372	0.7426
ZIP – NLMIXED	-0.3856	0.2233	0.0881	0.3327	0.1924	0.0876
Poisson hurdle						
(Non-zero model)	0.2068	0.2675	0.4417	0.05125	0.1415	0.7182
(Zeros model)	-0.5544	0.4073	0.1773	0.4531	0.3344	0.1792

Model	PNS2	SE	P-value	YNS*PNS	SE	P-value
Normal	0.04484	0.03376	0.1882	-0.128	0.07945	0.1114
Normal with ln(count+1)	0.005406	0.0132	0.6832	-0.0106	0.03105	0.733
Poisson	0.04433	0.02645	0.0979	-0.1334	0.05935	0.0275
Poisson DSCALE	0.0443	0.0341	0.1936	-0.1334	0.0765	0.0812
Poisson PSCALE	0.0443	0.0348	0.2032	-0.1334	0.0782	0.0879
ZIP – GENMOD	0.1093	0.0321	0.0007	-0.2935	0.0676	<.0001
Gen. Poisson	-0.00084	0.03585	0.9814	0.00143	0.08541	0.9867
ZIP – NLMIXED	0.08838	0.03028	0.0046	-0.2844	0.06743	<.0001
Poisson hurdle						
(Non-zero model)	-0.02583	0.03937	0.5136	0.1214	0.09836	0.2209
(Zeros model)	0.1148	0.05466	0.0388	-0.4557	0.1534	0.0039

Table C.4 May 2006 Parameter Estimates

Model	AIC	Intercept	SE	P-value	YNS	SE	P-value
Normal	246.4	0.6533	0.1331	<.0001	-1.98	1.6922	0.2456
Normal with ln(count+1)	120.5	0.3487	0.05816	<.0001	-1.0429	0.7394	0.1625
Poisson	198.37	-0.4257	0.1424	0.0038	-25.0944	806.86	0.9753
Poisson DSCALE	130.802	-0.4257	0.1779	0.0167	-47.0943	0.3237	<.0001
Poisson PSCALE	102.8648	-0.4257	0.2024	0.0354	-47.0943	0.3683	<.0001
ZIP – GENMOD	195.0774	0.2201	0.2027	0.2776	-8.2175	10.8301	0.448
Gen. Poisson	184.94	-0.4459	0.1969	0.0264	-24.6658	842.75	0.9767
ZIP – NLMIXED	196.6	0.1531	0.2168	0.4819	-28.0991	1811.36	0.9877
Poisson hurdle	200						
(Non-zero model)		-0.7606	0.1907	0.0001	-18.7616	33.1948	0.5735
(Zeros model)		0.2198	0.2027	0.2817	0.0236	NA	NA

Model	PNS	SE	P-value	YNS2	SE	P-value
Normal	0.3467	1.1604	0.7659	1.3267	0.9137	0.1506
Normal with ln(count+1)	0.3444	0.507	0.499	0.6942	0.3992	0.0861
Poisson	0.4257	1.0102	0.6747	12.8269	403.43	0.9747
Poisson DSCALE	0.4257	1.2577	0.735	NA	NA	NA
Poisson PSCALE	0.4257	1.431	0.7661	NA	NA	NA
ZIP – GENMOD	-0.2201	1.0203	0.8292	4.2262	5.4185	0.4354
Gen. Poisson	0.7672	1.0175	0.4532	12.6528	421.37	0.9761
ZIP – NLMIXED	-0.07656	0.5116	0.8814	14.1845	905.68	0.9875
Poisson hurdle						
(Non-zero model)	22.5099	0	<.0001	10.438	33.1948	0.754
(Zeros model)	-18.0633	0.4778	<.0001	0.04719	NA	NA

Model	PNS2	SE	P-value	YNS*PNS	SE	P-value
Normal	NA	NA	NA	NA	NA	NA
Normal with ln(count+1)	NA	NA	NA	NA	NA	NA
Poisson	NA	NA	NA	NA	NA	NA
Poisson DSCALE	NA	NA	NA	NA	NA	NA
Poisson PSCALE	NA	NA	NA	NA	NA	NA
ZIP – GENMOD	NA	NA	NA	NA	NA	NA
Gen. Poisson	NA	NA	NA	NA	NA	NA
ZIP – NLMIXED	-0.07656	0.5116	0.8814	NA	NA	NA
Poisson hurdle						
(Non-zero model)	22.5099	0	<.0001	0	0	NA
(Zeros model)	-18.0633	0.4778	<.0001	0	0	NA

Table C.5 July 2006 Parameter Estimates

Model	AIC	Intercept	SE	P-value	YNS	SE	P-value
Normal	238.8	0.6077	0.1724	0.0007	-0.05132	0.1311	0.6965
Normal with ln(count+1)	136	0.3346	0.08608	0.0002	-0.02117	0.06544	0.7472
Poisson	176.09	-0.4922	0.2426	0.0461	-0.1048	0.197	0.5965
Poisson DSCALE	137.2566	-0.4922	0.2776	0.0763	-0.1048	0.2255	0.6423
Poisson PSCALE	113.4259	-0.4922	0.3085	0.1107	-0.1048	0.2506	0.6759
ZIP – GENMOD	180.1912	0.0691	0.3295	0.8339	-0.2562	0.4491	0.5684
Gen. Poisson	172.53	-0.5377	0.2926	0.0701	-0.1111	0.2328	0.6347
ZIP – NLMIXED	176	-0.1226	0.3361	0.7162	-0.09069	0.2246	0.6875
Poisson hurdle	178.9						
(Non-zero model)		-0.7138	0.3102	0.024	-0.1349	0.2444	0.5824
(Zeros model)		0.02052	0.38	0.9571	-0.01315	0.4912	0.9787

Model	PNS	SE	P-value	YNS2	SE	P-value
Normal	0.008264	0.1178	0.9442	-0.0021	0.02085	0.9186
Normal with ln(count+1)	0.02383	0.0588	0.6865	-0.003	0.01041	0.7712
Poisson	0.03299	0.1657	0.8427	-0.007	0.03262	0.8297
Poisson DSCALE	0.033	0.1896	0.8619	-0.007	0.0373	0.8504
Poisson PSCALE	0.033	0.2107	0.8756	-0.007	0.0415	0.8653
ZIP – GENMOD	-0.0963	0.2079	0.6432	0.05	0.0787	0.5254
Gen. Poisson	0.1288	0.1863	0.4914	-0.0185	0.03733	0.6226
ZIP – NLMIXED	-0.00104	0.1742	0.9952	-0.0049	0.0369	0.8946
Poisson hurdle						
(Non-zero model)	0.1812	0.2137	0.399	-0.0255	0.04012	0.5273
(Zeros model)	-0.2992	0.3795	0.4329	0.01397	0.09543	0.884

Model	PNS2	SE	P-value	YNS*PNS	SE	P-value
Normal	-0.00293	0.01787	0.8703	0.01599	0.03549	0.6535
Normal with ln(count+1)	-0.00321	0.008923	0.7204	0.01084	0.01772	0.5425
Poisson	-0.01073	0.02763	0.6988	0.03827	0.05921	0.5201
Poisson DSCALE	-0.0107	0.0316	0.7344	0.0383	0.0678	0.5723
Poisson PSCALE	-0.0107	0.0351	0.7601	0.0383	0.0753	0.6114
ZIP – GENMOD	-0.0112	0.0358	0.7534	0.0466	0.0771	0.546
Gen. Poisson	-0.02616	0.03348	0.4372	0.06489	0.07397	0.3832
ZIP – NLMIXED	-0.00784	0.02871	0.7856	0.03045	0.06281	0.6291
Poisson hurdle						
(Non-zero model)	-0.02968	0.03679	0.4221	0.08722	0.07879	0.2716
(Zeros model)	-0.00273	0.06631	0.9673	0.01661	0.134	0.9017

Table C.6 September 2006 Parameter Estimates

Model	AIC	Intercept	SE	P-value	YNS	SE	P-value
Normal	219.7	0.2431	0.1681	0.1525	0.142	0.2784	0.6116
Normal with ln(count+1)	114.3	0.1441	0.08246	0.0847	0.05507	0.1365	0.6879
Poisson	148.98	-1.3802	0.3586	0.0002	0.3977	0.5454	0.4682
Poisson DSCALE	119.5923	-1.3802	0.4046	0.0006	0.3977	0.6155	0.5181
Poisson PSCALE	86.2	-1.3802	0.4872	0.0046	0.3977	0.7411	0.5915
ZIP – GENMOD	140.8276	0.0732	0.5587	0.8958	0.7809	0.7866	0.3208
Gen. Poisson	138.38	-1.3624	0.4655	0.0045	0.2019	0.6622	0.7614
ZIP – NLMIXED	137.9	-0.299	0.5301	0.5744	0.7168	0.6656	0.2847
Poisson hurdle	141.1						
(Non-zero model)		-1.7451	0.4595	0.0003	0.05923	0.6827	0.9311
(Zeros model)		0.05977	0.5693	0.9167	1.3869	1.0107	0.1738

Model	PNS	SE	P-value	YNS2	SE	P-value
Normal	0.02807	0.164	0.8645	-0.04141	0.08967	0.6456
Normal with ln(count+1)	0.001598	0.08042	0.9842	-0.0108	0.04398	0.8066
Poisson	0.1869	0.2747	0.4983	-0.1205	0.1895	0.527
Poisson DSCALE	0.1869	0.3099	0.5465	-0.1205	0.2138	0.5733
Poisson PSCALE	0.1869	0.3732	0.6165	-0.1205	0.2575	0.64
ZIP – GENMOD	0.0062	0.3438	0.9855	-0.4445	0.2657	0.0943
Gen. Poisson	0.1421	0.3519	0.6875	-0.01175	0.2022	0.9538
ZIP – NLMIXED	0.1599	0.324	0.623	-0.2735	0.2356	0.2491
Poisson hurdle						
(Non-zero model)	0.1328	0.3848	0.731	0.04664	0.1978	0.8142
(Zeros model)	-0.1135	0.4544	0.8034	-0.9249	0.5374	0.0891

Model	PNS2	SE	P-value	YNS*PNS	SE	P-value
Normal	0.03501	0.04484	0.4374	-0.02585	0.08921	0.7728
Normal with ln(count+1)	0.0199	0.02199	0.3684	-0.0134	0.04376	0.7603
Poisson	0.02934	0.06879	0.6709	-0.04736	0.1366	0.7298
Poisson DSCALE	0.0293	0.0776	0.7054	-0.0474	0.1541	0.7586
Poisson PSCALE	0.0293	0.0935	0.7535	-0.0474	0.1856	0.7986
ZIP – GENMOD	-0.0763	0.0867	0.3788	0.2794	0.1794	0.1193
Gen. Poisson	0.03902	0.08449	0.6456	-0.06146	0.1584	0.6991
ZIP – NLMIXED	0.005495	0.09744	0.9552	-0.00734	0.1964	0.9703
Poisson hurdle						
(Non-zero model)	0.04348	0.0903	0.6315	-0.0459	0.1733	0.7917
(Zeros model)	-0.04654	0.1476	0.7534	0.3596	0.3609	0.3221

Appendix D - SAS Code

```
***********************************************;
* Importing the data.                          ;
***********************************************;
proc import out = work.<dfile>
      datafile = "datafile.xls" DBMS=EXCEL replace;
      GETNAMES = yes;
run;


***********************************************;
* Creating the logged (rkn+1) data as well as   ;
* the "interaction" and "squared" terms for our ;
* model. YNS^2, PNS^2, and YNS*PNS.             ;
***********************************************;
data <datafile>;
      set <dfile>;
      logrkn = log(rkn+1);
      yns2 = yns**2;
      pns2 = pns**2;
      ynspns = yns*pns;
run;


***********************************************;
* Histogram of the nematode counts for the data ;
***********************************************;

proc univariate data = <datafile>;
      var rkn;
      histogram rkn / barlabel = count midpoints = 1 to 5 by 1;
run;



***********************************************;
* The linear model for the standard nematode    ;
* counts for the data with the raw,             ;
* pearson, and studentized residual histograms  ;
* and normal quantile plots                     ;
***********************************************;

ods html;
ods graphics on;
proc mixed data = <datafile> plots(unpack) = (residualpanel
                  studentpanel pearsonpanel);
      model rkn = yns pns yns2 pns2 ynspns / solution
                  outpm = mixout residual;
run;
ods graphics off;
ods html close;
```

```
**********************************************;
* Procedure to test the normality of the       ;
* different residuals                          ;
**********************************************;
proc univariate data = mixout normal;
      var resid;
      histogram resid;
run;



**********************************************;
* The linear model for the logged(rkn+1)       ;
* nematode counts for the data with the raw,   ;
* pearson, and studentized residual histograms ;
* and normal quantile plots                    ;
**********************************************;

ods html;
ods graphics on;
proc mixed data = <datafile> plots(unpack) = (residualpanel
                  studentpanel pearsonpanel);
      model logrkn = yns pns yns2 pns2 ynspns / solution
                  outpm = mixout residual;
run;
ods graphics off;
ods html close;

**********************************************;
* Procedure to test the normality of the       ;
* different residuals                          ;
**********************************************;
proc univariate data = mixout normal;
      var resid;
      histogram resid;
run;



**********************************************;
* The generalized linear model with a LOG link ;
* and a Poisson random component for the data  ;
**********************************************;

ods html;
ods graphics on;
proc glimmix data = <datafile> plots = (residualpanel(unpack)
                  studentpanel(unpack) pearsonpanel(unpack));
      model rkn = yns pns yns2 pns2 ynspns / dist = poisson
                  link = log solution;
      output out = mixout residual = resd;
run;
ods graphics off;
ods html close;
```

```
**********************************************;
* Procedure to test the normality of the       ;
* different residuals                          ;
**********************************************;
proc univariate data = mixout normal;
      var resd;
      histogram resd;
run;



**********************************************;
* The generalized linear model with a LOG link  ;
* and a Poisson random component and the DSCALE ;
* option which allows for modeling over-        ;
* dispersed distribution for the data           ;
**********************************************;

ods html;
ods graphics on;
proc genmod data = <datafile> plots(unpack) = (predicted
            reschi(xbeta) resdev(xbeta) reslik(xbeta) resraw(xbeta)
            STDRESCHI(xbeta) STDRESDEV(xbeta));
      model rkn = yns pns yns2 pns2 ynspns /  link = log
                  dist = poisson DSCALE p r;
      * Outputting the raw, pearson, deviane, and likelihood residuals;
      output out = mixout resraw = resd reschi = resch
                  resdev = rsdv reslik = rslk   stdreschi = stdrsch
                  stdresdev = stdrsdv;
run;
ods graphics off;
ods html close;

**********************************************;
* Procedure to test the normality of the       ;
* different residuals                          ;
**********************************************;
proc univariate data = mixout normal;
      var resd resch rsdv rslk stdrsch stdrsdv;
      histogram resd;
      histogram resch;
      histogram rsdv;
      histogram rslk;
      histogram stdrsch;
      histogram stdrsdv;
run;



**********************************************;
* The generalized linear model with a LOG link  ;
* and a Poisson random component and the PSCALE ;
* option which allows for modeling over-        ;
* dispersed distribution for the data           ;
**********************************************;

ods html;
```

```
ods graphics on;
proc genmod data = <datafile> plots(unpack) = (predicted
            reschi(xbeta) resdev(xbeta) reslik(xbeta) resraw(xbeta)
            STDRESCHI(xbeta) STDRESDEV(xbeta));
      model rkn = yns pns yns2 pns2 ynspns /  link = log
                  dist = poisson PSCALE p r;
      * Outputting the raw, pearson, deviane, and likelihood residuals;
      output out = mixout resraw = resd reschi = resch
                  resdev = rsdv reslik = rslk   stdreschi = stdrsch
                  stdresdev = stdrsdv;
run;
ods graphics off;
ods html close;

***********************************************;
* Procedure to test the normality of the       ;
* different residuals                          ;
***********************************************;
proc univariate data = mixout normal;
      var resd resch rsdv rslk stdrsch stdrsdv;
      histogram resd;
      histogram resch;
      histogram rsdv;
      histogram rslk;
      histogram stdrsch;
      histogram stdrsdv;
run;



***********************************************;
* The generalized linear model with a LOG link  ;
* and the built in ZIP random component in PROC ;
* GENMOD for the data                          ;
***********************************************;

ods html;
ods graphics on;
proc genmod data = <datafile> plots(unpack) = (predicted
            reschi(xbeta) resdev(xbeta) reslik(xbeta) resraw(xbeta)
            STDRESCHI(xbeta) STDRESDEV(xbeta));
      model rkn = yns pns yns2 pns2 ynspns /  link = log
                  dist = zip p r;
      zeromodel yns pns yns2 pns2 ynspns;
      output out = mixout resraw = resd reschi = resch;
run;
ods graphics off;
ods html close;

***********************************************;
* Procedure to test the normality of the       ;
* different residuals                          ;
***********************************************;
proc univariate data = mixout normal;
      var resd resch;
      histogram resd;
      histogram resch;
```

```
run;



**********************************************;
* The generalized poisson linear model for the  ;
* data (Schabenberger, 2008)                    ;
**********************************************;

ods html;
ods graphics on;
proc glimmix data = <datafile> method = quad plots =
                  (residualpanel(unpack) studentpanel(unpack)
                  pearsonpanel(unpack));
      model rkn = yns pns yns2 pns2 ynspns / link = log s;
      xi = (1 - 1/exp(_phi_));
      * Setting up the user-defined variance of the model;
      _variance_ = _mu_ / (1-xi)/(1-xi);
      if (_mu_ = .) or (_linp_ = .) then _logl_ = .;
      else do;
            mustar = _mu_ - xi*(_mu_ - rkn);
            if(mustar < 1E-12) or (_mu_*(1-xi) < 1e-12)
                        then _logl_ = -1e20;
            else do;
                  _logl_ = log(_mu_*(1-xi)) + (rkn-1)*log(mustar)
                              - mustar - lgamma(rkn+1);
            end;
      end;
      output out = mixoutgenP / allstats;
run;
ods graphics off;
ods html close;

**********************************************;
* Procedure to test the normality of the        ;
* different residuals                           ;
**********************************************;
proc univariate data = mixoutgenP normal;
      var resid;
      histogram resid;
run;



**********************************************;
* The ZIP linear model in PROC NLMIXED for      ;
* data. Litell et al., (2006).                  ;
**********************************************;

ods html;
ods graphics on;
proc nlmixed data = <datafile>;
      parms infl = 0 b0 = 0 b1 = 0 b2 = 0 b3 = 0 b4 = 0 b5 = 0;
      * linear predictor for the inflation probability;
      linpinfl = infl;
      * infprob = inflation probability for zeros;
```

```
      *              = logistic transform of the linear predictor;
      infprob = 1/(1+exp(-linpinfl));
      * Poisson mean;
      lambda = exp(b0 + b1*yns + b2*pns + b3*yns2 + b4*pns2
            + b5*ynspns);
      * Building the ZIP log-likelihood;
      if rkn = 0 then
            ll = log(infprob + (1-infprob)*exp(-lambda));
      else ll = log(1-infprob) + rkn*log(lambda) - lgamma(rkn+1)
            - lambda;
      model rkn ~ general(ll);
      predict ll out = mixout;
run;
ods graphics off;
ods html close;

data data2;
      set mixout;
      resd = rkn - pred;
      *stud = (rkn - pred) / stderrpred;
      id = _N_;
run;

***********************************************;
* Procedure to test the normality of the       ;
* different residuals                          ;
***********************************************;
proc univariate data = data2 normal;
      var resd;
      histogram resd;
      *histogram stud;
run;



***********************************************;
* The hurdle model in PROC NLMIXED for the data ;
* Litell et al., (2006).                        ;
***********************************************;

ods html;
ods graphics on;
proc nlmixed data = <datafile>;
      parms a0 = 0 a1 = 0 a2 = 0 a3 = 0 a4 = 0 a5 = 0
            b0 = 0 b1 = 0 b2 = 0 b3 = 0 b4 = 0 b5 = 0;
      * linear predictor for the data consisting of only zeros;
      linpzero = a0 + a1*yns + a2*pns + a3*yns2 + a4*pns2
            + a5*ynspns;
      * linear predictor for the data consisting of non-zeros;
      linpnozero = b0 + b1*yns + b2*pns + b3*yns2 + b4*pns2
            + b5*ynspns;
      * mean of the model for the data with only zeros;
      muzero = exp(linpzero);
      * mean of the model for the data with only non-zeros;
      munozero = exp(linpnozero);
      * Building the hurdle log-likelihoods;
      f10 = exp(-muzero);
```

```
      f20 = exp(-munozero);
      logpnozero = log(1-f10) - log(1-f20) - munozero -
                  lgamma(rkn+1) + rkn*log(munozero);
      if rkn = 0 then ll = -muzero;
      else ll = logpnozero;
      model rkn ~ general(ll);
      predict ll out = mixout;
run;
ods graphics off;
ods html close;

data data2;
      set mixout;
      resd = rkn - pred;
      *stud = (rkn - pred) / stderrpred;
run;

************************************************;
* Procedure to test the normality of the        ;
* different residuals                           ;
************************************************;
proc univariate data = data2 normal;
      var resd;
      histogram resd;
      *histogram stud;
run;


quit;
```

Appendix E - Residual Plots

E.1 May 2005 Residual Plots

E.1.1 May 2005 Model 1 Residual Plots

Figure E.1.1.1 Histogram of the raw residuals

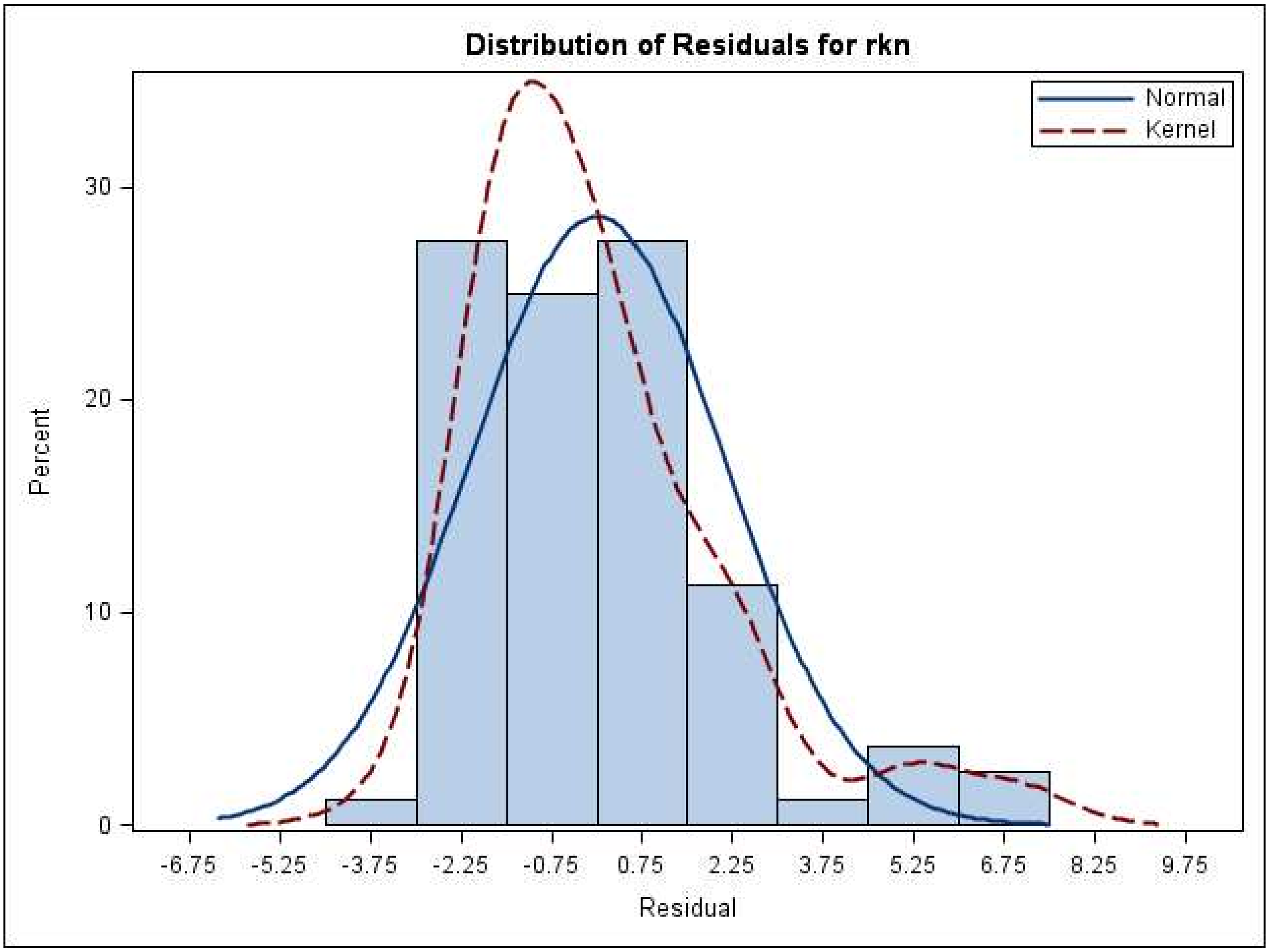


Figure E.1.1.2 Normal quantile plot of the raw residuals

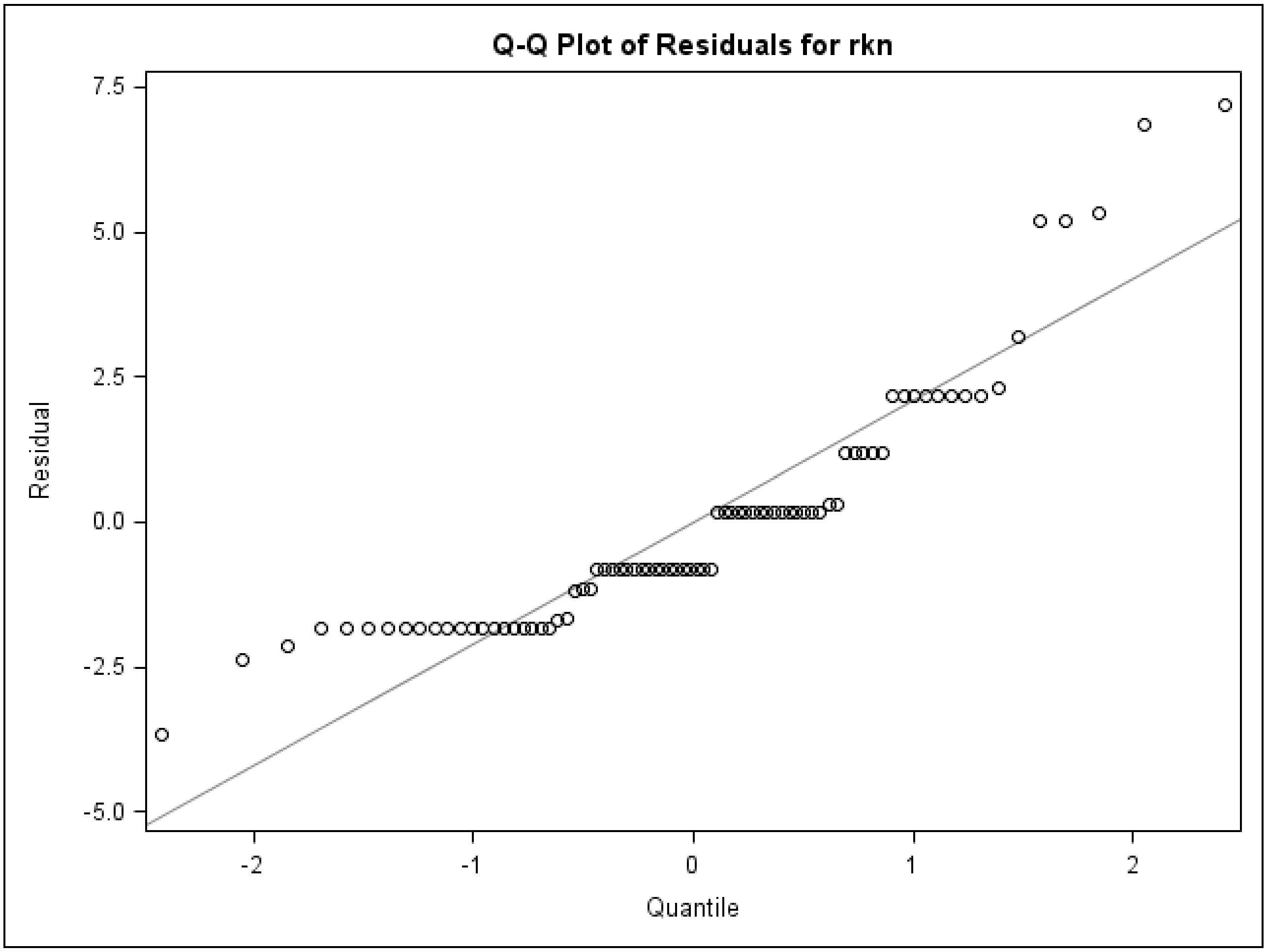


Figure E.1.1.3 Histogram of the Studentized residuals

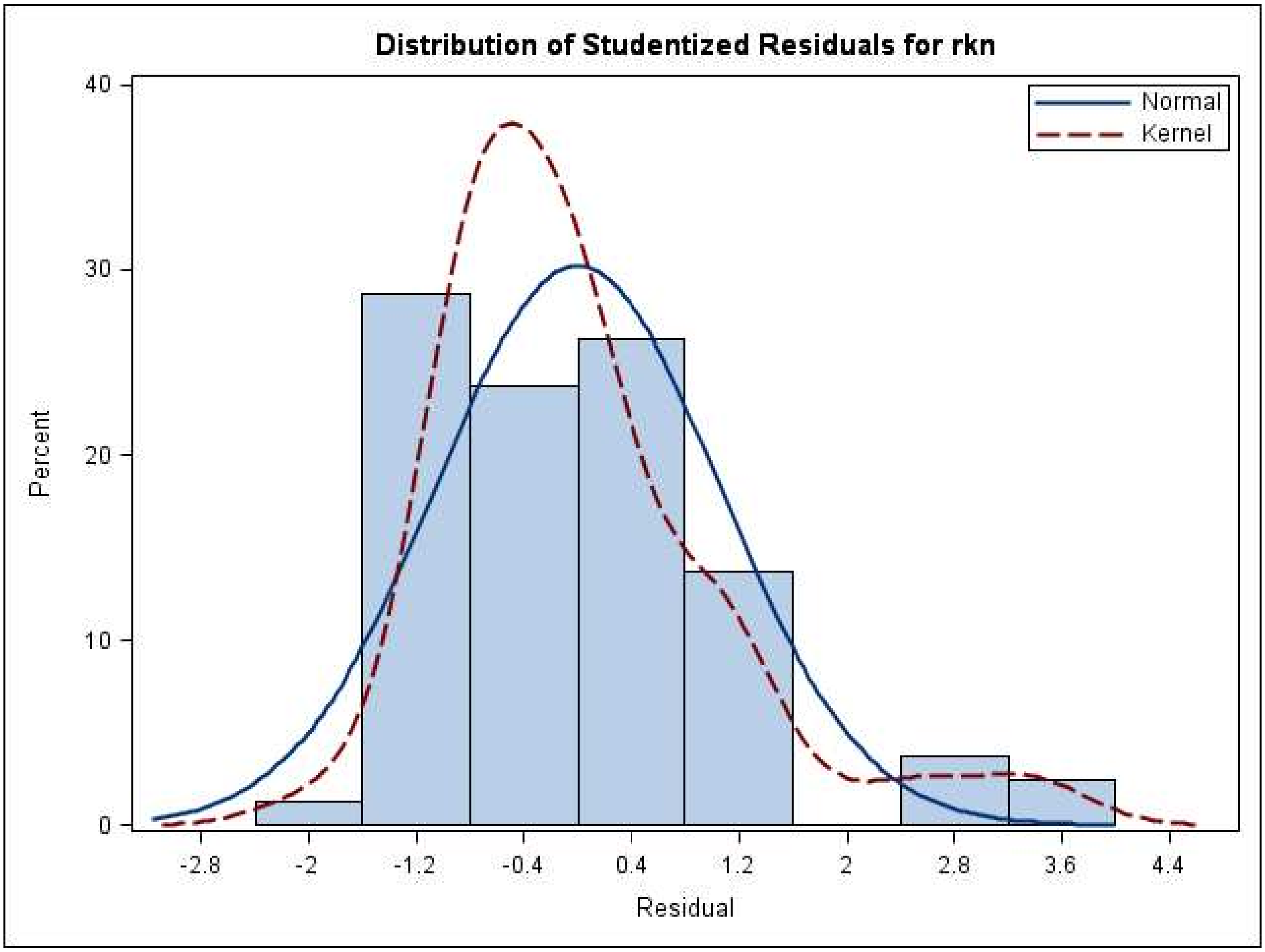


Figure E.1.1.4 Normal quantile plot of the Studentized residuals

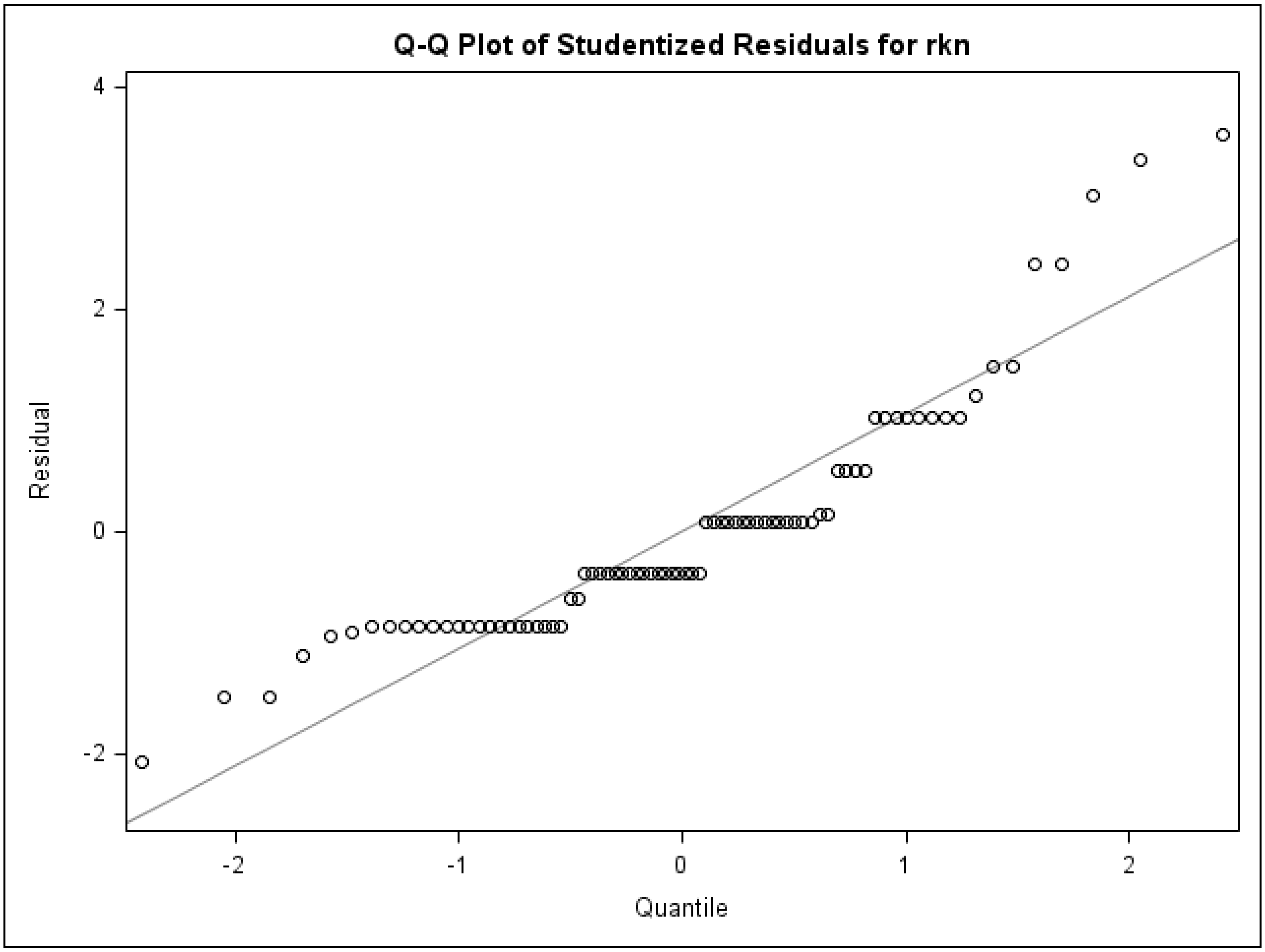


Figure E.1.1.5 Histogram of the Pearson residuals

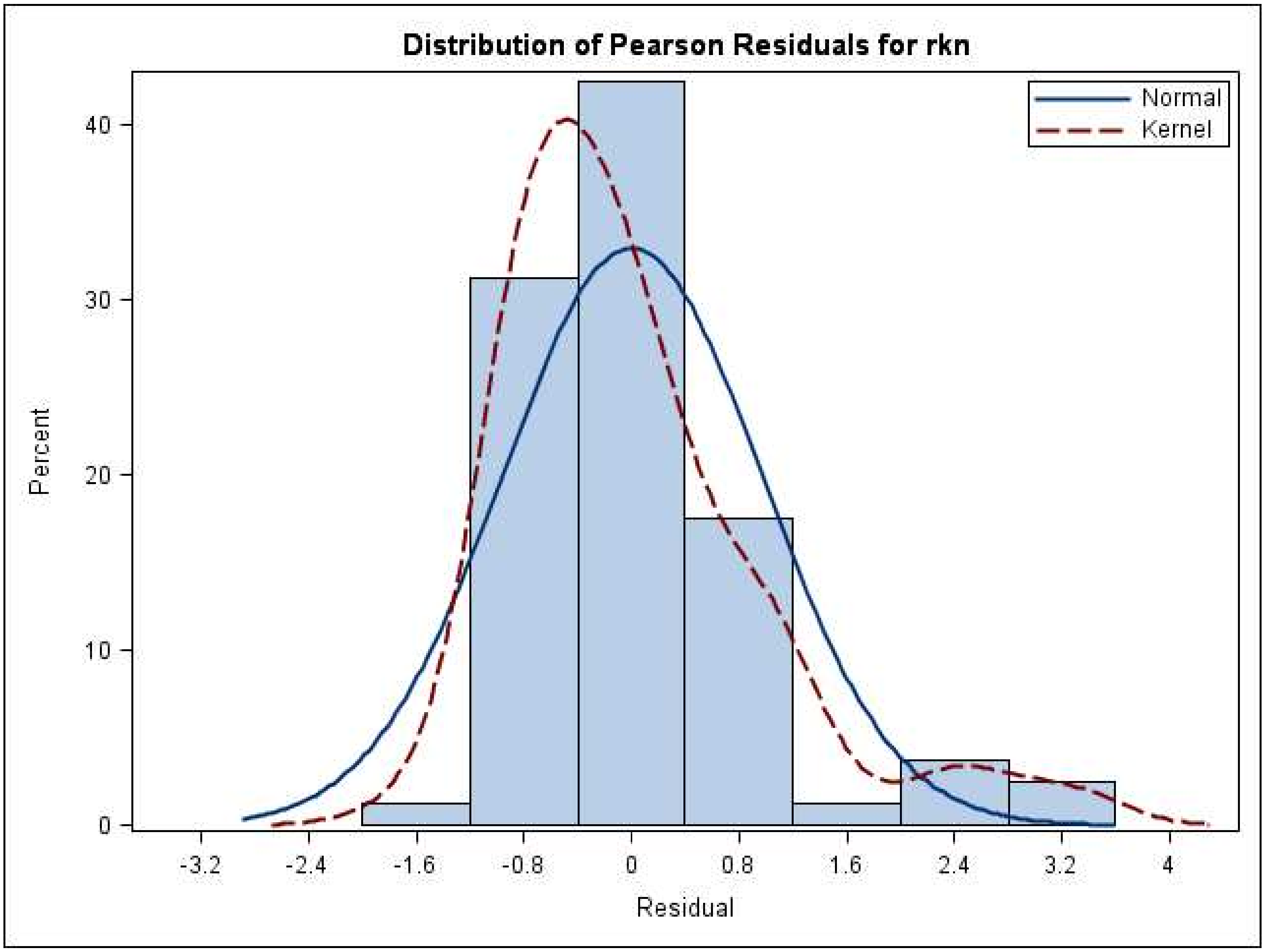
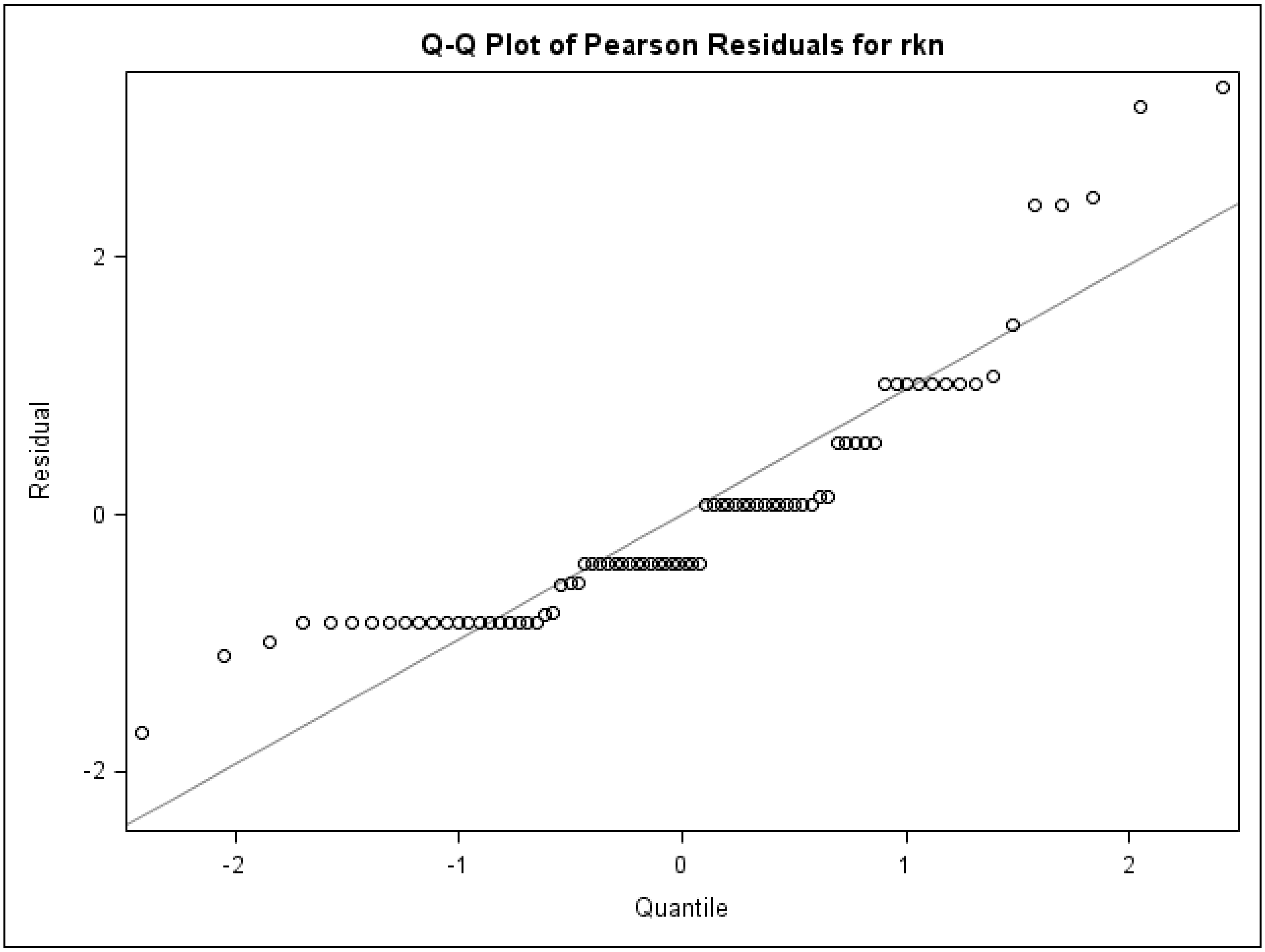


Figure E.1.1.6 Normal quantile plot of the Pearson residuals



E.1.2 May 2005 Model 2 Residual Plots

Figure E.1.2.1 Histogram of the raw residuals

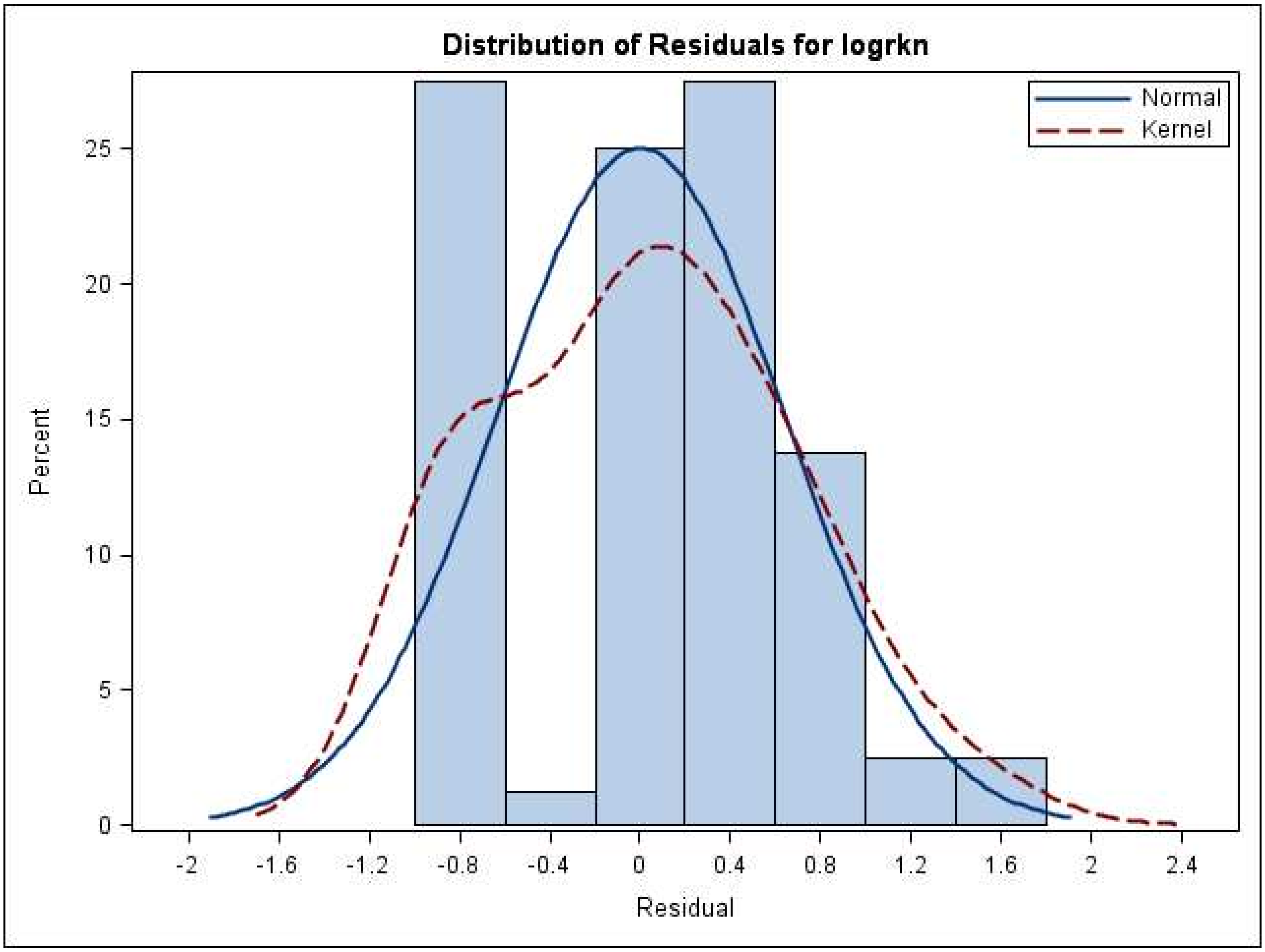


Figure E.1.2.2 Normal quantile plot of the raw residuals

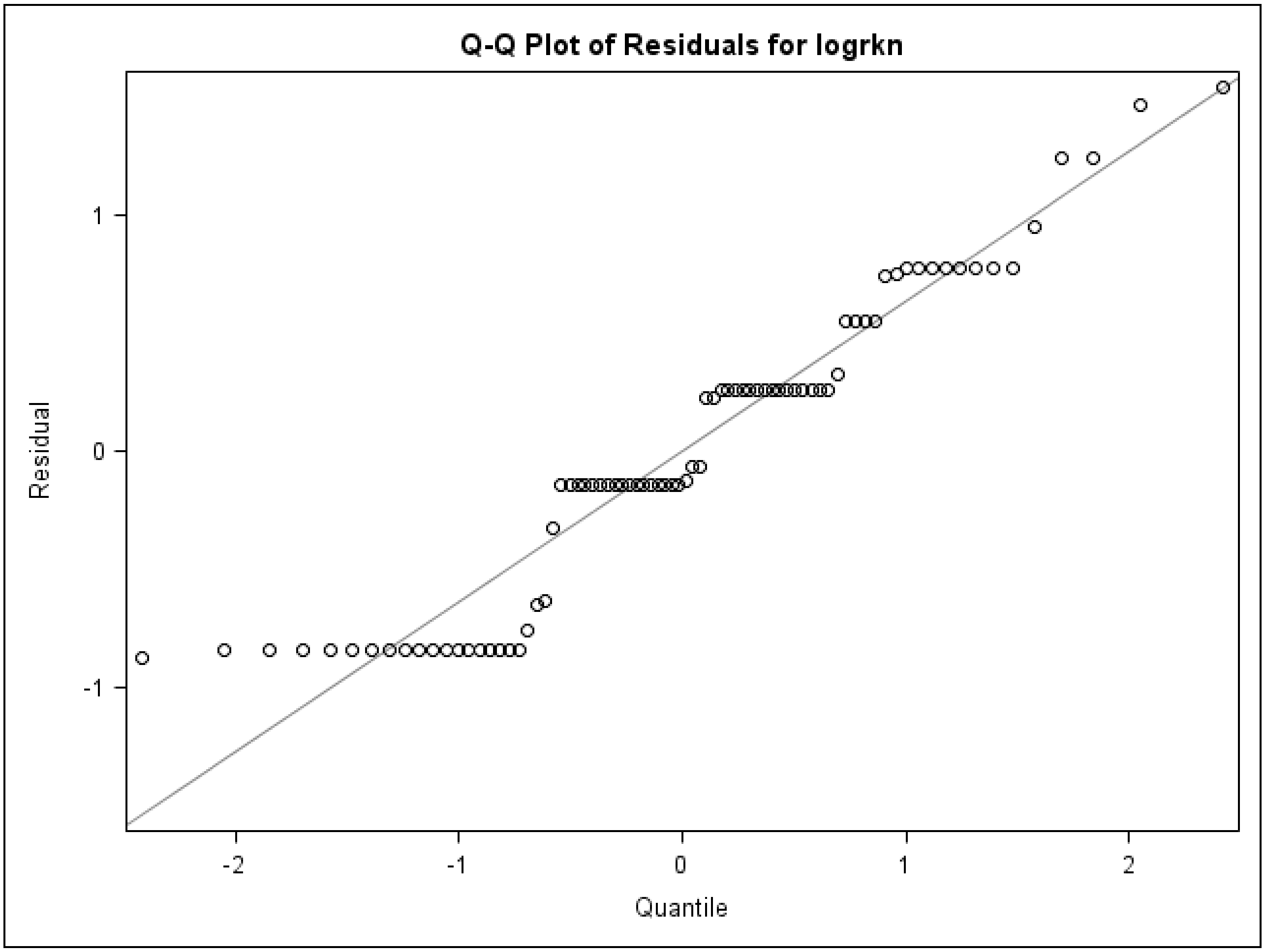


Figure E.1.2.3 Histogram of the Studentized residuals

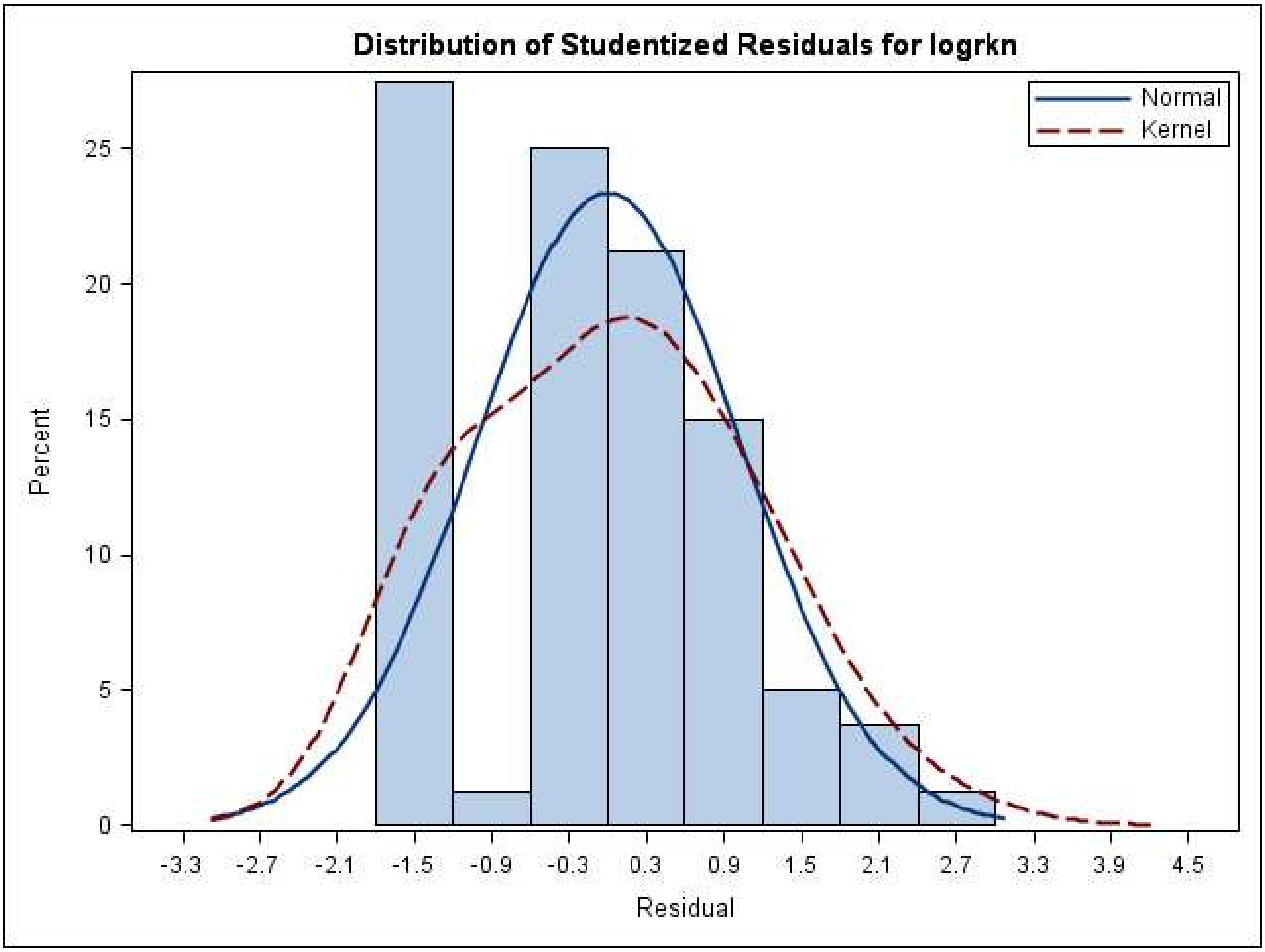


Figure E.1.2.4 Normal quantile plot of the Studentized residuals

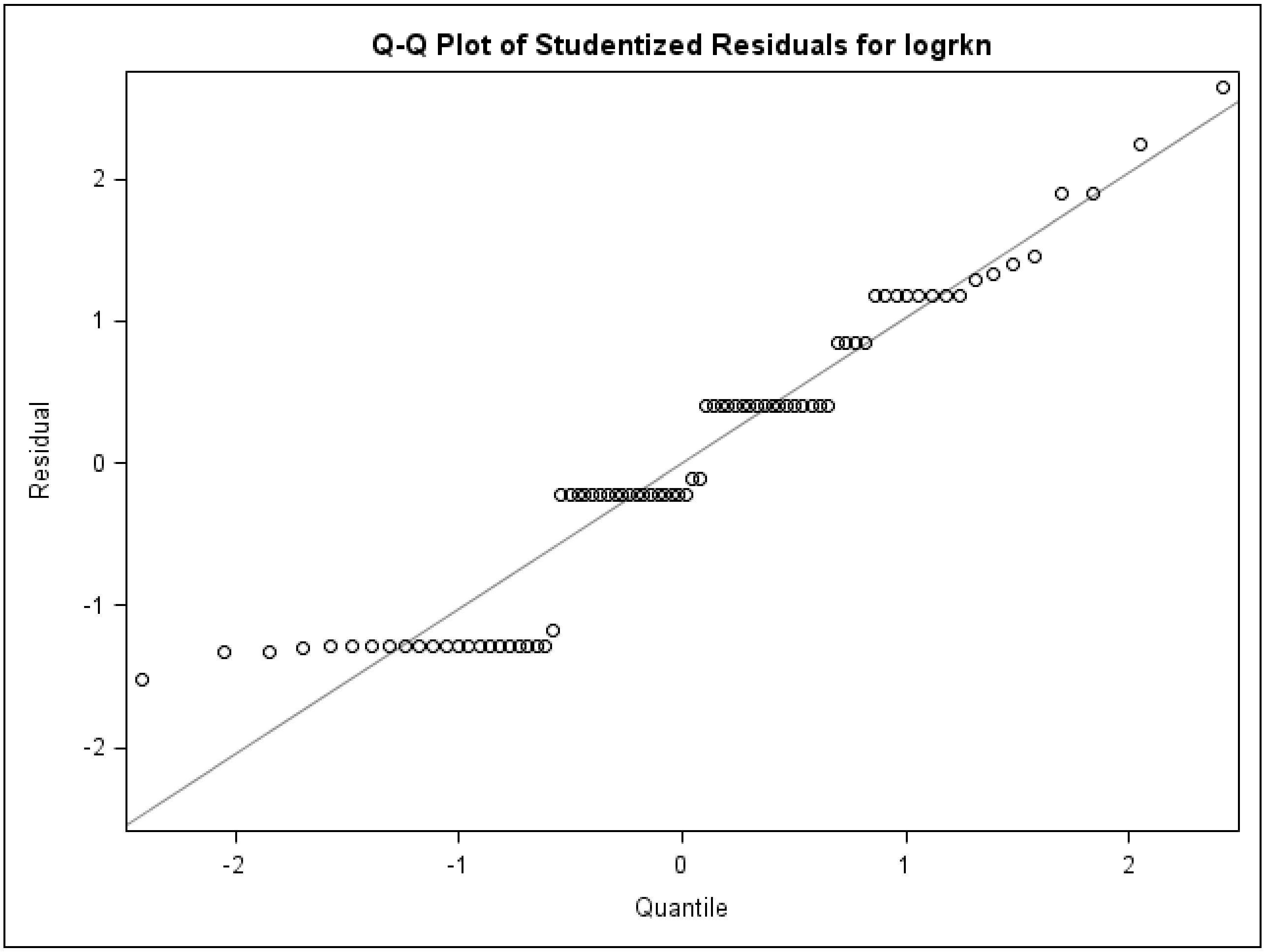


Figure E.1.2.5 Histogram of the Pearson residuals

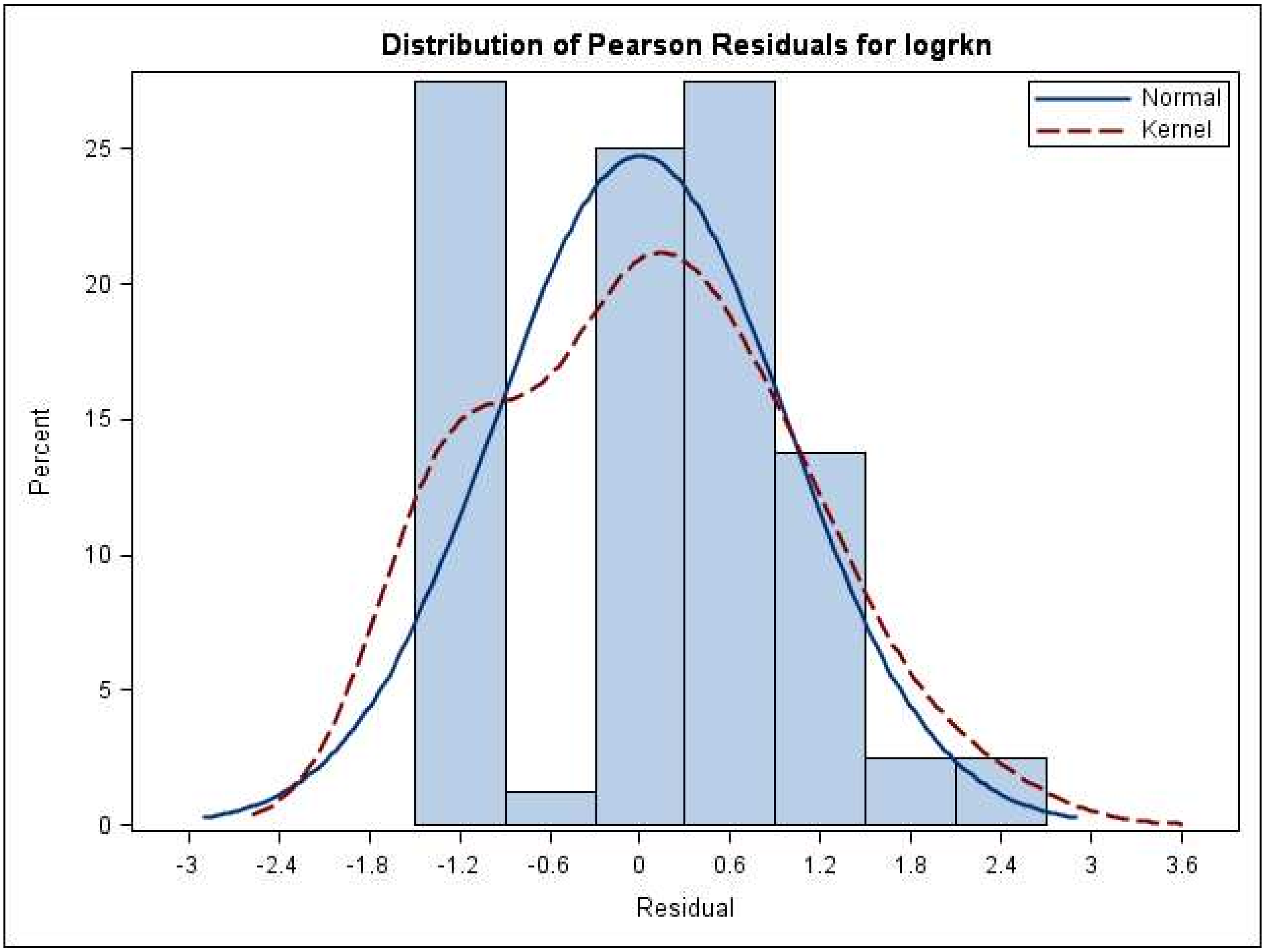
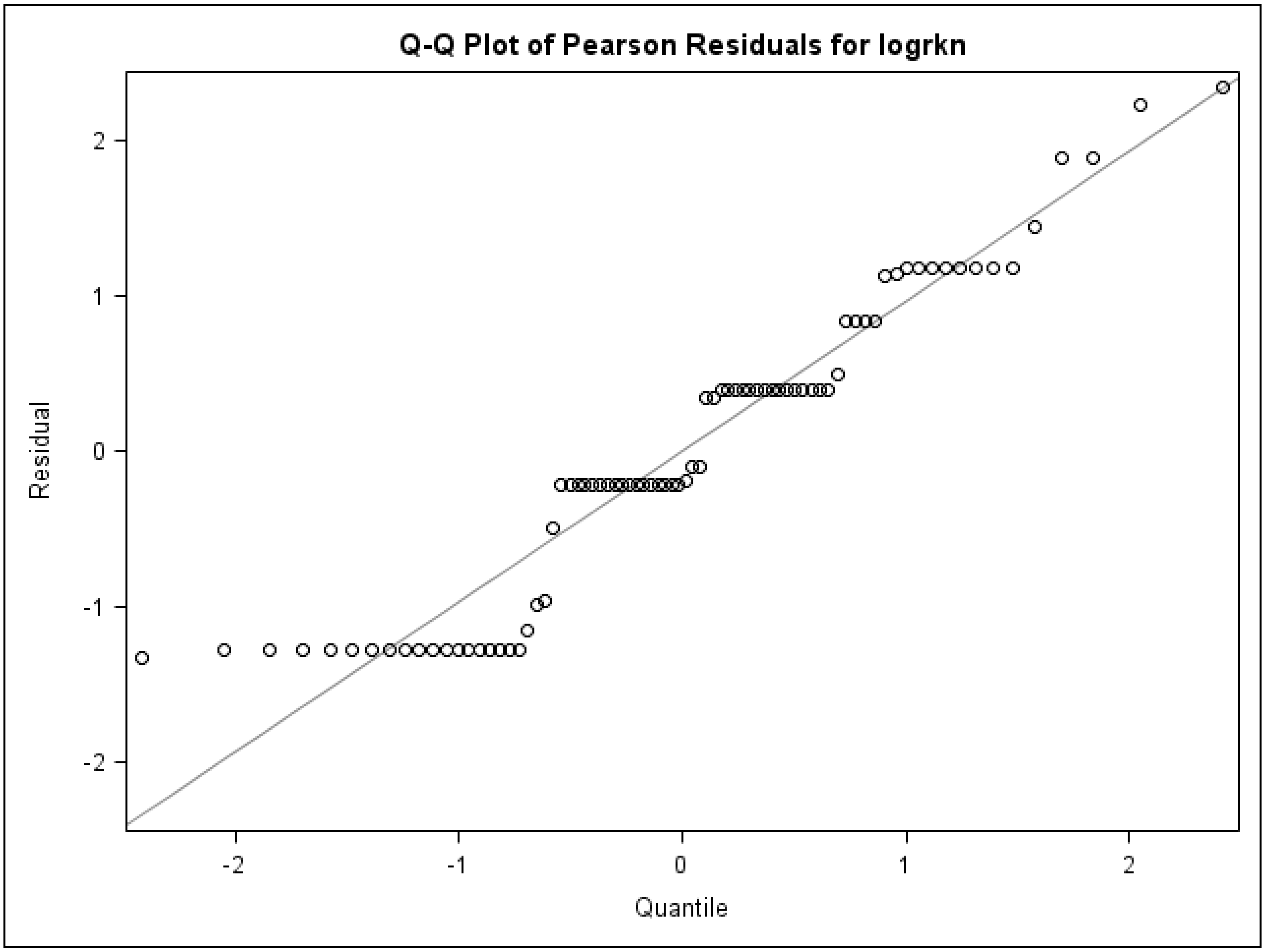


Figure E.1.2.6 Normal quantile plot of the Pearson residuals



E.1.3 May 2005 Model 3 Residual Plots

Figure E.1.3.1 Histogram of the raw residuals

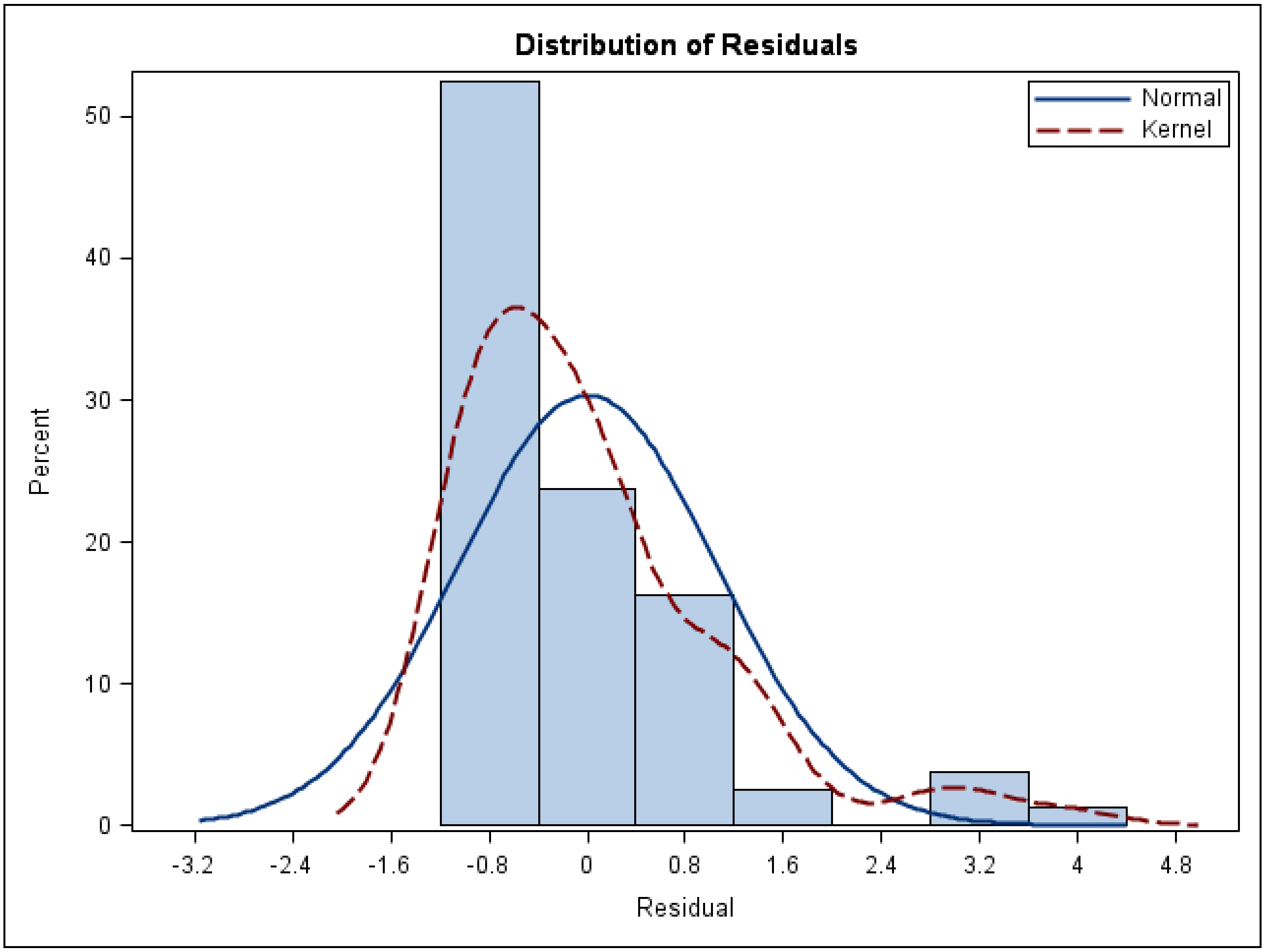


Figure E.1.3.2 Normal quantile plot of the raw residuals

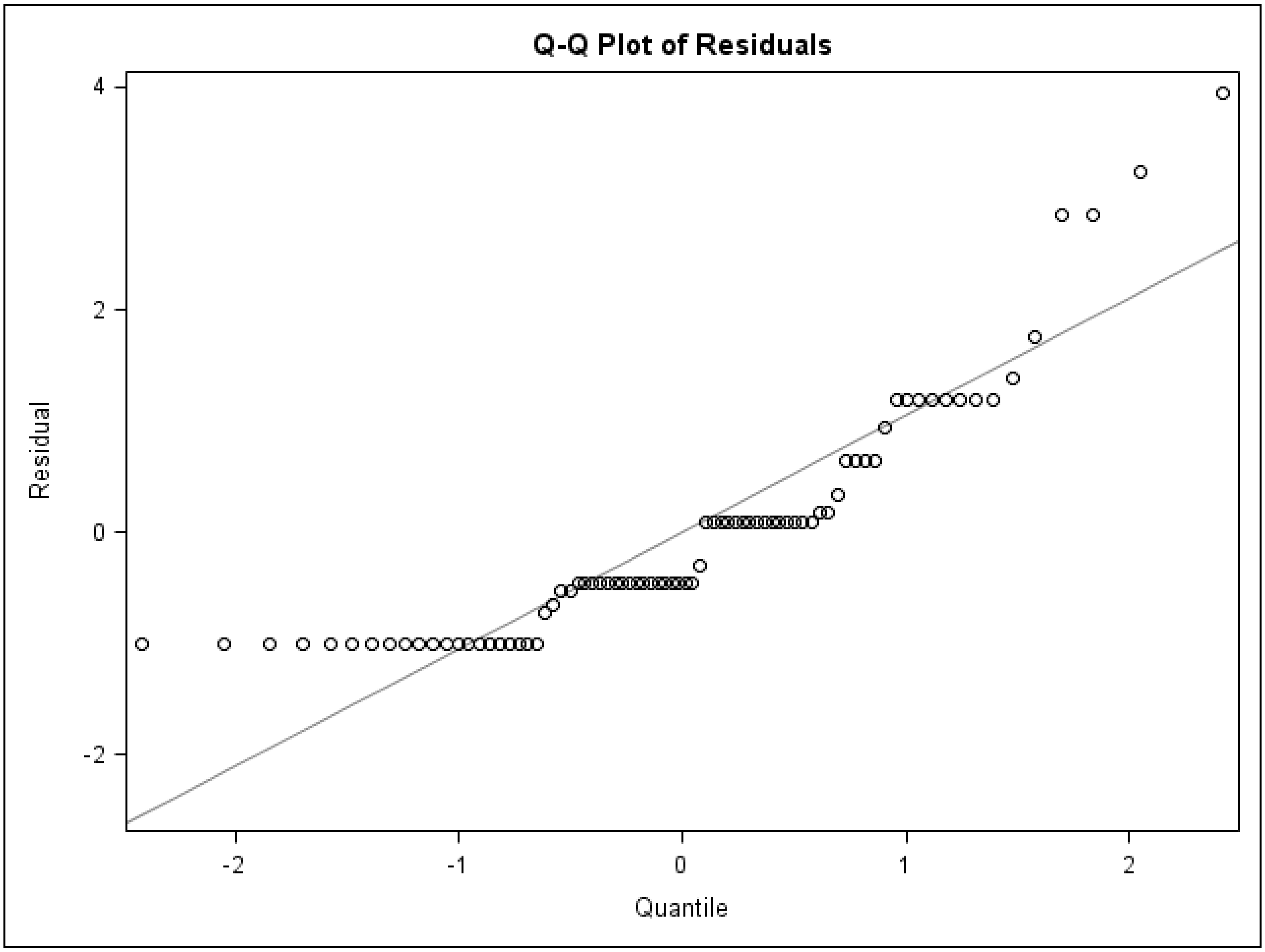


Figure E.1.3.3 Histogram of the Studentized residuals

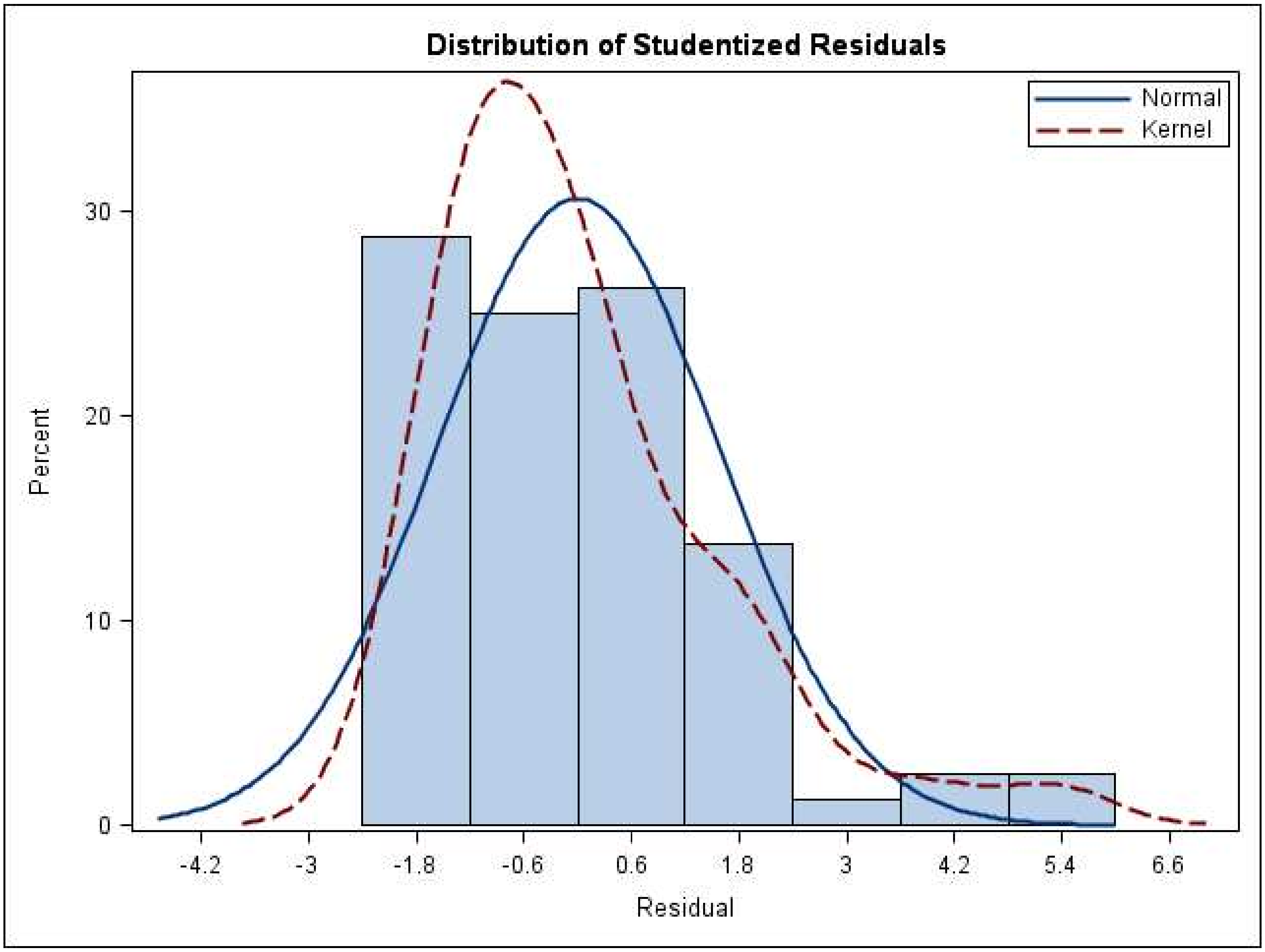


Figure E.1.3.4. Normal quantile plot of the Studentized residuals

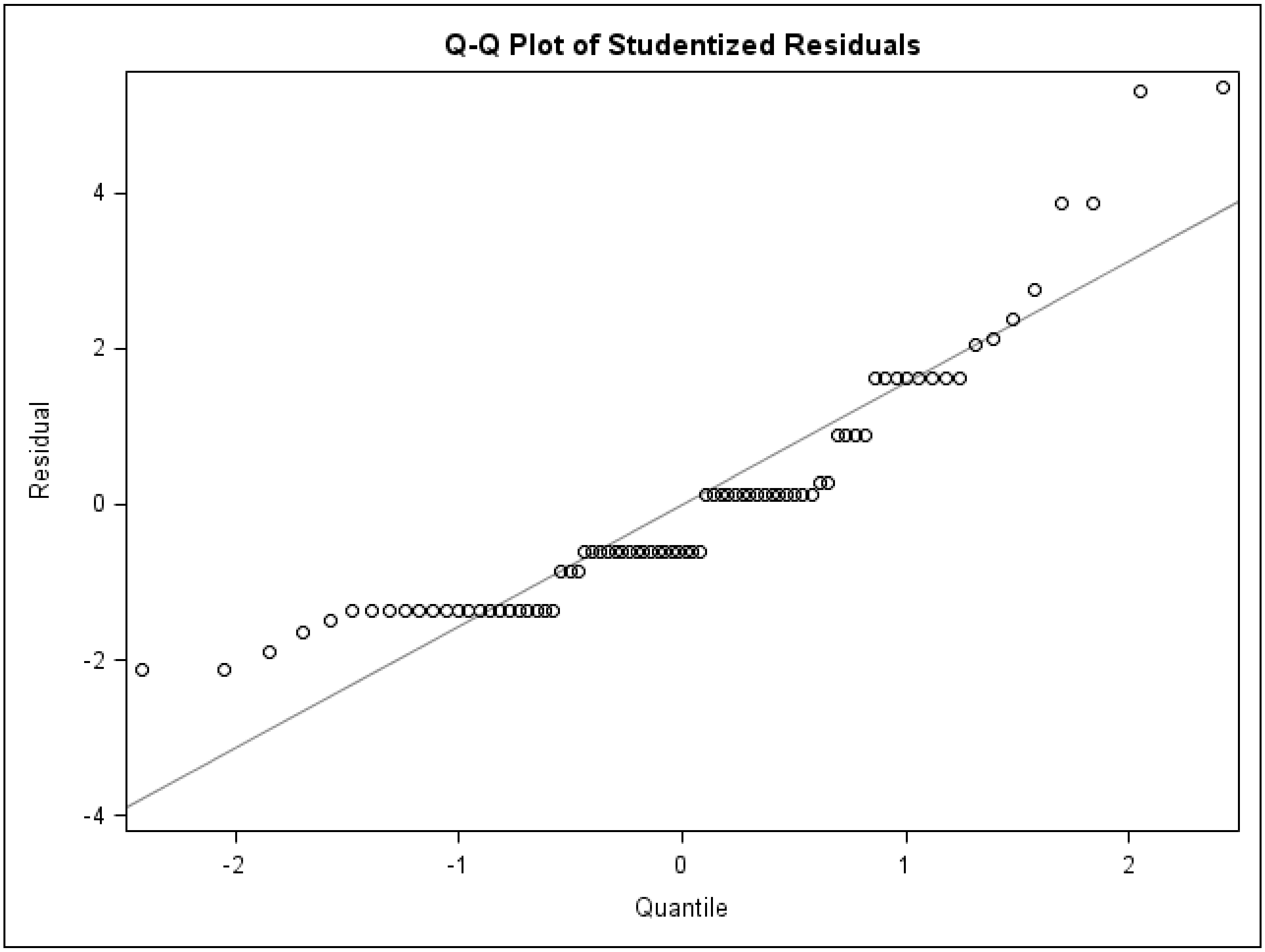


Figure E.1.3.5 Histogram of the Pearson residuals

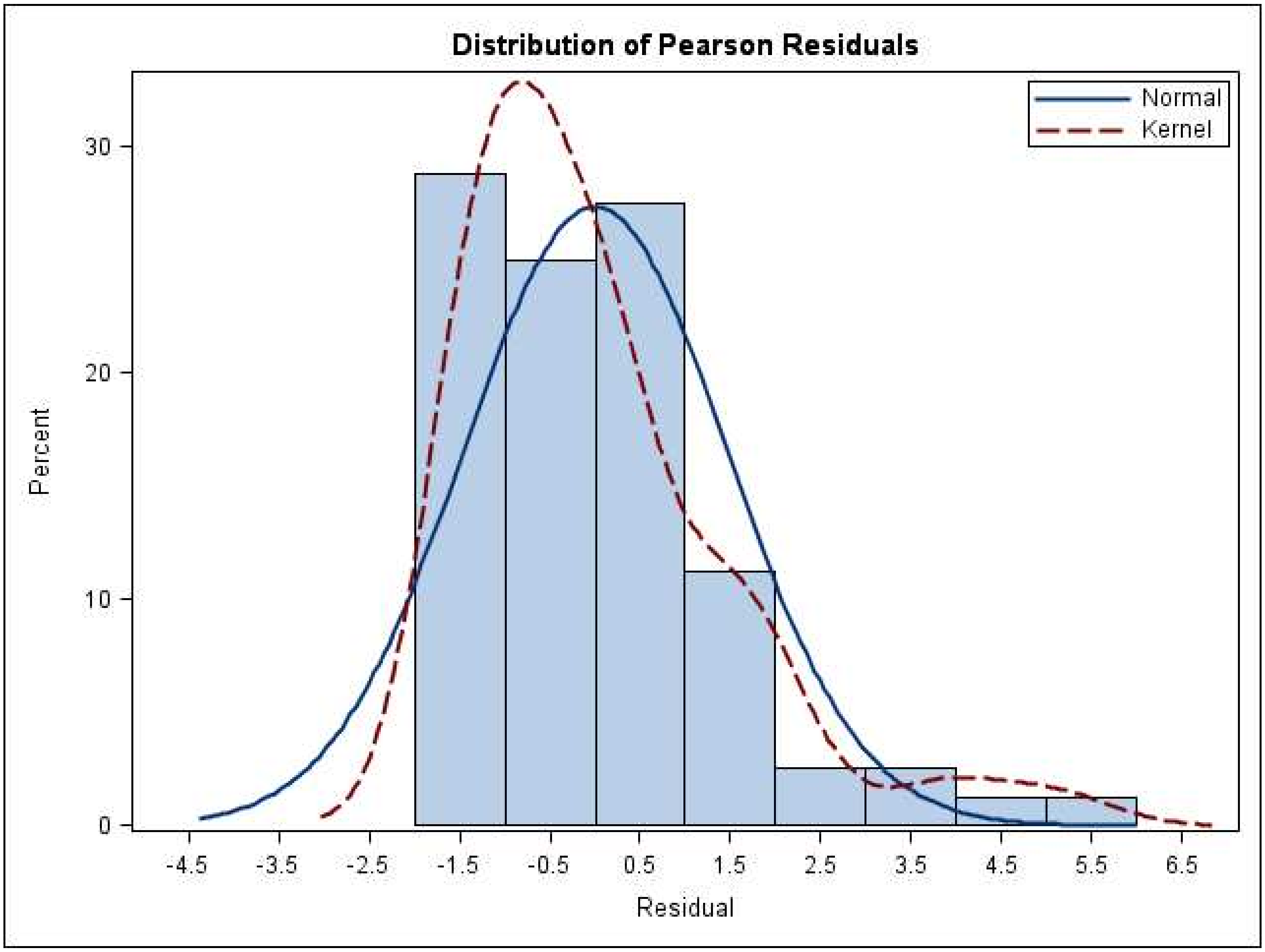
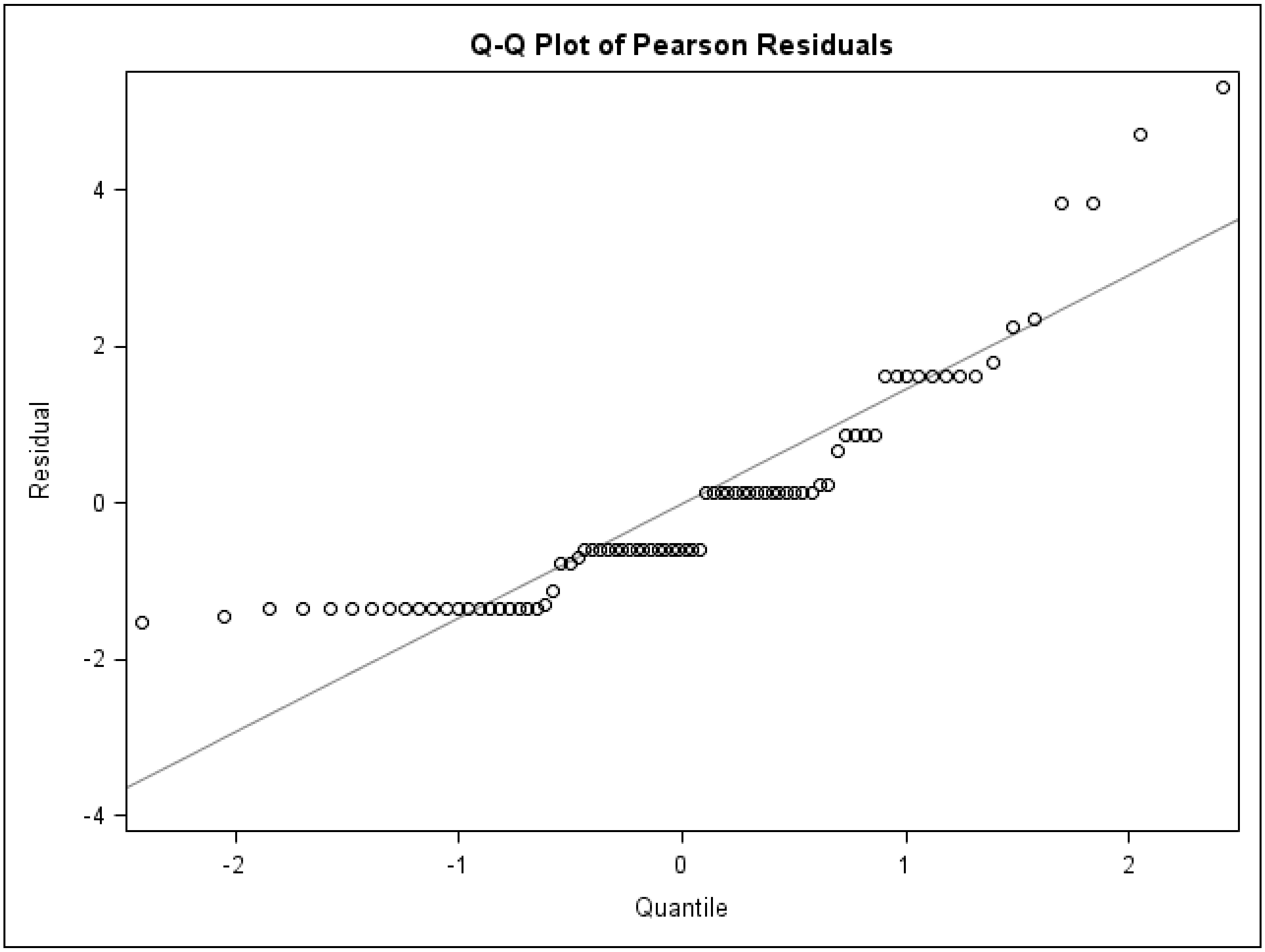


Figure E.1.3.6 Normal quantile plot of the Pearson residuals



E.1.4 May 2005 Model 4 Residual Plots

Figure E.1.4.1 Histogram of the raw residuals

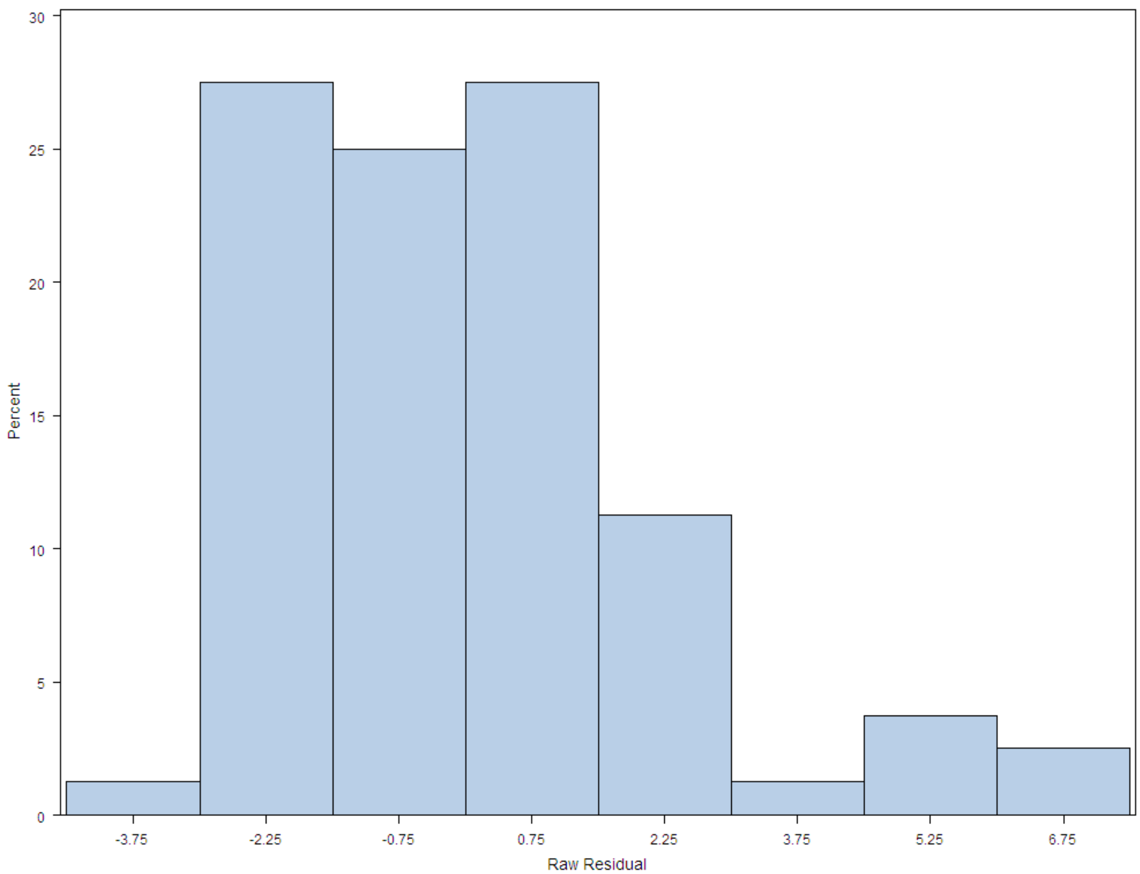


Figure E.1.4.2 Histogram of the Pearson residuals

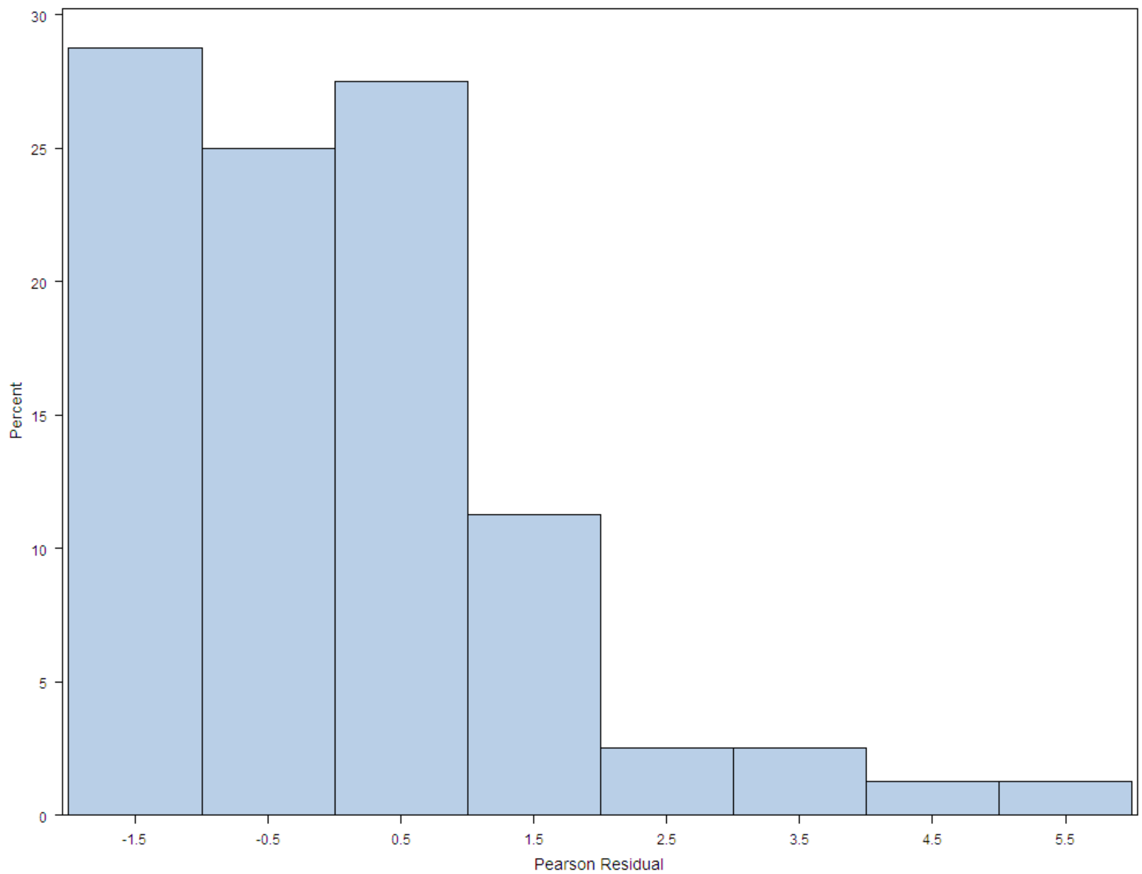


Figure E.1.4.3 Histogram of the deviance residuals

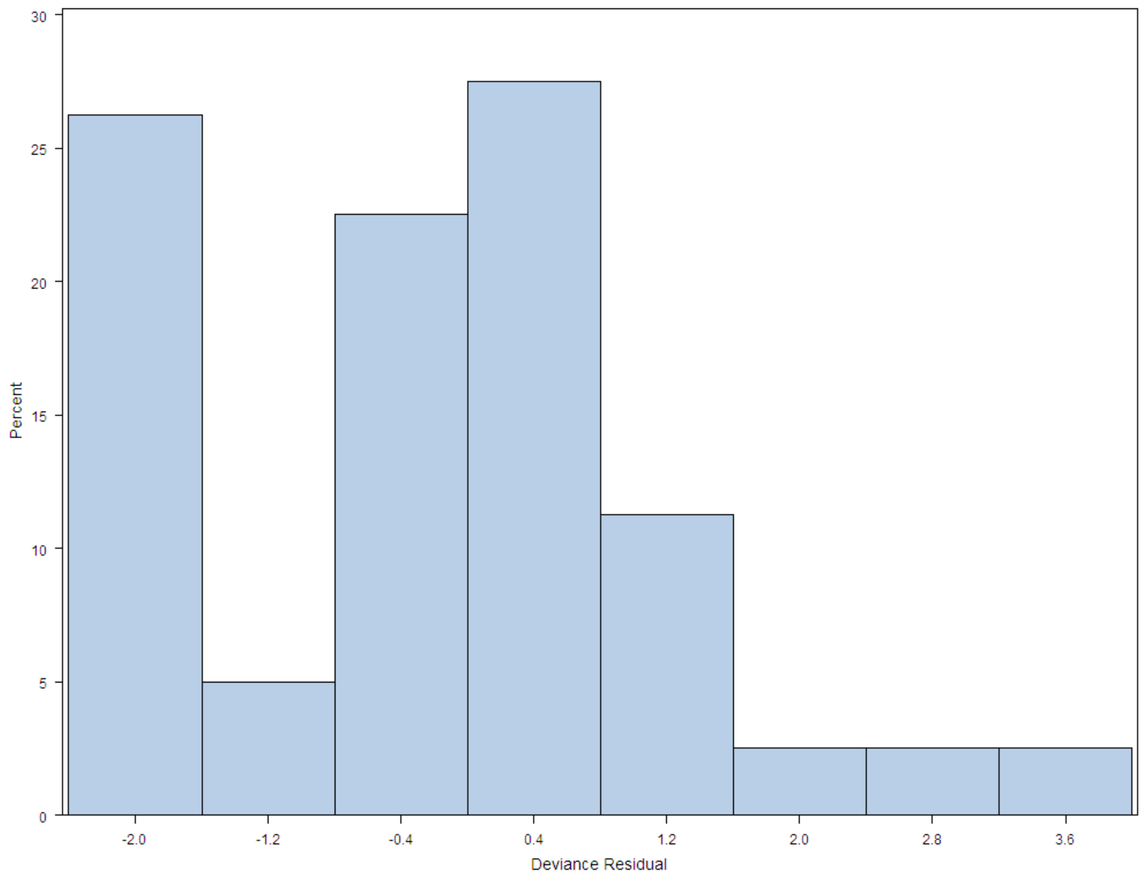


Figure E.1.4.4 Histogram of the likelihood residuals

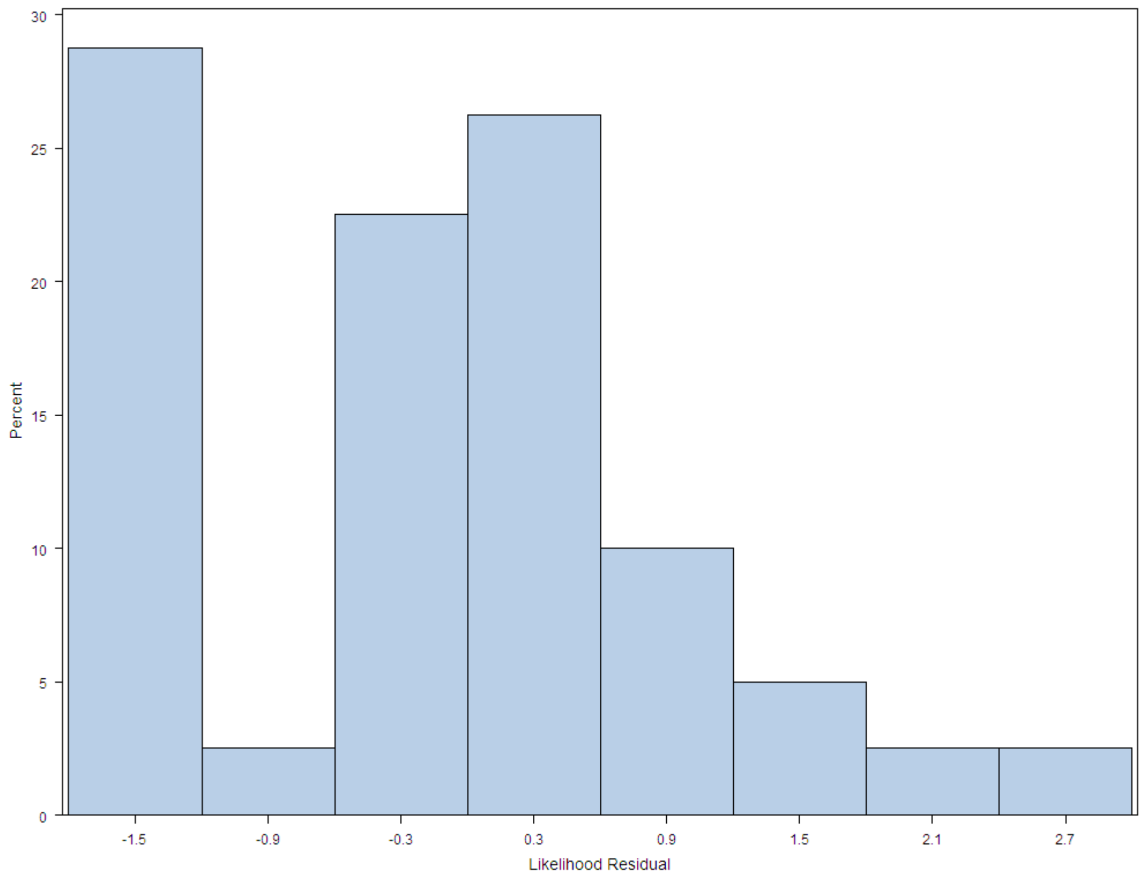


Figure E.1.4.5 Histogram of the standardized Pearson residuals

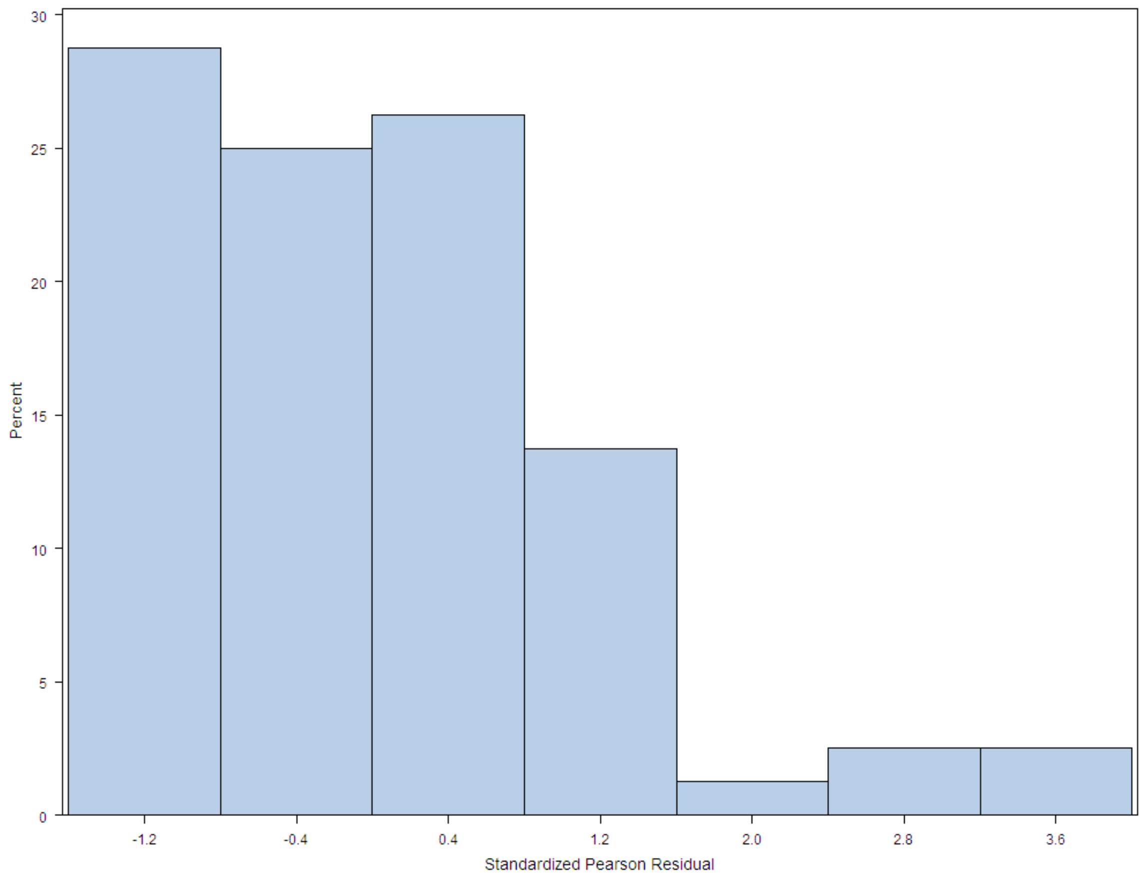
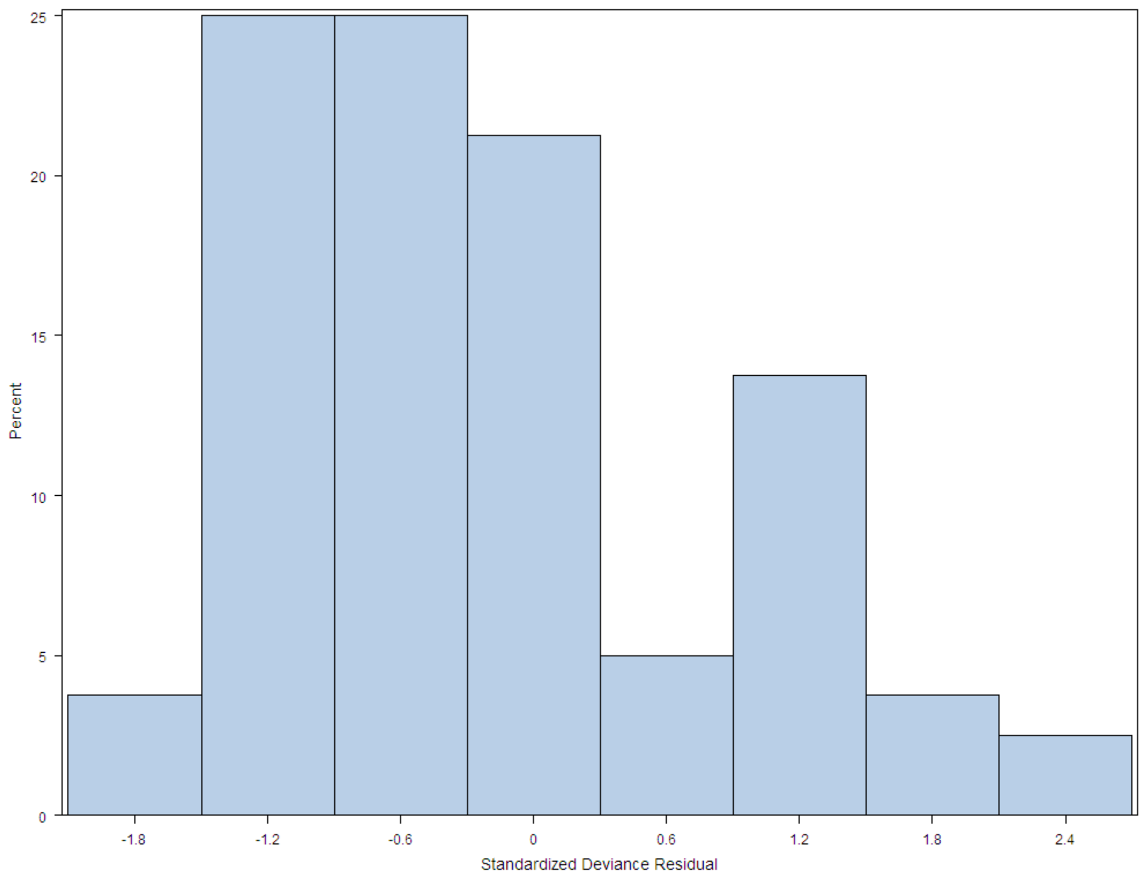


Figure E.1.4.6 Histogram of the standardized deviance residuals



E.1.5 May 2005 Model 5 Residual Plots

Figure E.1.5.1 Histogram of the raw residuals

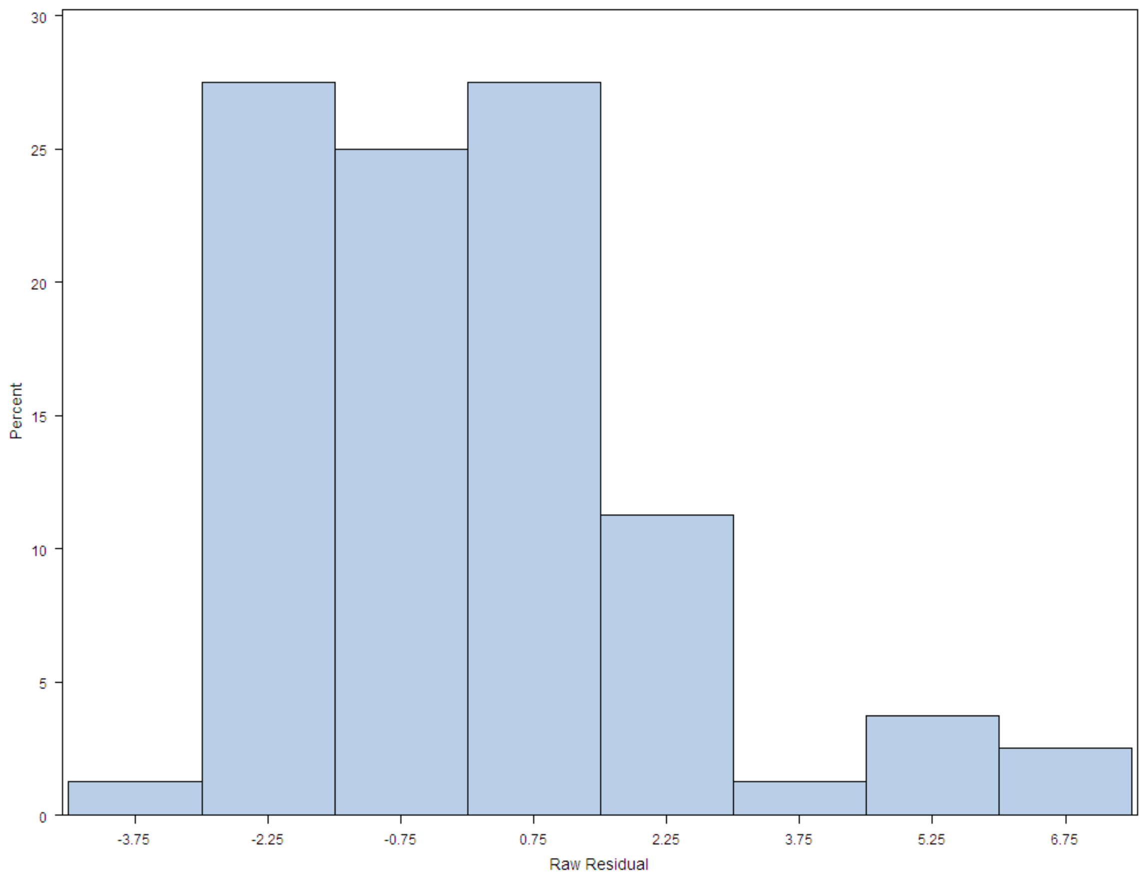


Figure E.1.5.2 Histogram of the Pearson residuals

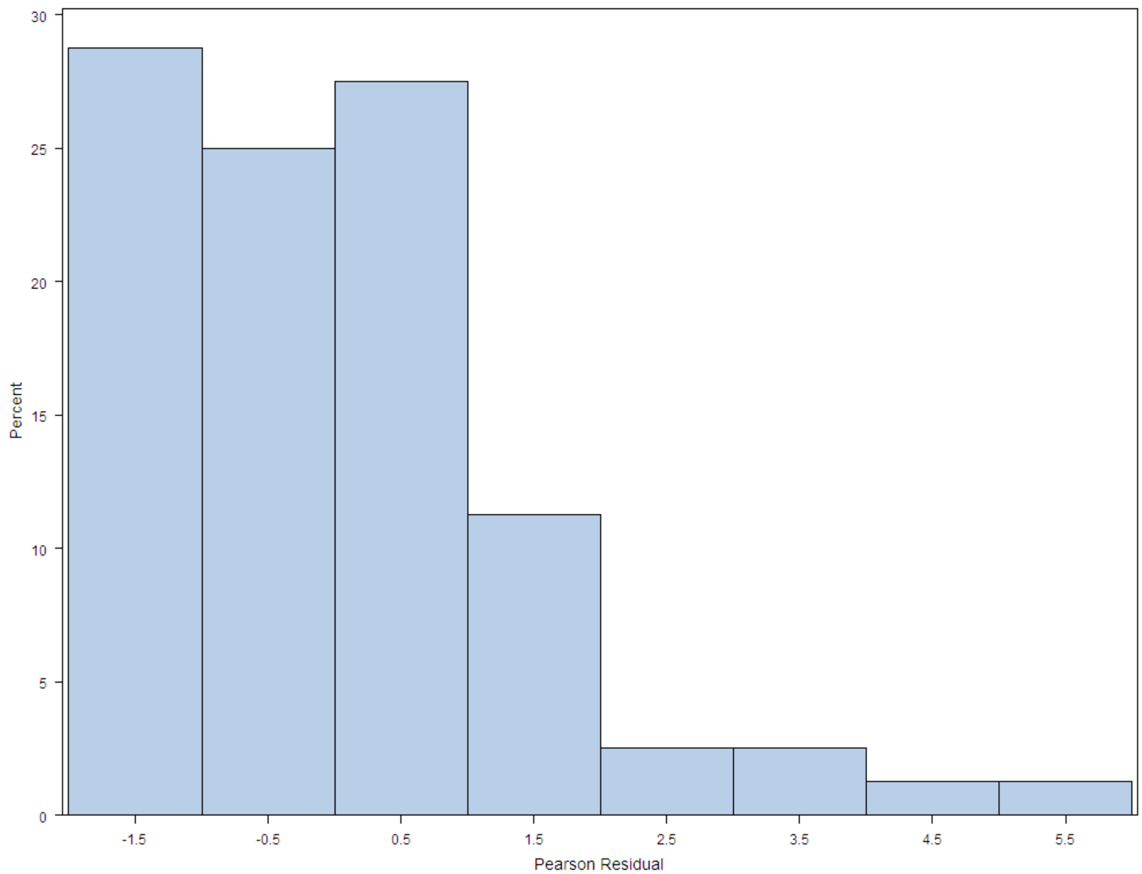


Figure E.1.5.3 Histogram of the deviance residuals

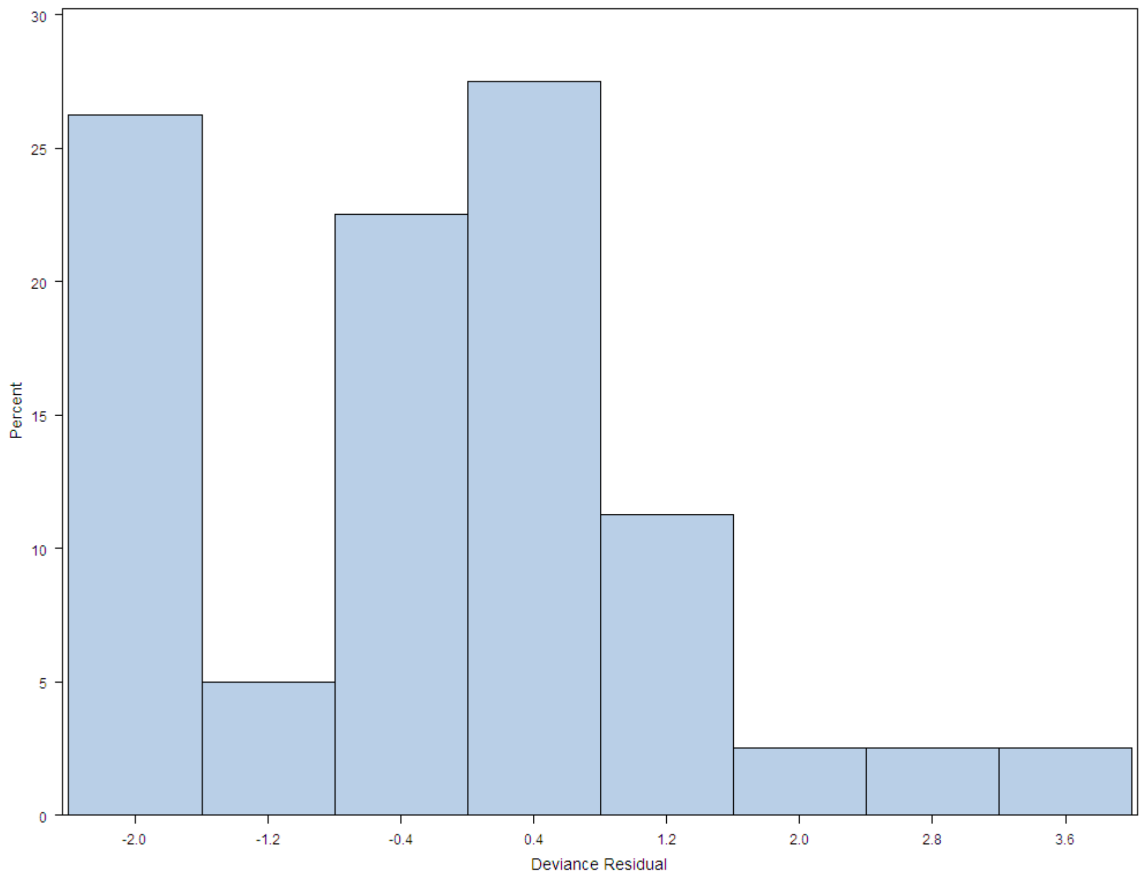


Figure E.1.5.4 Histogram of the likelihood residuals

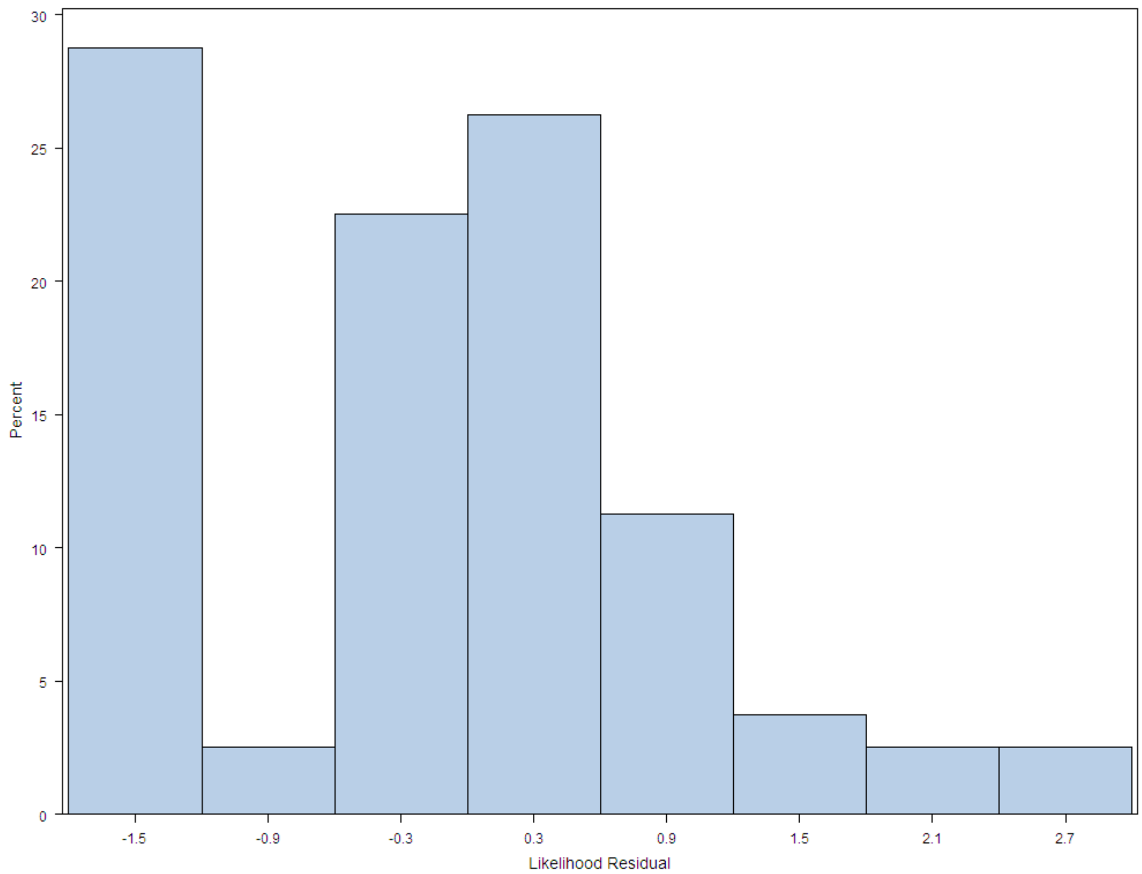


Figure E.1.5.5 Histogram of the standardized Pearson residuals

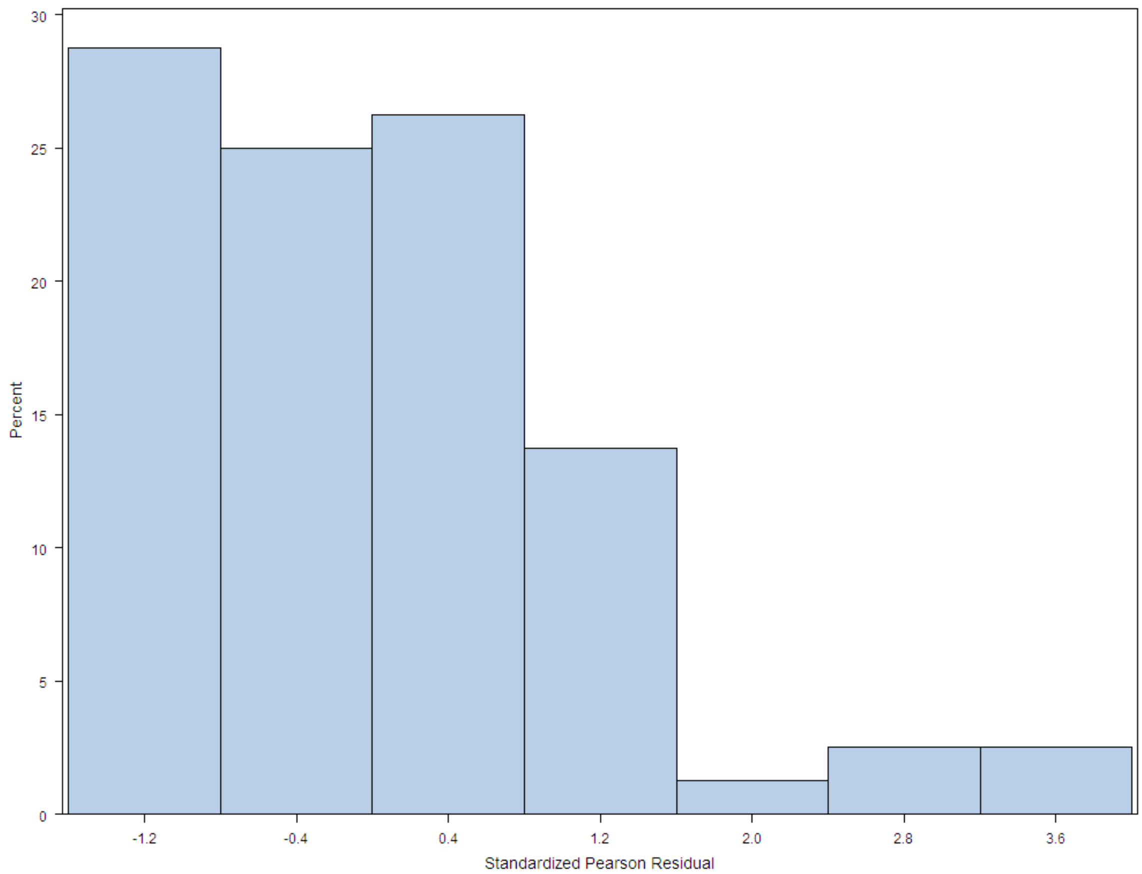
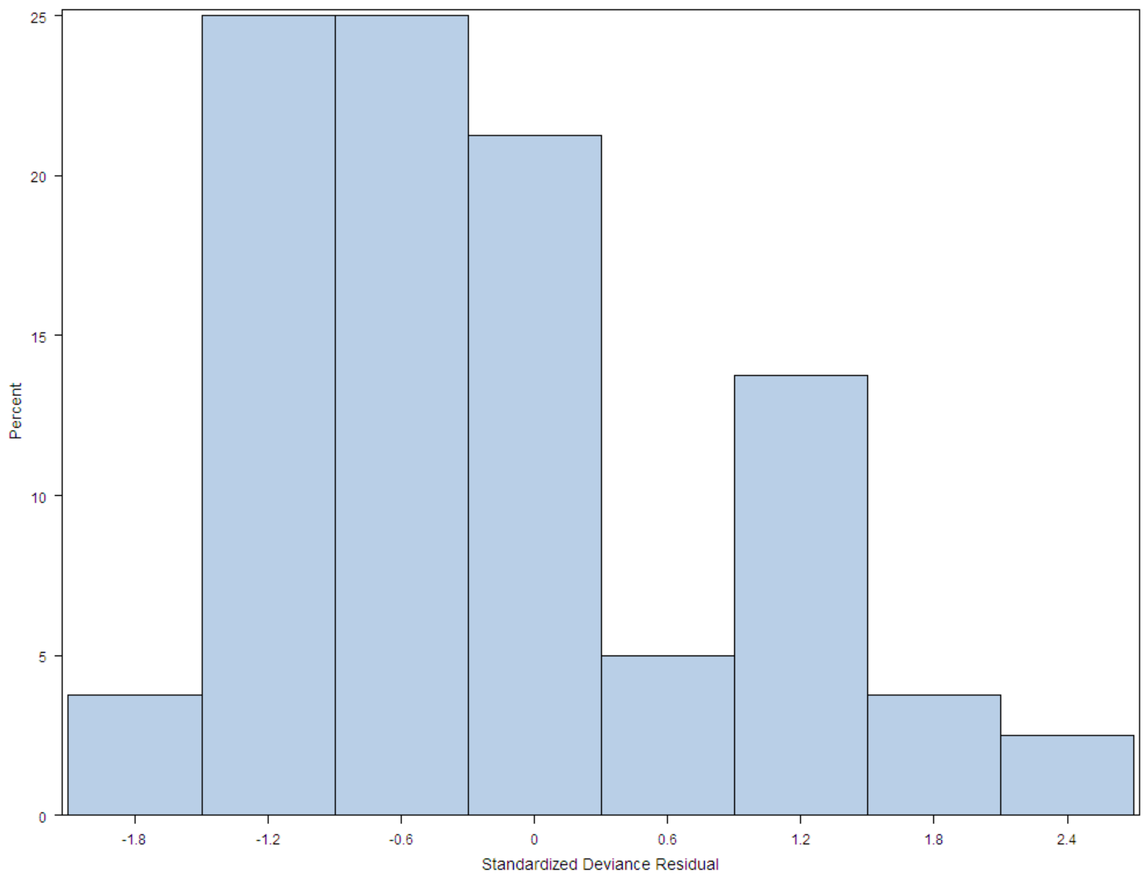


Figure E.1.5.6 Histogram of the standardized deviance residuals



E.1.6 May 2005 Model 6 Residual Plots

Figure E.1.6.1 Histogram of the raw residuals

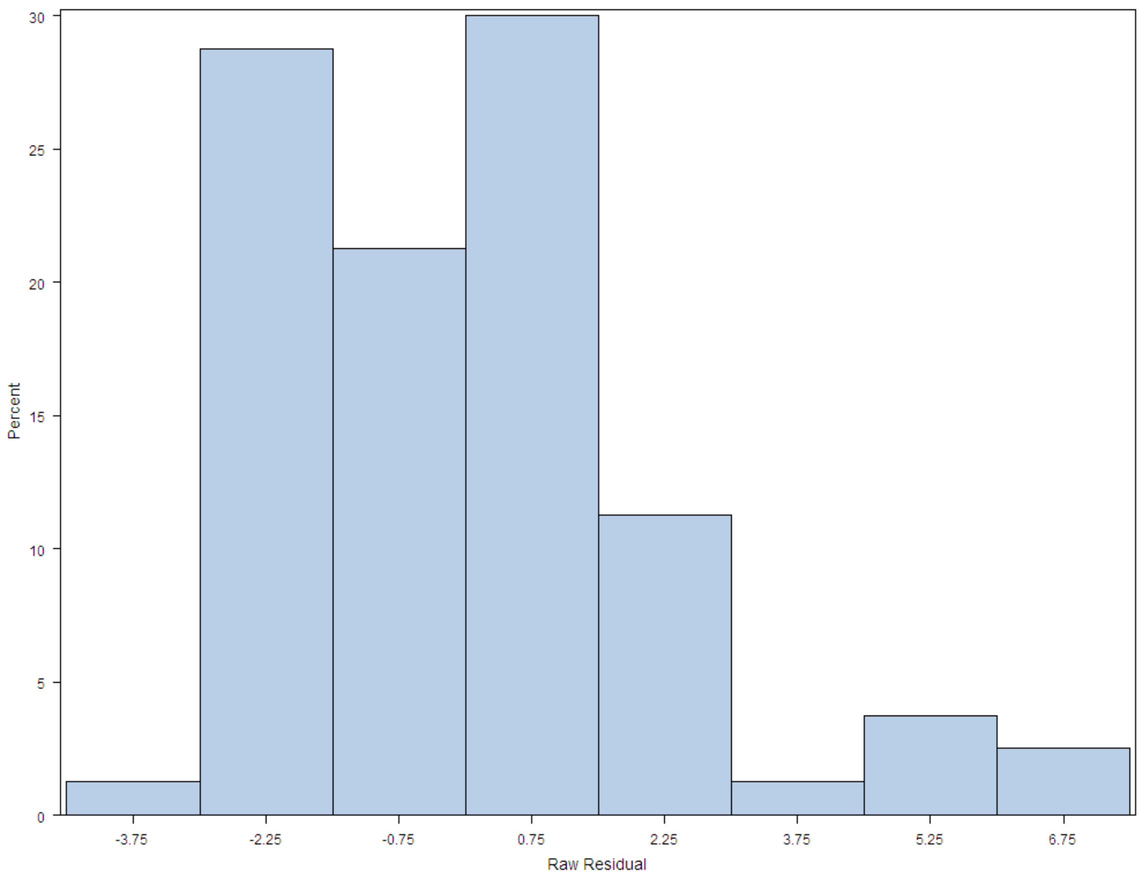
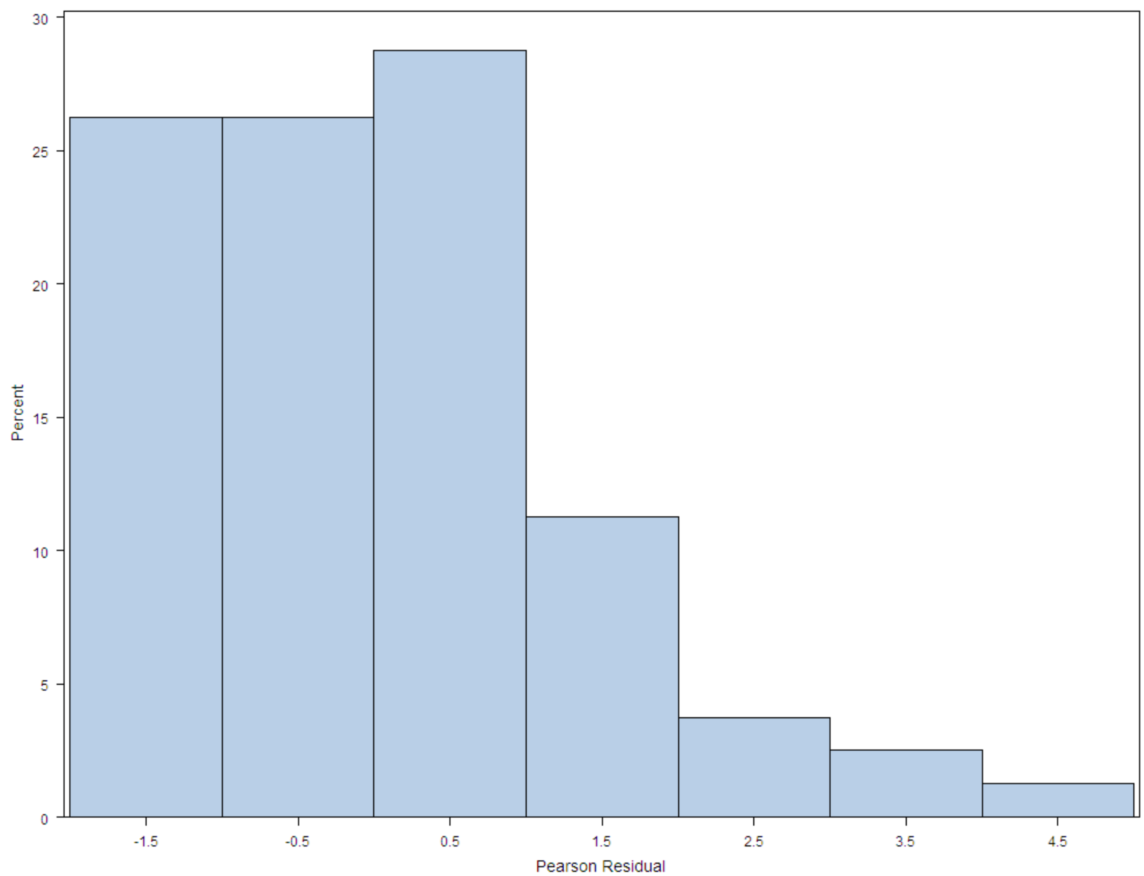


Figure E.1.6.2 Histogram of the Pearson residuals



E.1.7 May 2005 Model 7 Residual Plots

Figure E.1.7.1 Histogram of the raw residuals

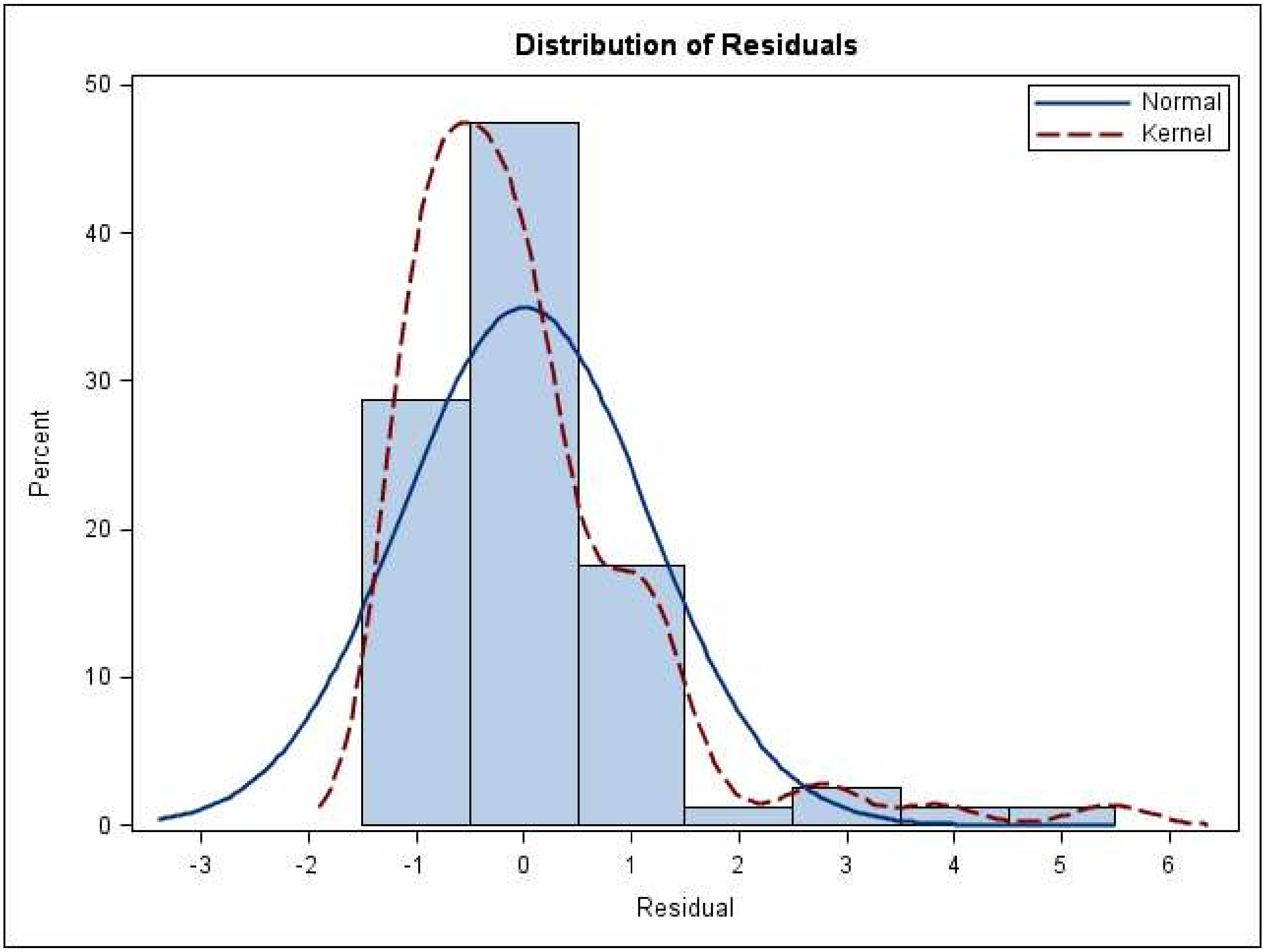


Figure E.1.7.2 Normal quantile plot of the raw residuals

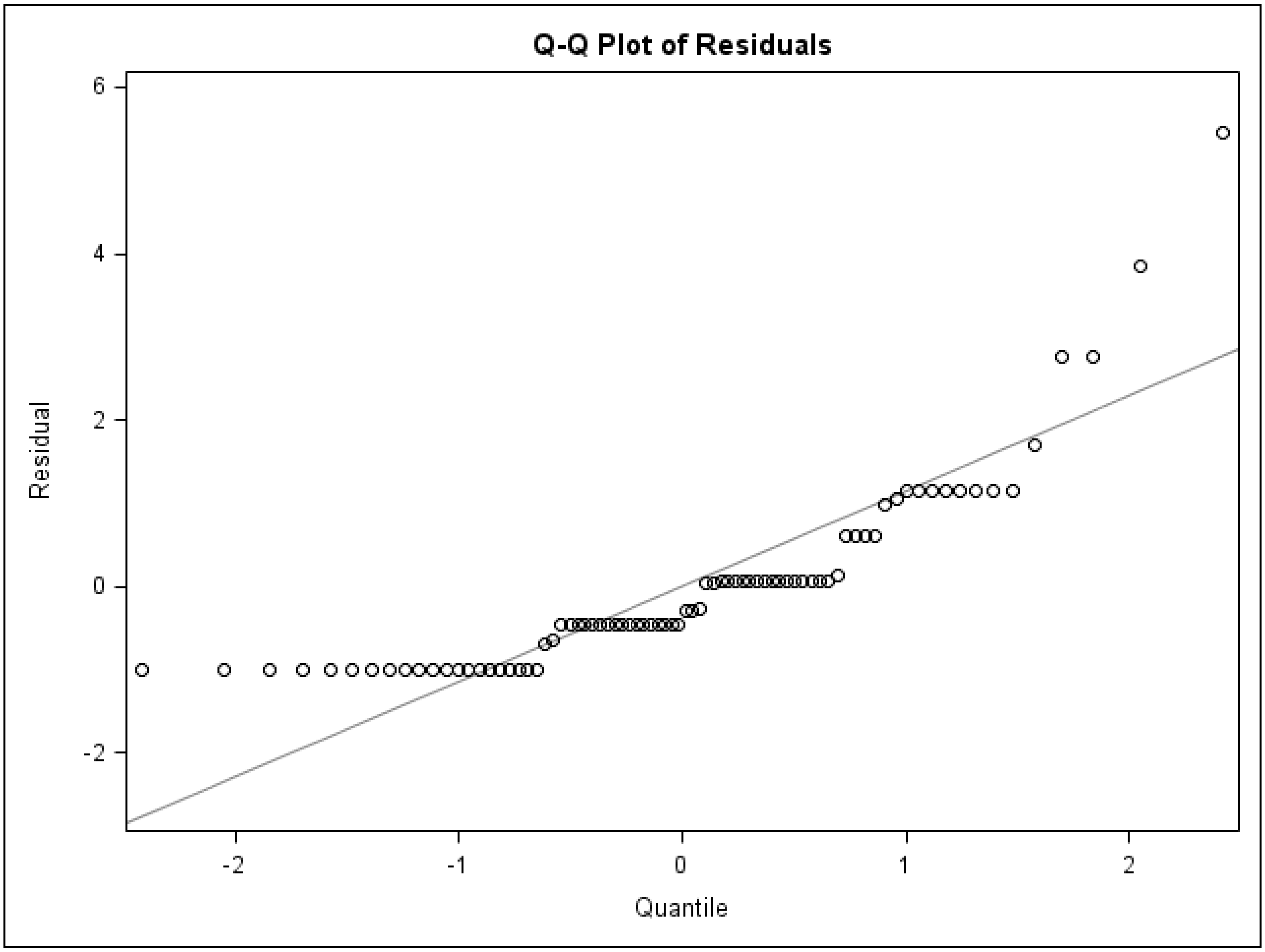


Figure E.1.7.3 Histogram of the Studentized residuals

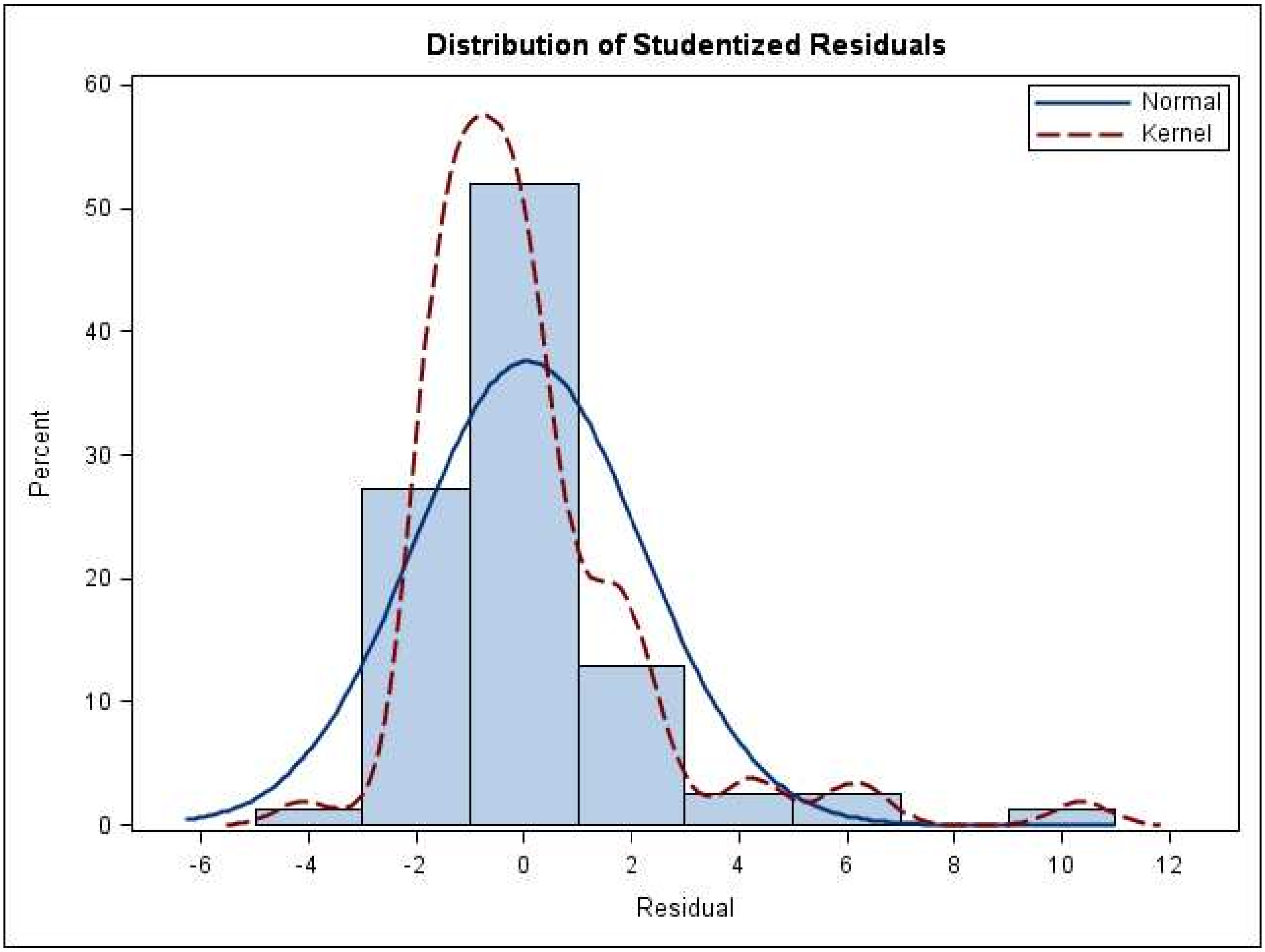


Figure E.1.7.4 Normal quantile plot of the Studentized residuals

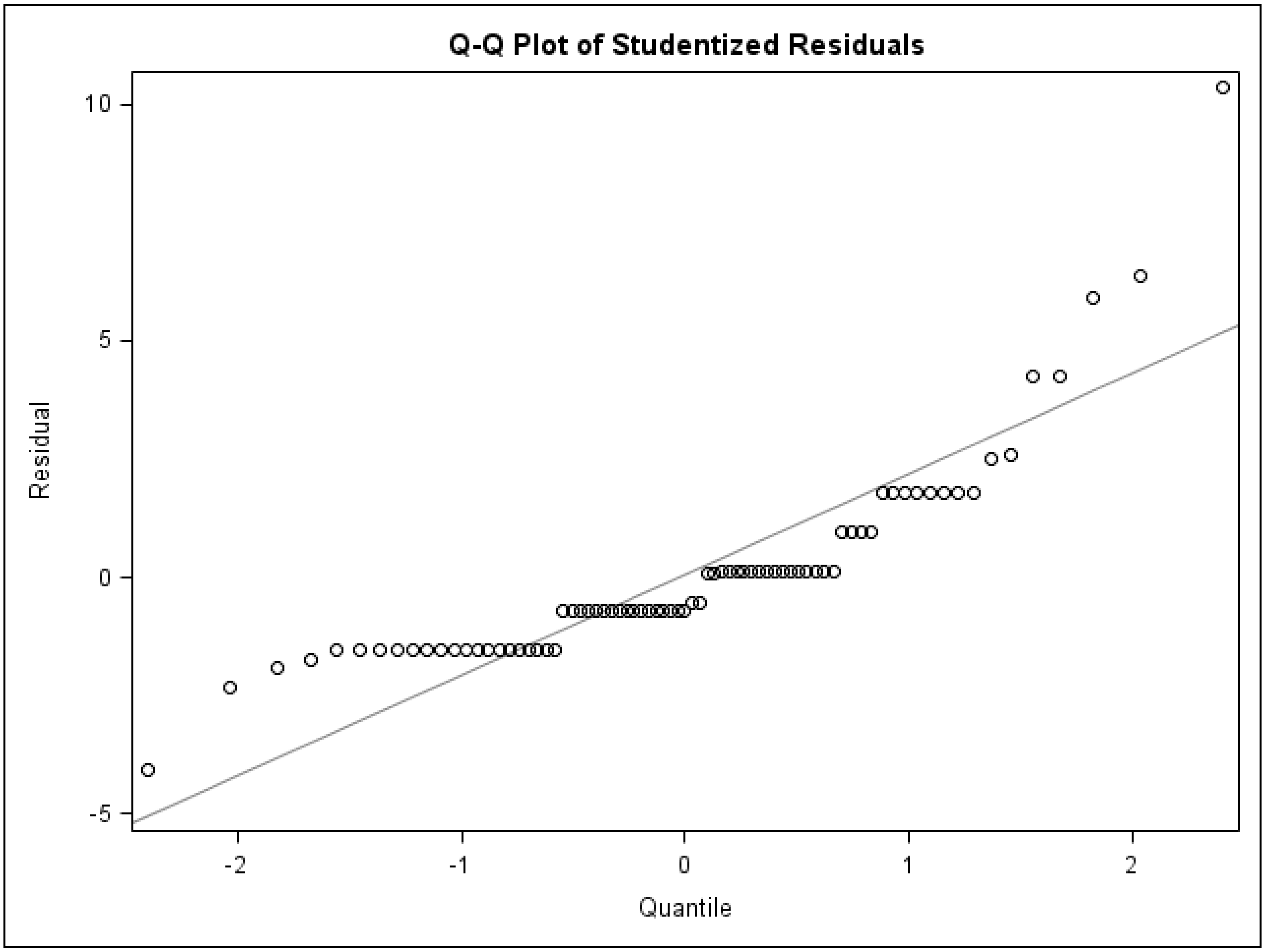


Figure E.1.7.5 Histogram of the Pearson residuals

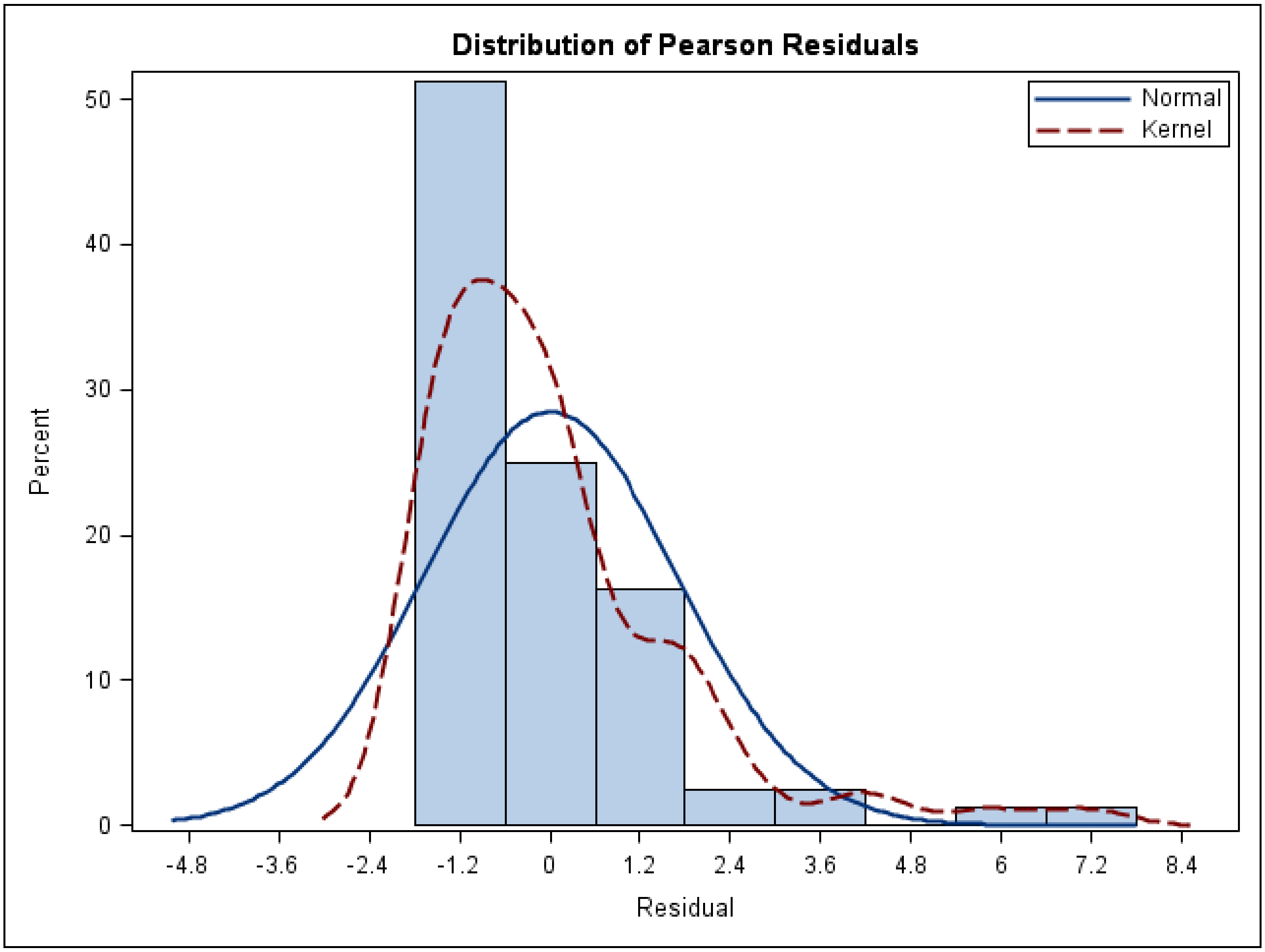
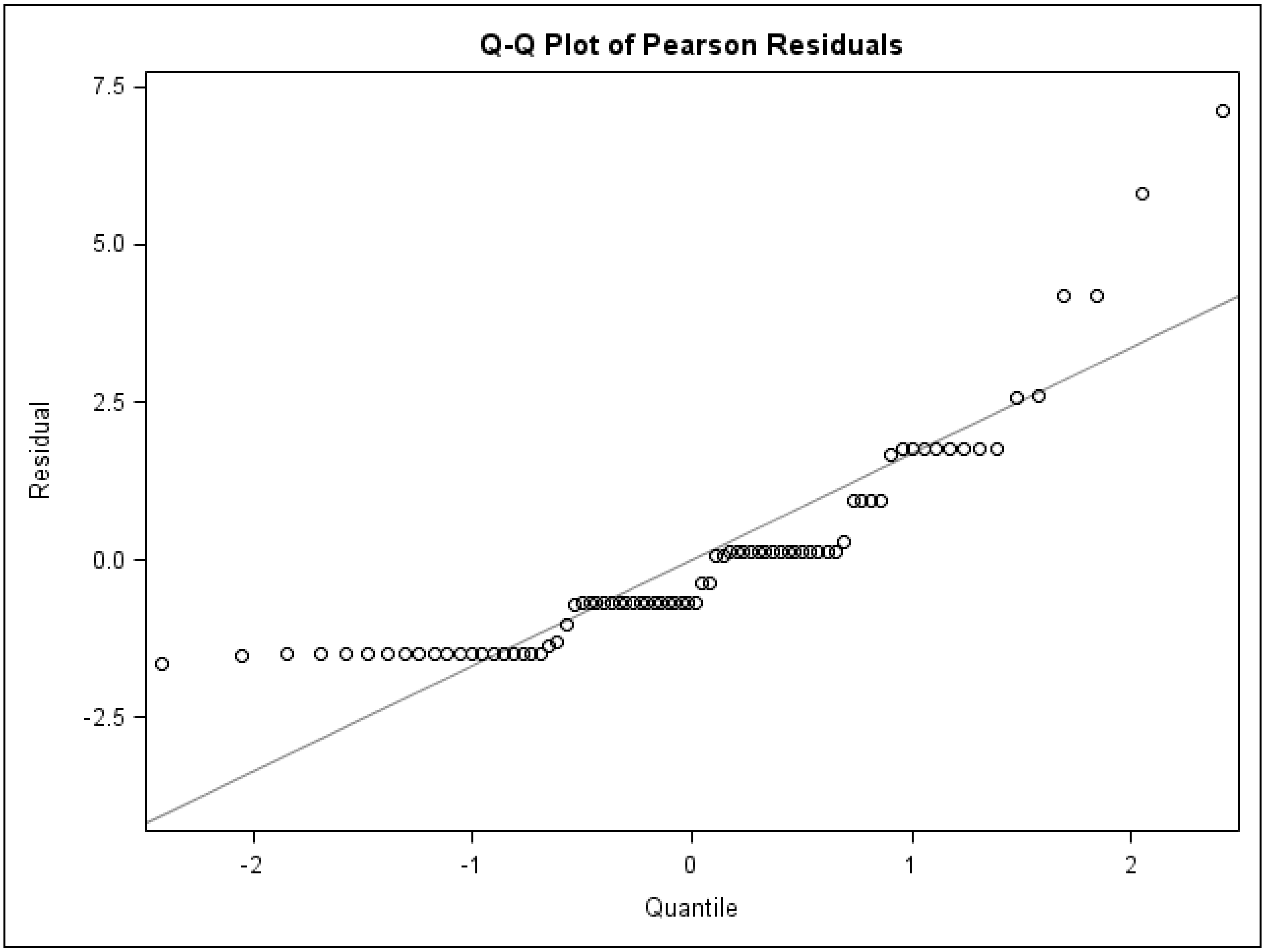
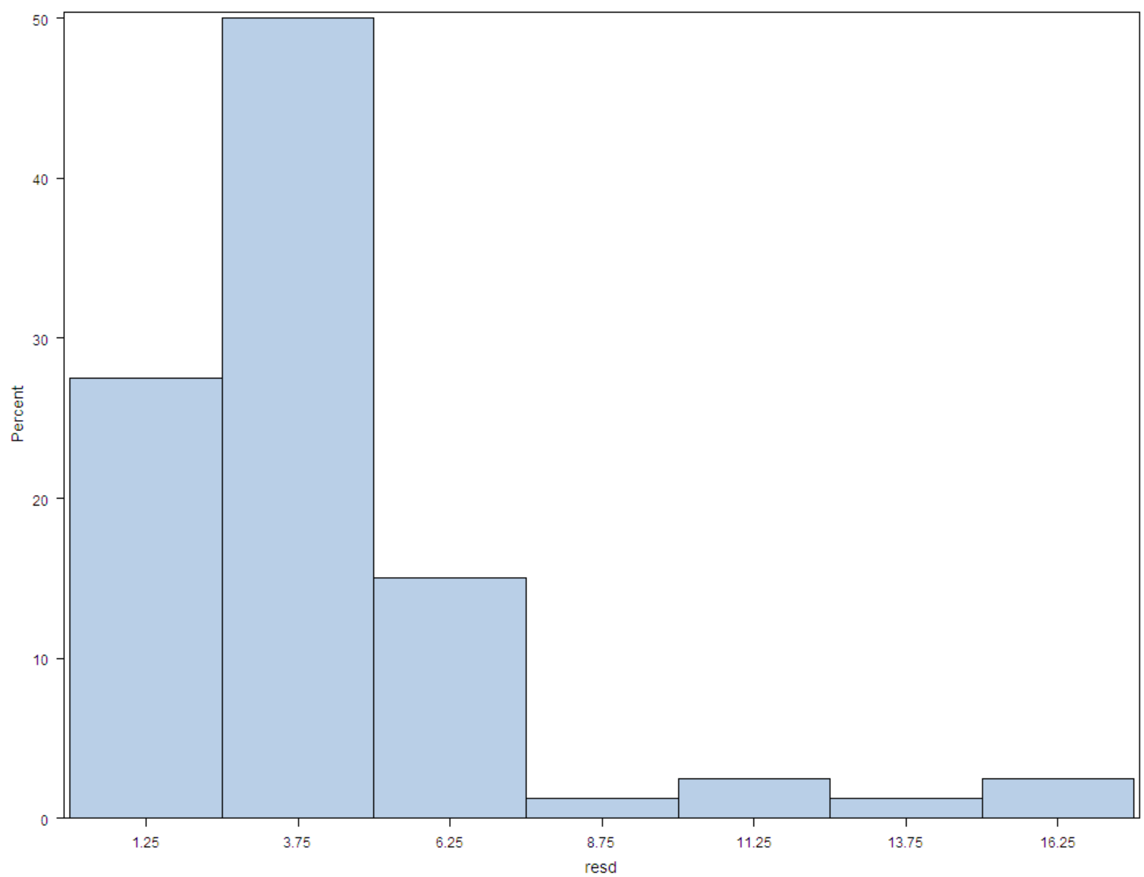


Figure E.1.7.6 Normal quantile plot of the Pearson residuals



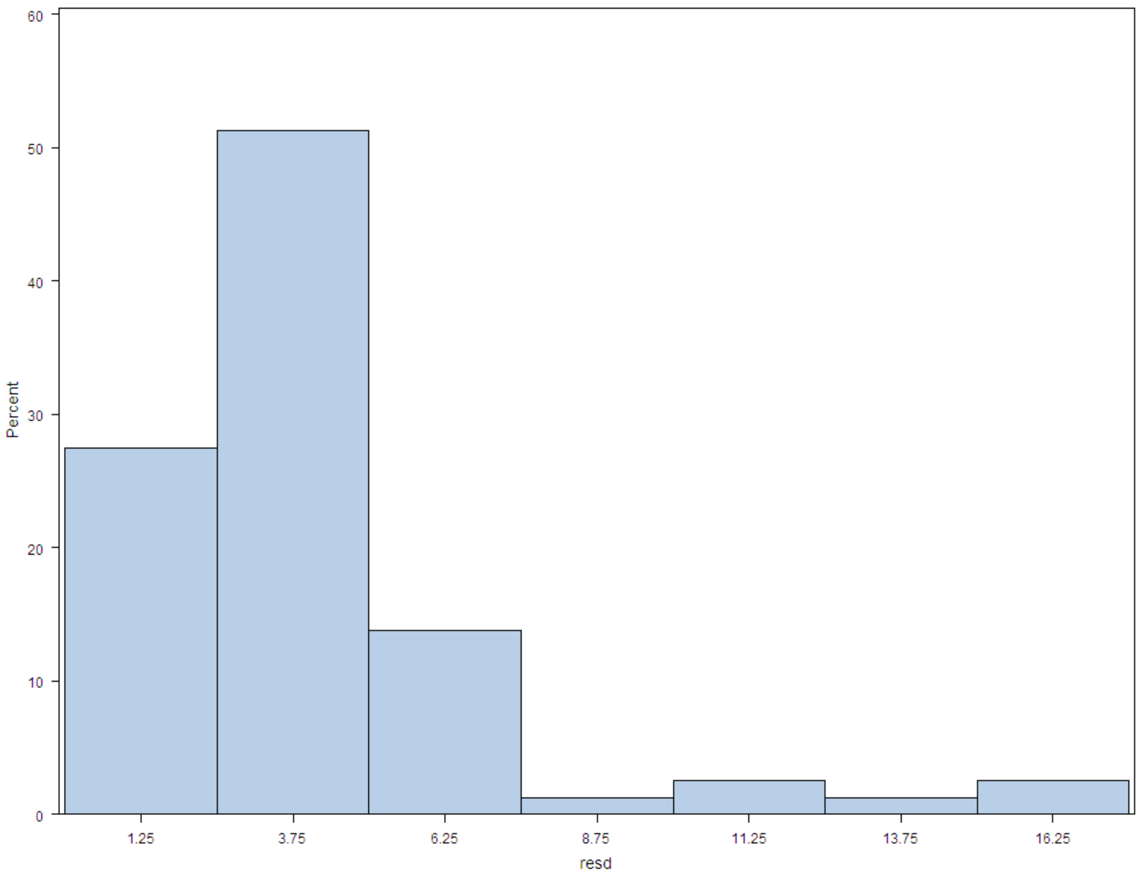
E.1.8 May 2005 Model 8 Residual Plots

Figure E.1.8.1 Histogram of the raw residuals



E.1.9 May 2005 Model 9 Residual Plots

Figure E.1.9.1 Histogram of the raw residuals



E.2 July 2005 Residual Plots

E.2.1 July 2005 Model 1 Residual Plots

Figure E.2.1.1 Histogram of the raw residuals

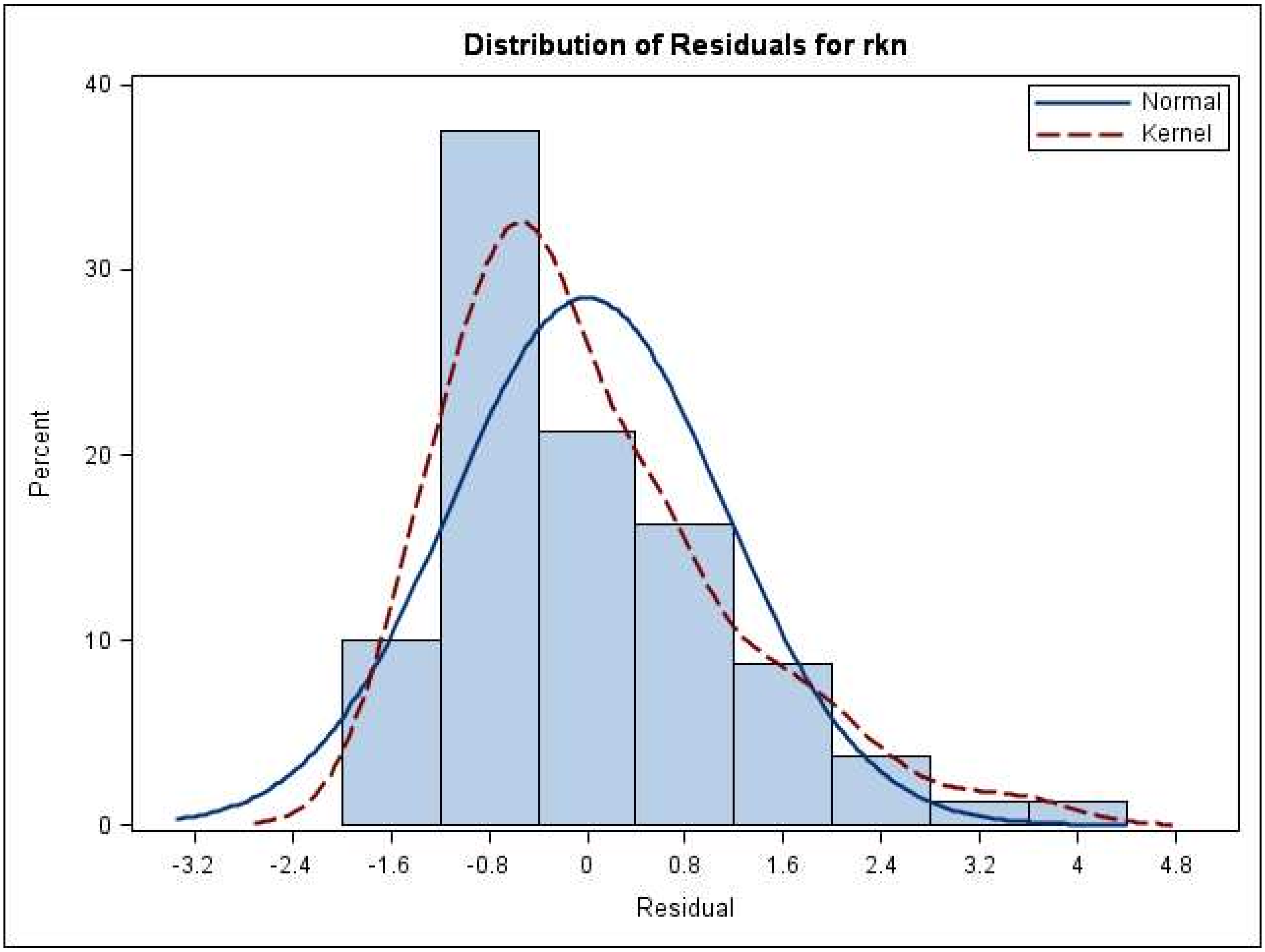


Figure E.2.1.2 Normal quantile plot of the raw residuals

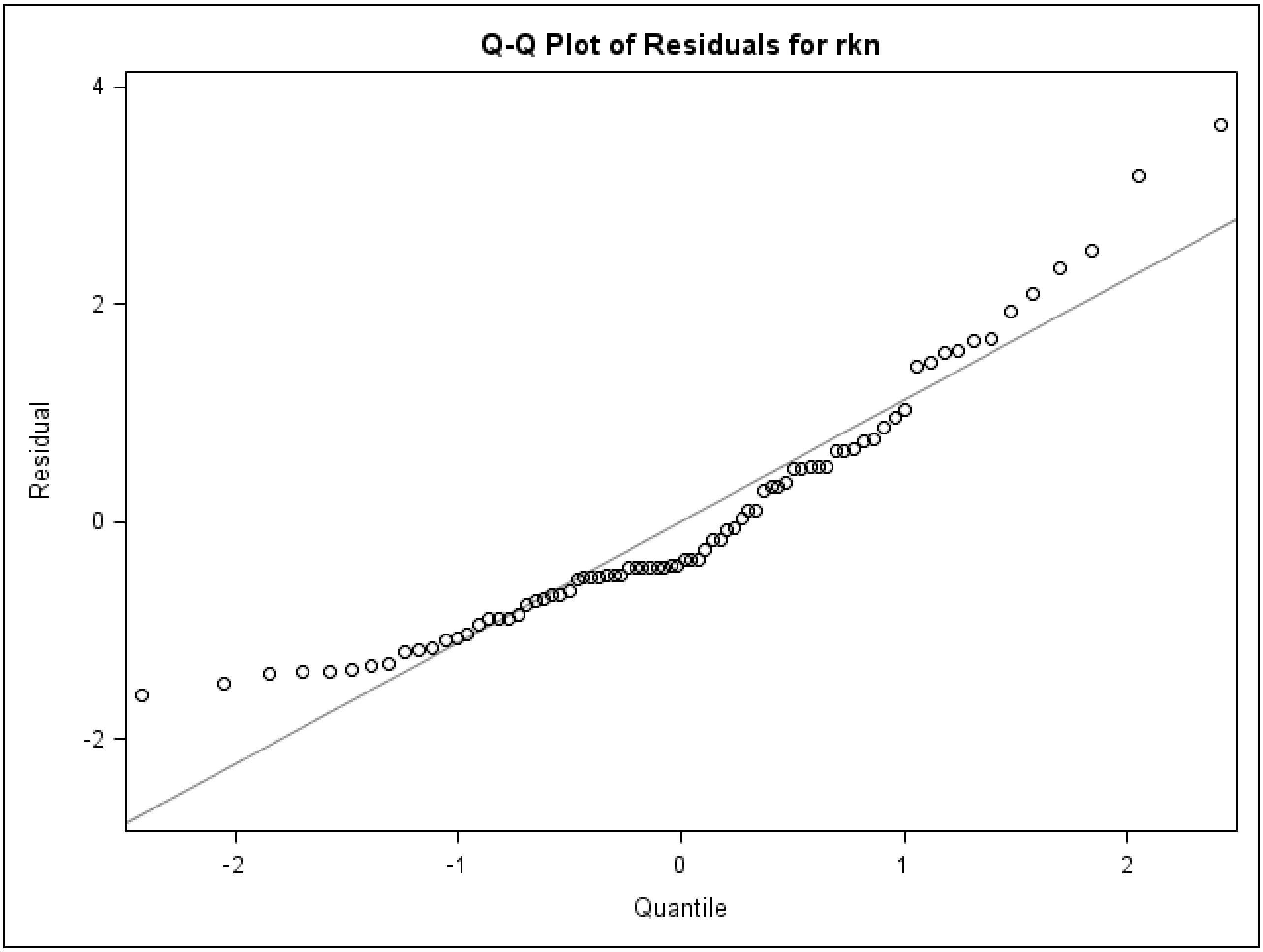


Figure E.2.1.3 Histogram of the Studentized residuals

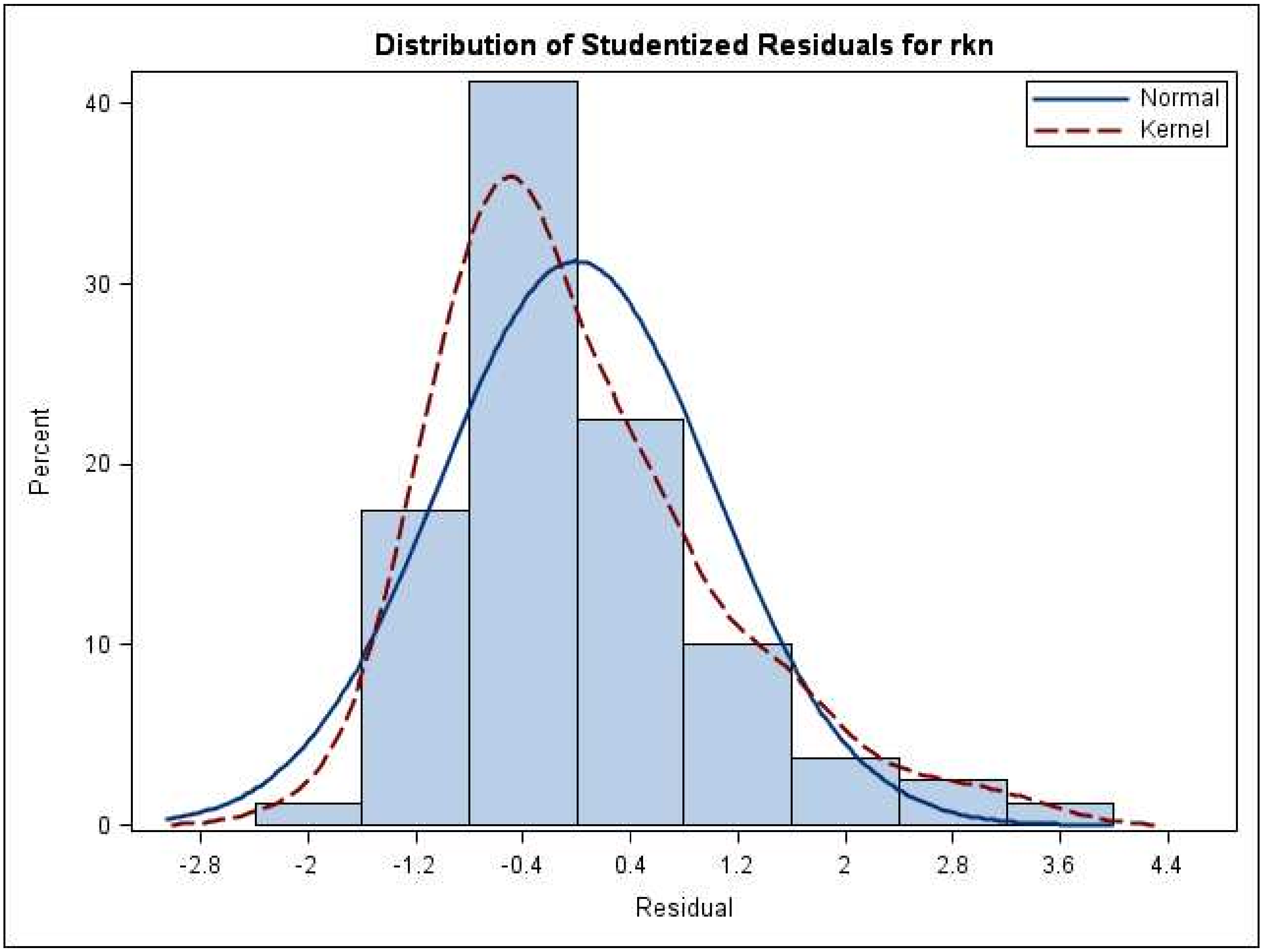


Figure E.2.1.4 Normal quantile plot of the Studentized residuals

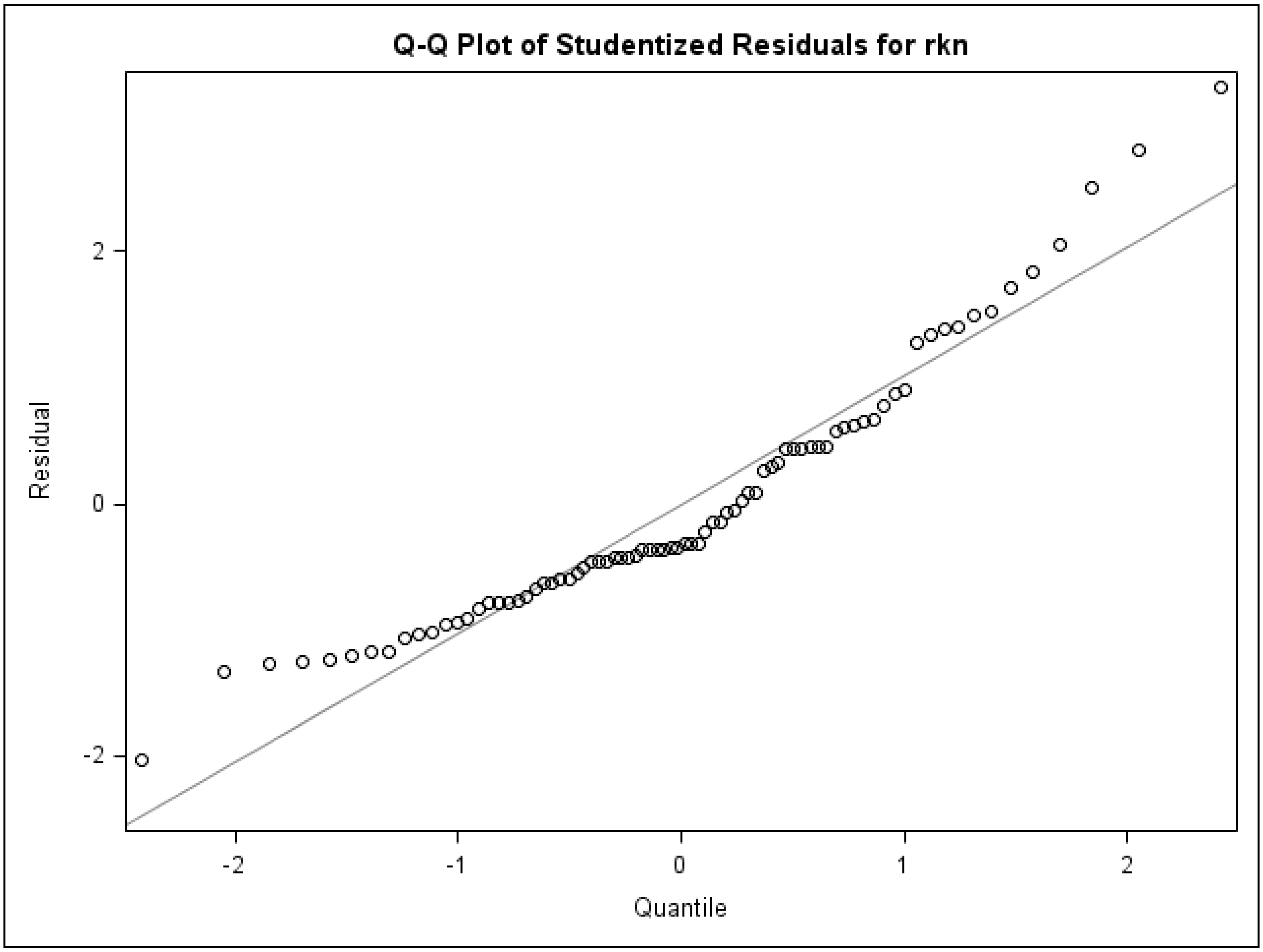


Figure E.2.1.5 Histogram of the Pearson residuals

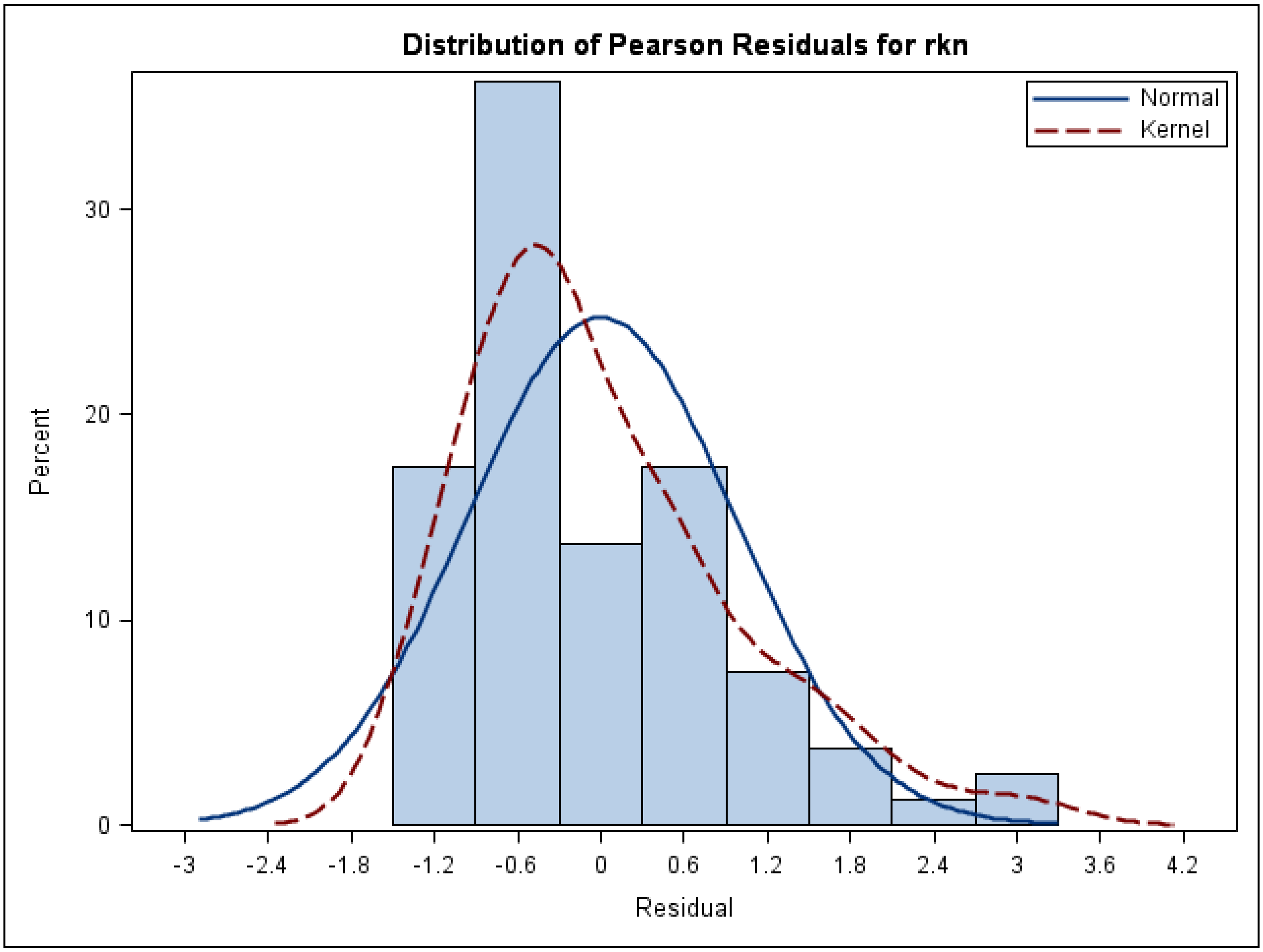
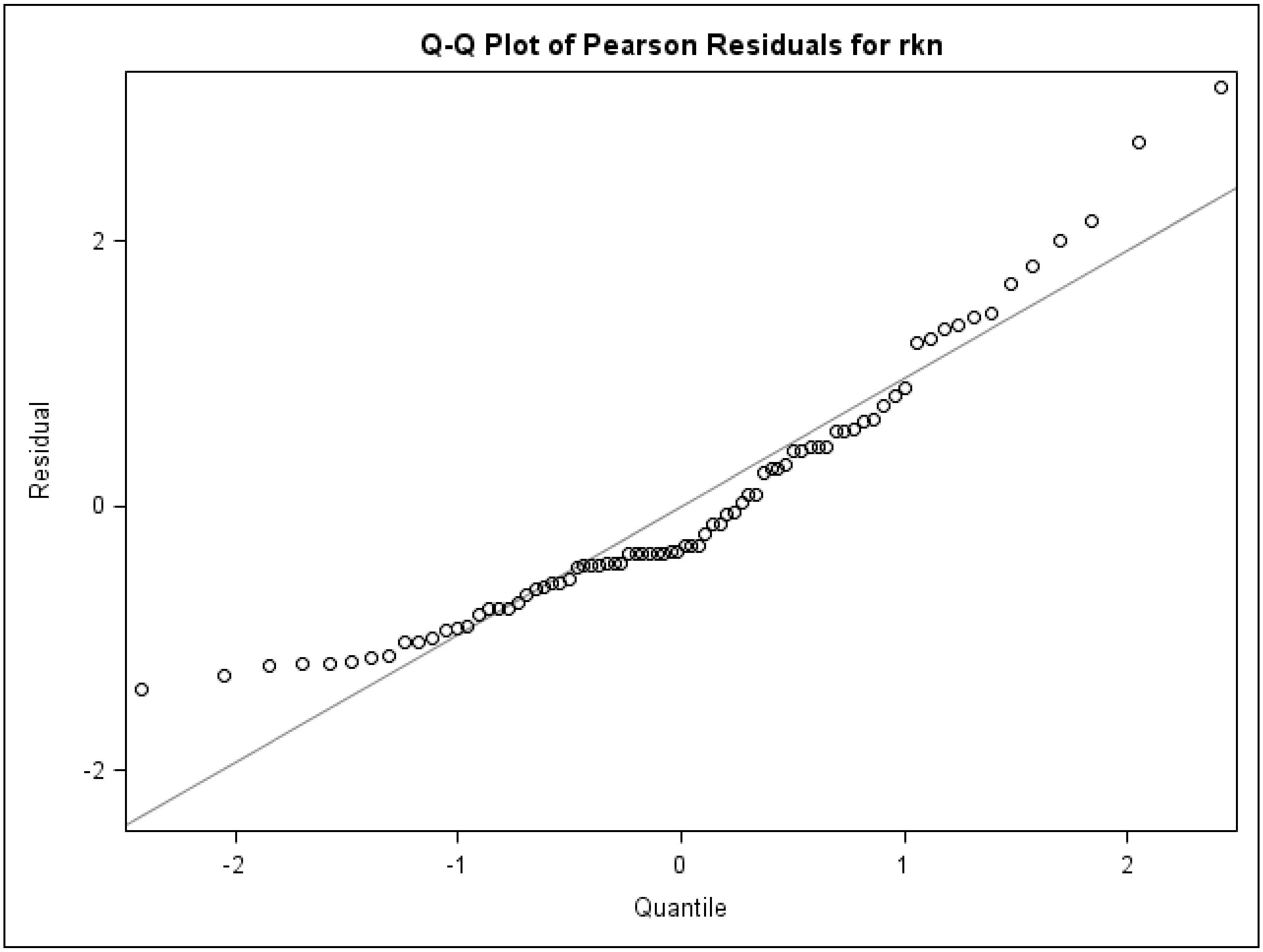


Figure E.2.1.6 Normal quantile plot of the Pearson residuals



E.2.2 July 2005 Model 2 Residual Plots

Figure E.2.2.1 Histogram of the raw residuals

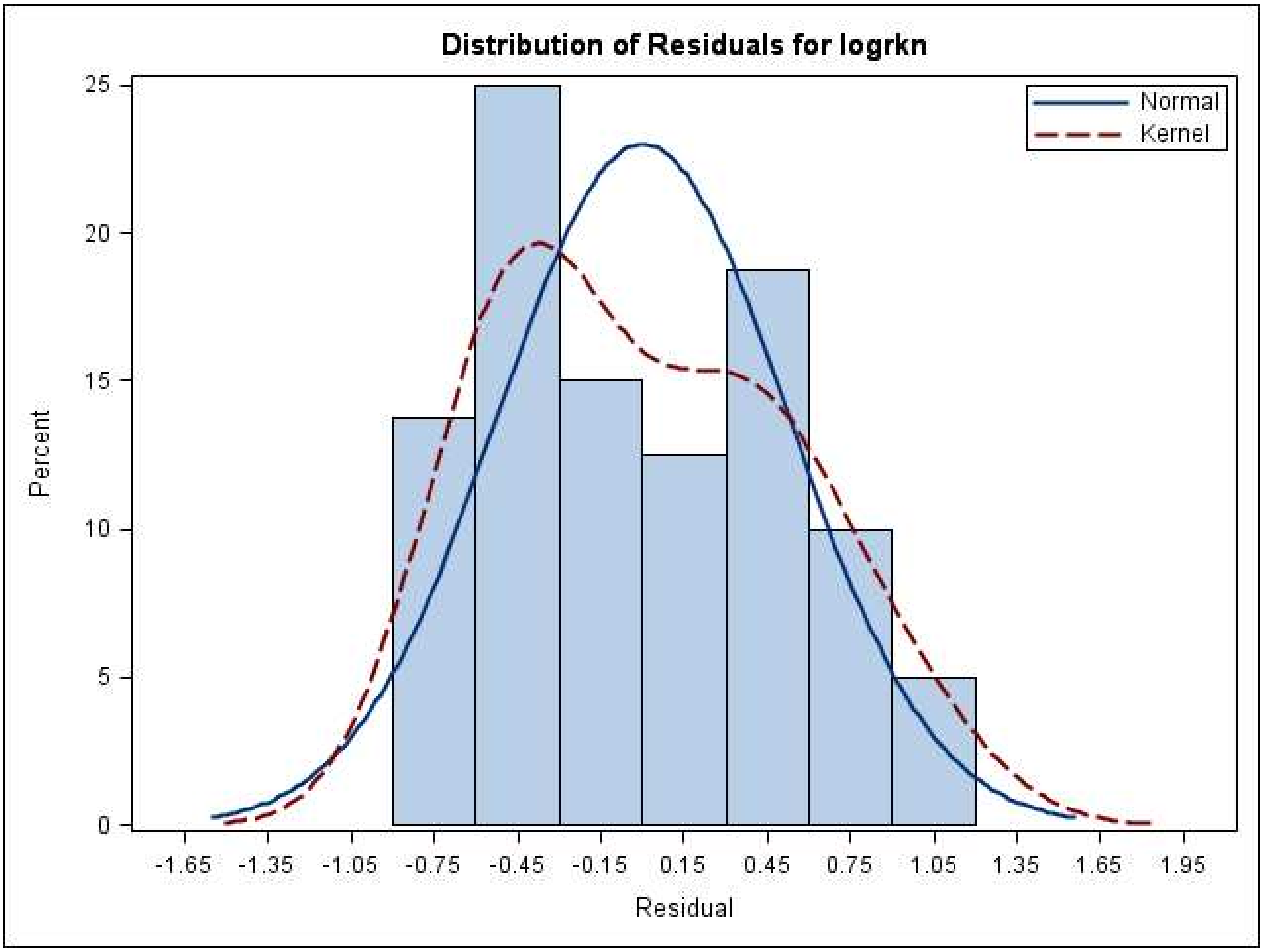


Figure E.2.2.2 Normal quantile plot of the raw residuals

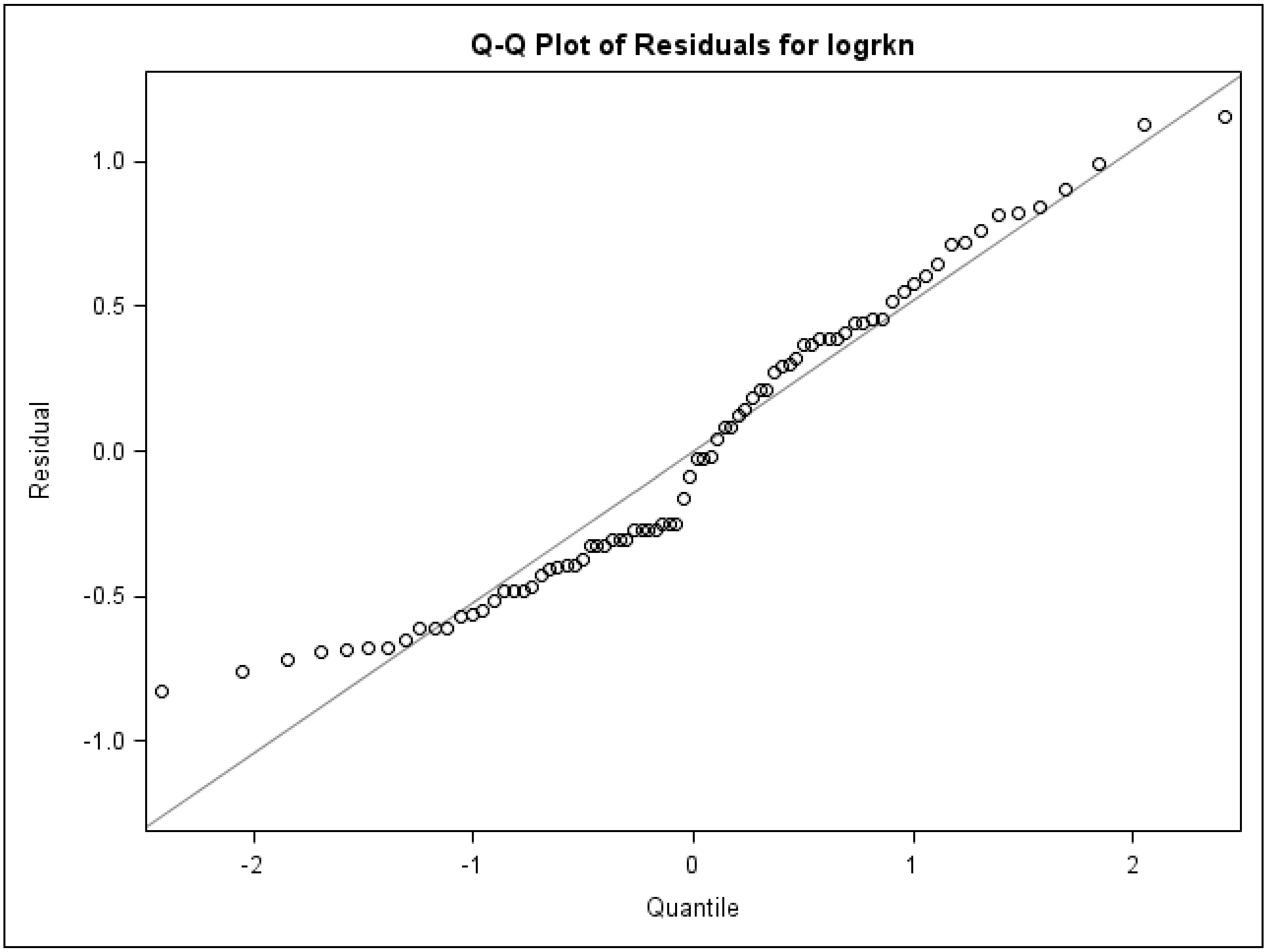


Figure E.2.2.3 Histogram of the Studentized residuals

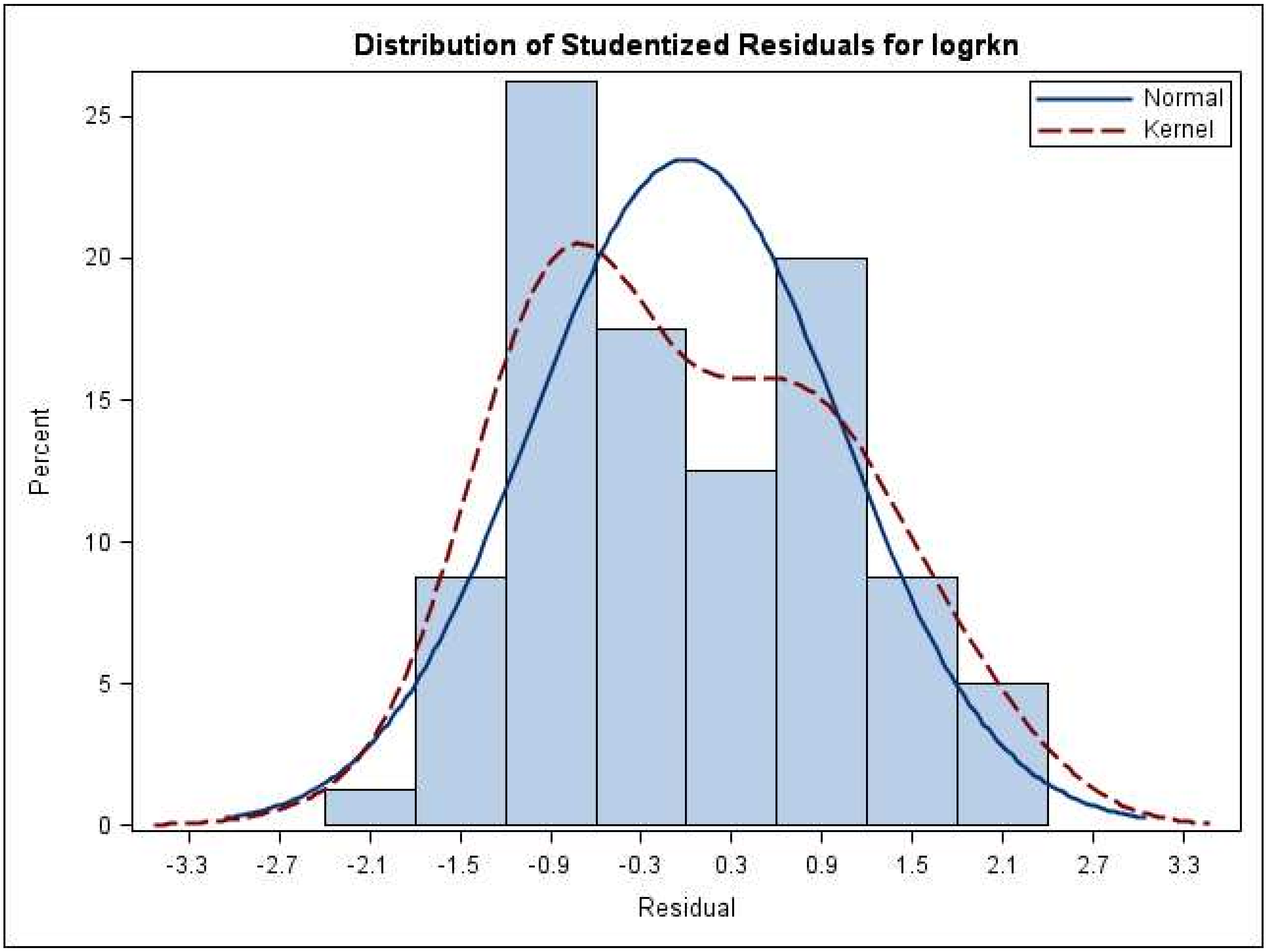


Figure E.2.2.4 Normal quantile plot of the Studentized residuals

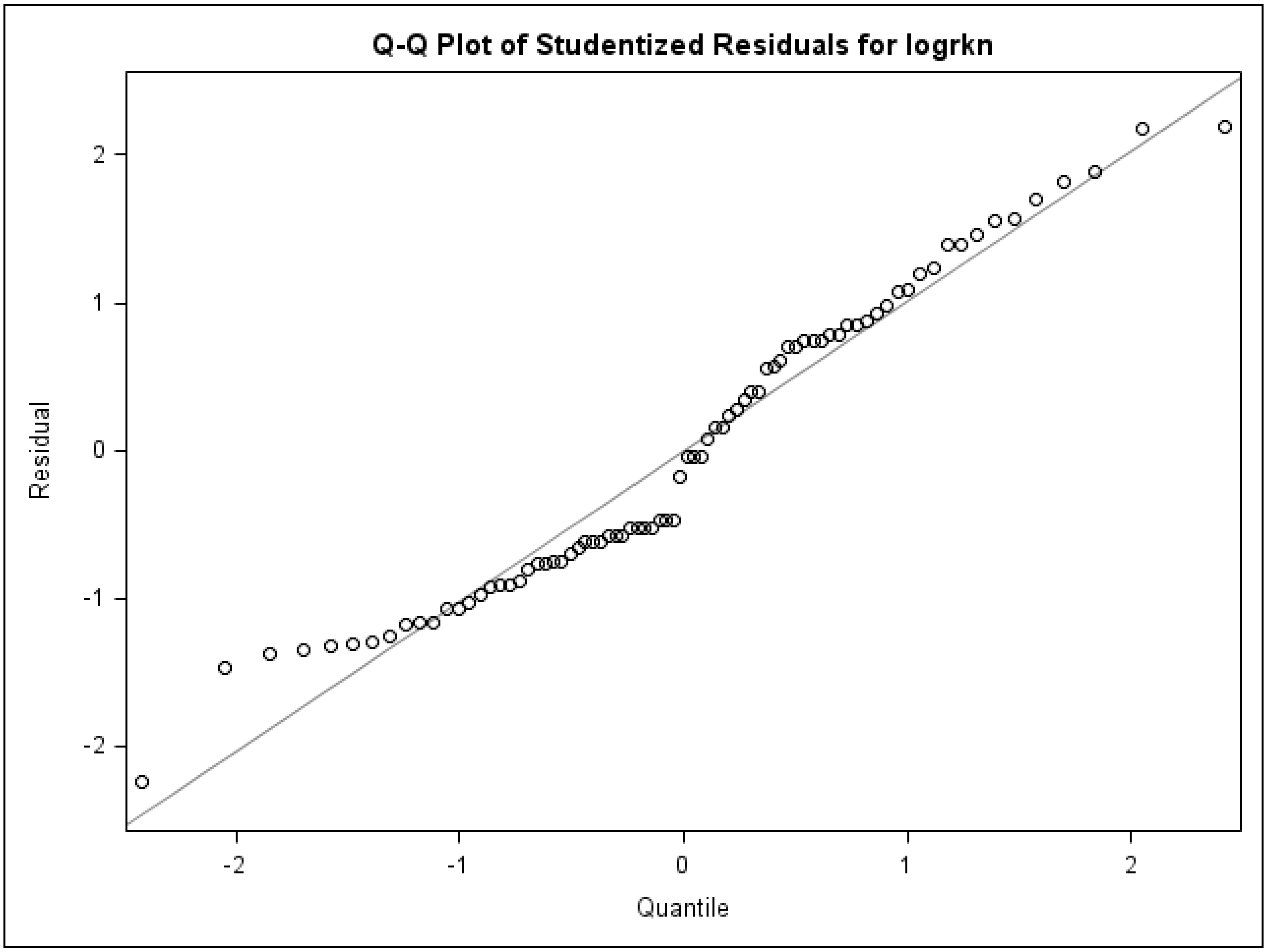


Figure E.2.2.5 Histogram of the Pearson residuals

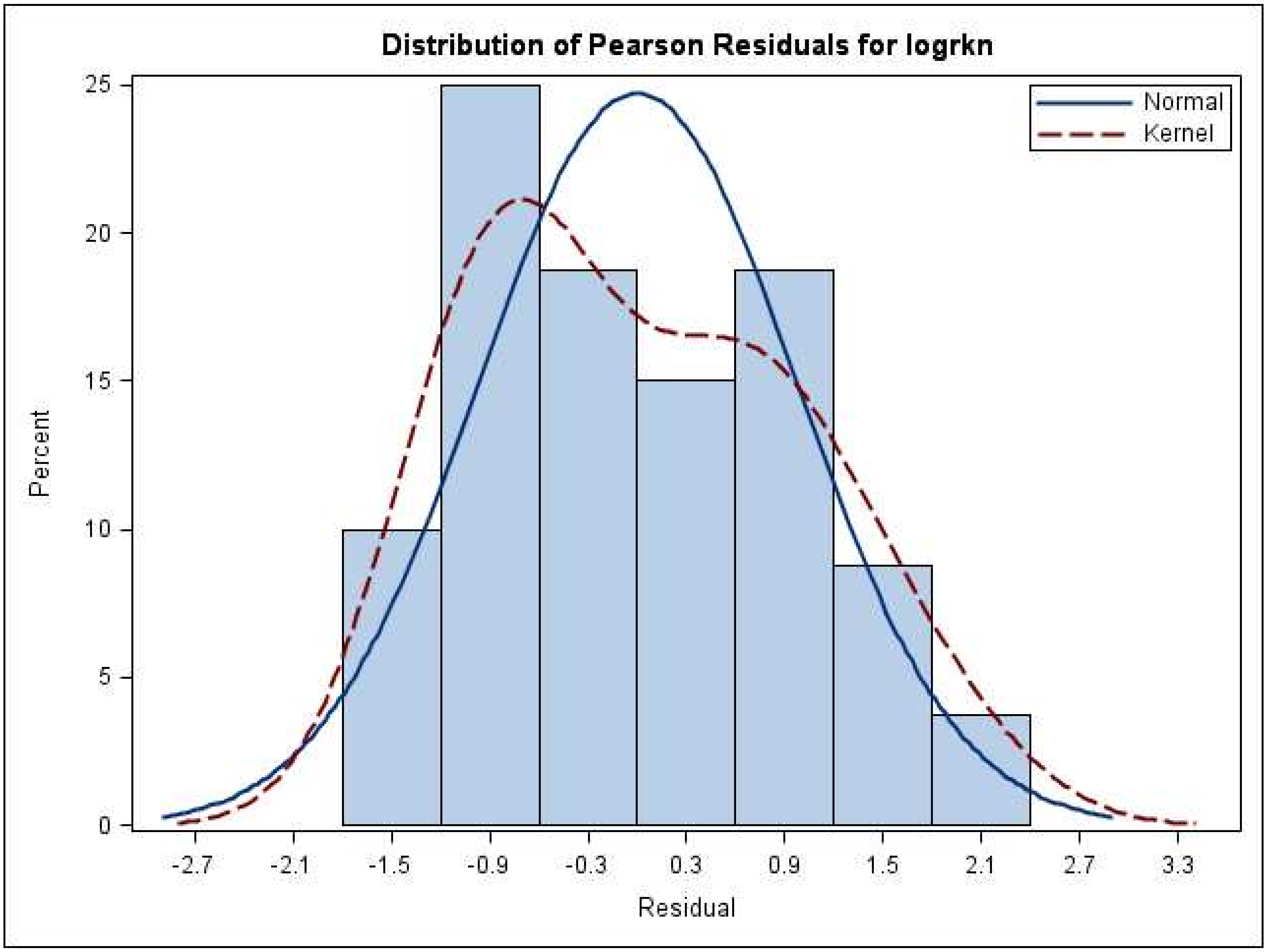
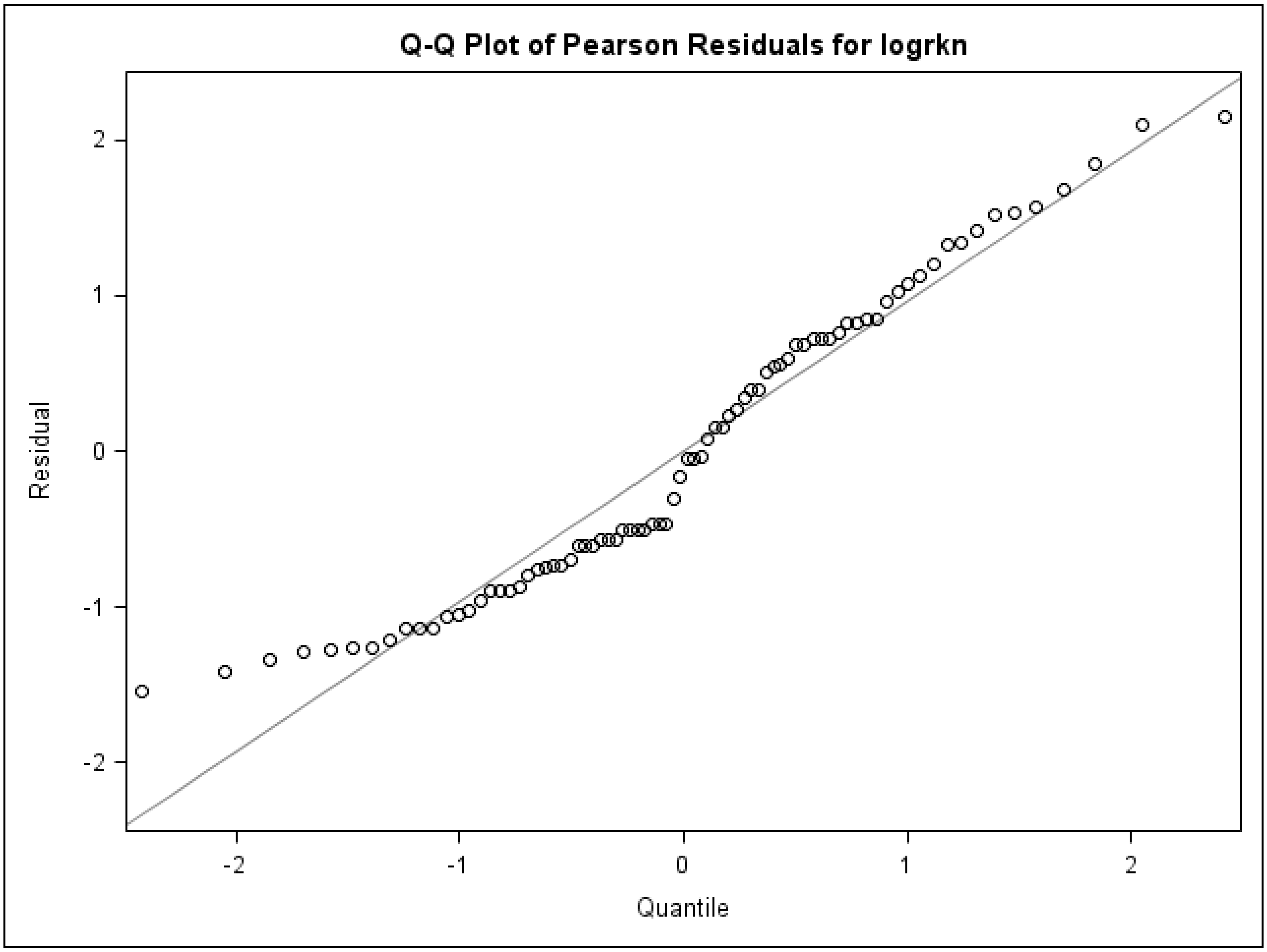


Figure E.2.2.6 Normal quantile plot of the Pearson residuals



E.2.3 July 2005 Model 3 Residual Plots

Figure E.2.3.1 Histogram of the raw residuals

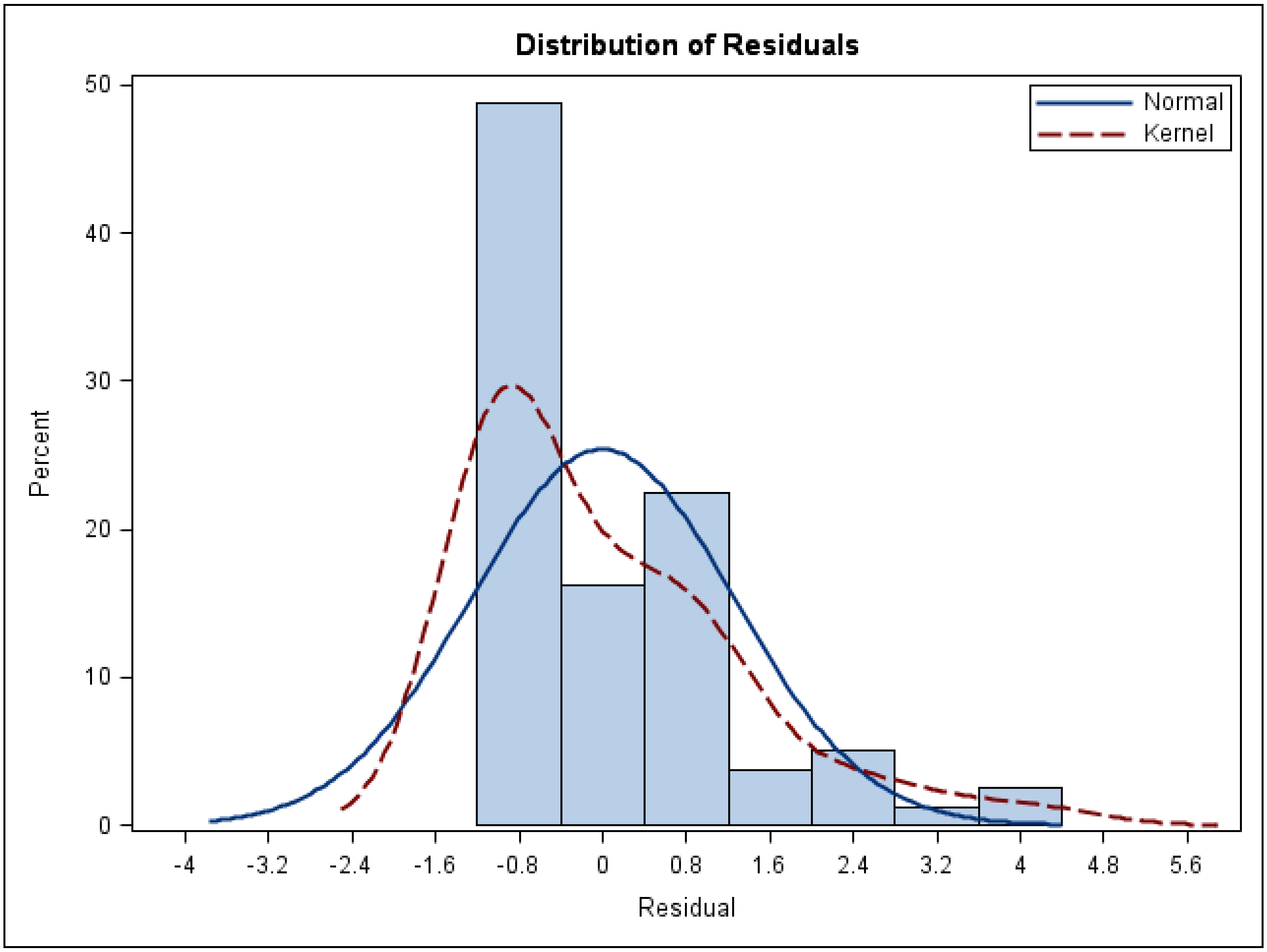


Figure E.2.3.2 Normal quantile plot of the raw residuals

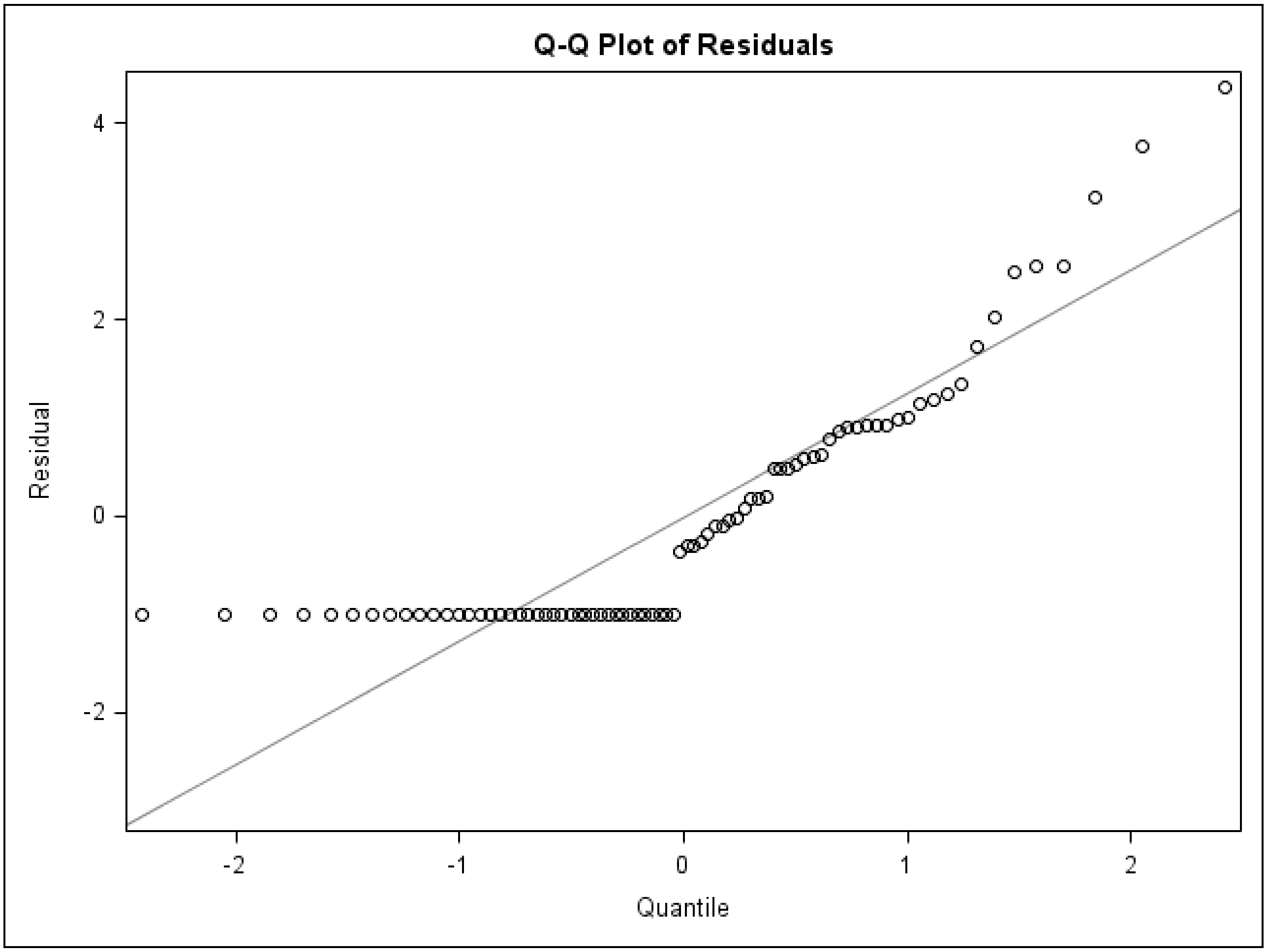


Figure E.2.3.3 Histogram of the Studentized residuals

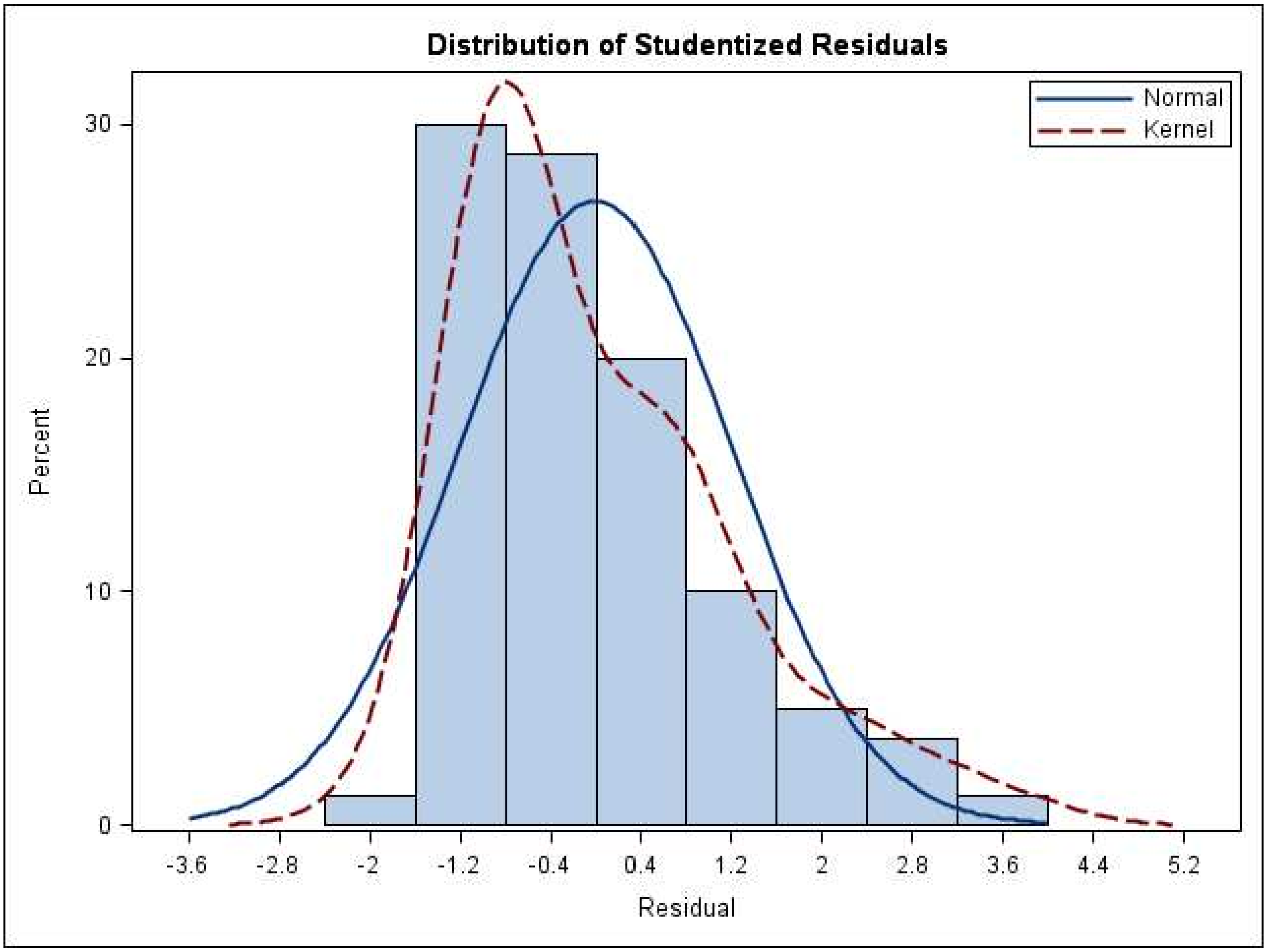


Figure E.2.3.4 Normal quantile plot of the Studentized residuals

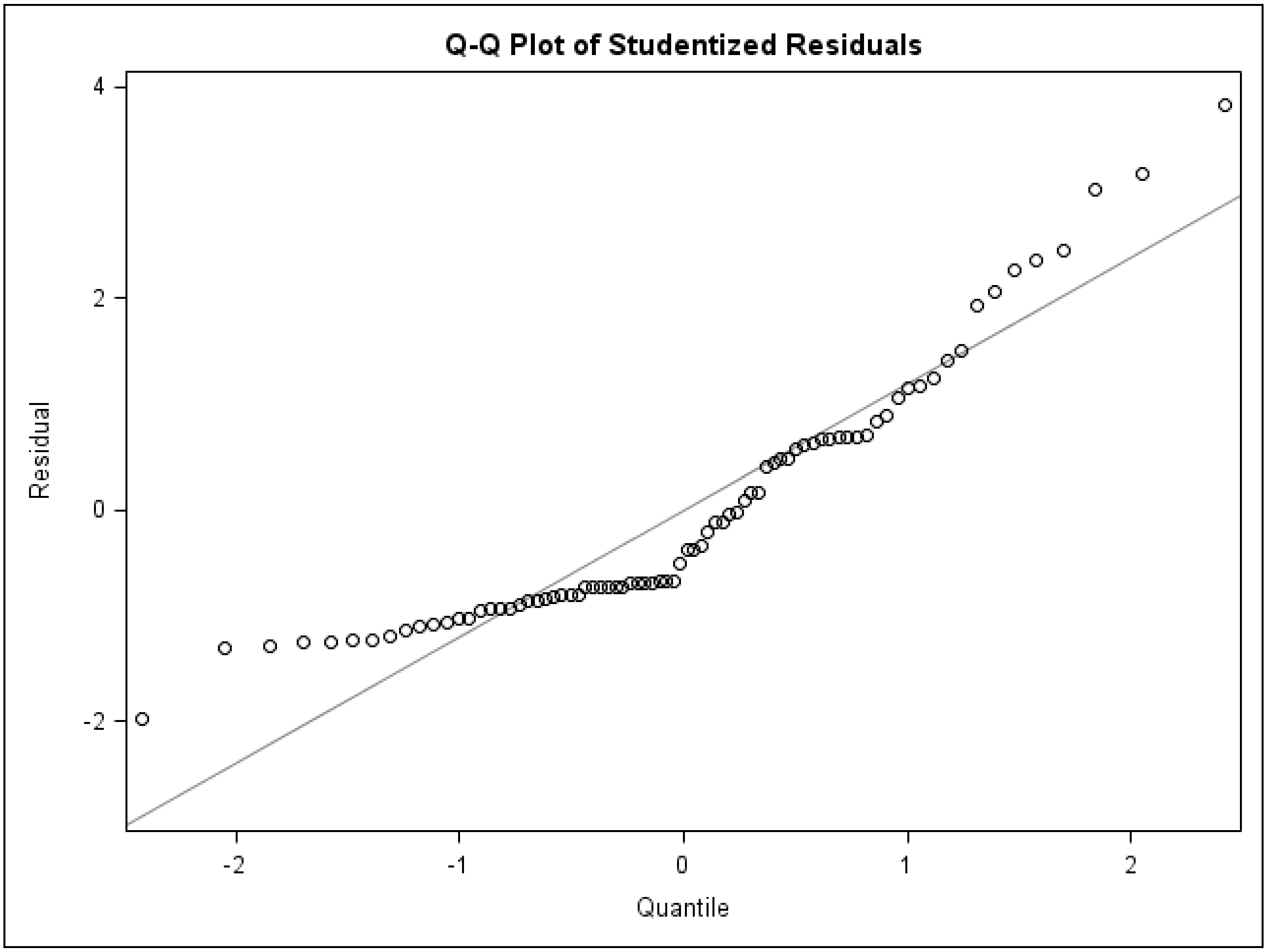


Figure E.2.3.5 Histogram of the Pearson residuals

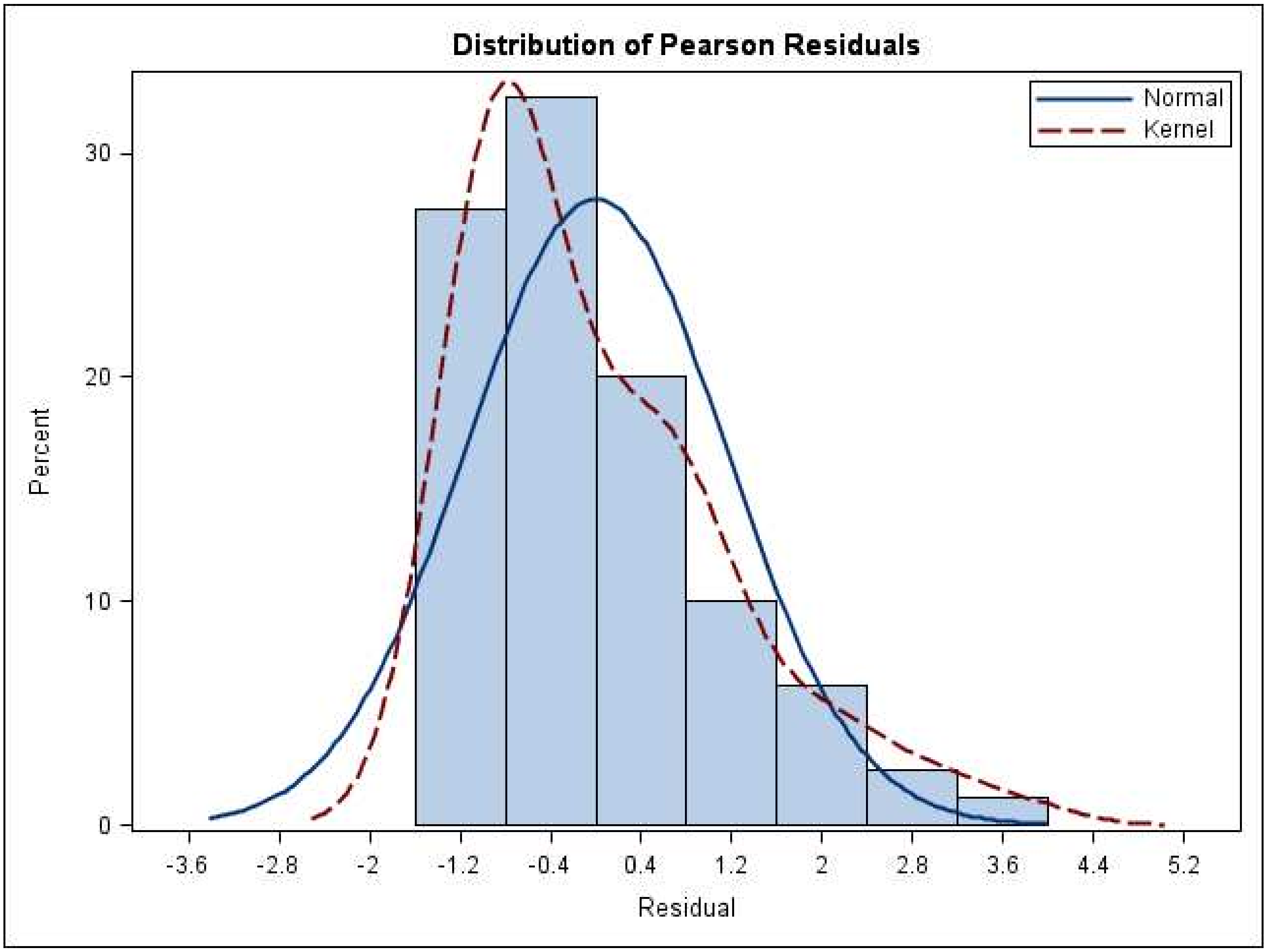
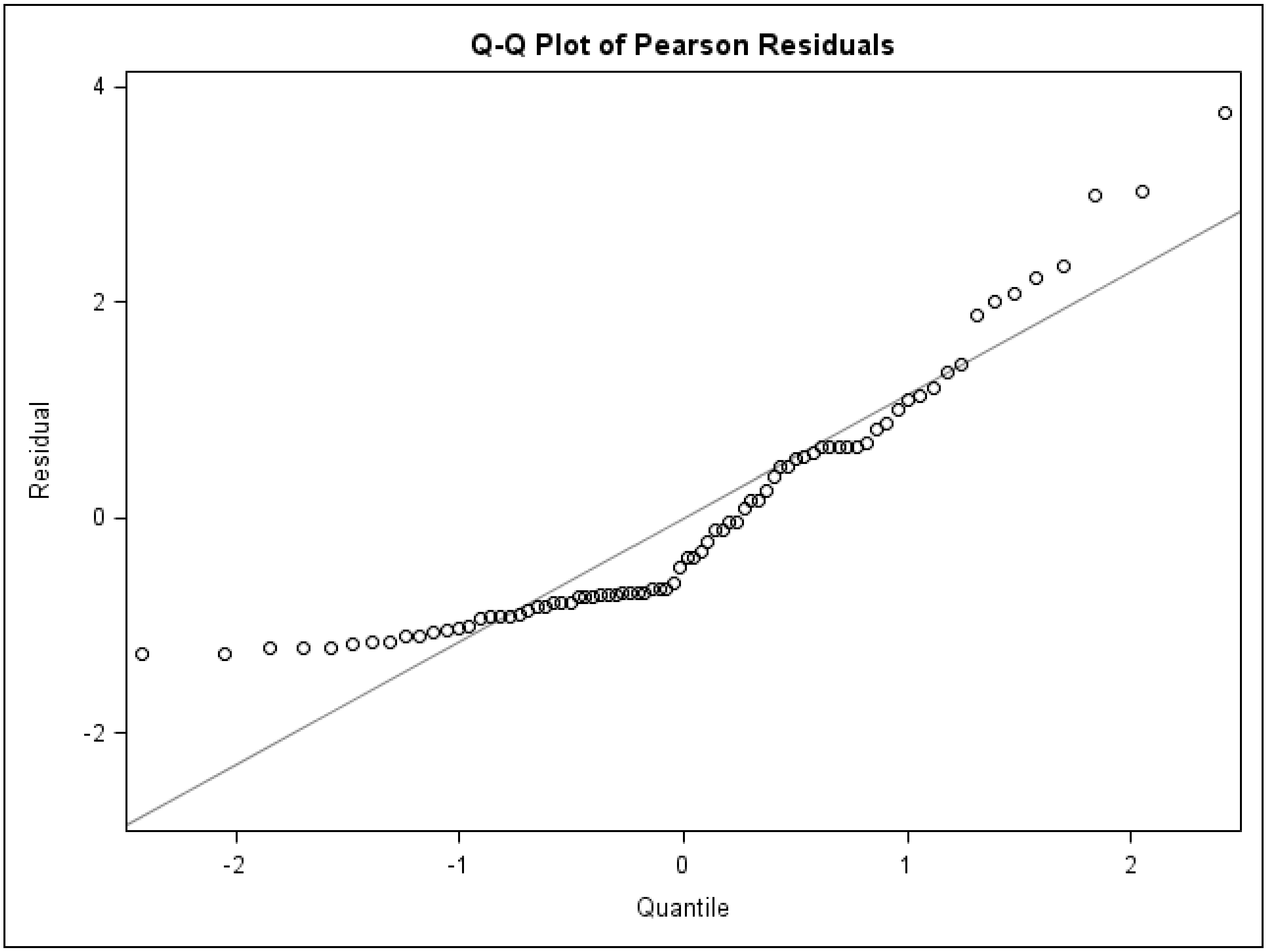


Figure E.2.3.6 Normal quantile plot of the Pearson residuals



E.2.4 July 2005 Model 4 Residual Plots

Figure E.2.4.1 Histogram of the raw residuals

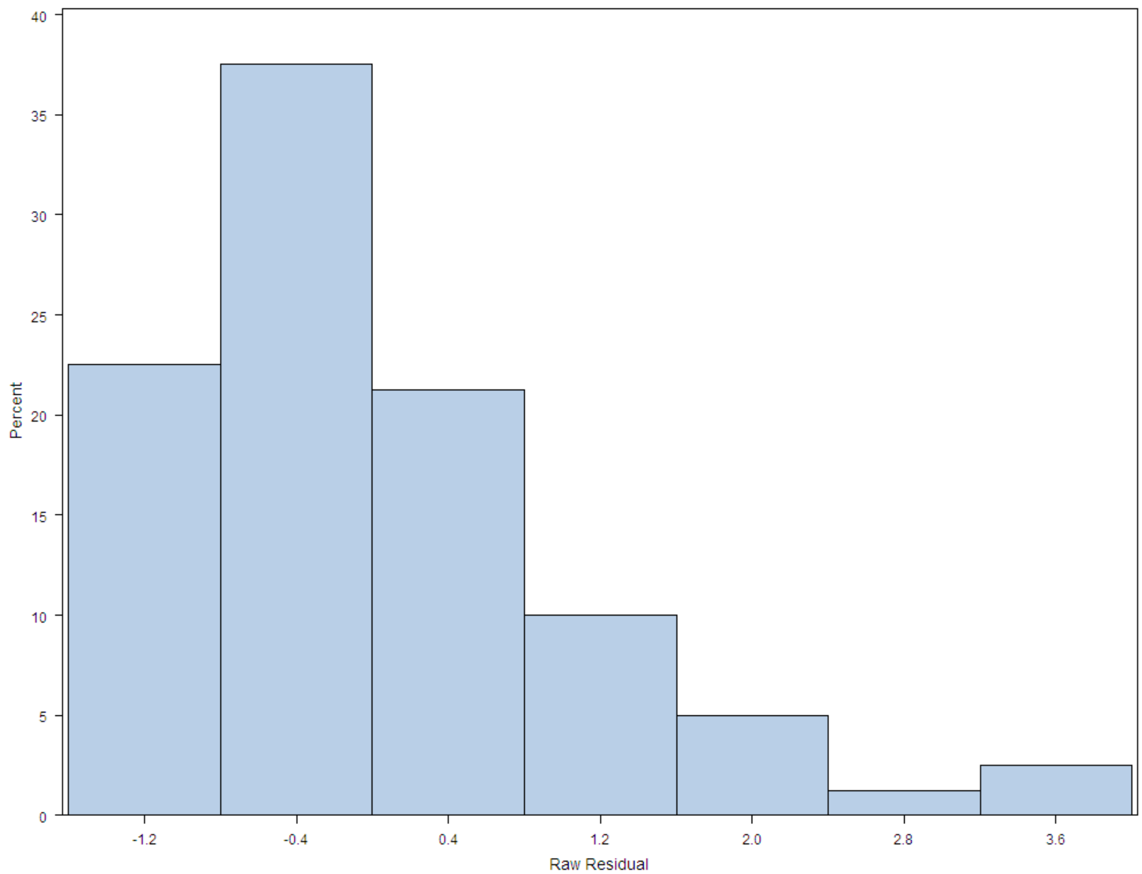


Figure E.2.4.2 Histogram of the Pearson residuals

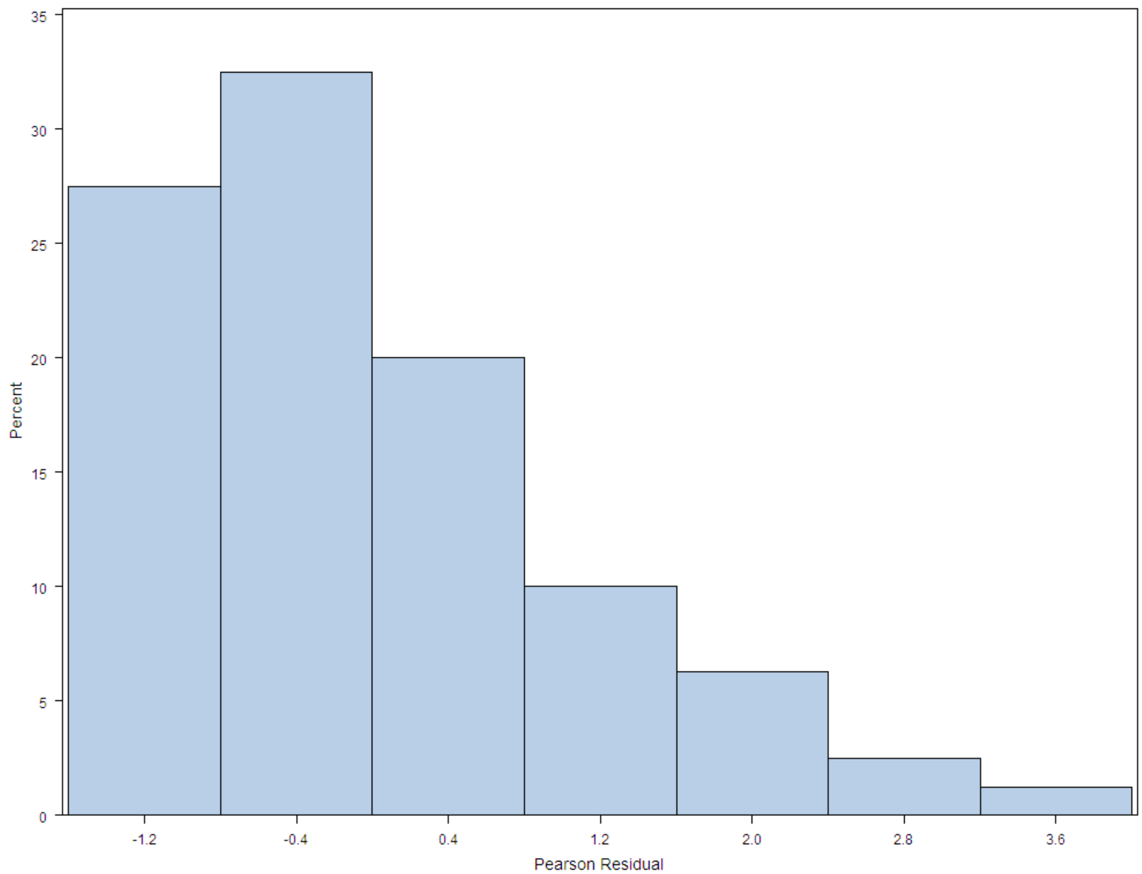


Figure E.2.4.3 Histogram of the deviance residuals

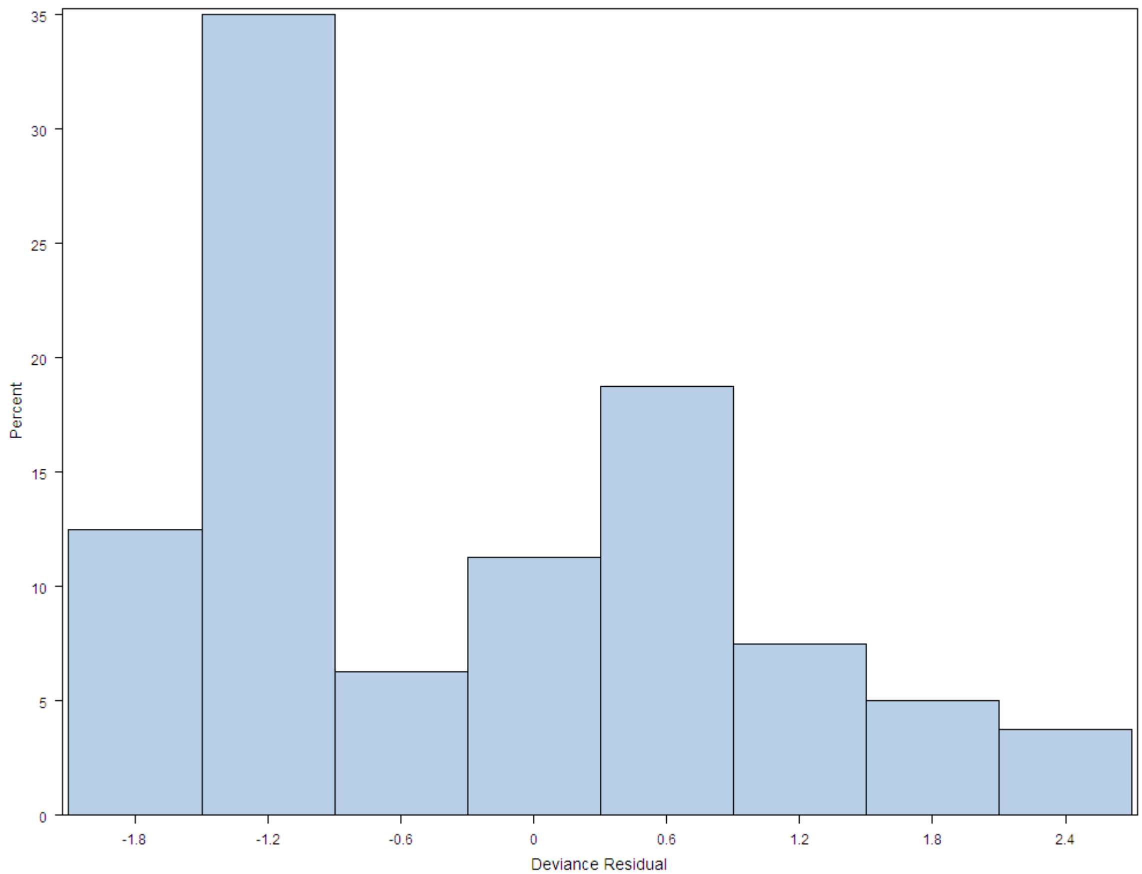


Figure E.2.4.4 Histogram of the likelihood residuals

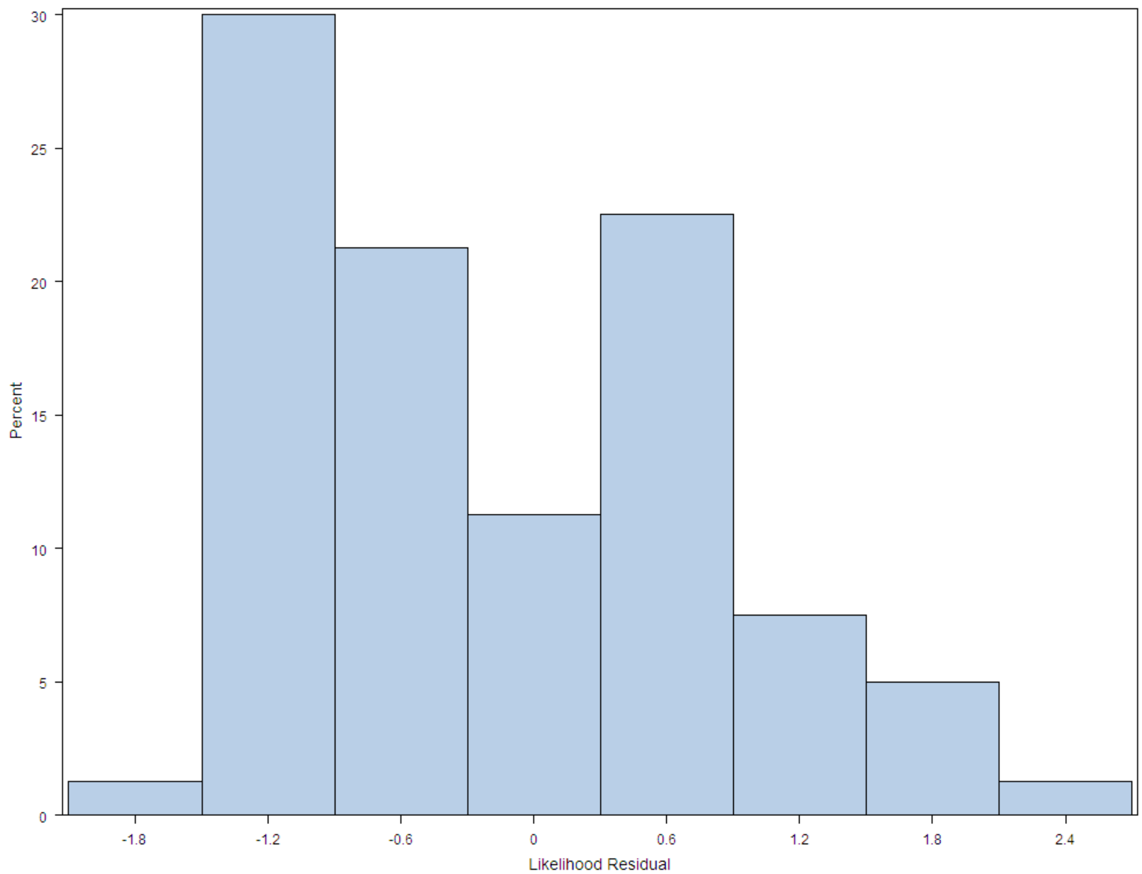


Figure E.2.4.5 Histogram of the standardized Pearson residuals

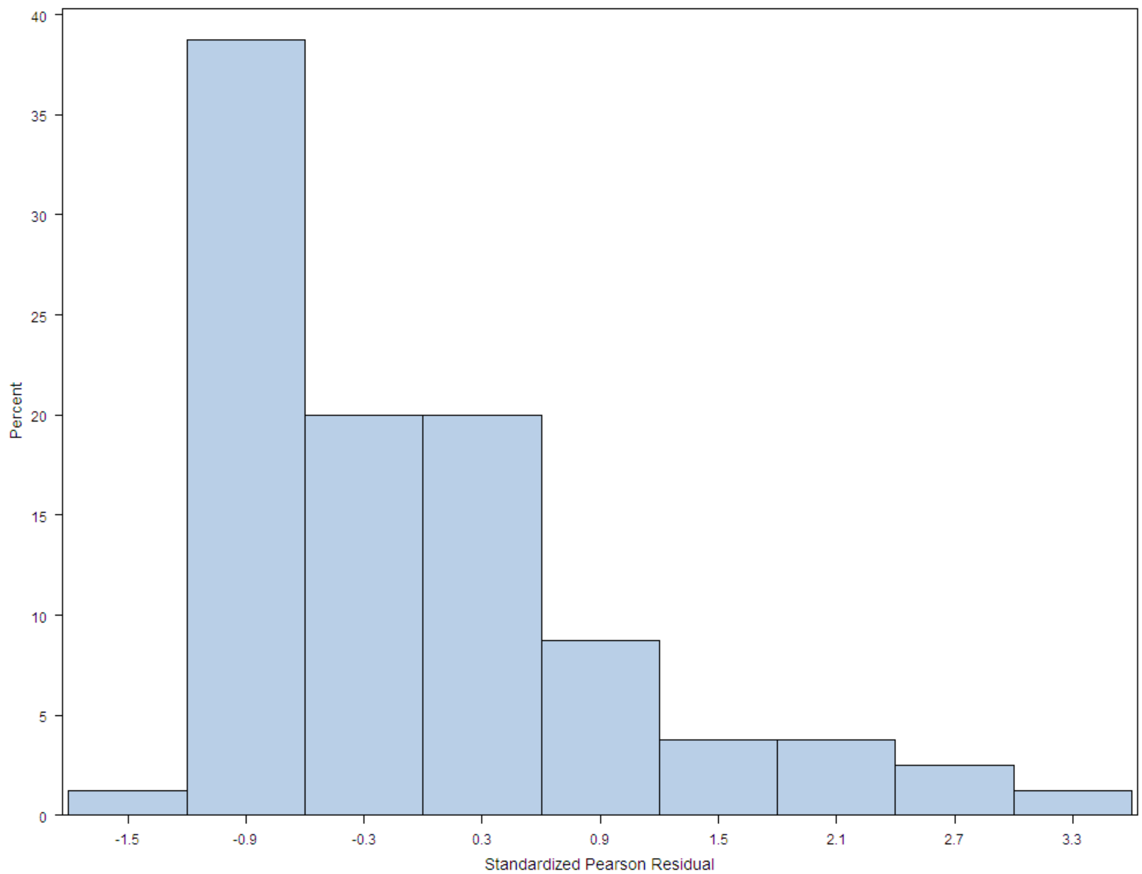
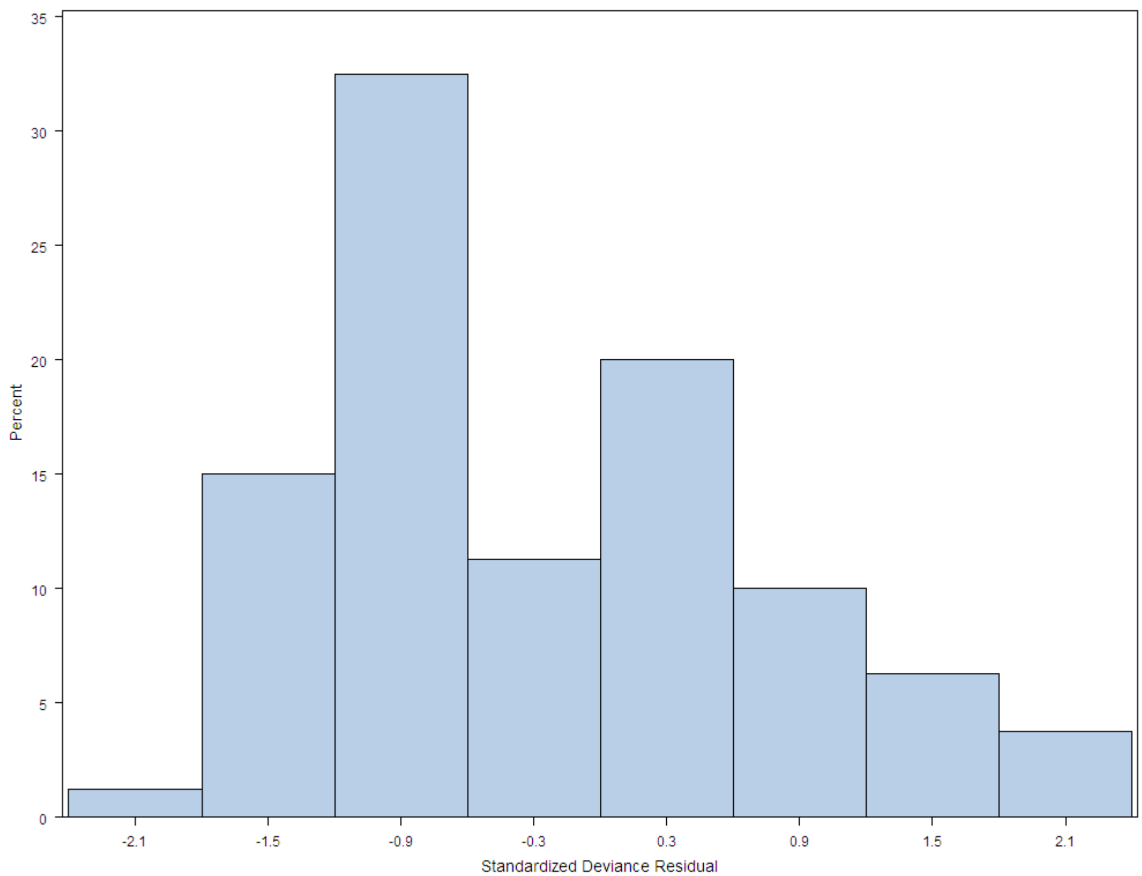


Figure E.2.4.6 Histogram of the standardized deviance residuals



E.2.5 July 2005 Model 5 Residual Plots

Figure E.2.5.1 Histogram of the raw residuals

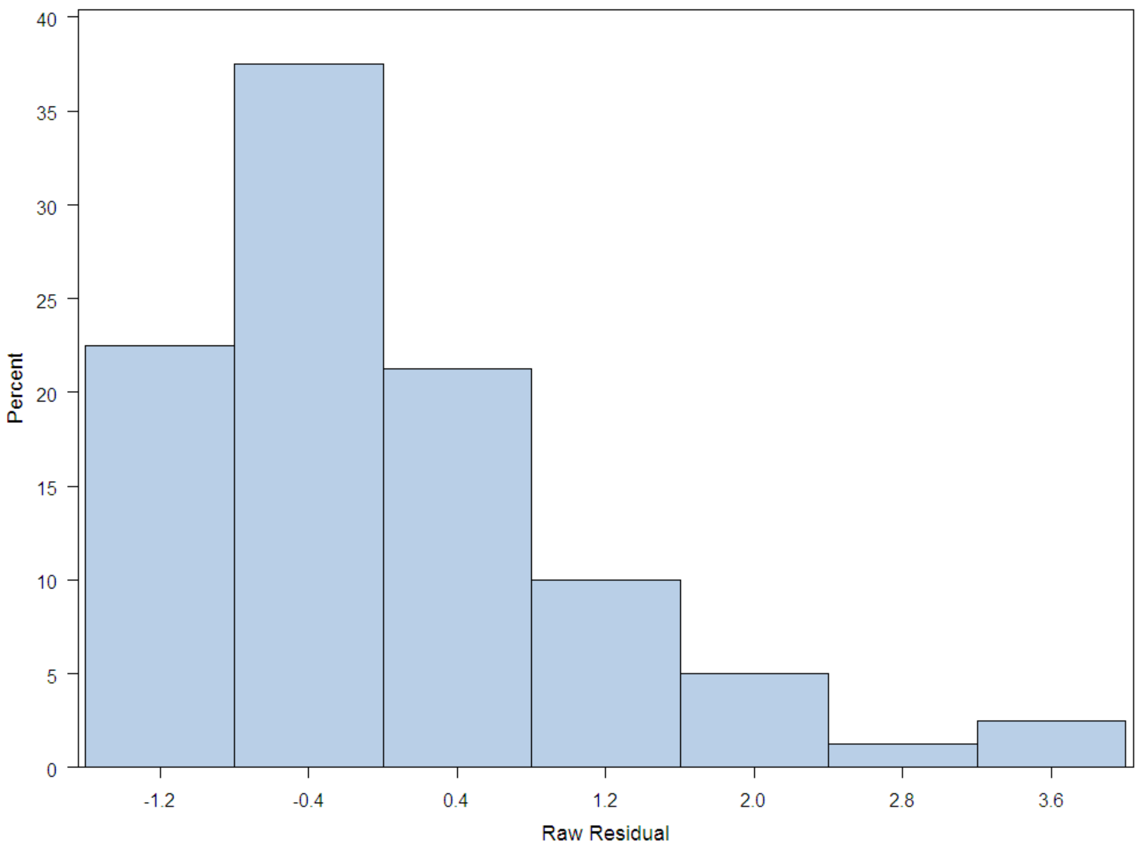


Figure E.2.5.2 Histogram of the Pearson residuals

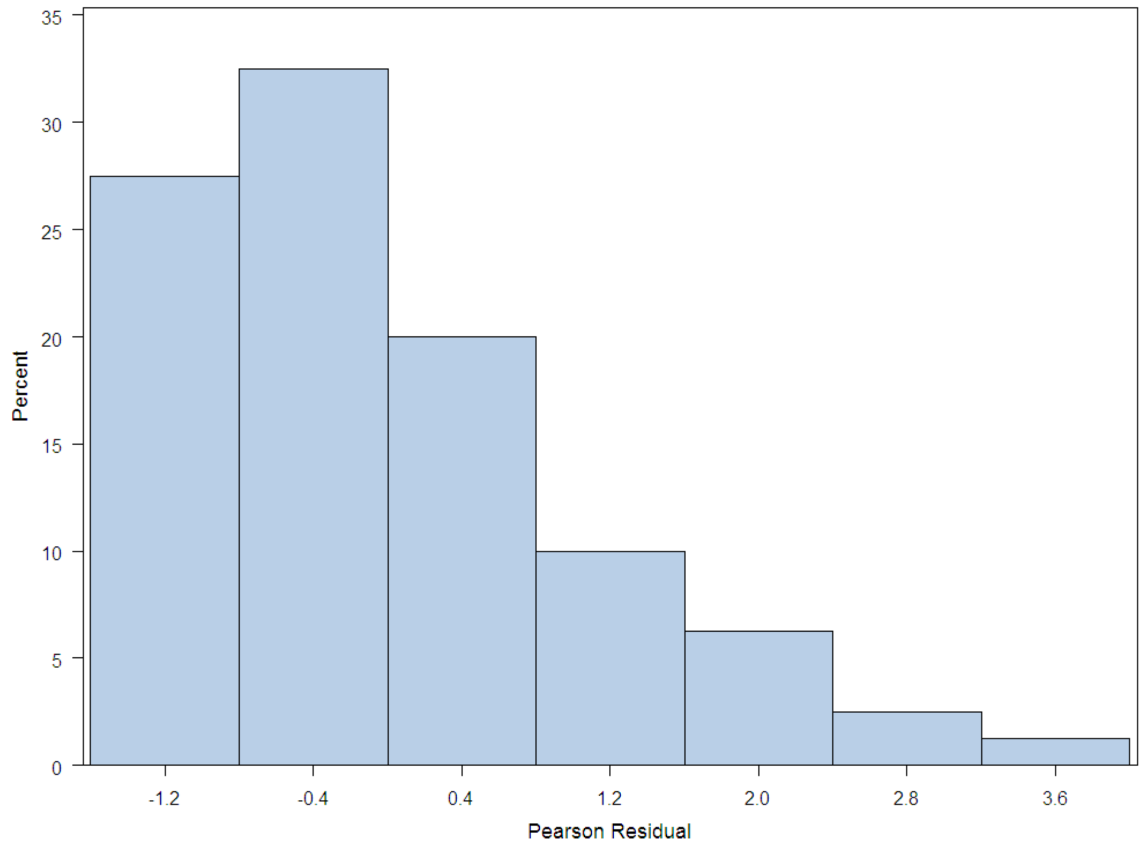


Figure E.2.5.3 Histogram of the deviance residuals

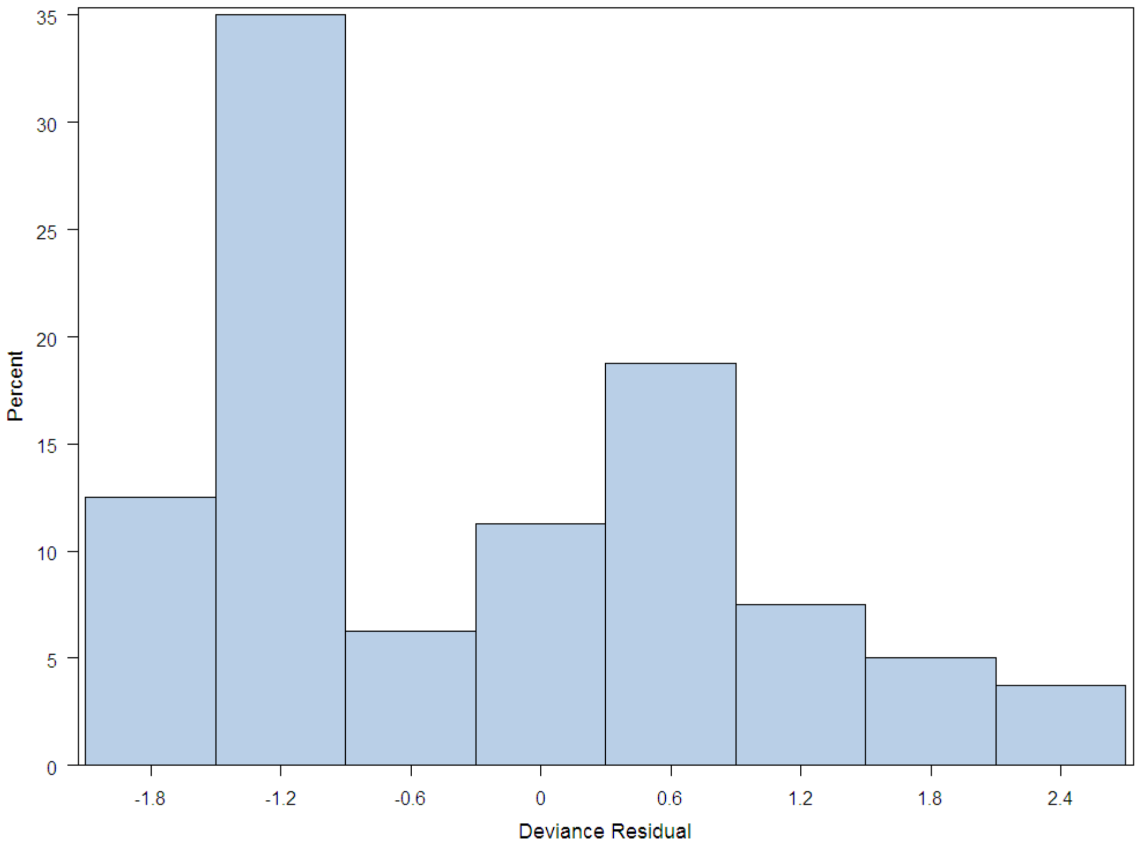


Figure E.2.5.4 Histogram of the likelihood residuals

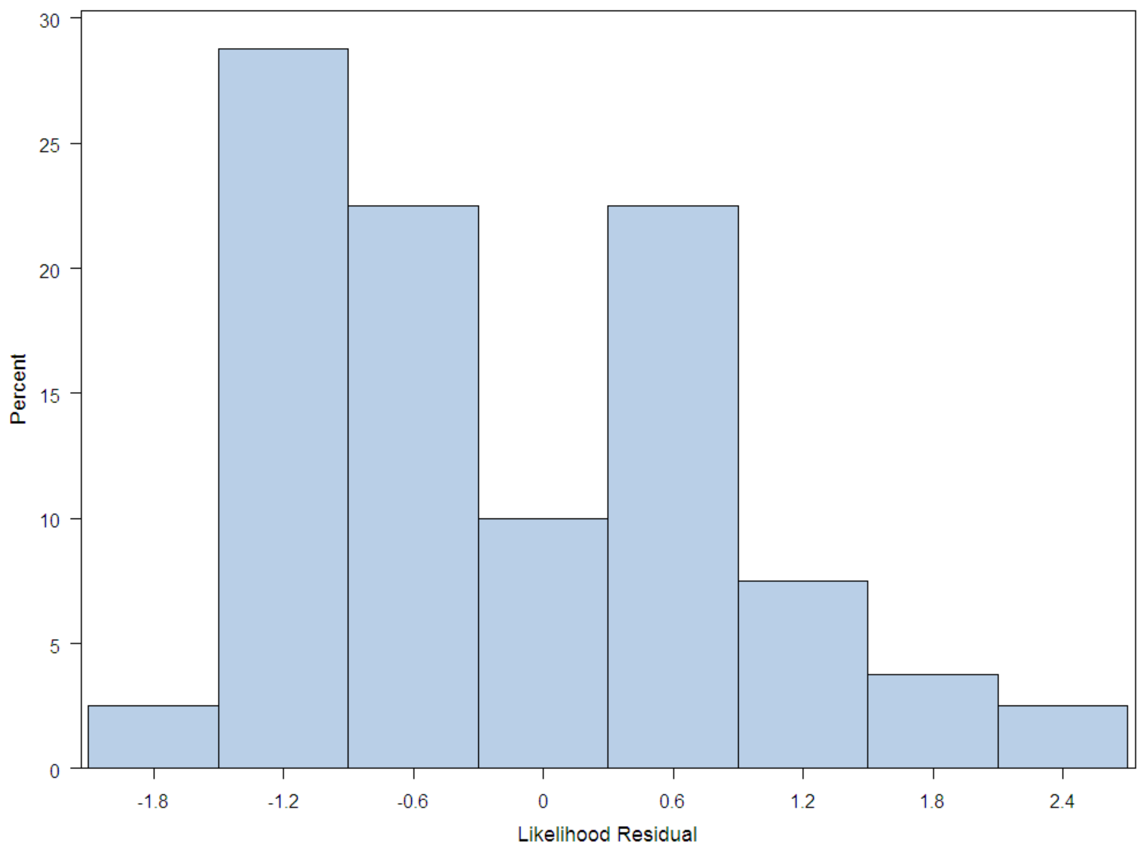


Figure E.2.5.5Histogram of the standardized Pearson residuals

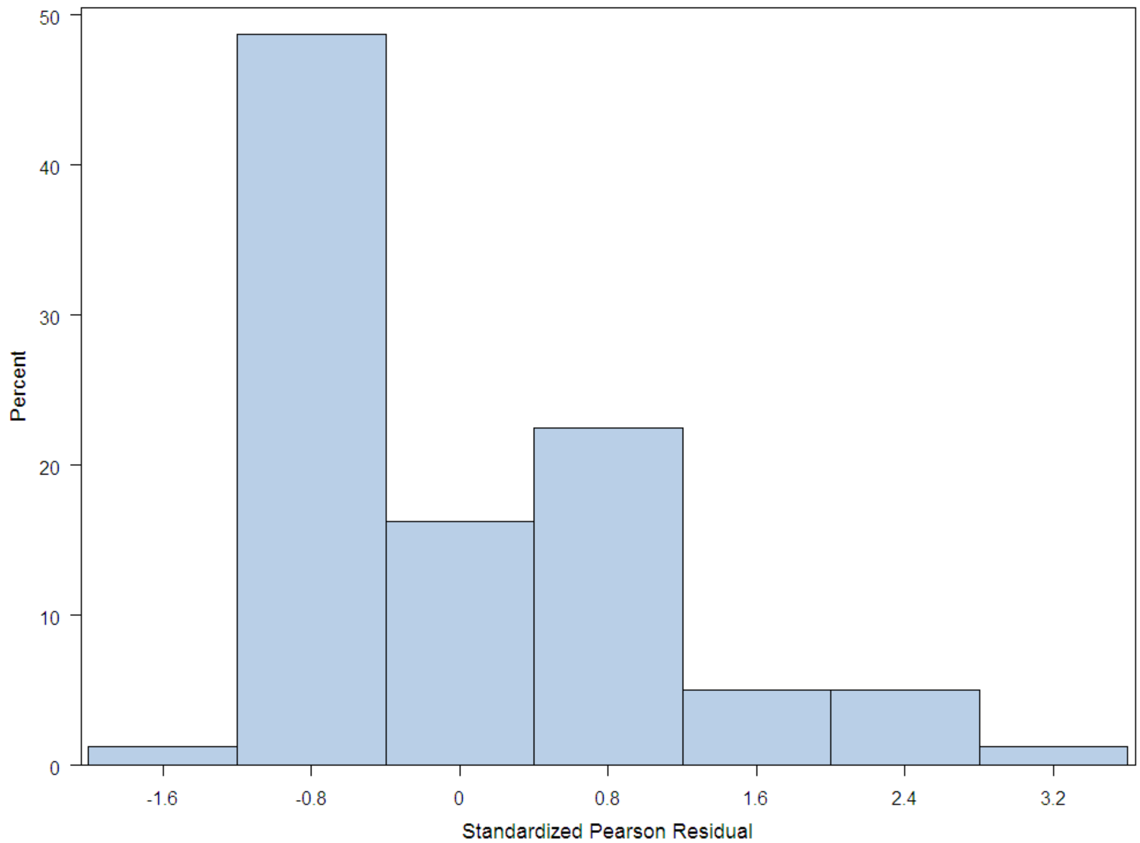
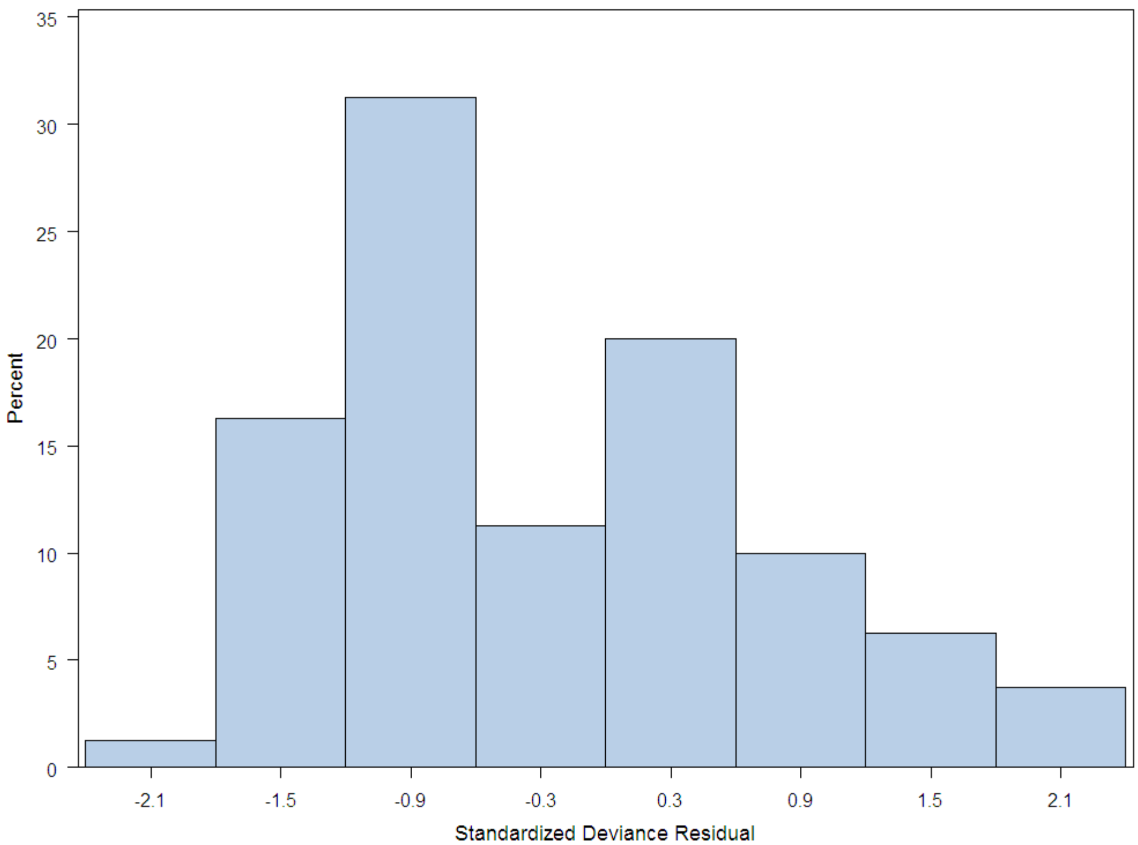


Figure E.2.5.6 Histogram of the standardized deviance residuals



E.2.6 July 2005 Model 6 Residual Plots

Figure E.2.6.1 Histogram of the raw residuals

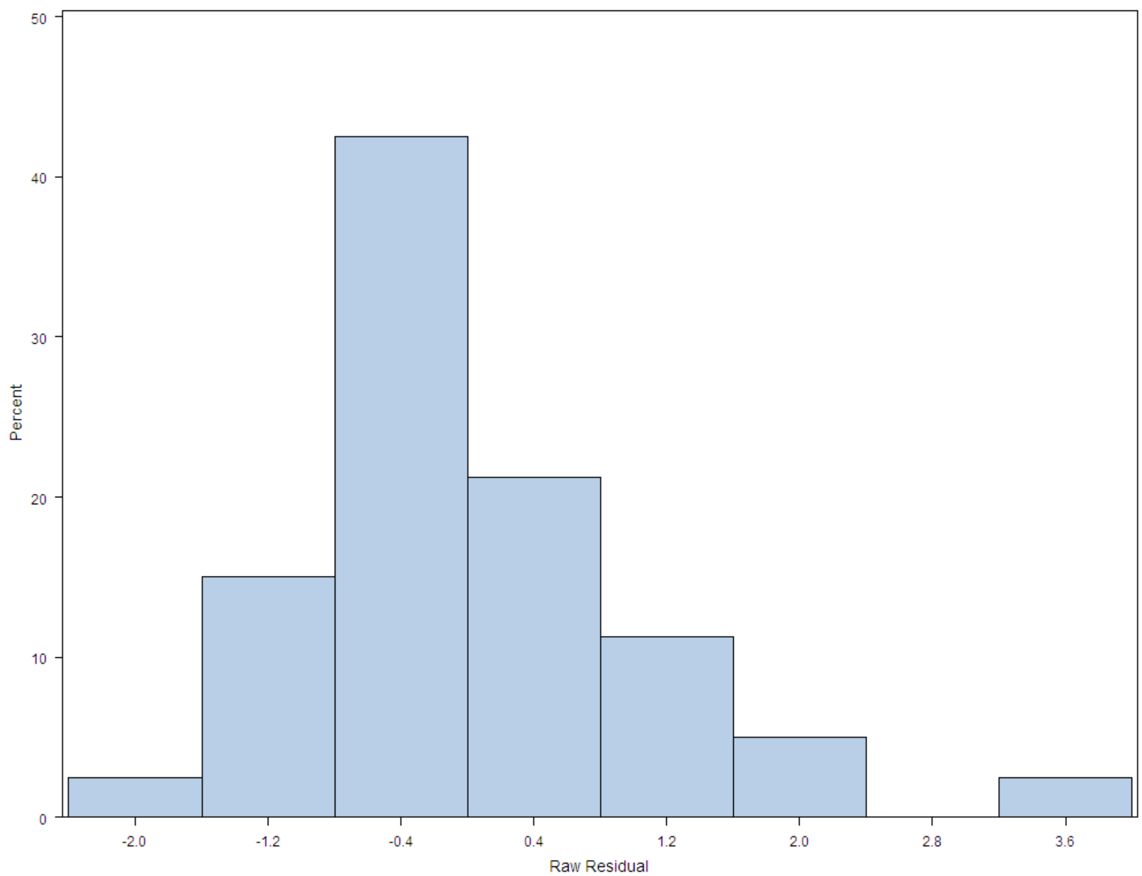
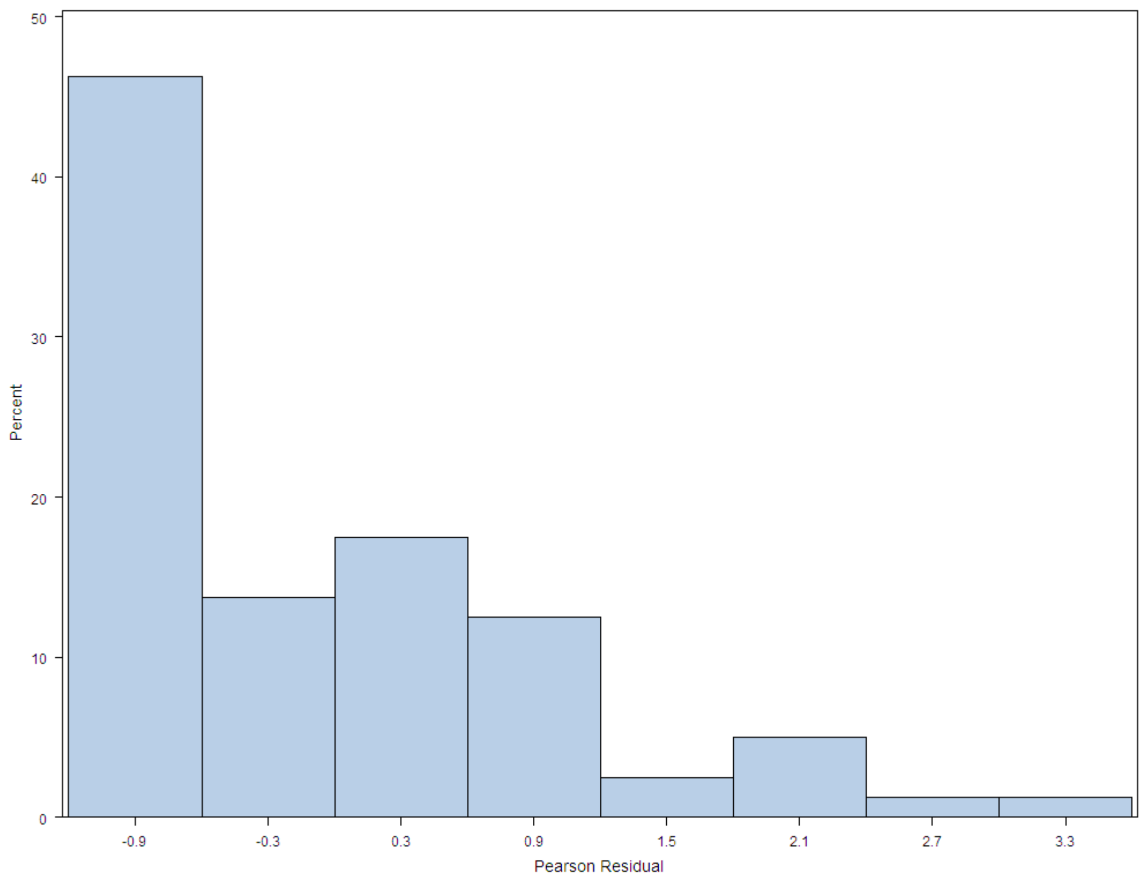


Figure E.2.6.2 Histogram of the Pearson residuals



E.2.7 July 2005 Model 7 Residual Plots

Figure E.2.7.1 Histogram of the raw residuals

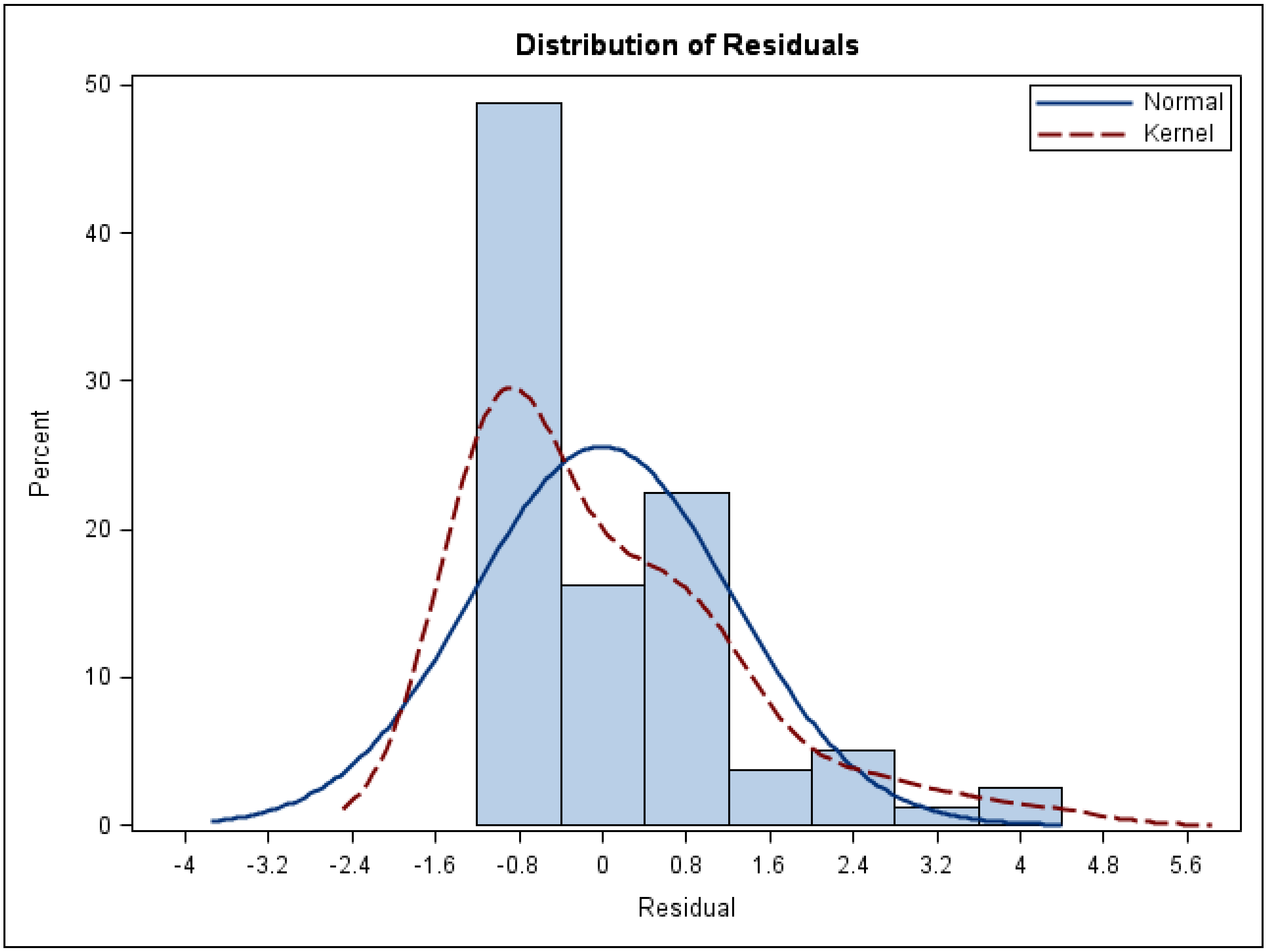


Figure E.2.7.2 Normal quantile plot of the raw residuals

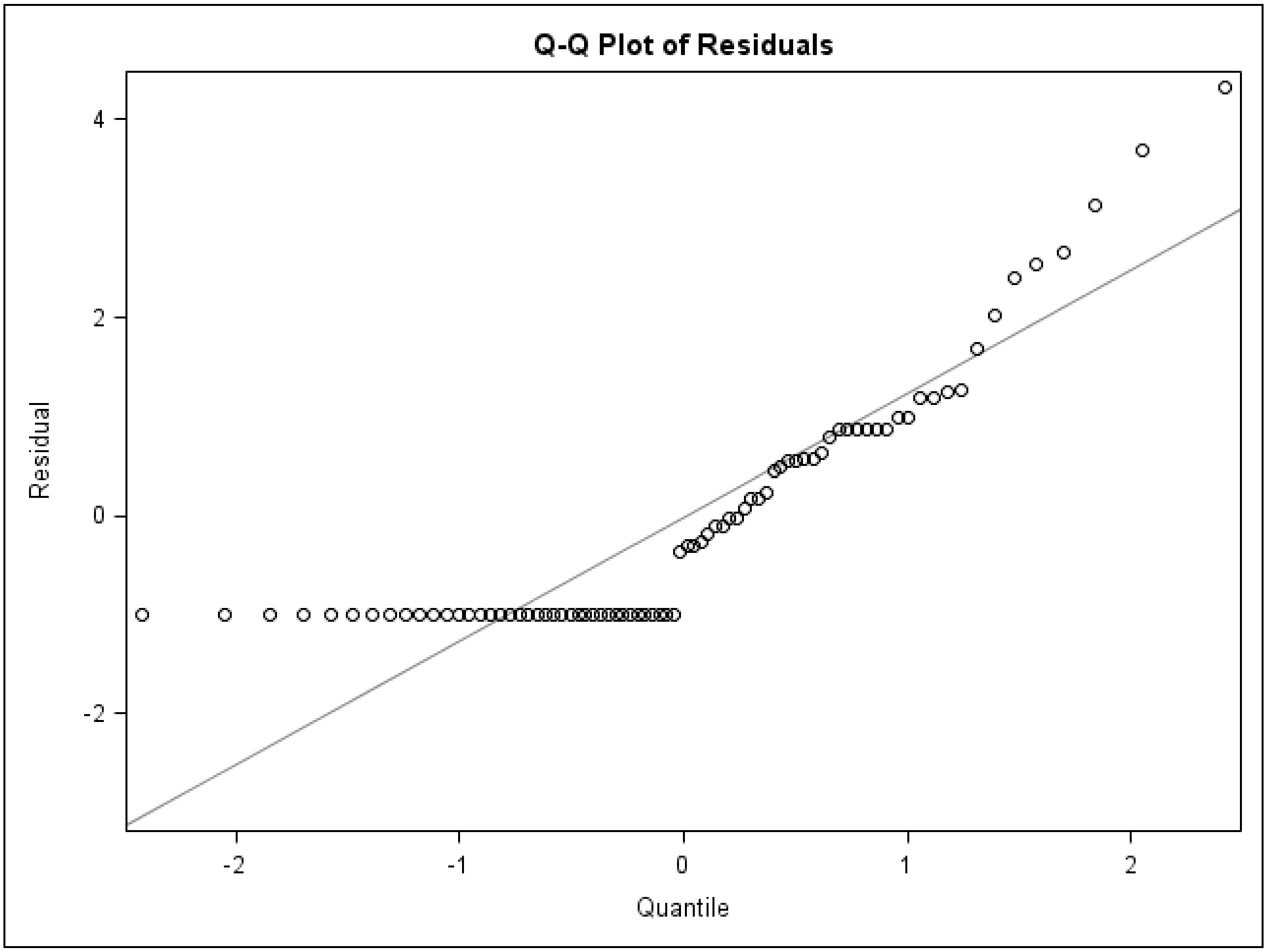


Figure E.2.7.3 Histogram of the Studentized residuals

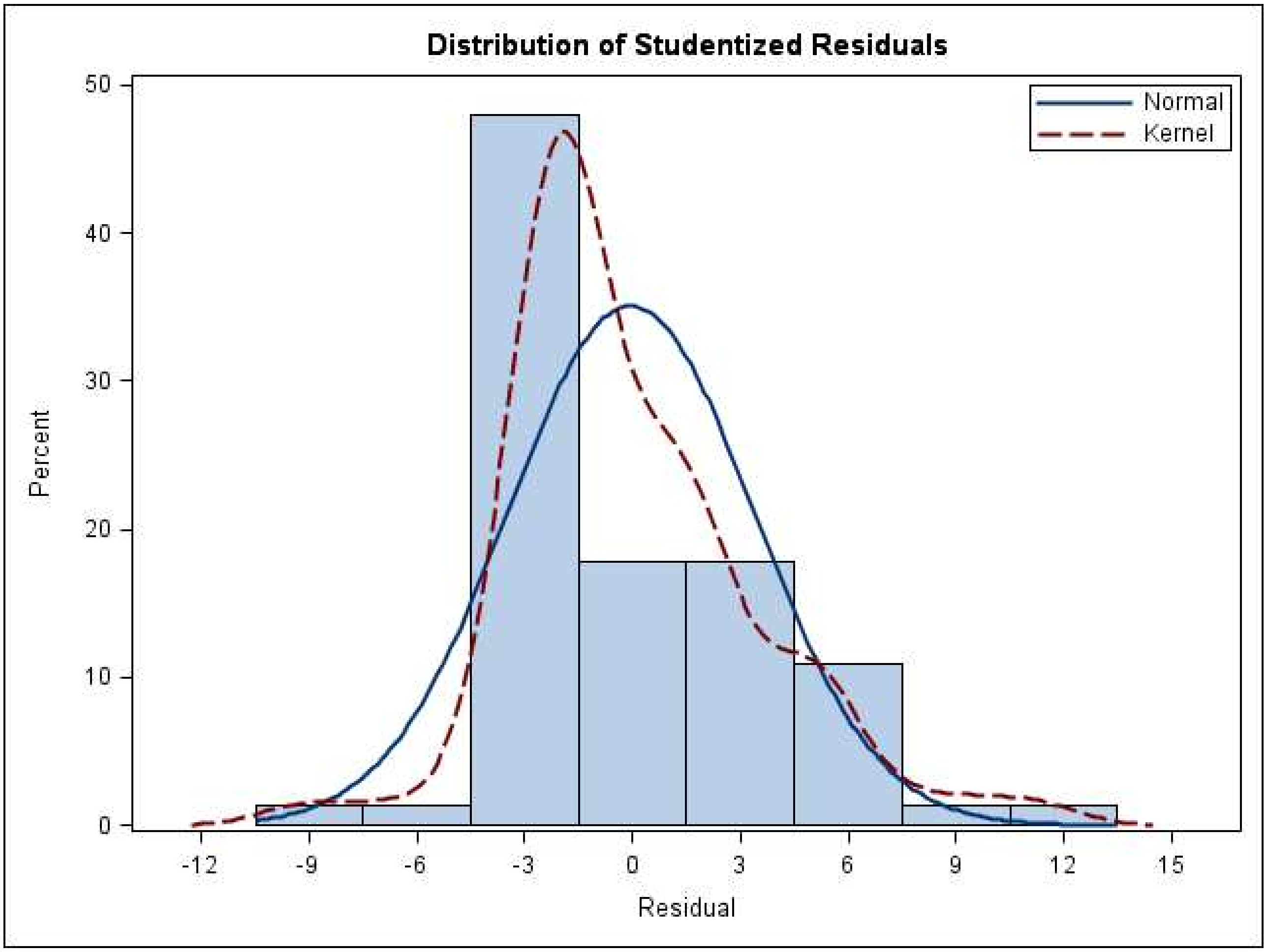


Figure E.2.7.4 Normal quantile plot of the Studentized residuals

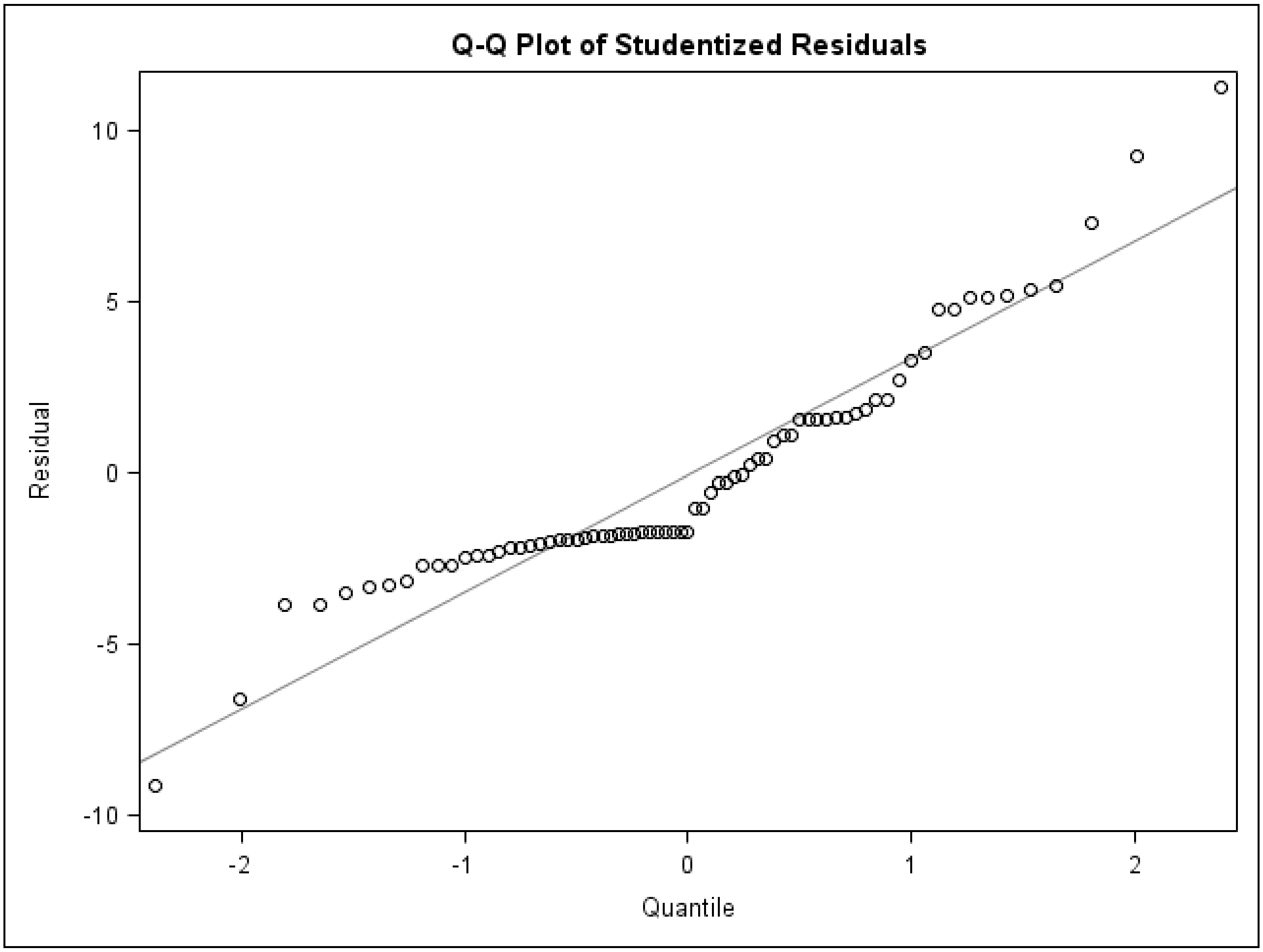


Figure E.2.7.5 Histogram of the Pearson residuals

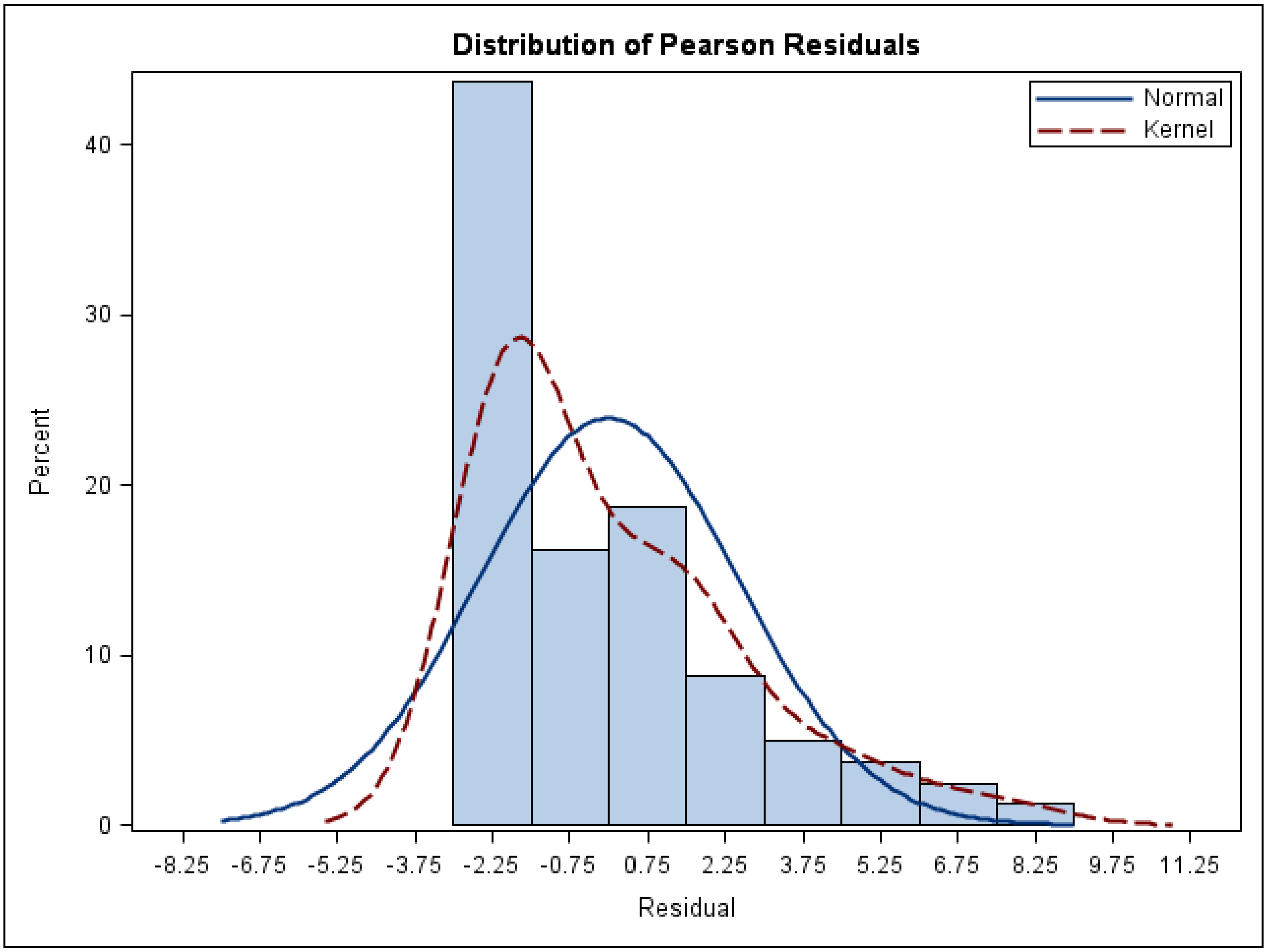
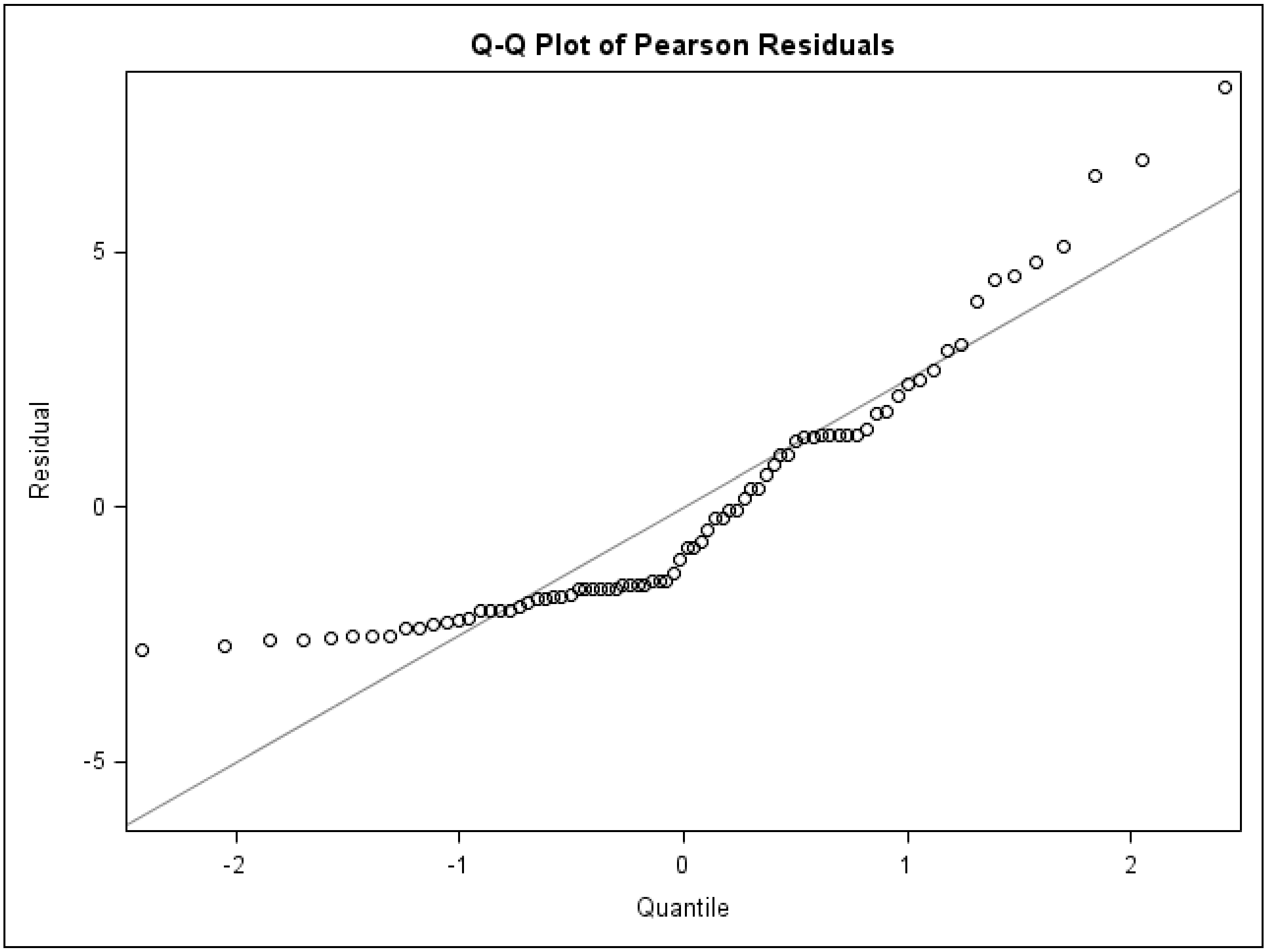
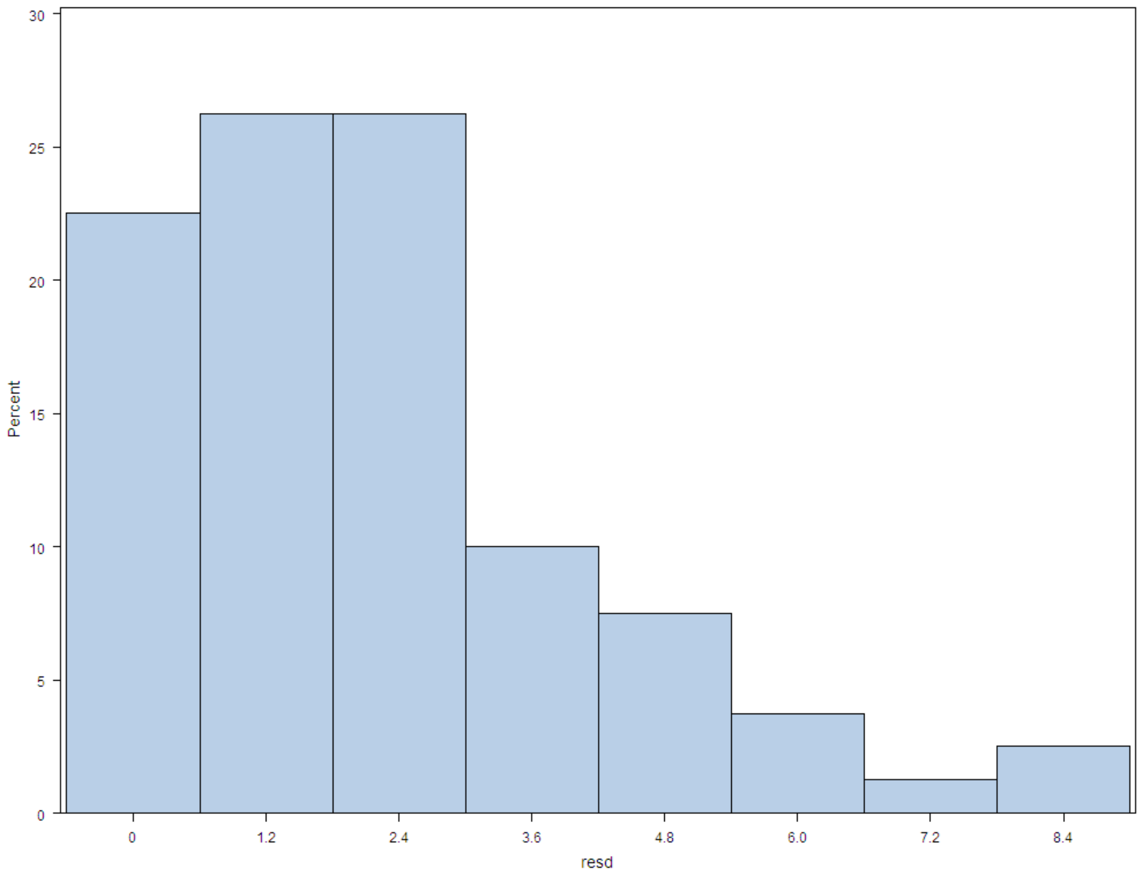


Figure E.2.7.6 Normal quantile plot of the Pearson residuals



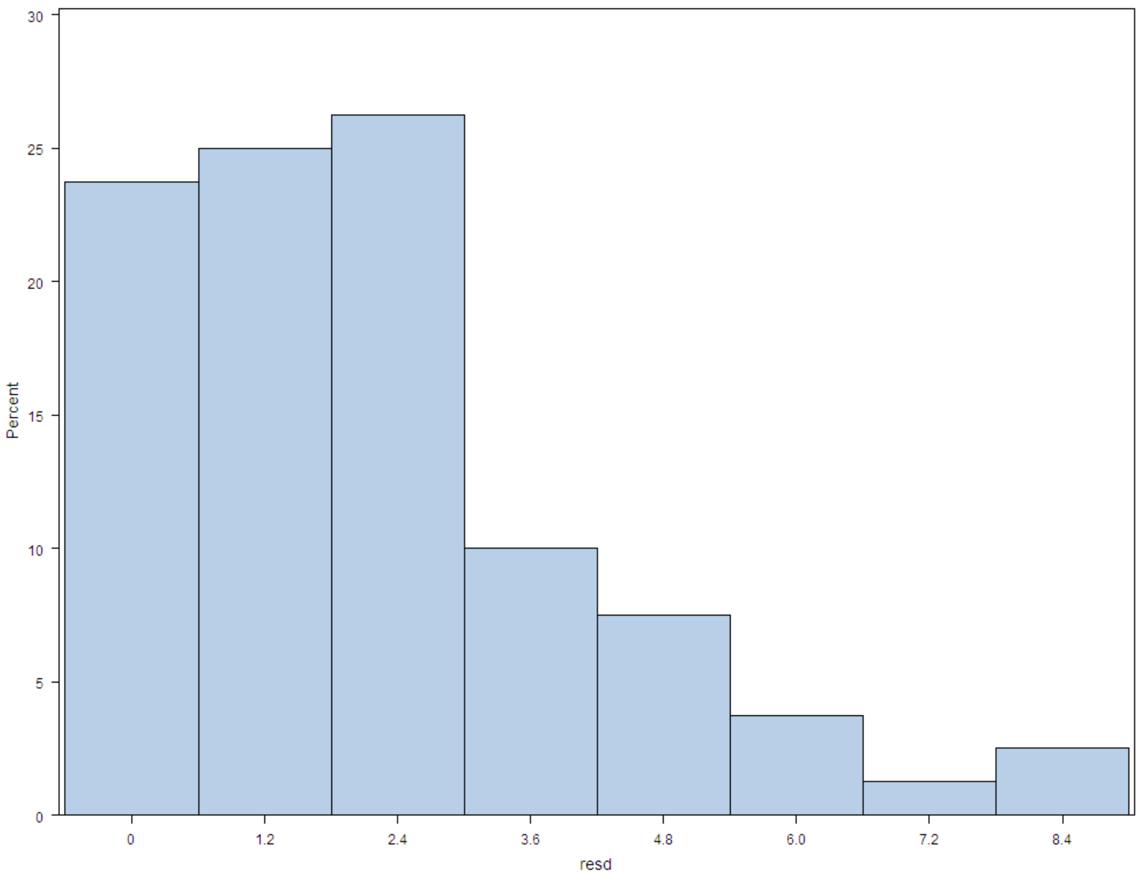
E.2.8 July 2005 Model 8 Residual Plots

Figure E.2.8.1 Histogram of the raw residuals



E.2.9 July 2005 Model 9 Residual Plots

Figure E.2.9.1 Histogram of the raw residuals



E.3 September 2005 Residual Plots

E.3.1 September 2005 Model 1 Residual Plots

Figure E.3.1.1 Histogram of the raw residuals

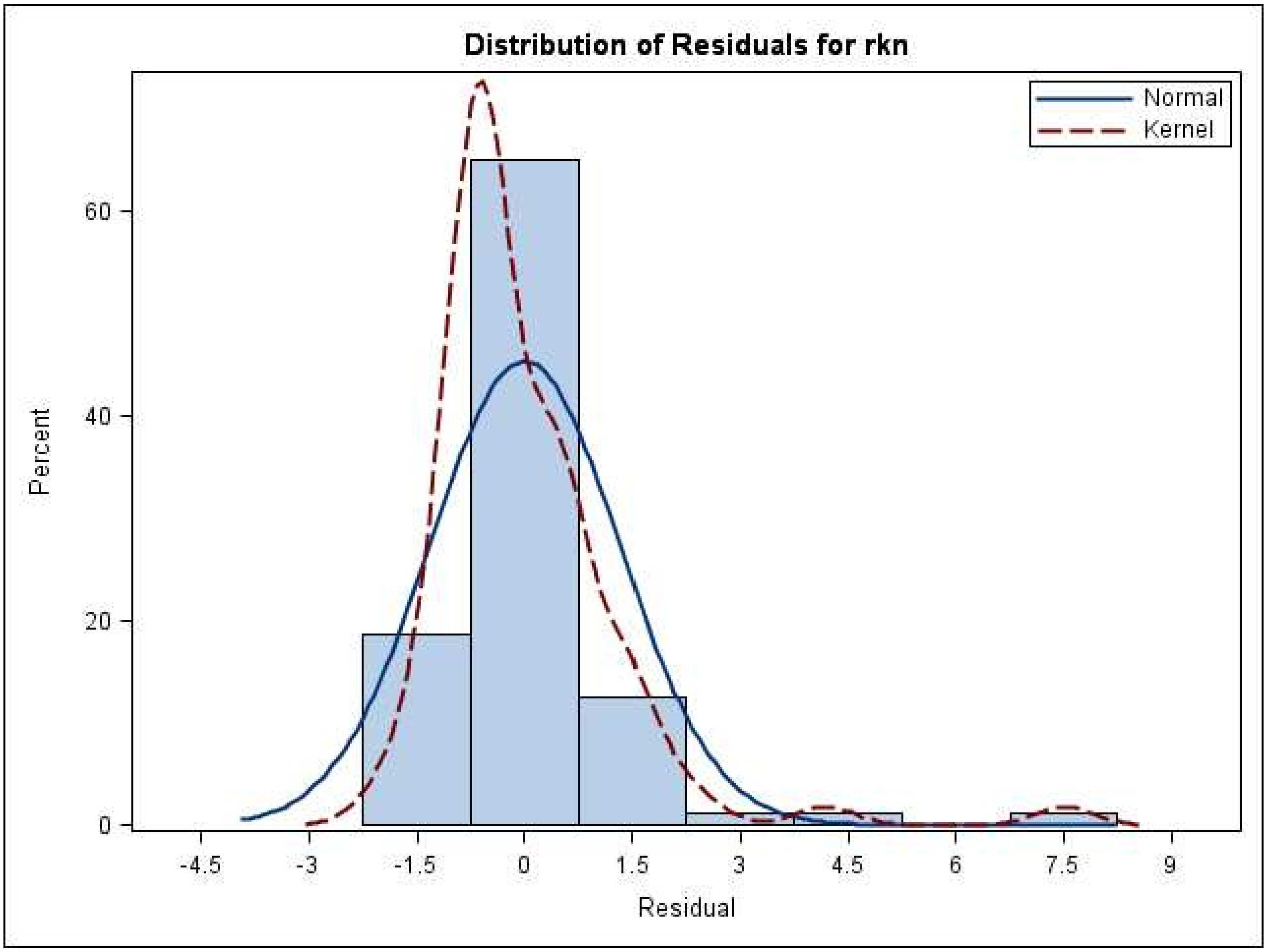


Figure E.3.1.2 Normal quantile plot of the raw residuals

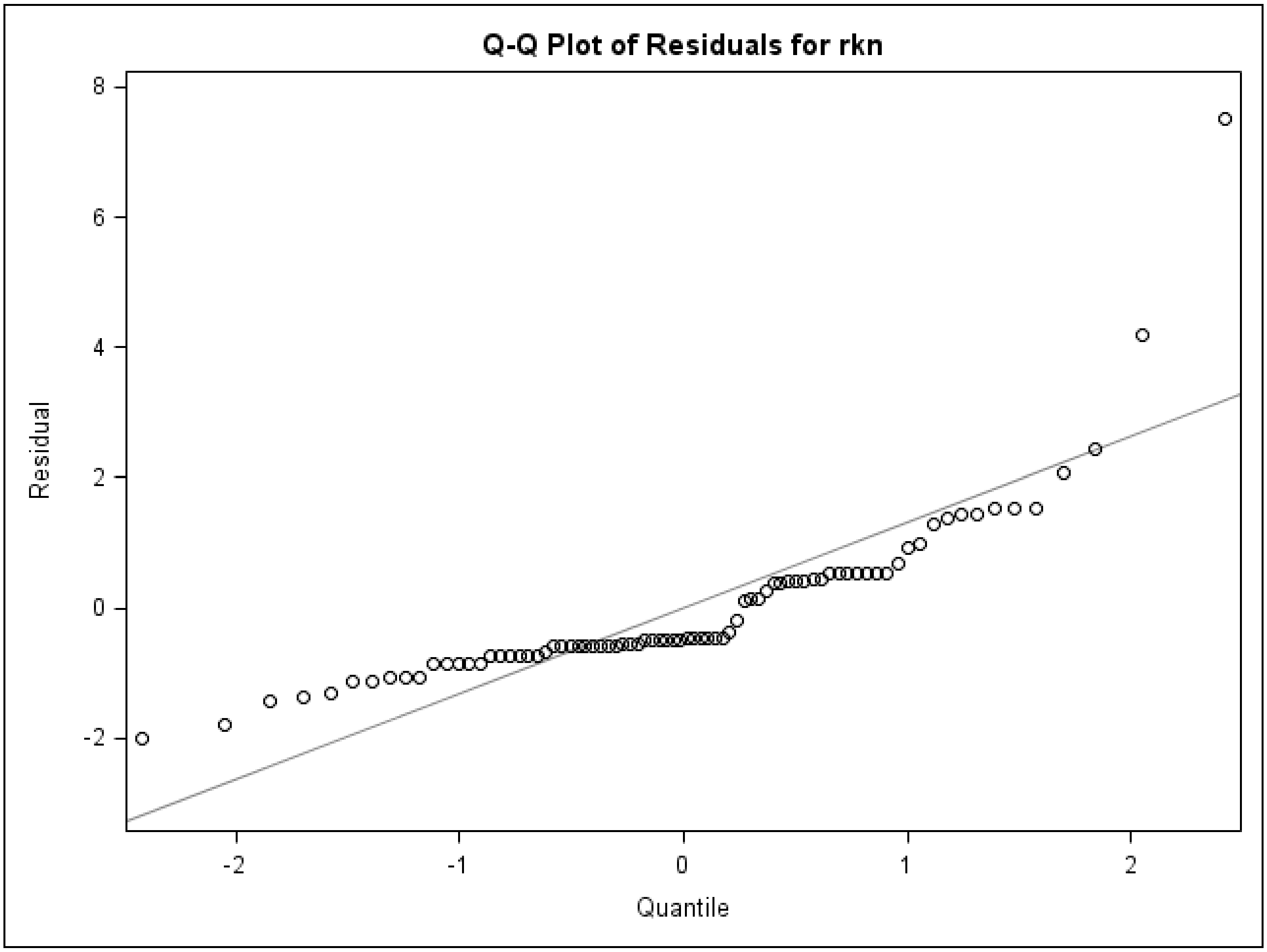


Figure E.3.1.3 Histogram of the Studentized residuals

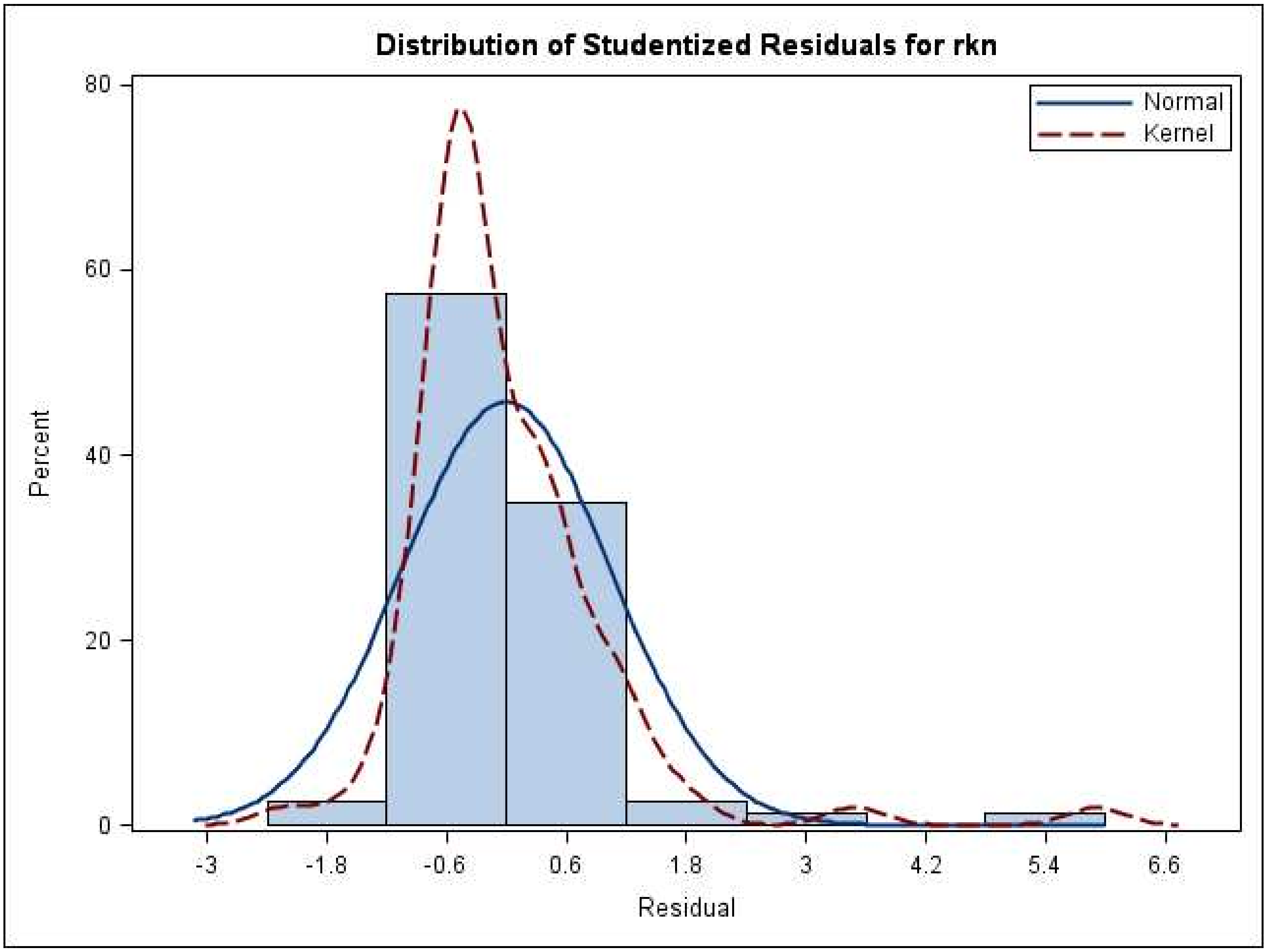


Figure E.3.1.4 Normal quantile plot of the Studentized residuals

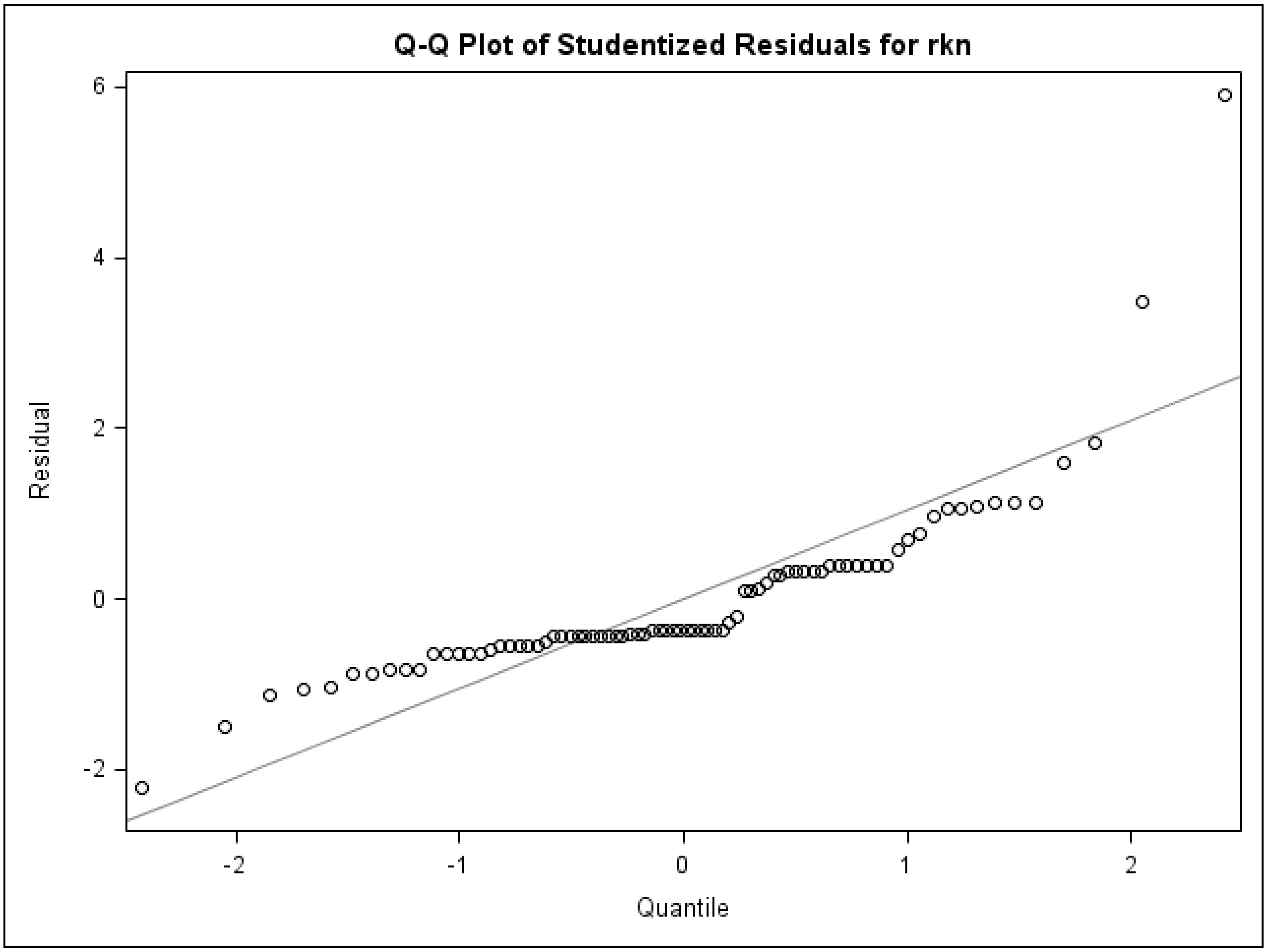


Figure E.3.1.5 Histogram of the Pearson residuals

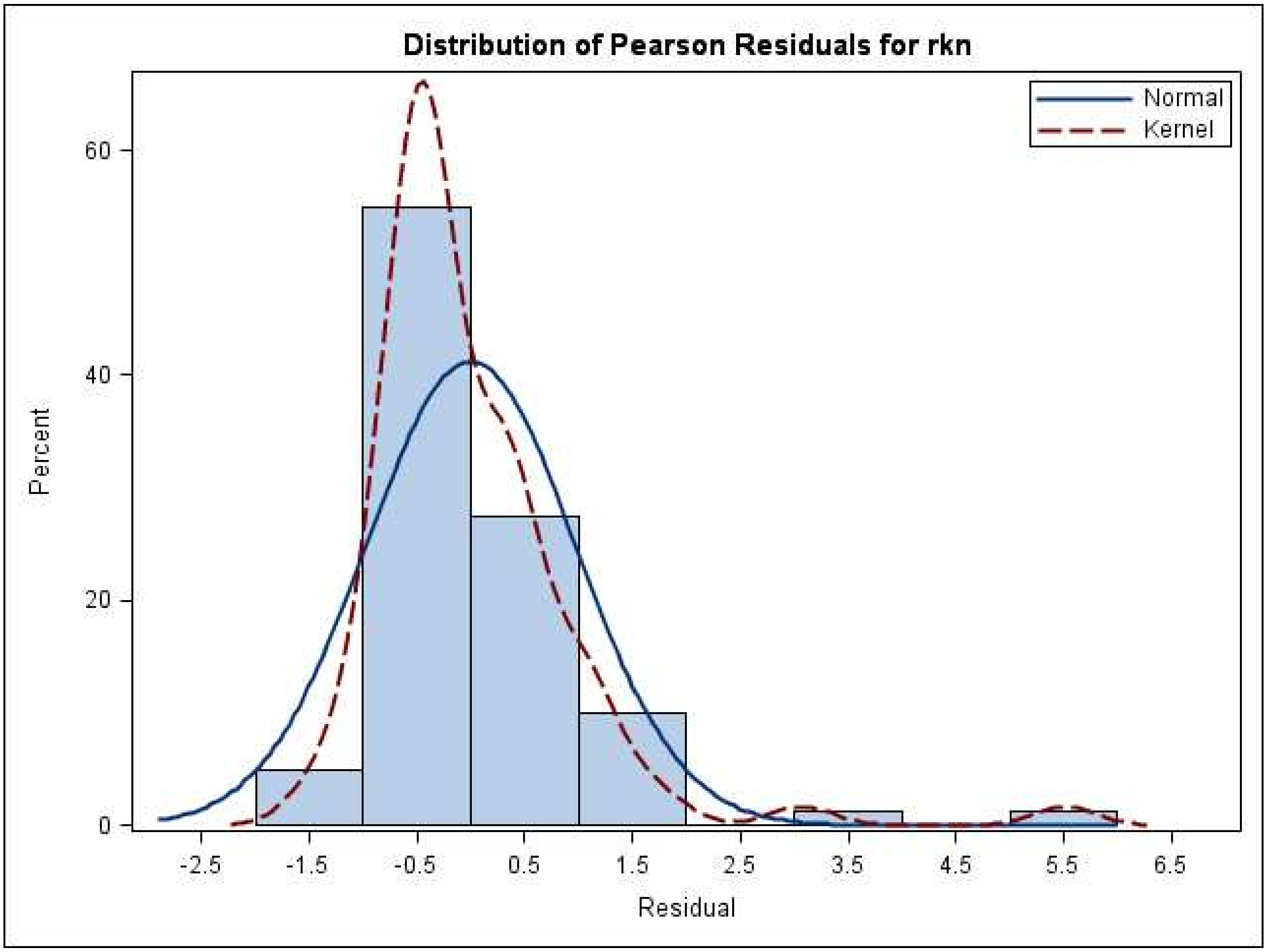
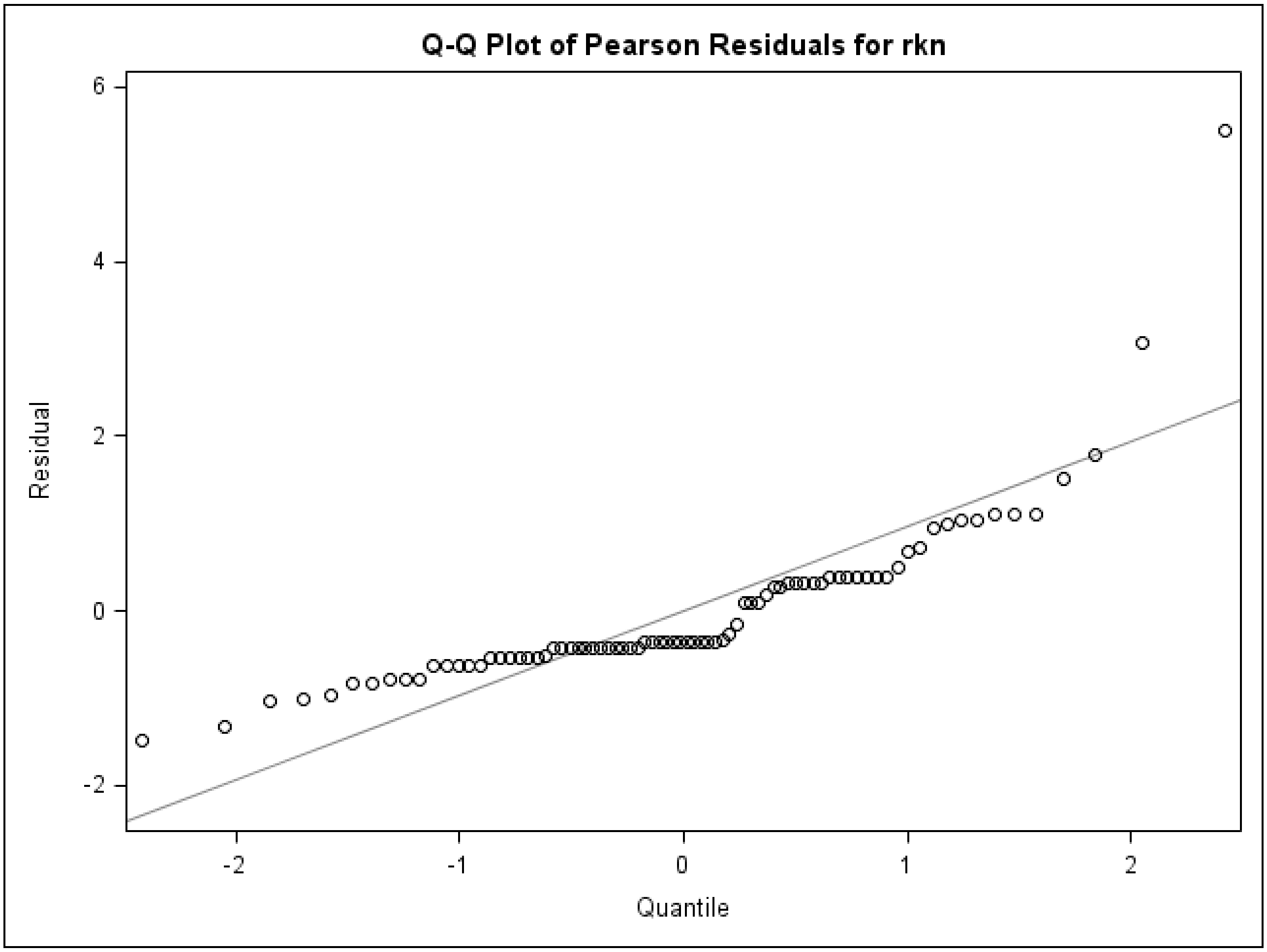


Figure E.3.1.6 Normal quantile plot of the Pearson residuals



E.3.2 September 2005 Model 2 Residual Plots

Figure E.3.2.1 Histogram of the raw residuals

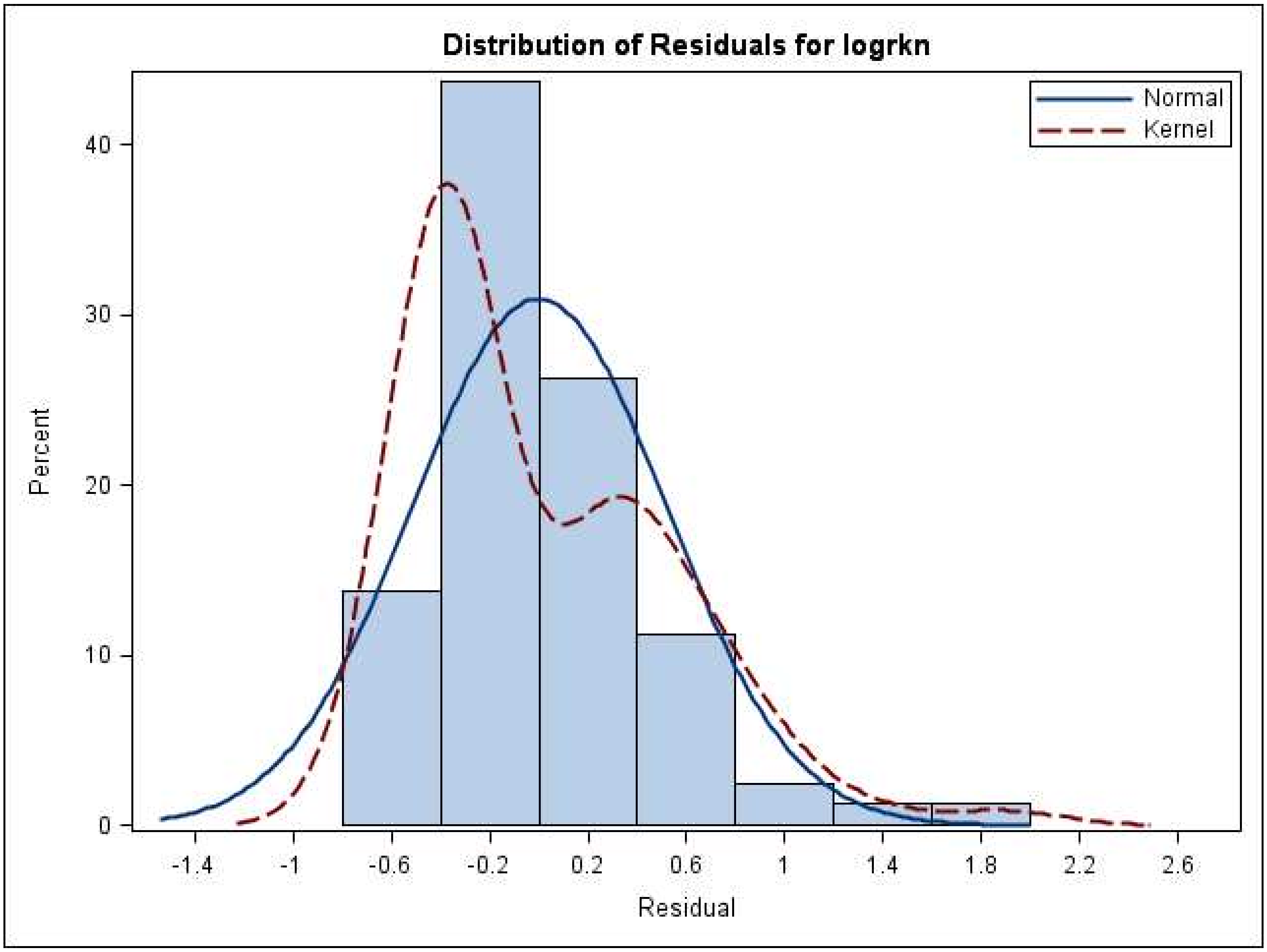


Figure E.3.2.2 Normal quantile plot of the raw residuals

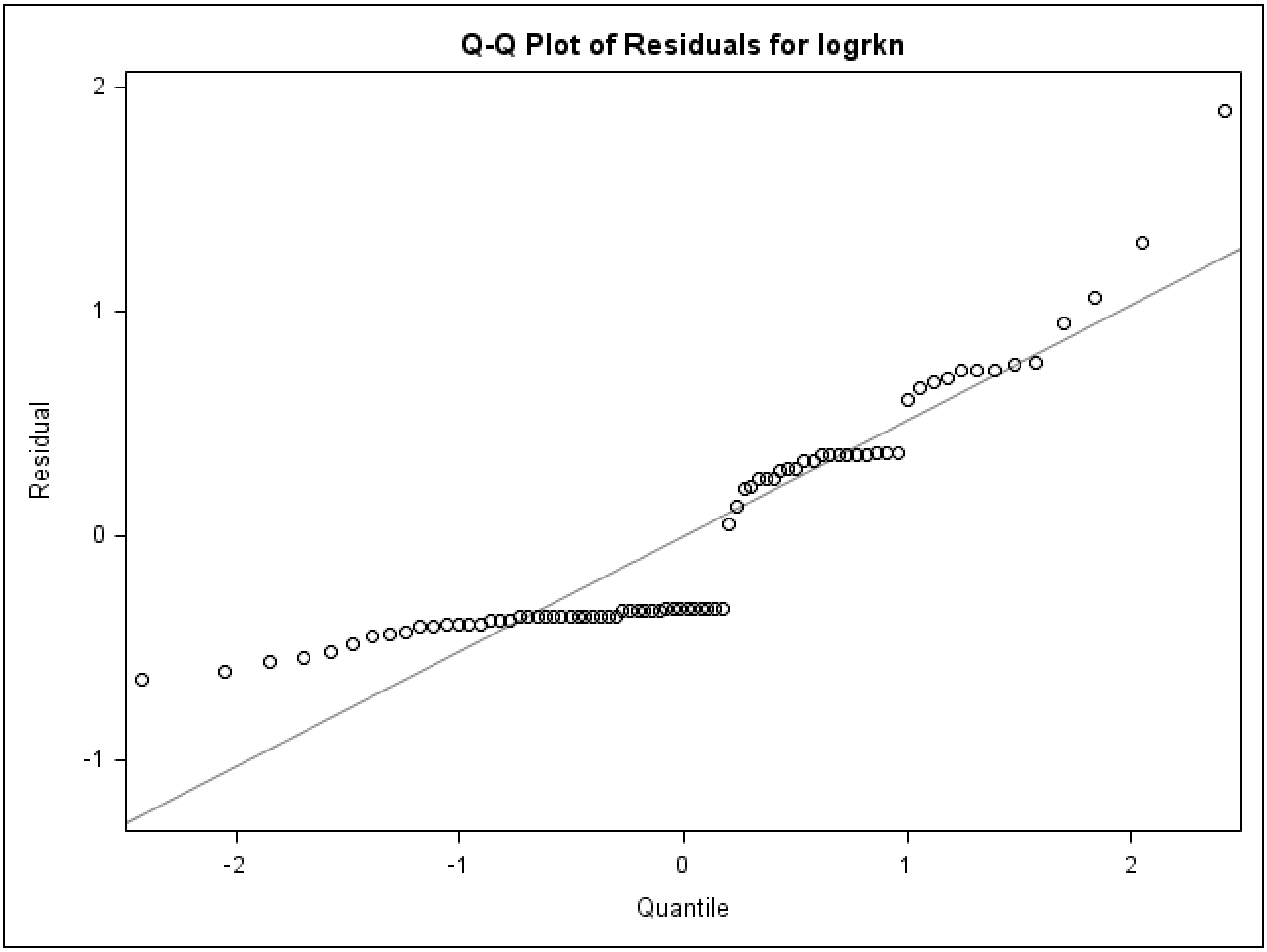


Figure E.3.2.3 Histogram of the Studentized residuals

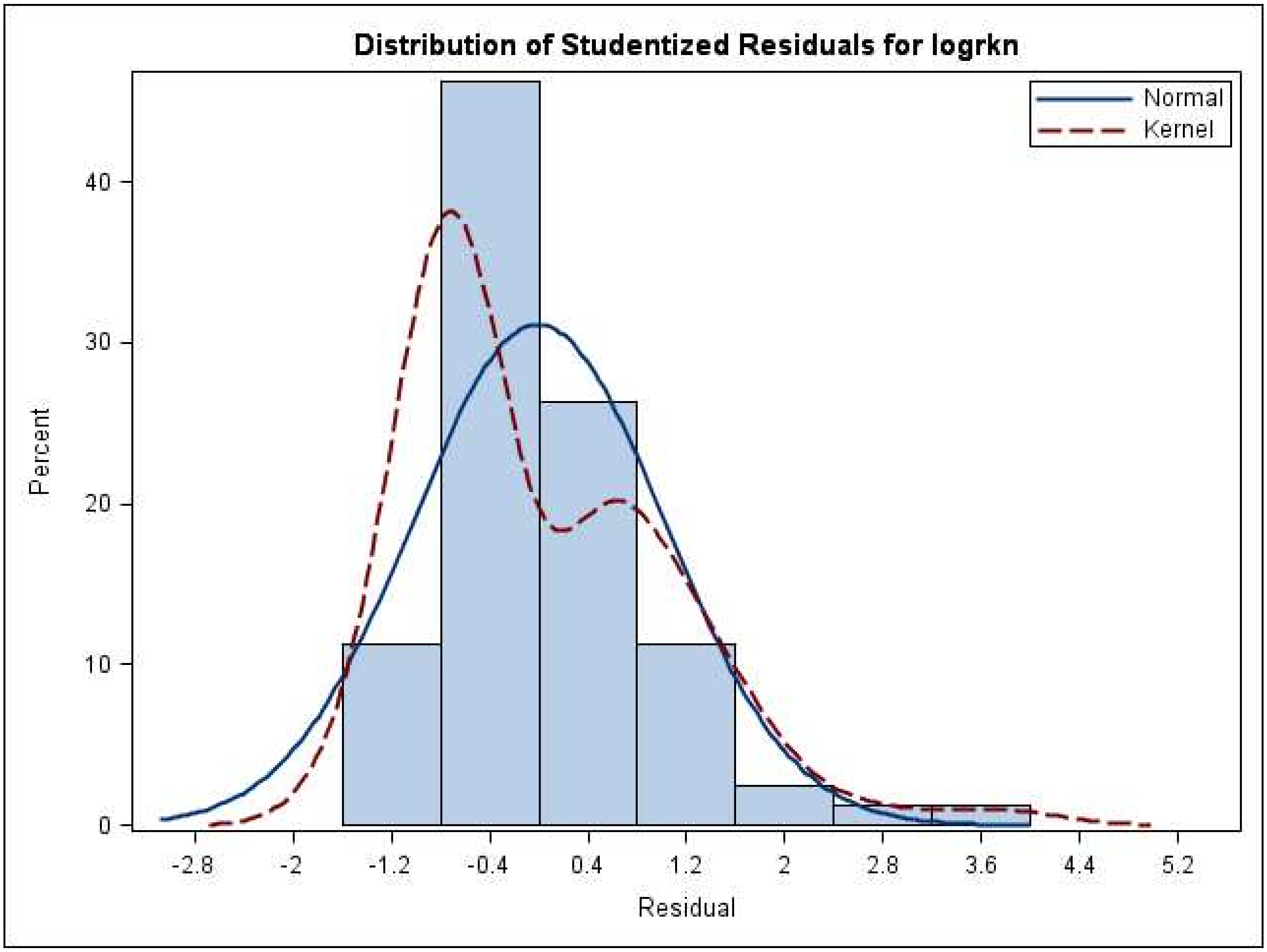


Figure E.3.2.4 Normal quantile plot of the Studentized residuals

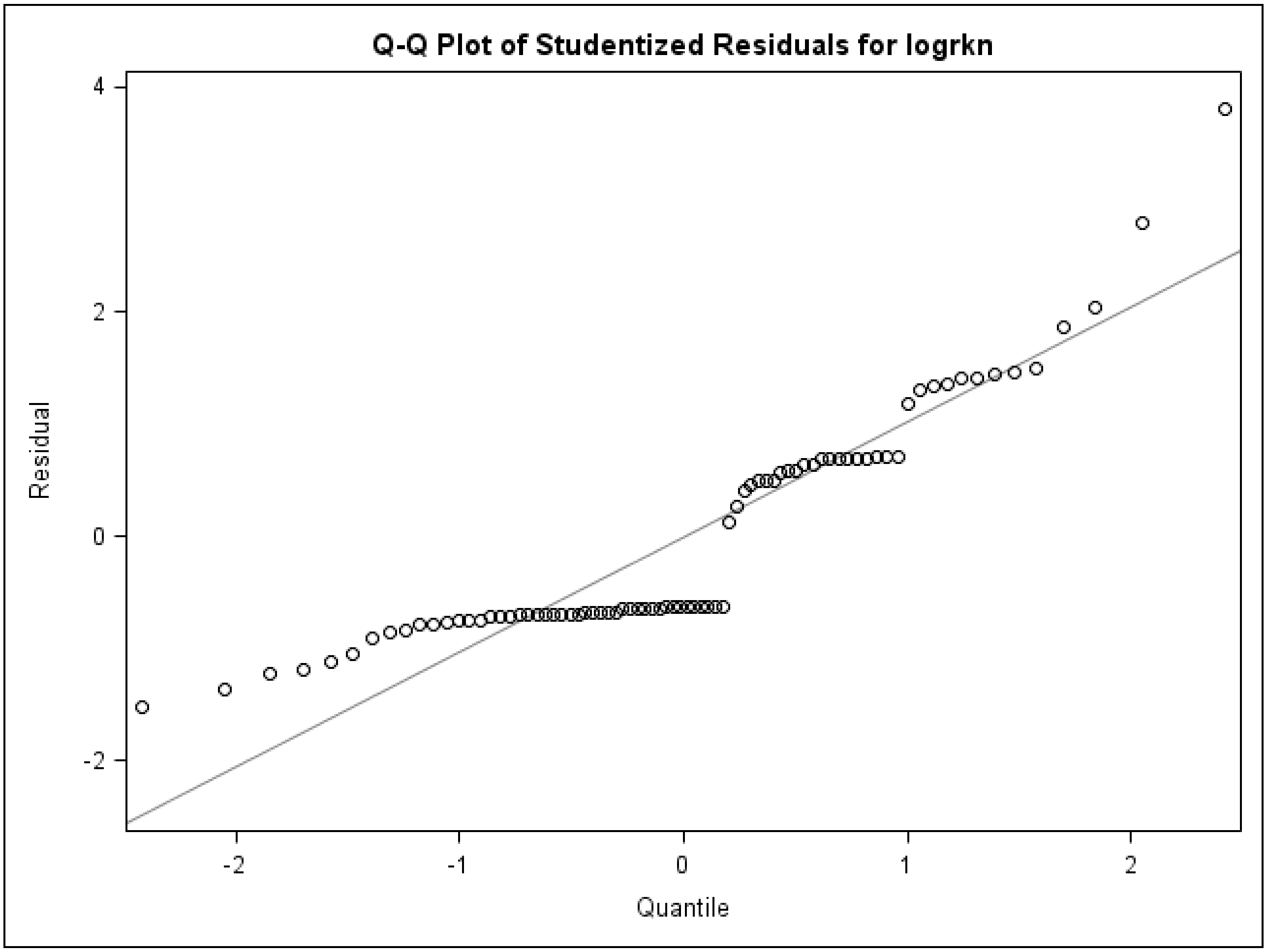


Figure E.3.2.5 Histogram of the Pearson residuals

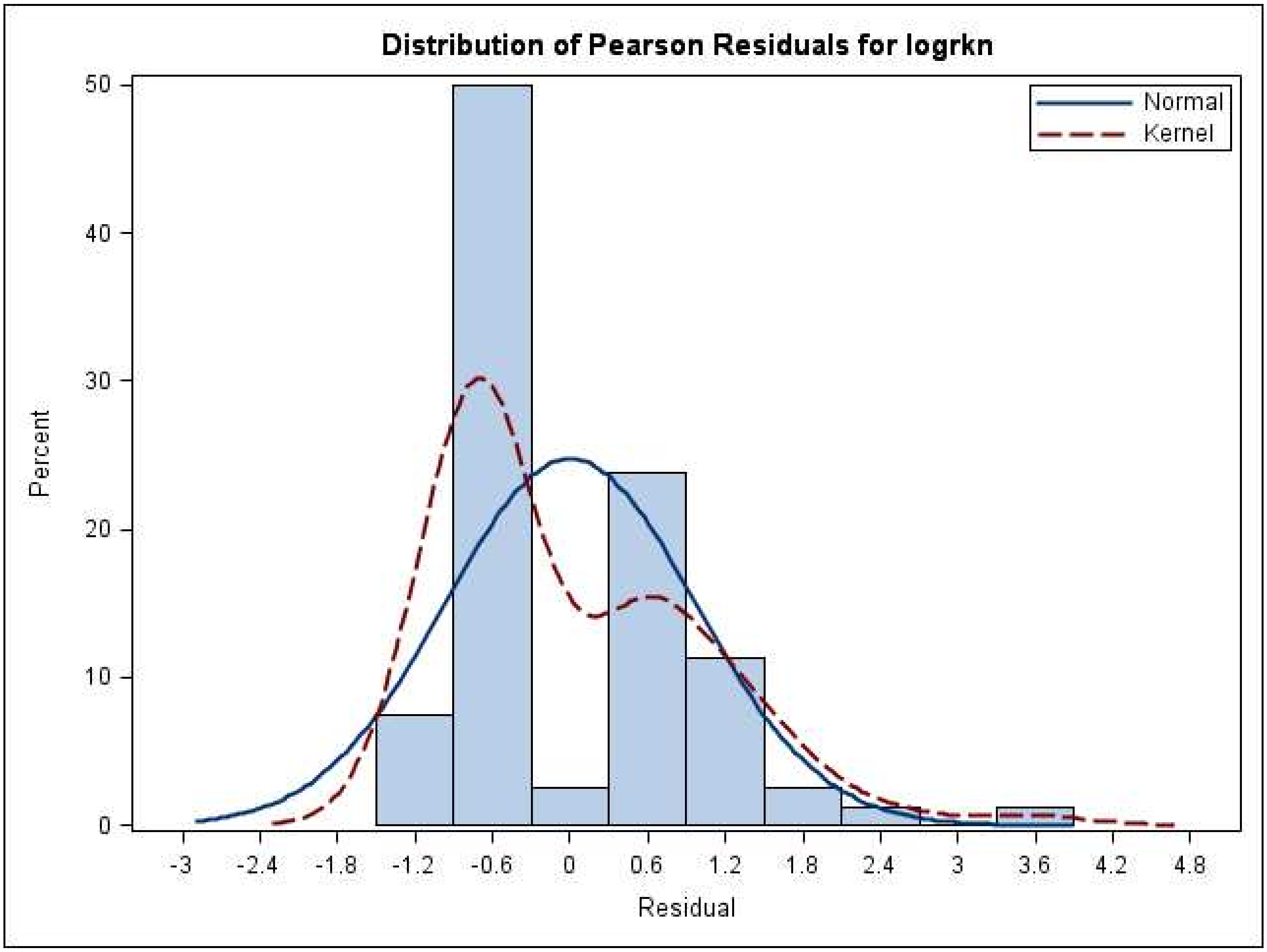
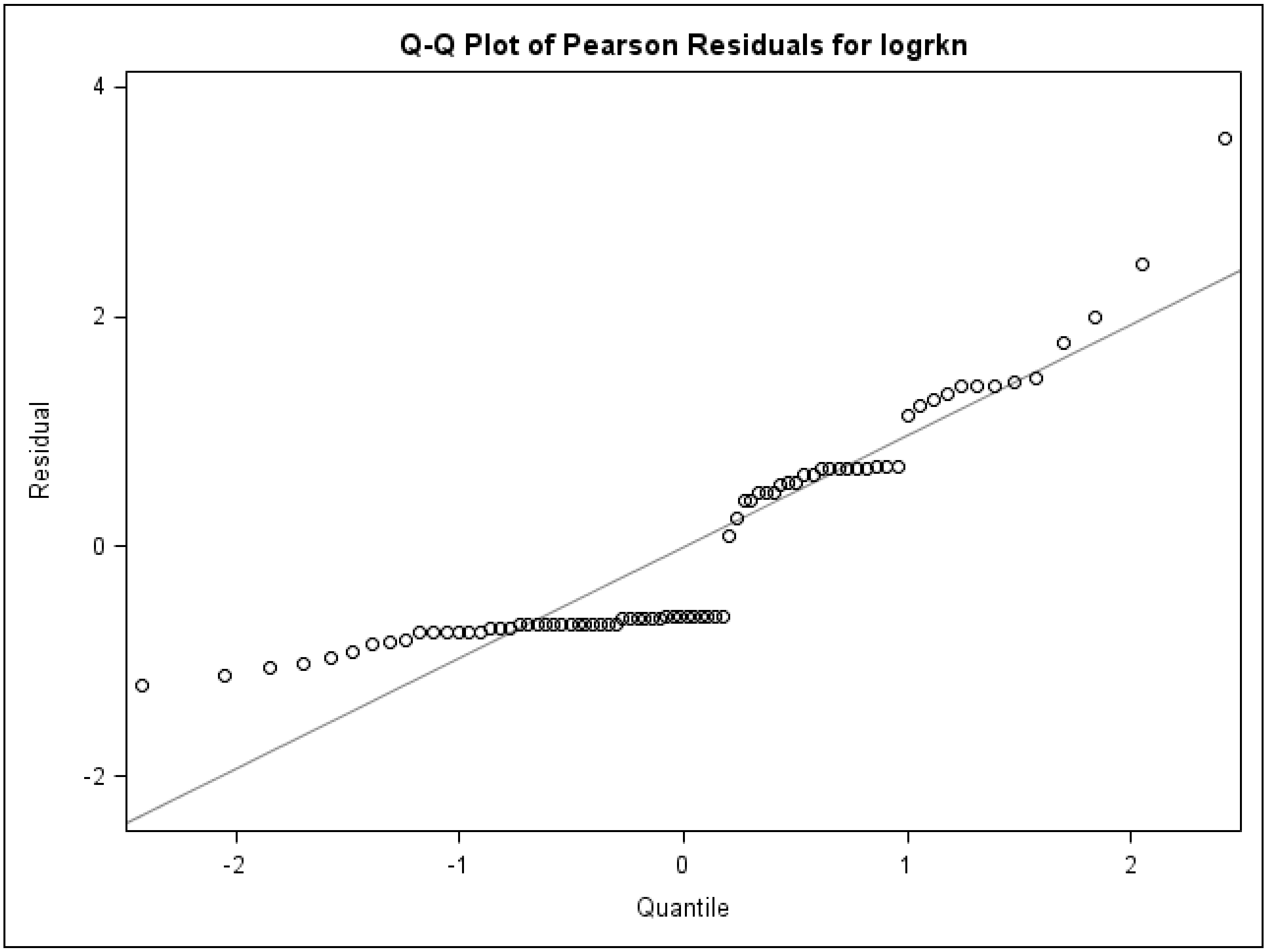


Figure E.3.2.6 Normal quantile plot of the Pearson residuals



E.3.3 September 2005 Model 3 Residual Plots

Figure E.3.3.1 Histogram of the raw residuals

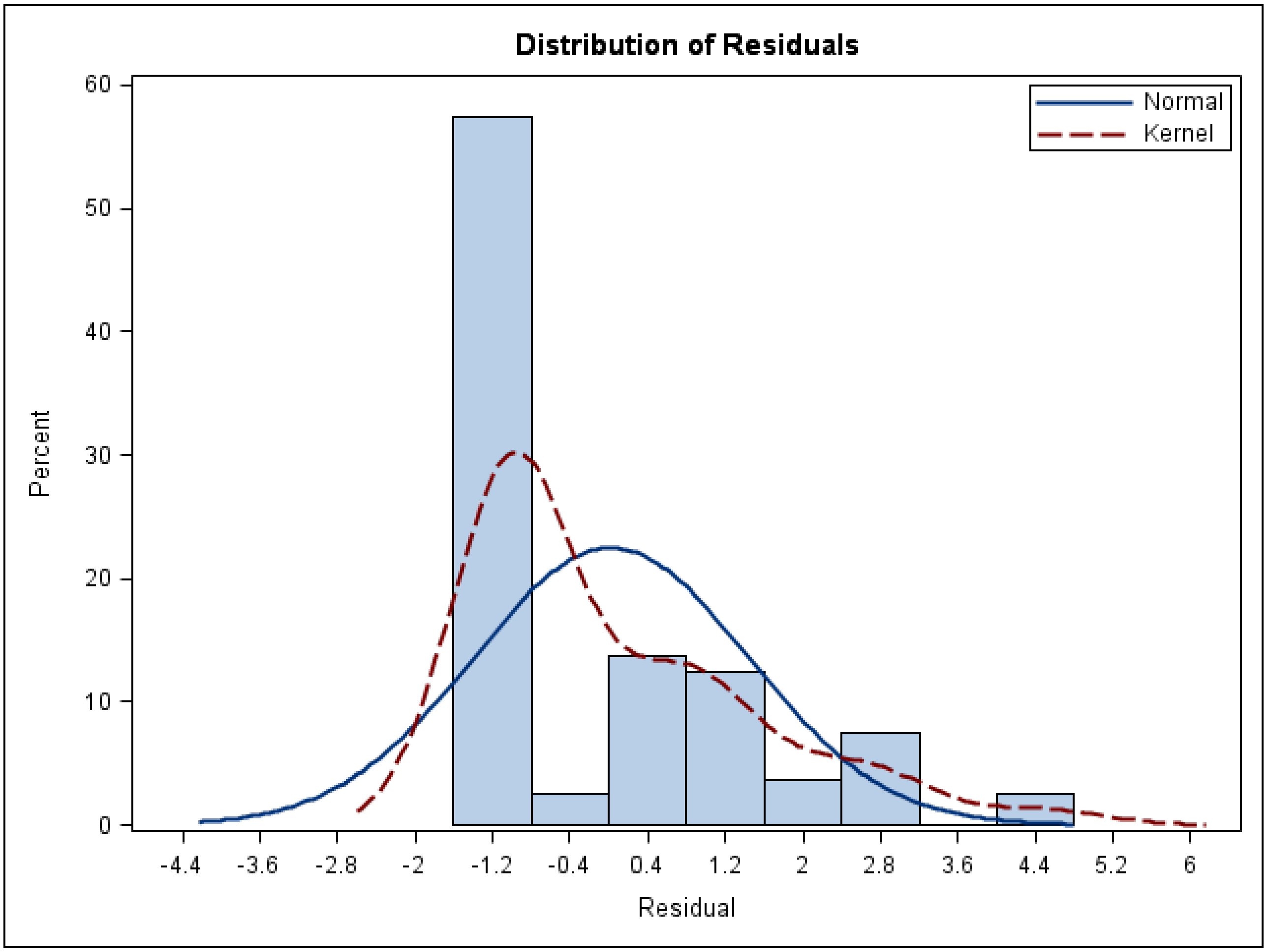


Figure E.3.3.2 Normal quantile plot of the raw residuals

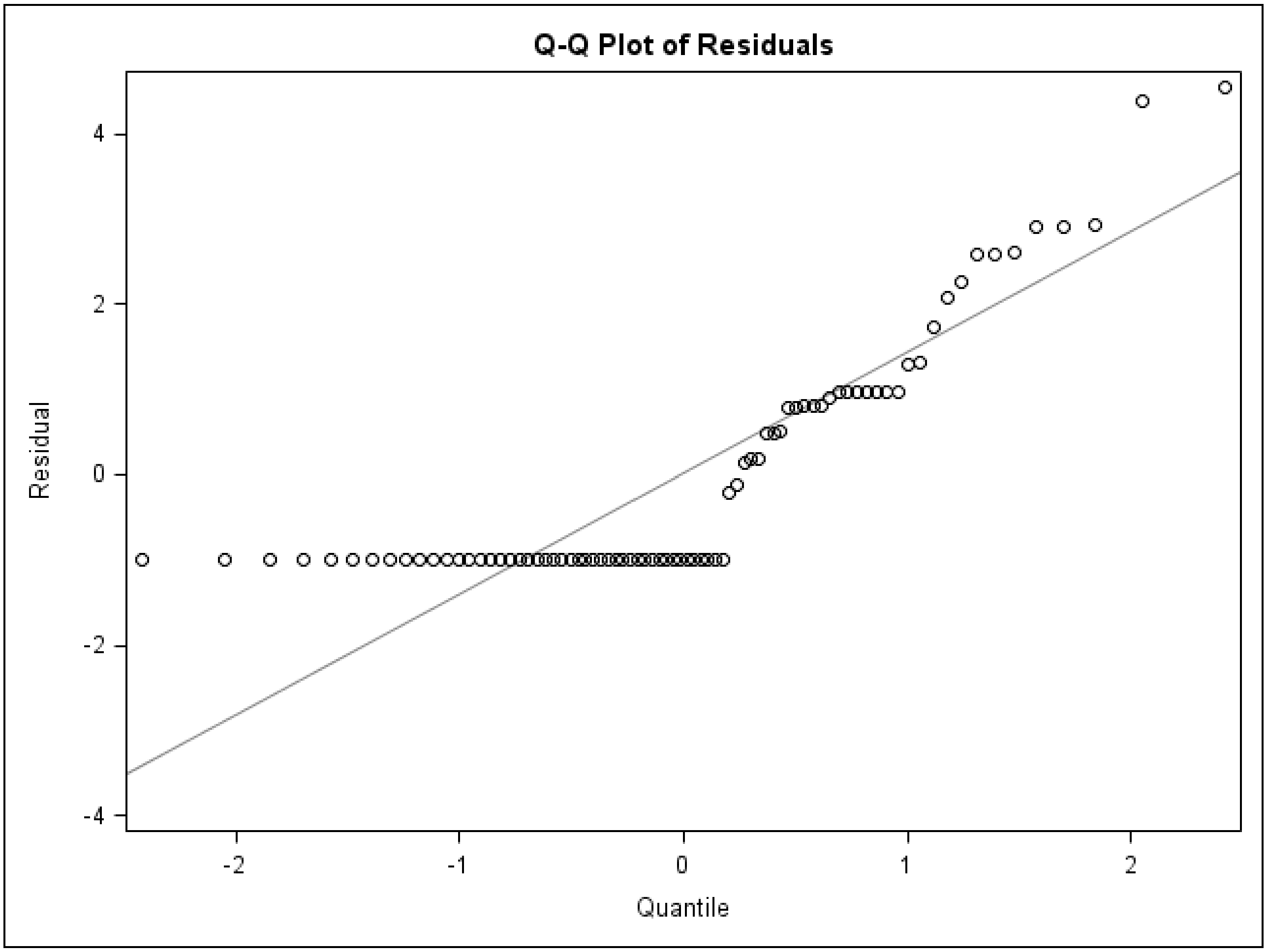


Figure E.3.3.3 Histogram of the Studentized residuals

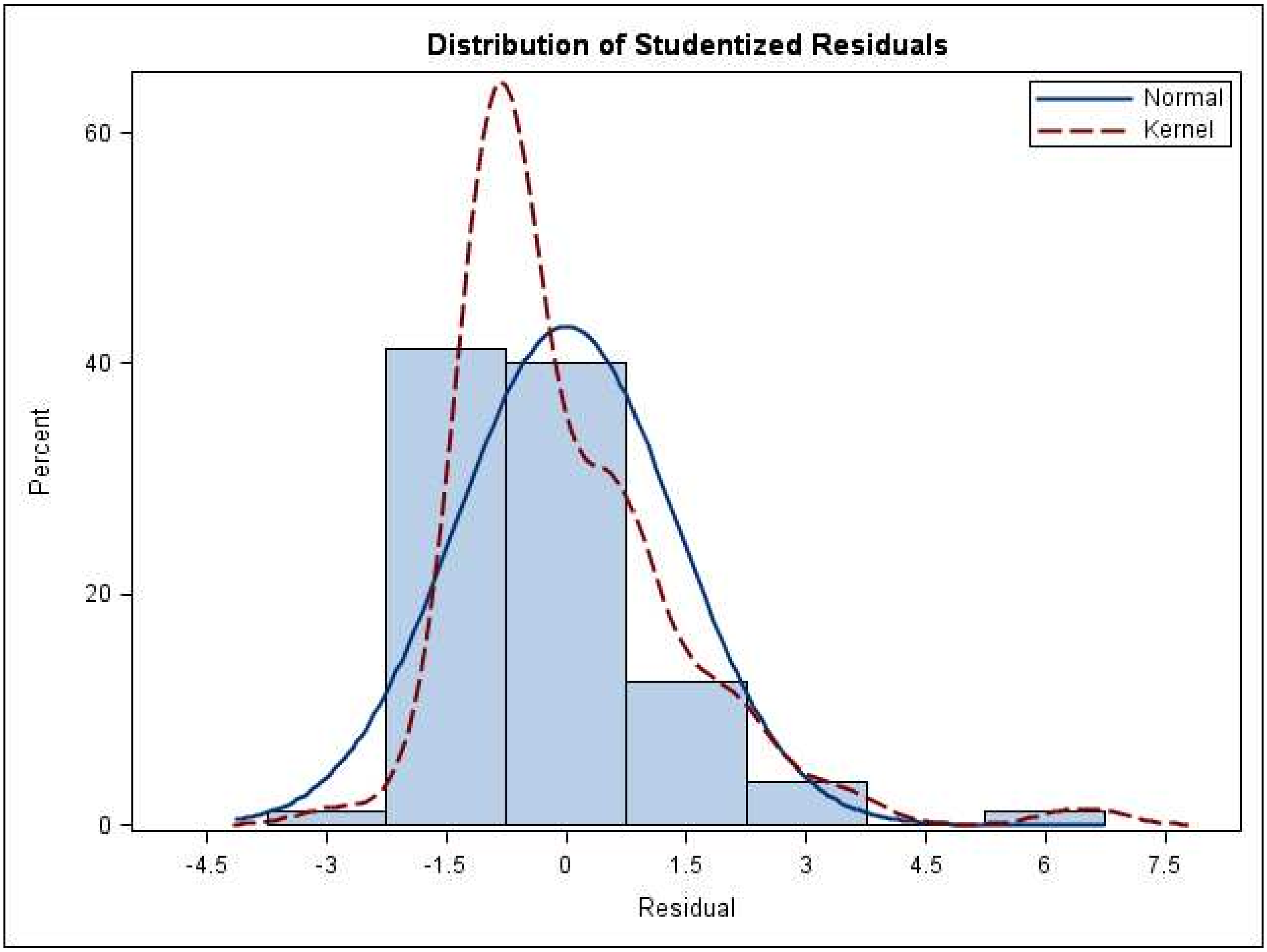


Figure E.3.3.4 Normal quantile plot of the Studentized residuals

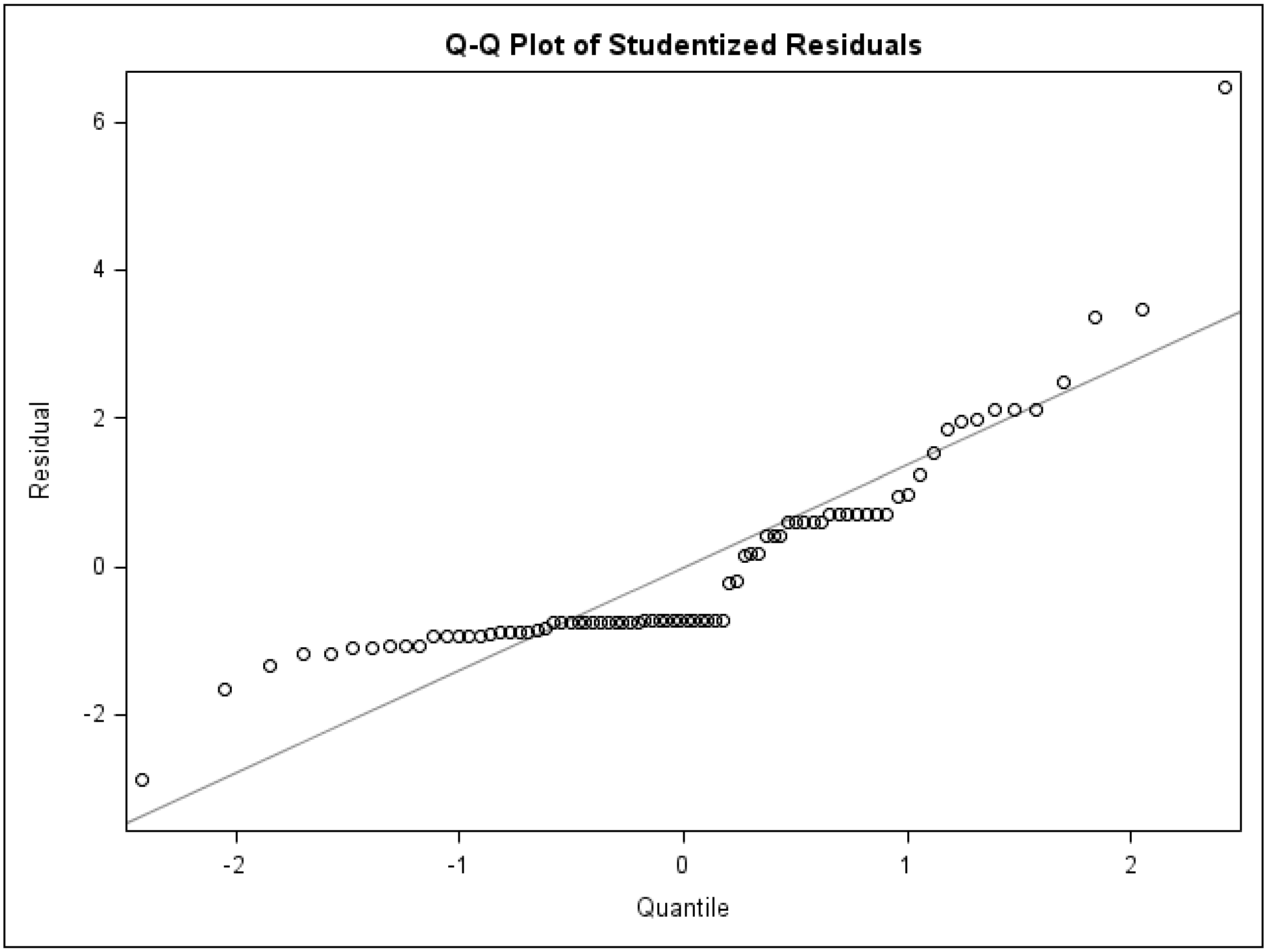


Figure E.3.3.5 Histogram of the Pearson residuals

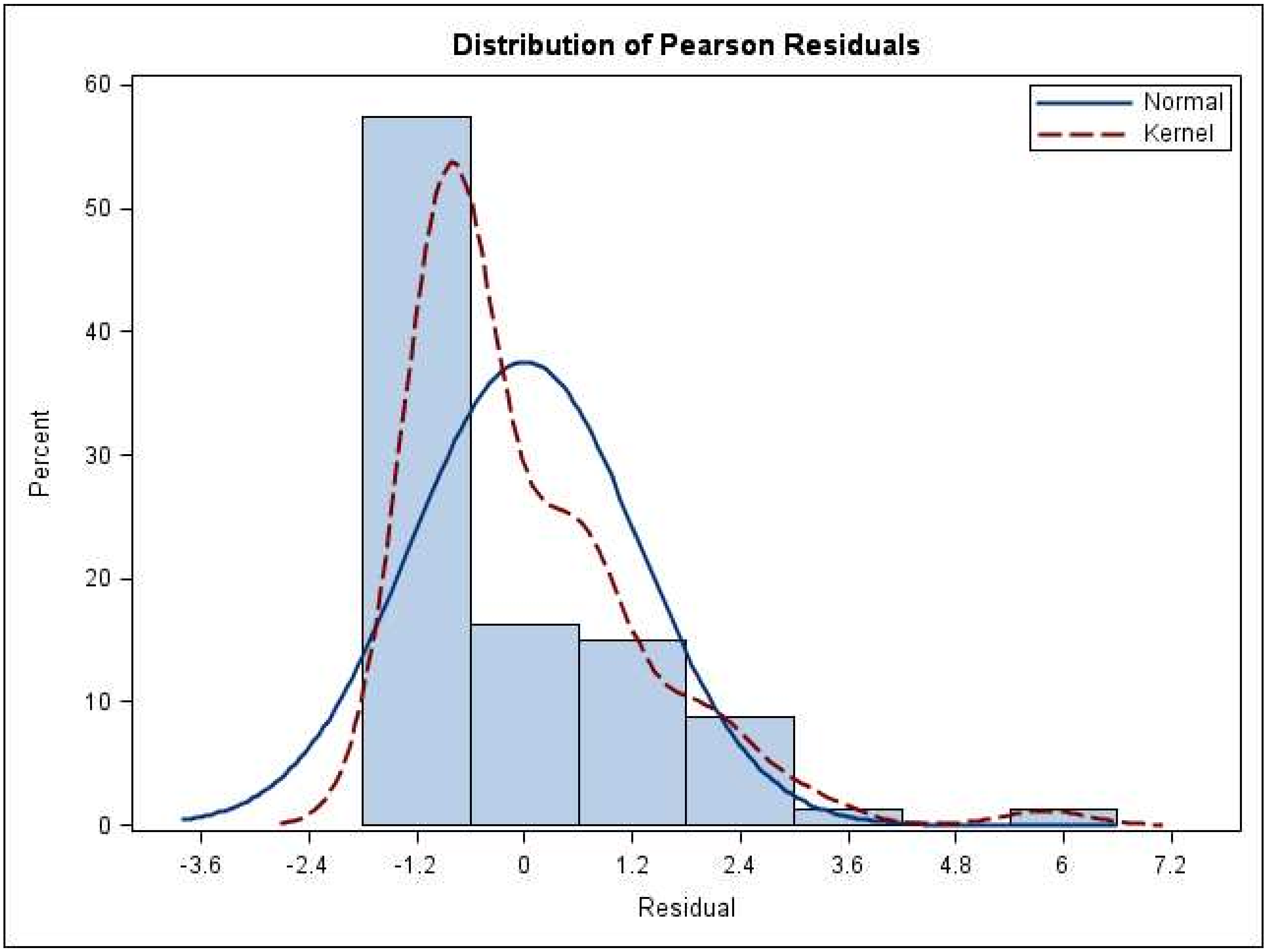
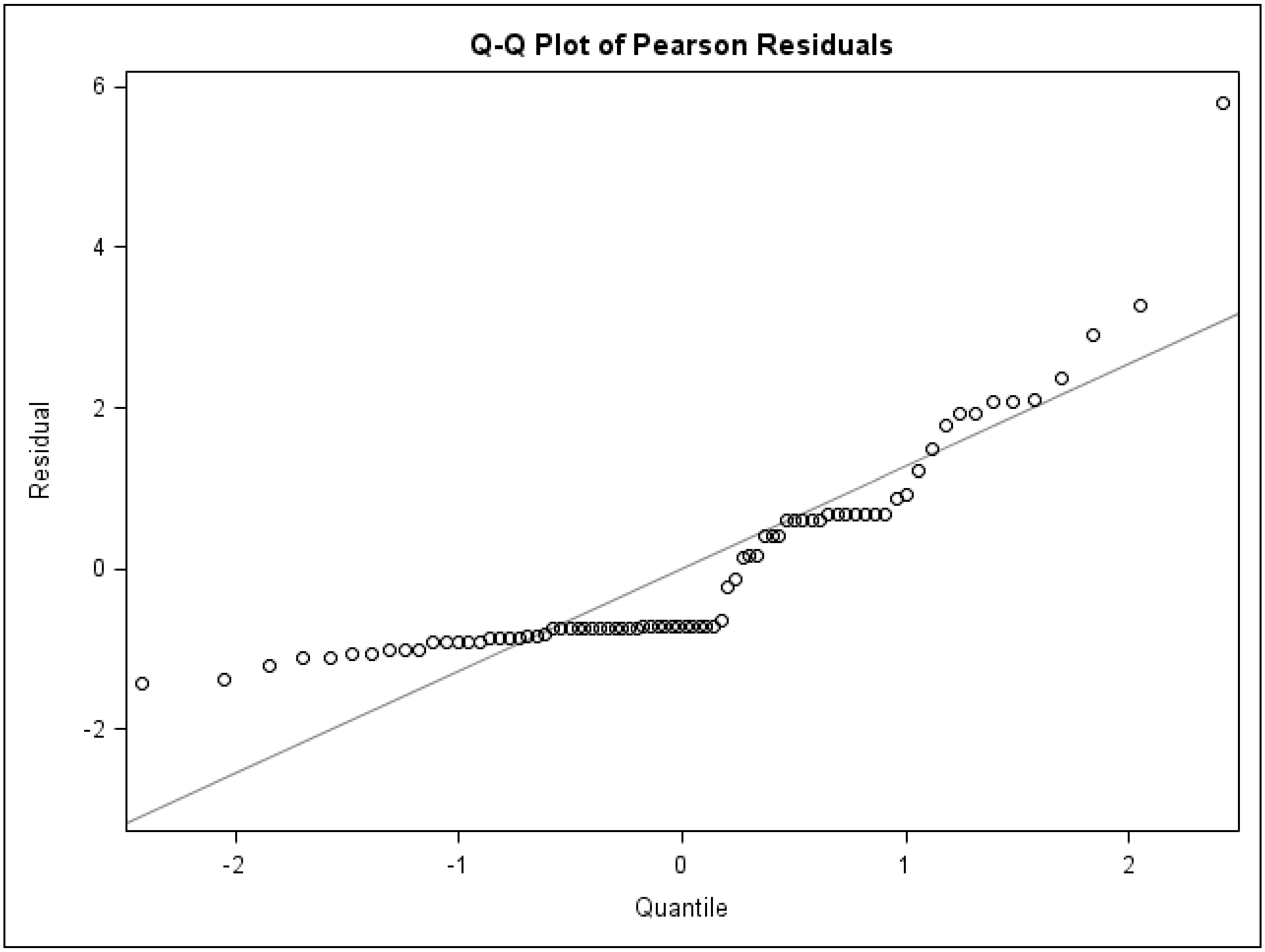


Figure E.3.3.6 Normal quantile plot of the Pearson residuals



E.3.4 September 2005 Model 4 Residual Plots

Figure E.3.4.1 Histogram of the raw residuals

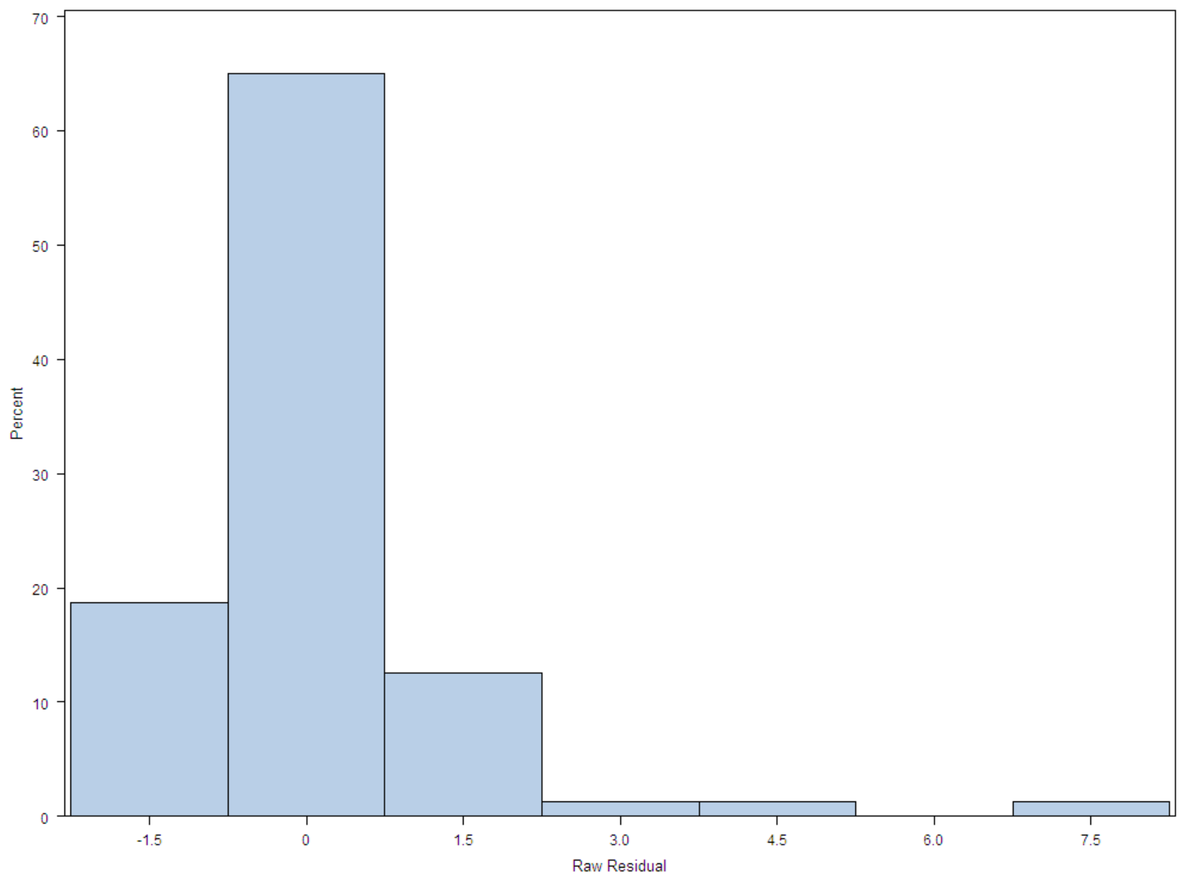


Figure E.3.4.2 Histogram of the Pearson residuals

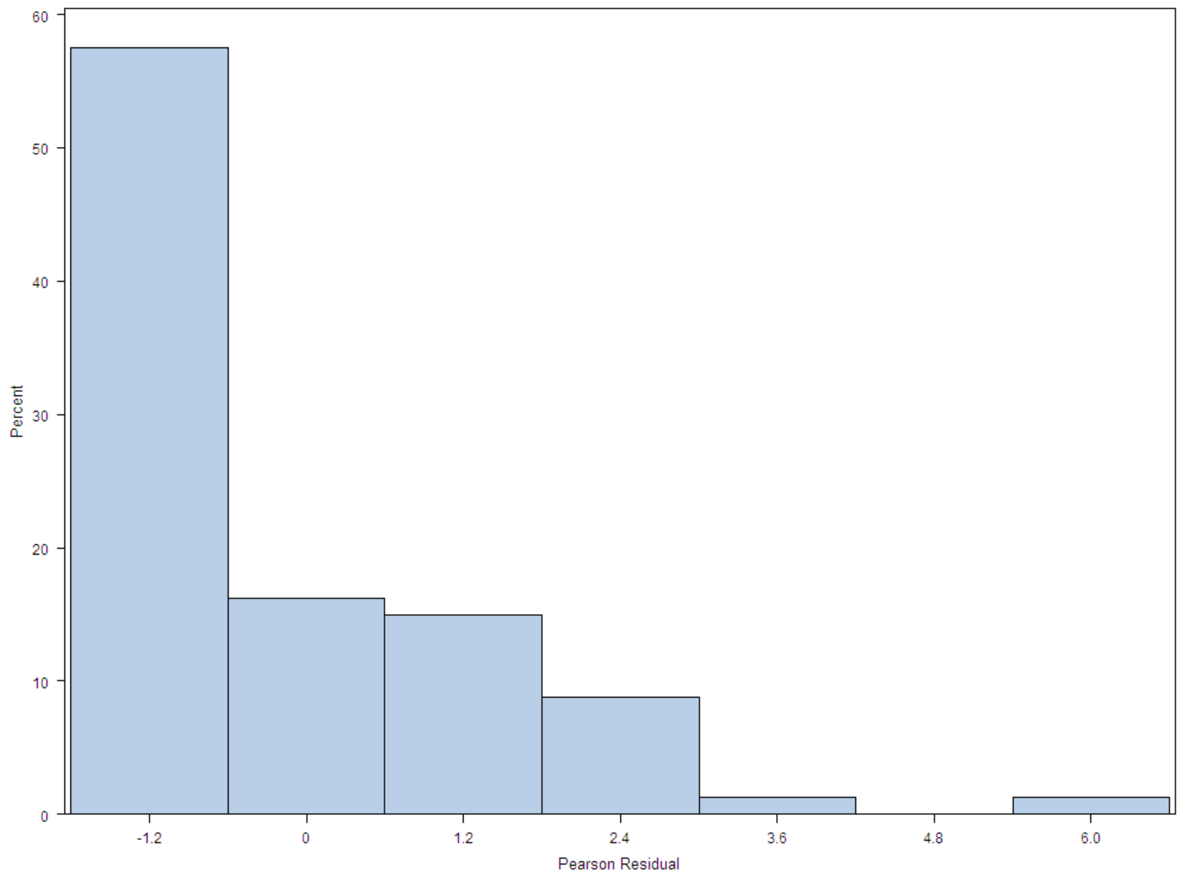


Figure E.3.4.3 Histogram of the deviance residuals

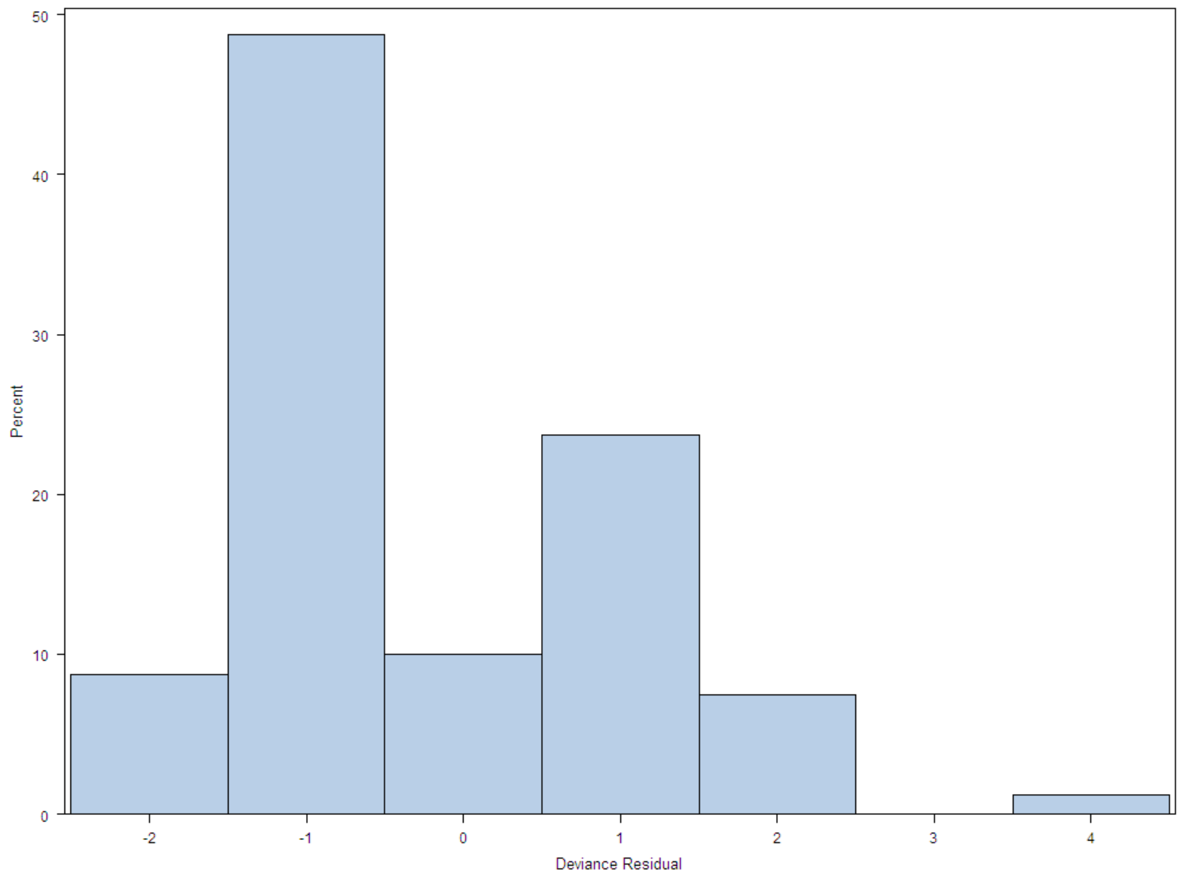


Figure E.3.4.4 Histogram of the likelihood residuals

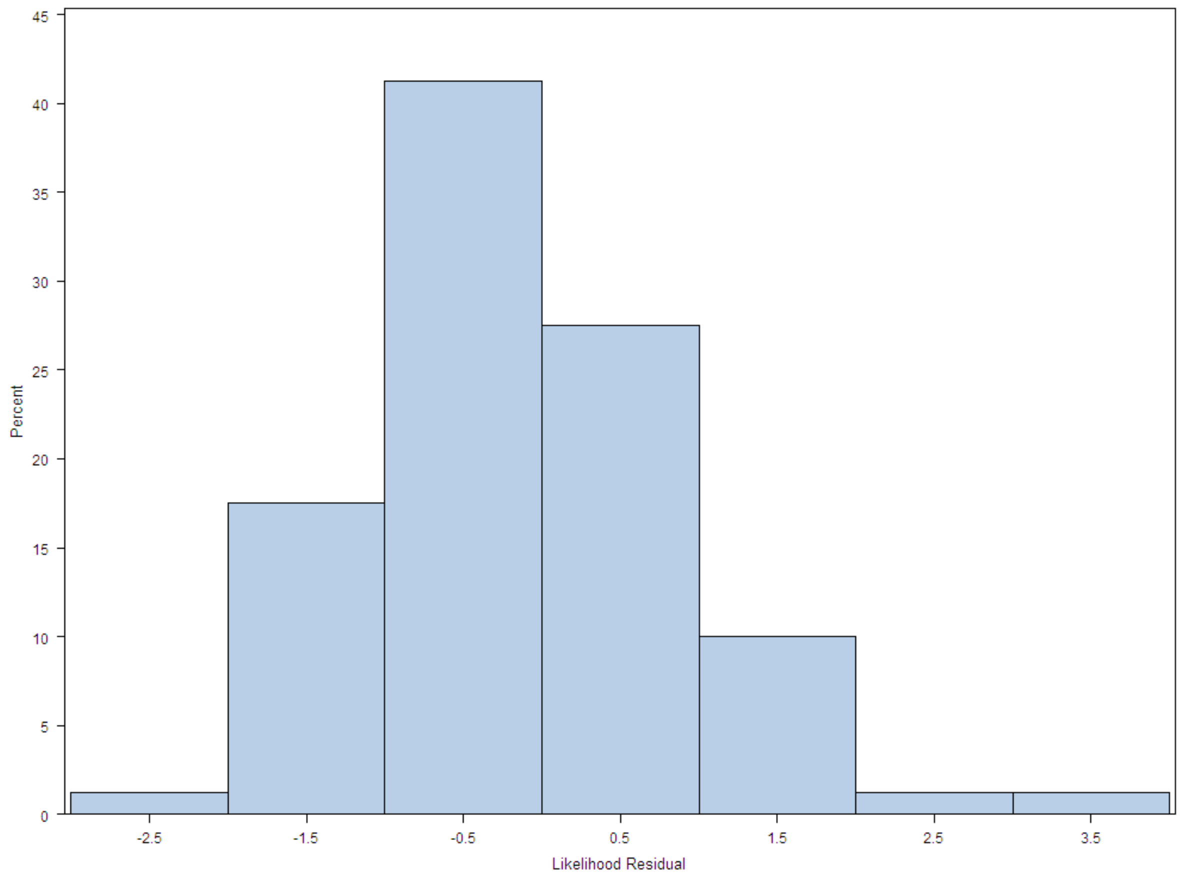


Figure E.3.4.5 Histogram of the standardized Pearson residuals

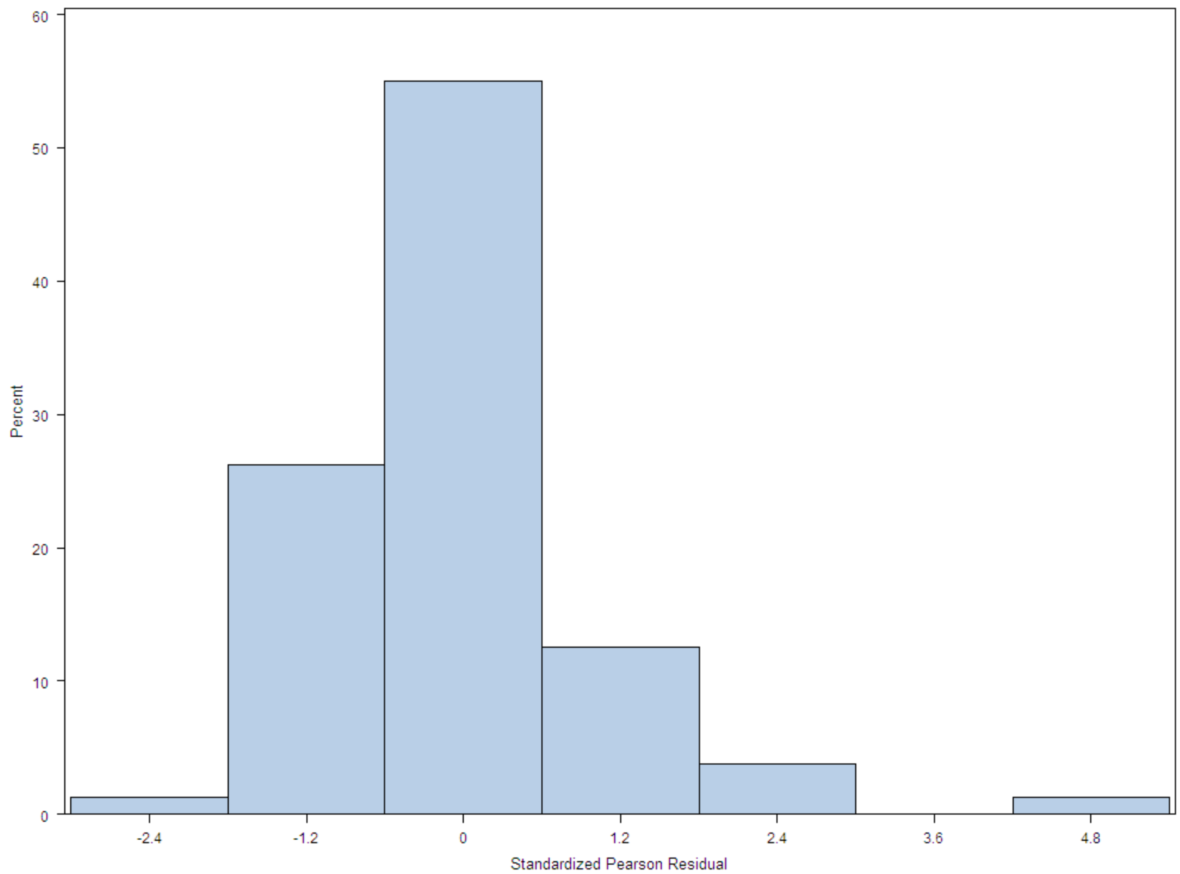
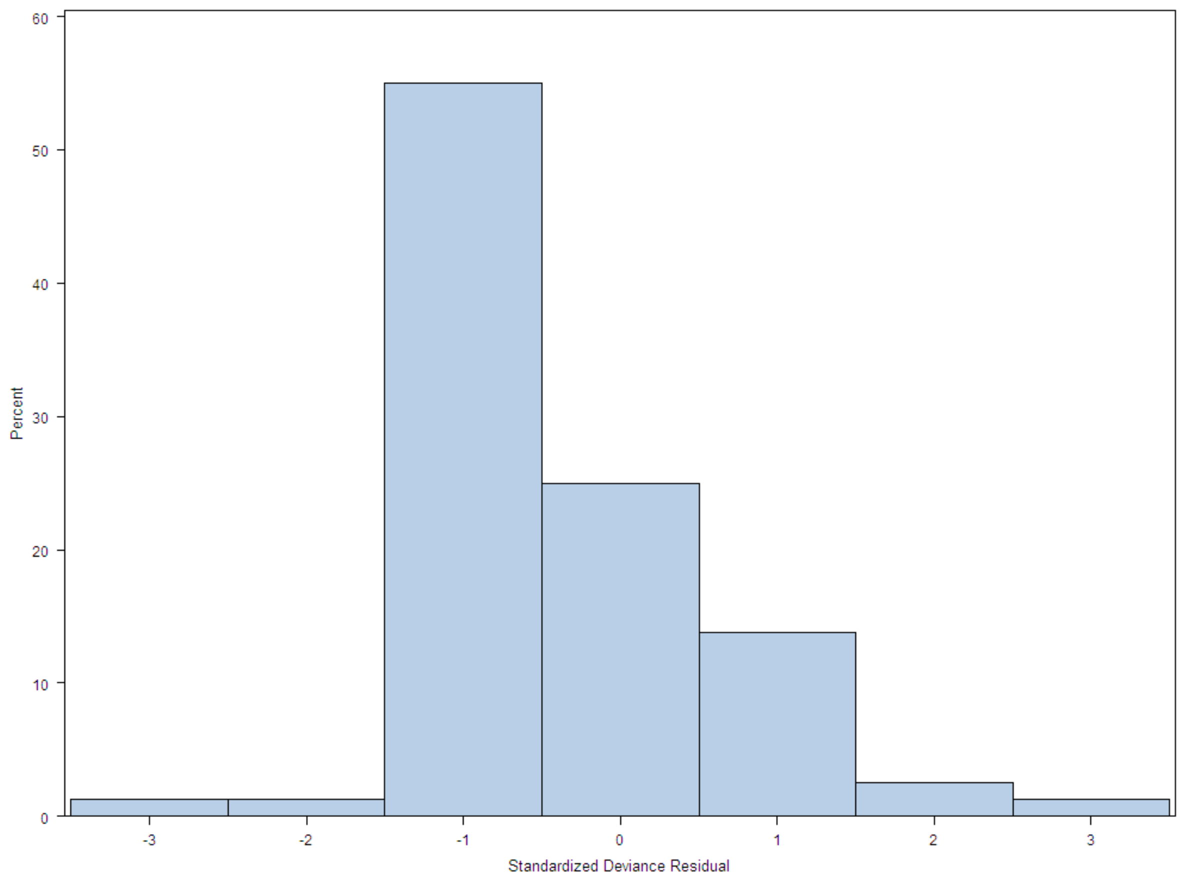


Figure E.3.4.6 Histogram of the standardized deviance residuals



E.3.5 September 2005 Model 5 Residual Plots

Figure E.3.5.1 Histogram of the raw residuals

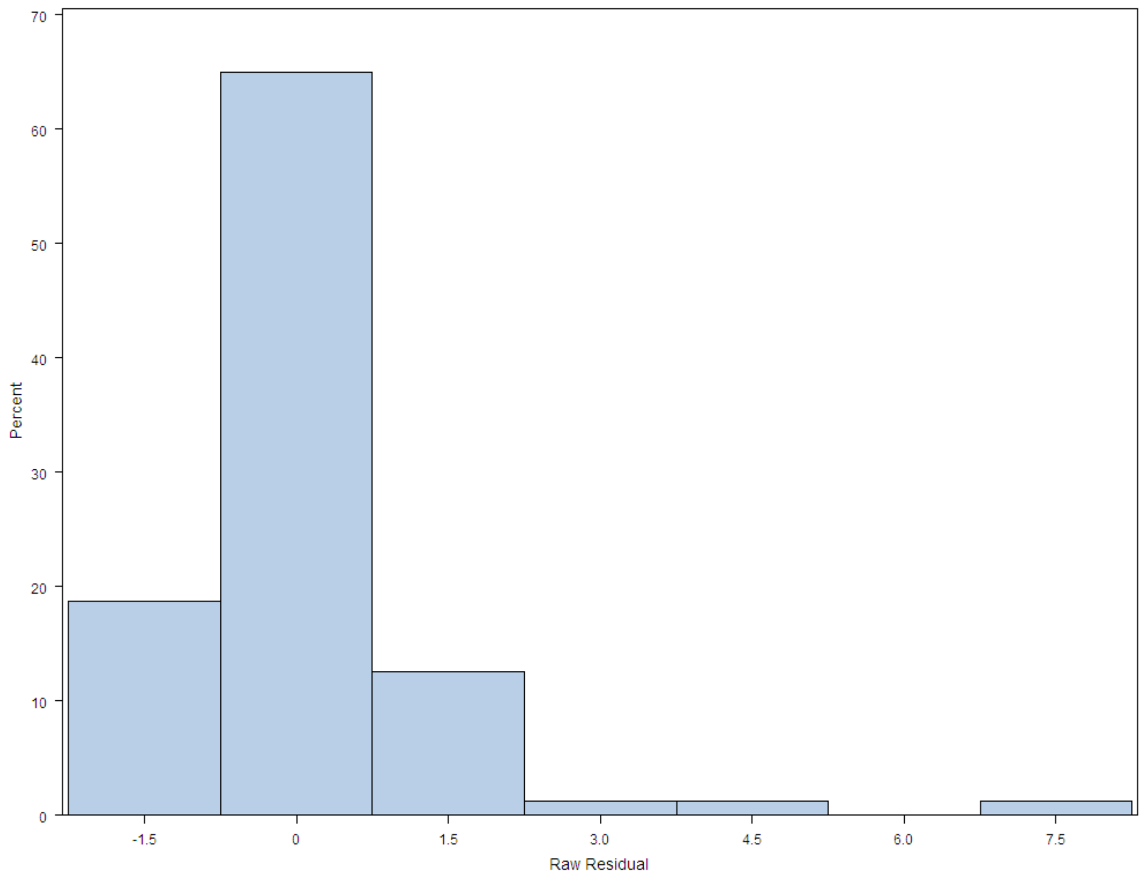


Figure E.3.5.2 Histogram of the Pearson residuals

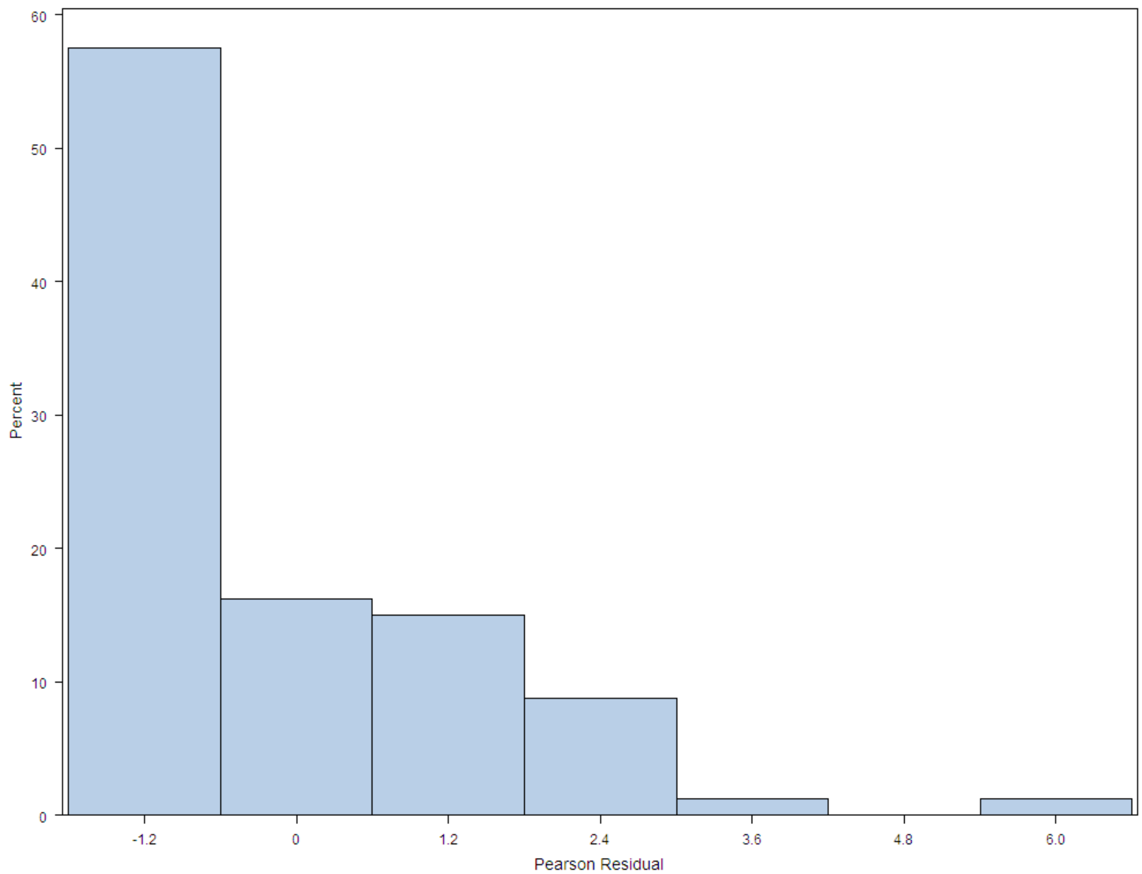


Figure E.3.5.3 Histogram of the deviance residuals

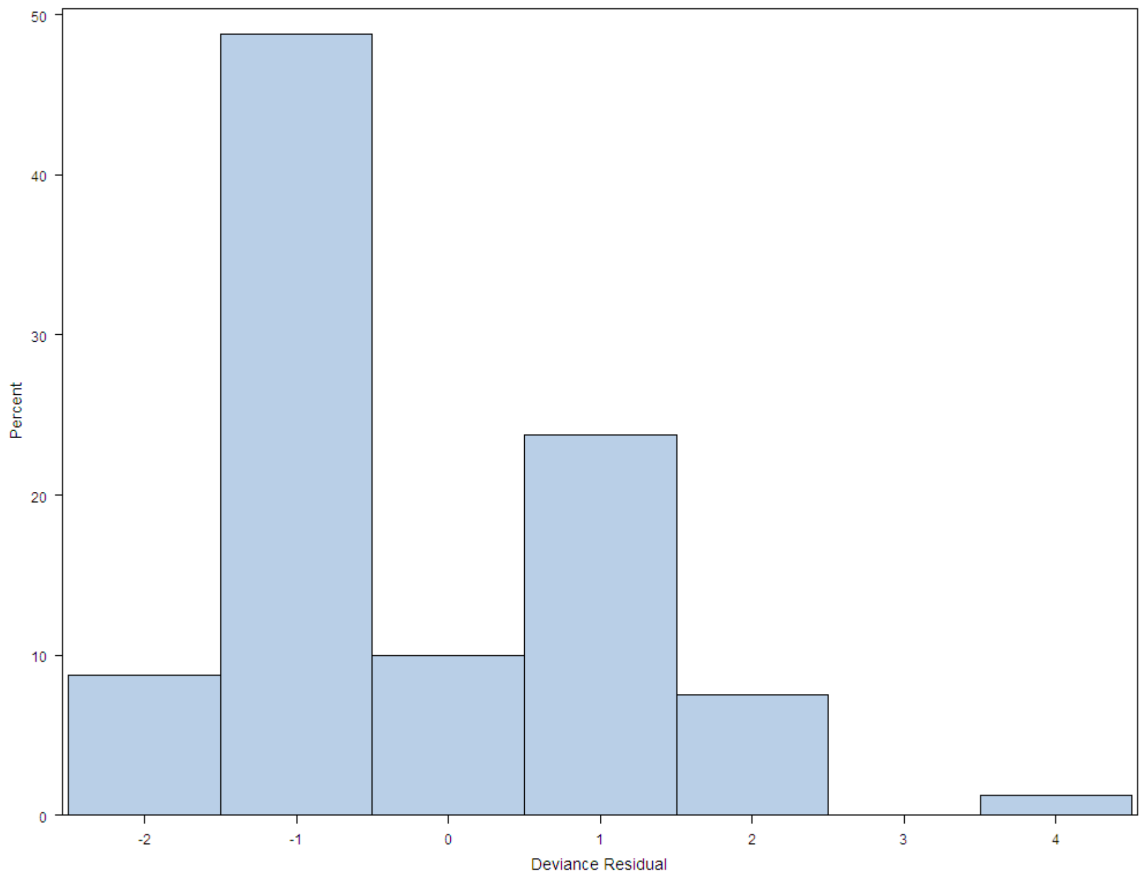


Figure E.3.5.4 Histogram of the likelihood residuals

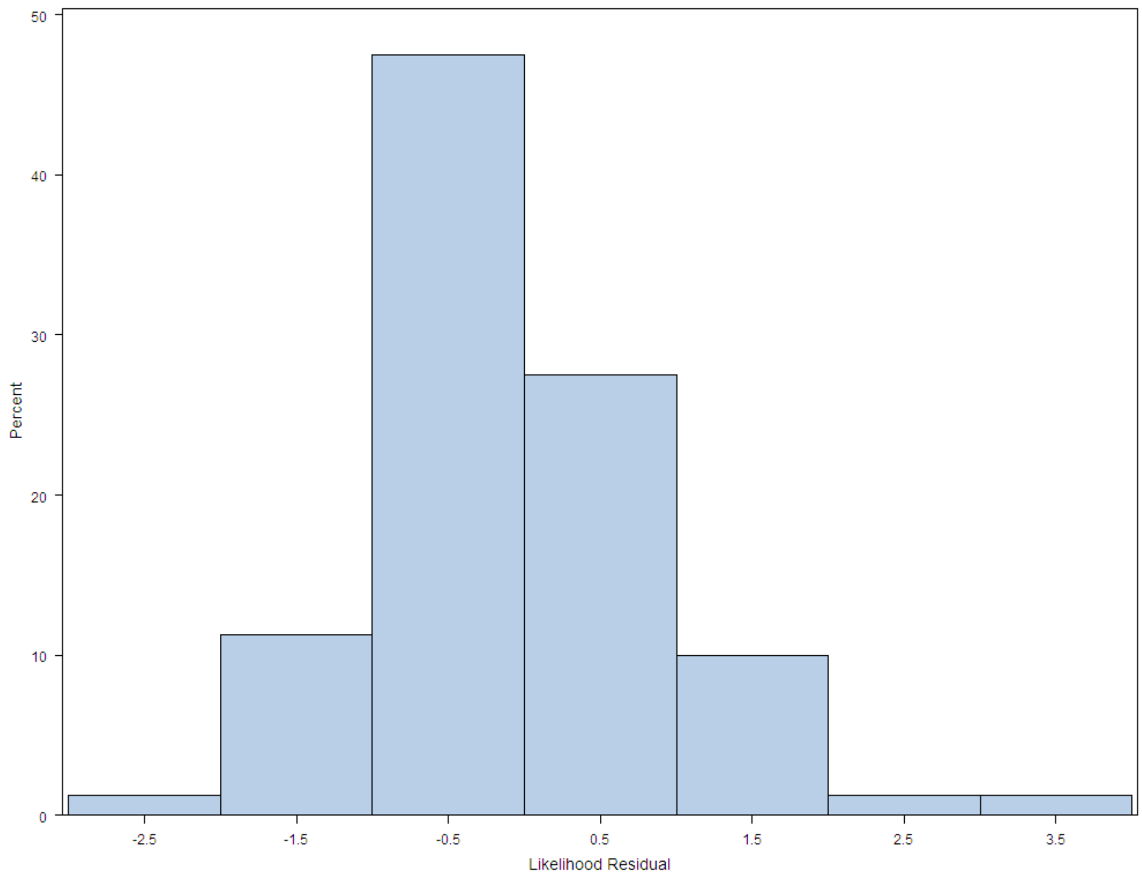


Figure E.3.5.5 Histogram of the standardized Pearson residuals

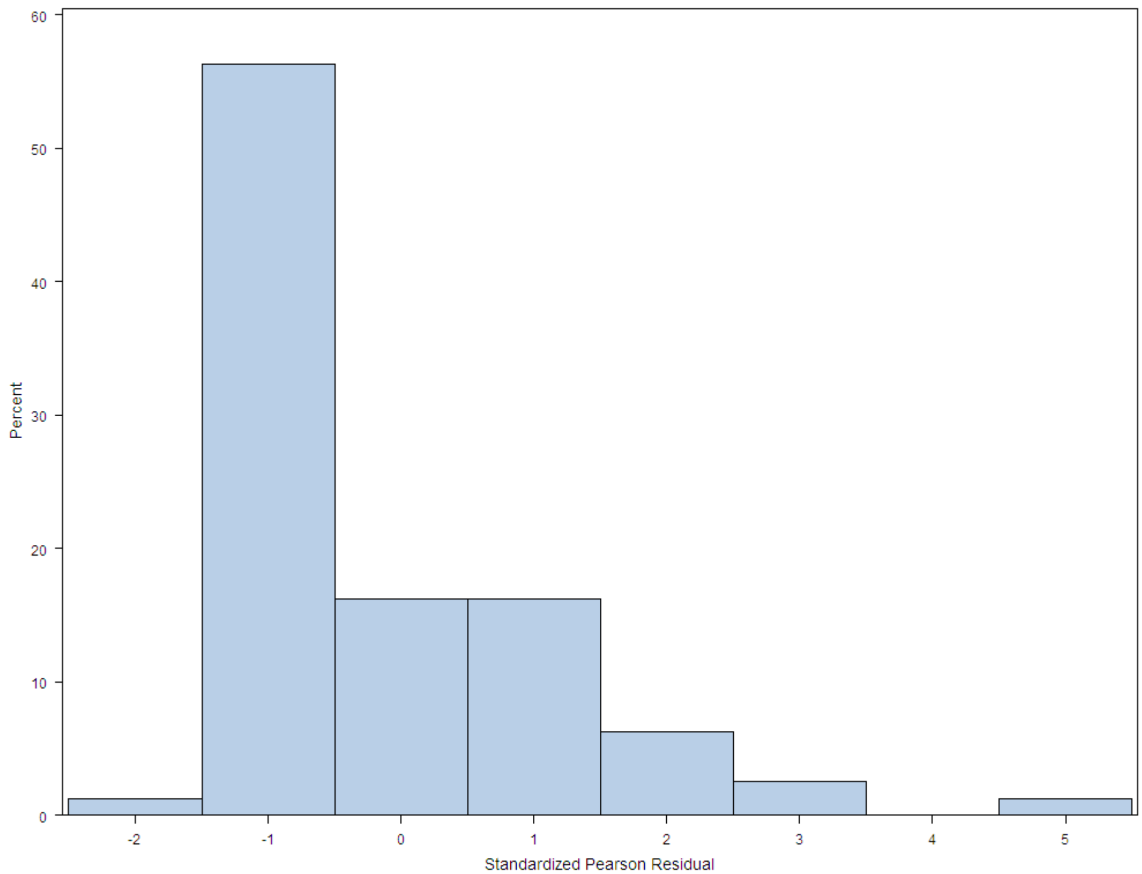
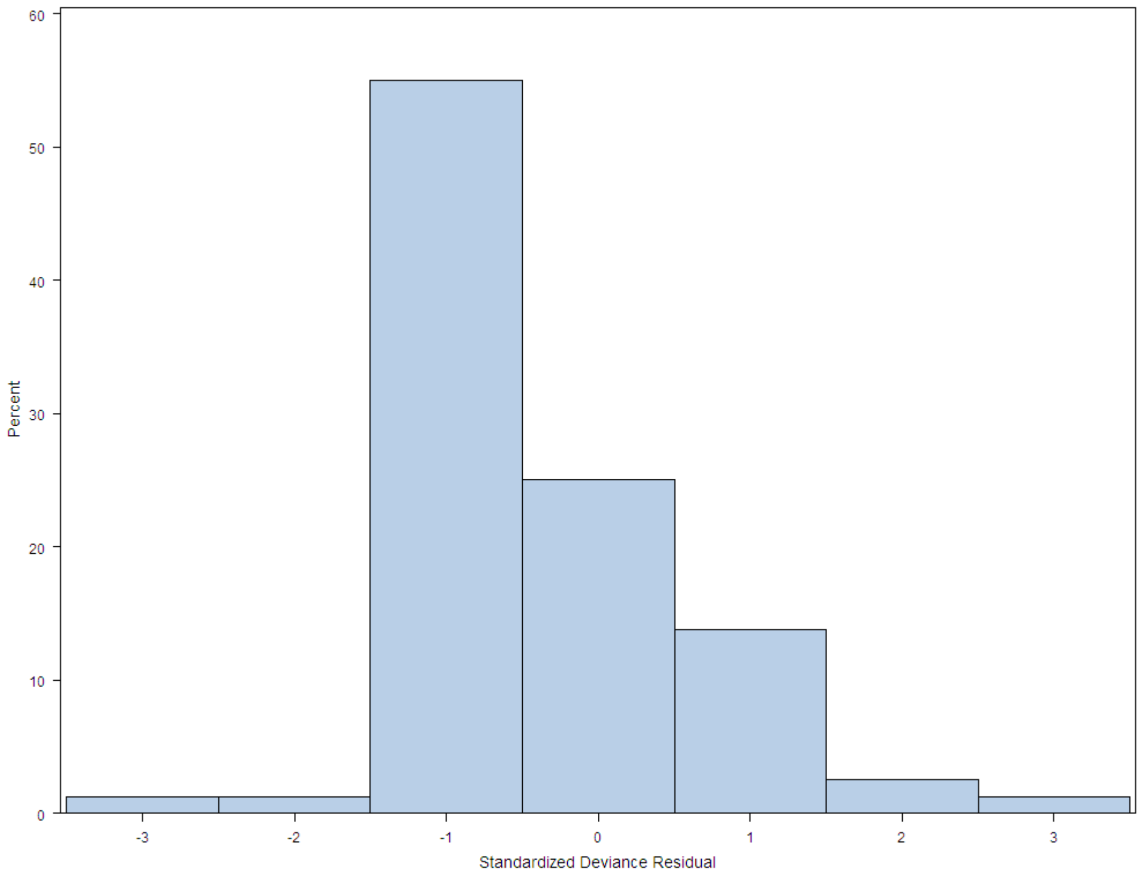


Figure E.3.5.6 Histogram of the standardized deviance residuals



E.3.6 September 2005 Model 6 Residual Plots

Figure E.3.6.1 Histogram of the raw residuals

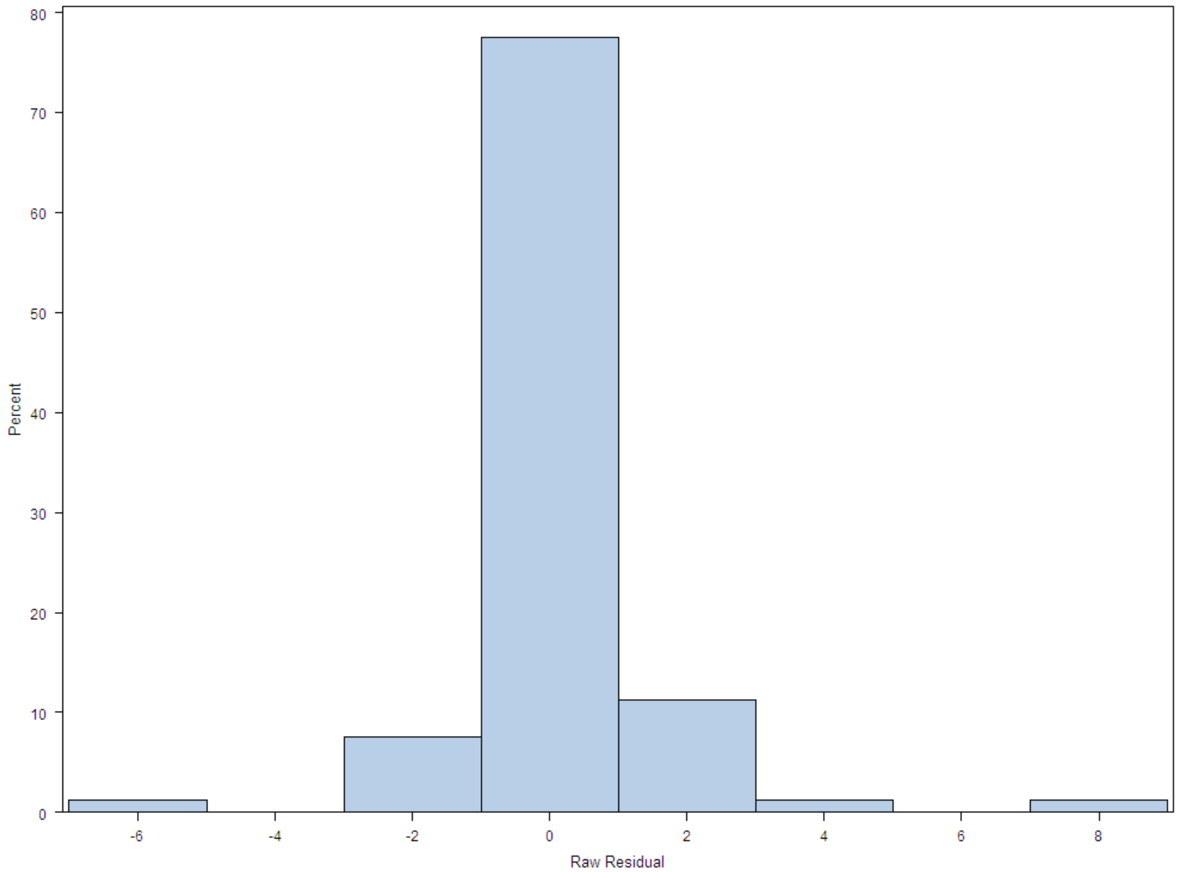
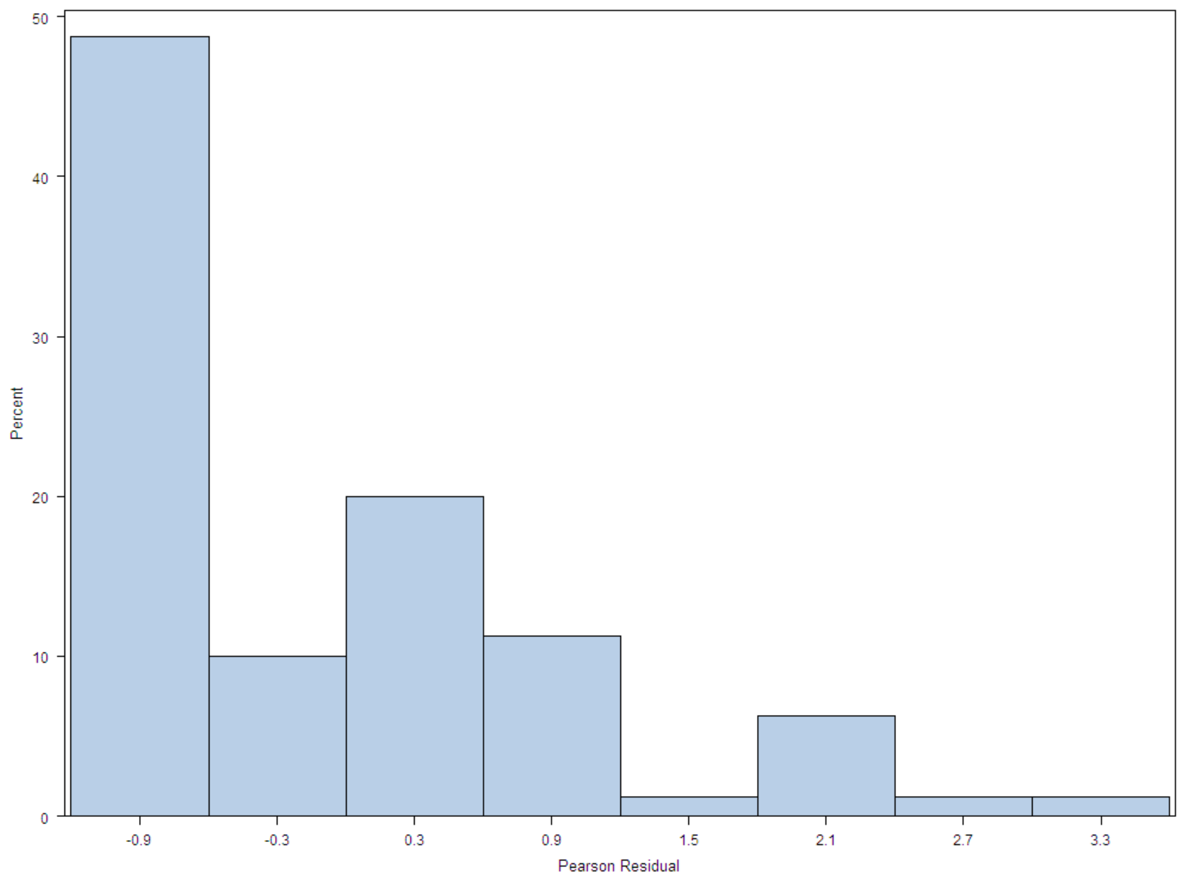


Figure E.3.6.2 Histogram of the Pearson residuals



E.3.7 September 2005 Model 7 Residual Plots

Figure E.3.7.1 Histogram of the raw residuals

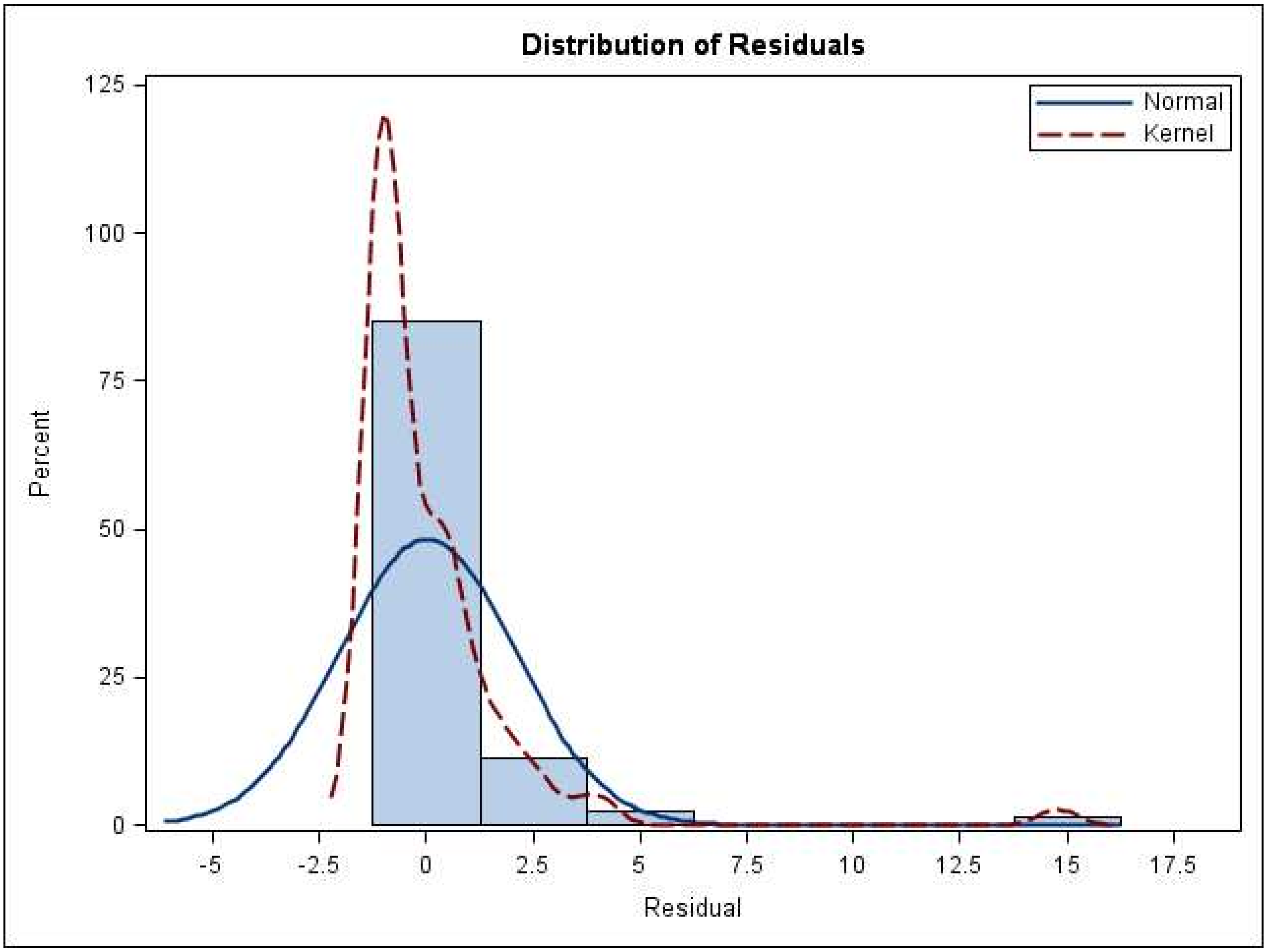


Figure E.3.7.2 Normal quantile plot of the raw residuals

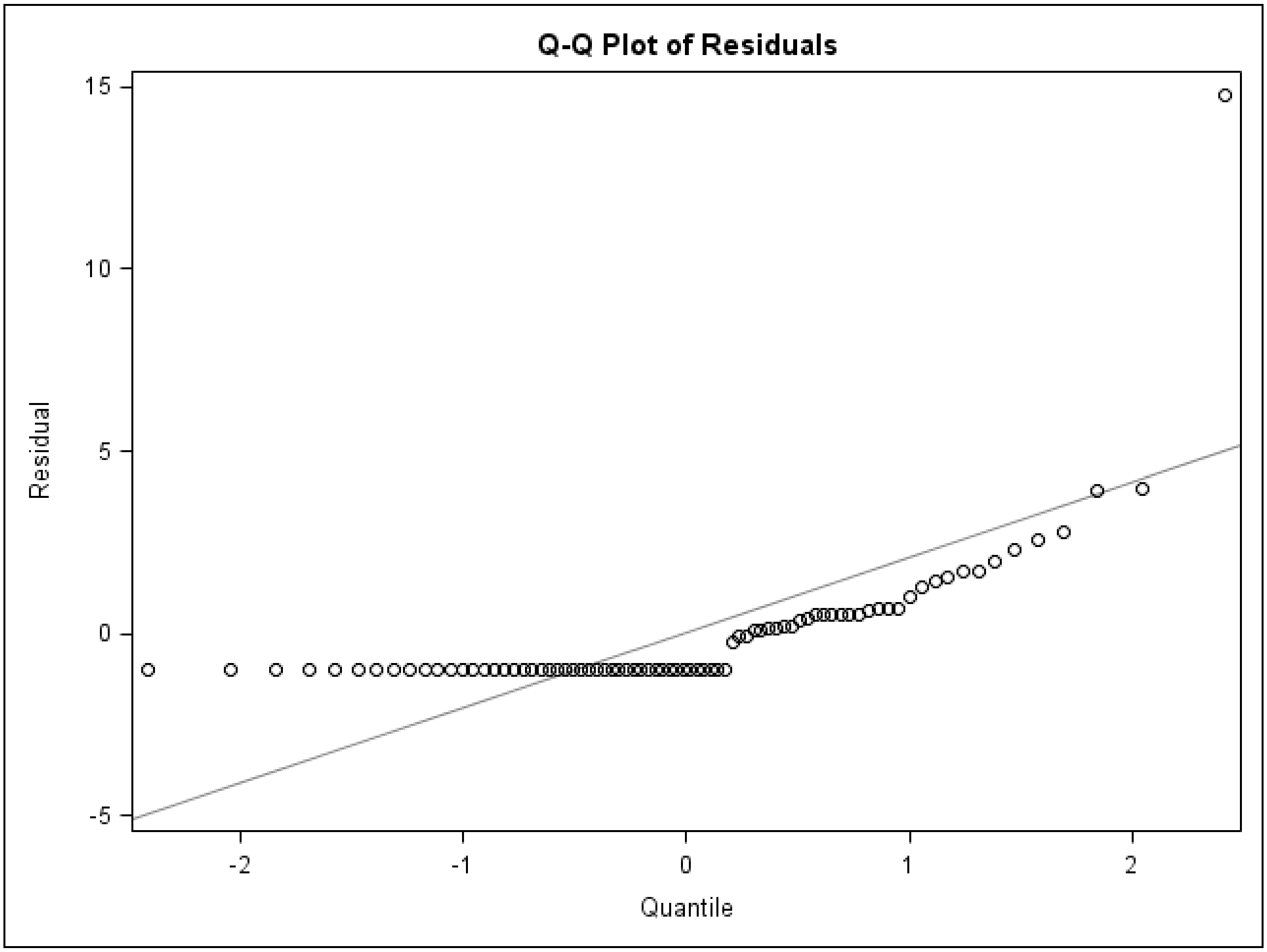


Figure E.3.7.3 Histogram of the Studentized residuals

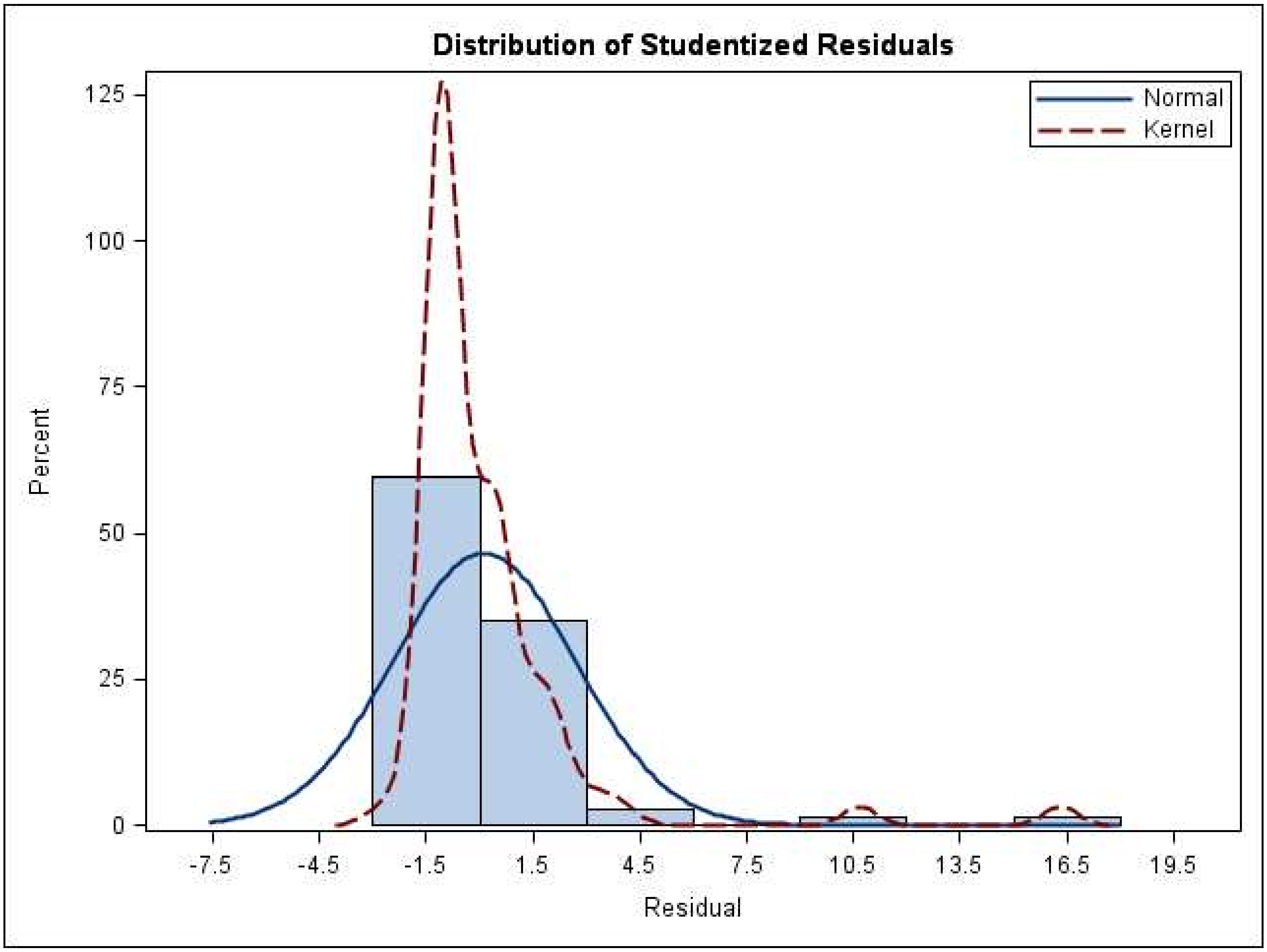


Figure E.3.7.4 Normal quantile plot of the Studentized residuals

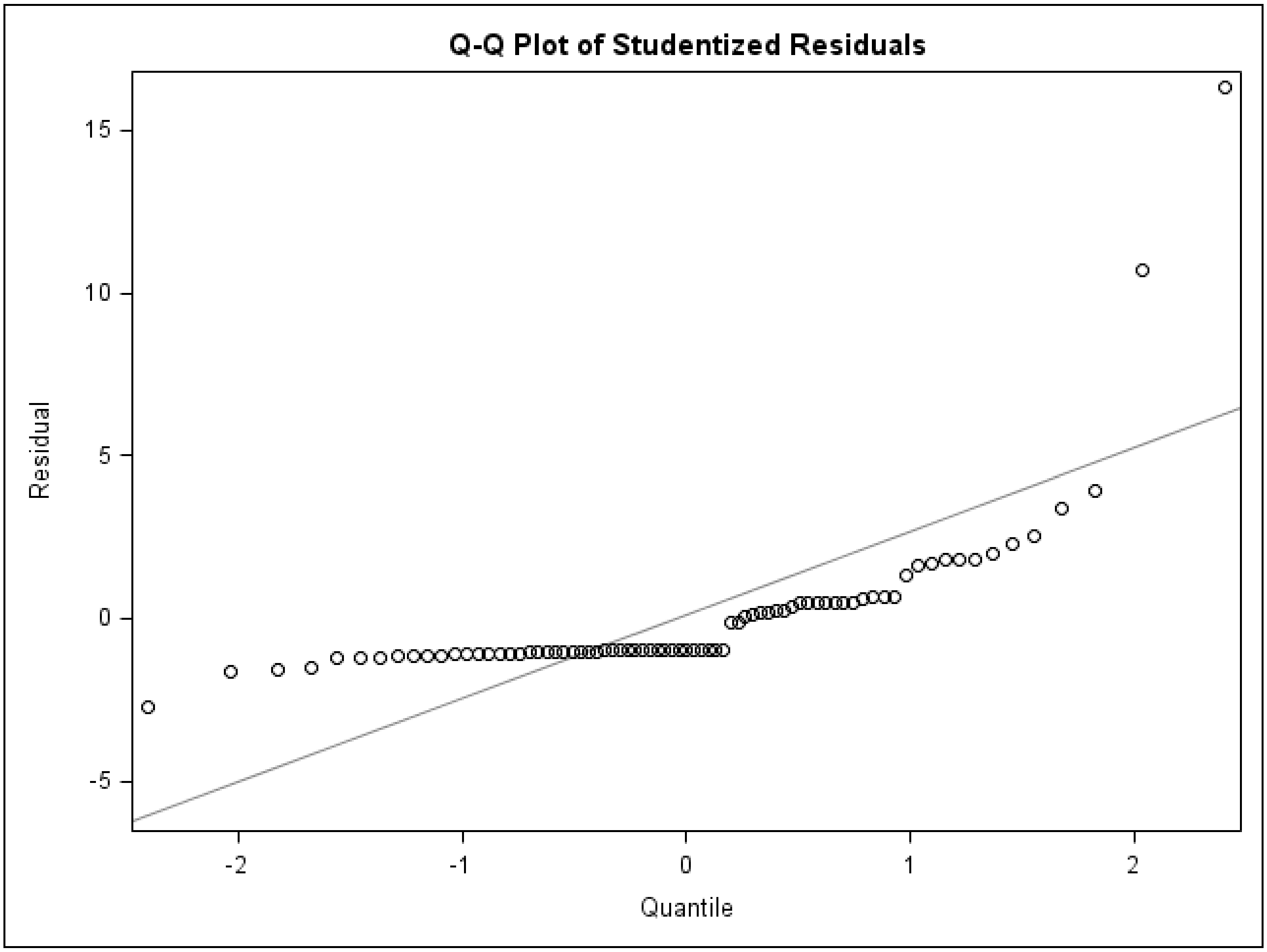


Figure E.3.7.5 Histogram of the Pearson residuals

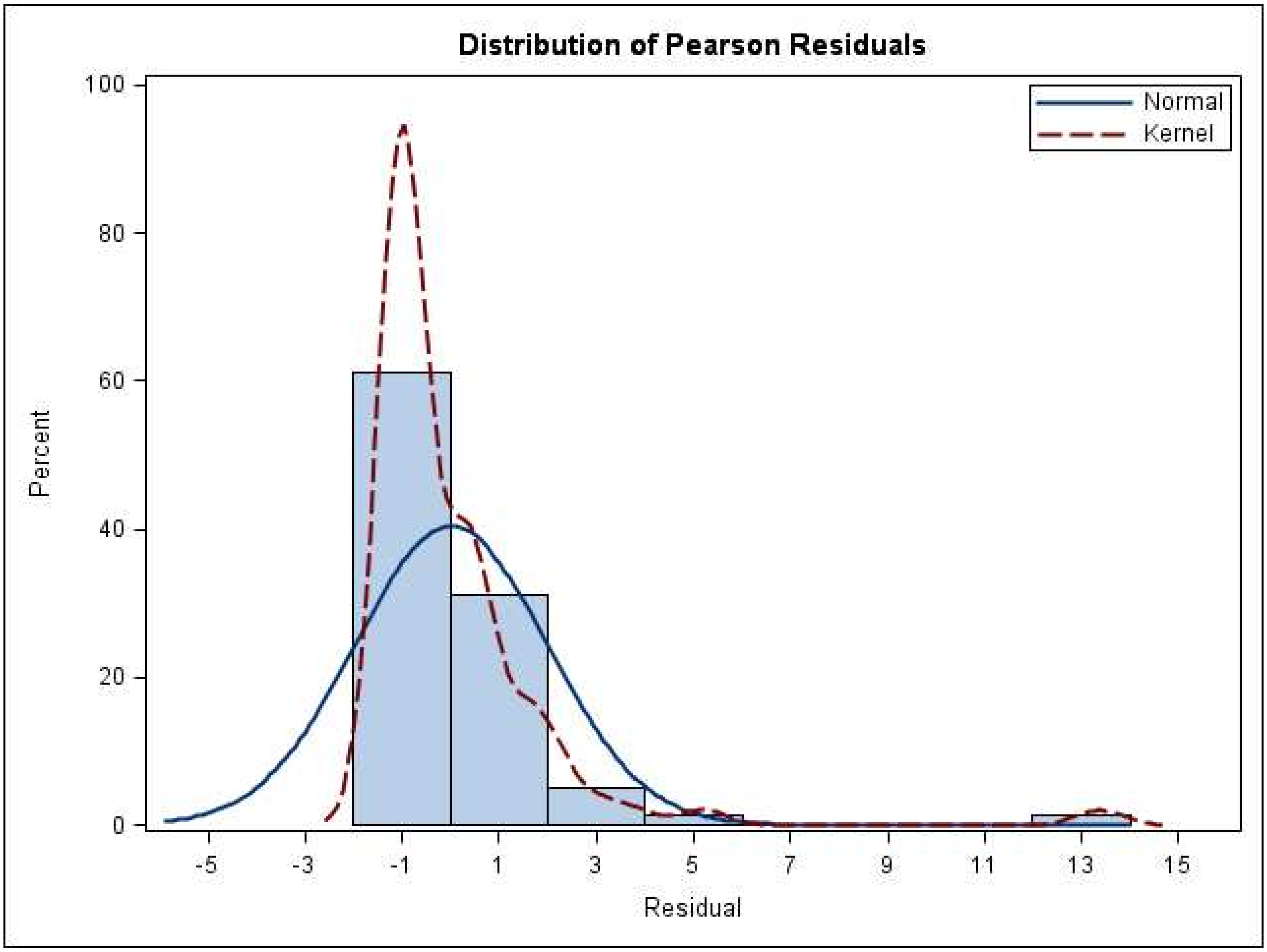
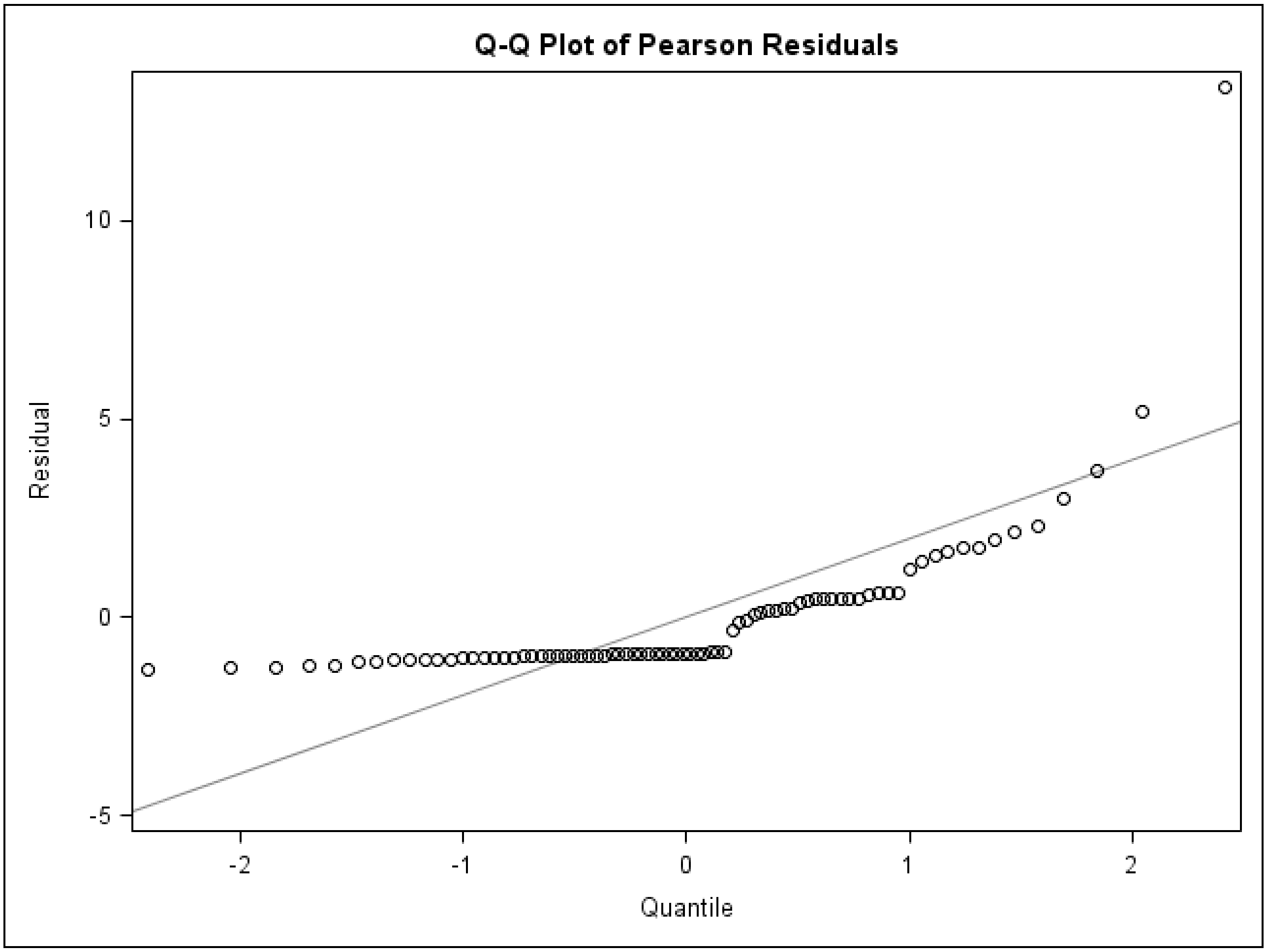
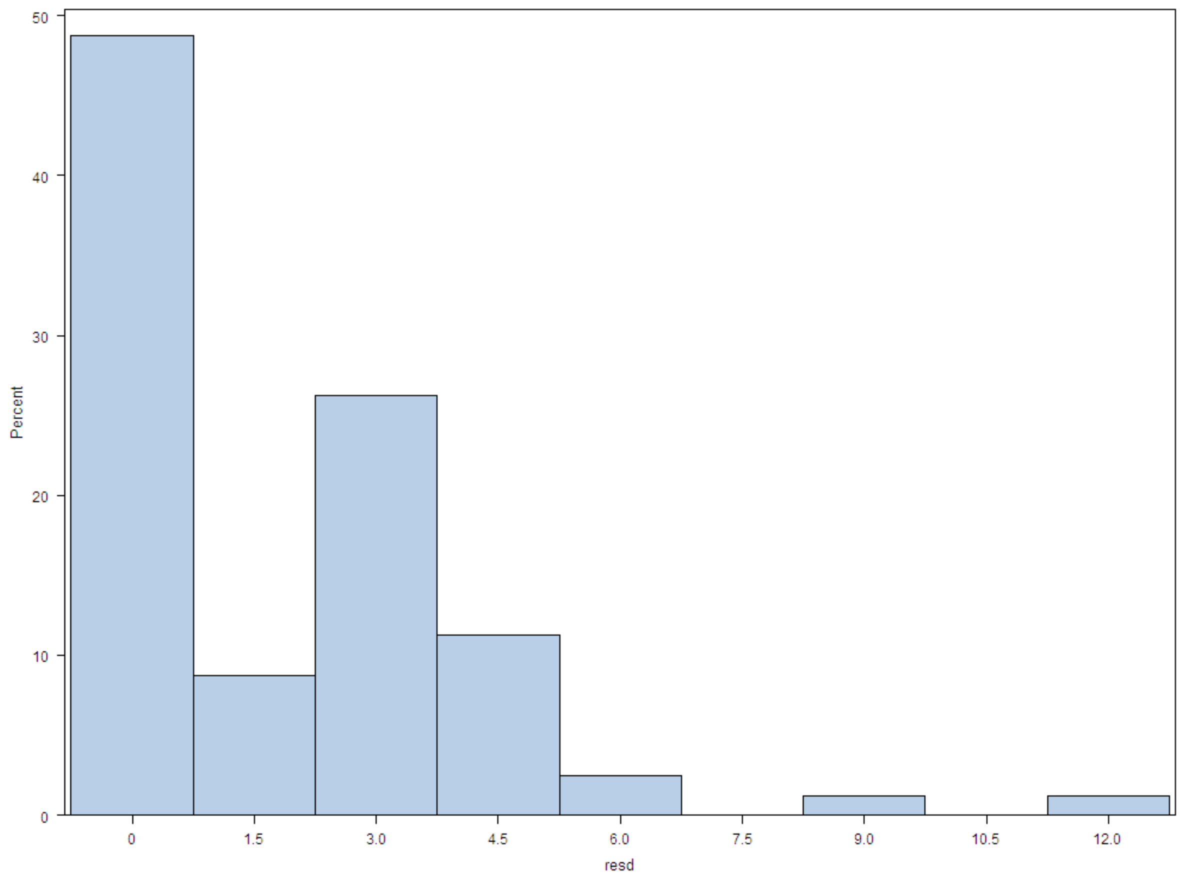


Figure E.3.7.6 Normal quantile plot of the Pearson residuals



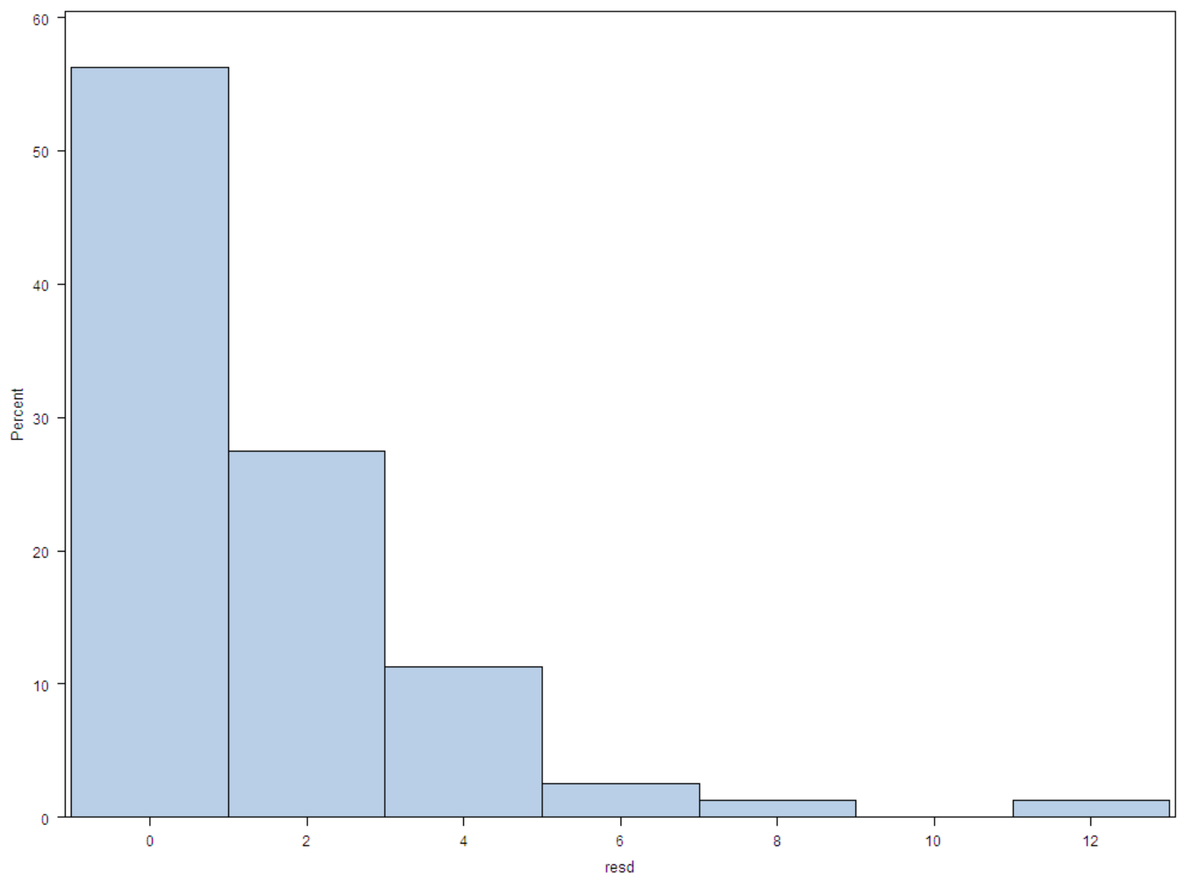
E.3.8 September 2005 Model 8 Residual Plots

Figure E.3.8.1 Histogram of the raw residuals



E.3.9 September 2005 Model 9 Residual Plots

Figure E.3.9.1 Histogram of the raw residuals



E.4 May 2006 Residual Plots

E.4.1 May 2006 Model 1 Residual Plots

Figure E.4.1.1 Histogram of the raw residuals

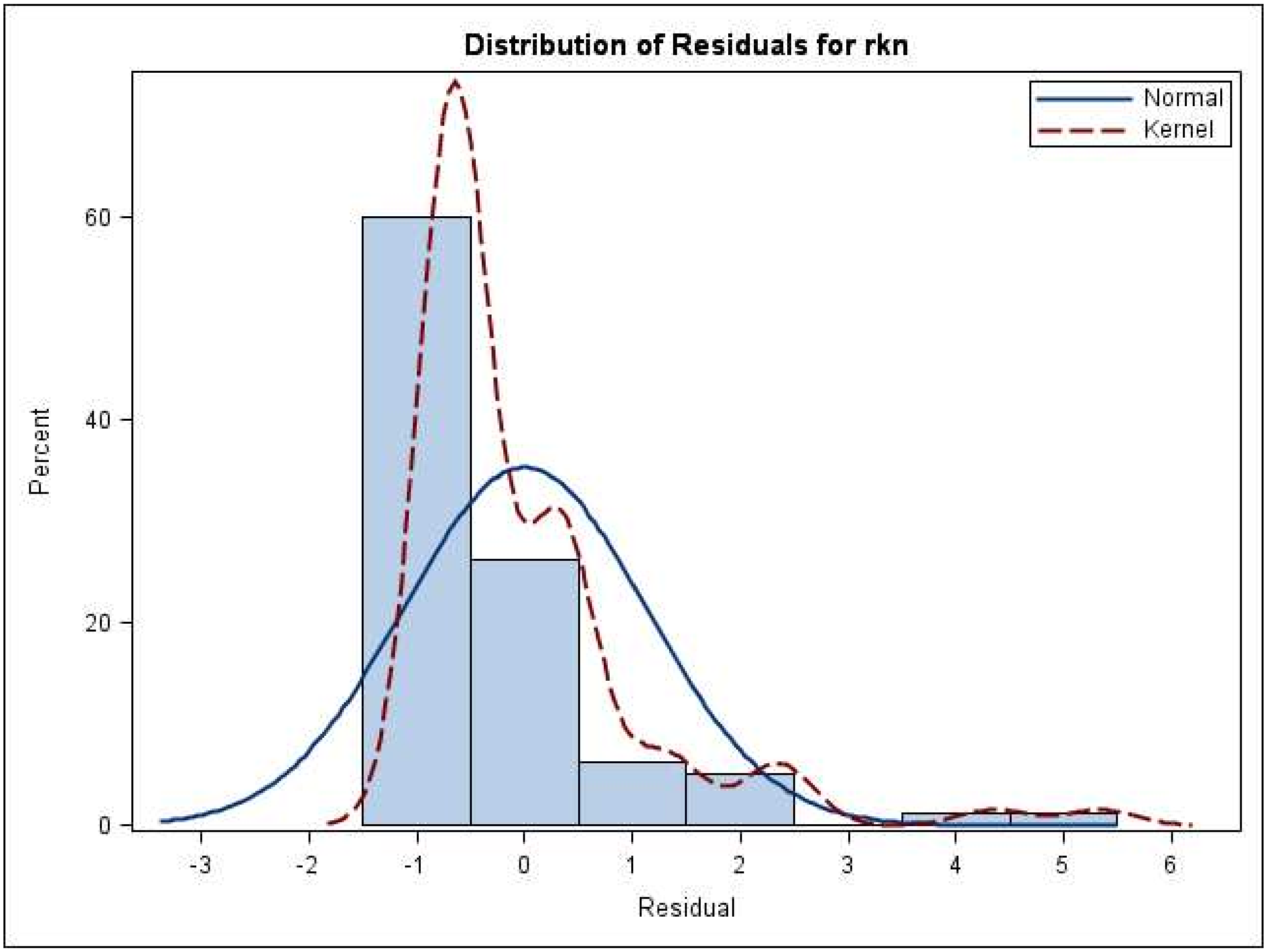


Figure E.4.1.2 Normal quantile plot of the raw residuals

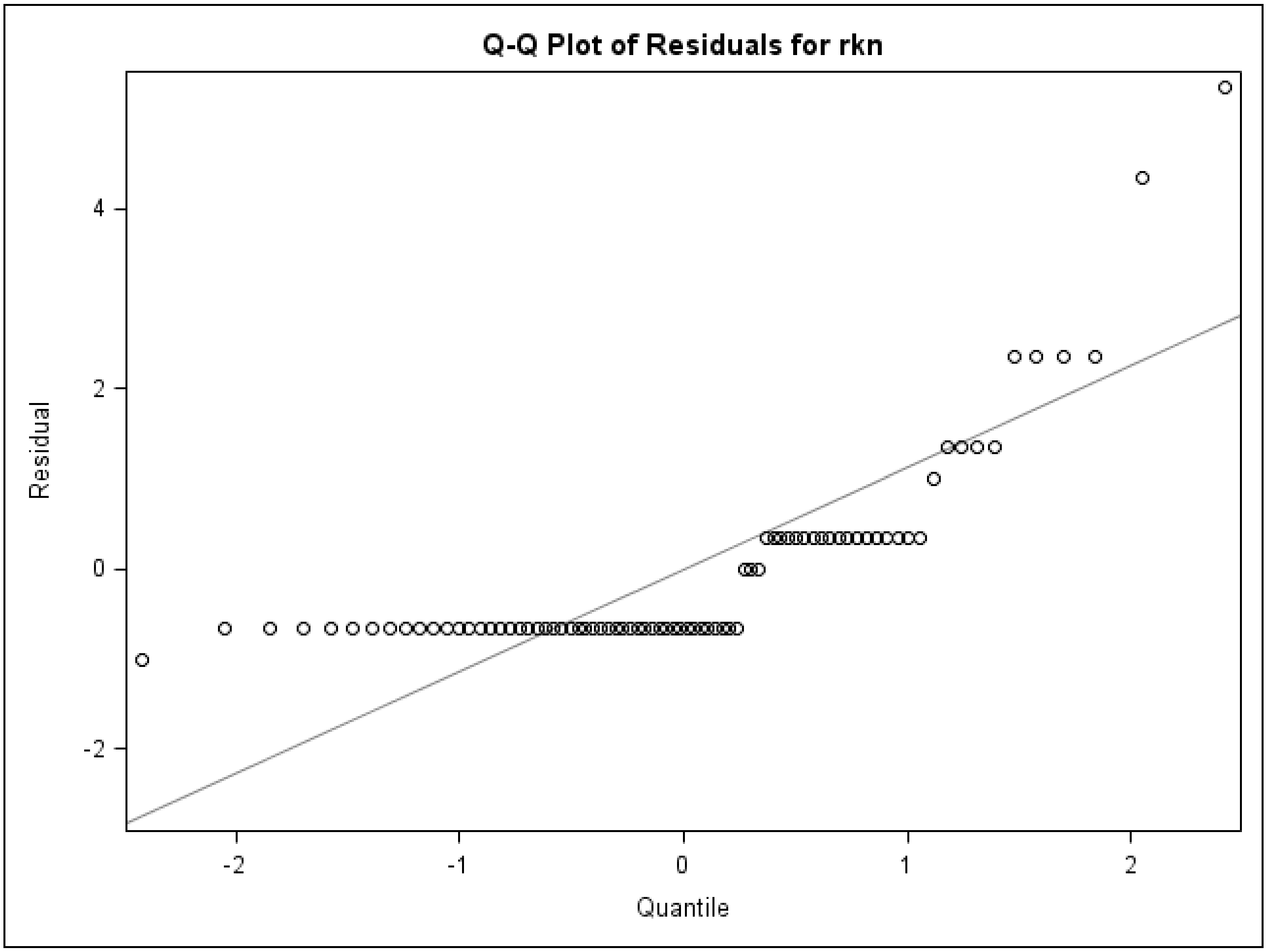


Figure E.4.1.3 Histogram of the Studentized residuals

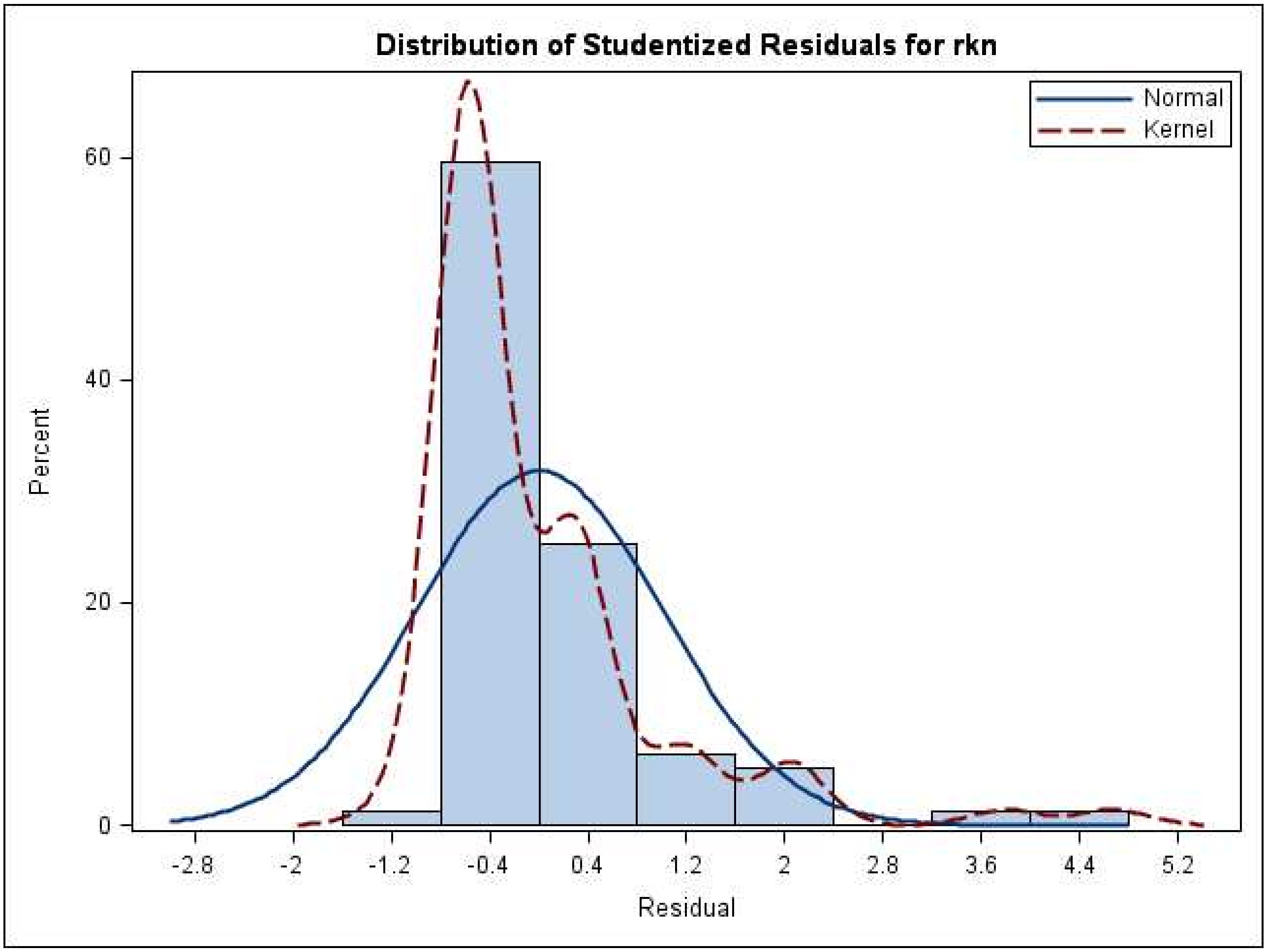


Figure E.4.1.4 Normal quantile plot of the Studentized residuals

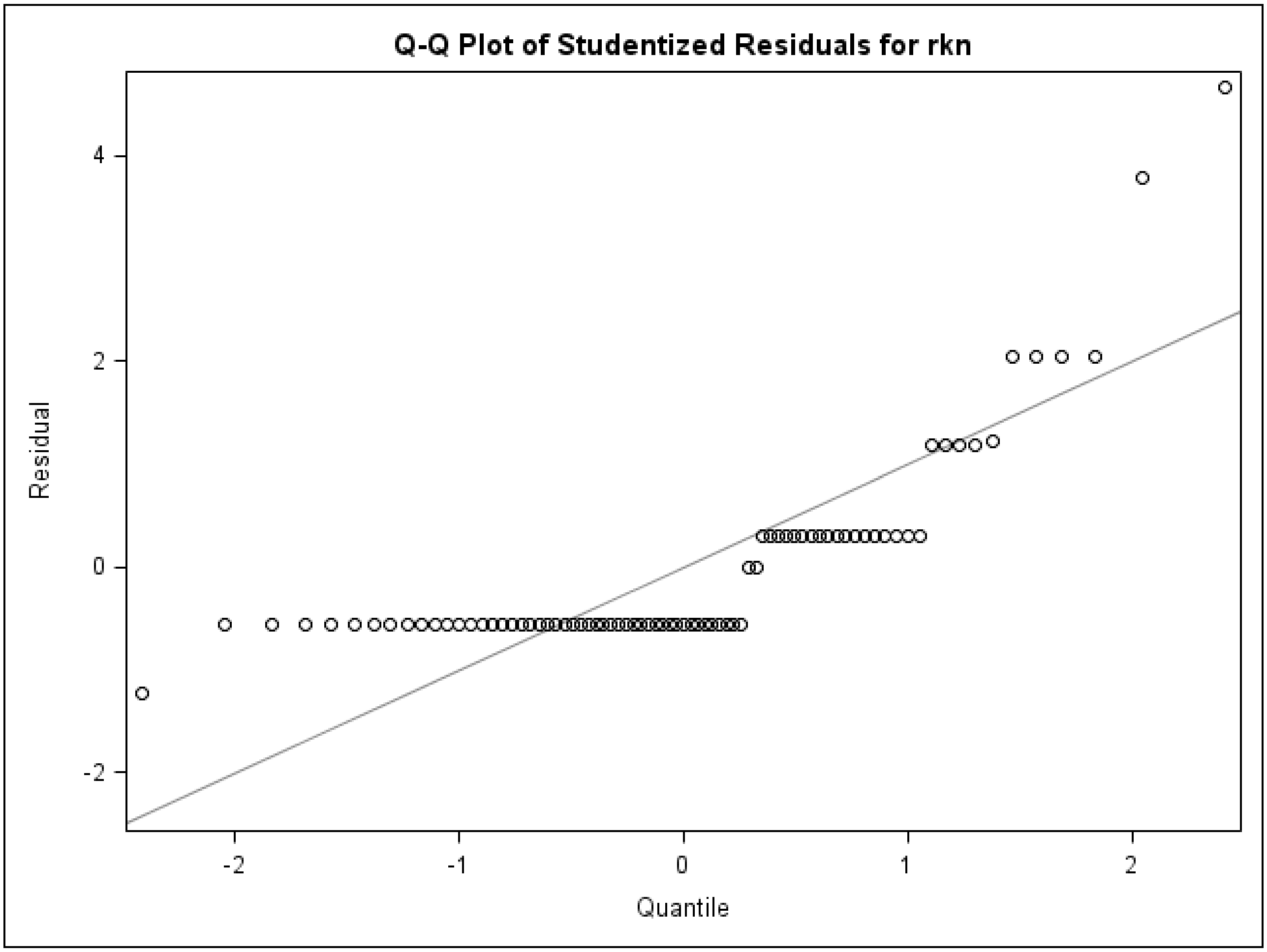


Figure E.4.1.5 Histogram of the Pearson residuals

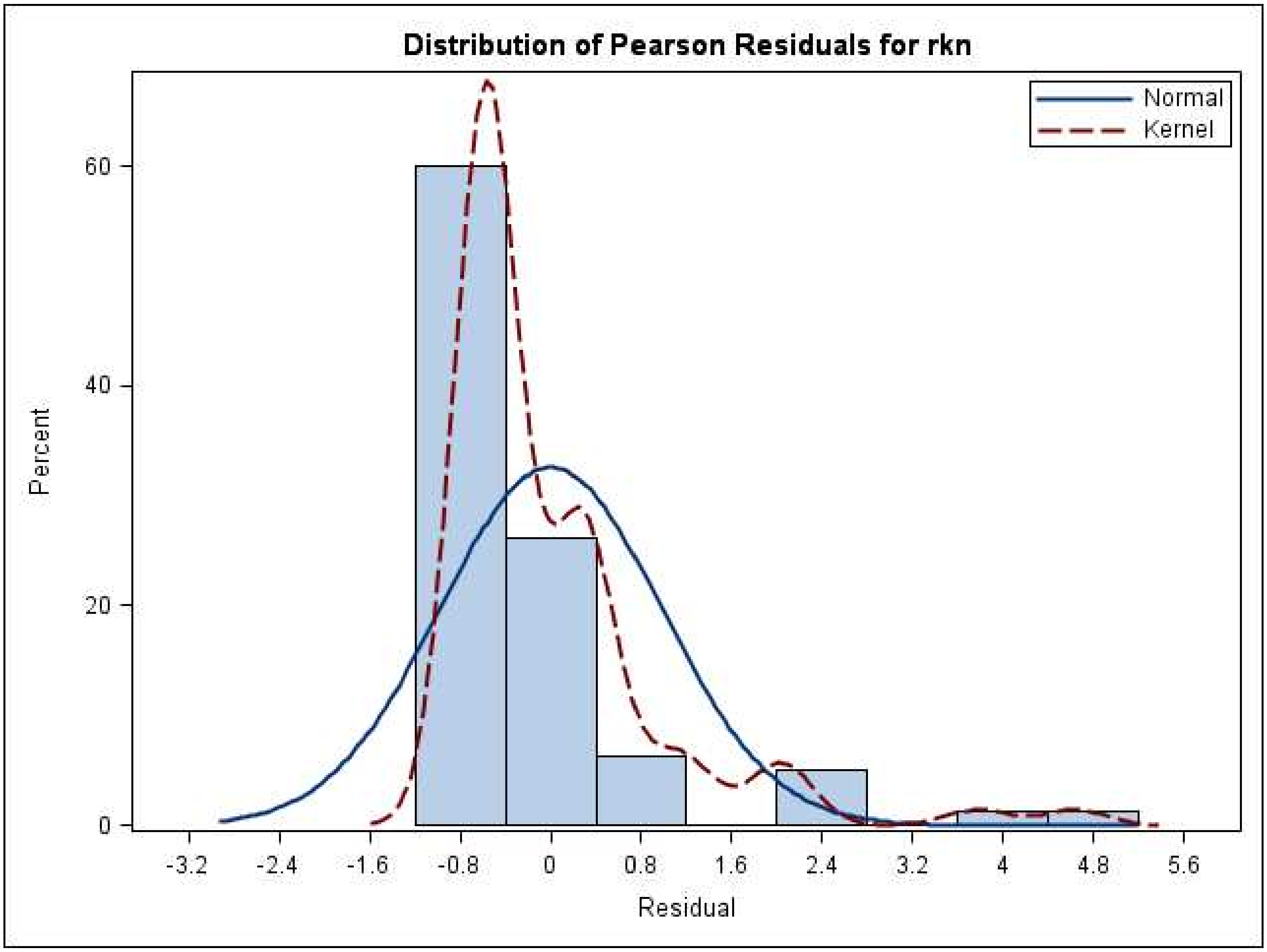
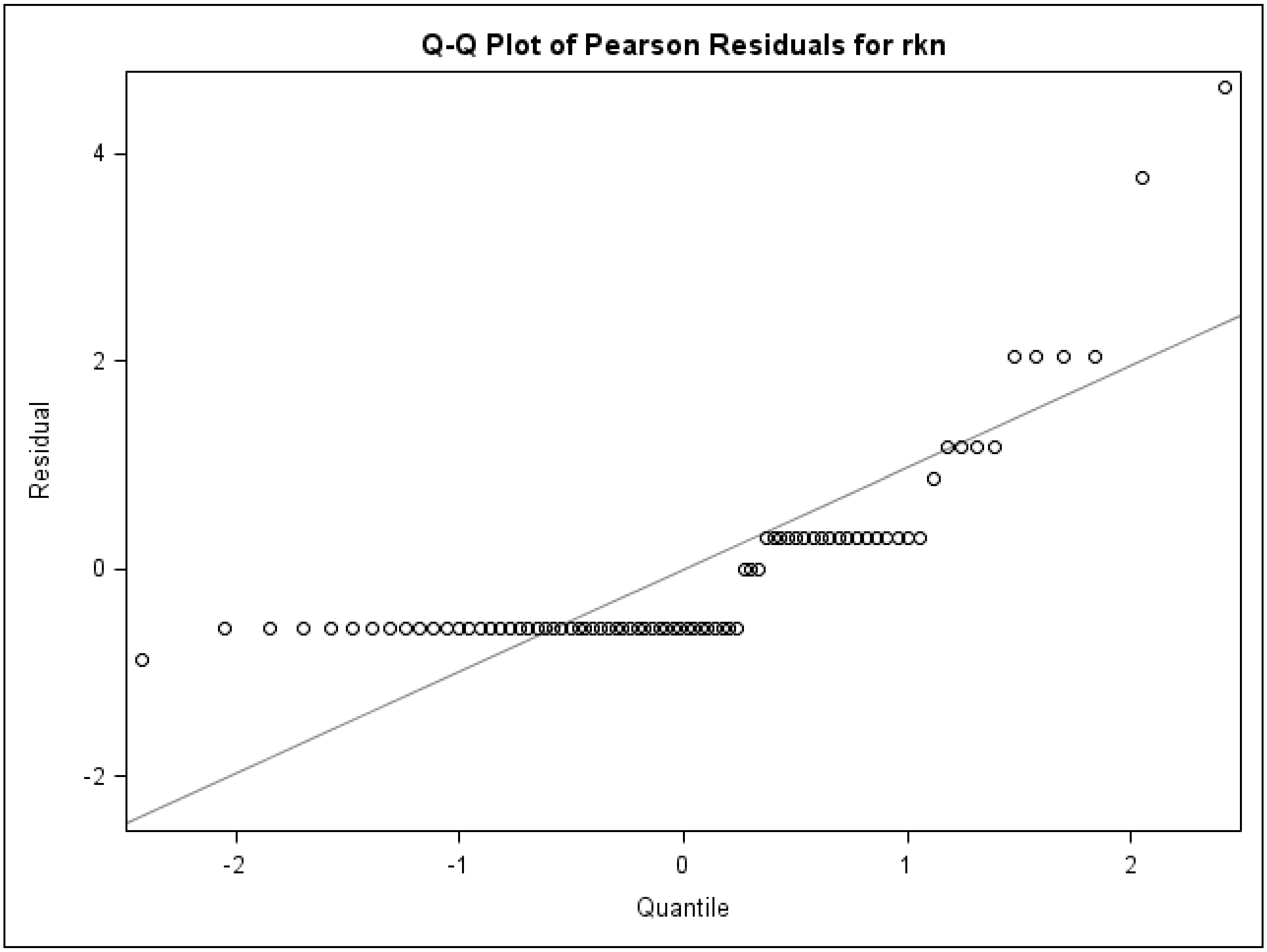


Figure E.4.1.6 Normal quantile plot of the Pearson residuals



E.4.2 May 2006 Model 2 Residual Plots

Figure E.4.2.1 Histogram of the raw residuals

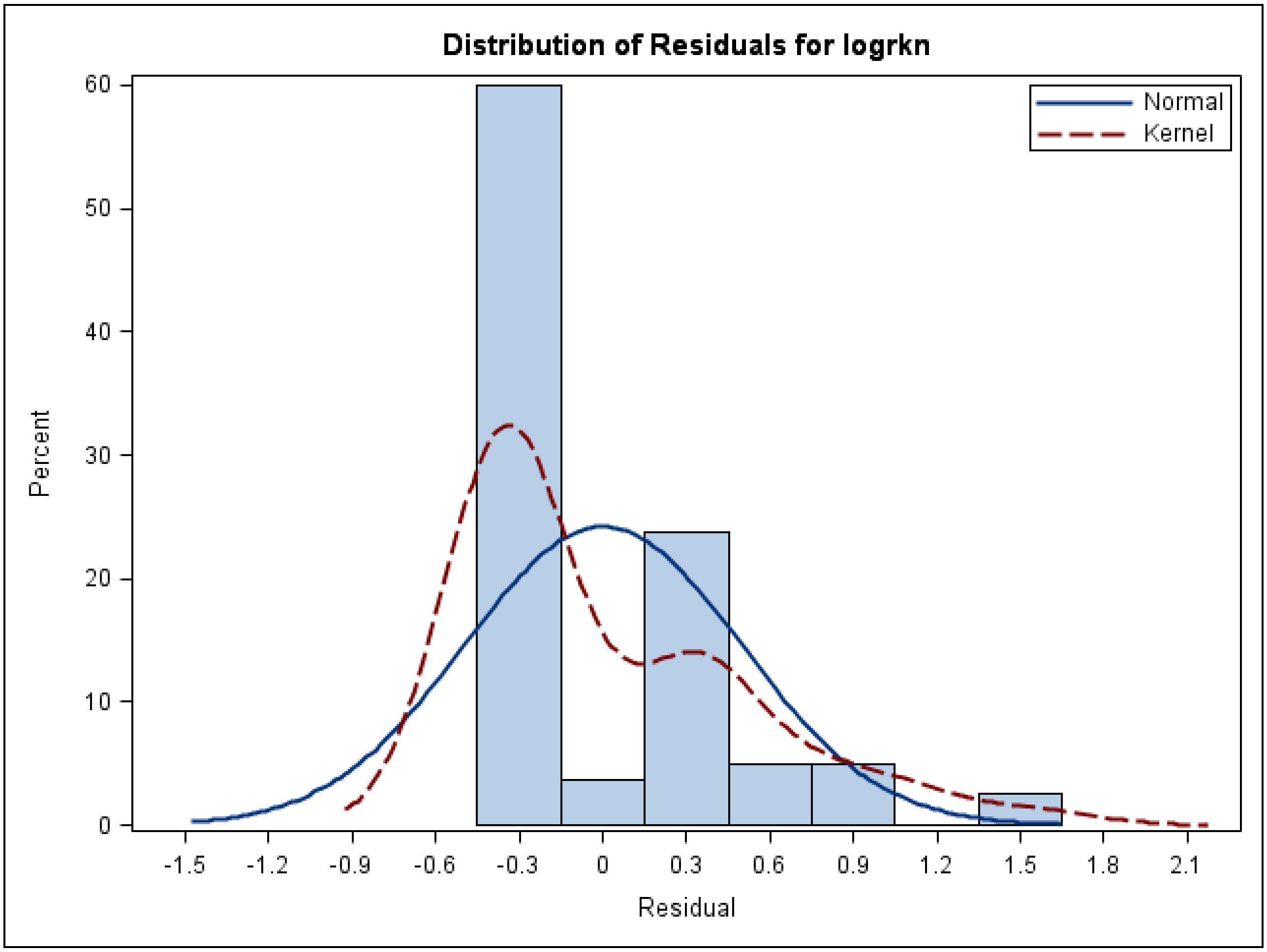


Figure E.4.2.2 Normal quantile plot of the raw residuals

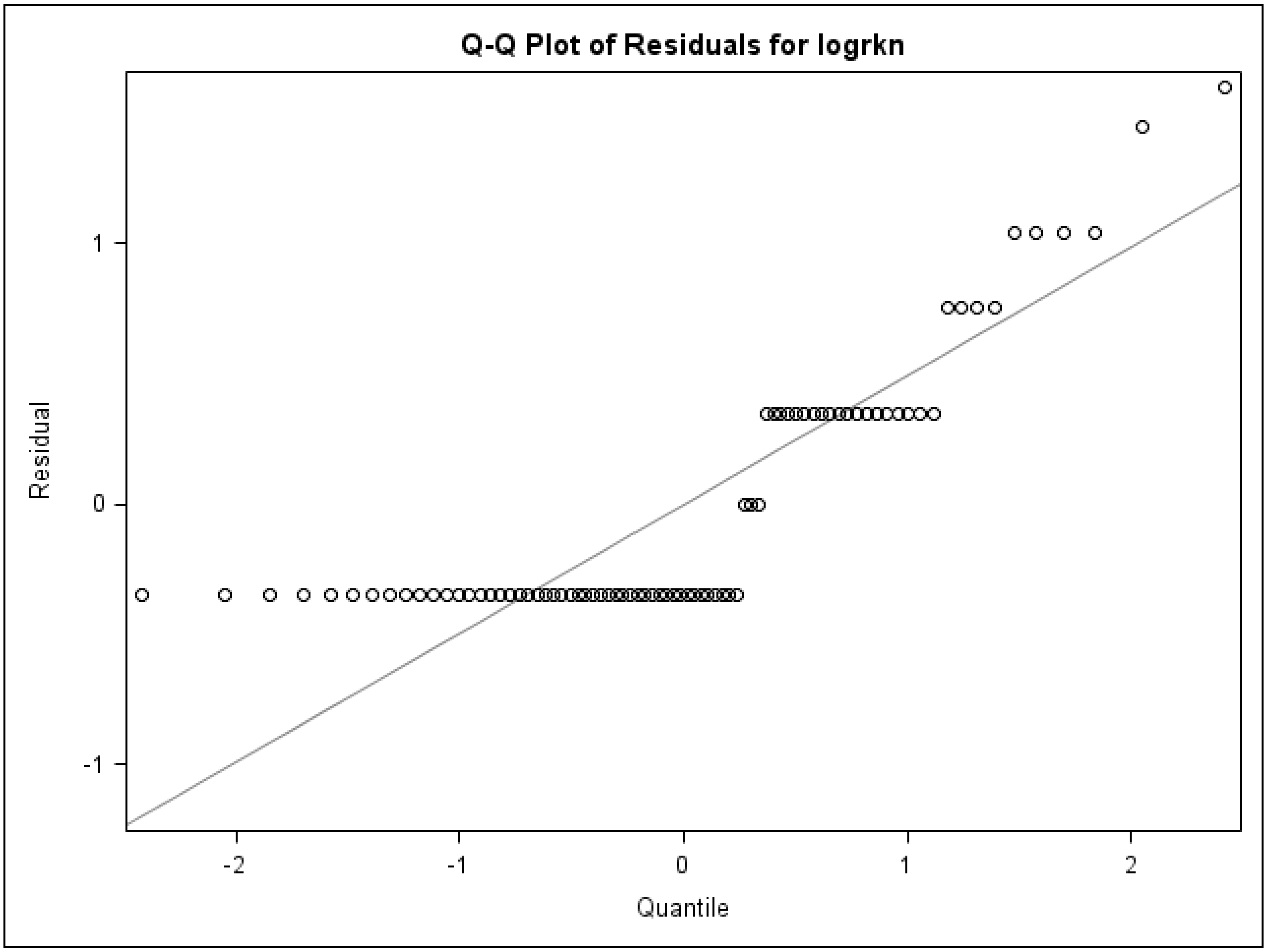


Figure E.4.2.3 Histogram of the Studentized residuals

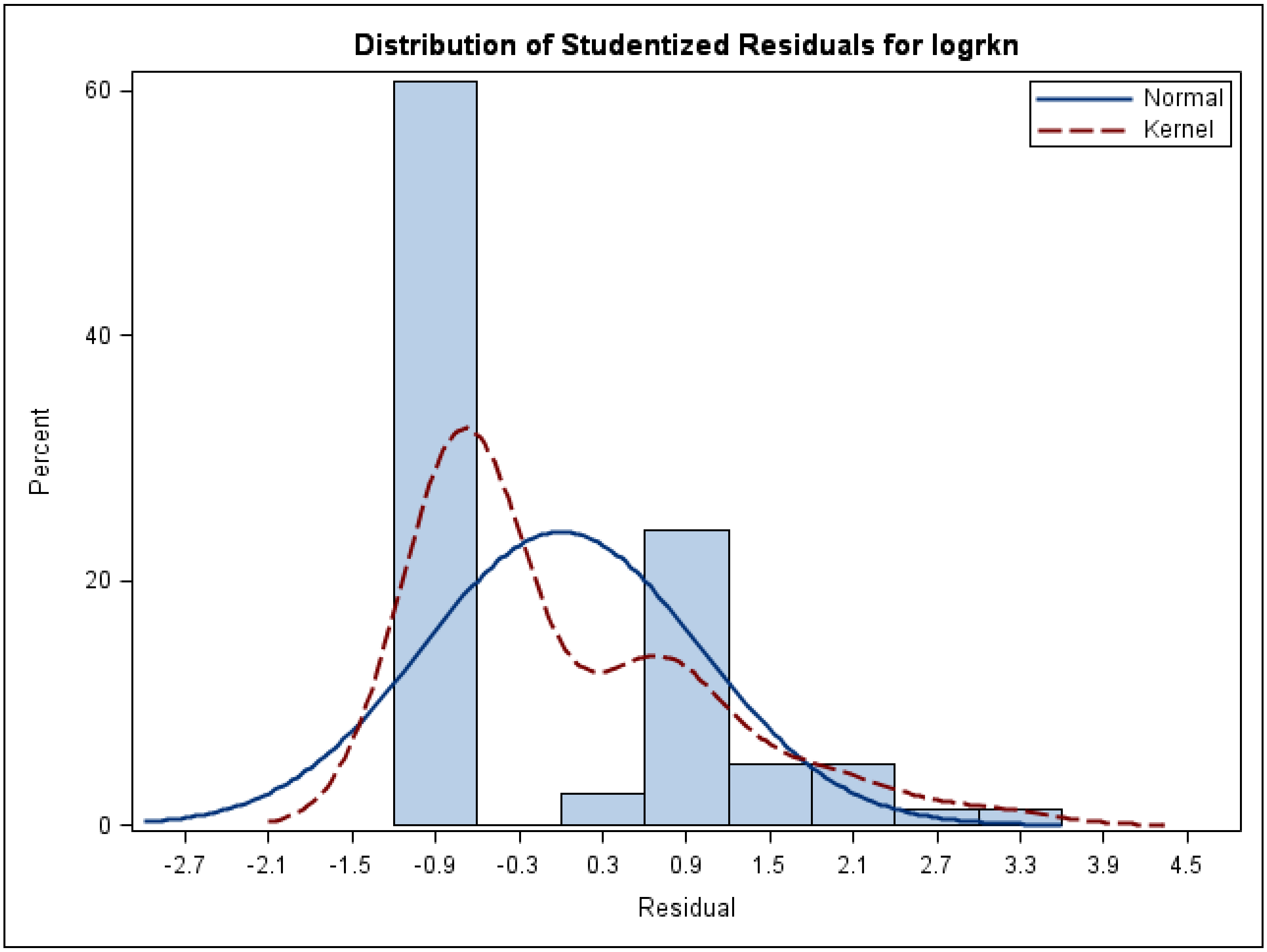


Figure E.4.2.4 Normal quantile plot of the Studentized residuals

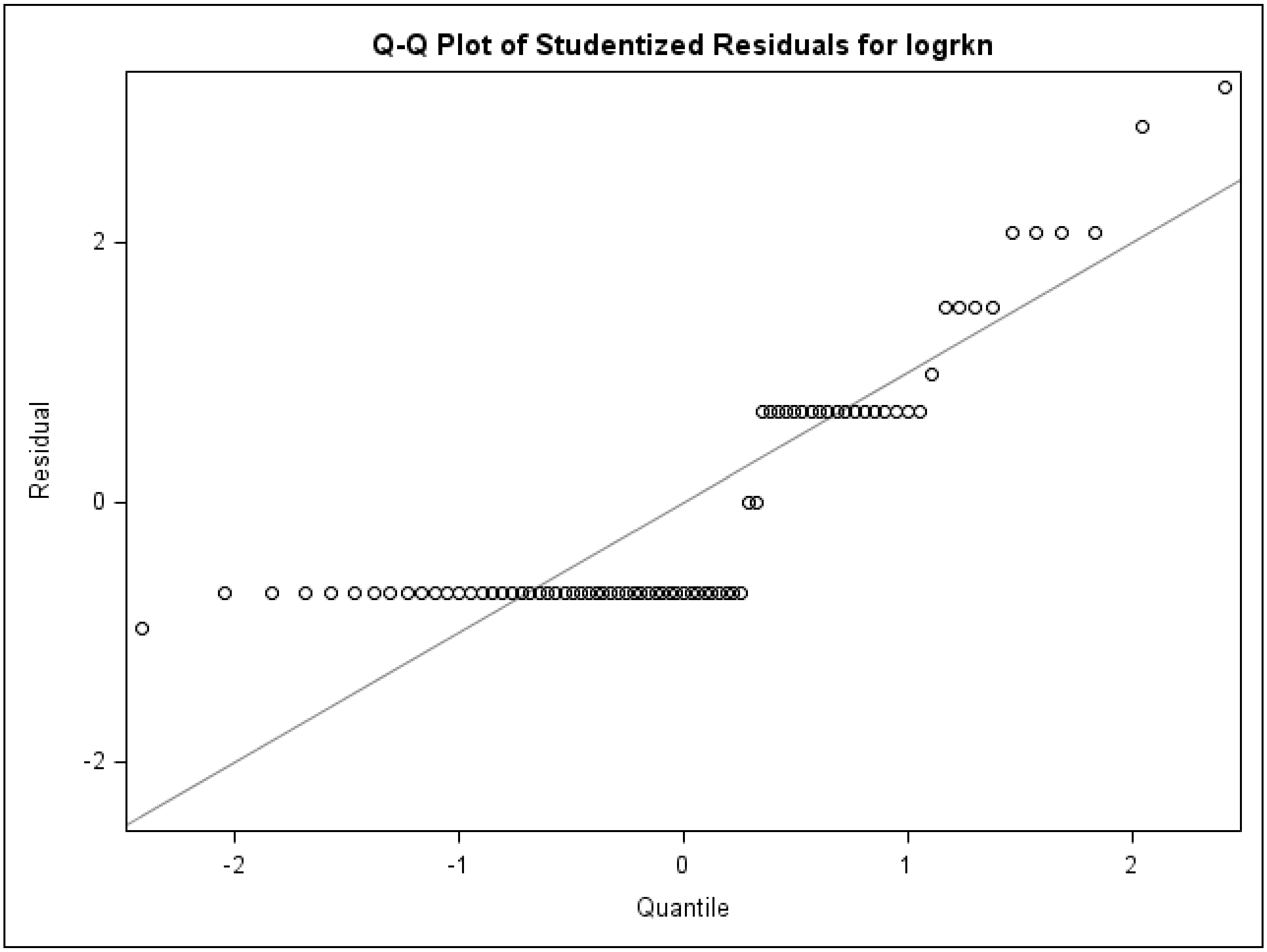


Figure E.4.2.5 Histogram of the Pearson residuals

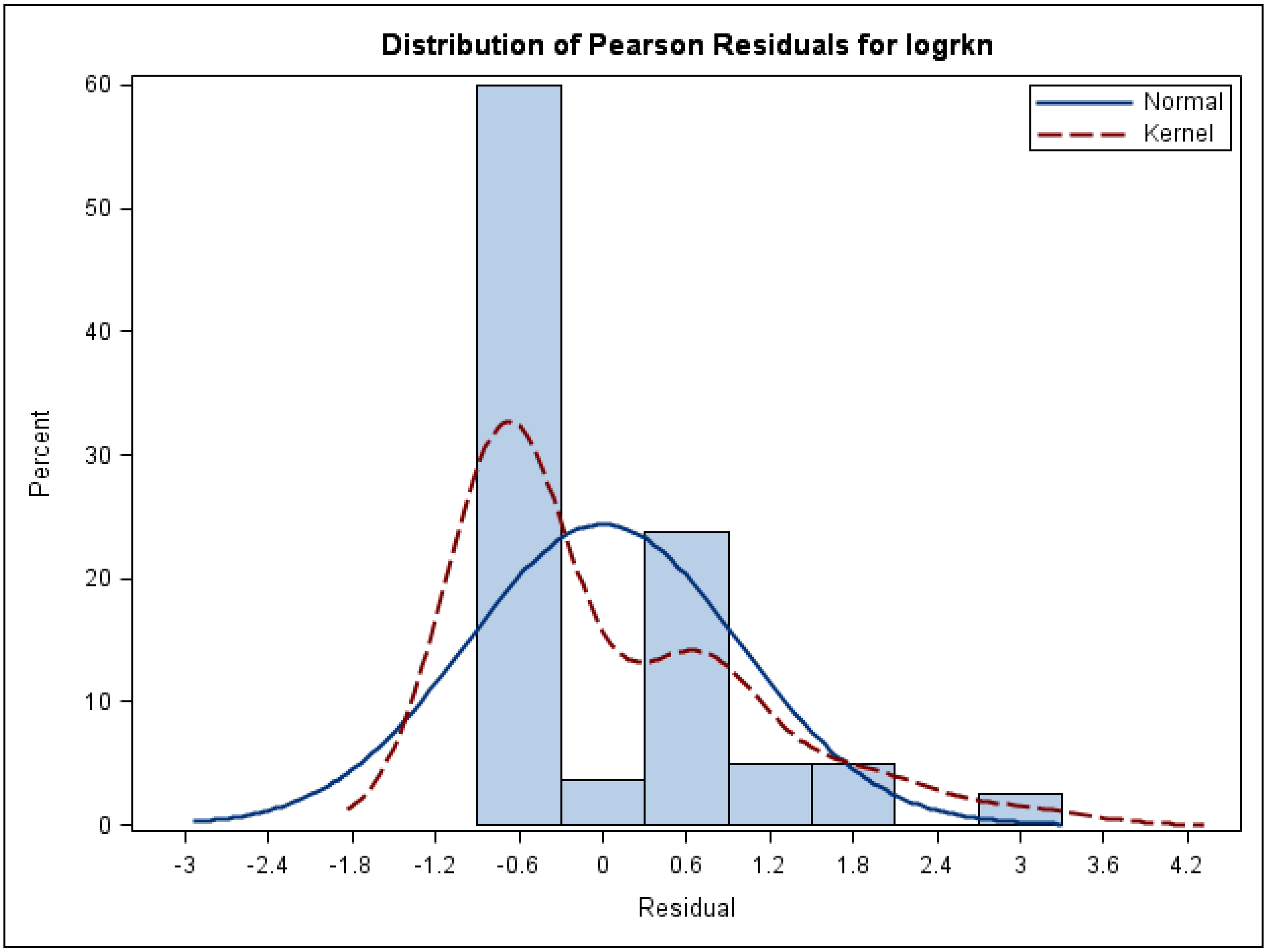
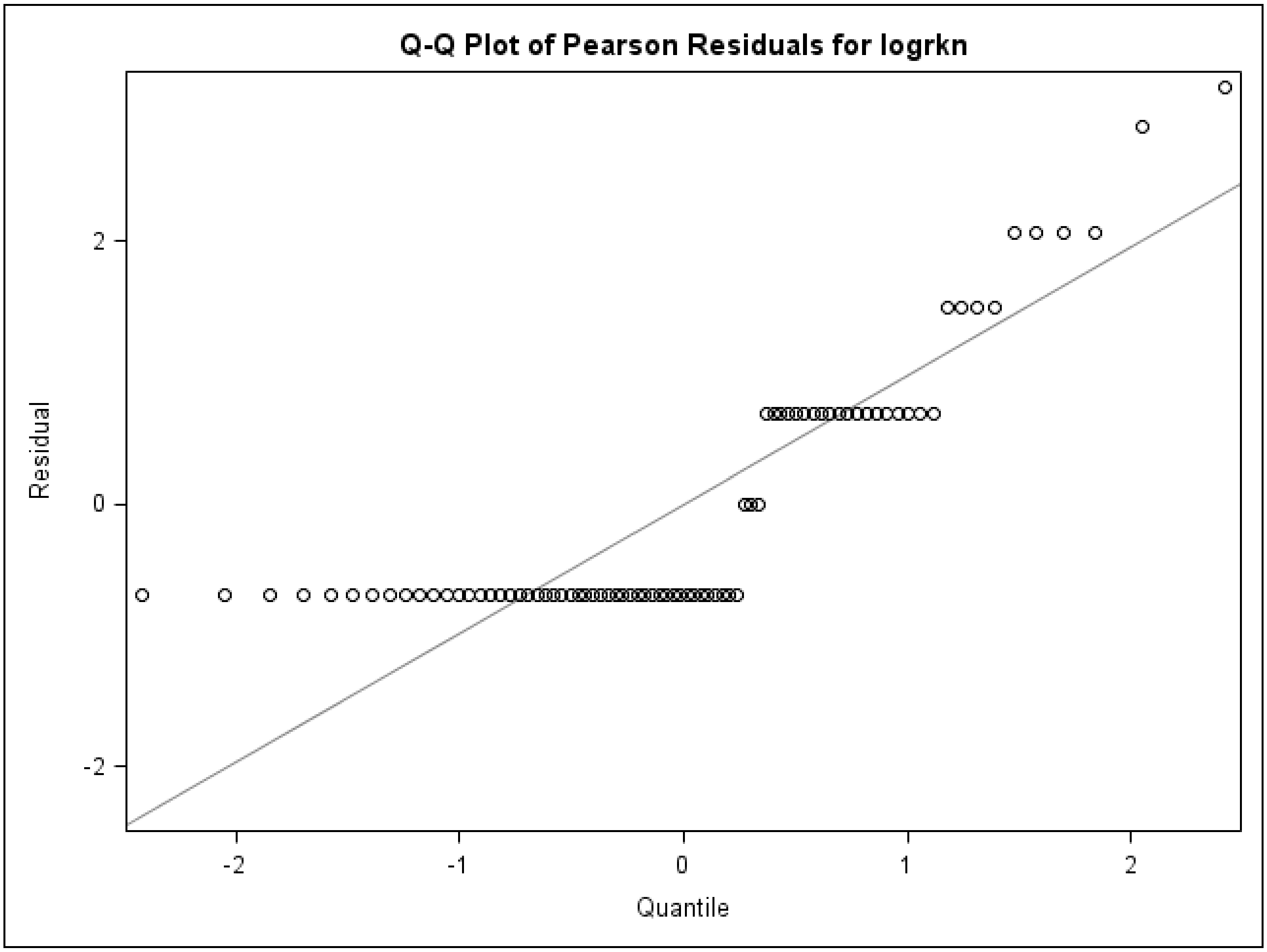


Figure E.4.2.6 Normal quantile plot of the Pearson residuals



E.4.3 May 2006 Model 3 Residual Plots

Figure E.4.3.1 Histogram of the raw residuals

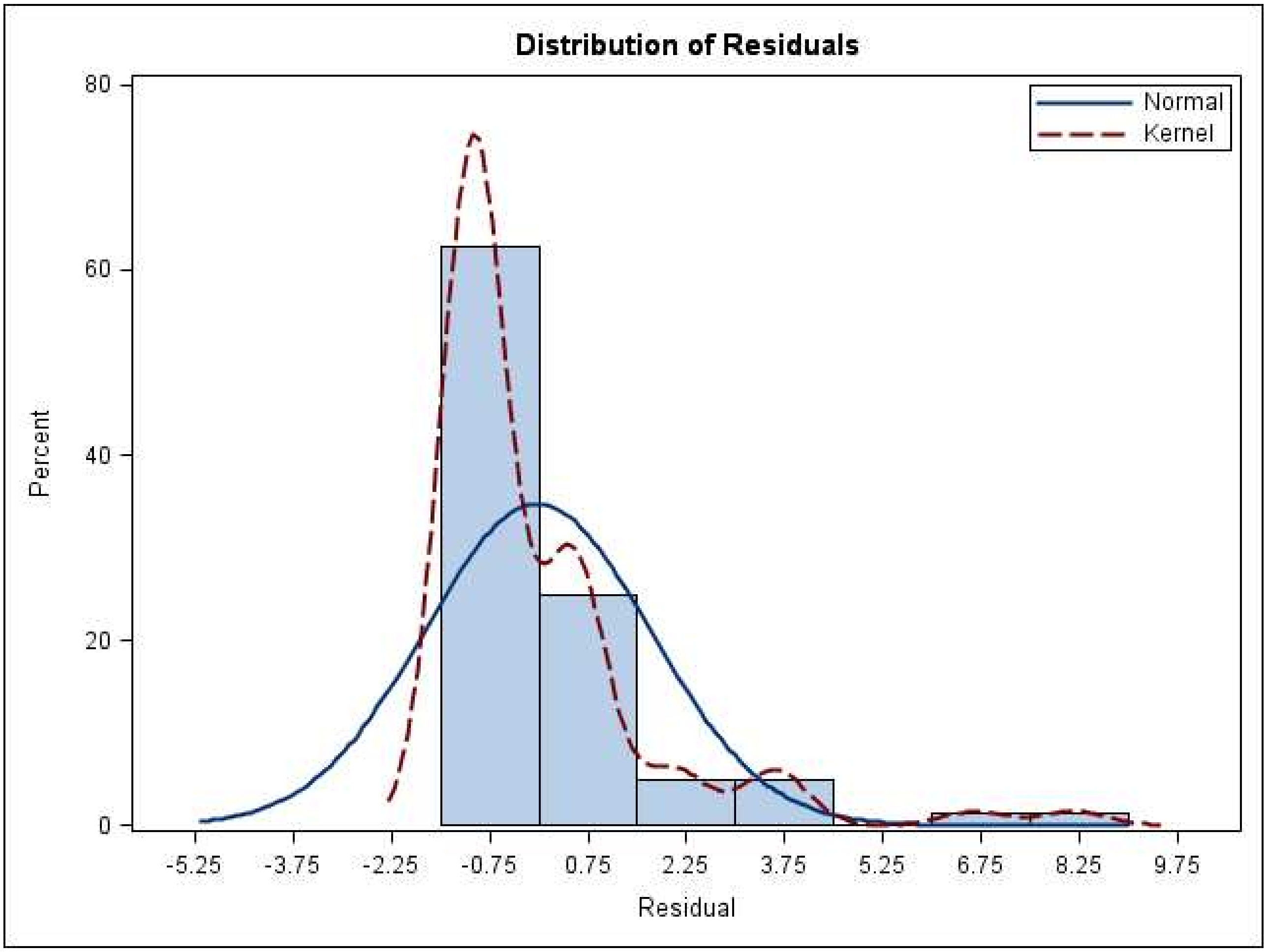


Figure E.4.3.2 Normal quantile plot of the raw residuals

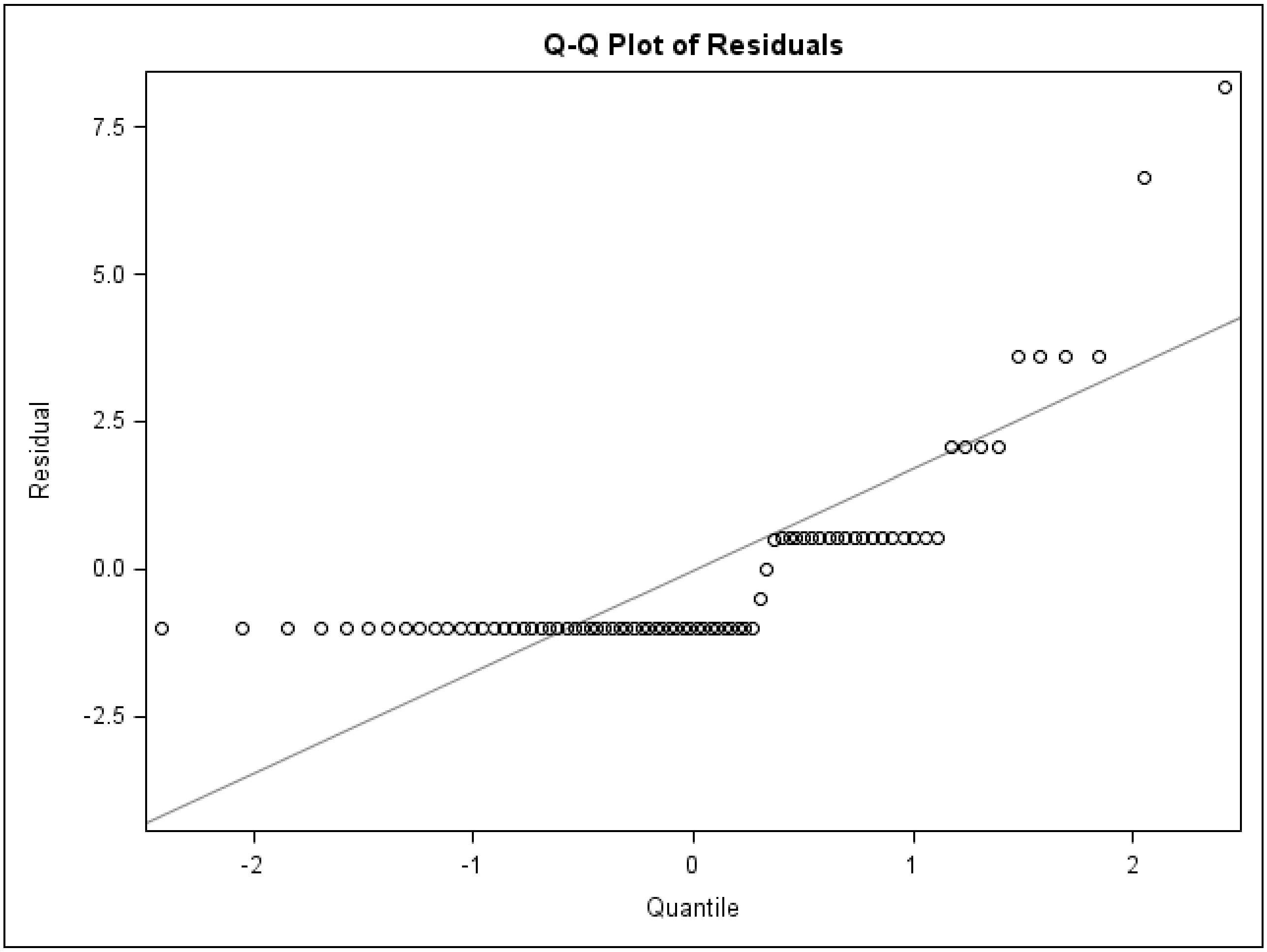


Figure E.4.3.3 Histogram of the Studentized residuals

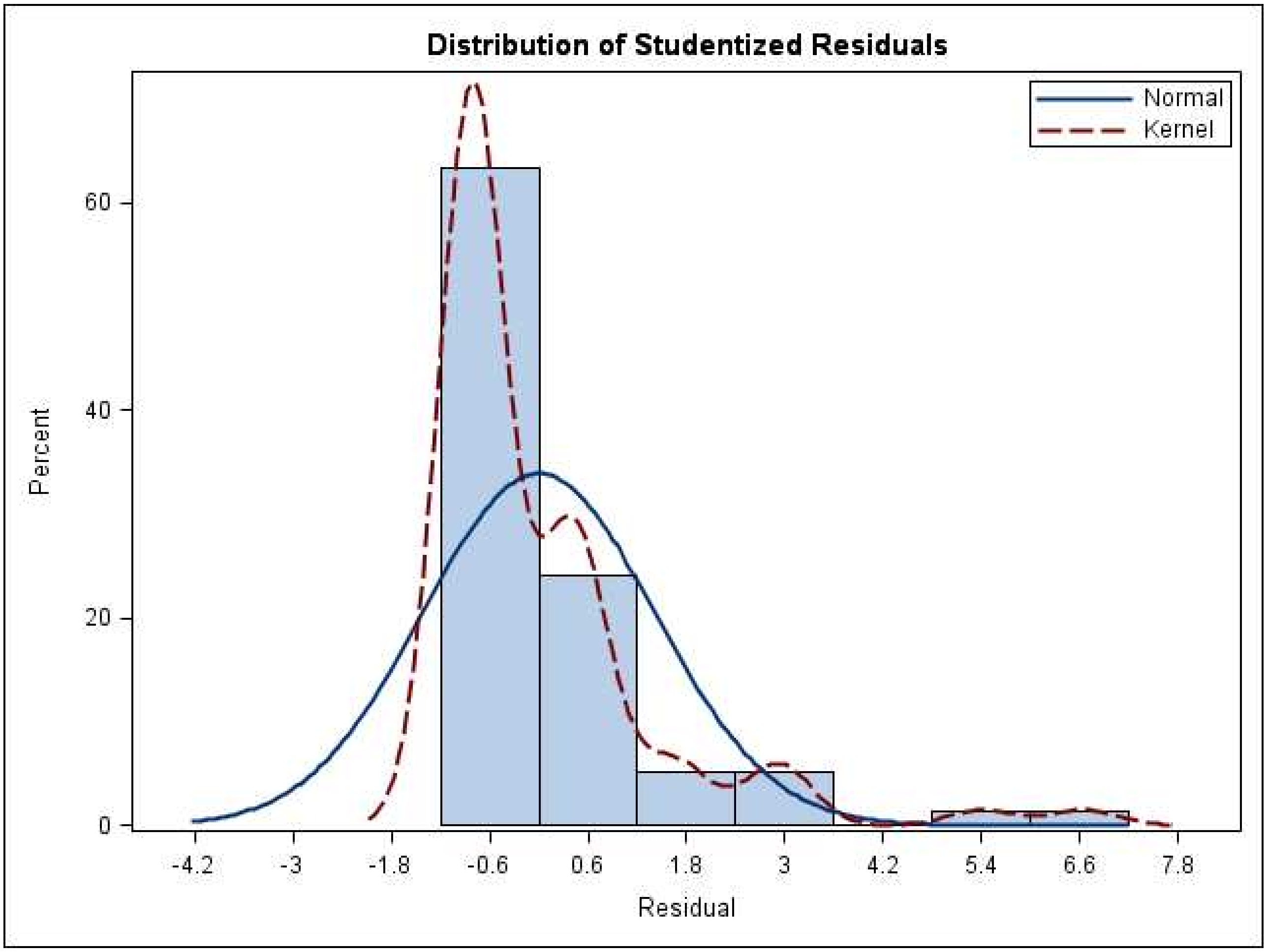


Figure E.4.3.4 Normal quantile plot of the Studentized residuals

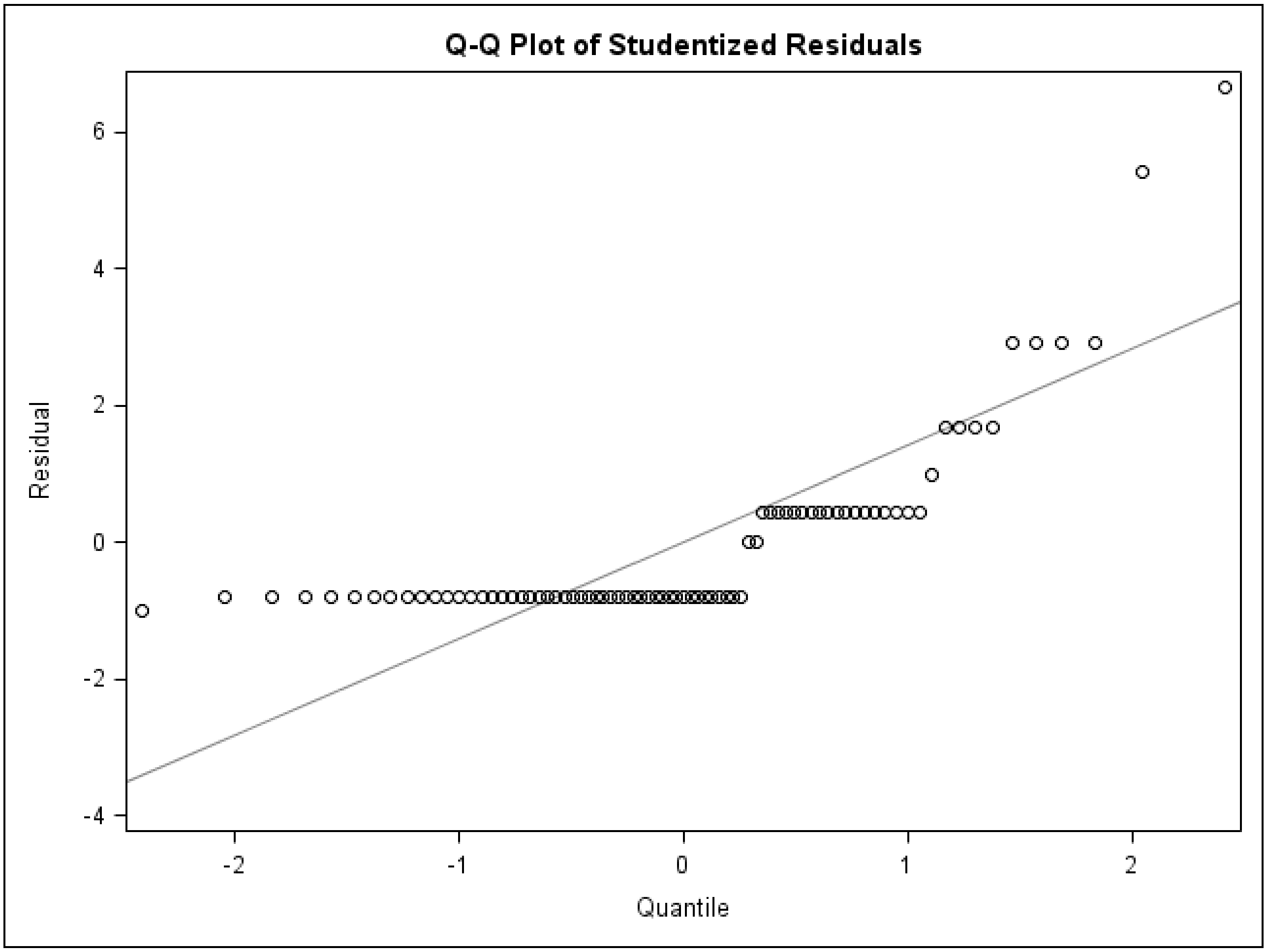


Figure E.4.3.5 Histogram of the Pearson residuals

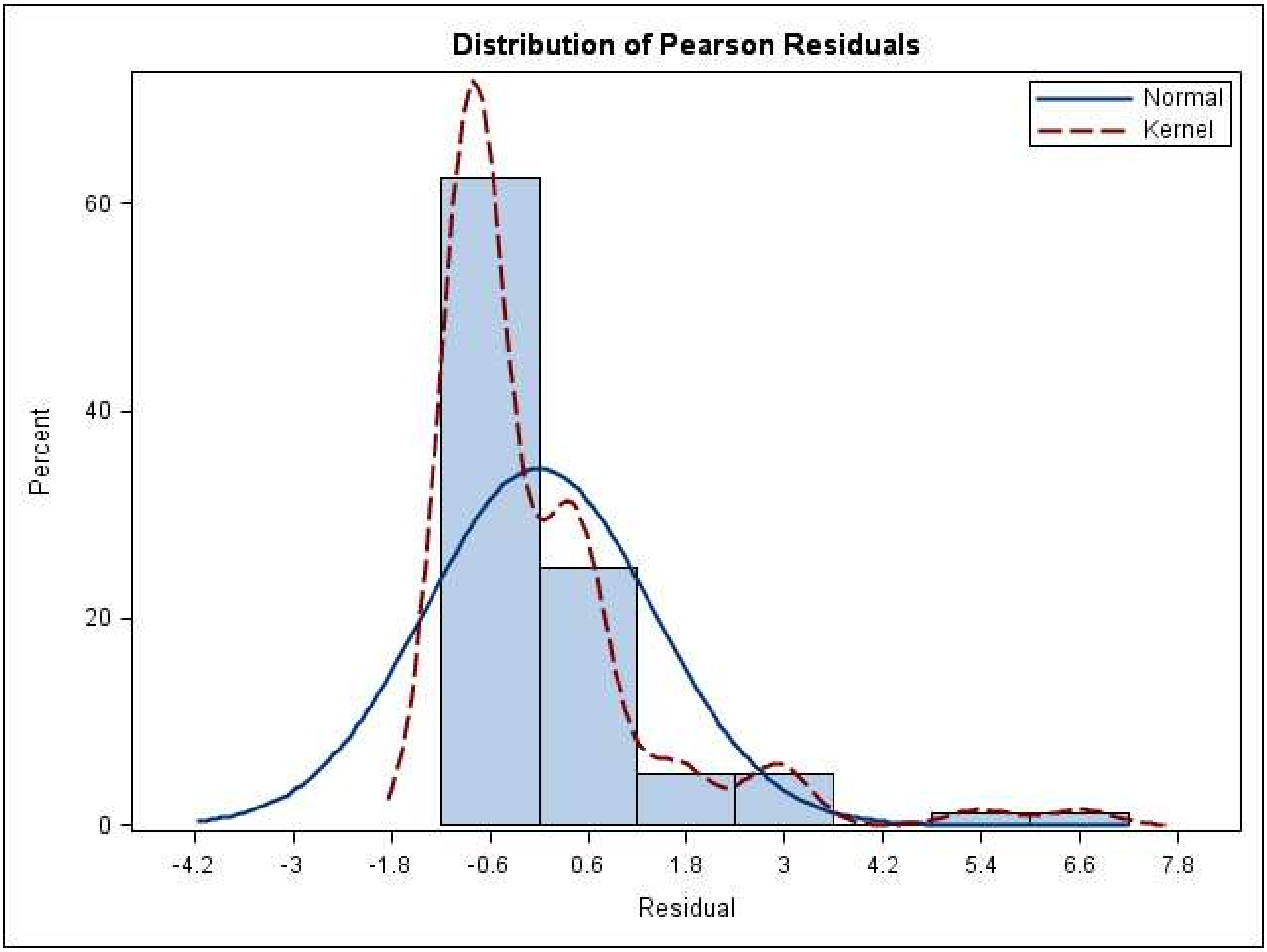
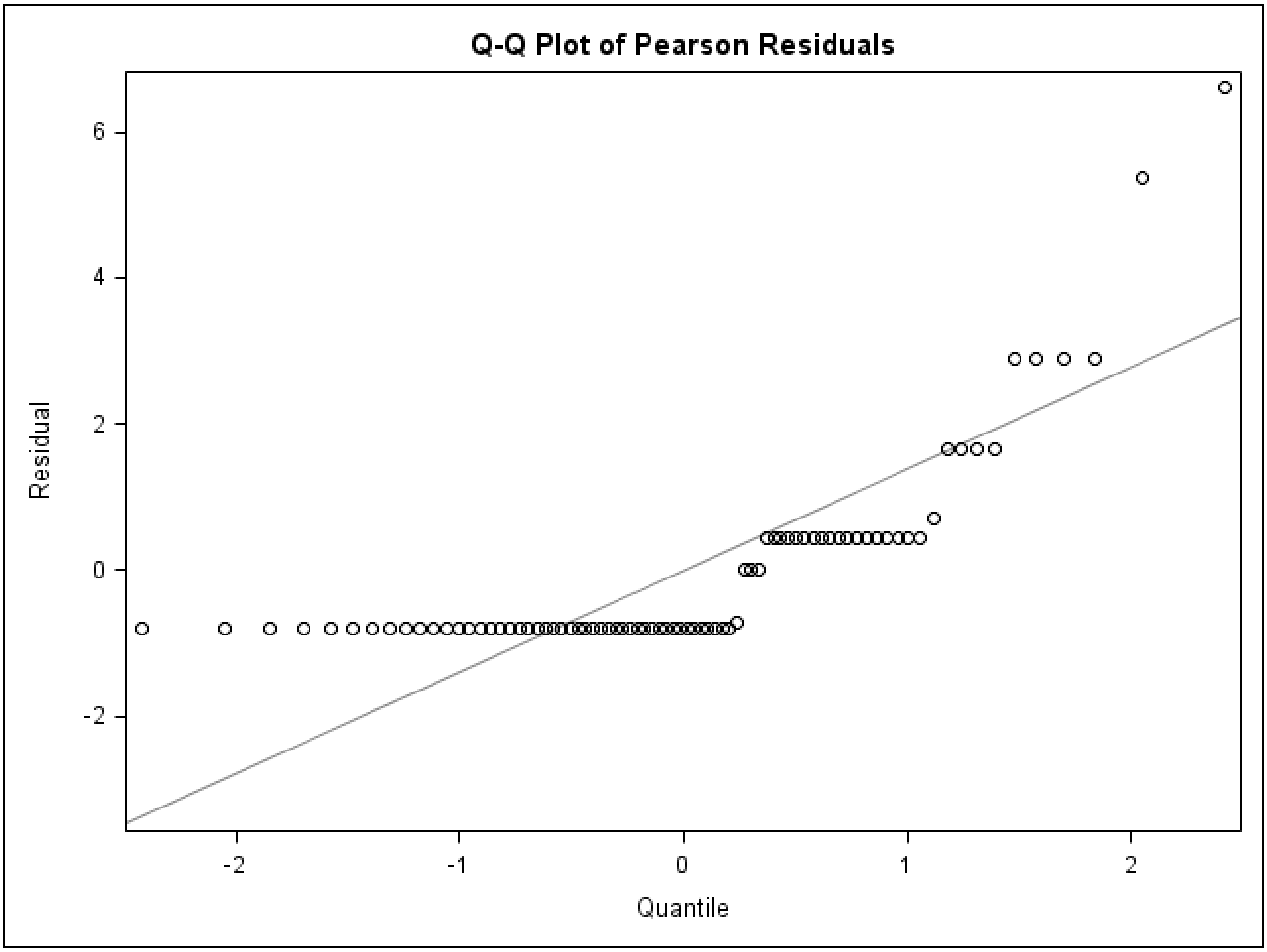


Figure E.4.3.6 Normal quantile plot of the Pearson residuals



E.4.4 May 2006 Model 4 Residual Plots

Figure E.4.4.1 Histogram of the raw residuals

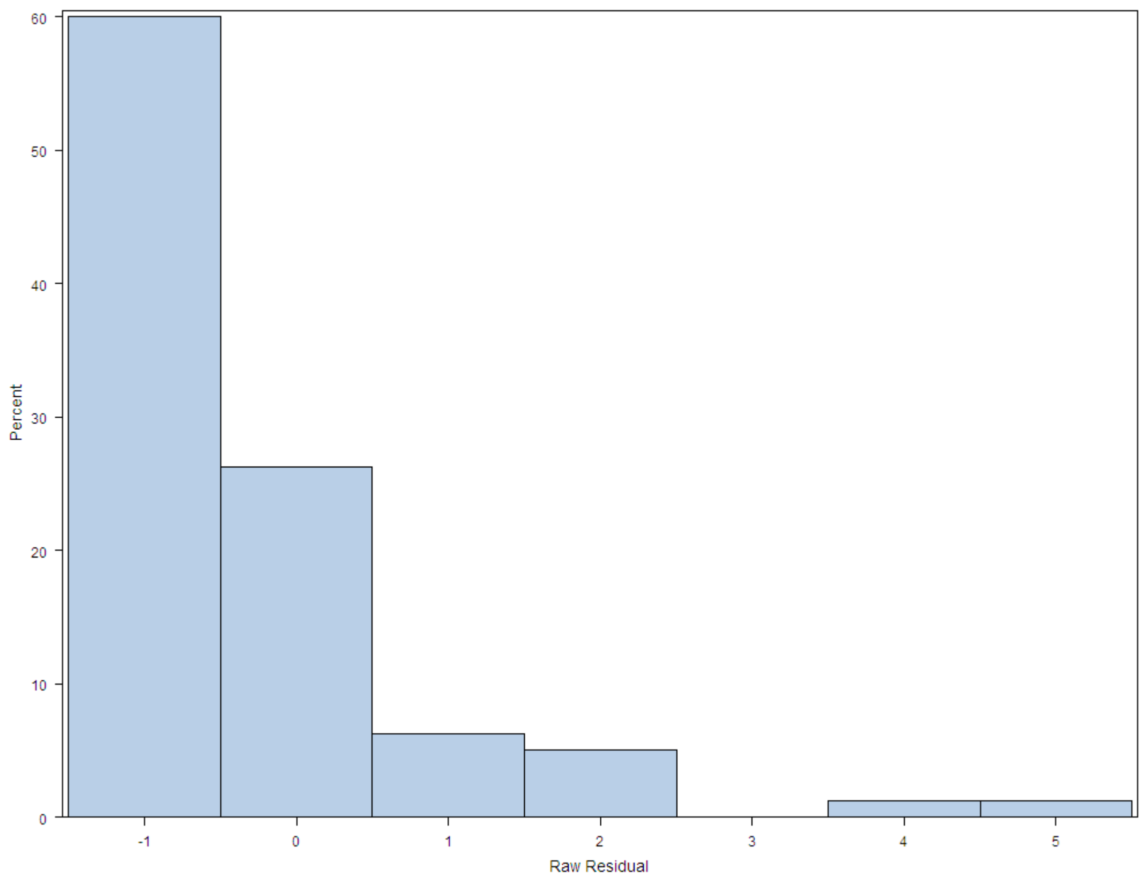


Figure E.4.4.2 Histogram of the Pearson residuals

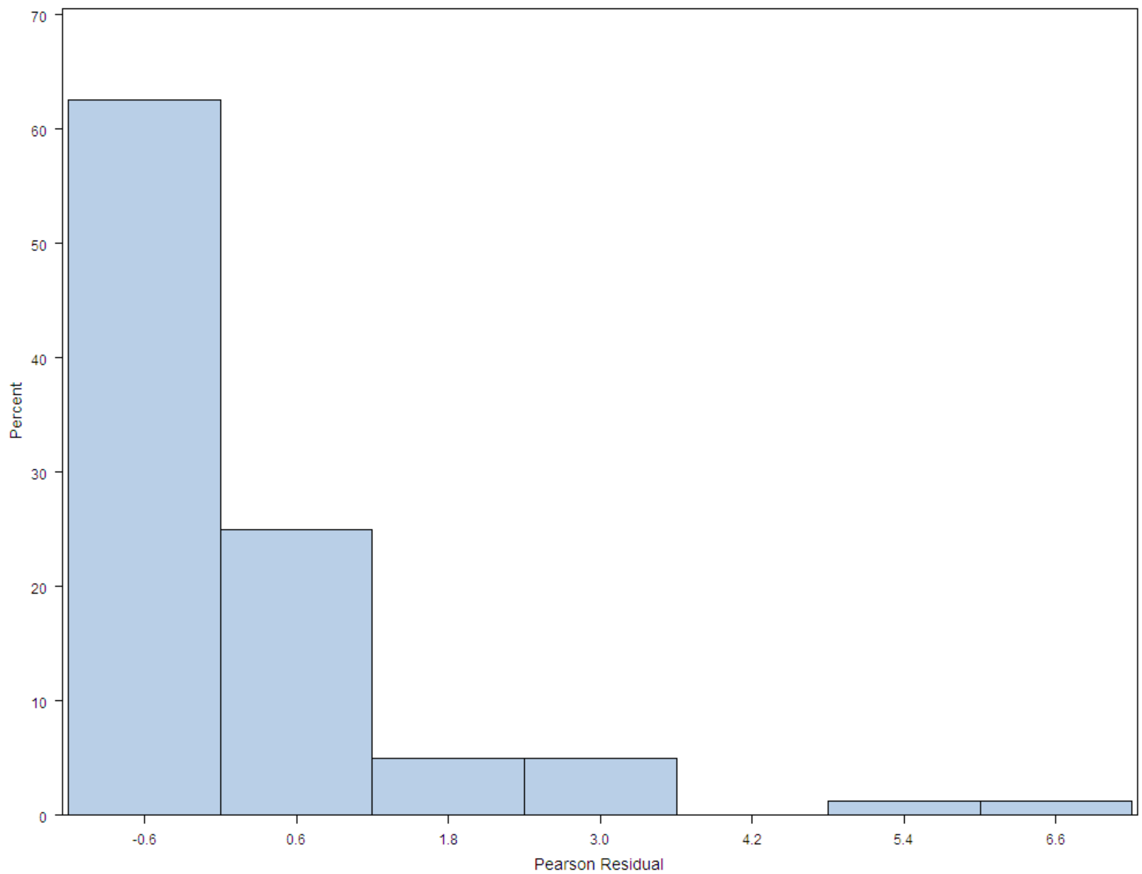


Figure E.4.4.3 Histogram of the deviance residuals

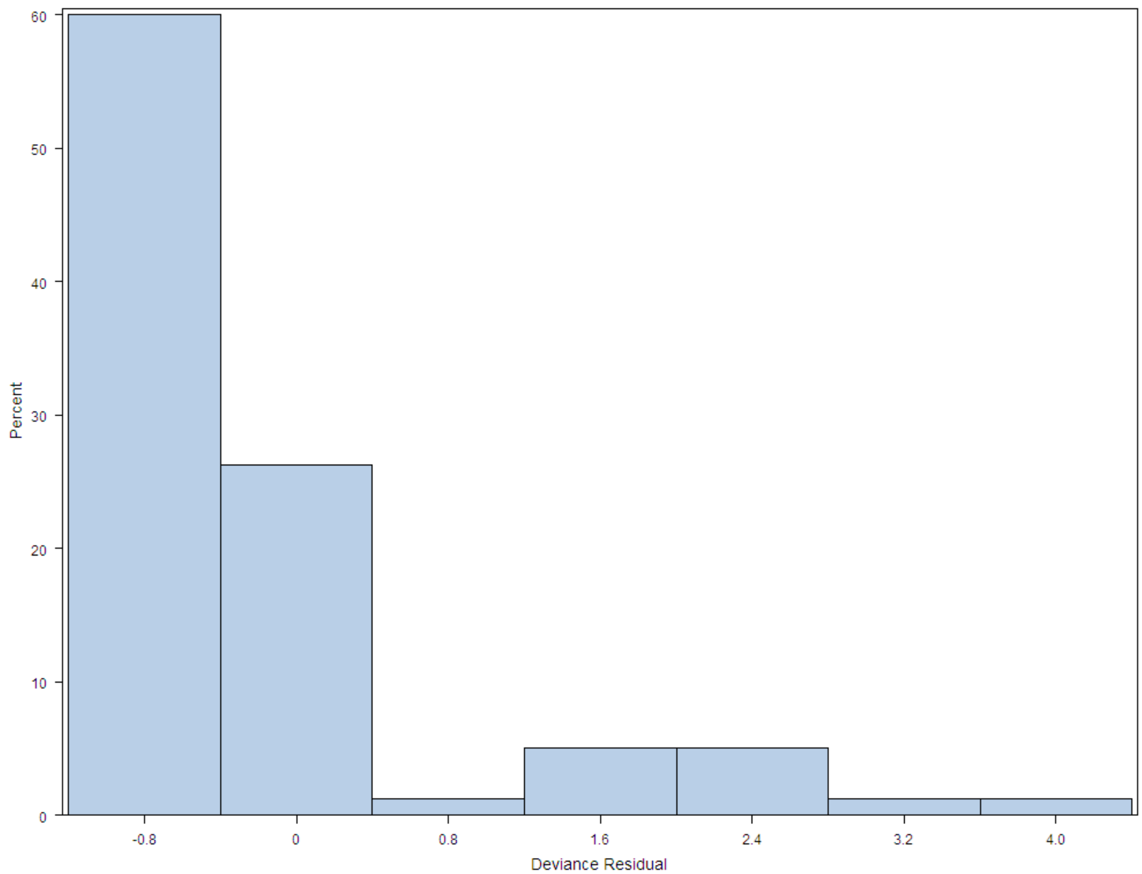


Figure E.4.4.4 Histogram of the likelihood residuals

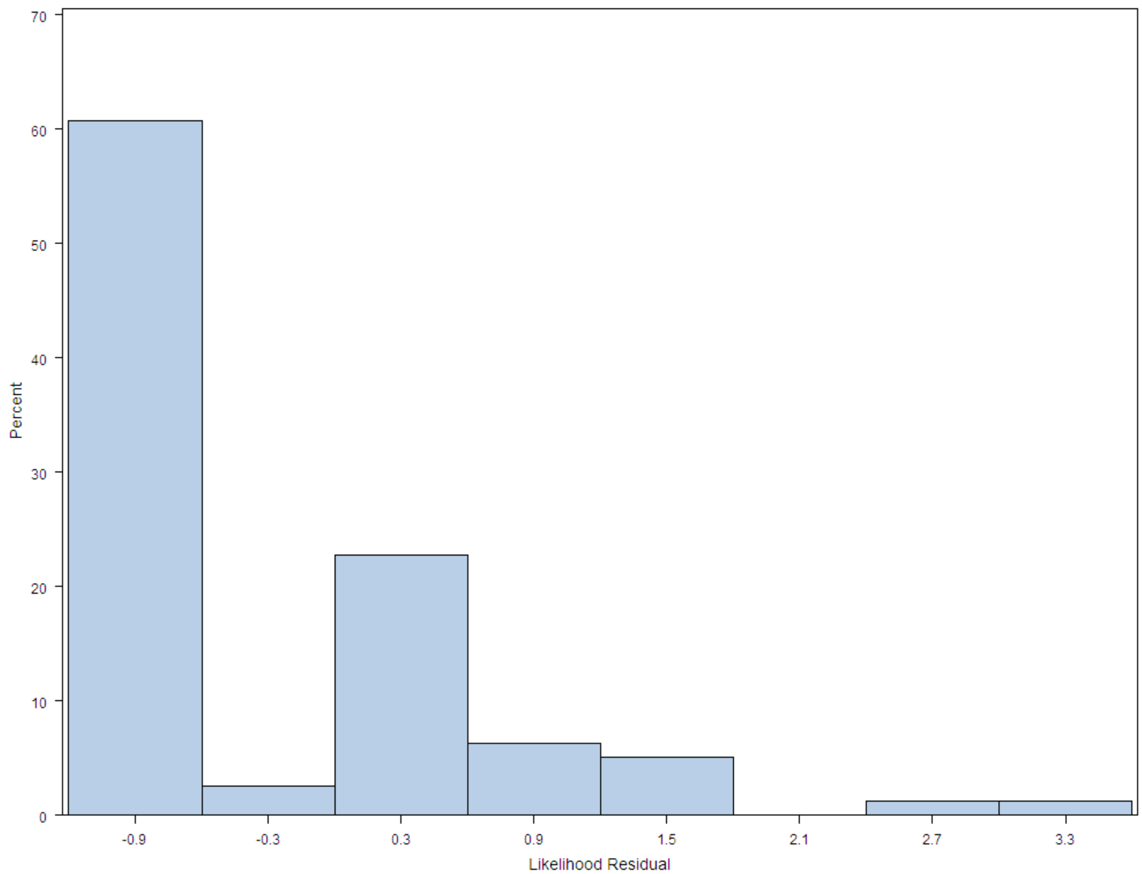


Figure E.4.4.5 Histogram of the standardized Pearson residuals

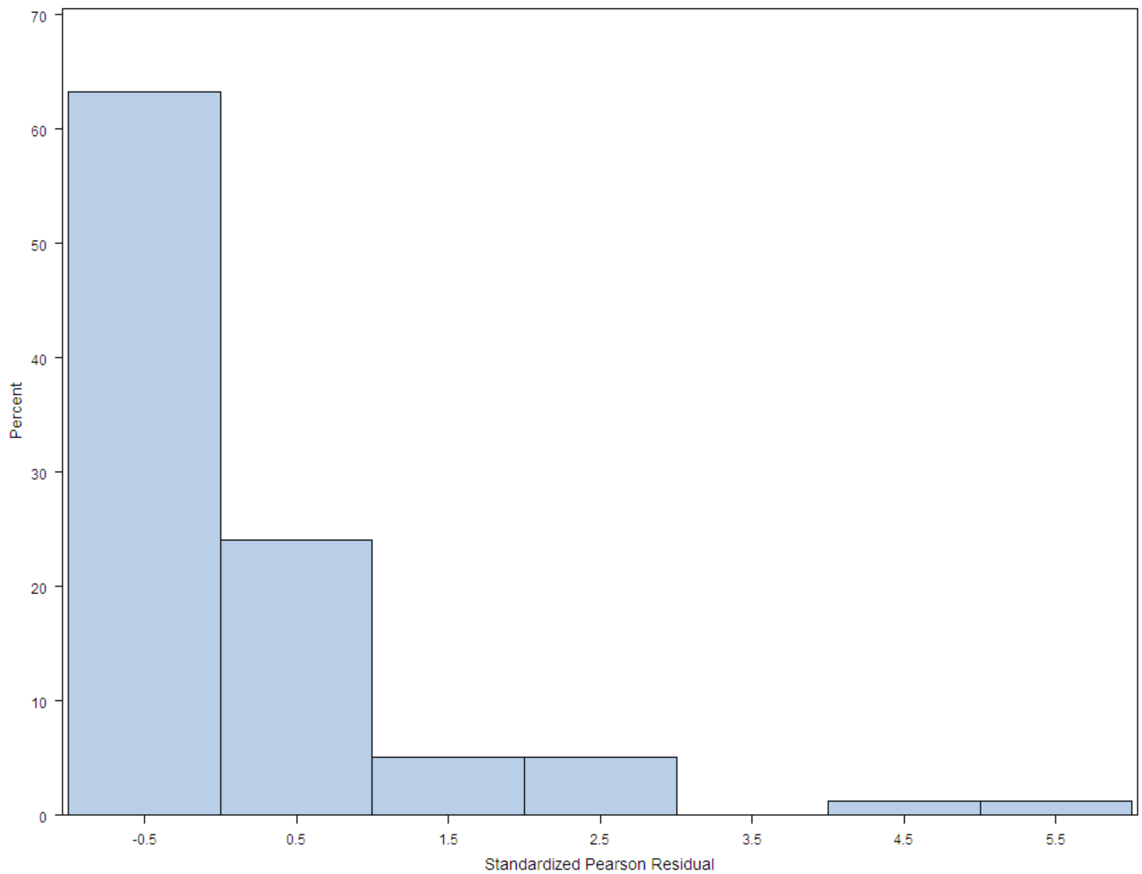
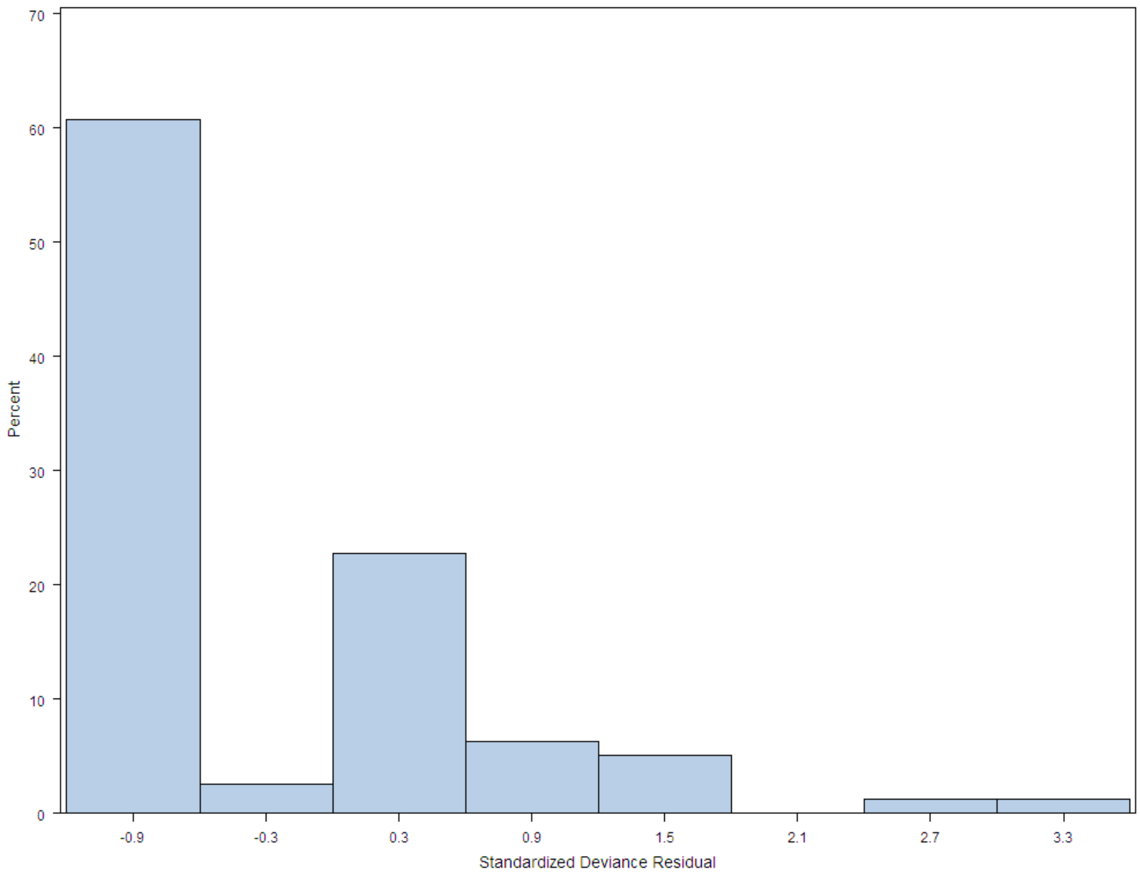


Figure E.4.4.6 Histogram of the standardized deviance residuals



E.4.5 May 2006 Model 5 Residual Plots

Figure E.4.5.1 Histogram of the raw residuals

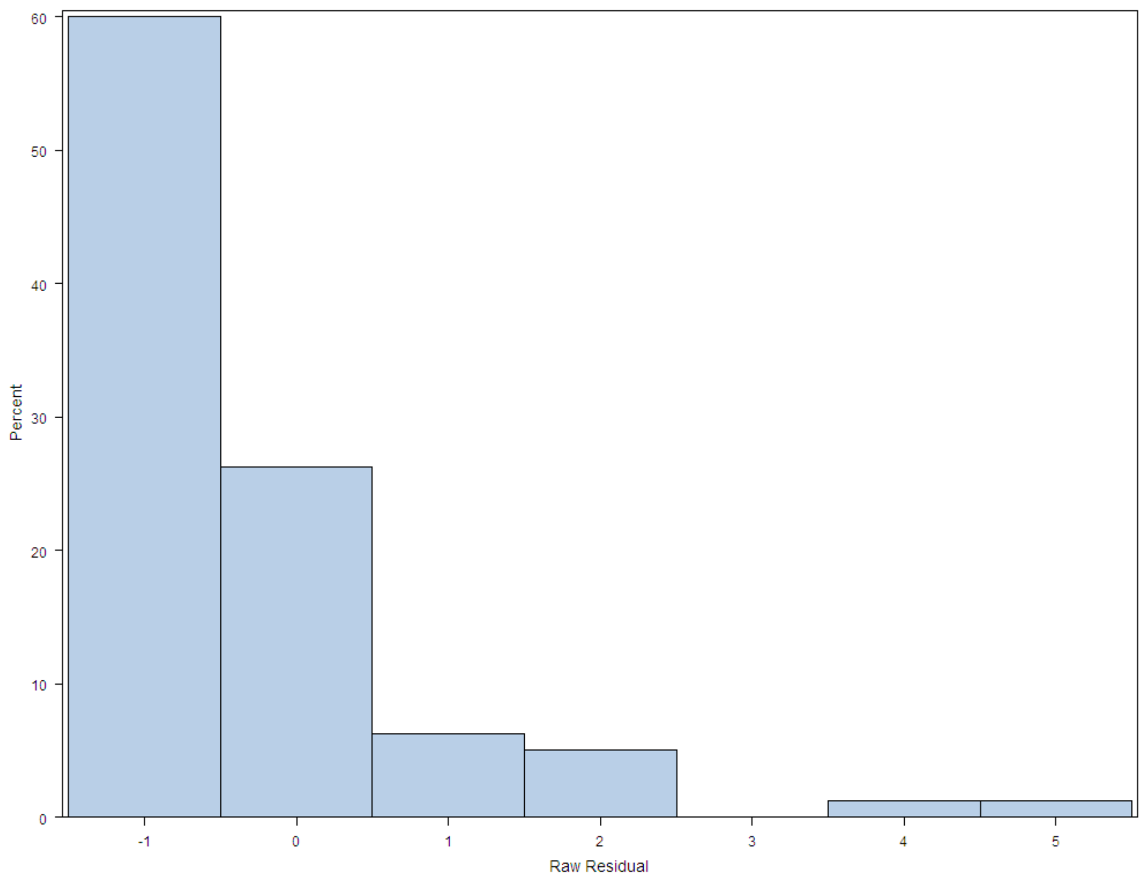


Figure E.4.5.2 Histogram of the Pearson residuals

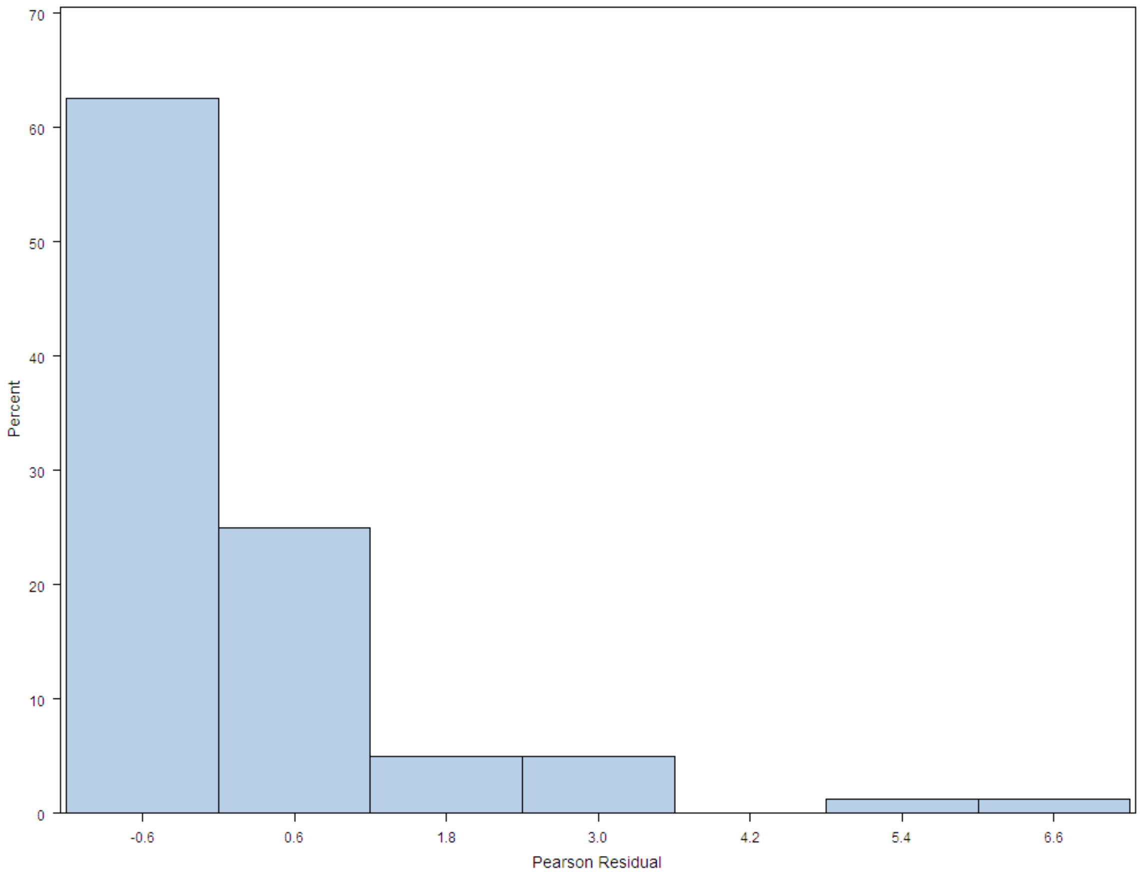


Figure E.4.5.3 Histogram of the deviance residuals

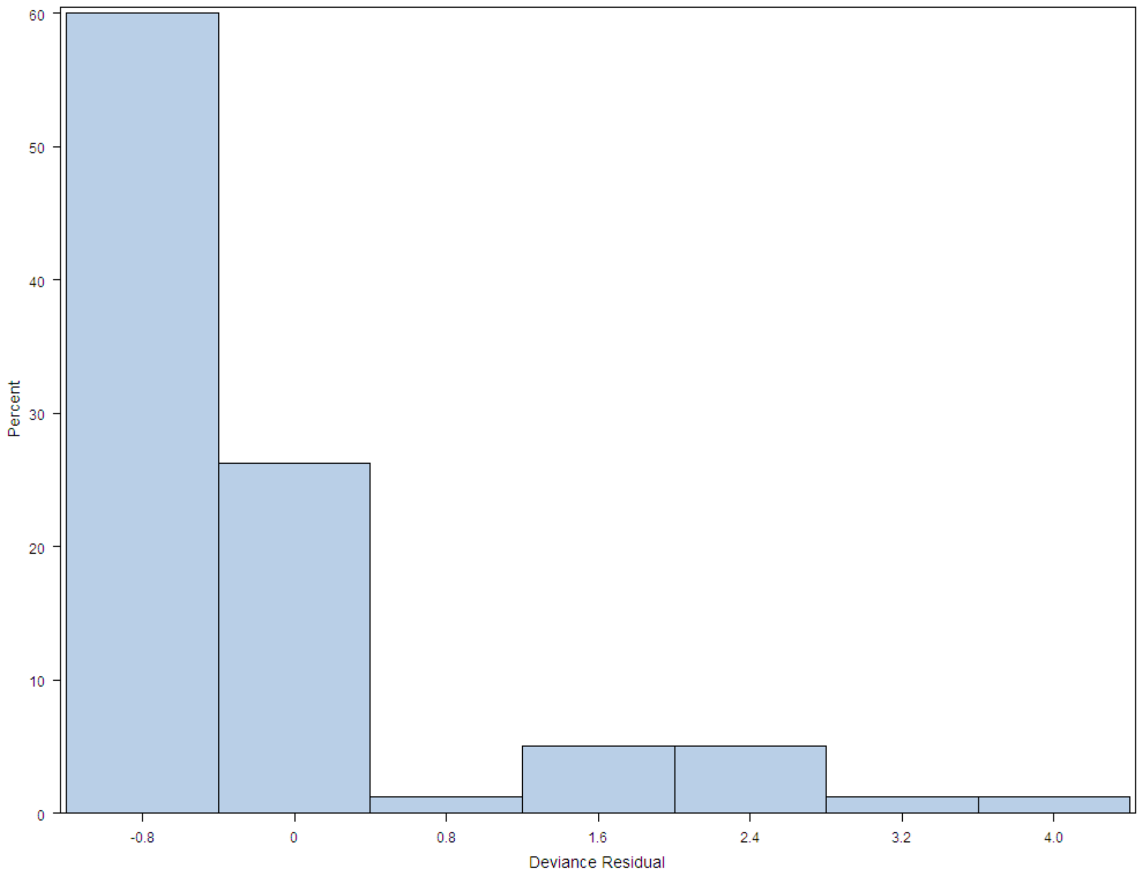


Figure E.4.5.4 Histogram of the likelihood residuals

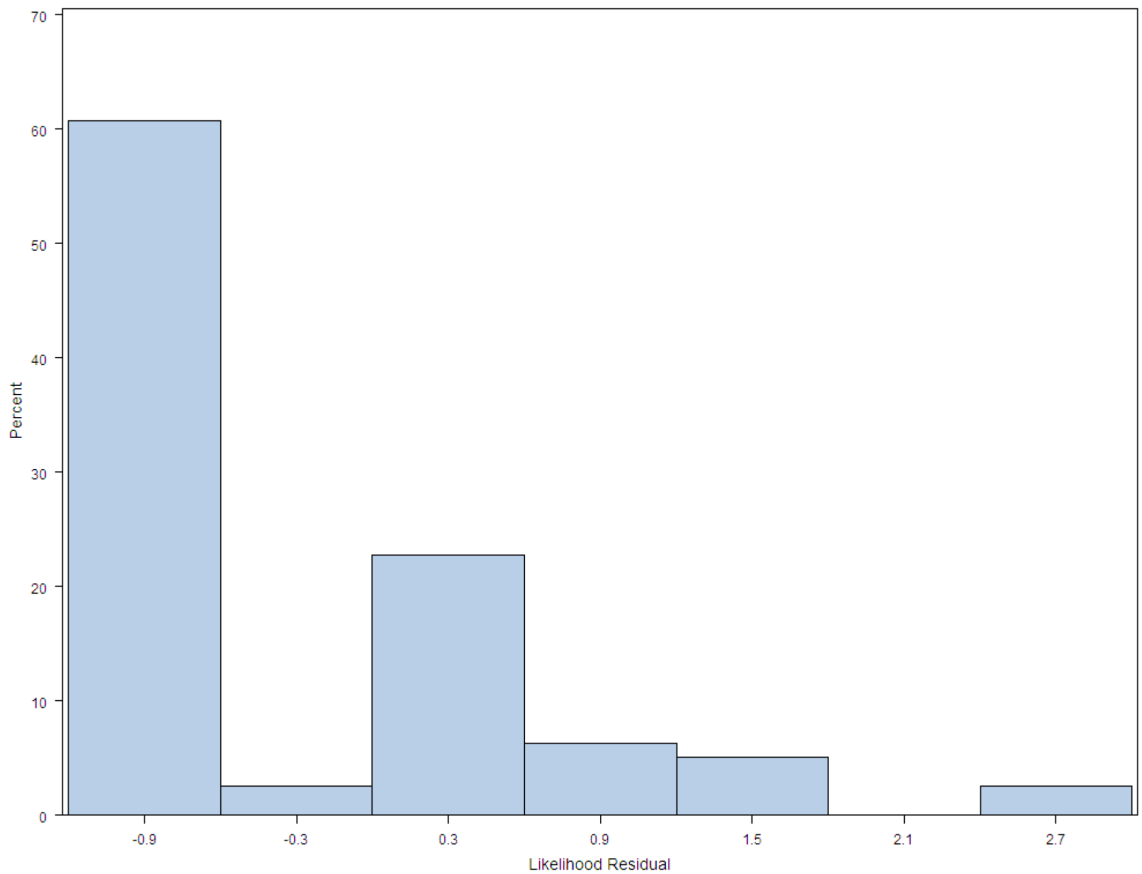


Figure E.4.5.5 Histogram of the standardized Pearson residuals

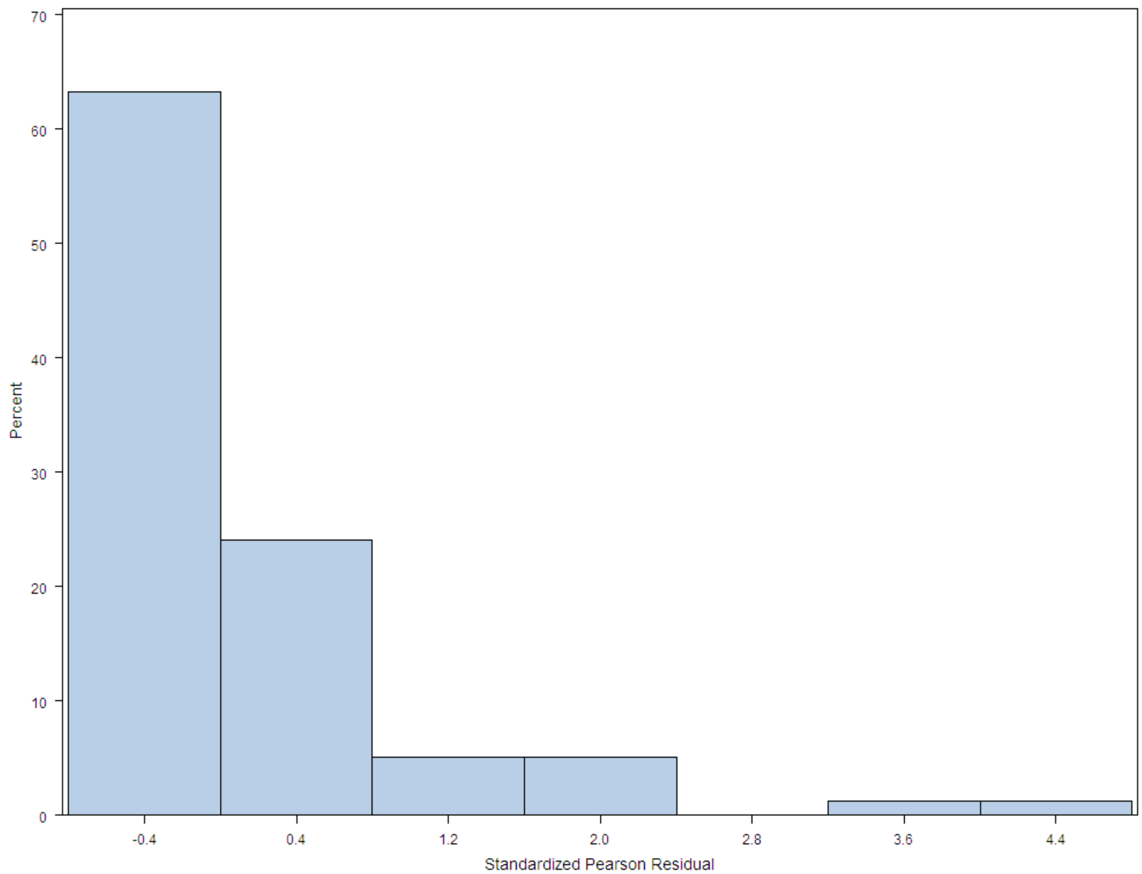
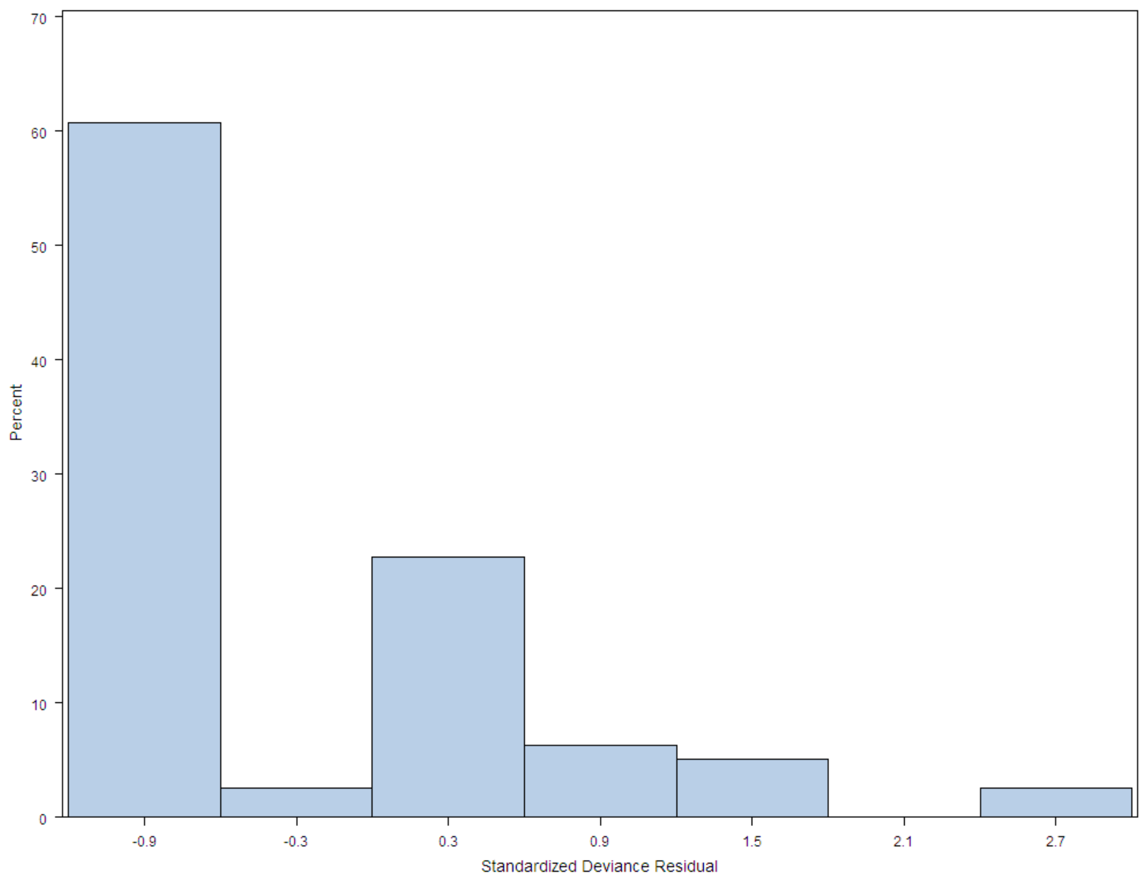


Figure E.4.5.6 Histogram of the standardized deviance residuals



E.4.6 May 2006 Model 6 Residual Plots

Figure E.4.6.1 Histogram of the raw residuals

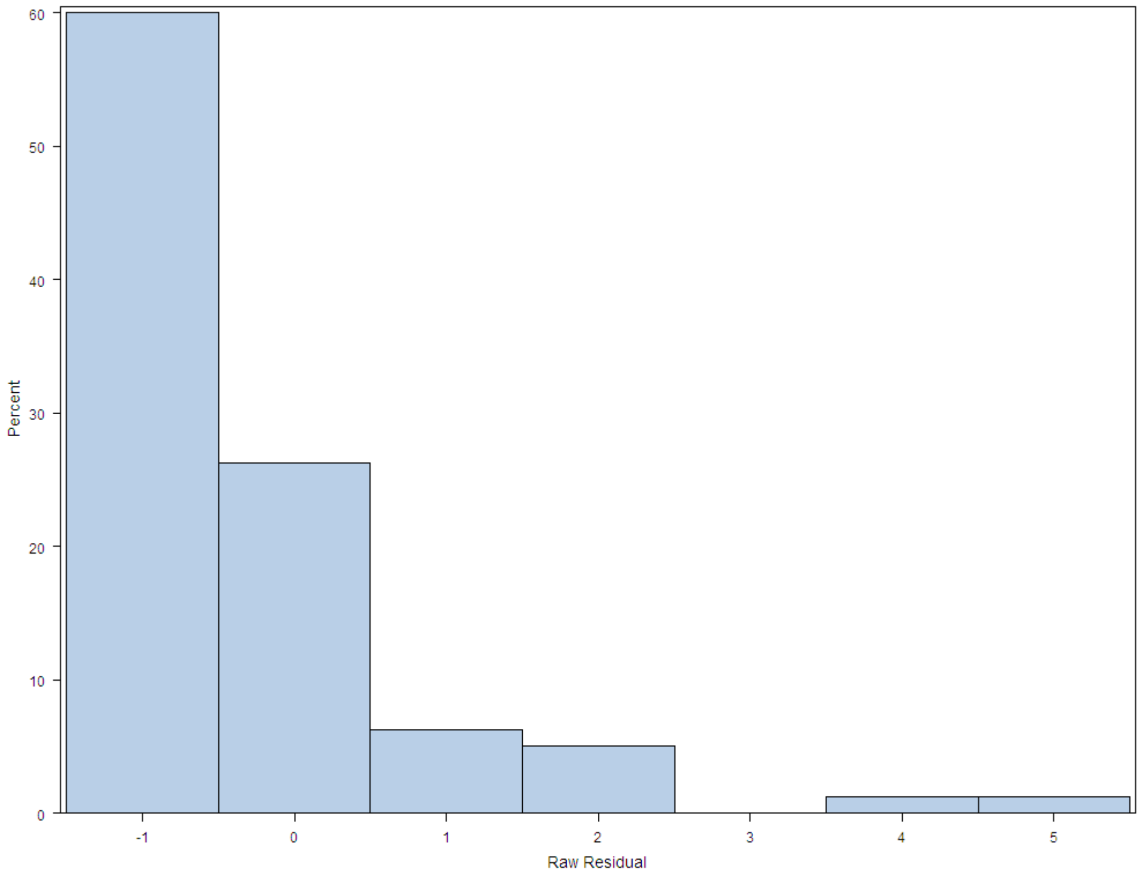
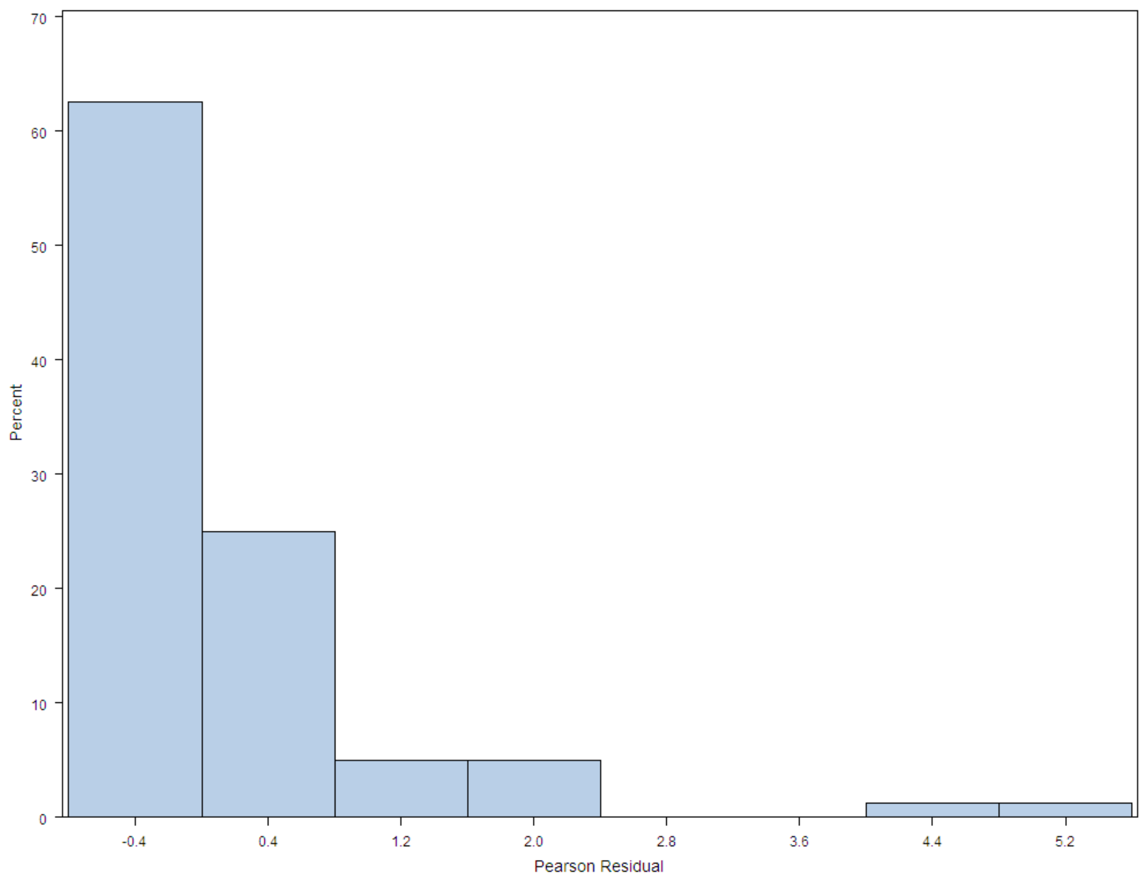


Figure E.4.6.2 Histogram of the Pearson residuals



E.4.7 May 2006 Model 7 Residual Plots

Figure E.4.7.1 Histogram of the raw residuals

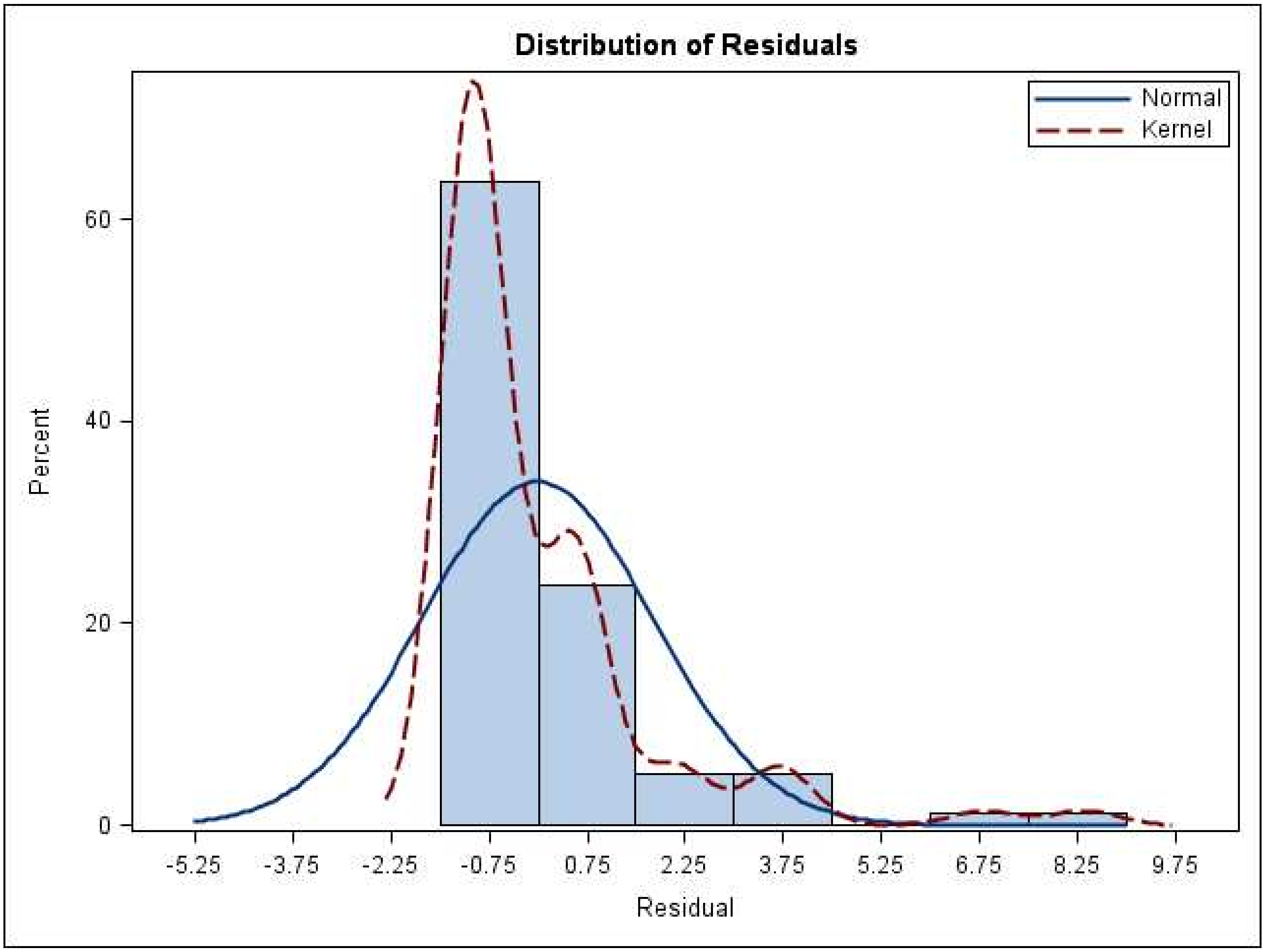


Figure E.4.7.2 Normal quantile plot of the raw residuals

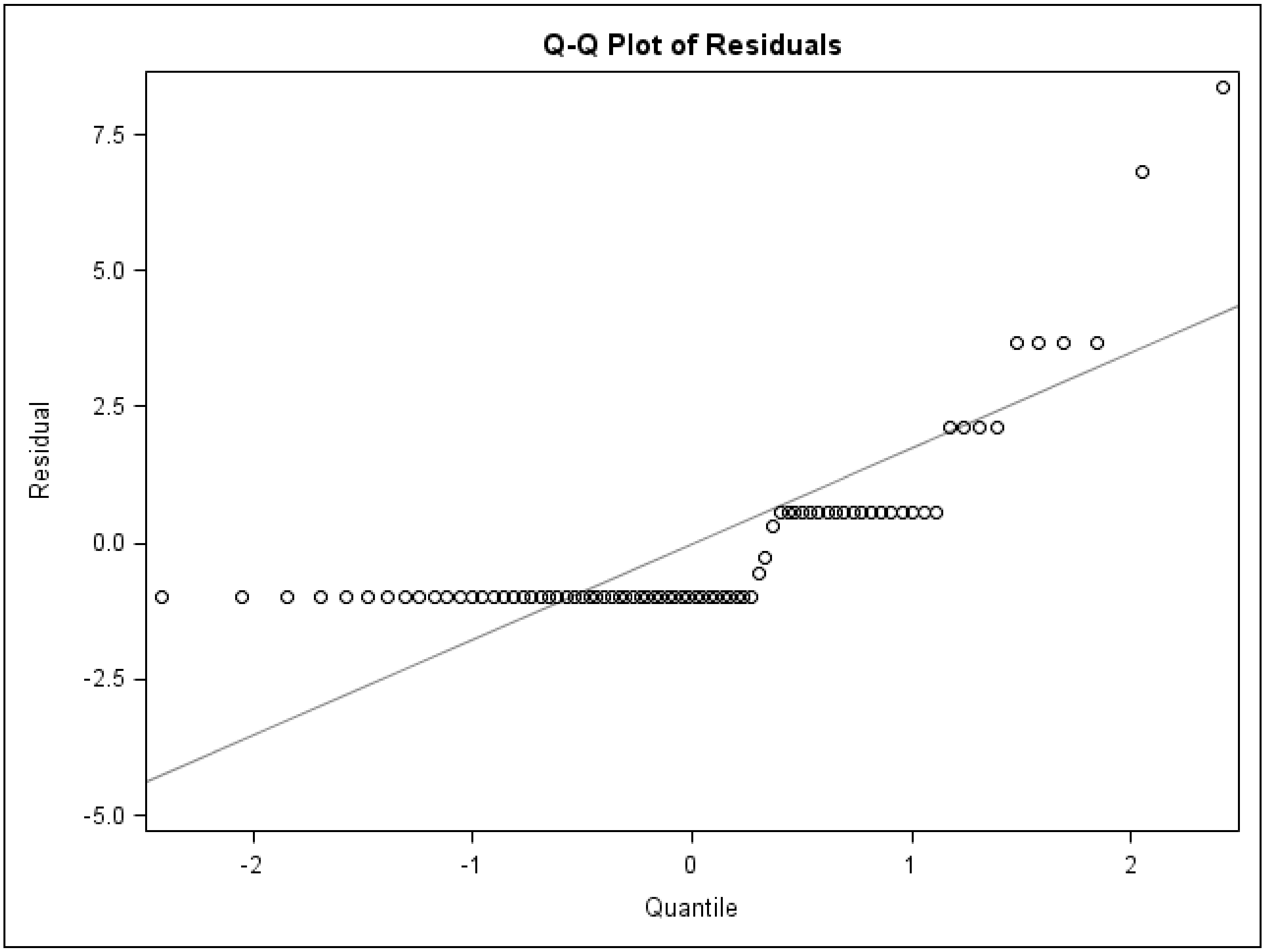


Figure E.4.7.3 Histogram of the Studentized residuals

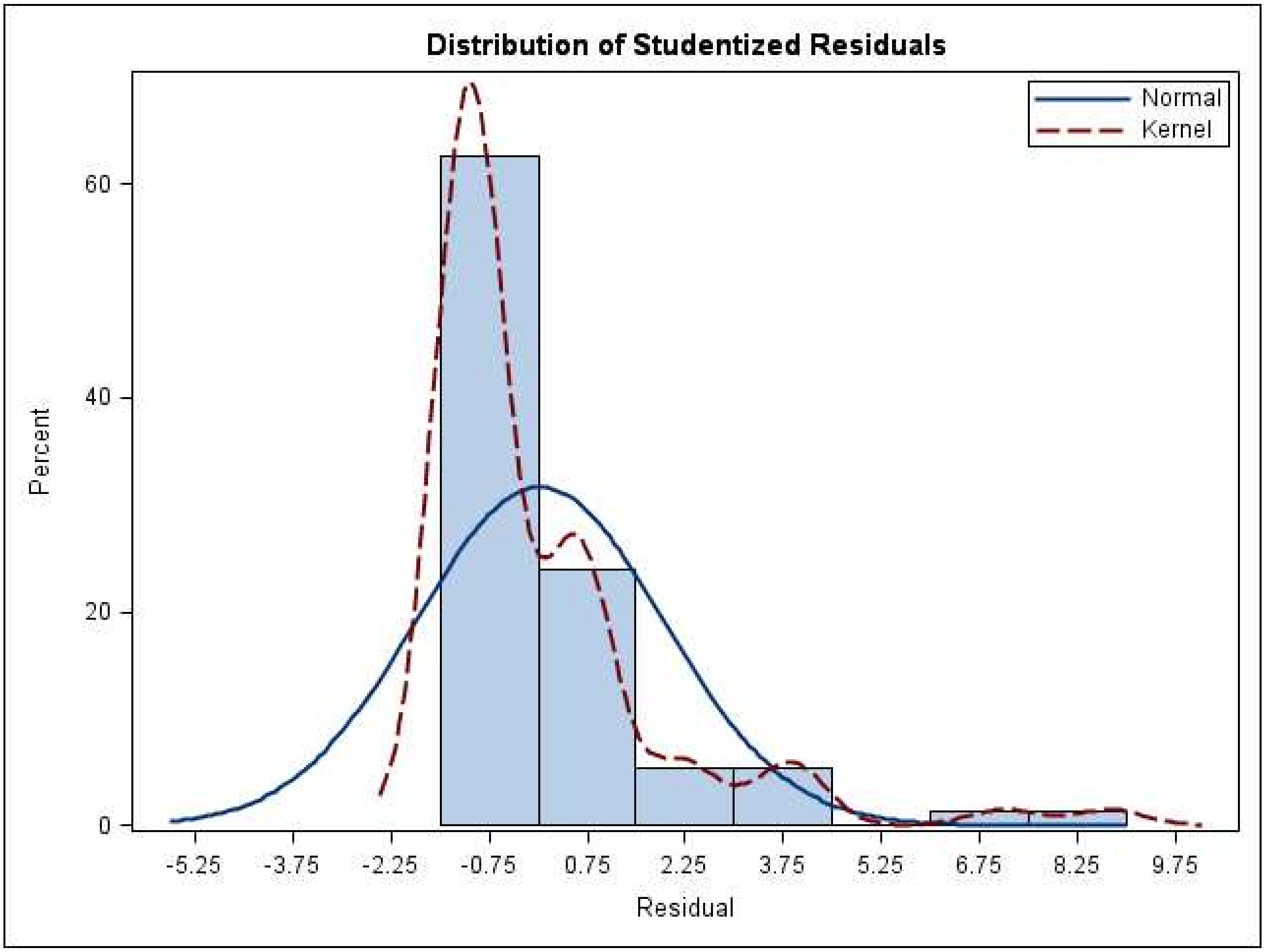


Figure E.4.7.4 Normal quantile plot of the Studentized residuals

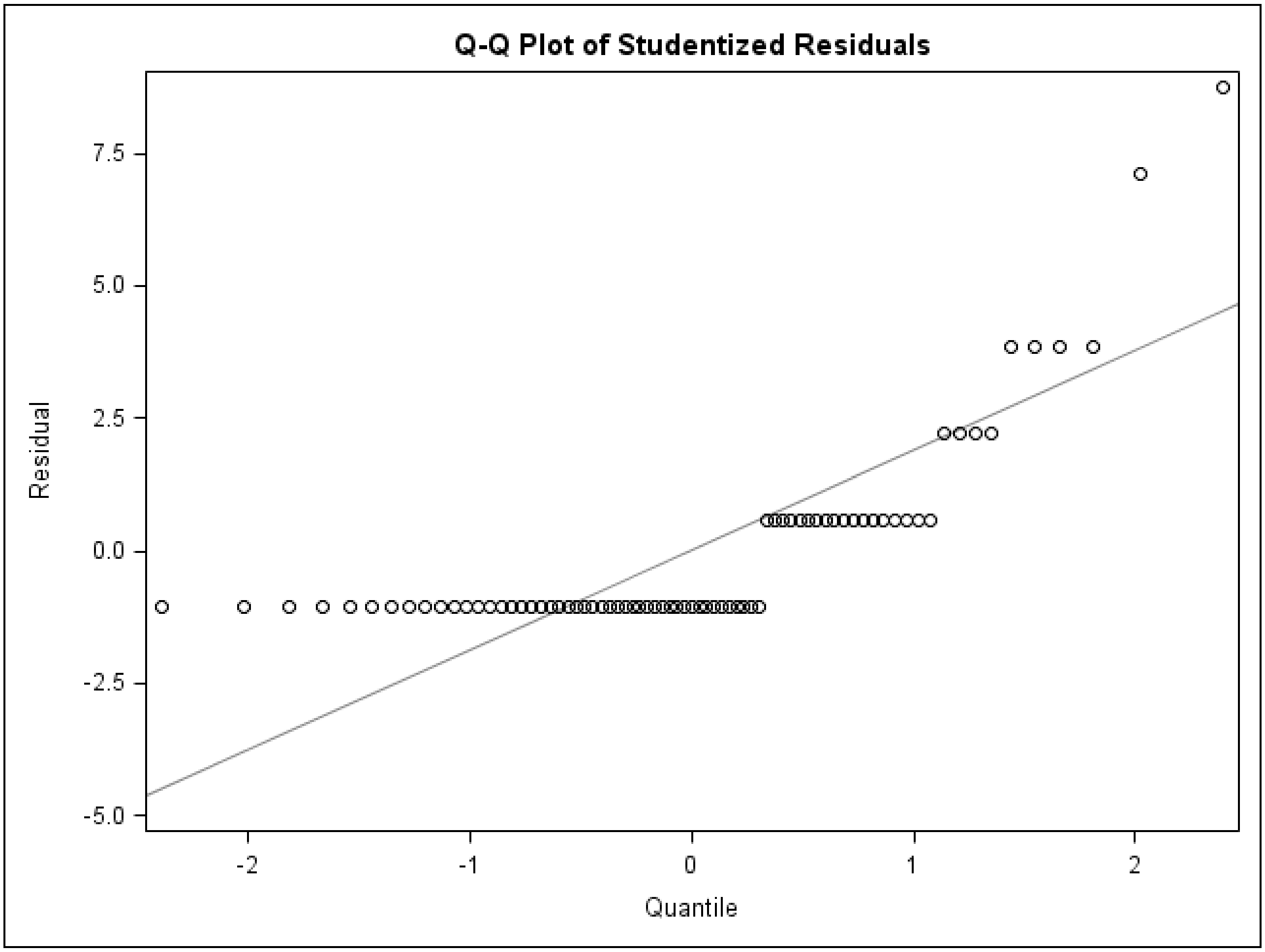


Figure E.4.7.5 Histogram of the Pearson residuals

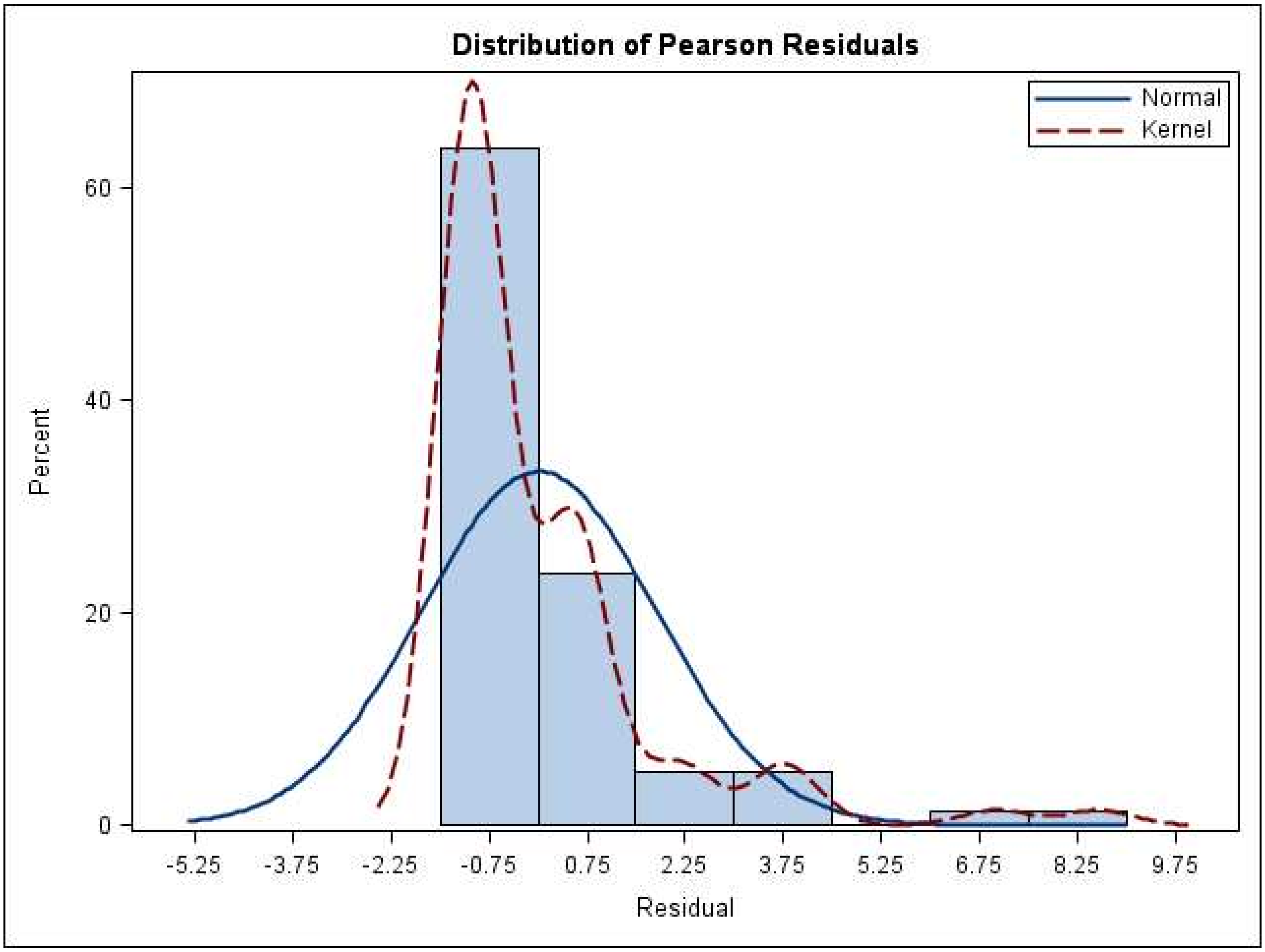
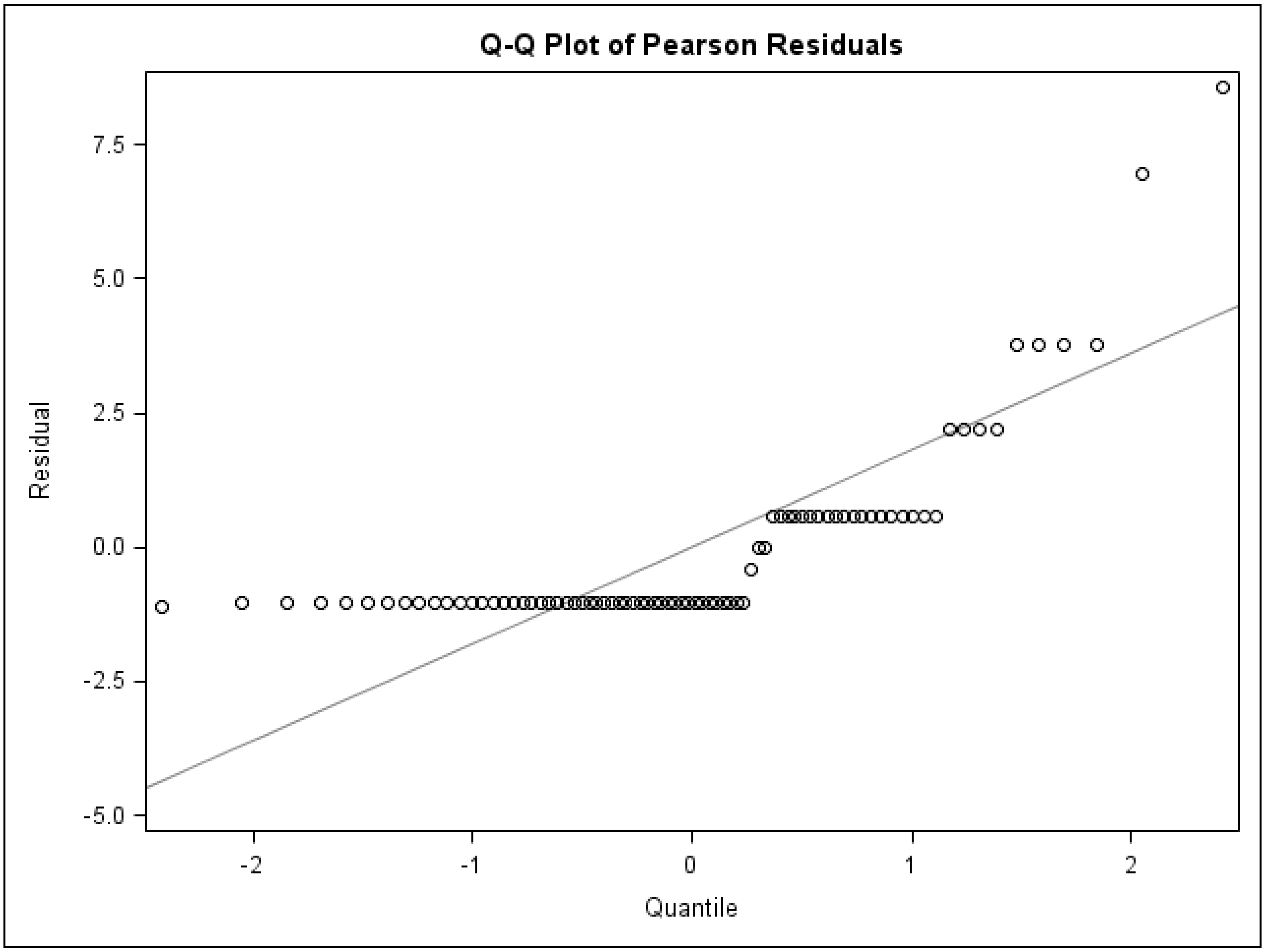
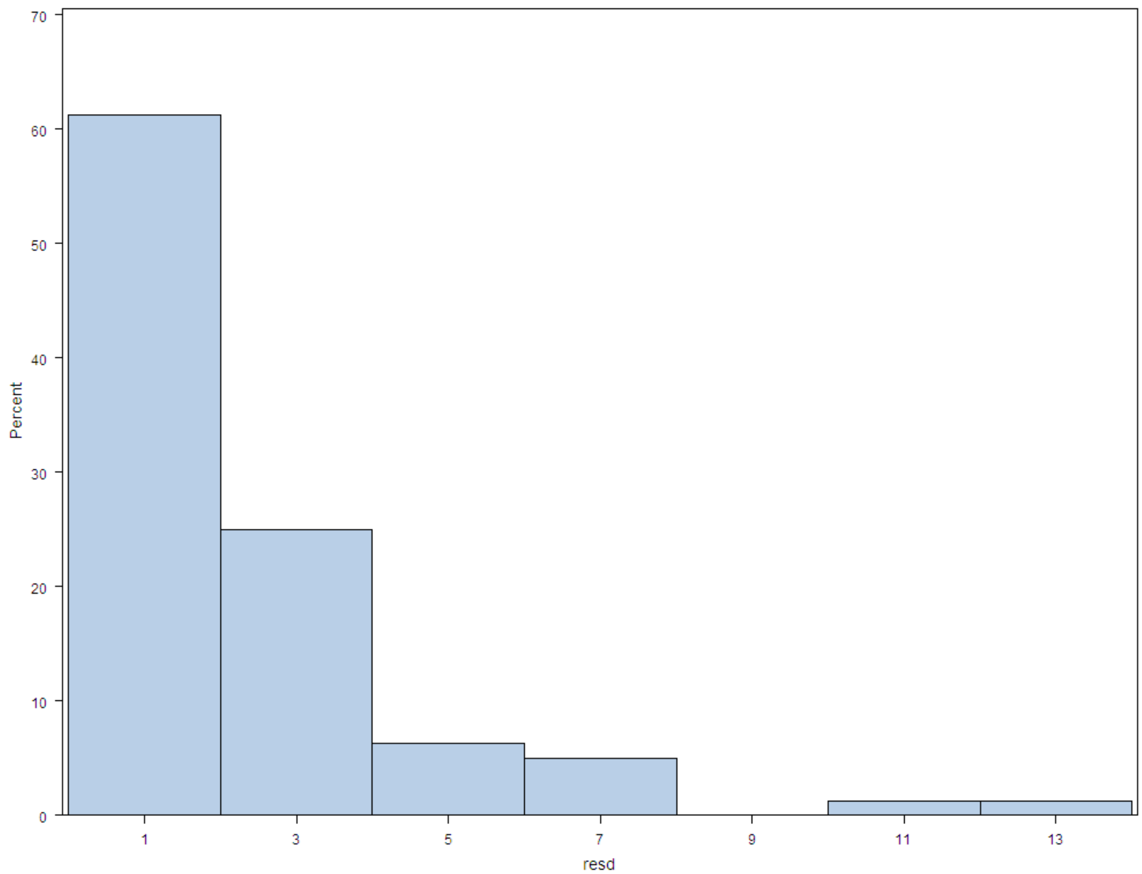


Figure E.4.7.6 Normal quantile plot of the Pearson residuals



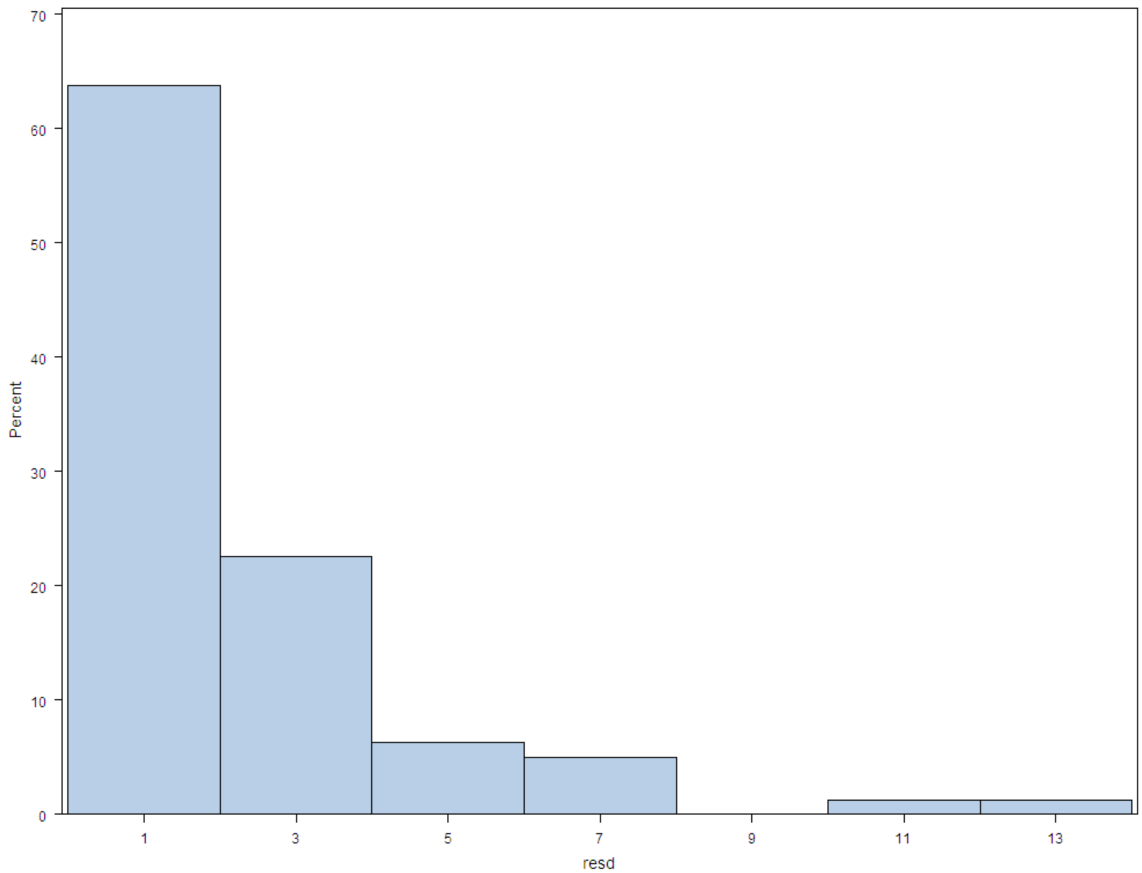
E.4.8 May 2006 Model 8 Residual Plots

Figure E.4.8.1 Histogram of the raw residuals



E.4.9 May 2006 Model 9 Residual Plots

Figure E.4.9.1 Histogram of the raw residuals



E.5 July 2006 Residual Plots

E.5.1 July 2006 Model 1 Residual Plots

Figure E.5.1.1 Histogram of the raw residuals

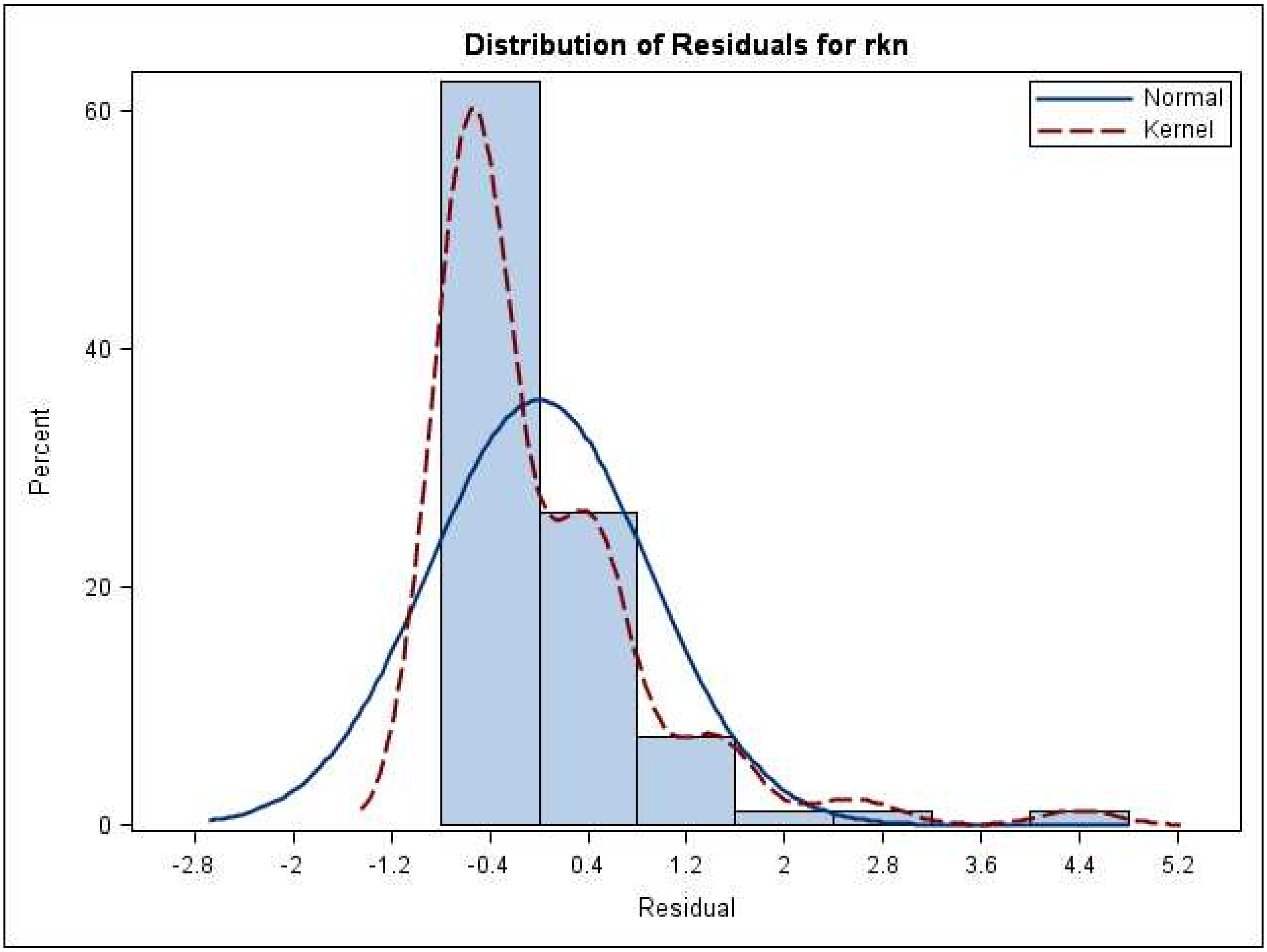


Figure E.5.1.2 Normal quantile plot of the raw residuals

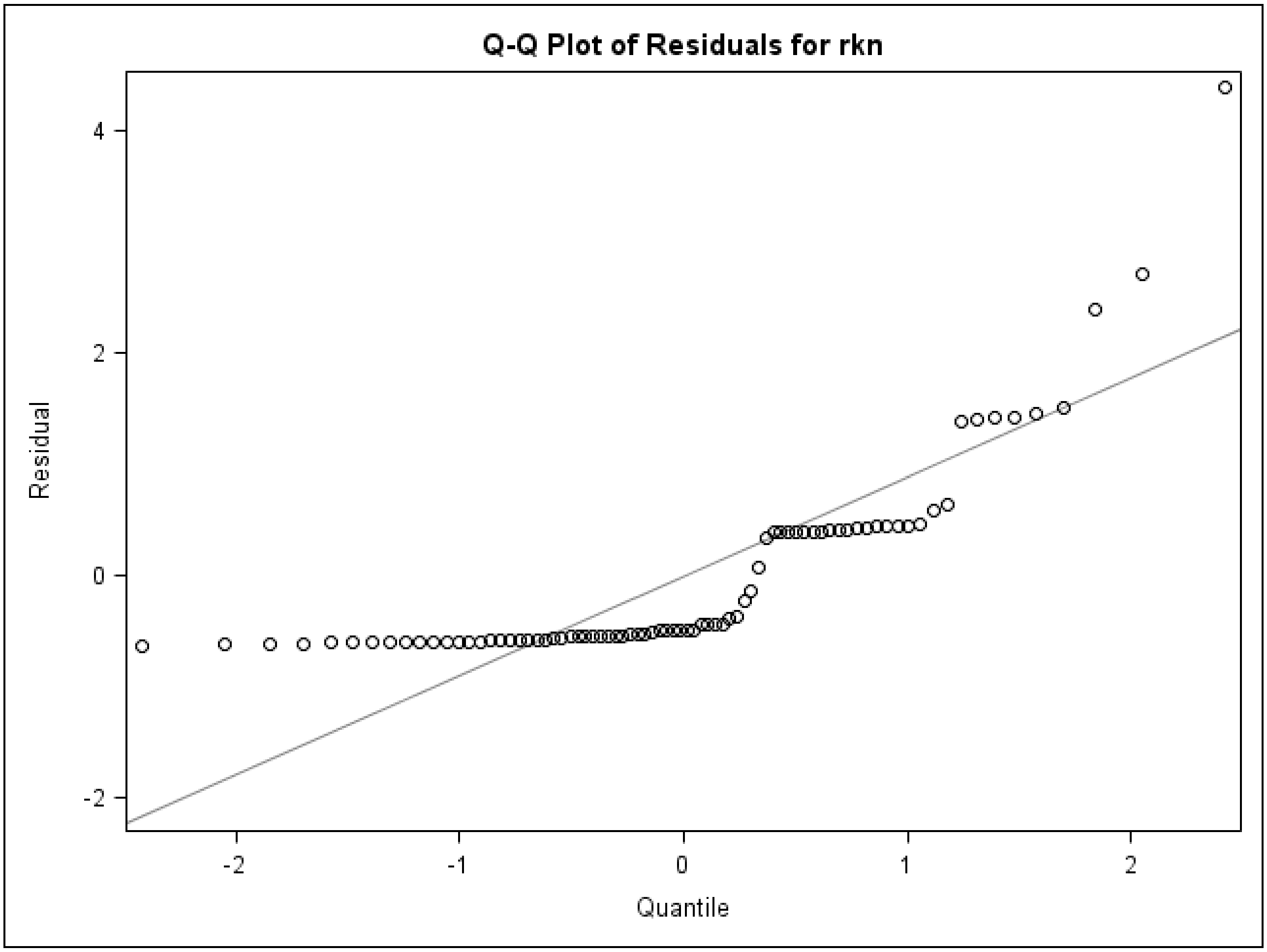


Figure E.5.1.3 Histogram of the Studentized residuals

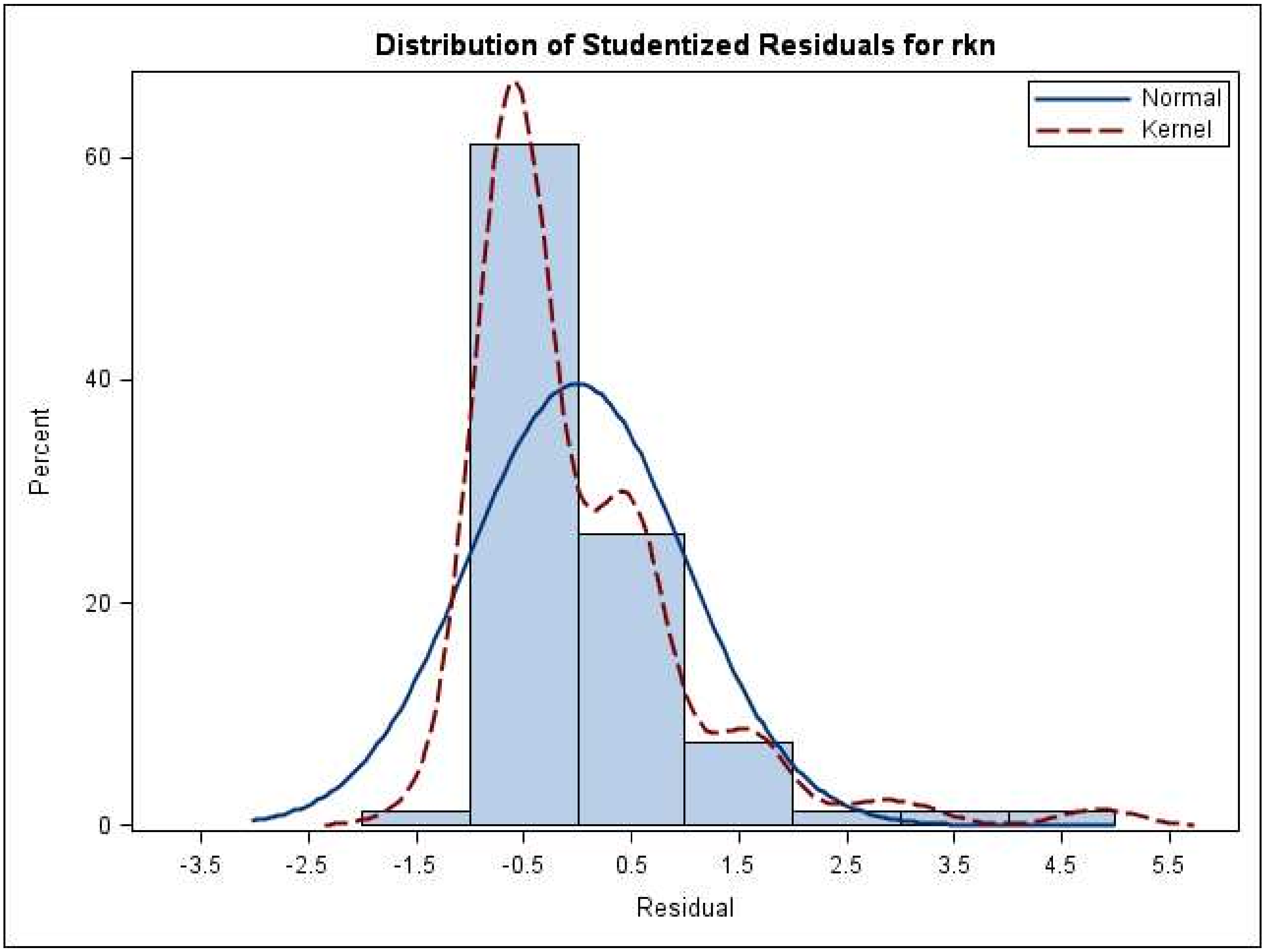


Figure E.5.1.4 Normal quantile plot of the Studentized residuals

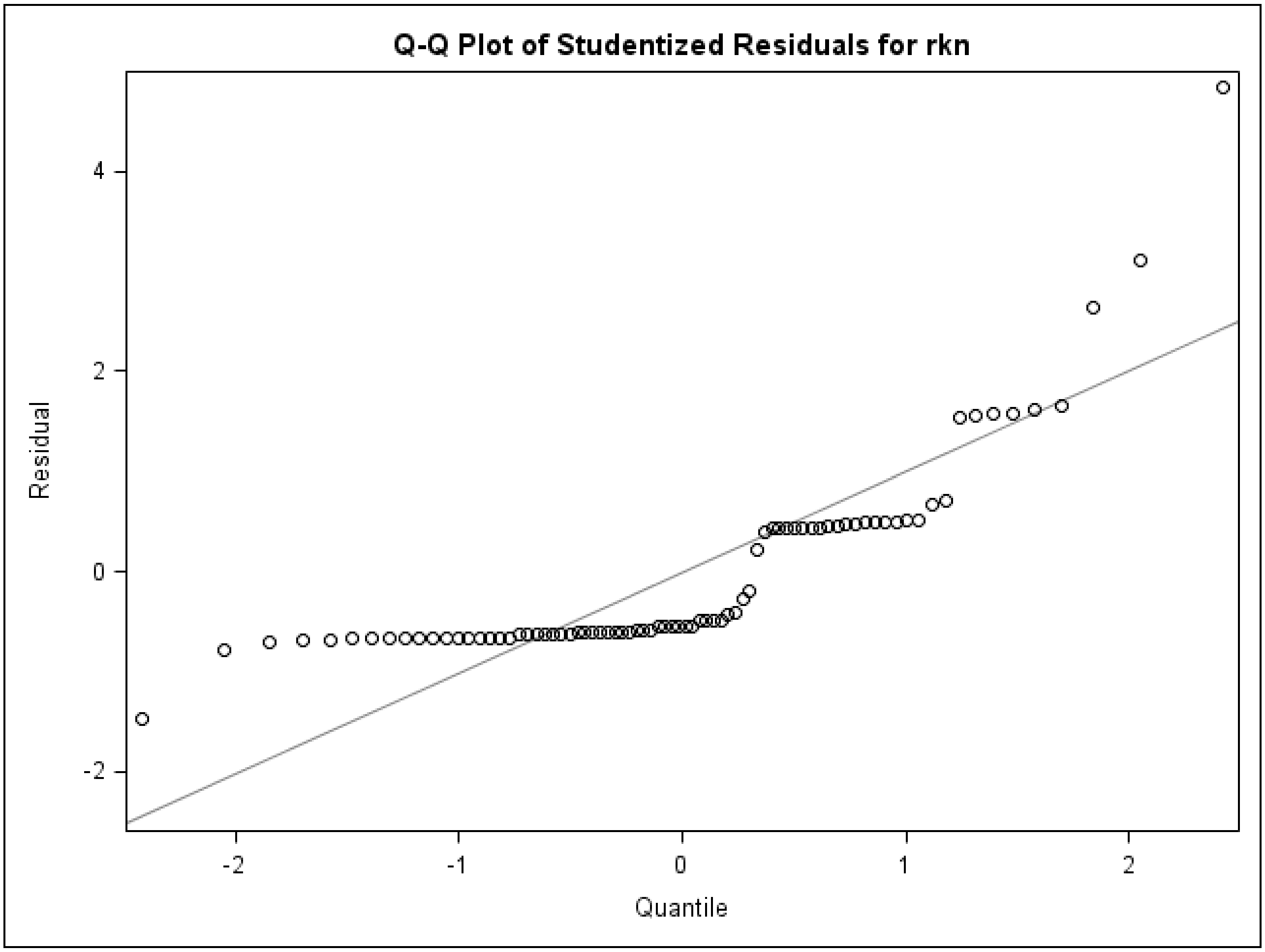


Figure E.5.1.5 Histogram of the Pearson residuals

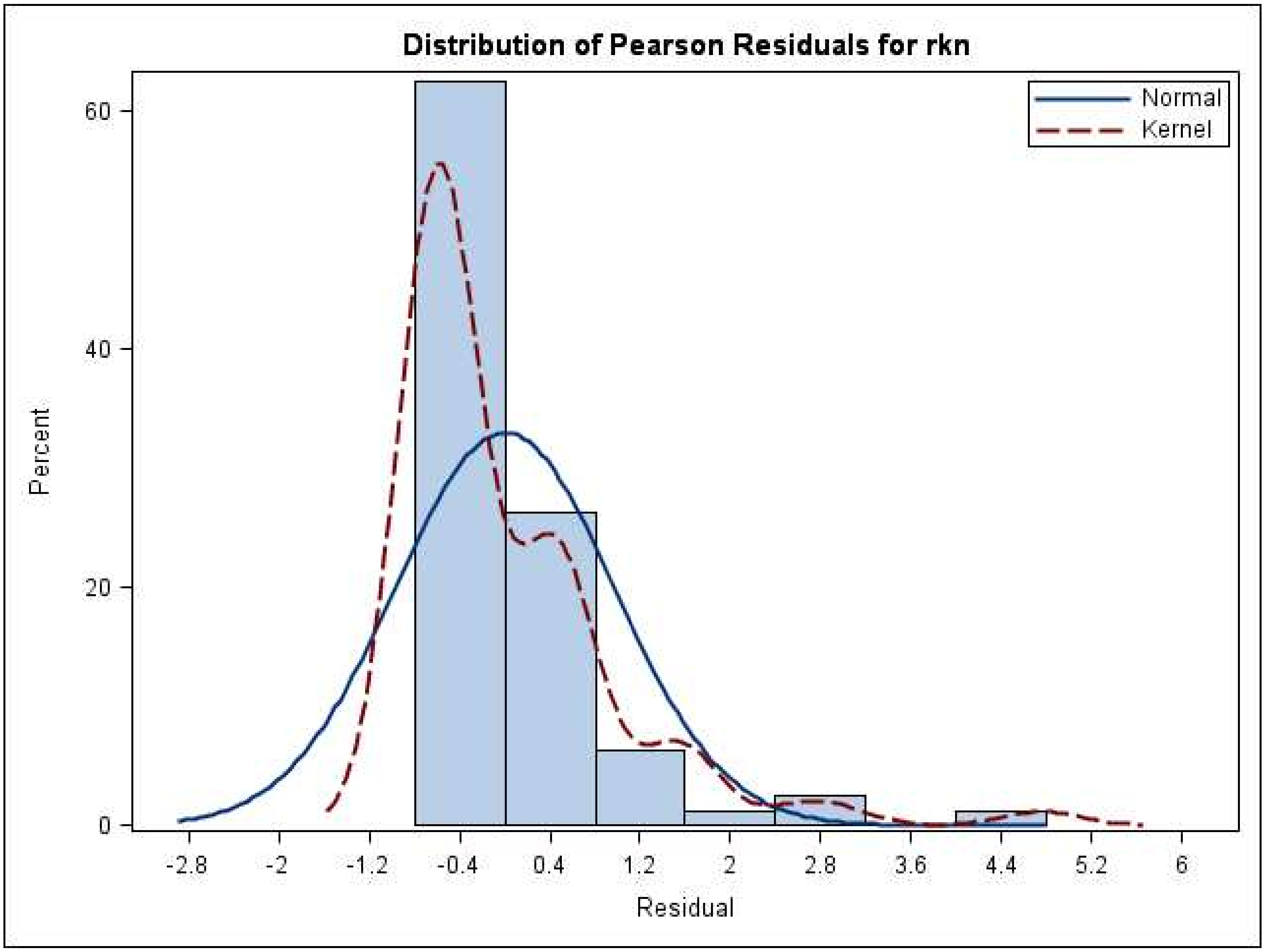
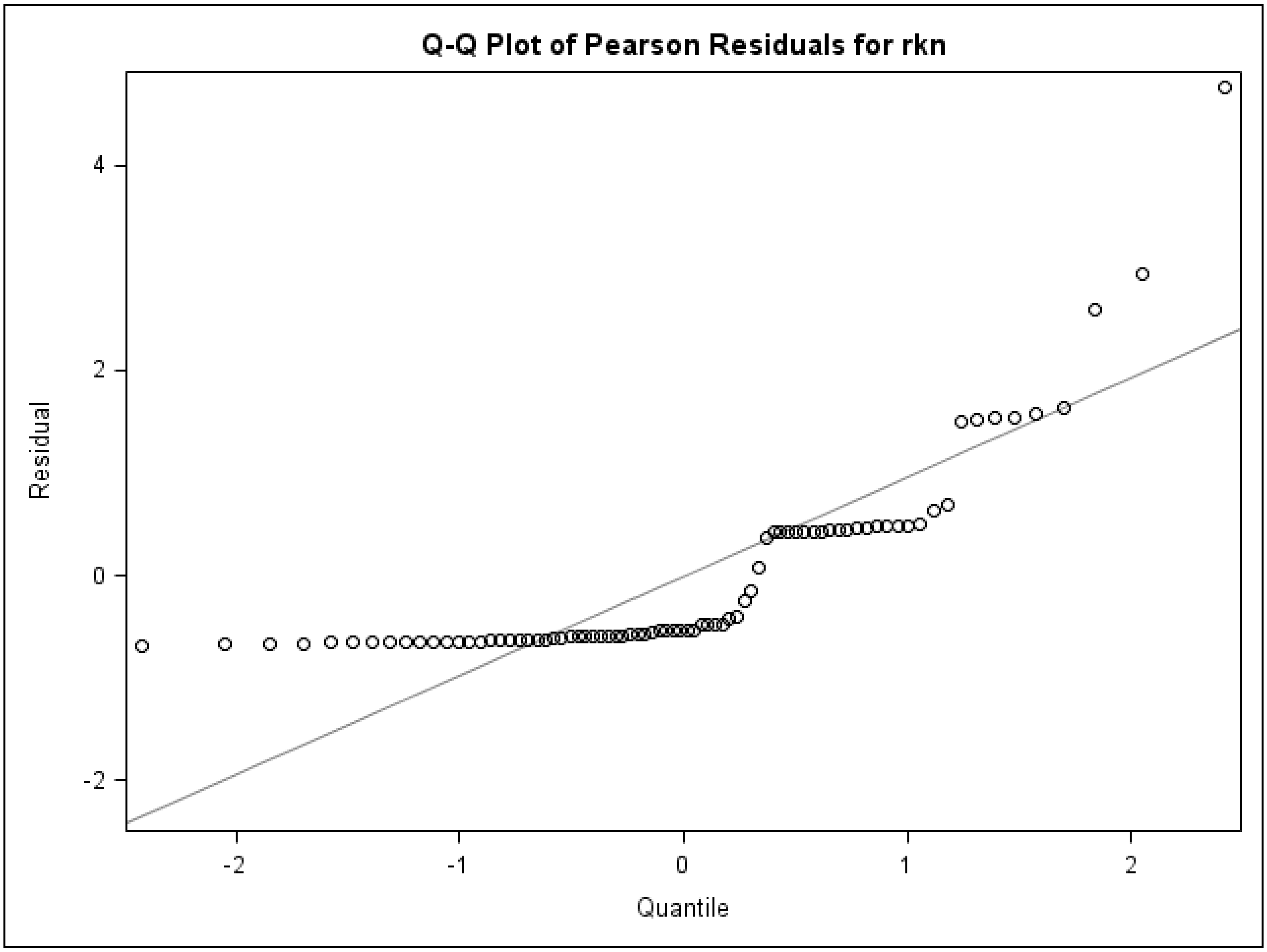


Figure E.5.1.6 Normal quantile plot of the Pearson residuals



E.5.2 July 2006 Model 2 Residual Plots

Figure E.5.2.1 Histogram of the raw residuals

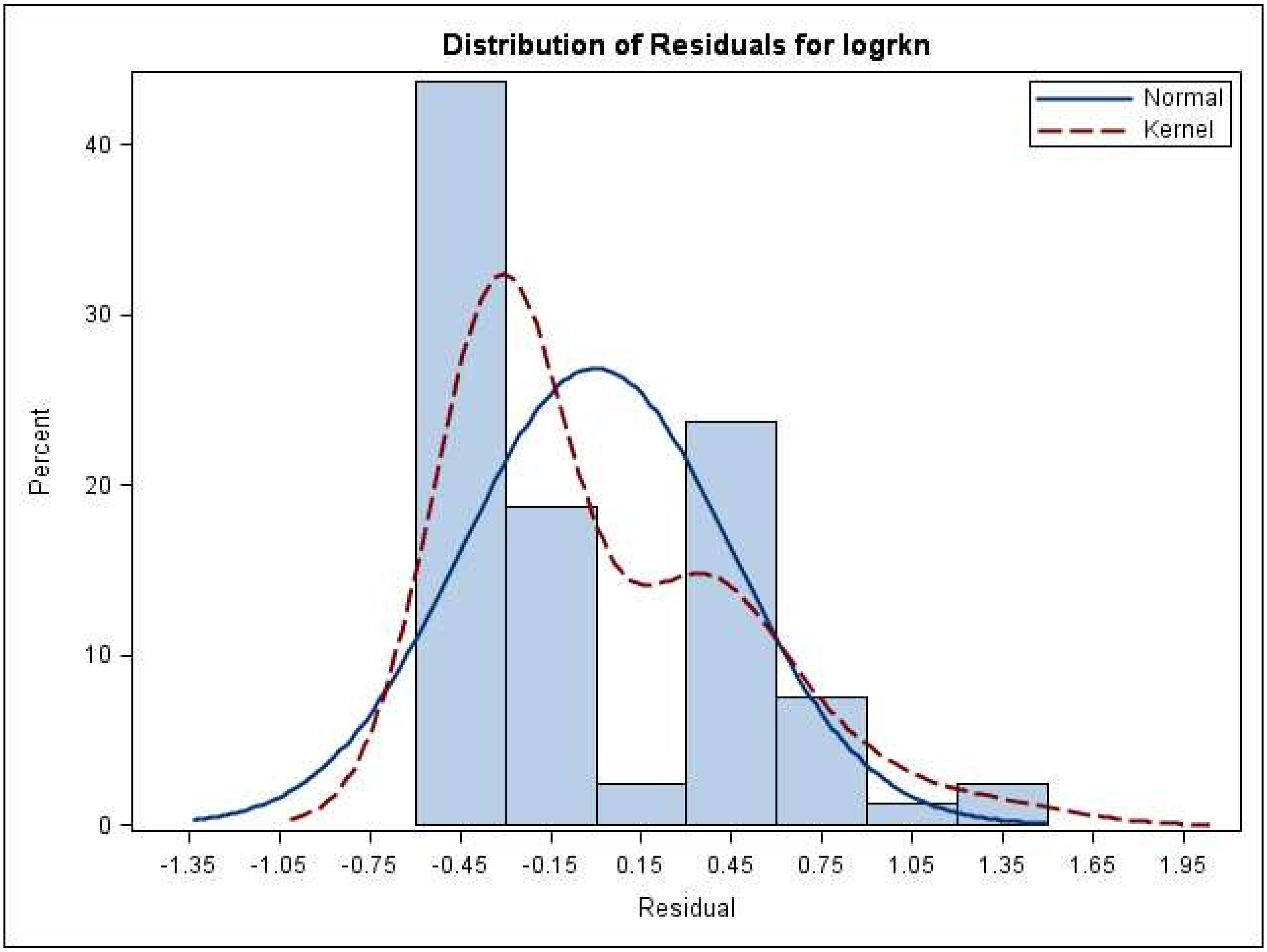


Figure E.5.2.2 Normal quantile plot of the raw residuals

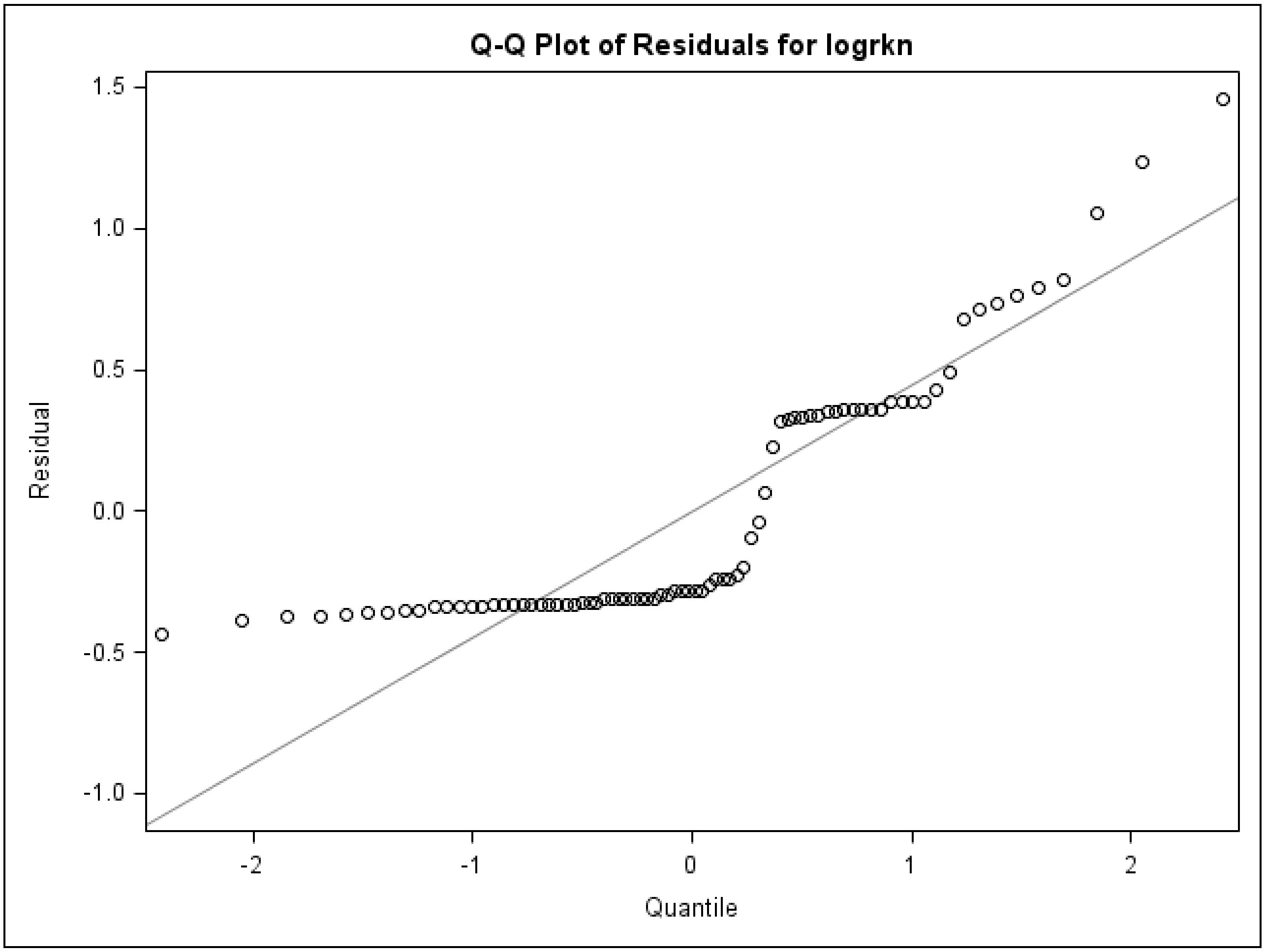


Figure E.5.2.3 Histogram of the Studentized residuals

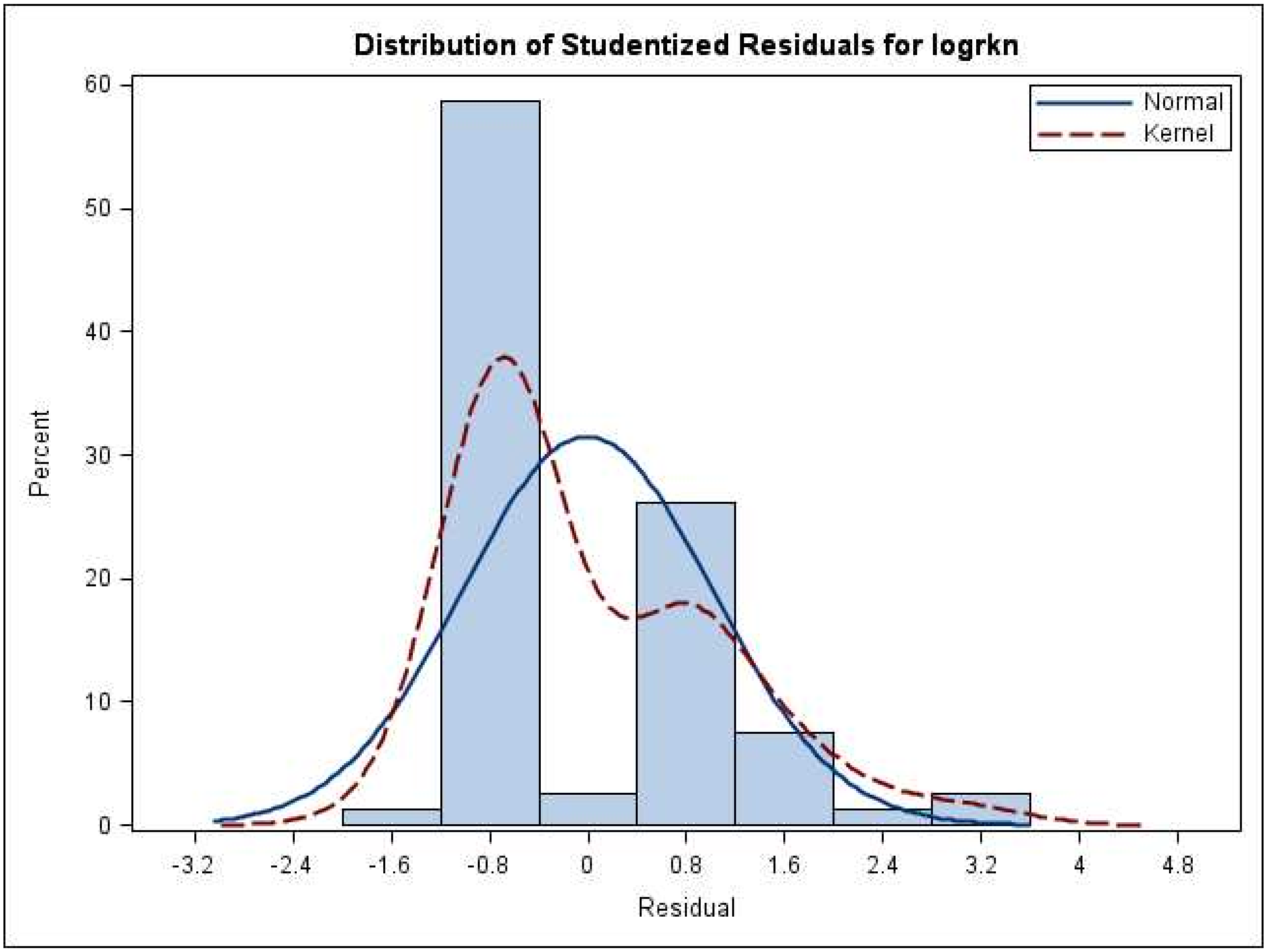


Figure E.5.2.4 Normal quantile plot of the Studentized residuals

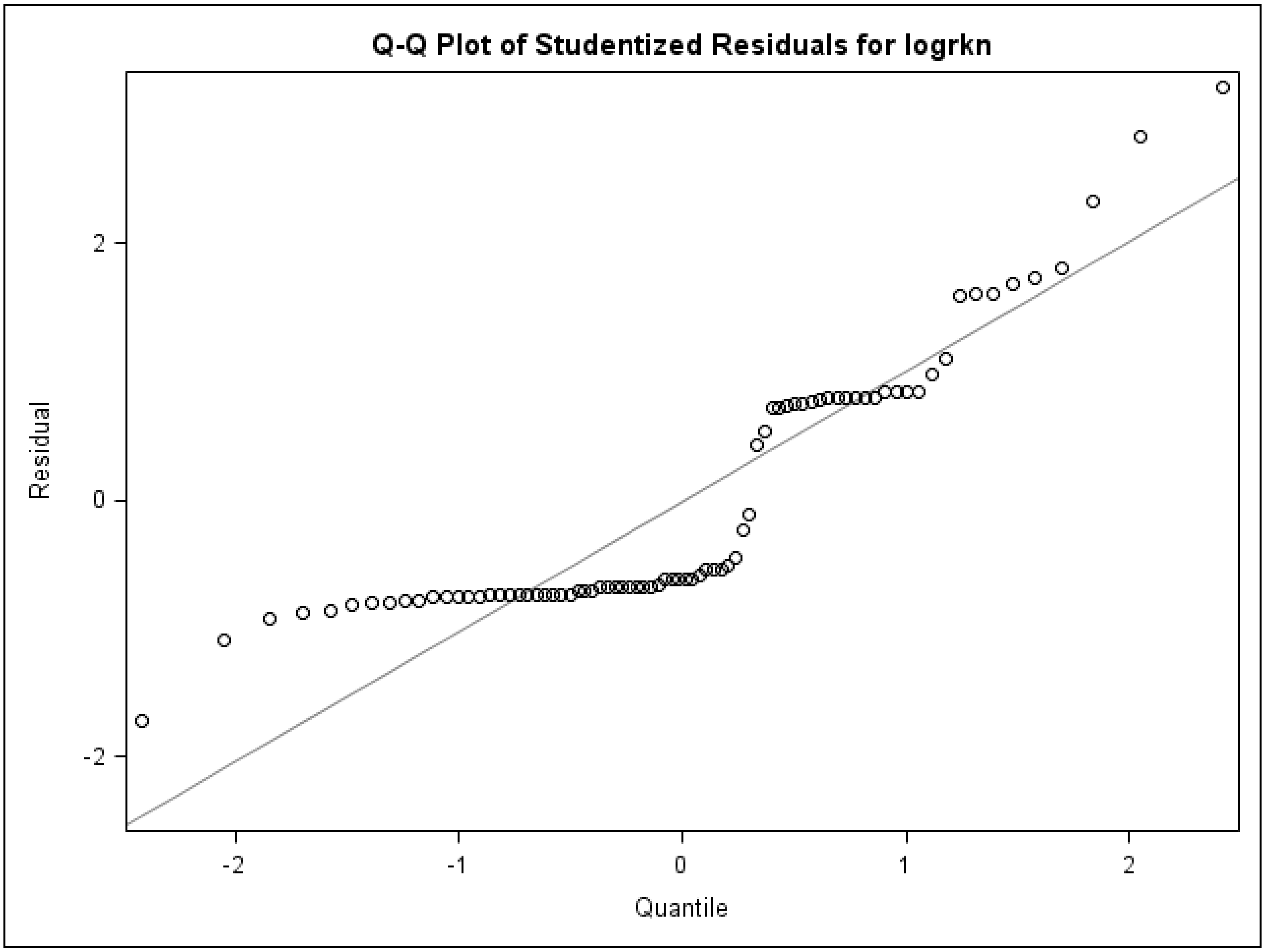


Figure E.5.2.5 Histogram of the Pearson residuals

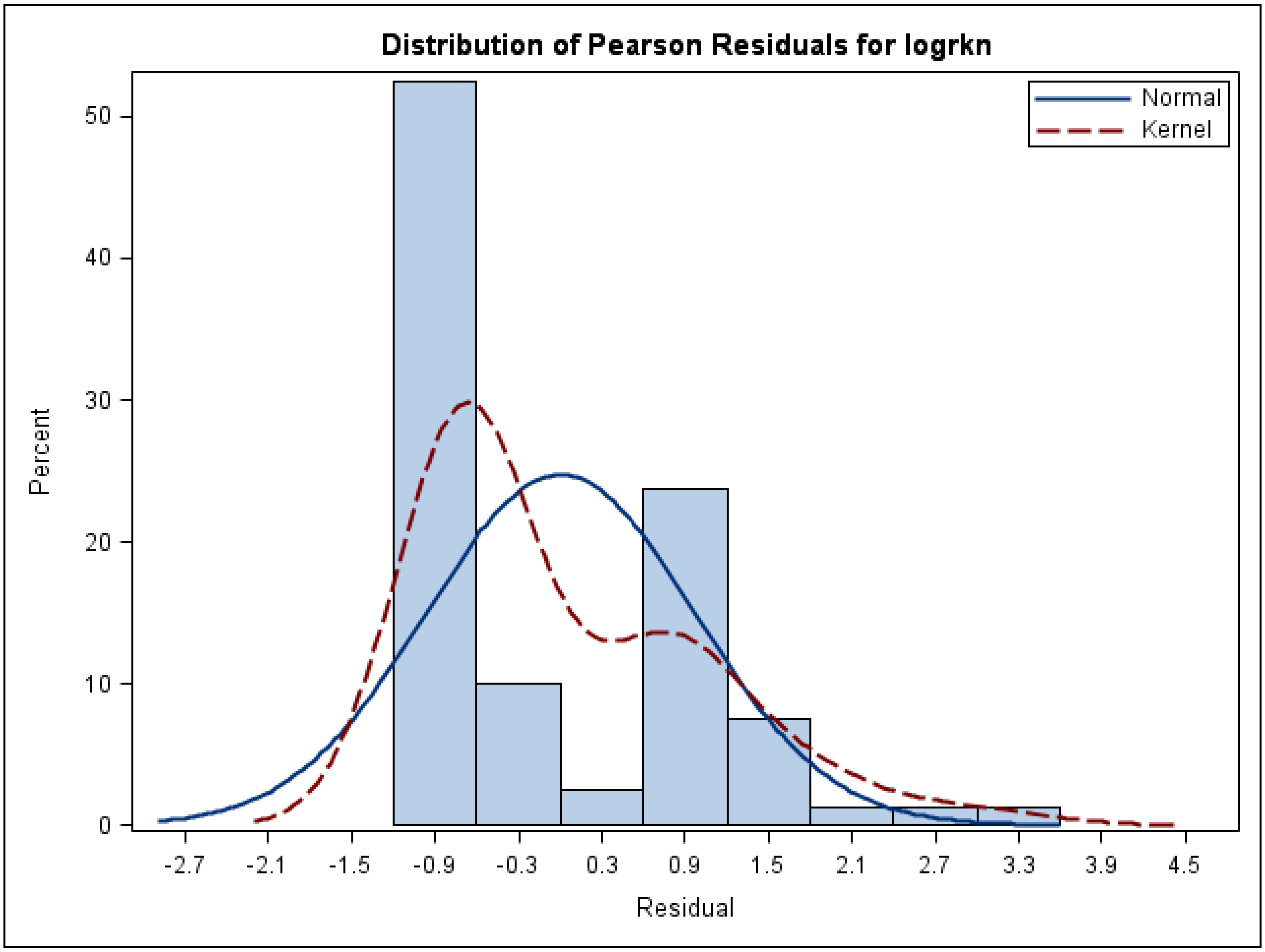
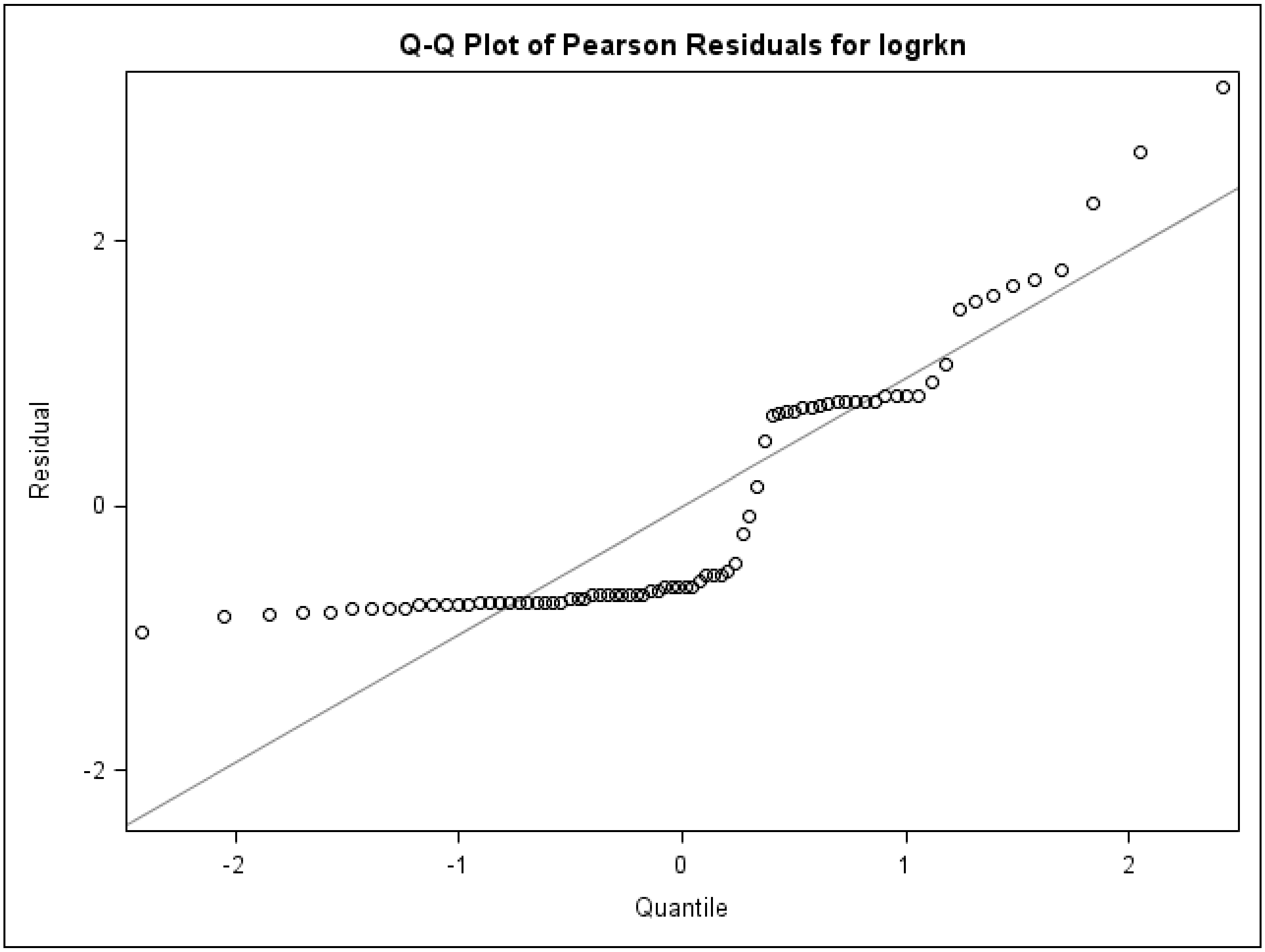


Figure E.5.2.6 Normal quantile plot of the Pearson residuals



E.5.3 July 2006 Model 3 Residual Plots

Figure E.5.3.1 Histogram of the raw residuals

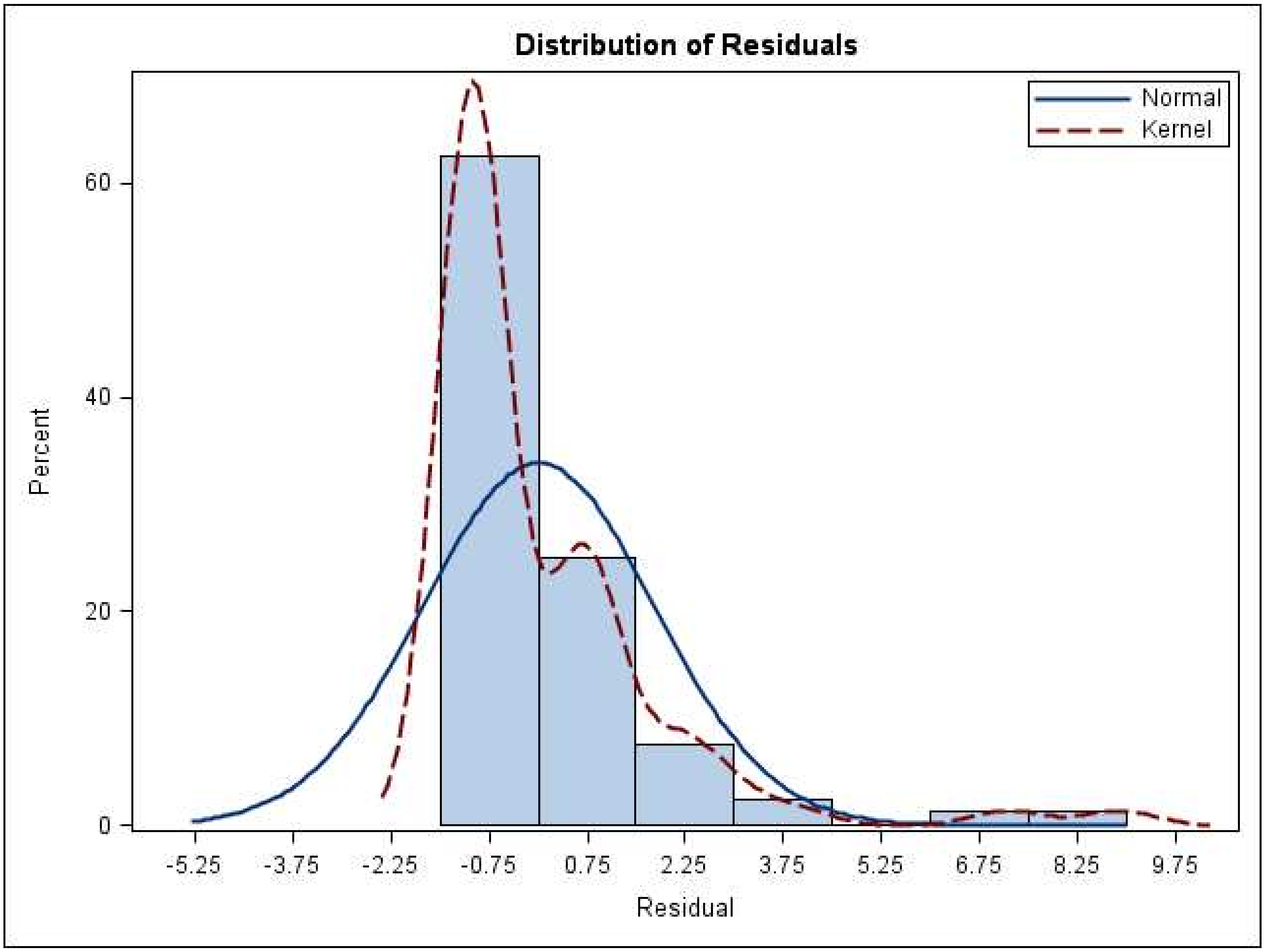


Figure E.5.3.2 Normal quantile plot of the raw residuals

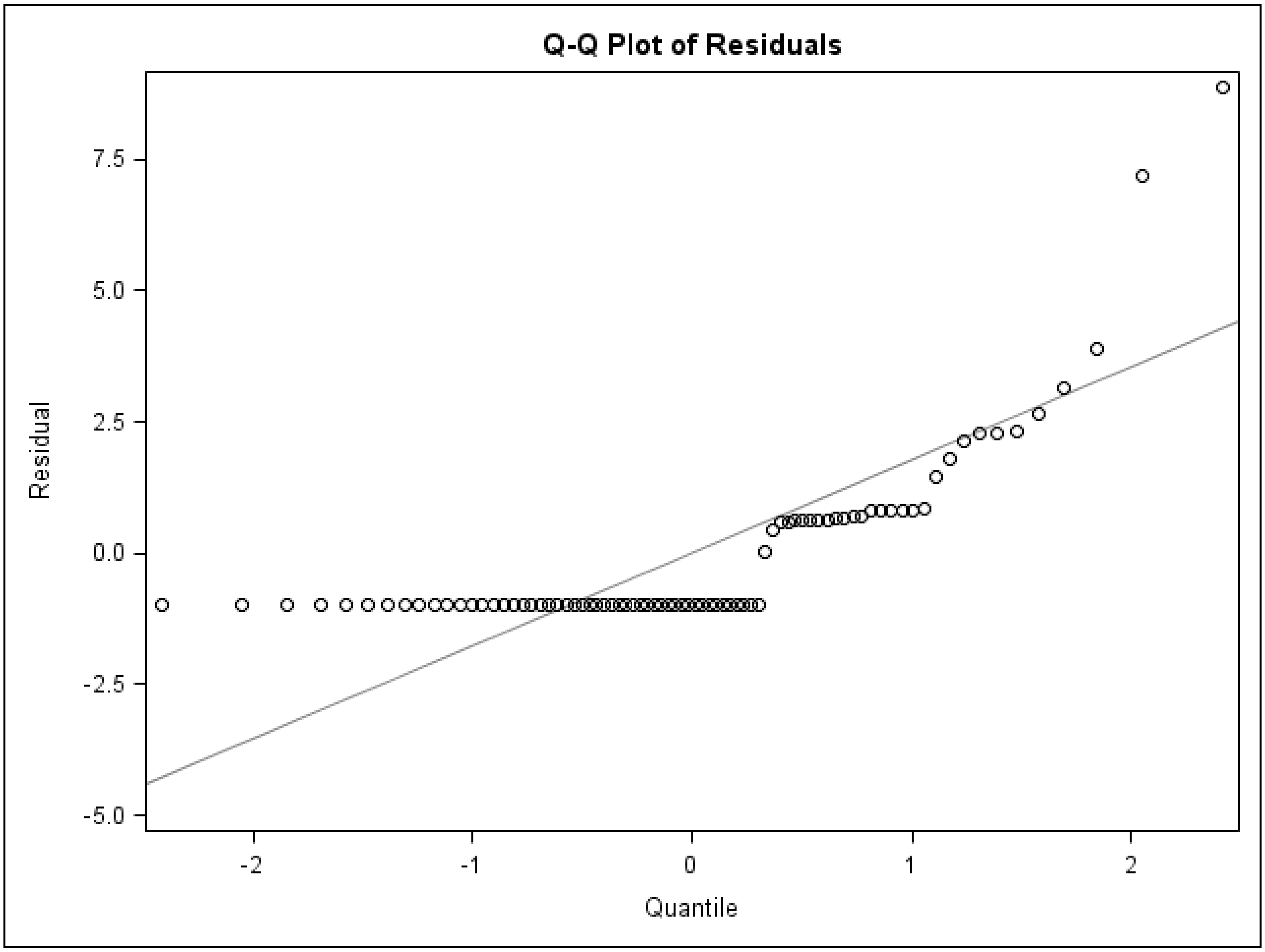


Figure E.5.3.3 Histogram of the Studentized residuals

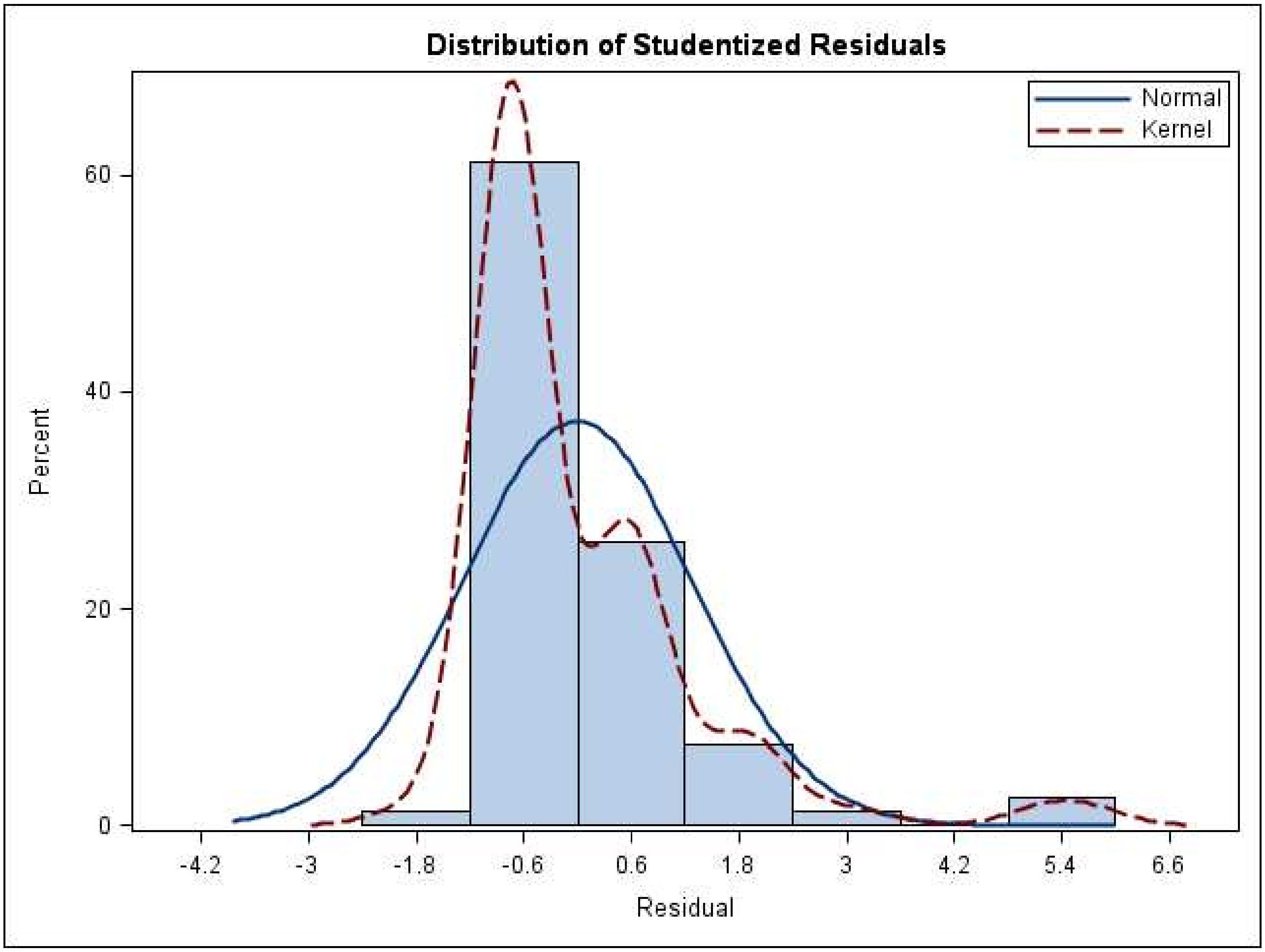


Figure E.5.3.4 Normal quantile plot of the Studentized residuals

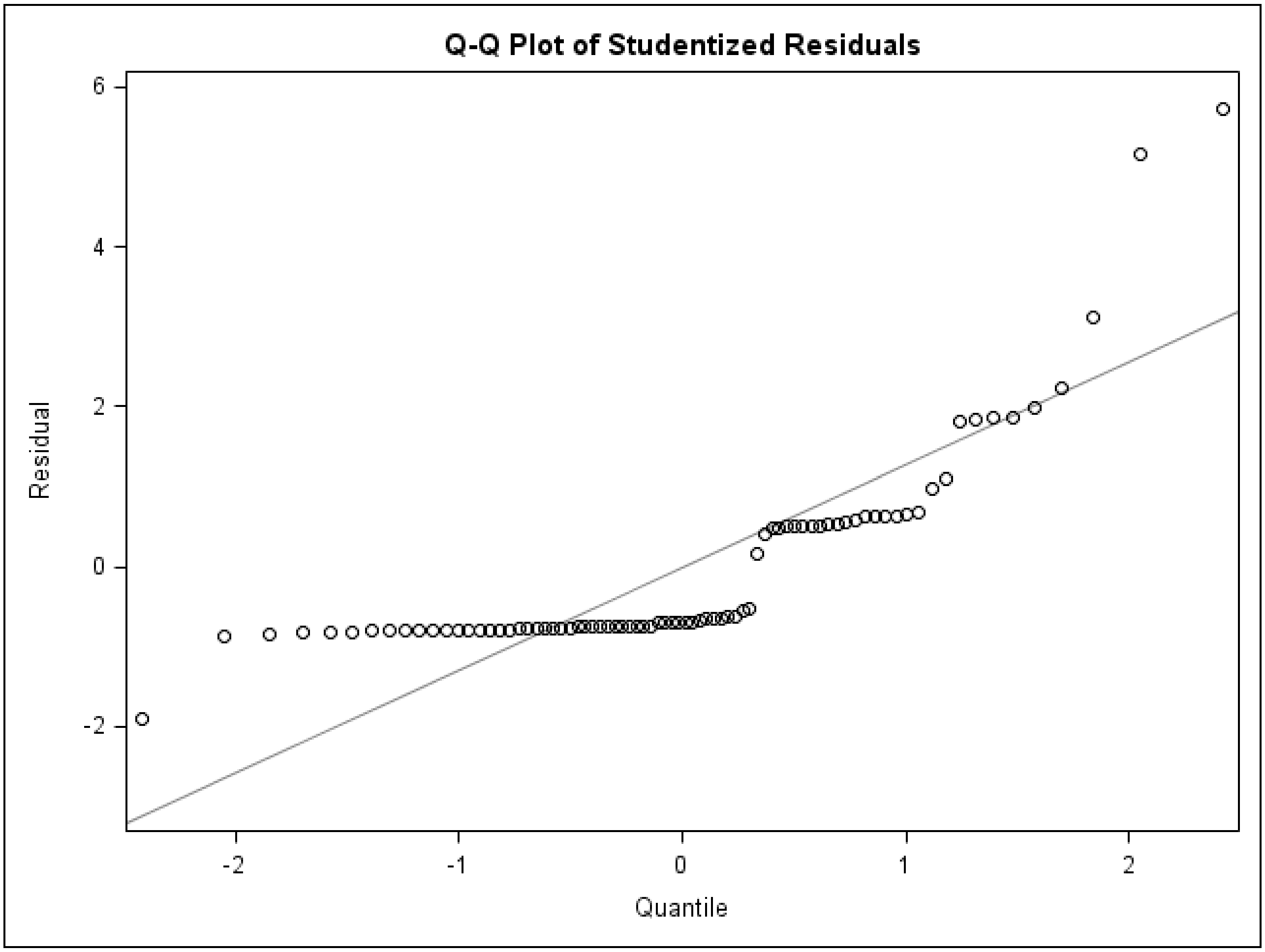


Figure E.5.3.5 Histogram of the Pearson residuals

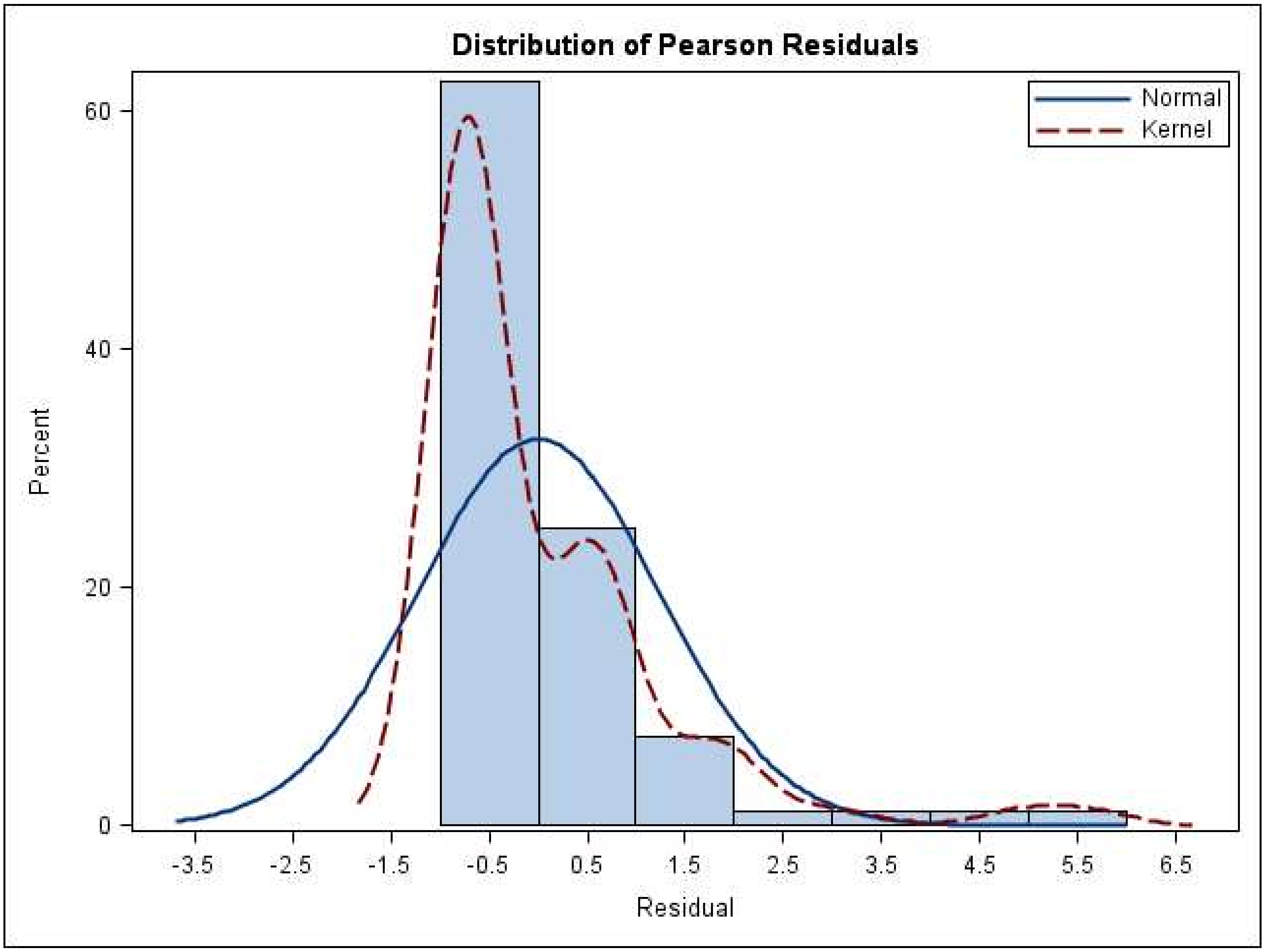
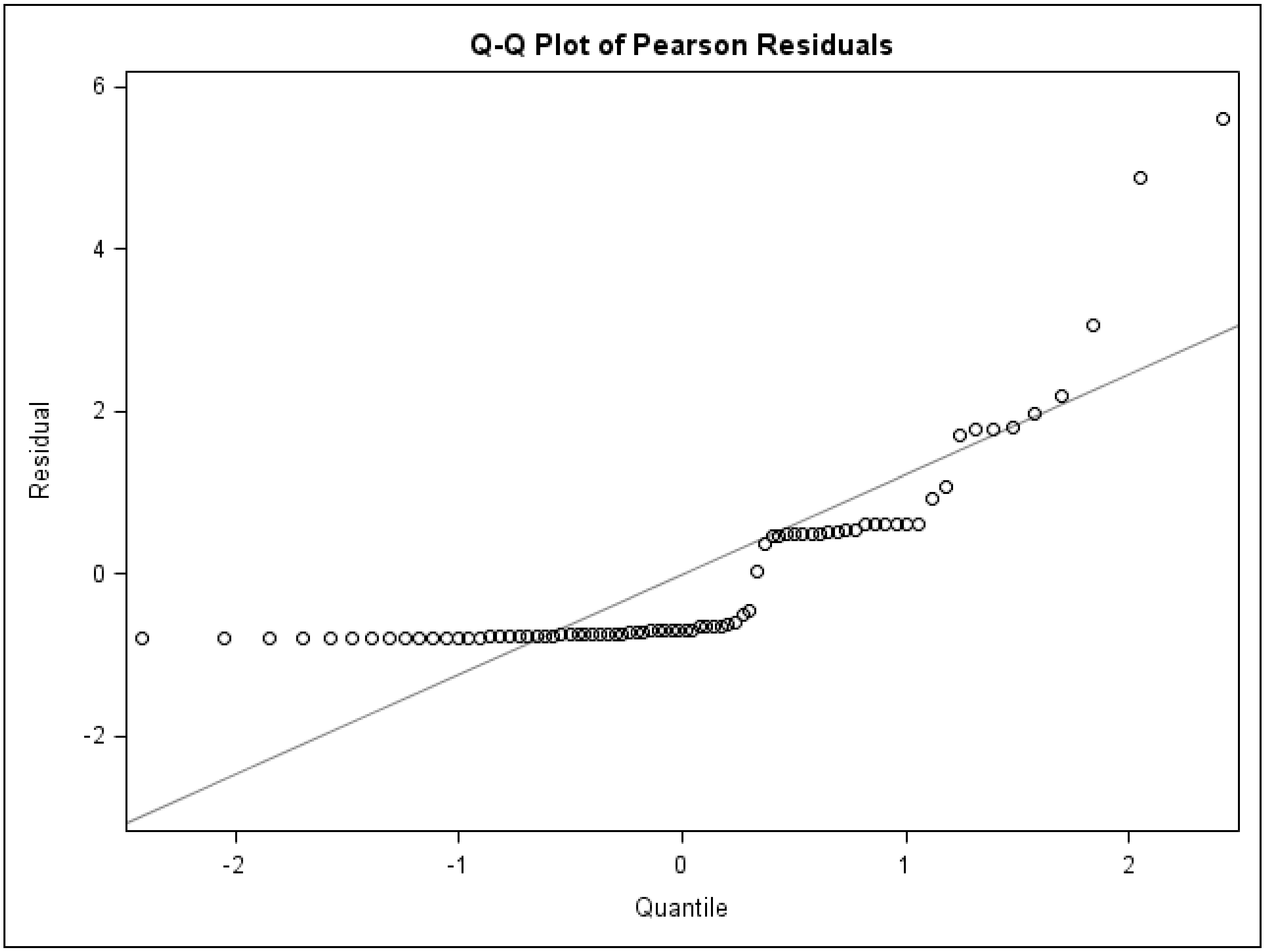


Figure E.5.3.6 Normal quantile plot of the Pearson residuals



E.5.4 July 2006 Model 4 Residual Plots

Figure E.5.4.1 Histogram of the raw residuals

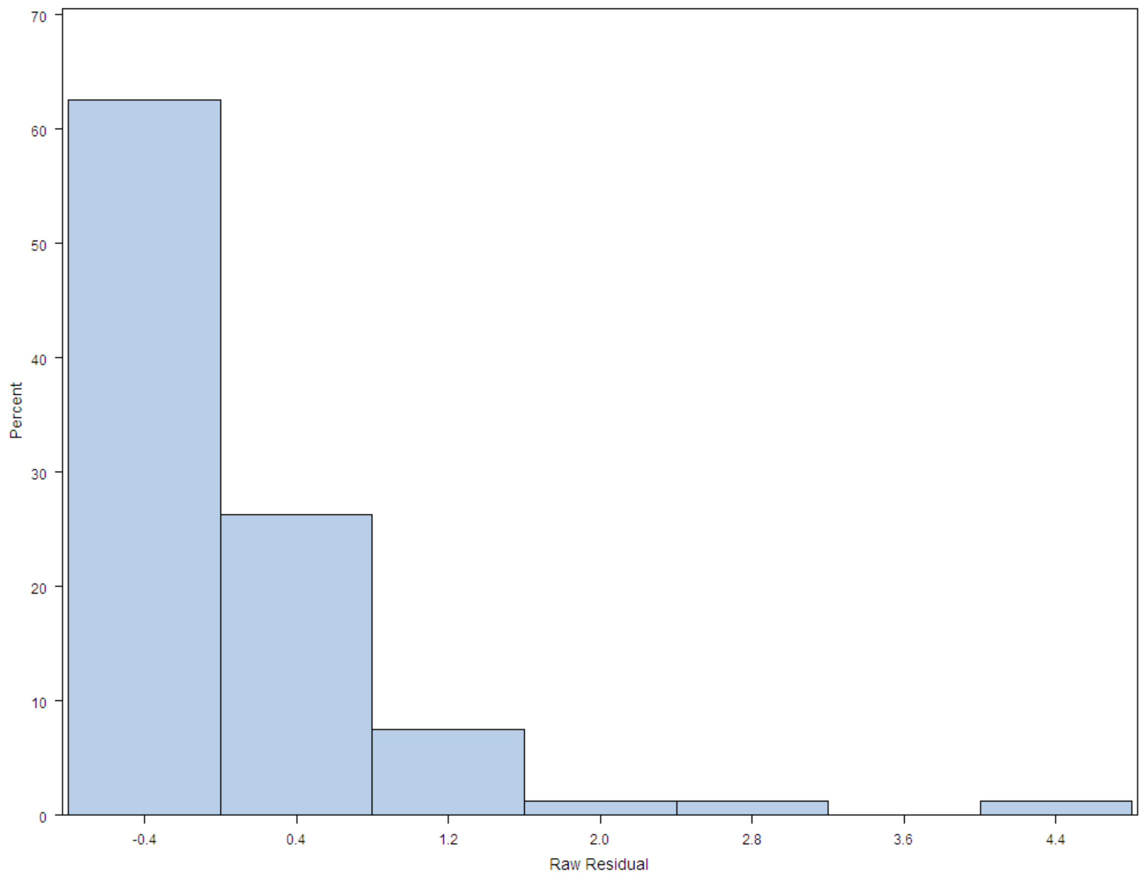


Figure E.5.4.2 Histogram of the Pearson residuals

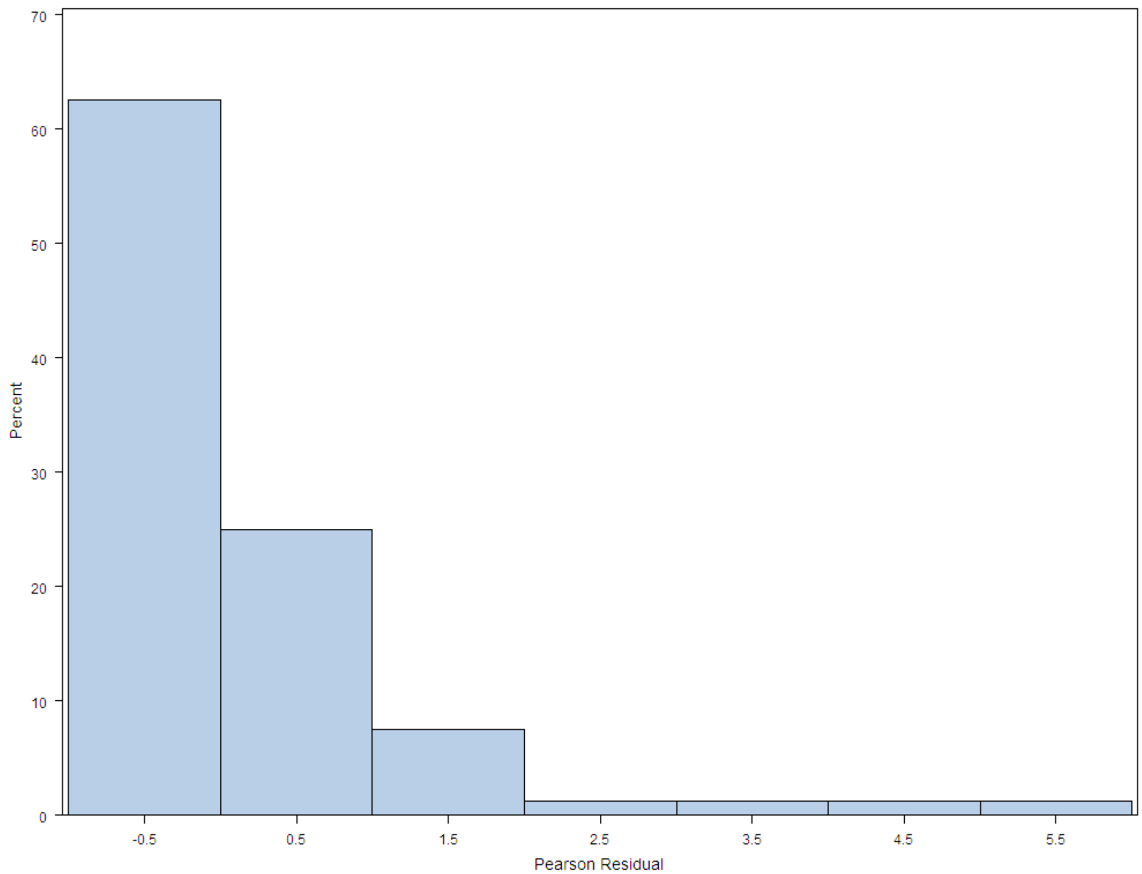


Figure E.5.4.3 Histogram of the deviance residuals

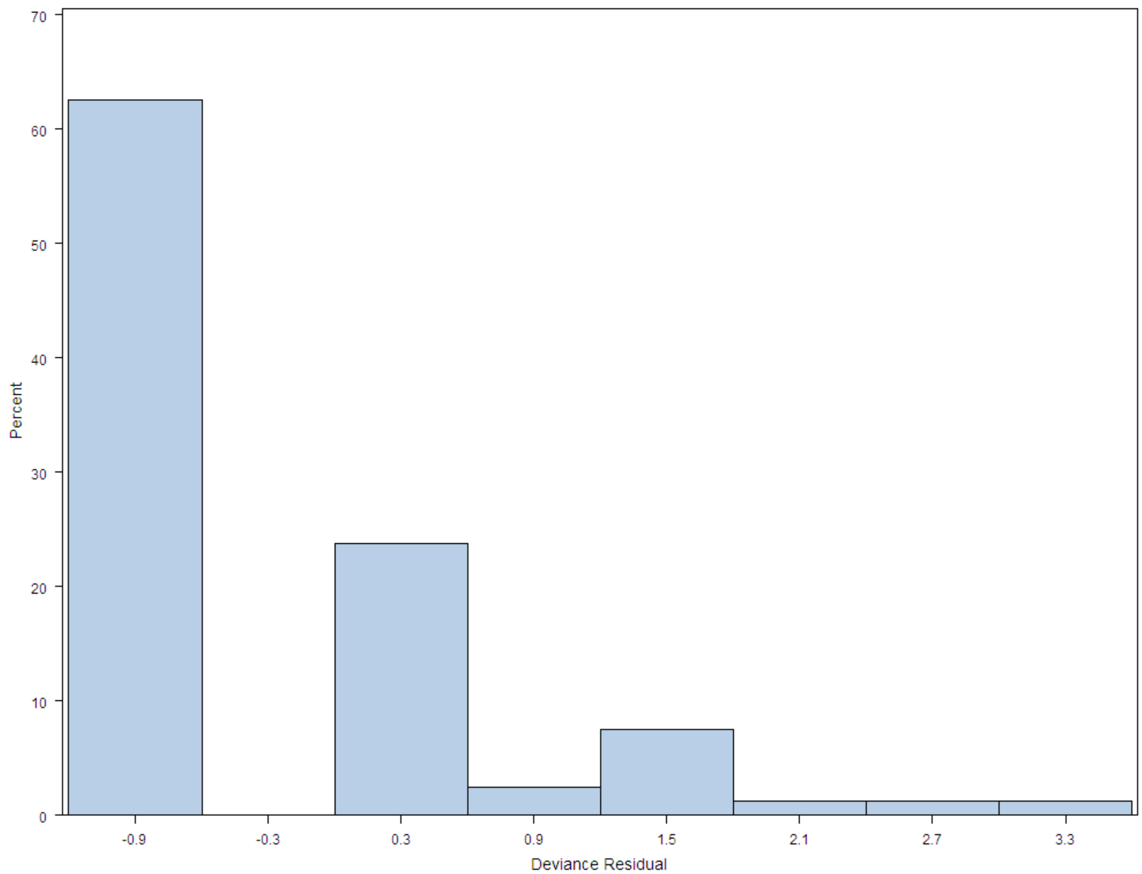


Figure E.5.4.4 Histogram of the likelihood residuals

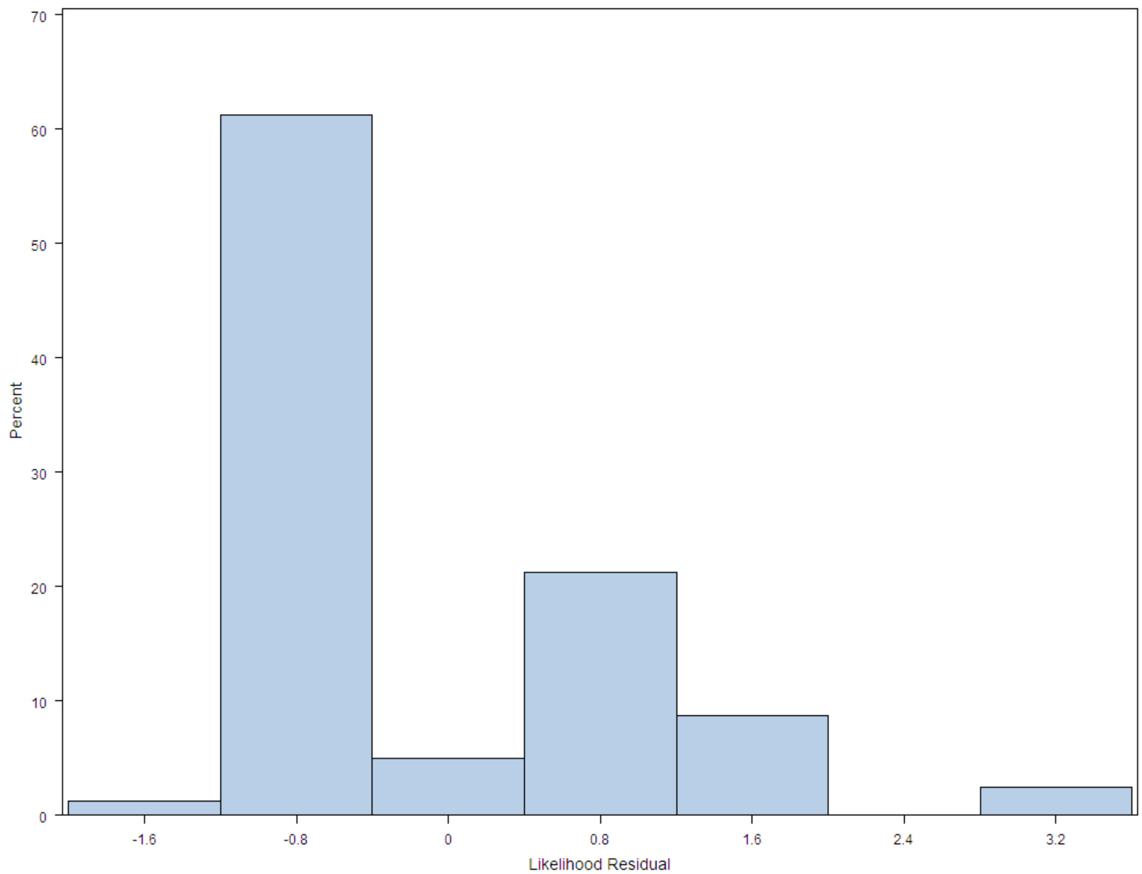


Figure E.5.4.5 Histogram of the standardized Pearson residuals

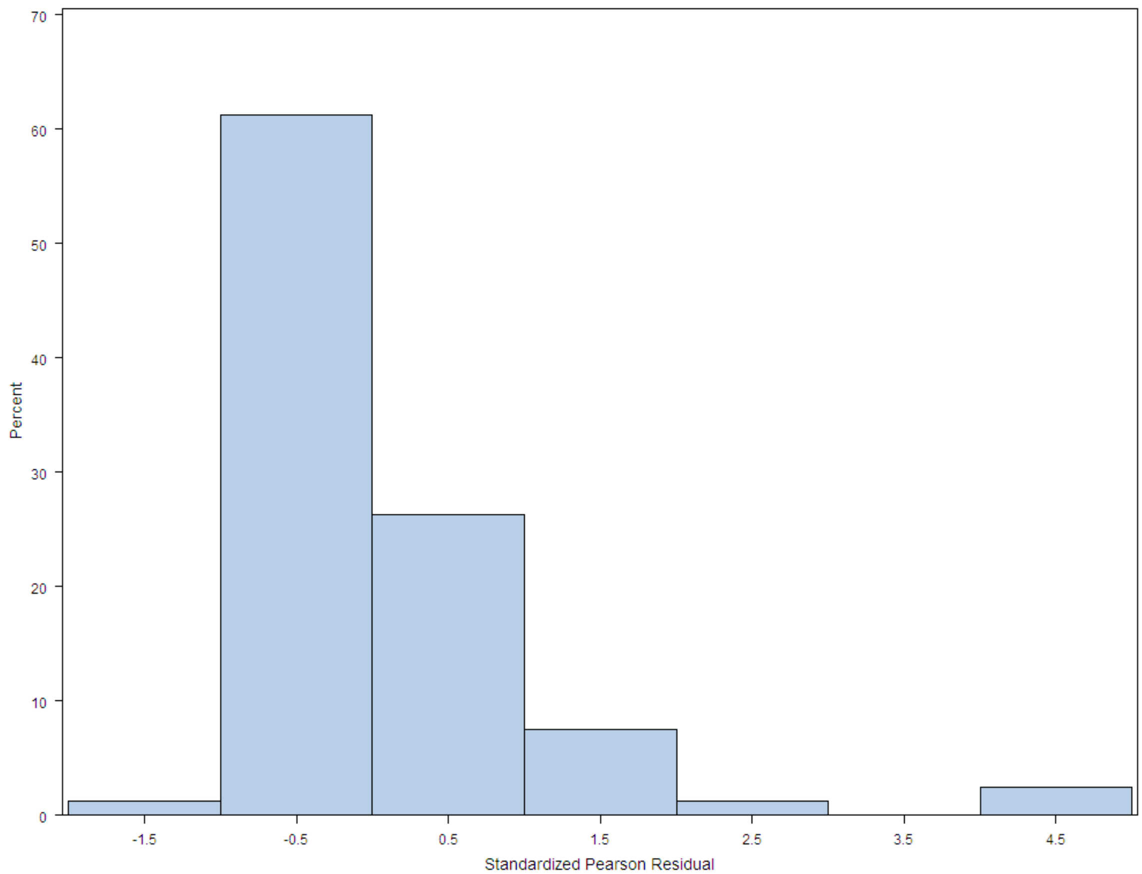
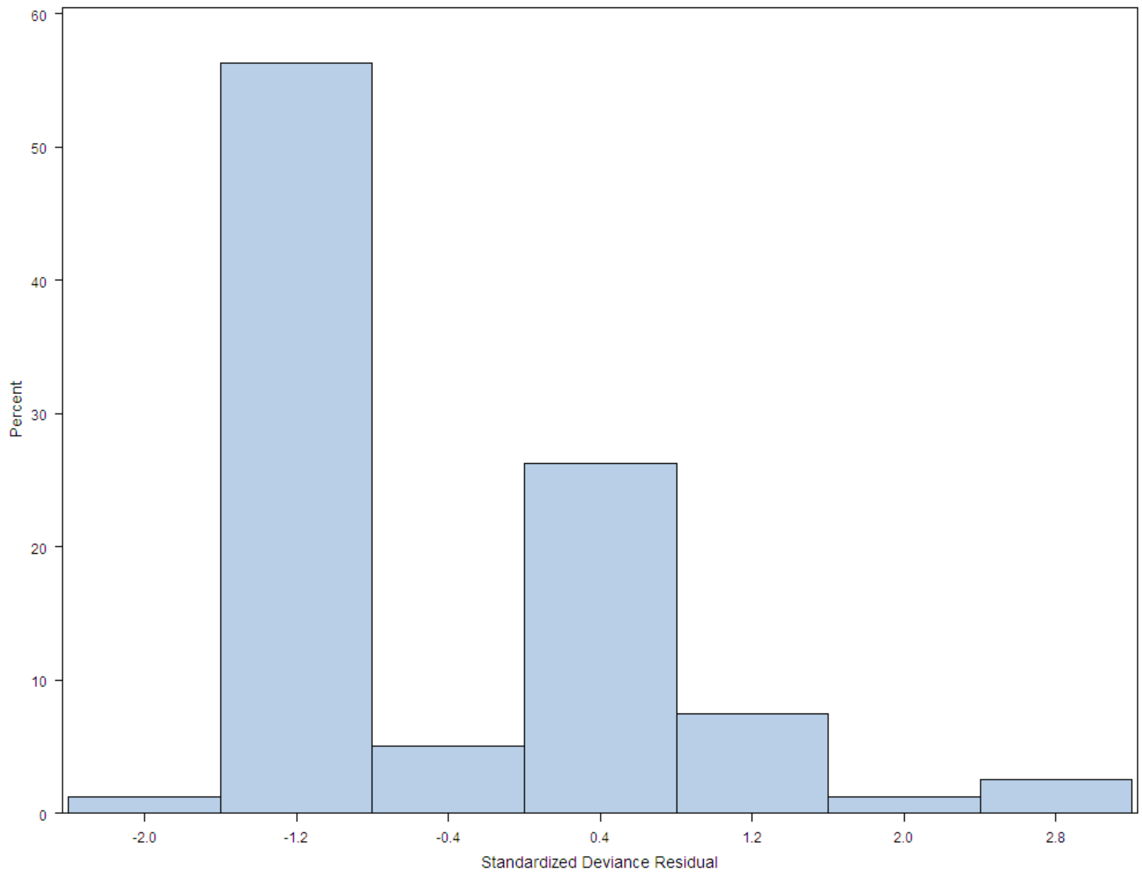


Figure E.5.4.6 Histogram of the standardized deviance residuals



E.5.5 July 2006 Model 5 Residual Plots

Figure E.5.5.1 Histogram of the raw residuals

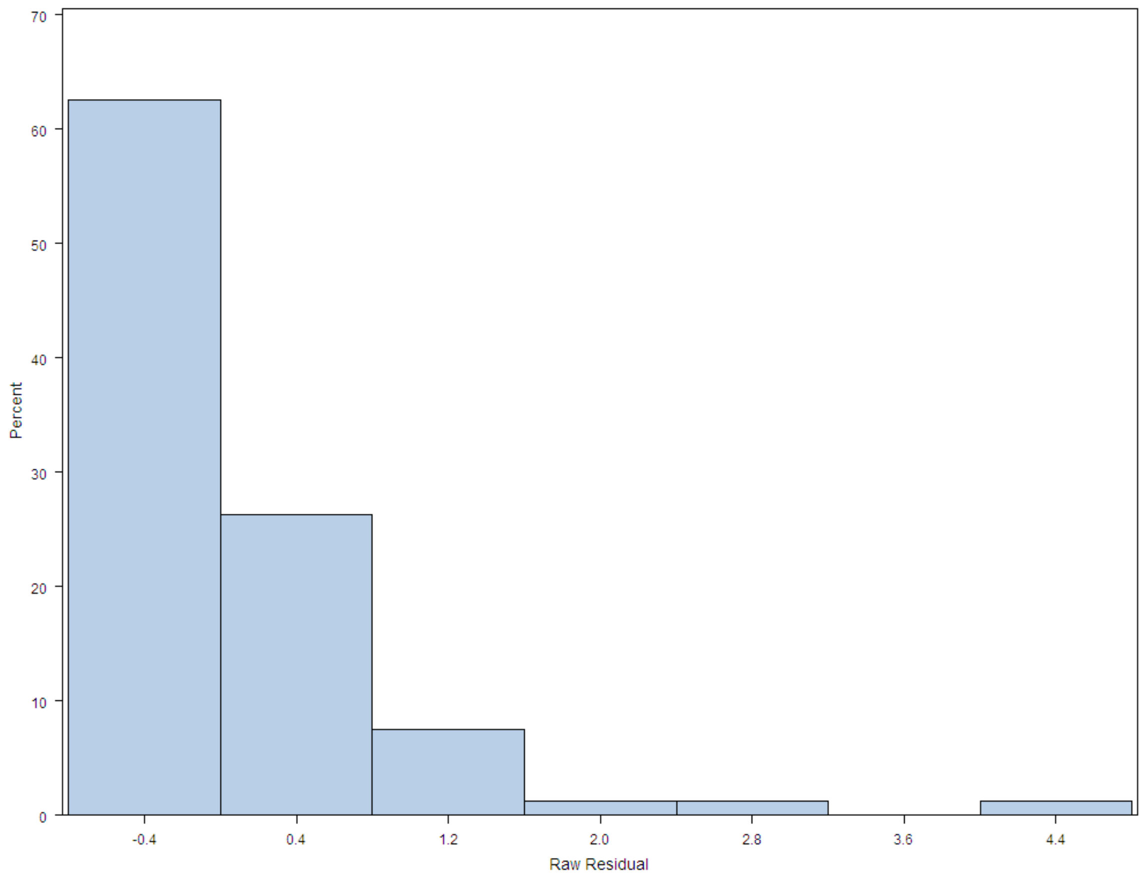


Figure E.5.5.2 Histogram of the Pearson residuals

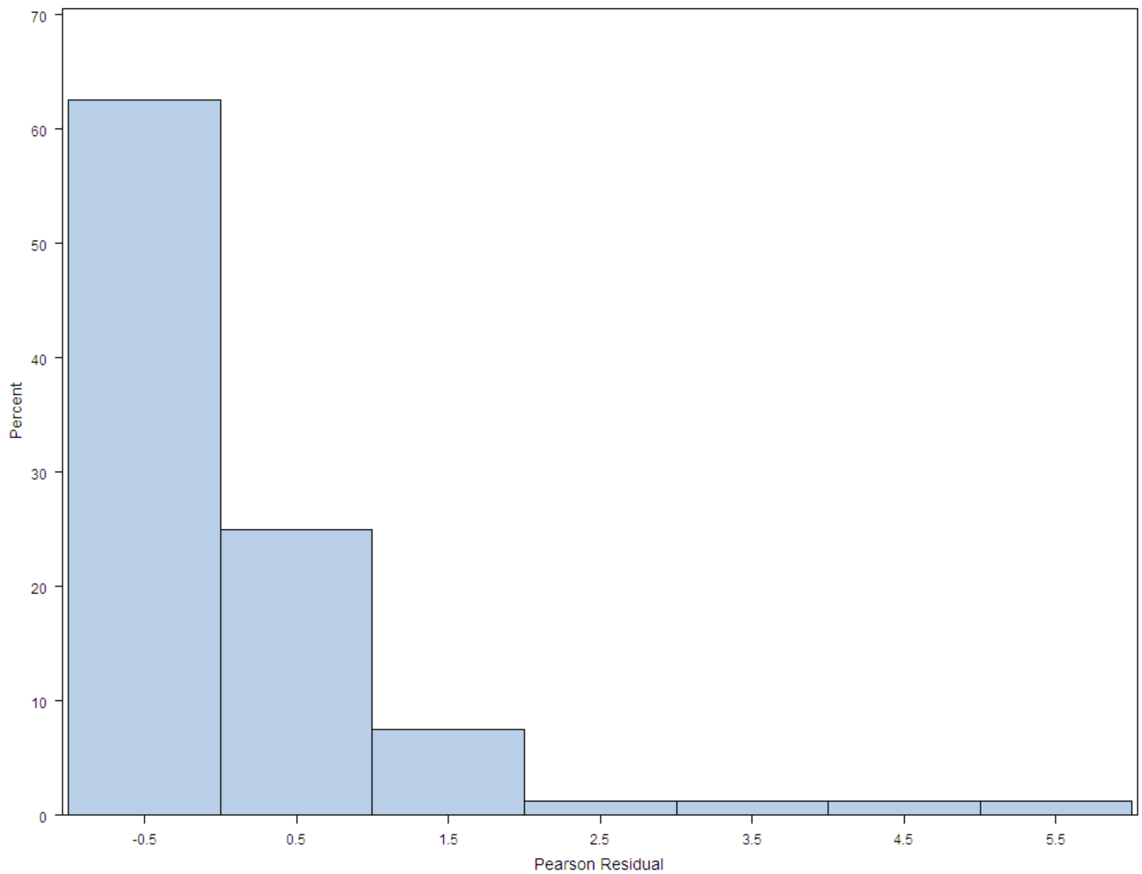


Figure E.5.5.3 Histogram of the deviance residuals

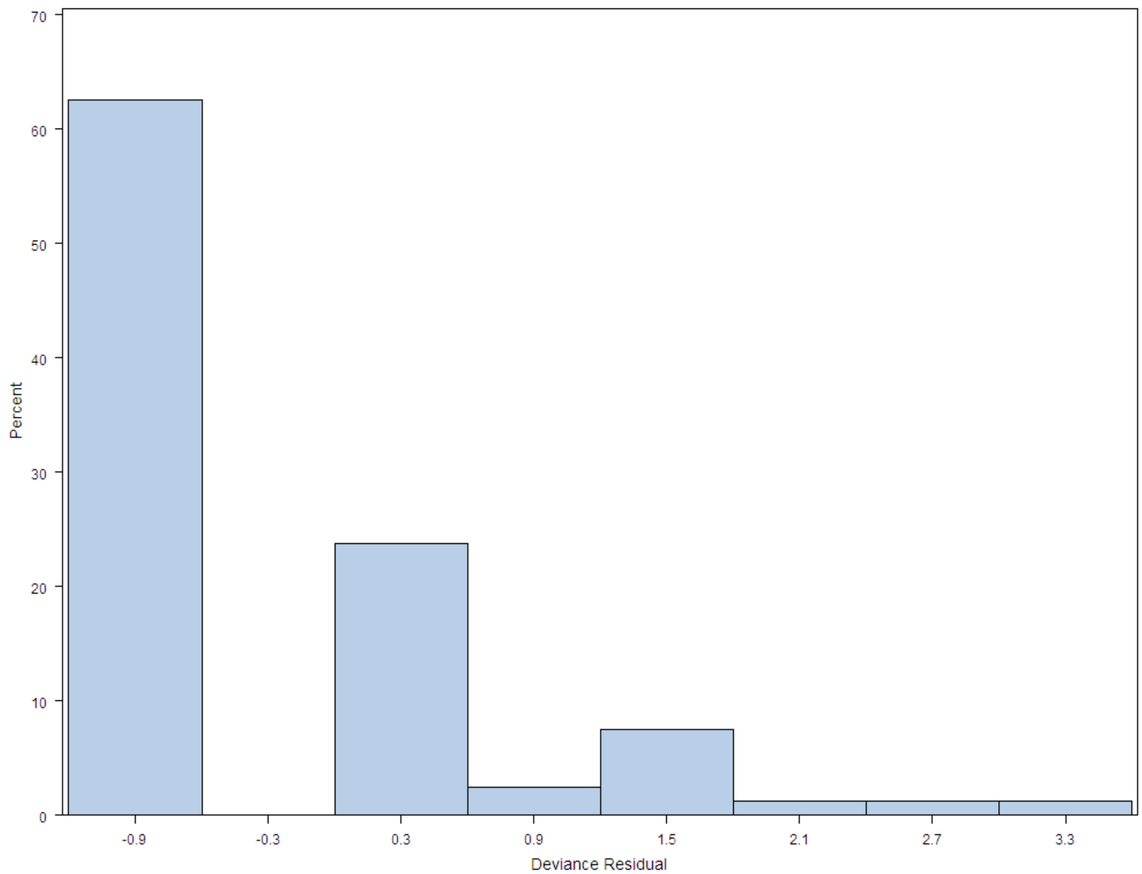


Figure E.5.5.4 Histogram of the likelihood residuals

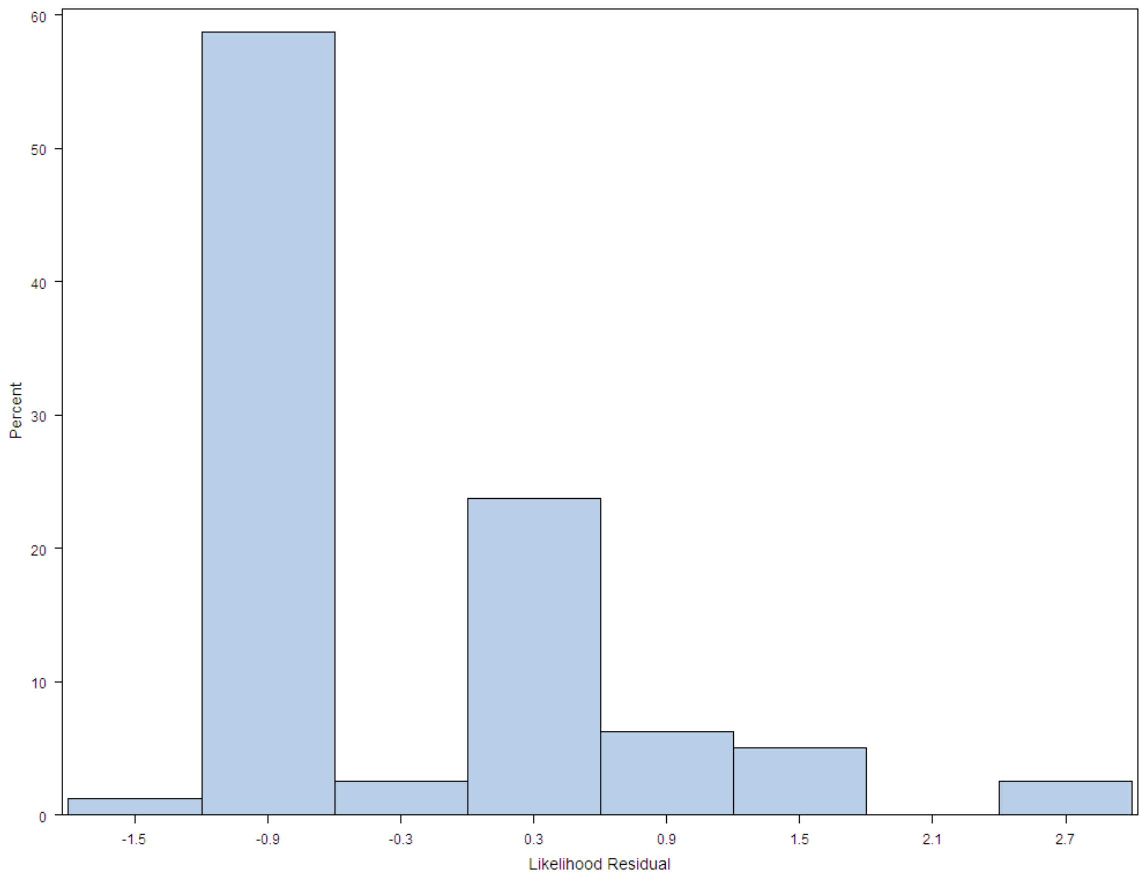


Figure E.5.5.5 Histogram of the standardized Pearson residuals

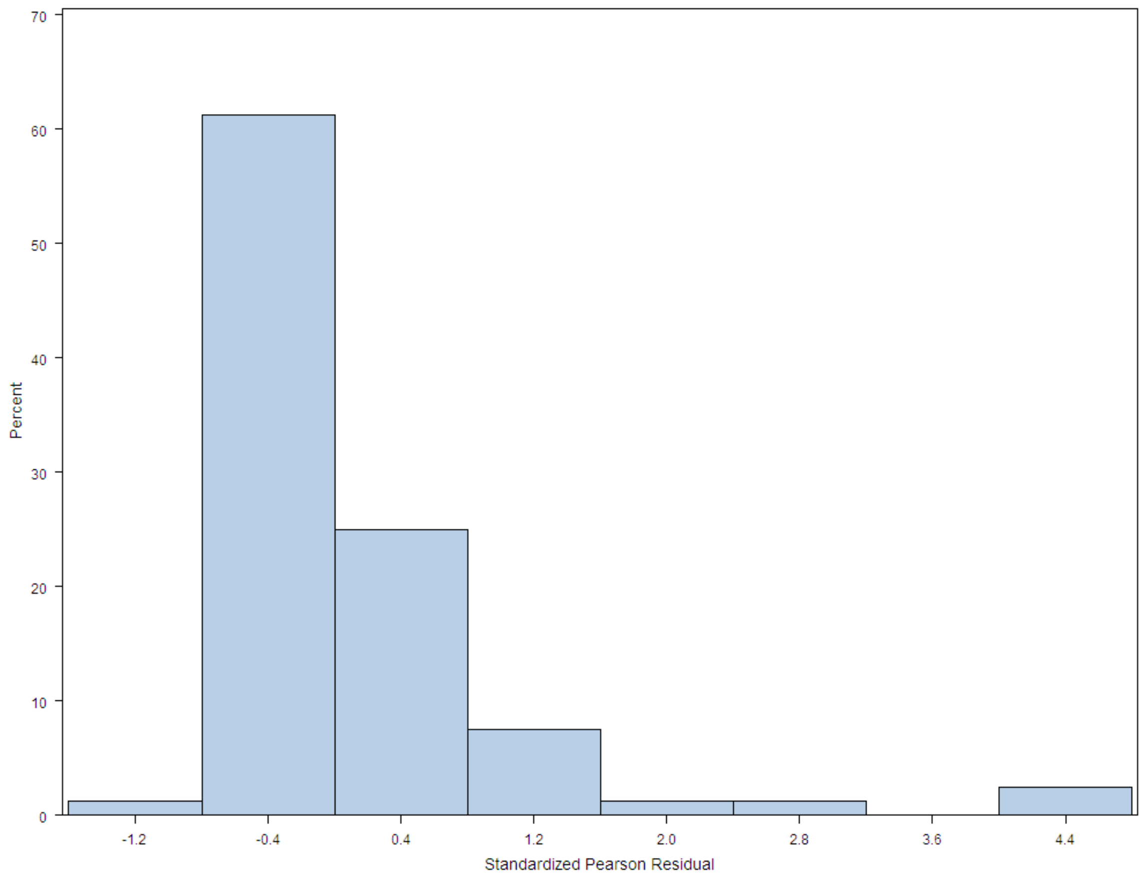
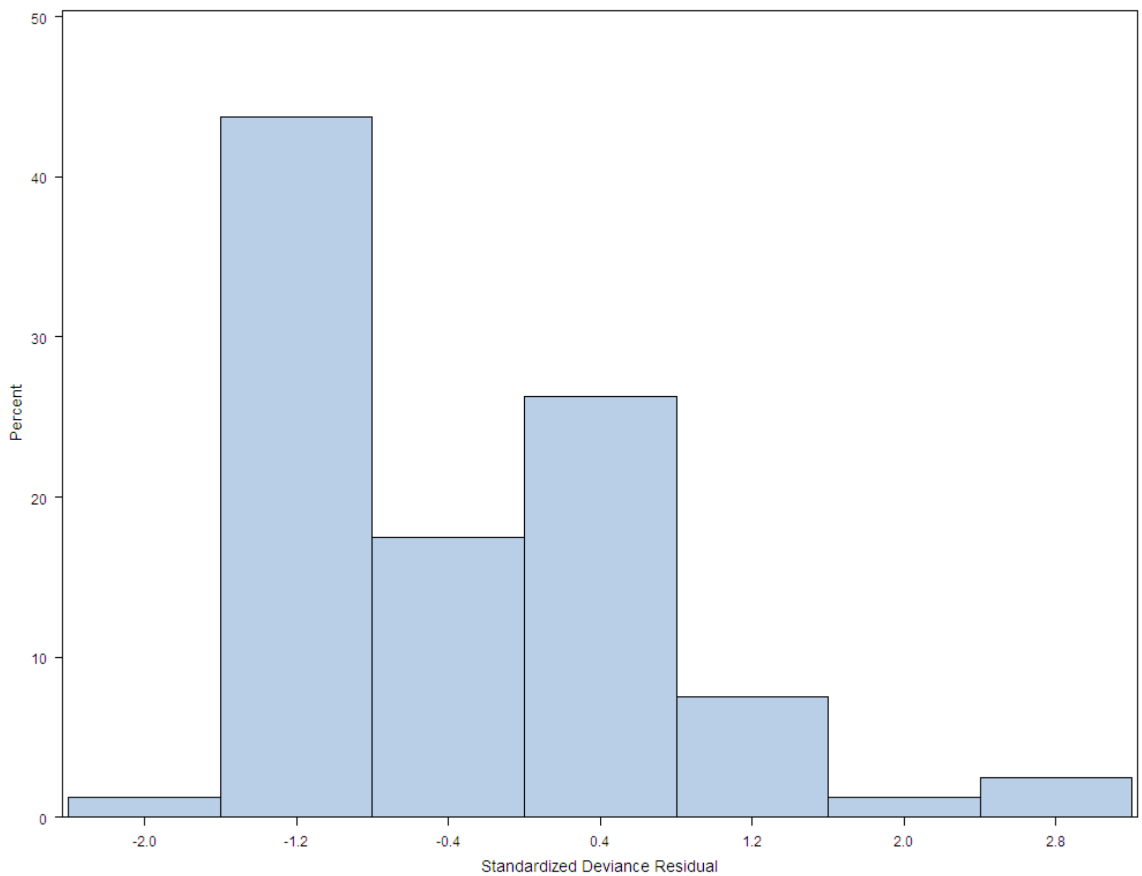


Figure E.5.5.6 Histogram of the standardized deviance residuals



E.5.6 July 2006 Model 6 Residual Plots

Figure E.5.6.1 Histogram of the raw residuals

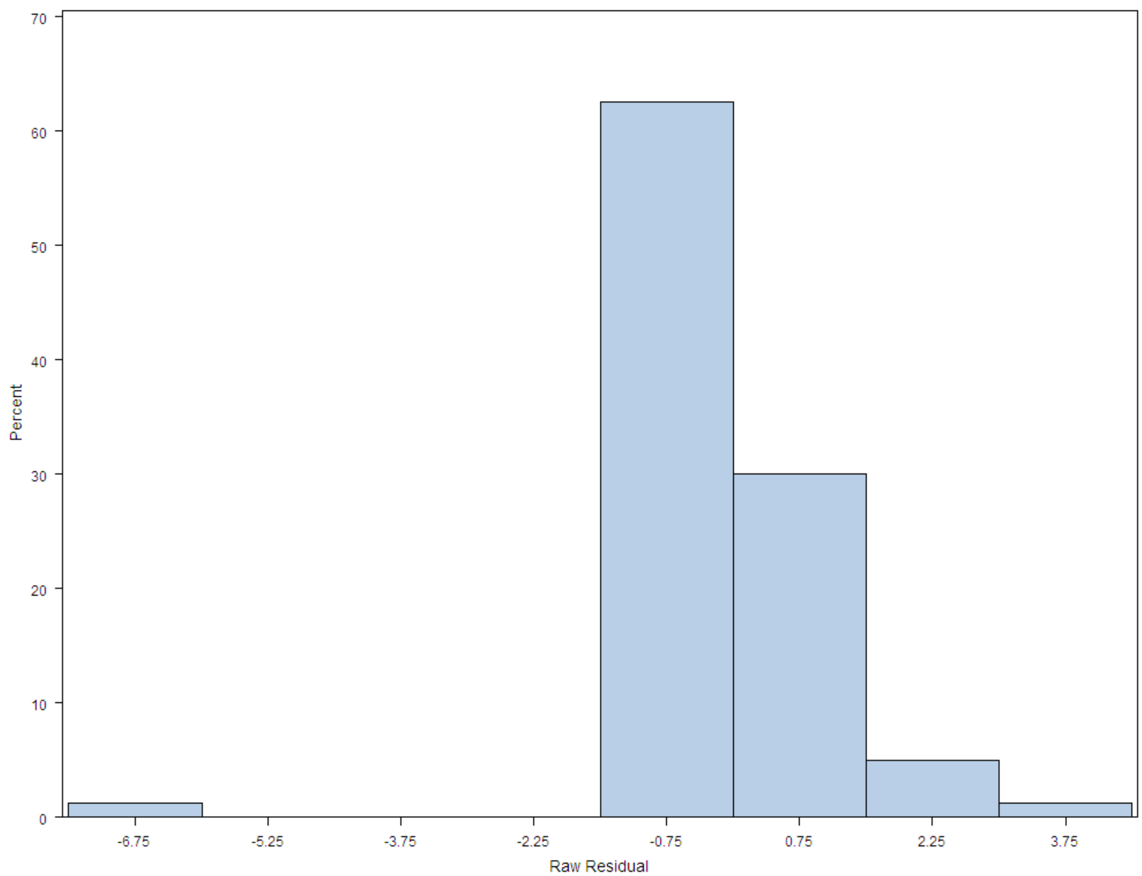
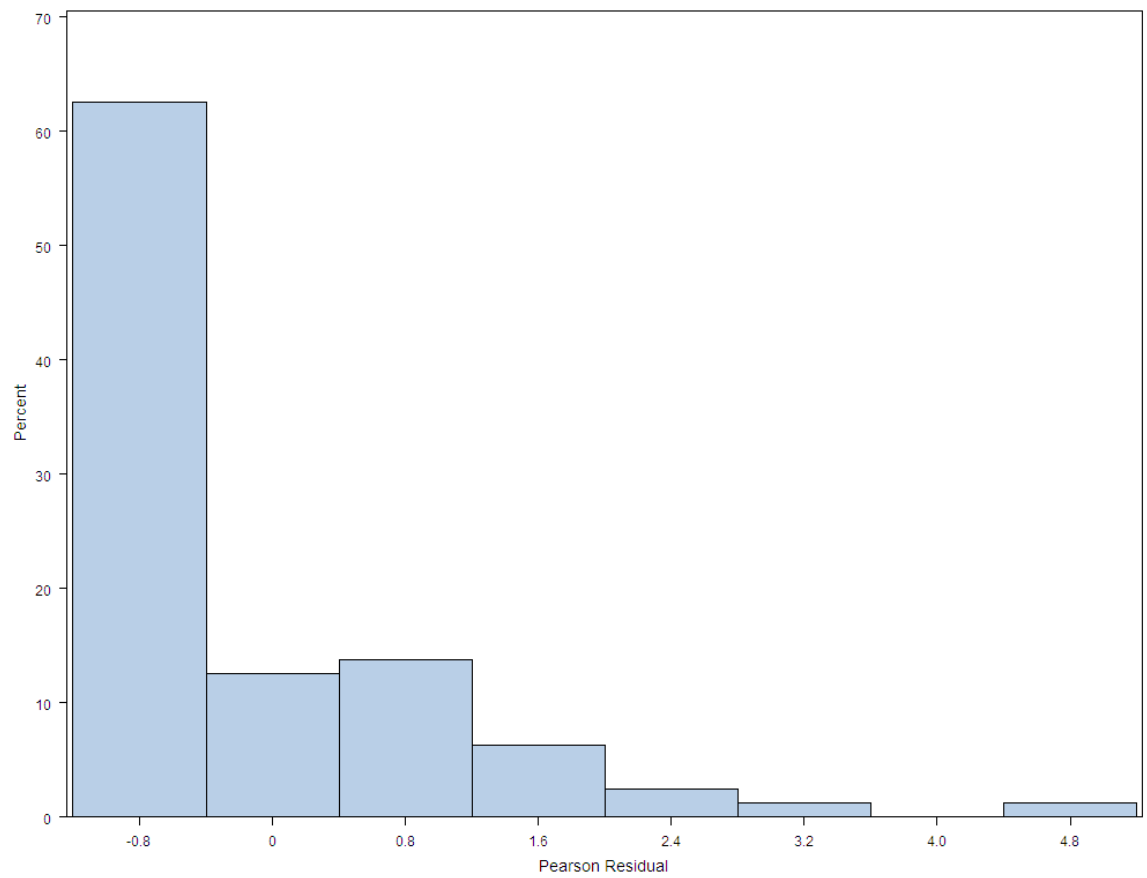


Figure E.5.6.2 Histogram of the Pearson residuals



E.5.7 July 2006 Model 7 Residual Plots

Figure E.5.7.1 Histogram of the raw residuals

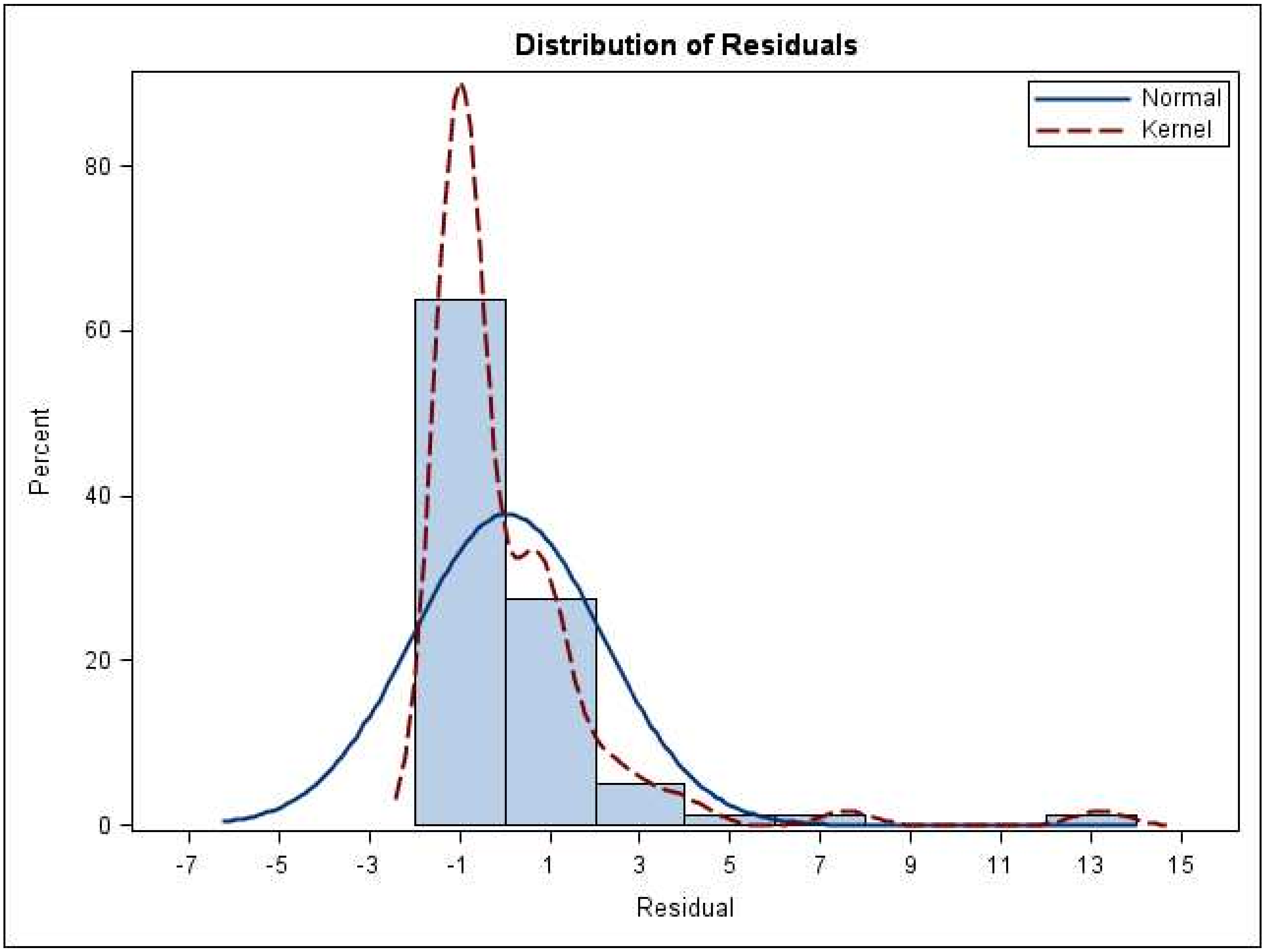


Figure E.5.7.2 Normal quantile plot of the raw residuals

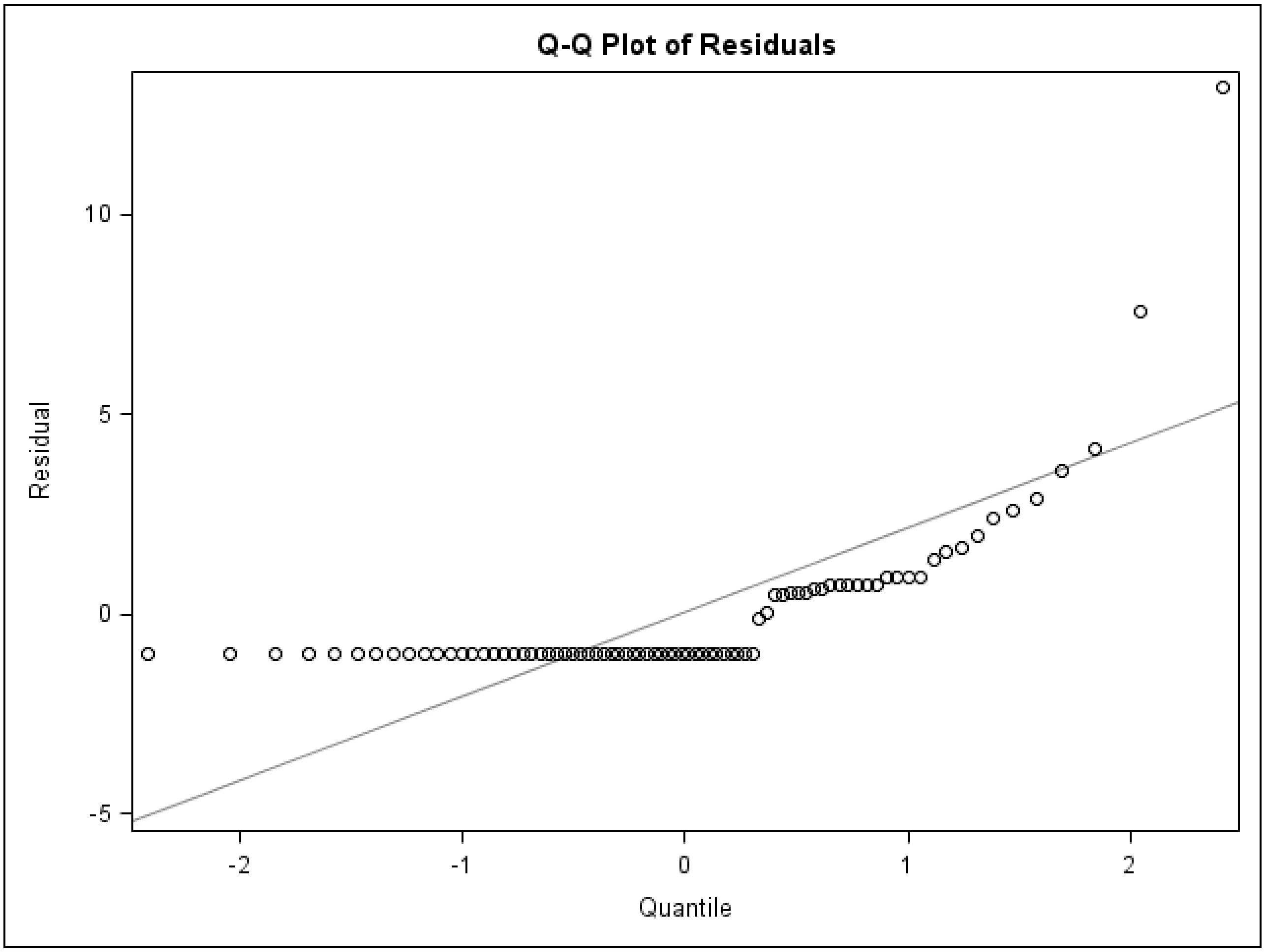


Figure E.5.7.3 Histogram of the Studentized residuals

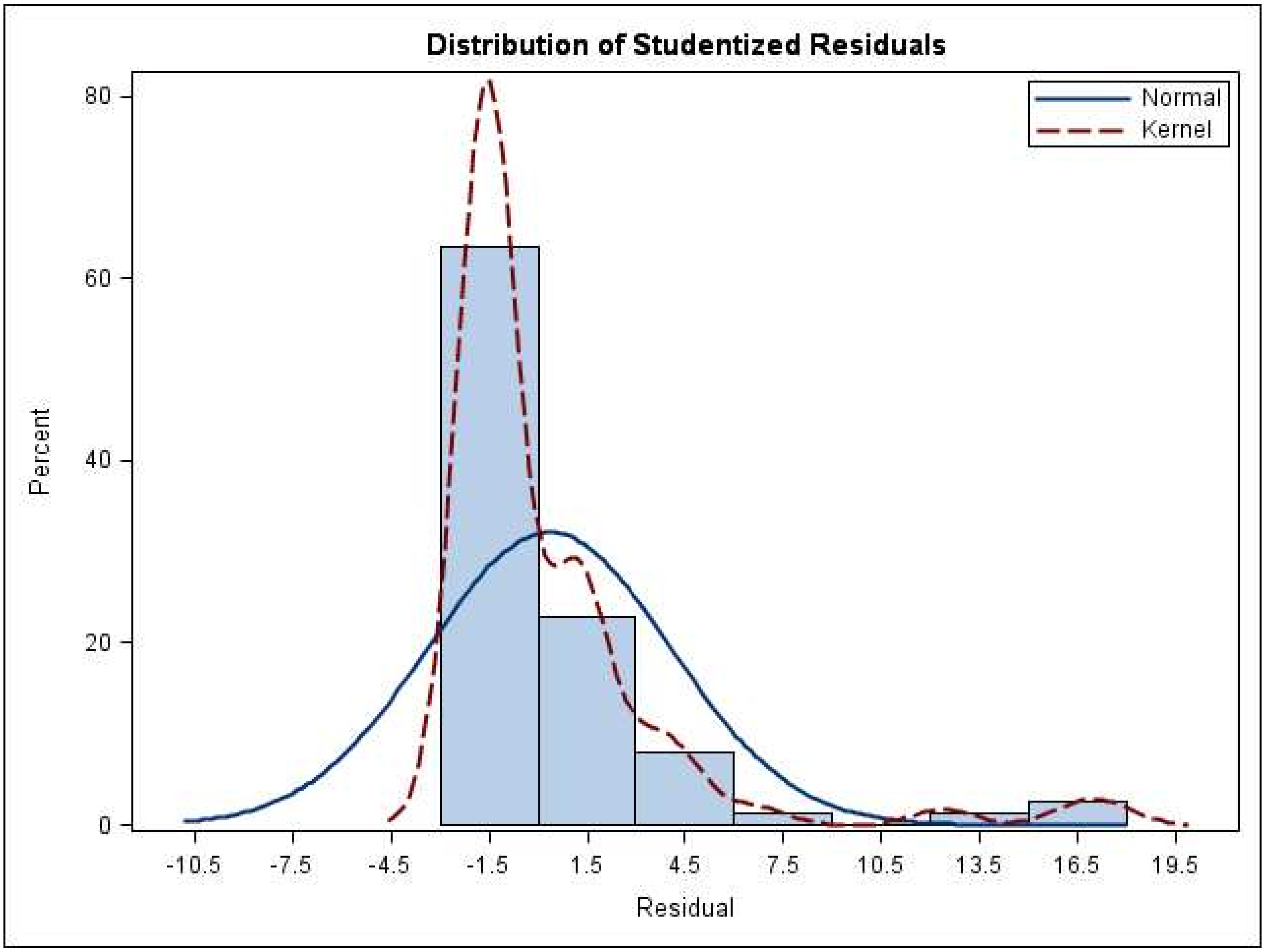


Figure E.5.7.4 Normal quantile plot of the Studentized residuals

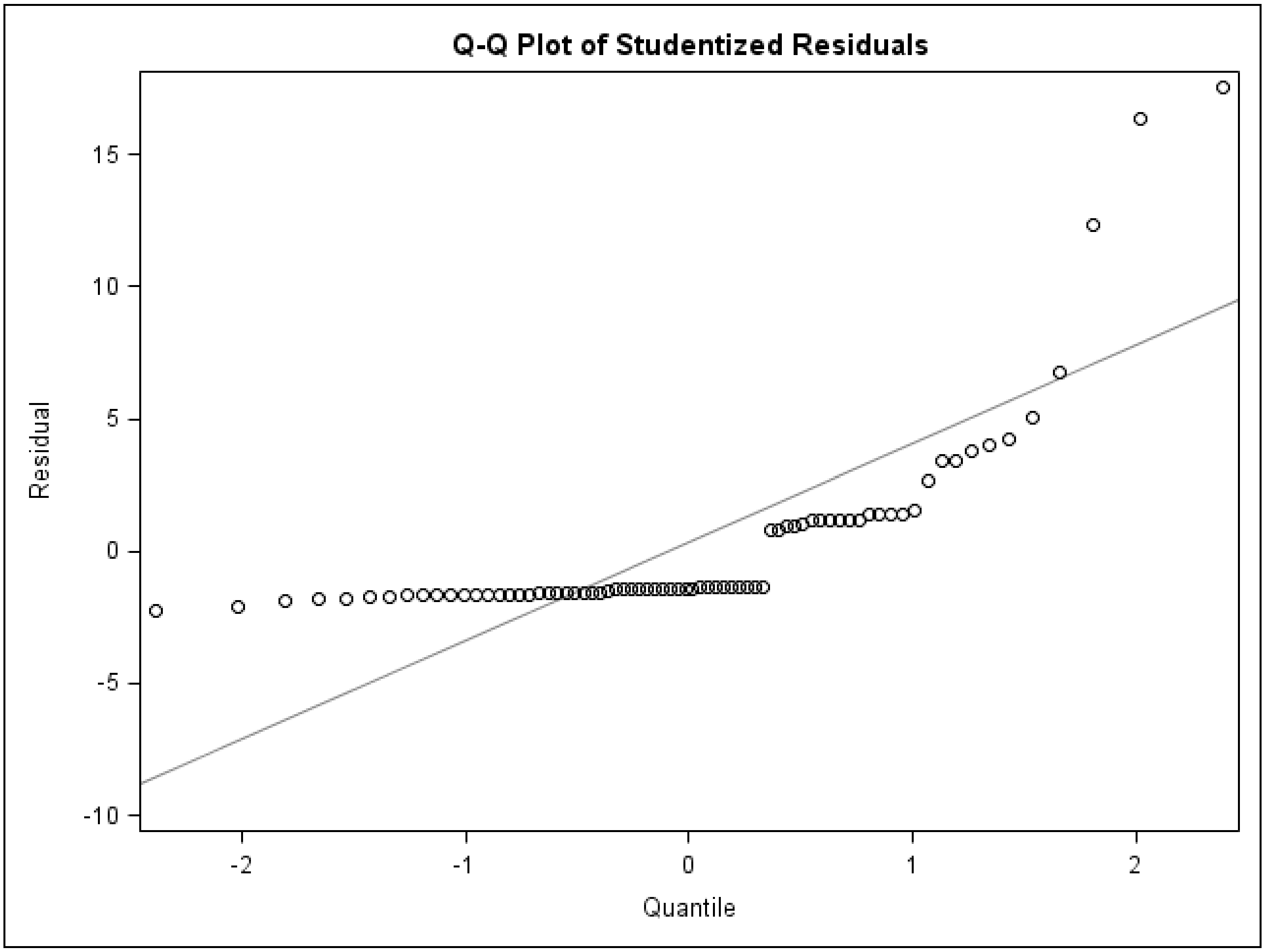


Figure E.5.7.5 Histogram of the Pearson residuals

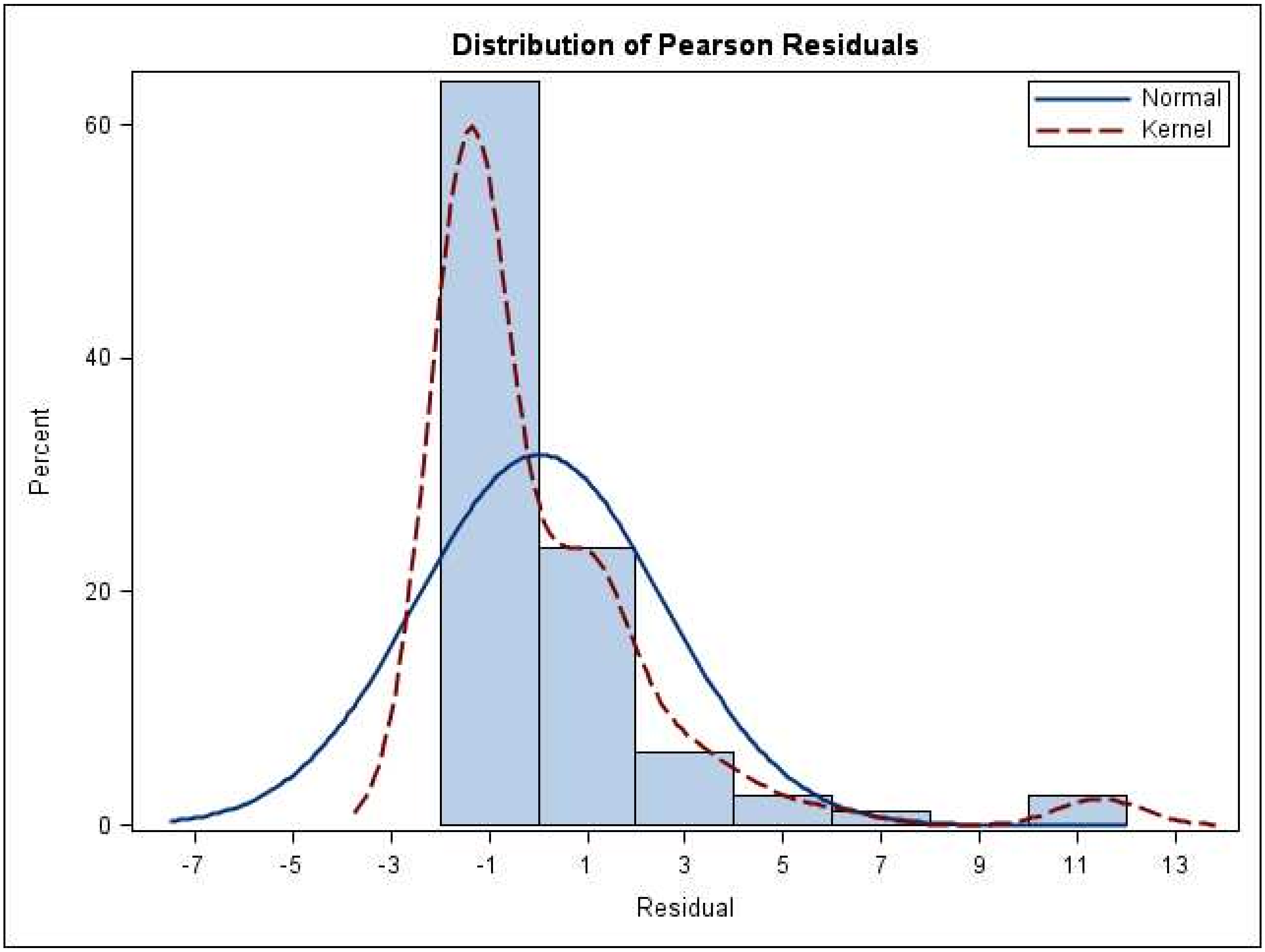
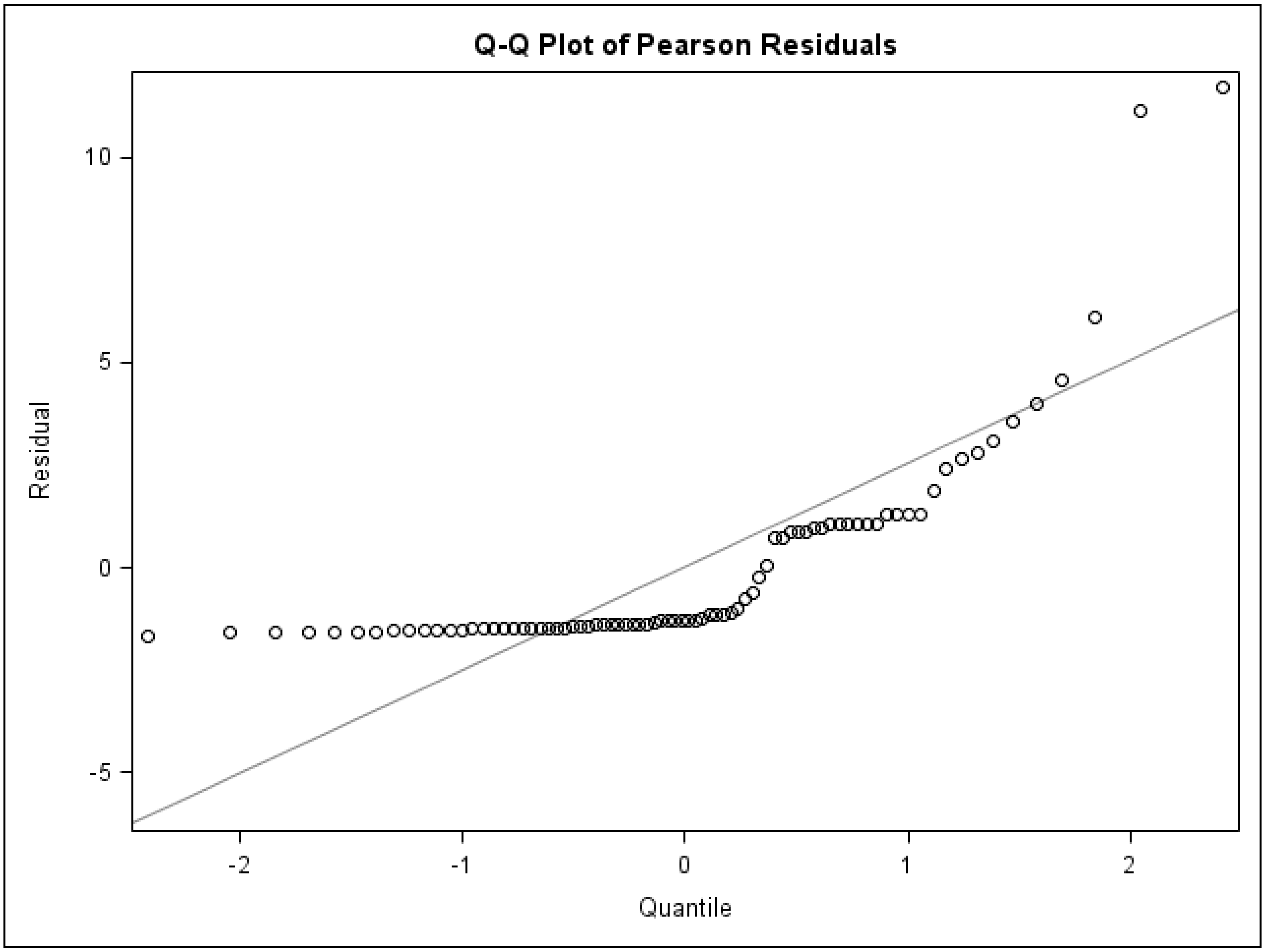
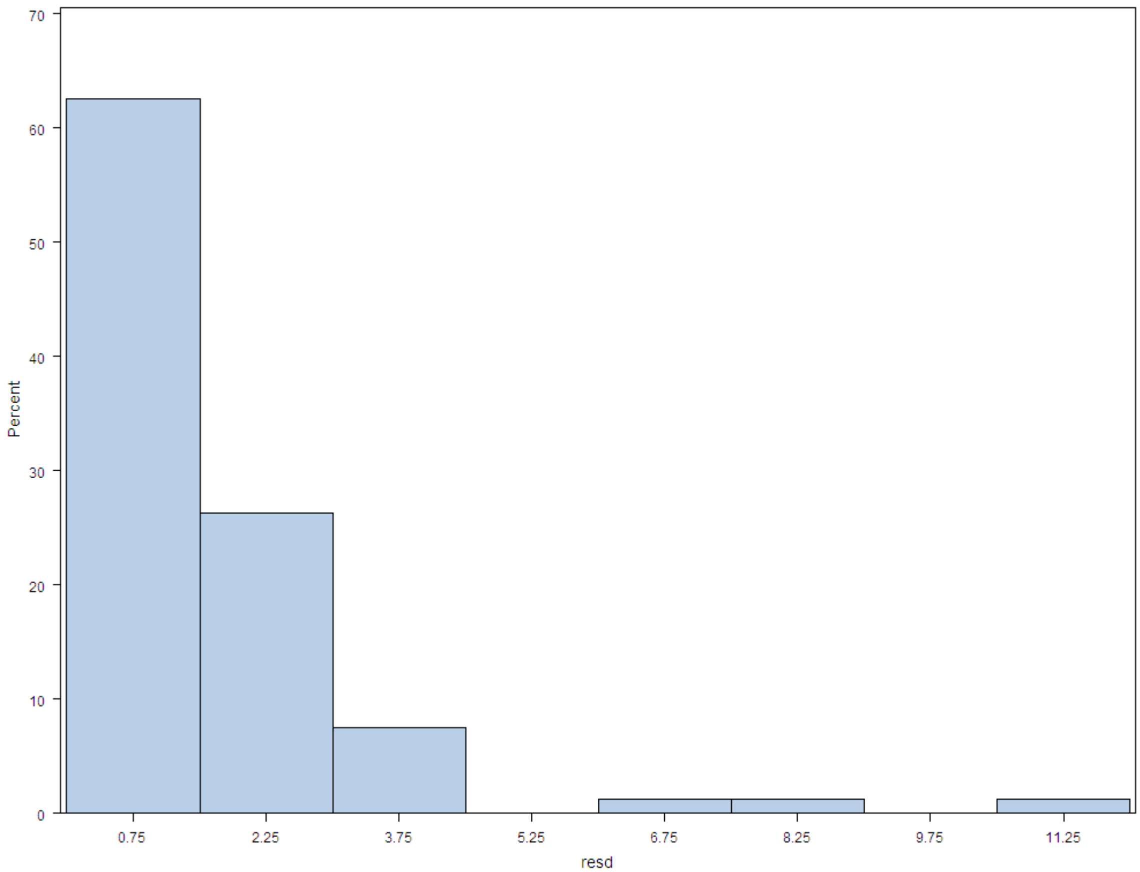


Figure E.5.7.6 Normal quantile plot of the Pearson residuals



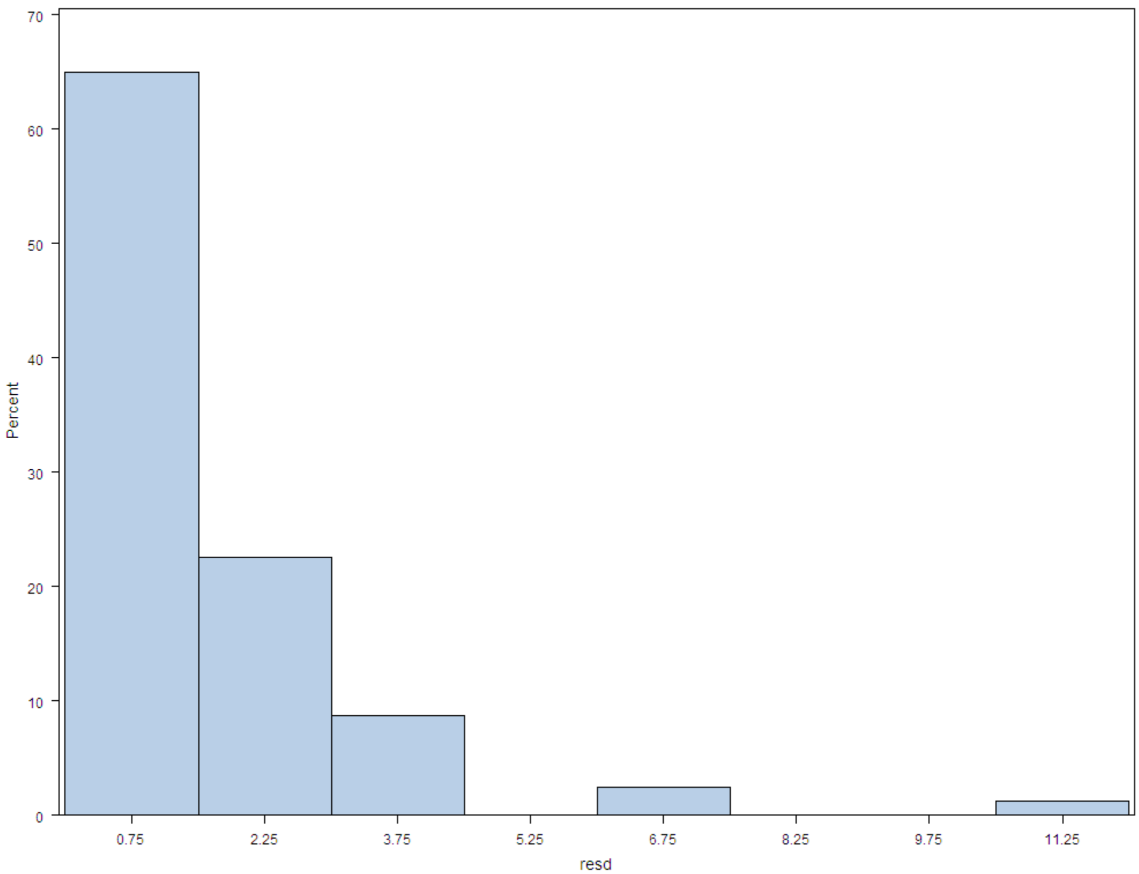
E.5.8 July 2006 Model 8 Residual Plots

Figure E.5.8.1 Histogram of the raw residuals



E.5.9 July 2006 Model 9 Residual Plots

Figure E.5.9.1 Histogram of the raw residuals



E.6 September 2006 Residual Plots

E.6.1 September 2006 Model 1 Residual Plots

Figure E.6.1.1 Histogram of the raw residuals

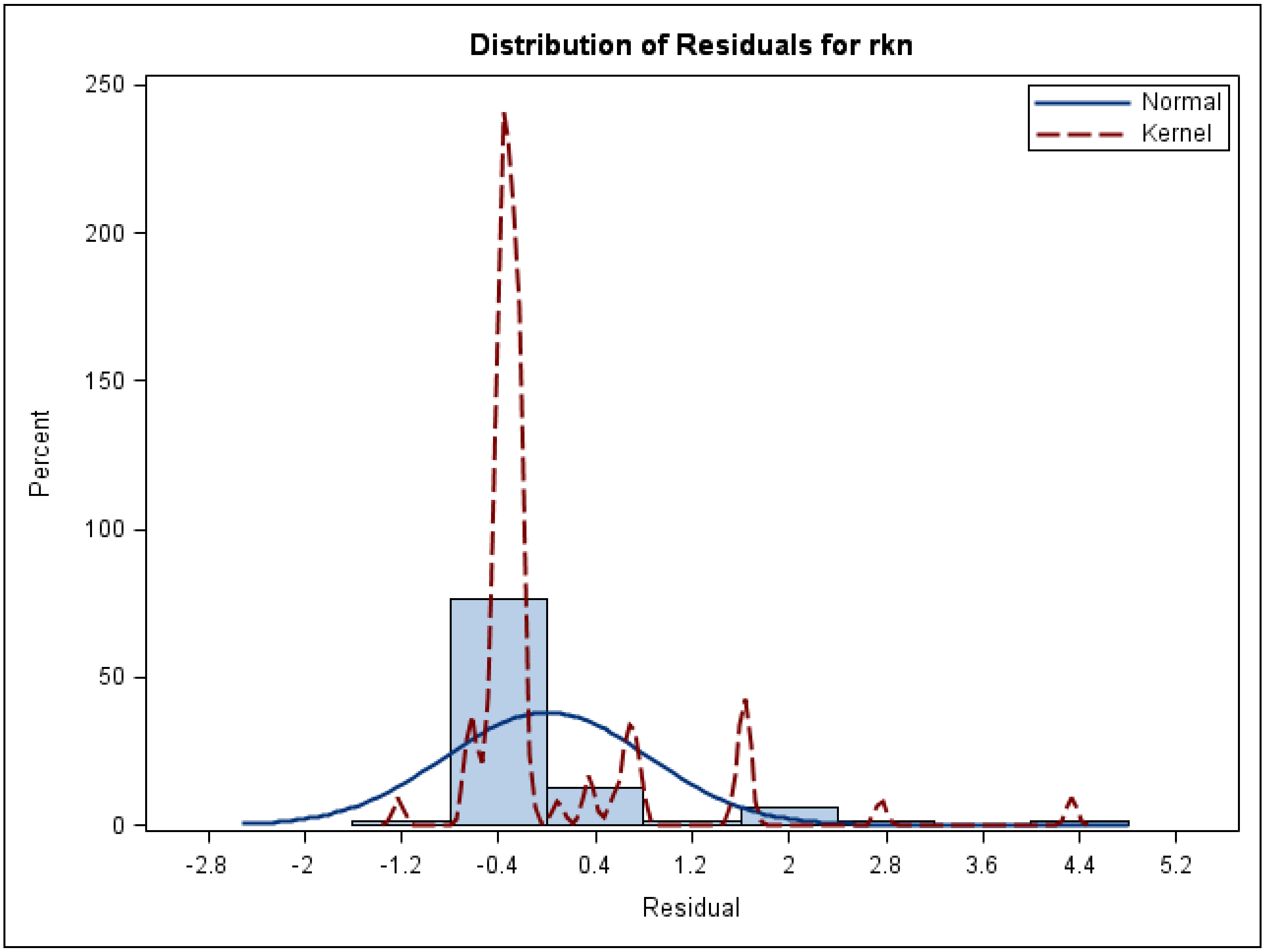


Figure E.6.1.2 Normal quantile plot of the raw residuals

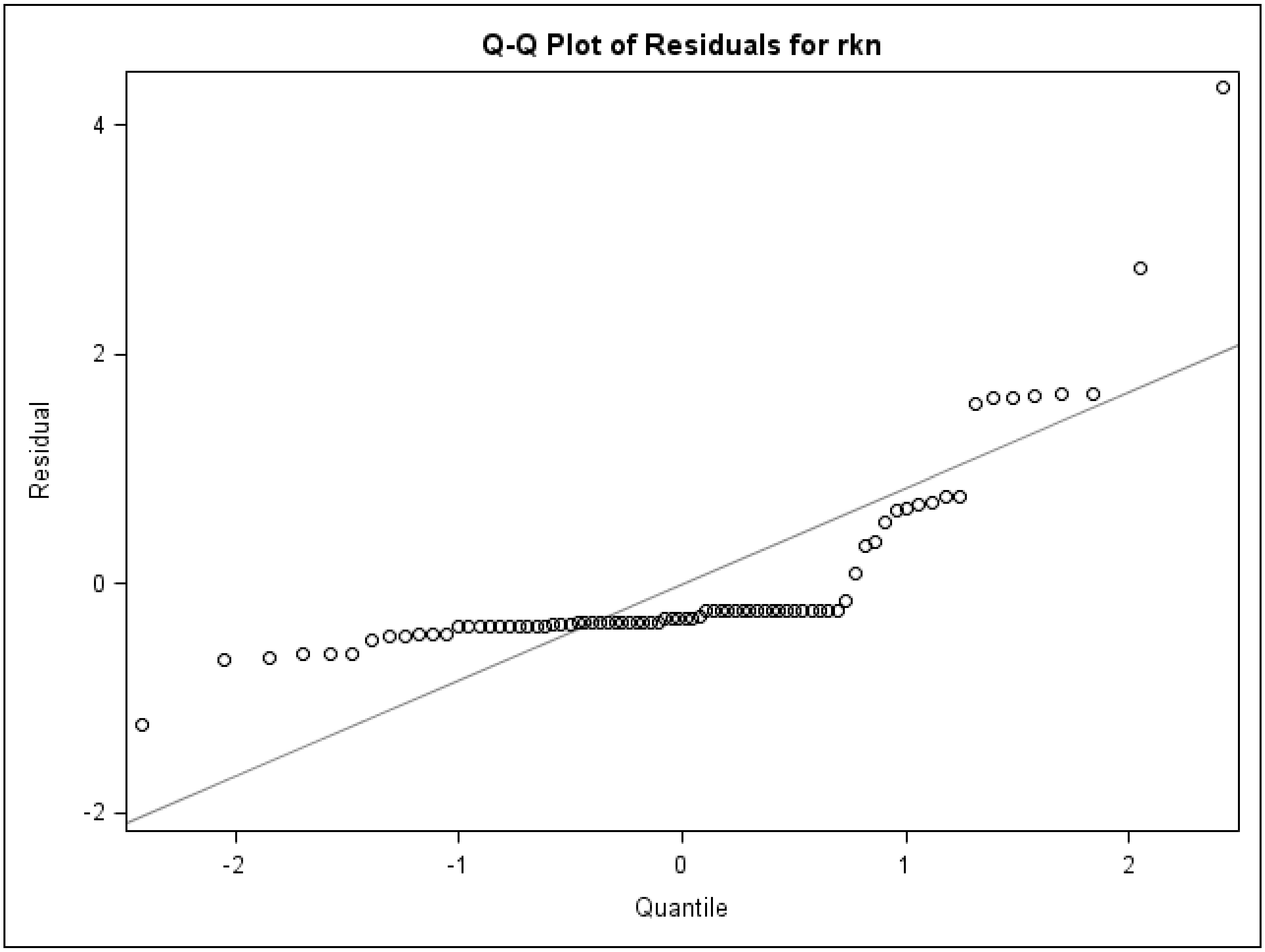


Figure E.6.1.3 Histogram of the Studentized residuals

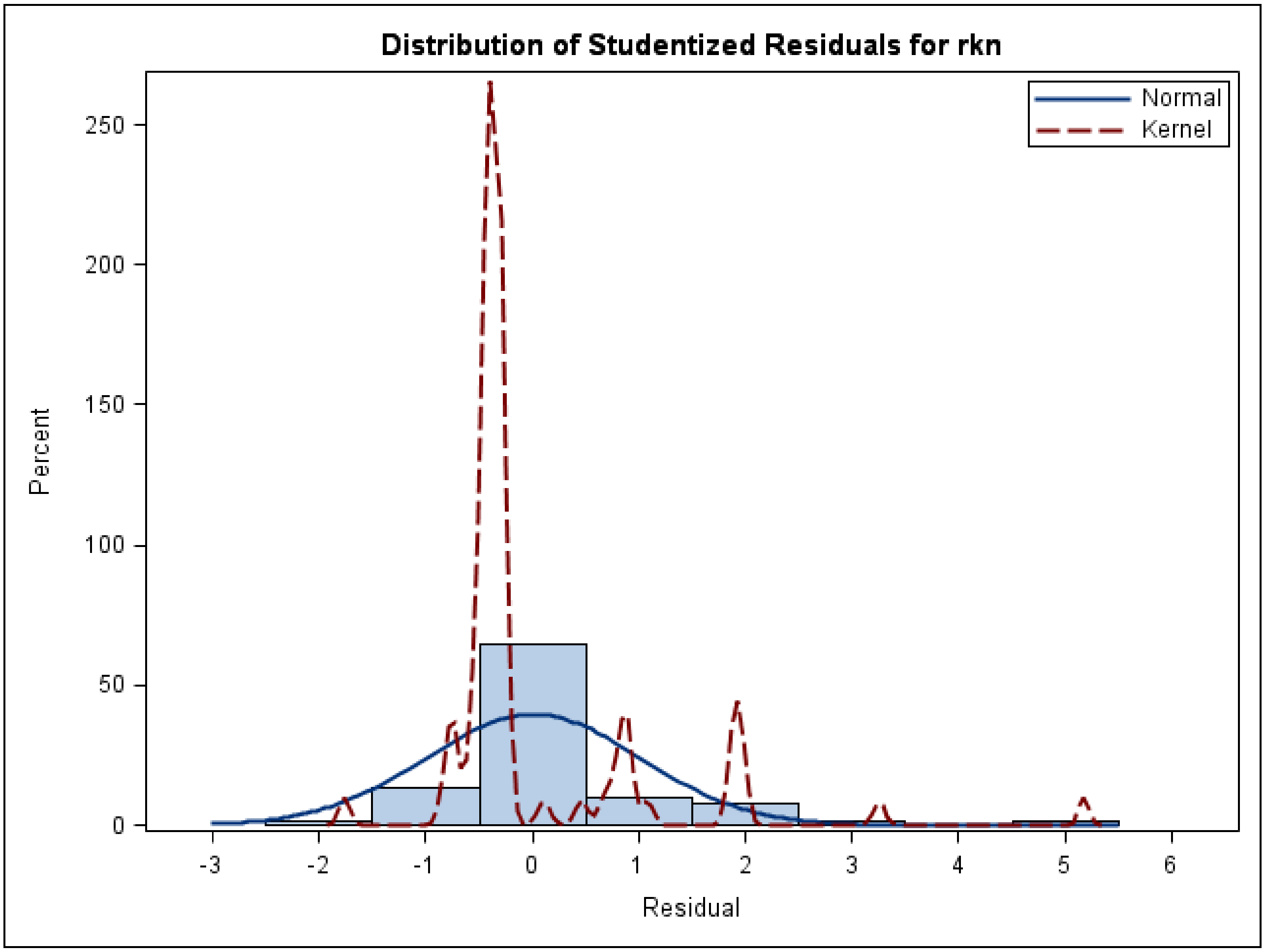


Figure E.6.1.4 Normal quantile plot of the Studentized residuals

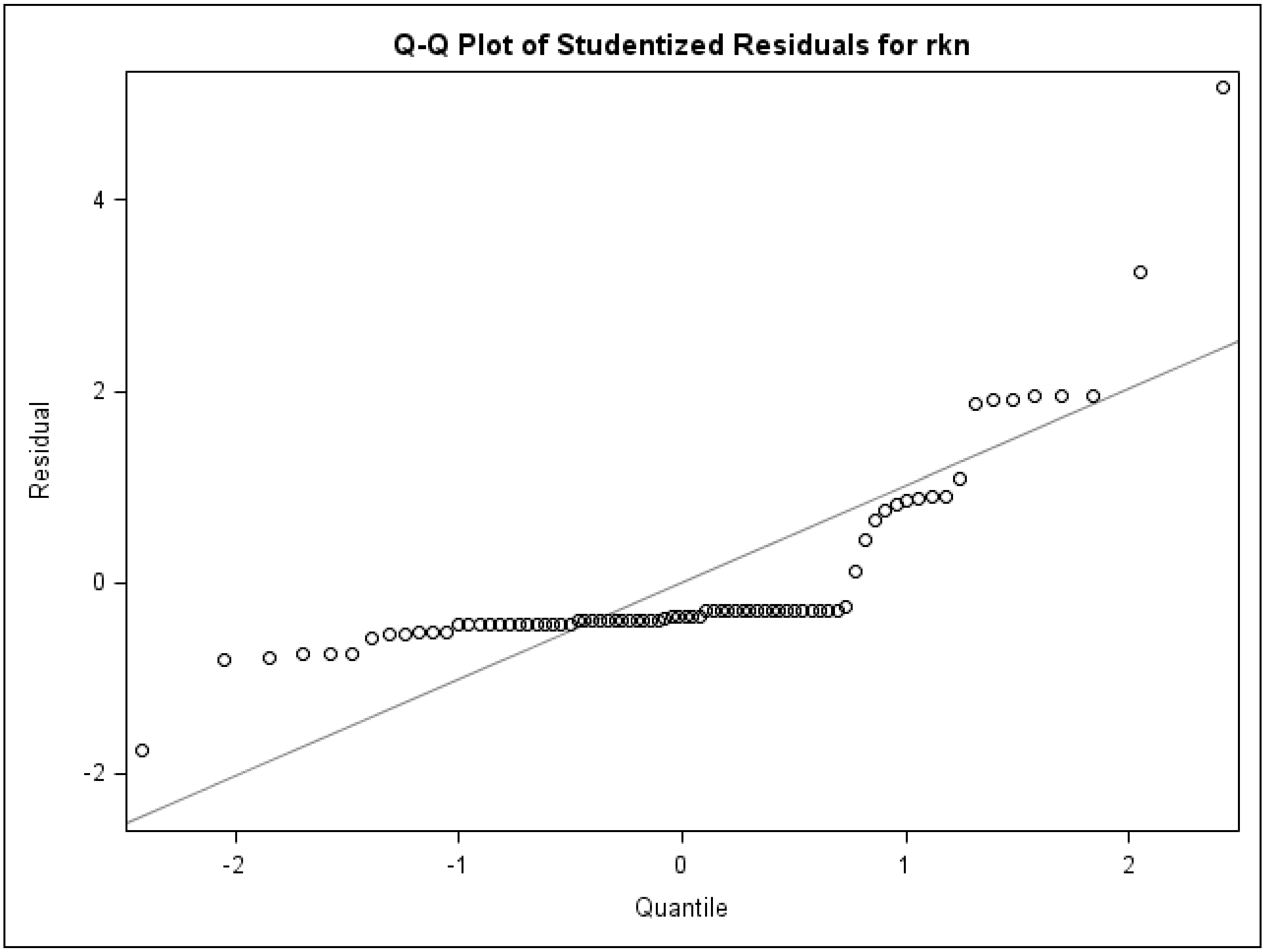


Figure E.6.1.5 Histogram of the Pearson residuals

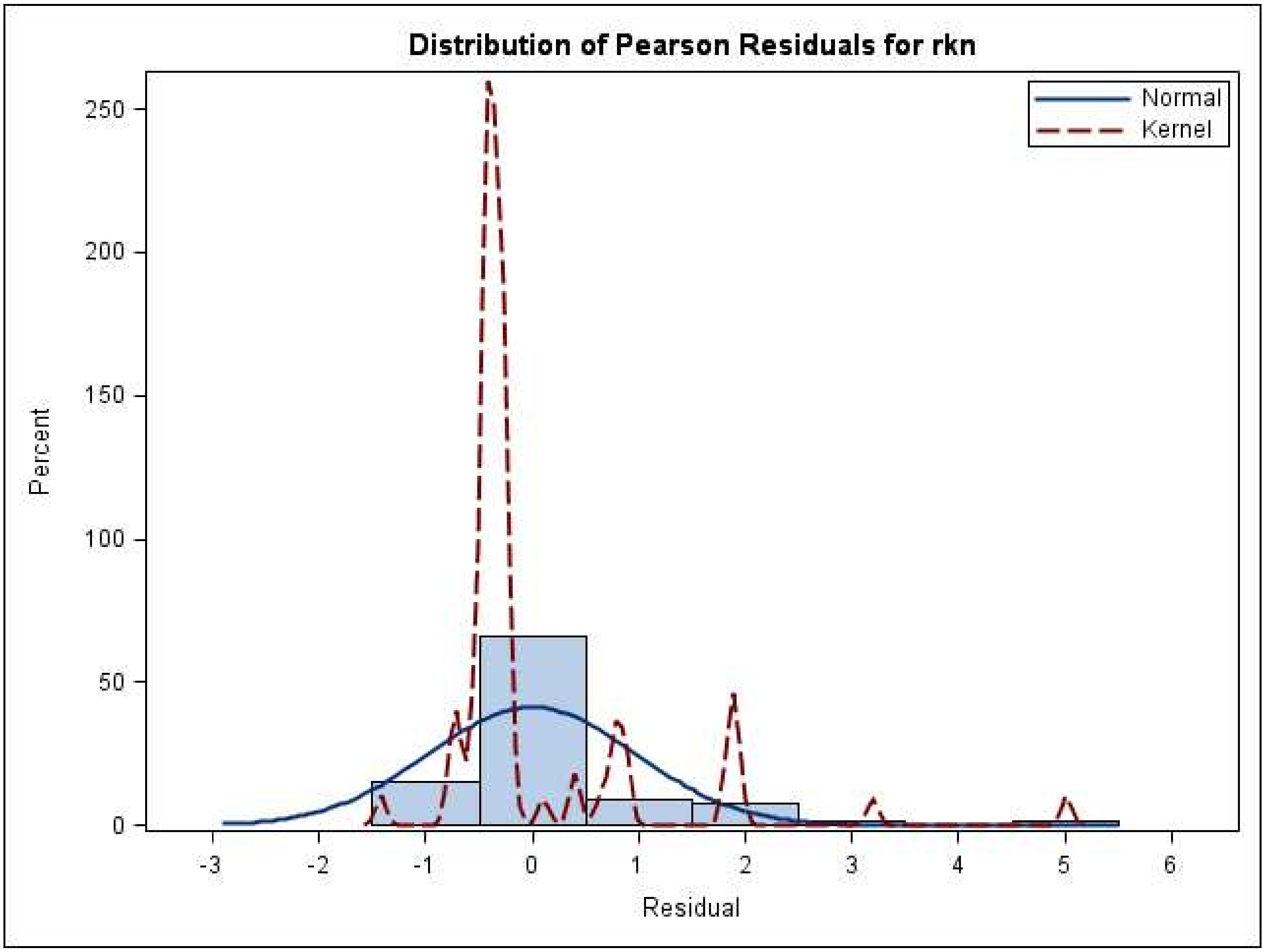
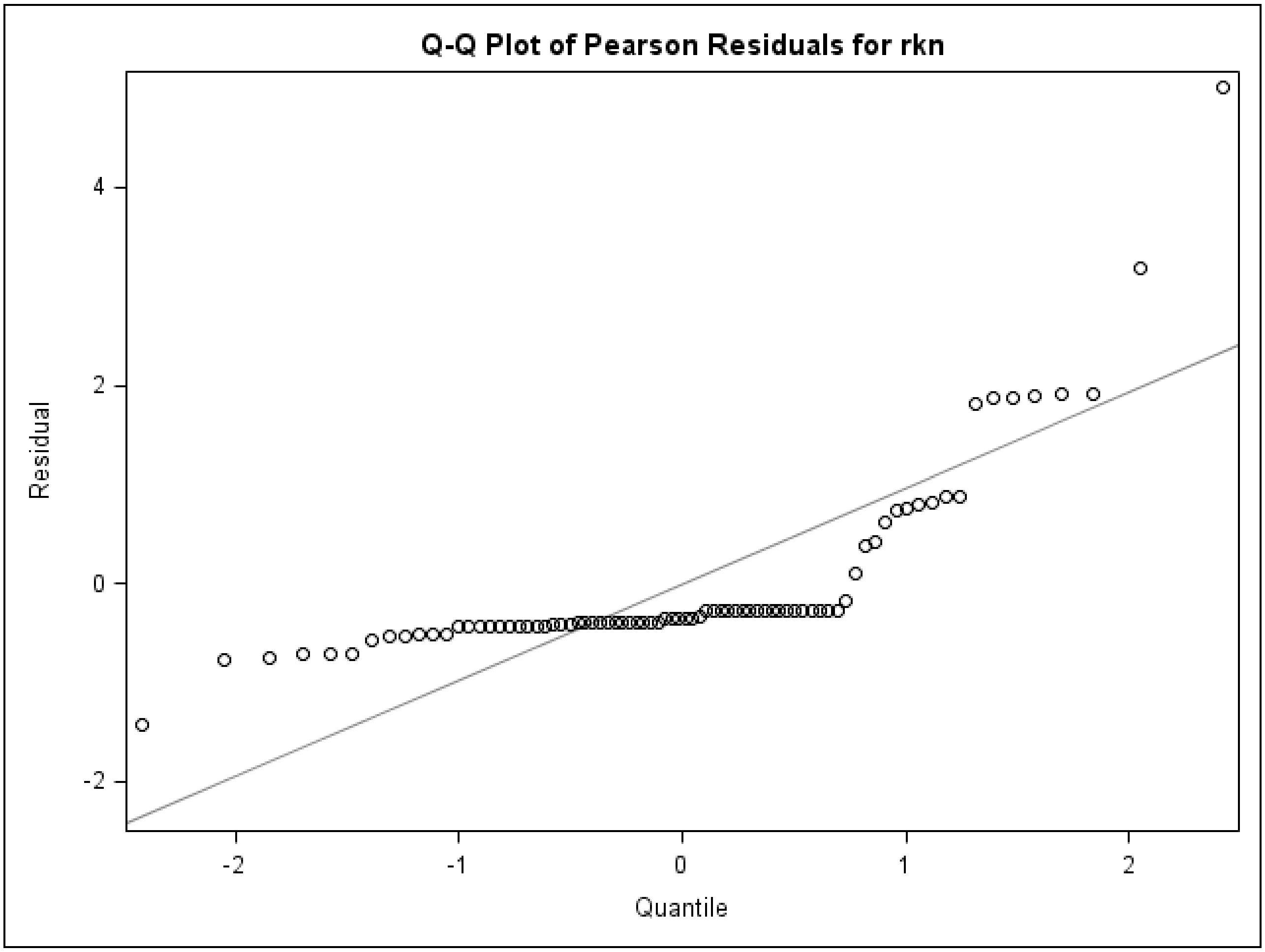


Figure E.6.1.6 Normal quantile plot of the Pearson residuals



E.6.2 September 2006 Model 2 Residual Plots

Figure E.6.2.1 Histogram of the raw residuals

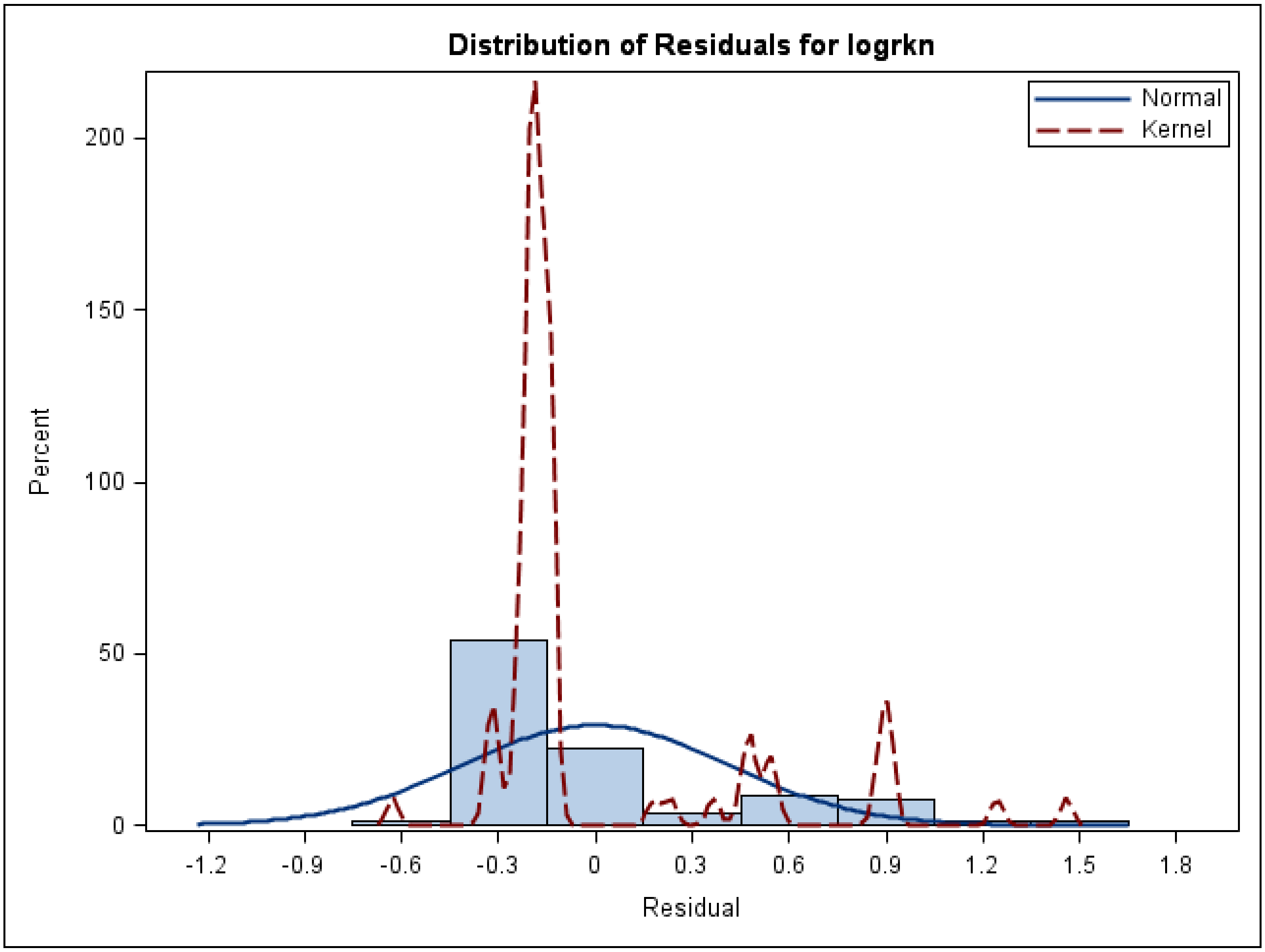


Figure E.6.2.2 Normal quantile plot of the raw residuals

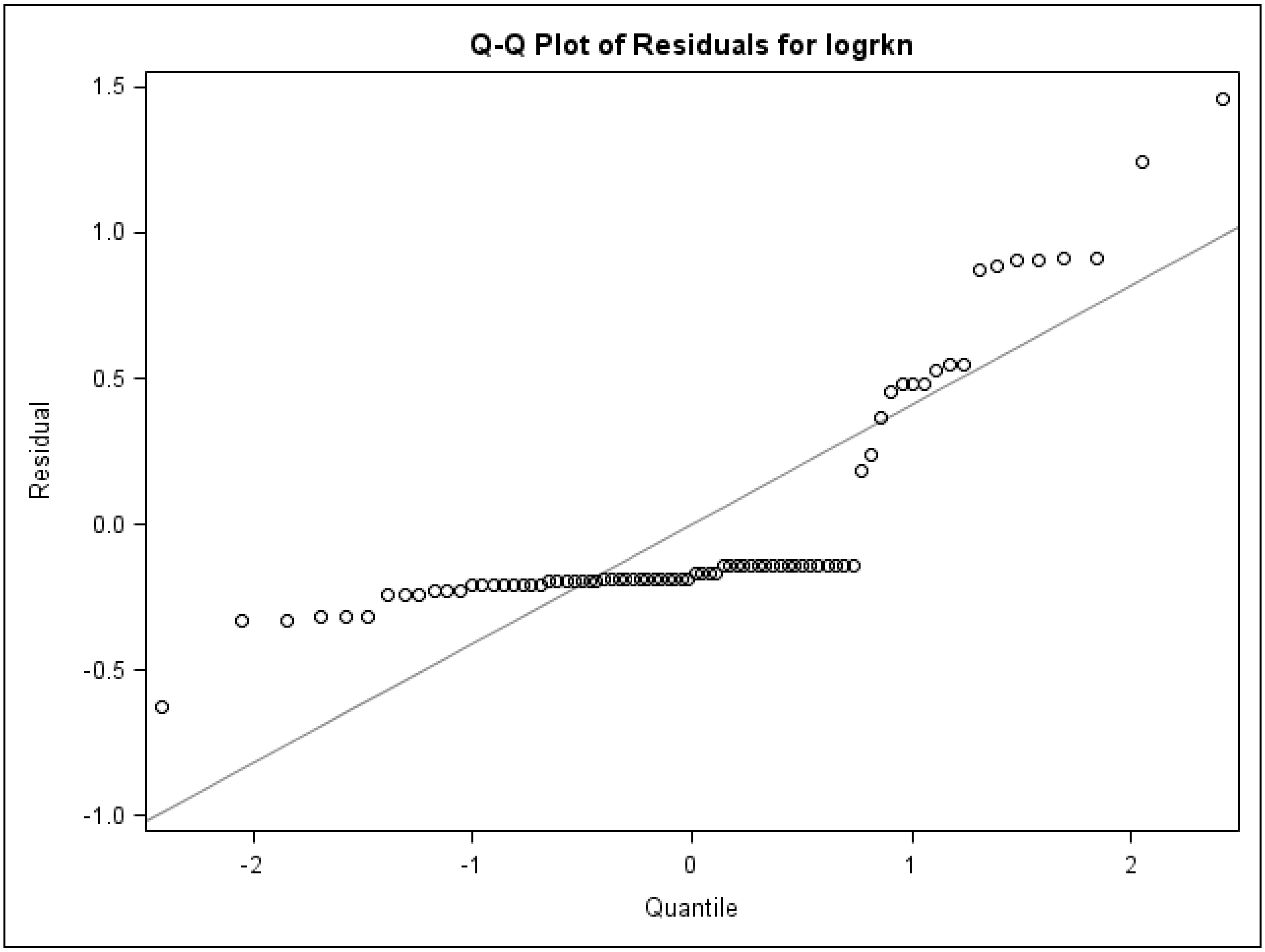


Figure E.6.2.3 Histogram of the Studentized residuals

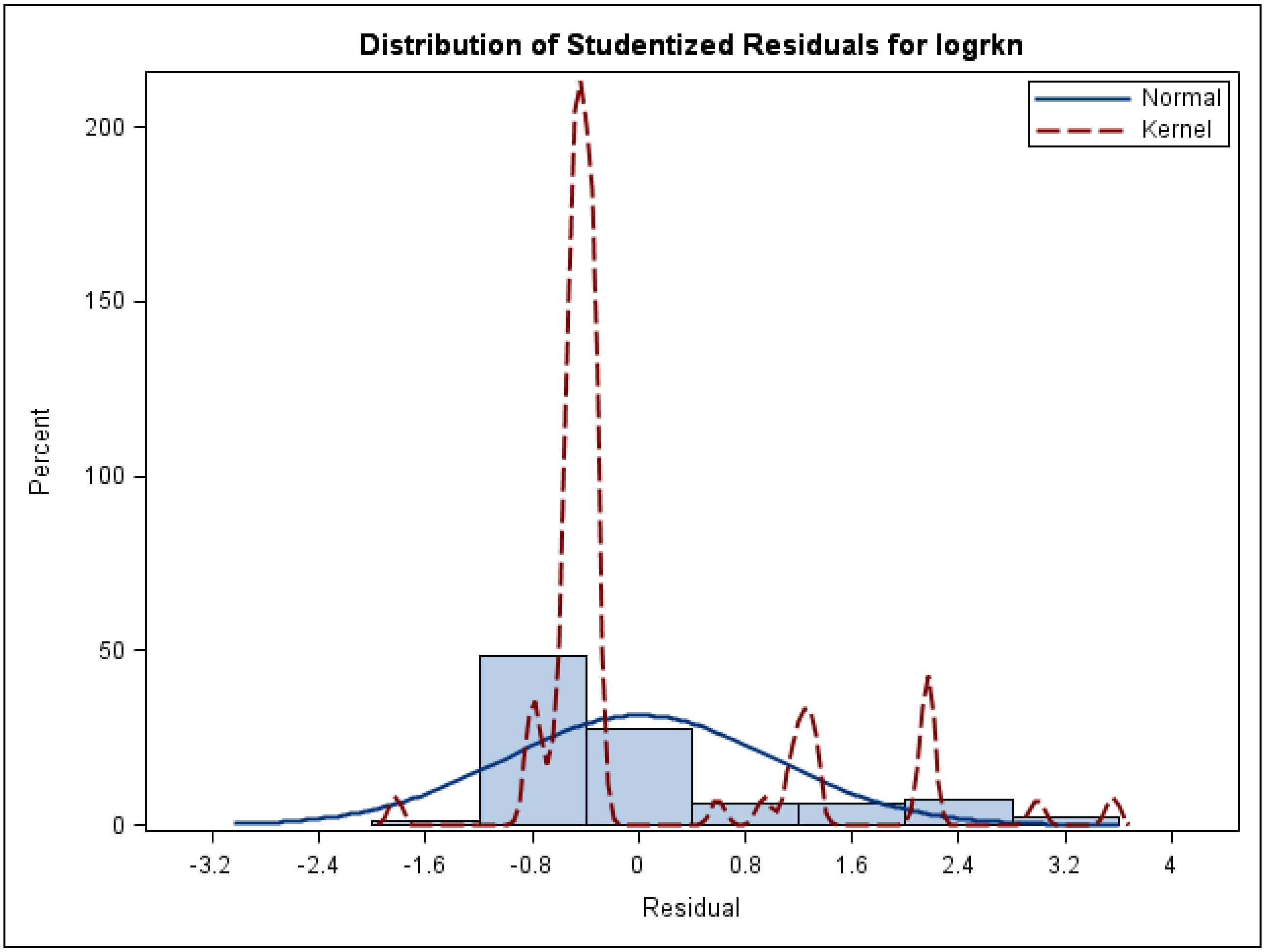


Figure E.6.2.4 Normal quantile plot of the Studentized residuals

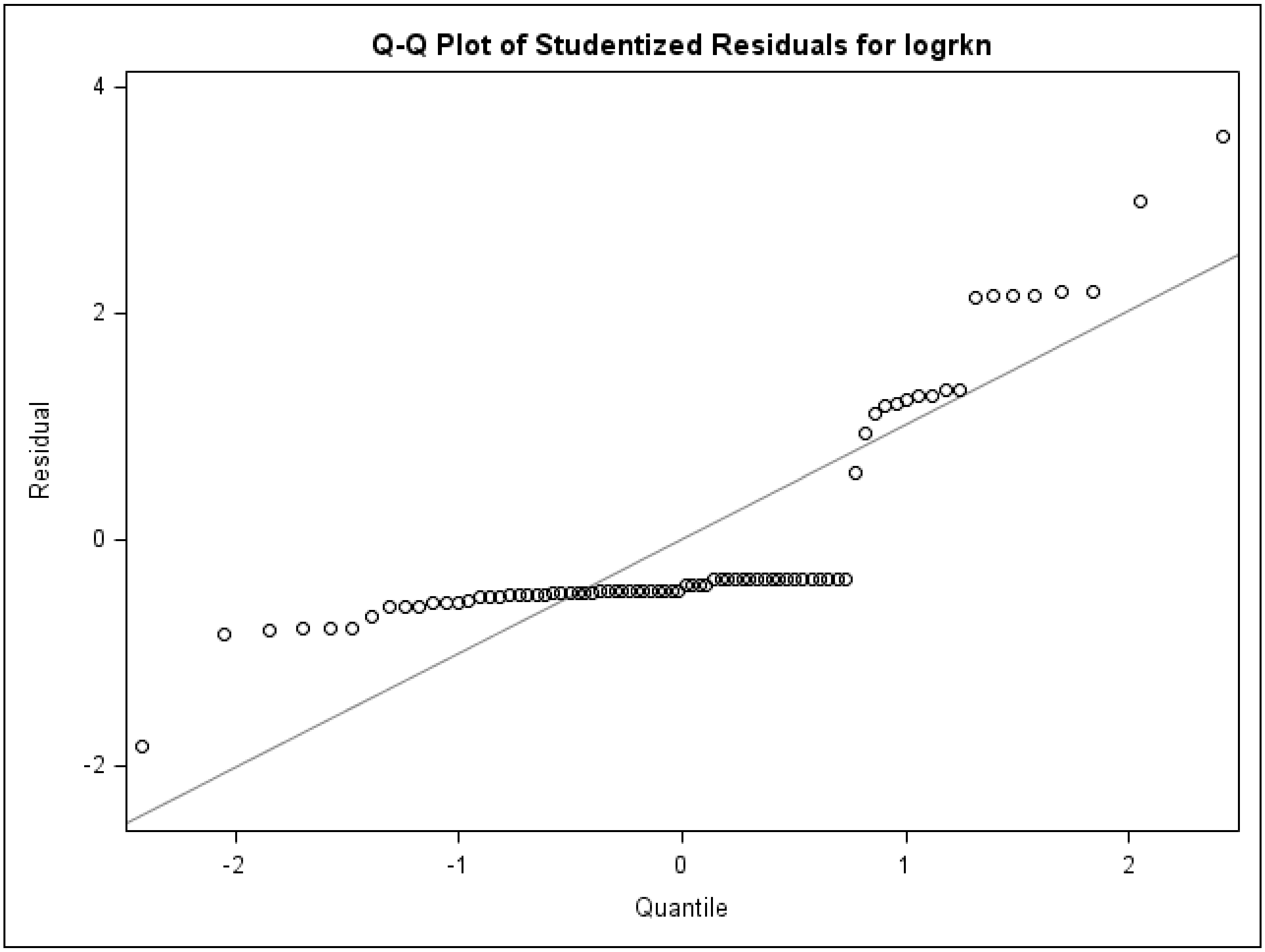


Figure E.6.2.5 Histogram of the Pearson residuals

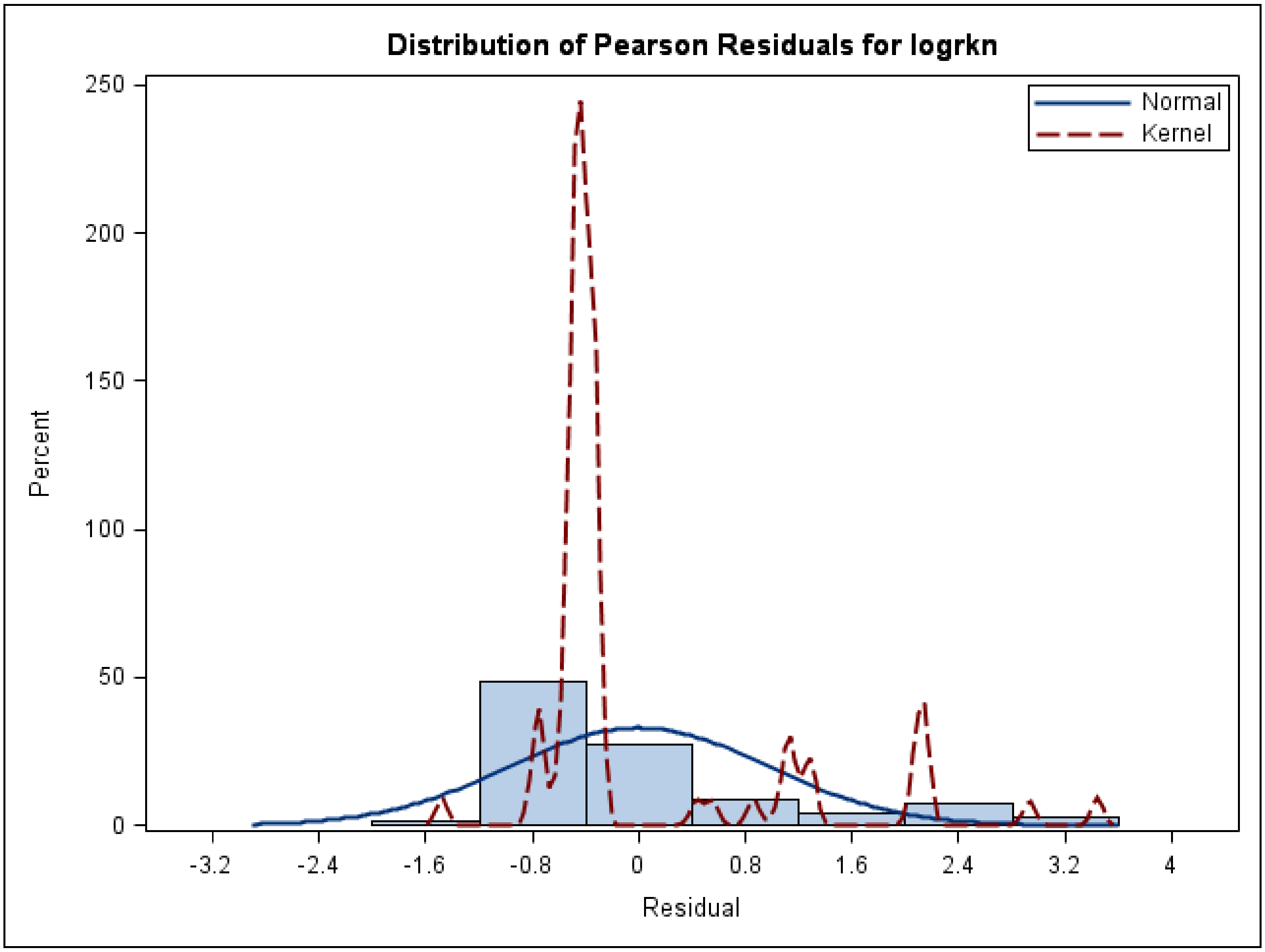
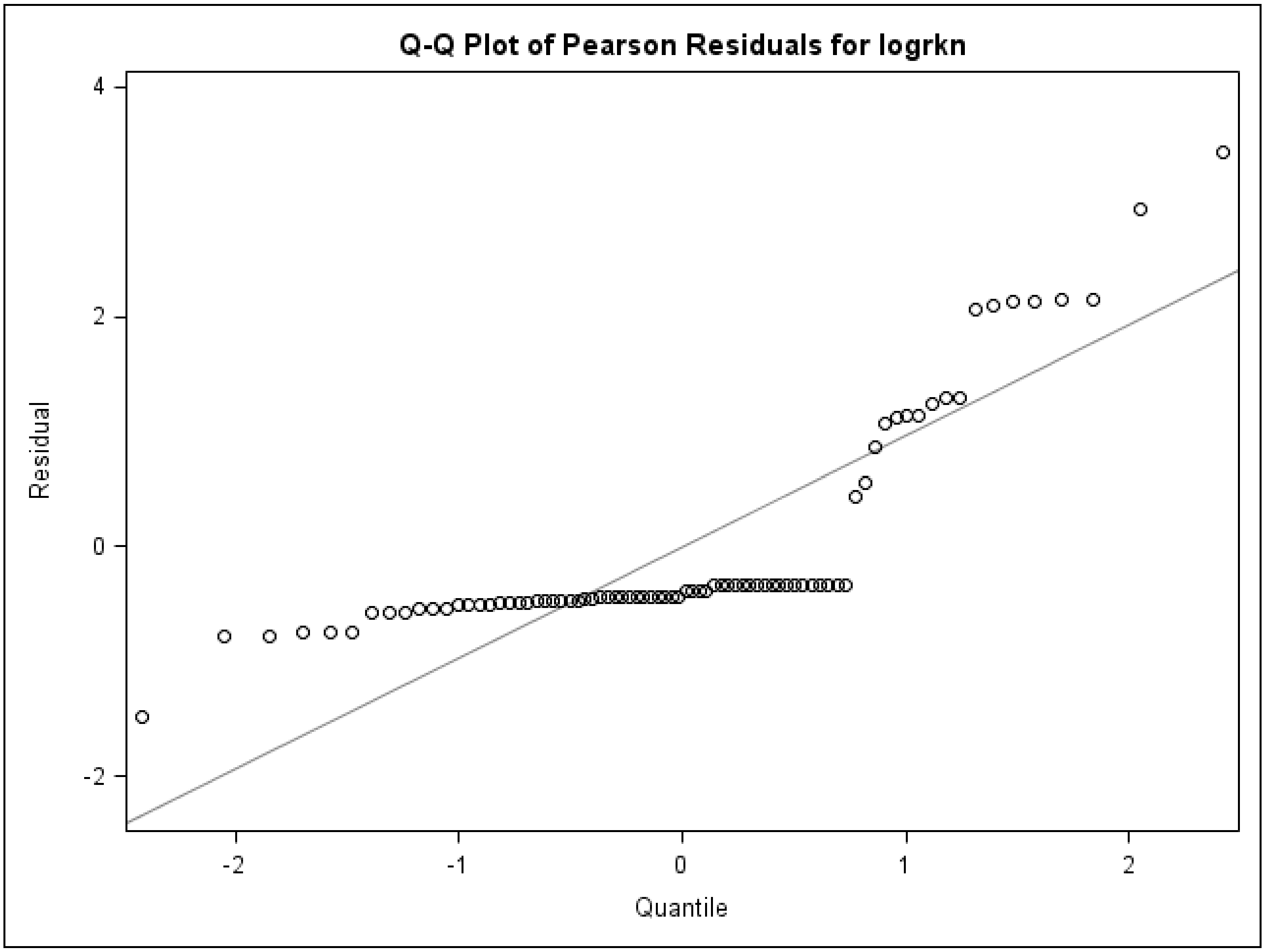


Figure E.6.2.6 Normal quantile plot of the Pearson residuals



E.6.3 September 2006 Model 3 Residual Plots

Figure E.6.3.1 Histogram of the raw residuals

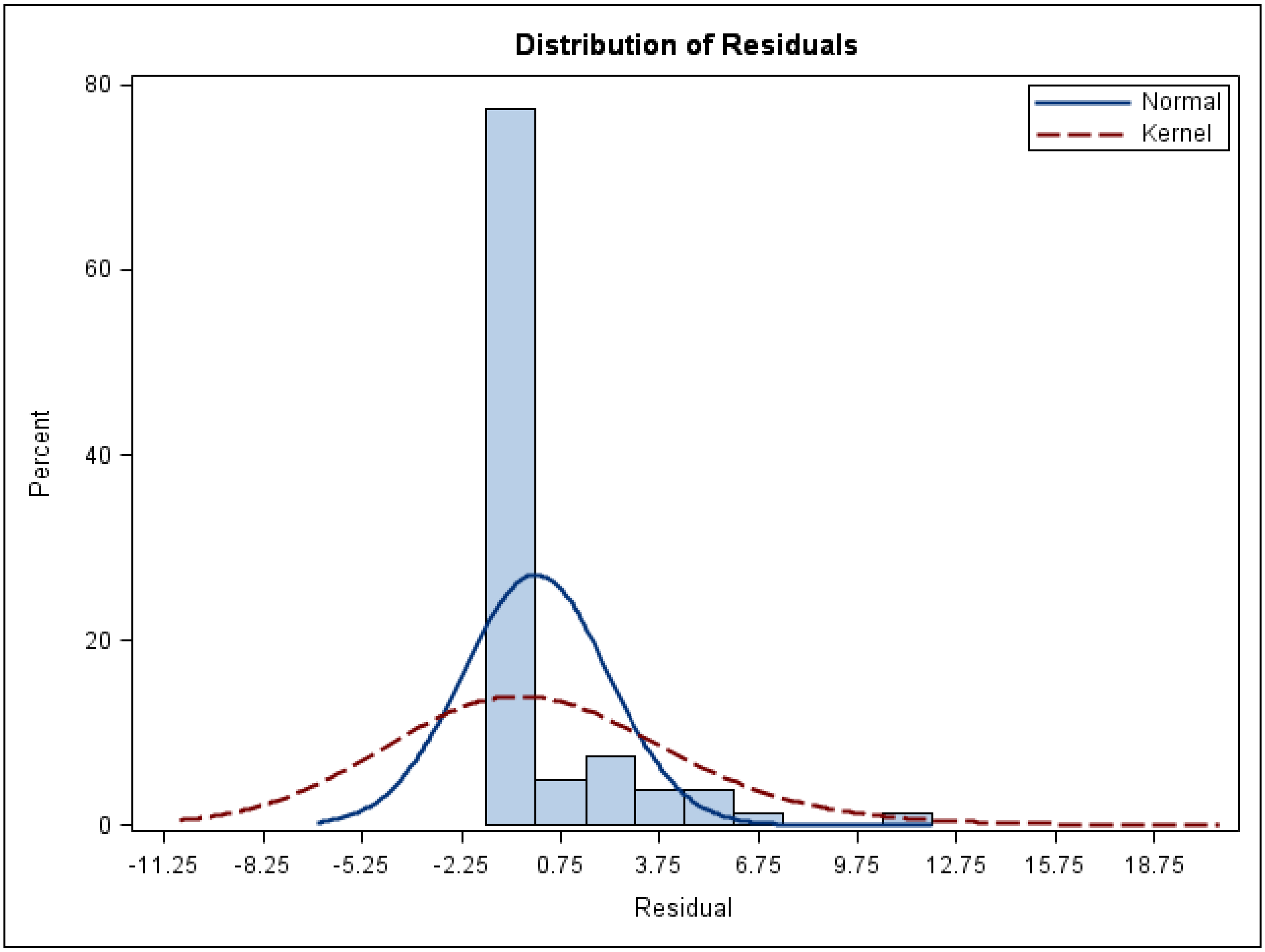


Figure E.6.3.2 Normal quantile plot of the raw residuals

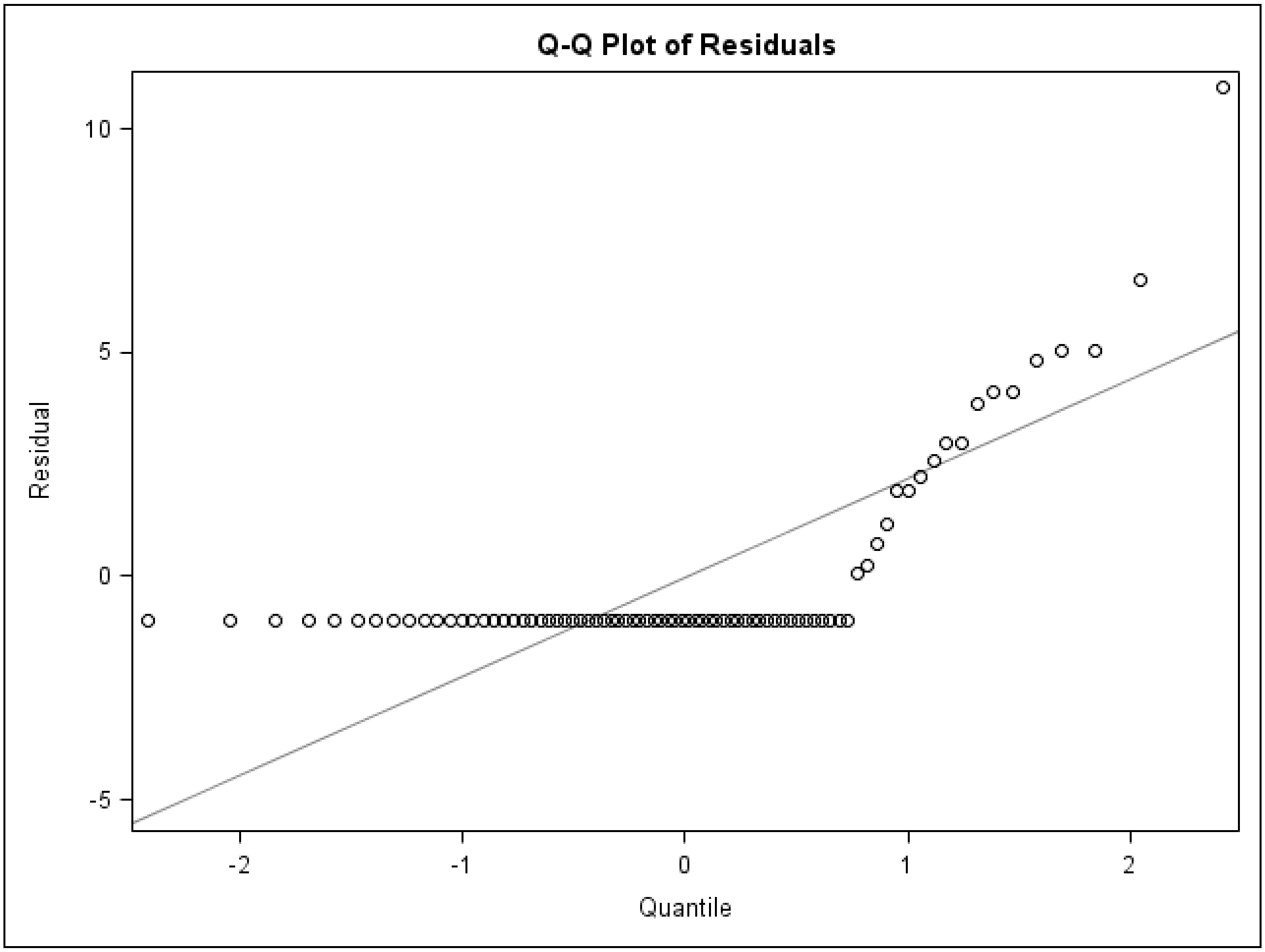


Figure E.6.3.3 Histogram of the Studentized residuals

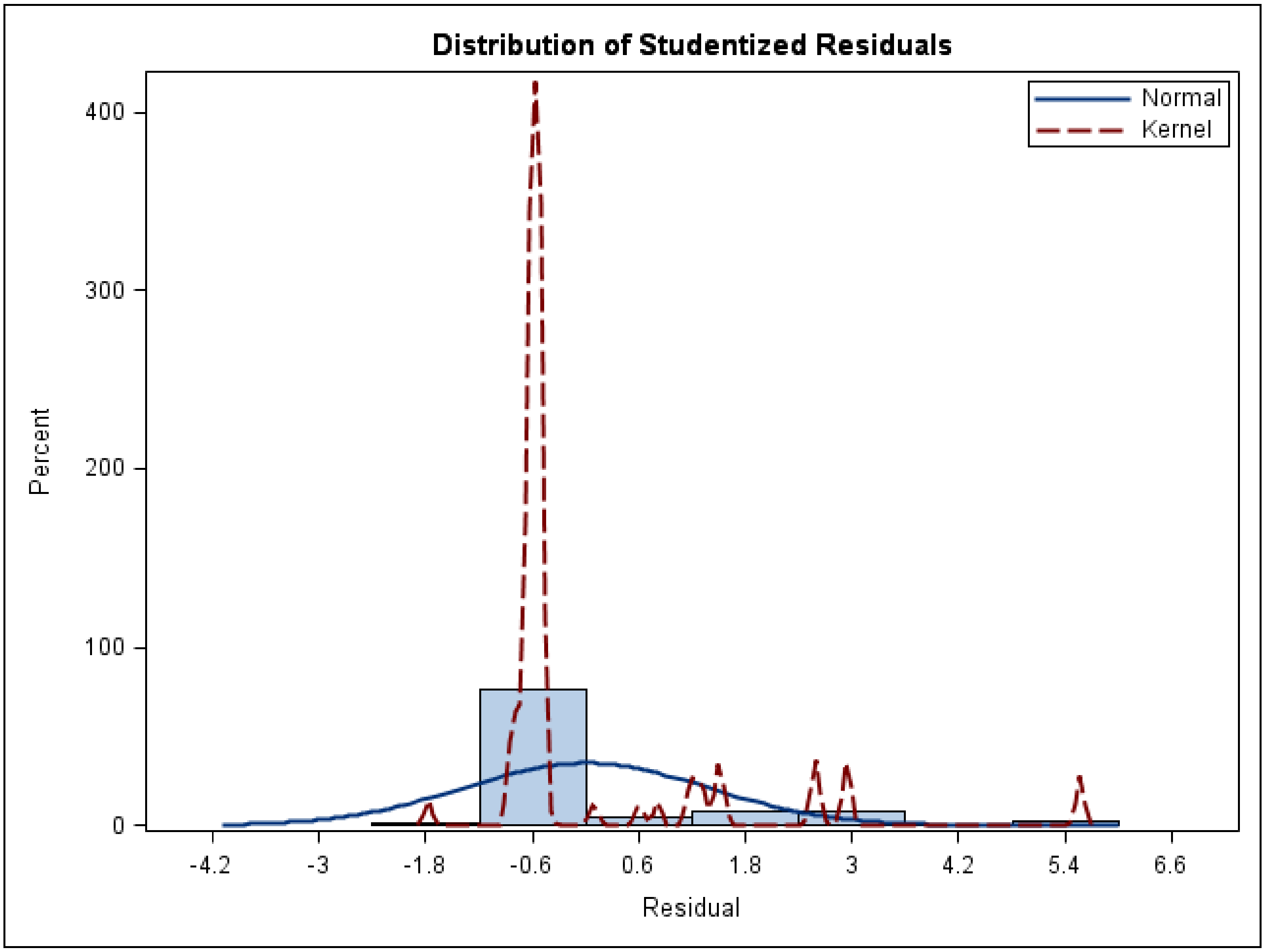


Figure E.6.3.4 Normal quantile plot of the Studentized residuals

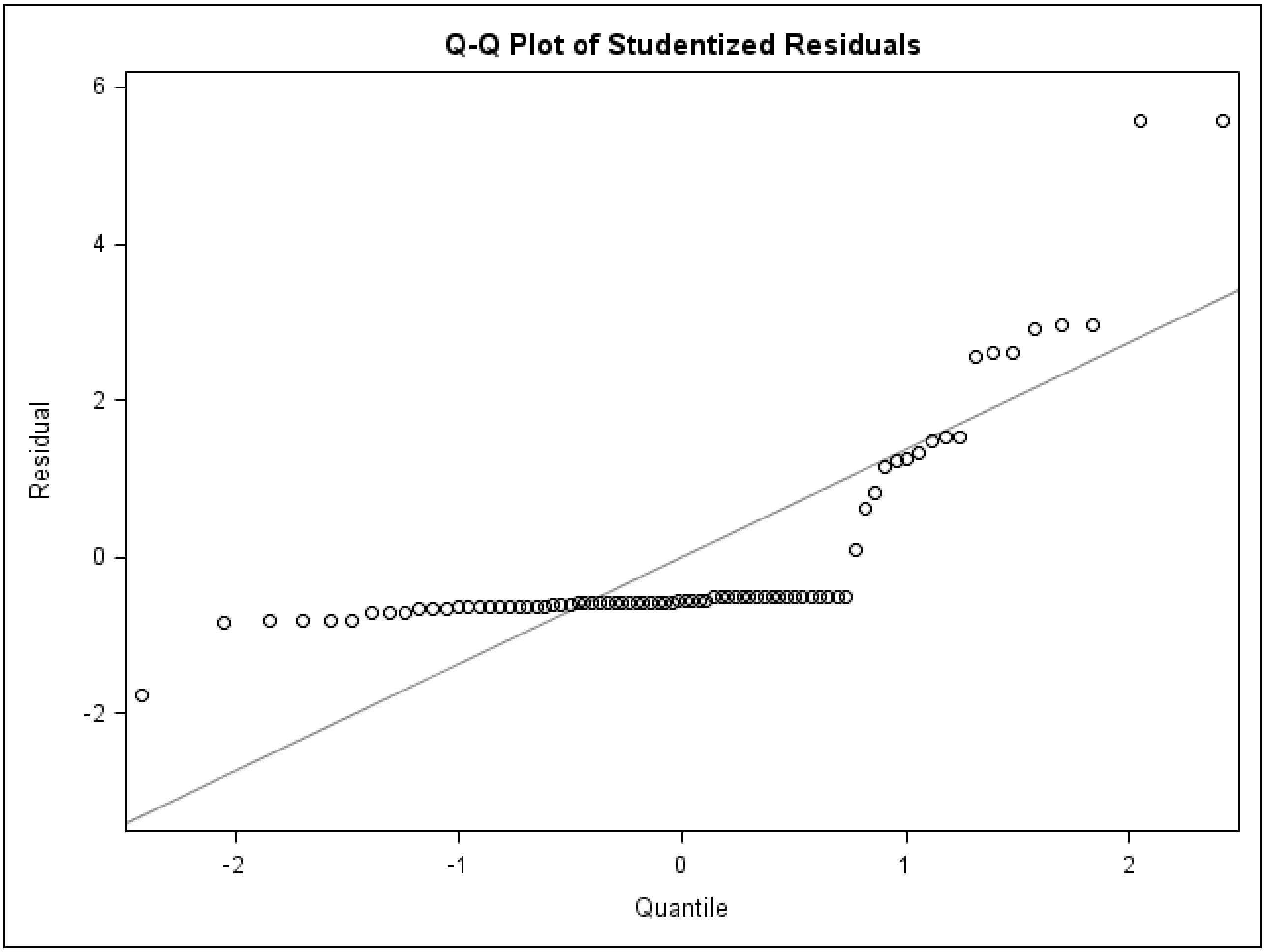


Figure E.6.3.5 Histogram of the Pearson residuals

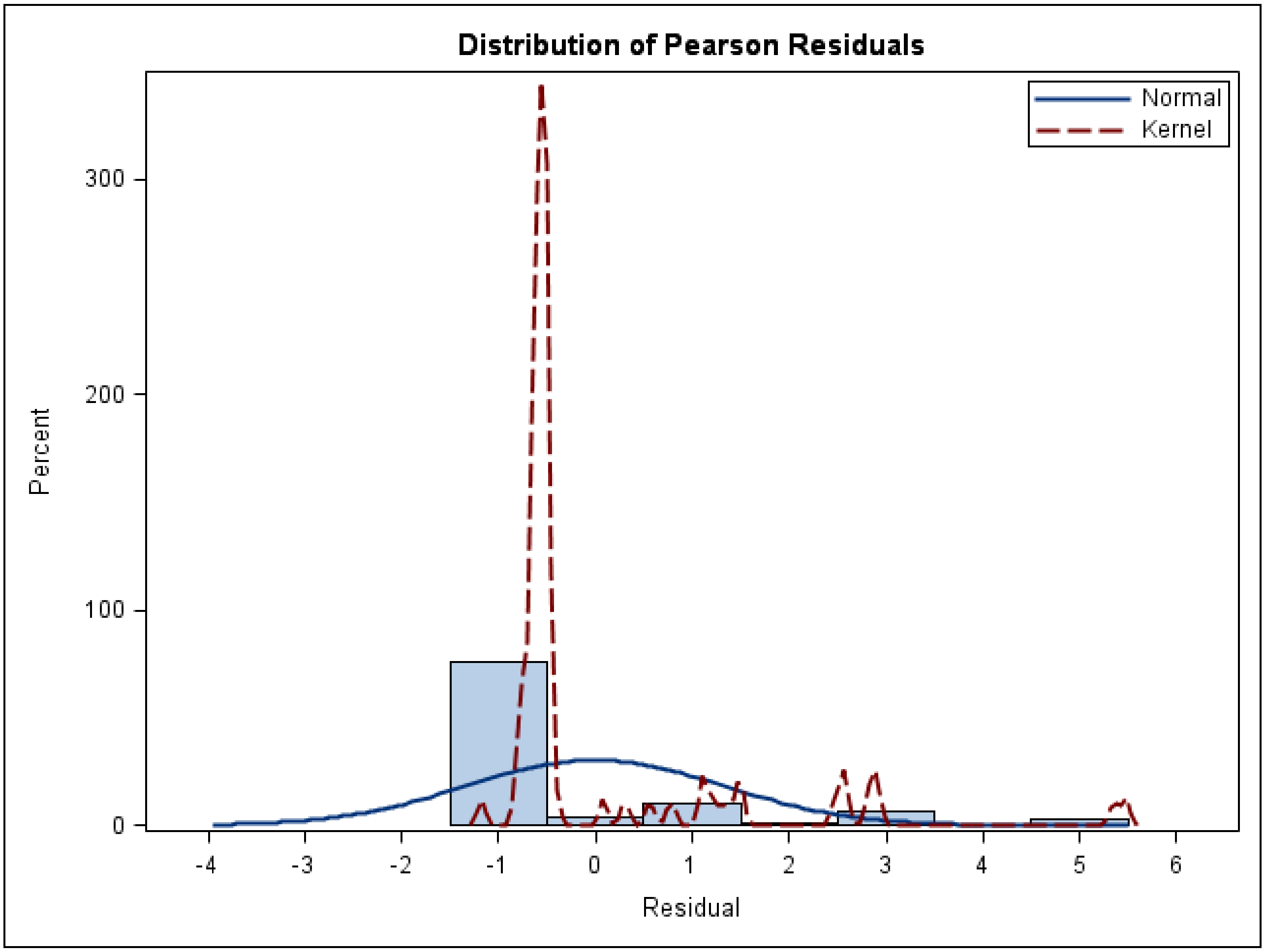
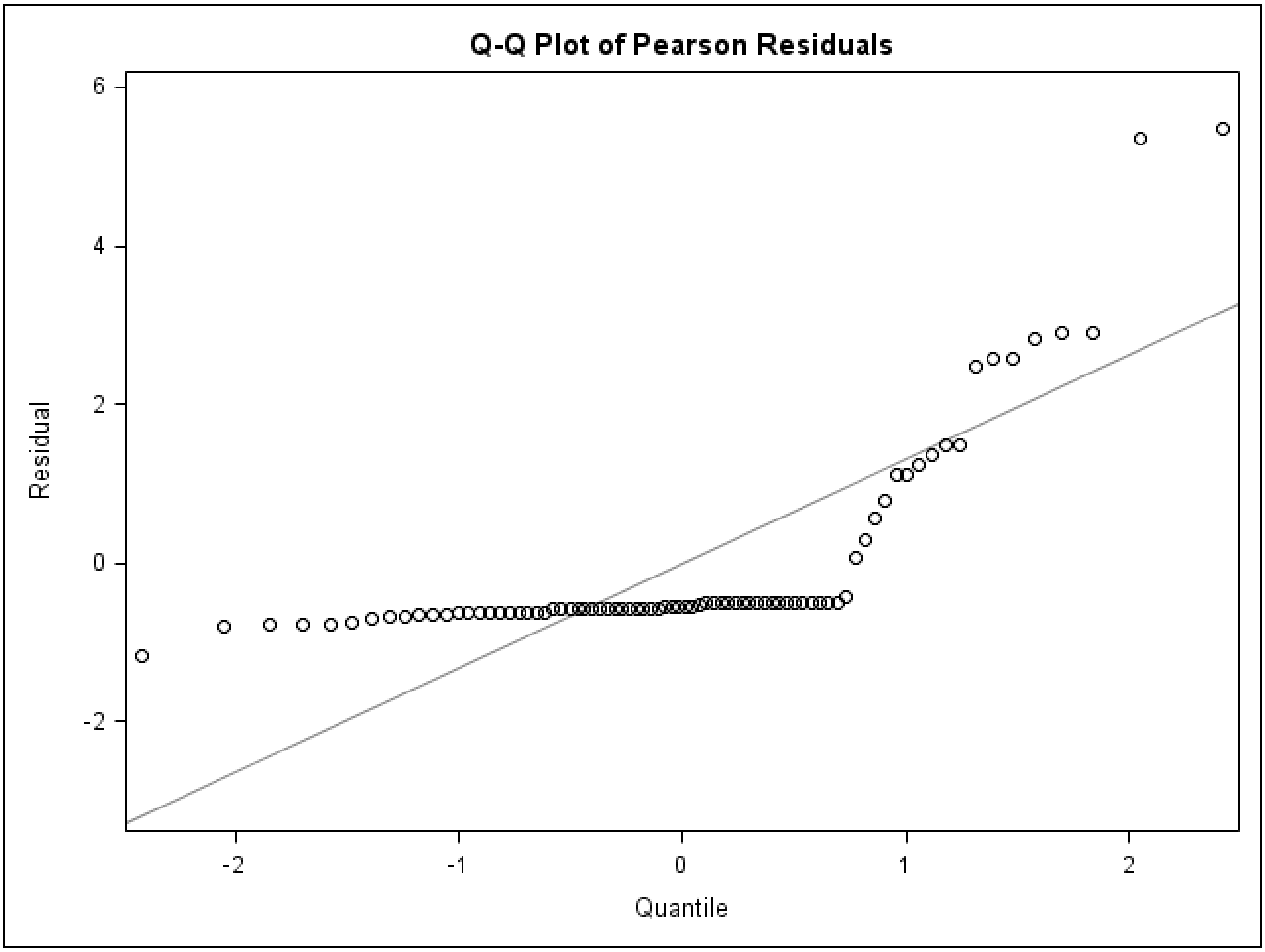


Figure E.6.3.6 Normal quantile plot of the Pearson residuals



E.6.4 September 2006 Model 4 Residual Plots

Figure E.6.4.1 Histogram of the raw residuals

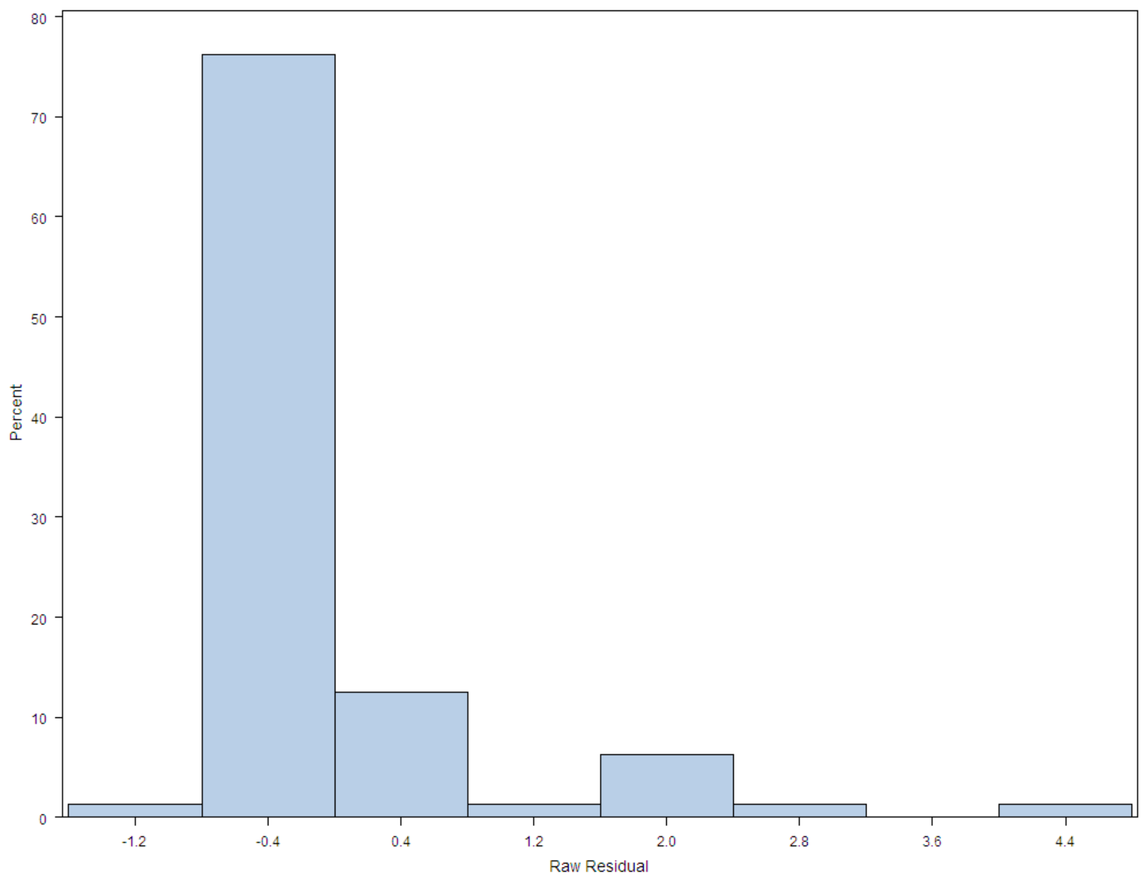


Figure E.6.4.2 Histogram of the Pearson residuals

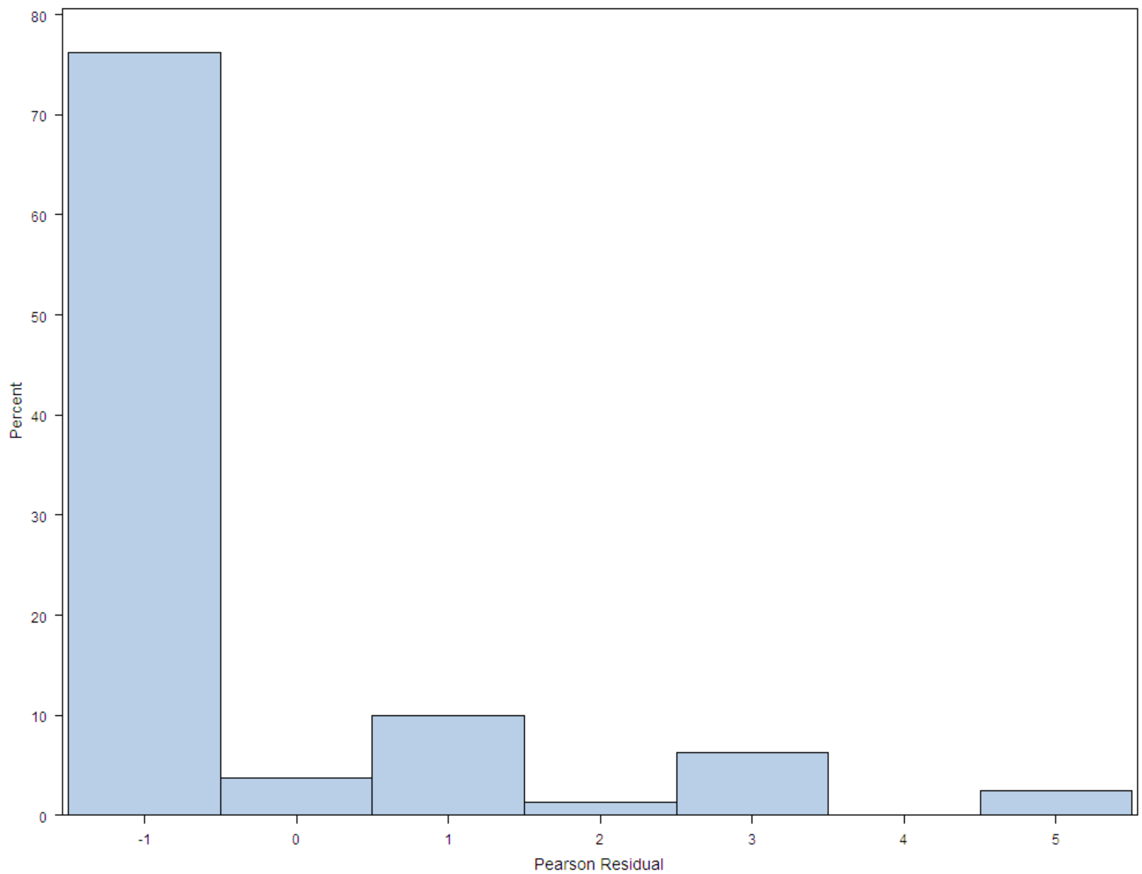


Figure E.6.4.3 Histogram of the deviance residuals

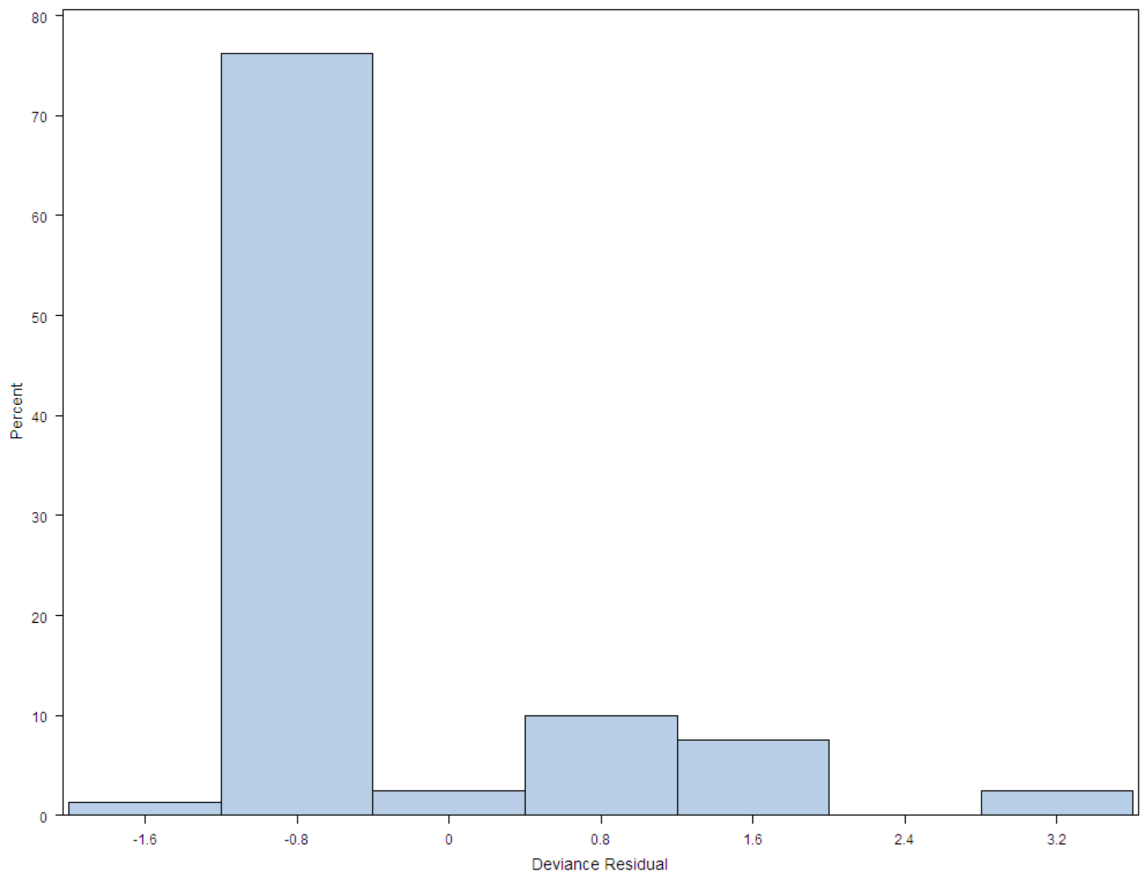


Figure E.6.4.4 Histogram of the likelihood residuals

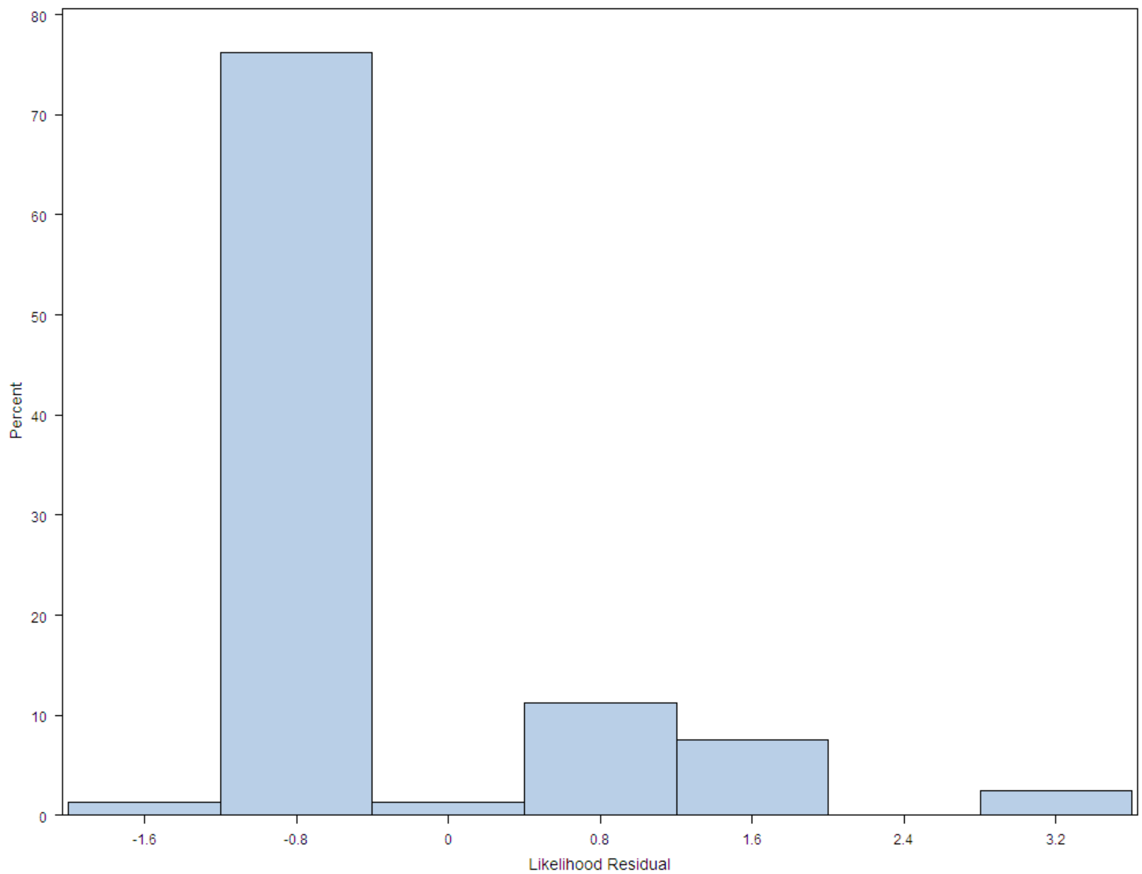


Figure E.6.4.5 Histogram of the standardized Pearson residuals

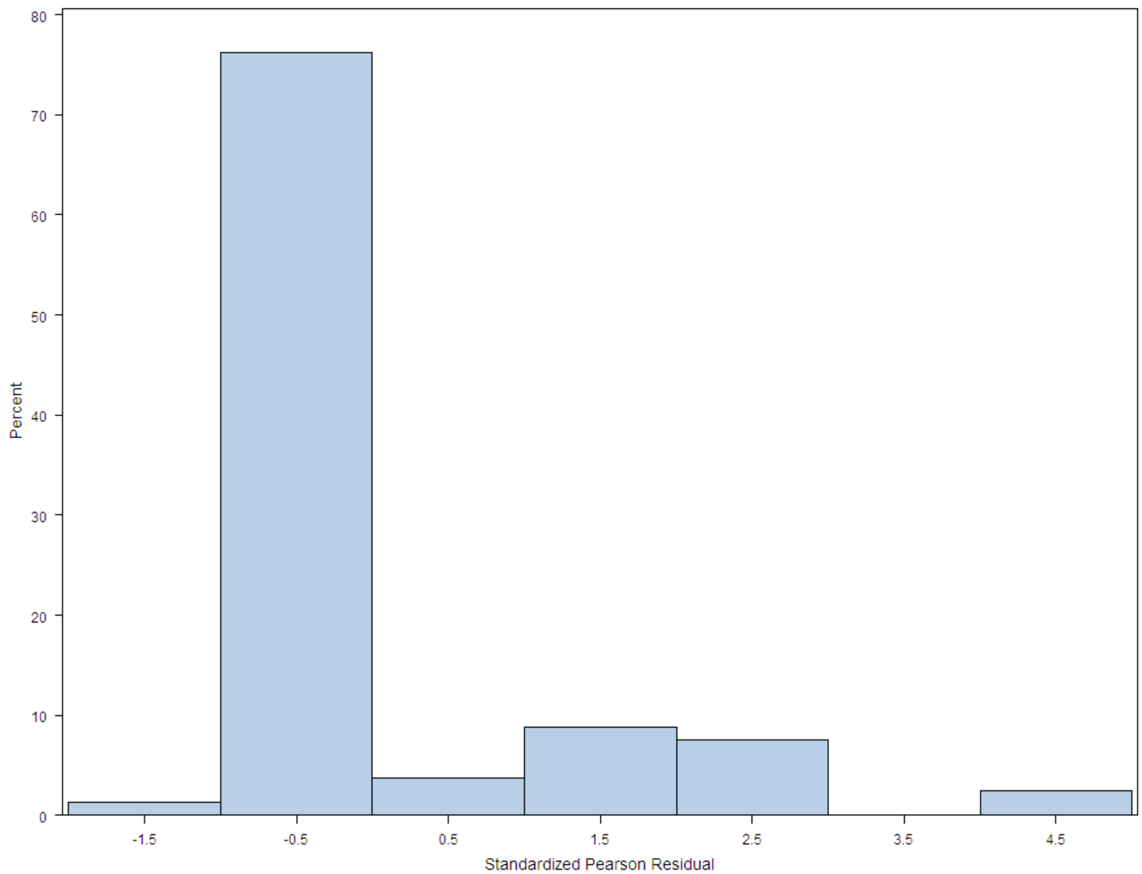
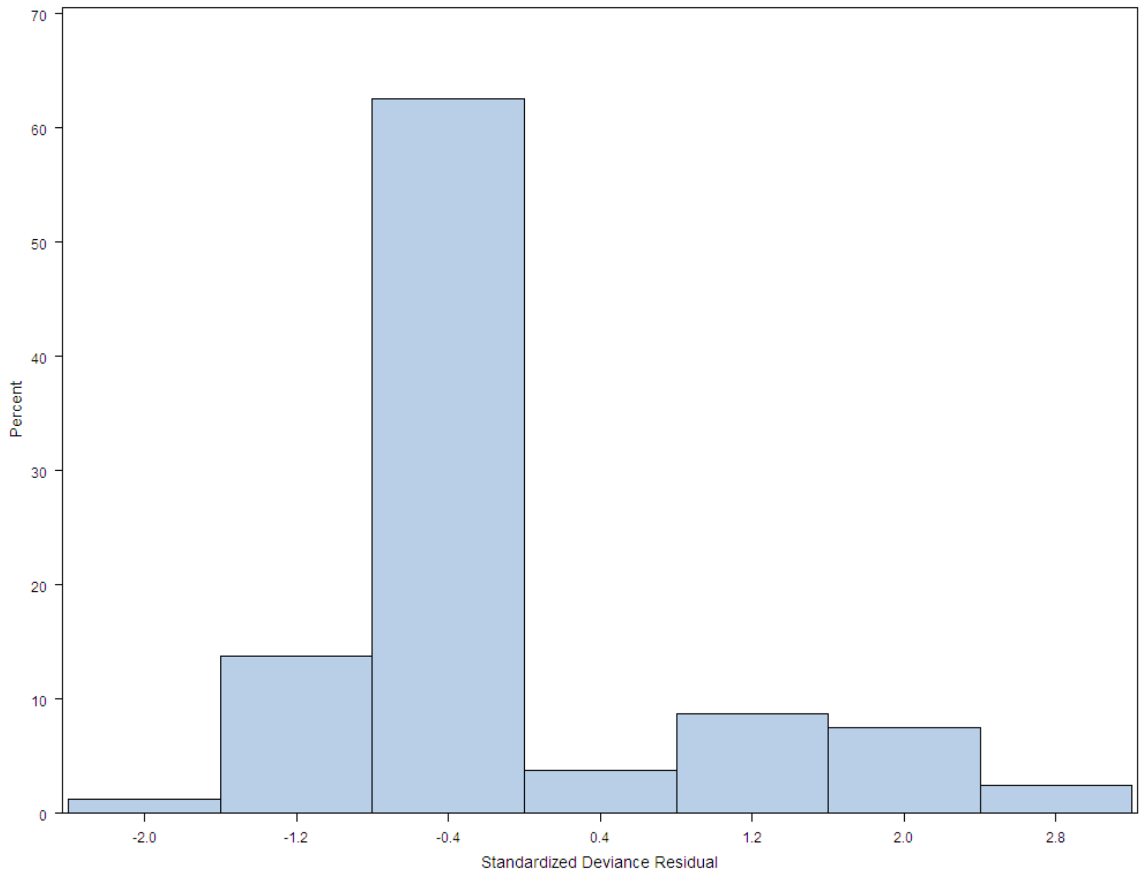


Figure E.6.4.6 Histogram of the standardized deviance residuals



E.6.5 September 2006 Model 5 Residual Plots

Figure E.6.5.1 Histogram of the raw residuals

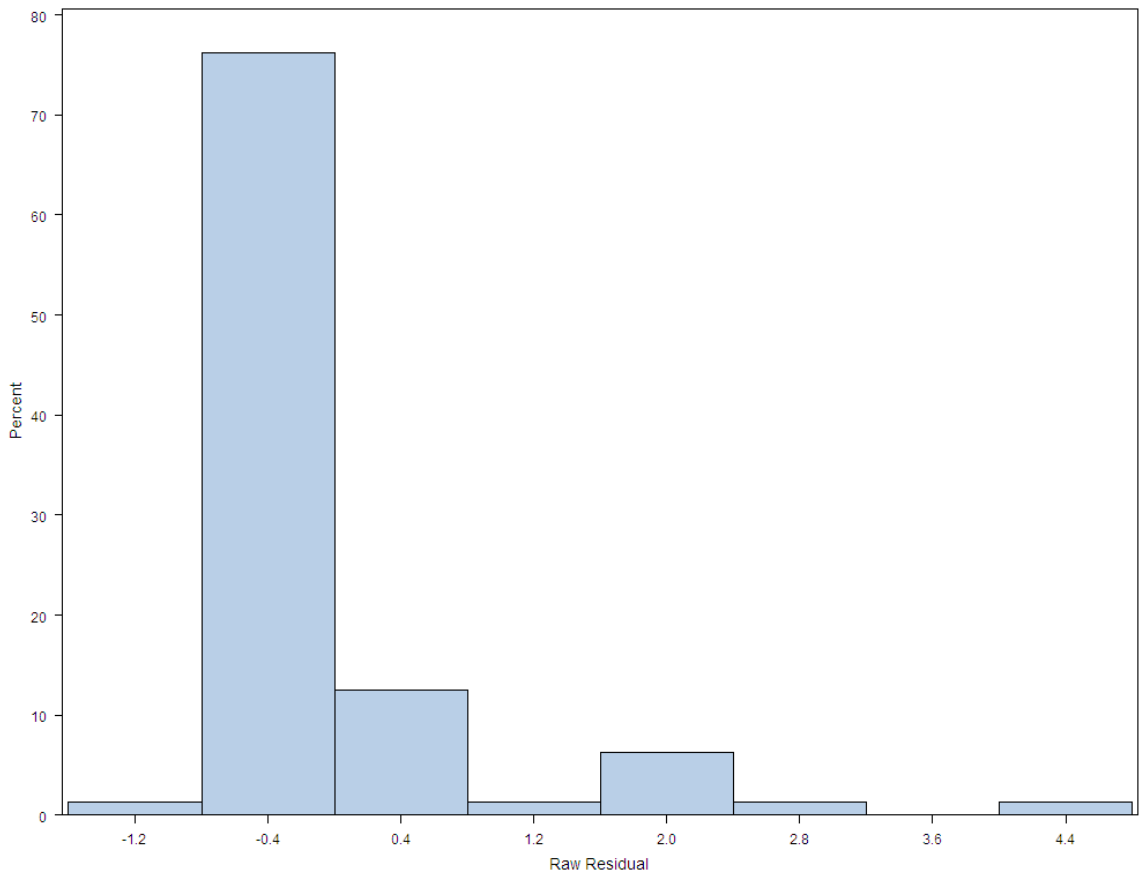


Figure E.6.5.2 Histogram of the Pearson residuals

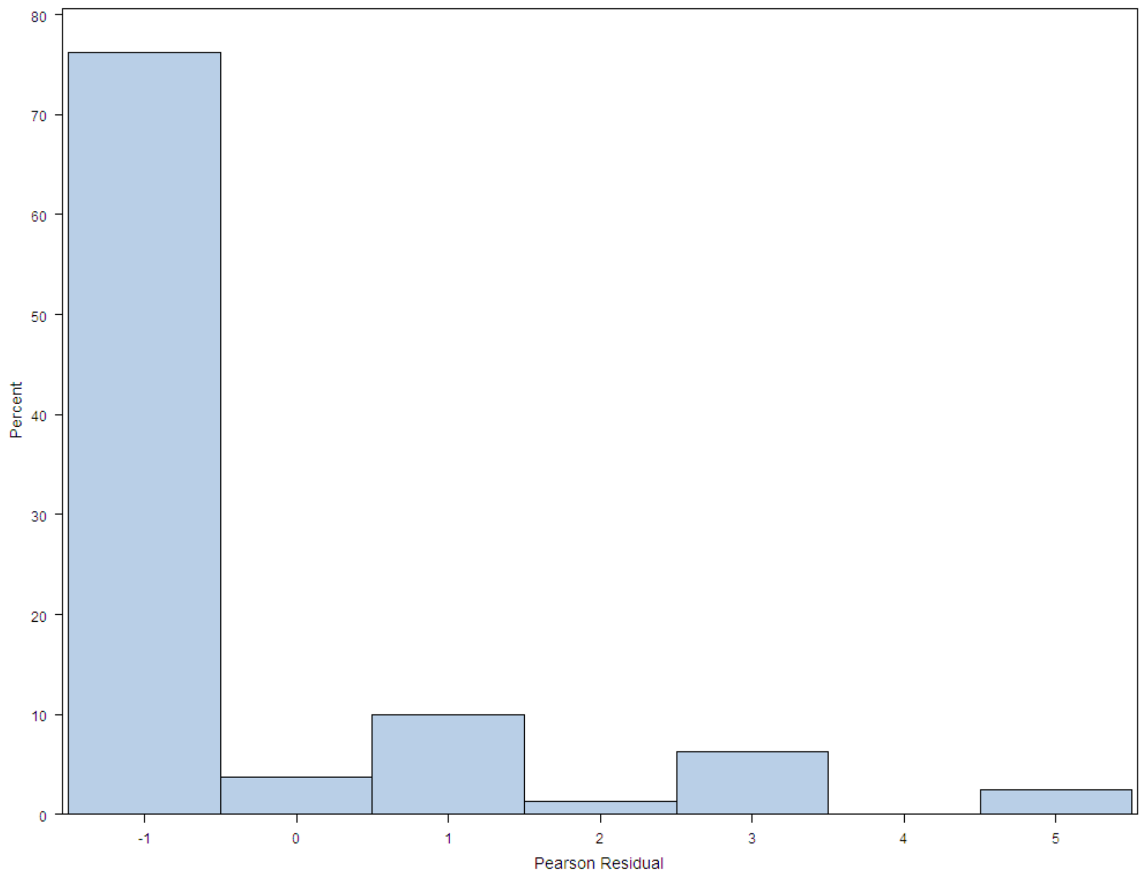


Figure E.6.5.3 Histogram of the deviance residuals

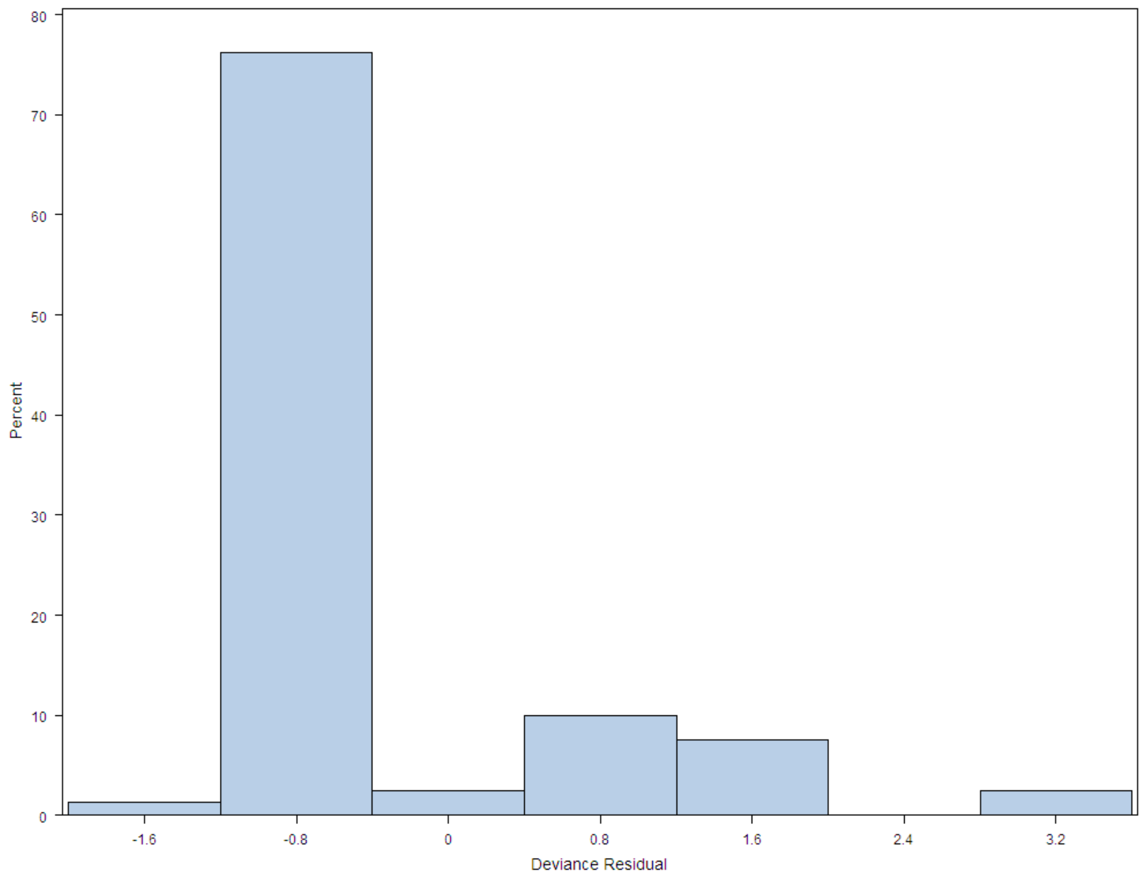


Figure E.6.5.4 Histogram of the likelihood residuals

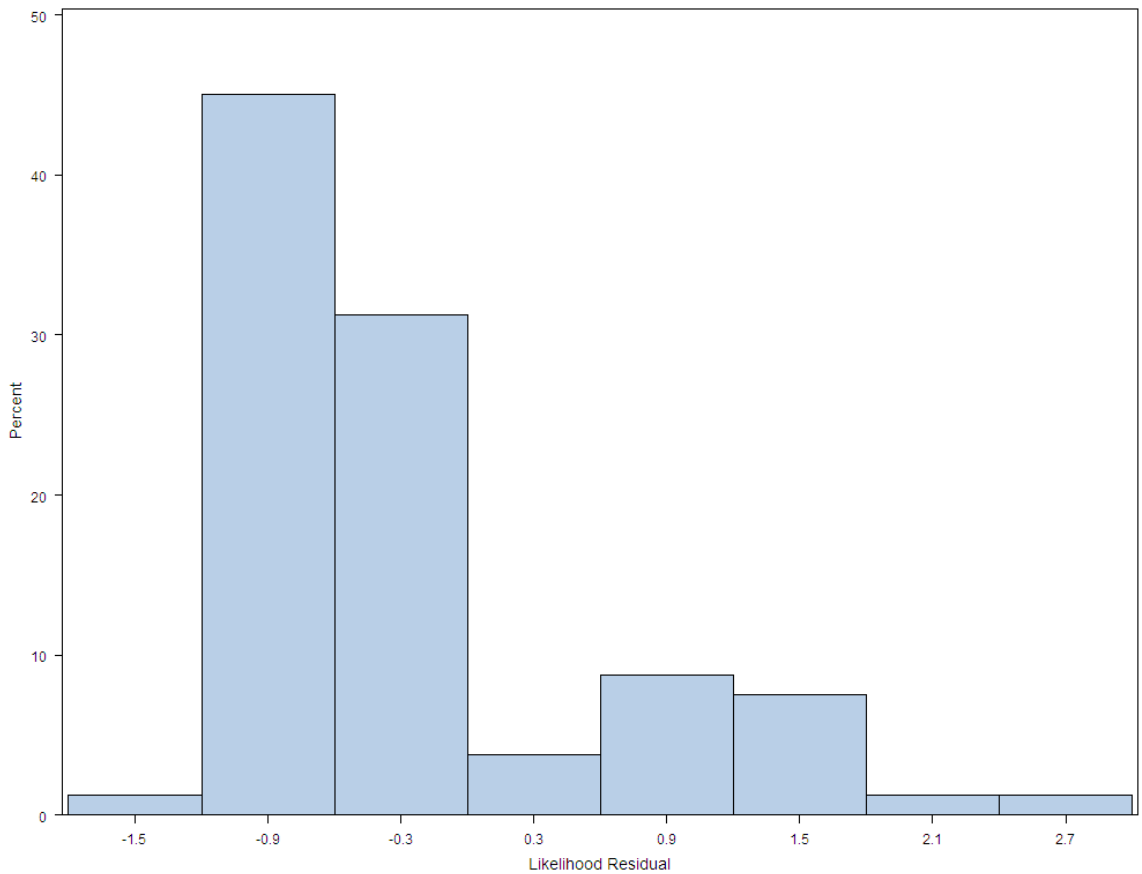


Figure E.6.5.5 Histogram of the standardized Pearson residuals

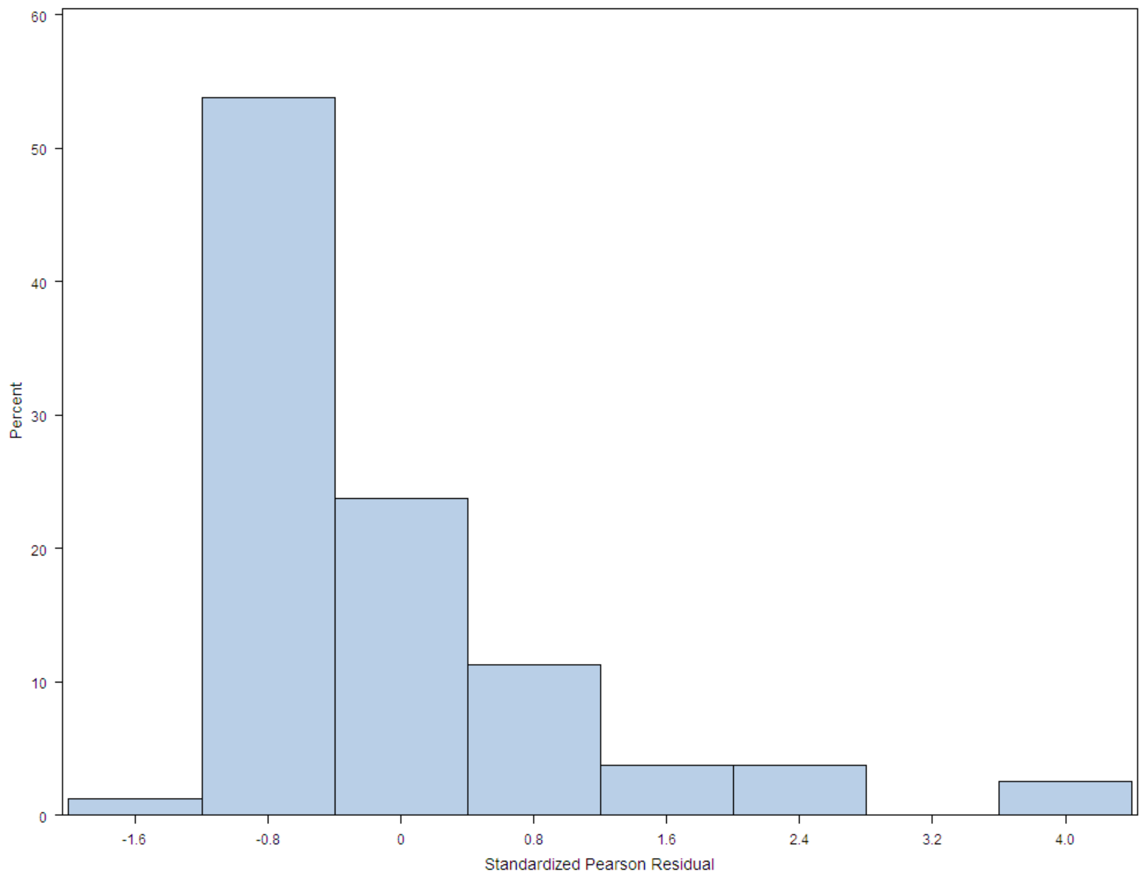
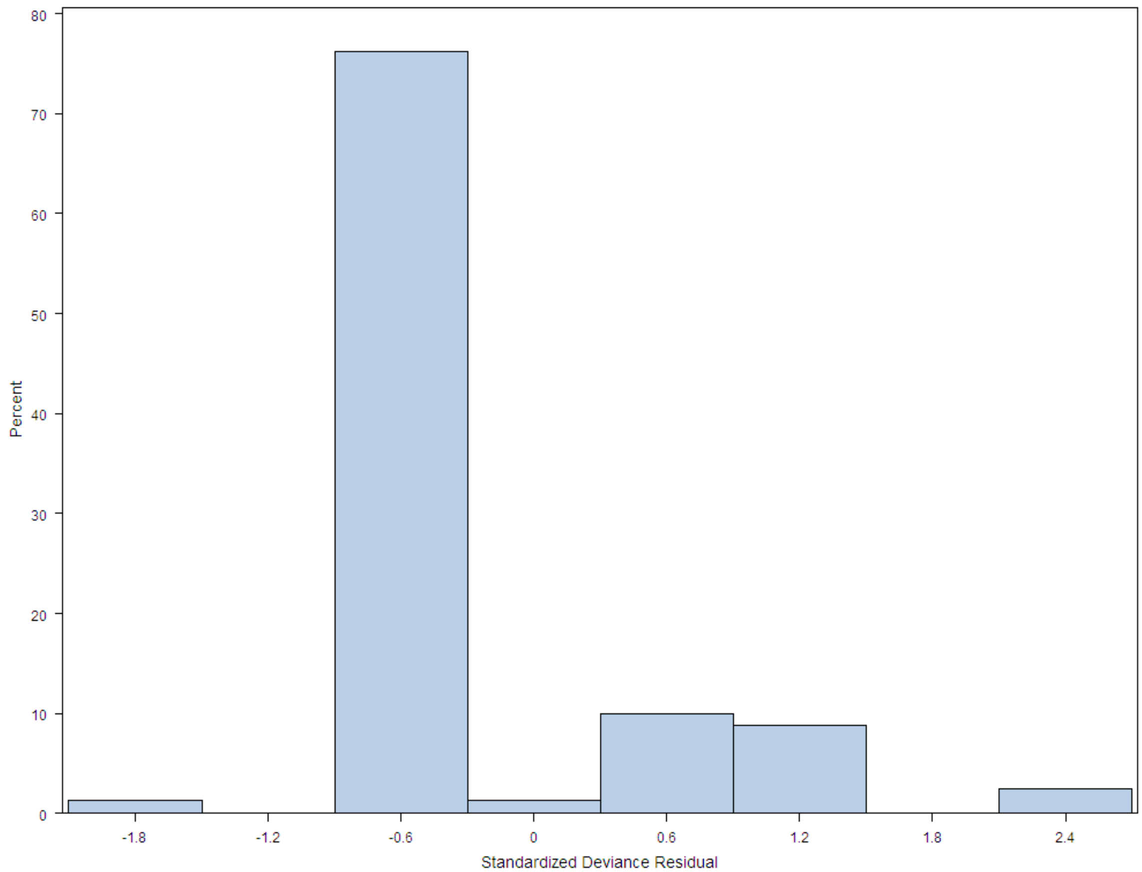


Figure E.6.5.6 Histogram of the standardized deviance residuals



E.6.6 September 2006 Model 6 Residual Plots

Figure E.6.6.1 Histogram of the raw residuals

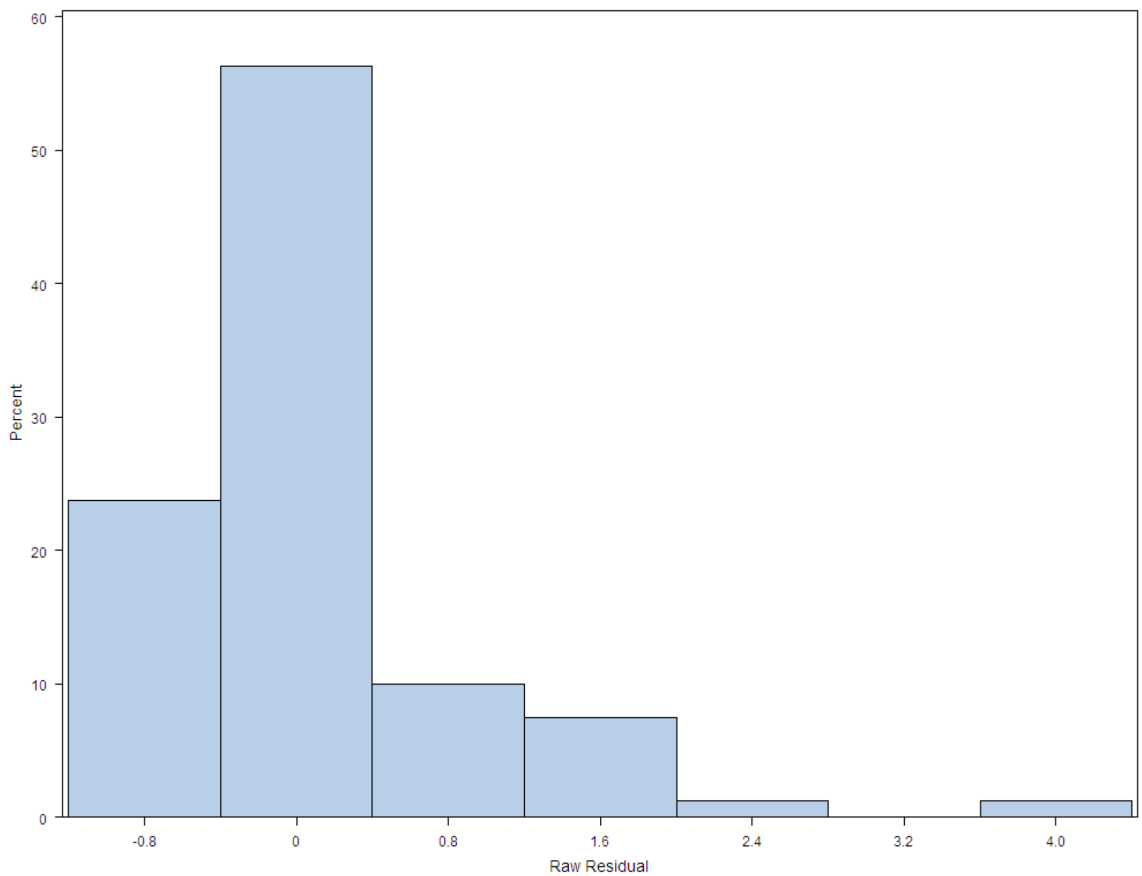
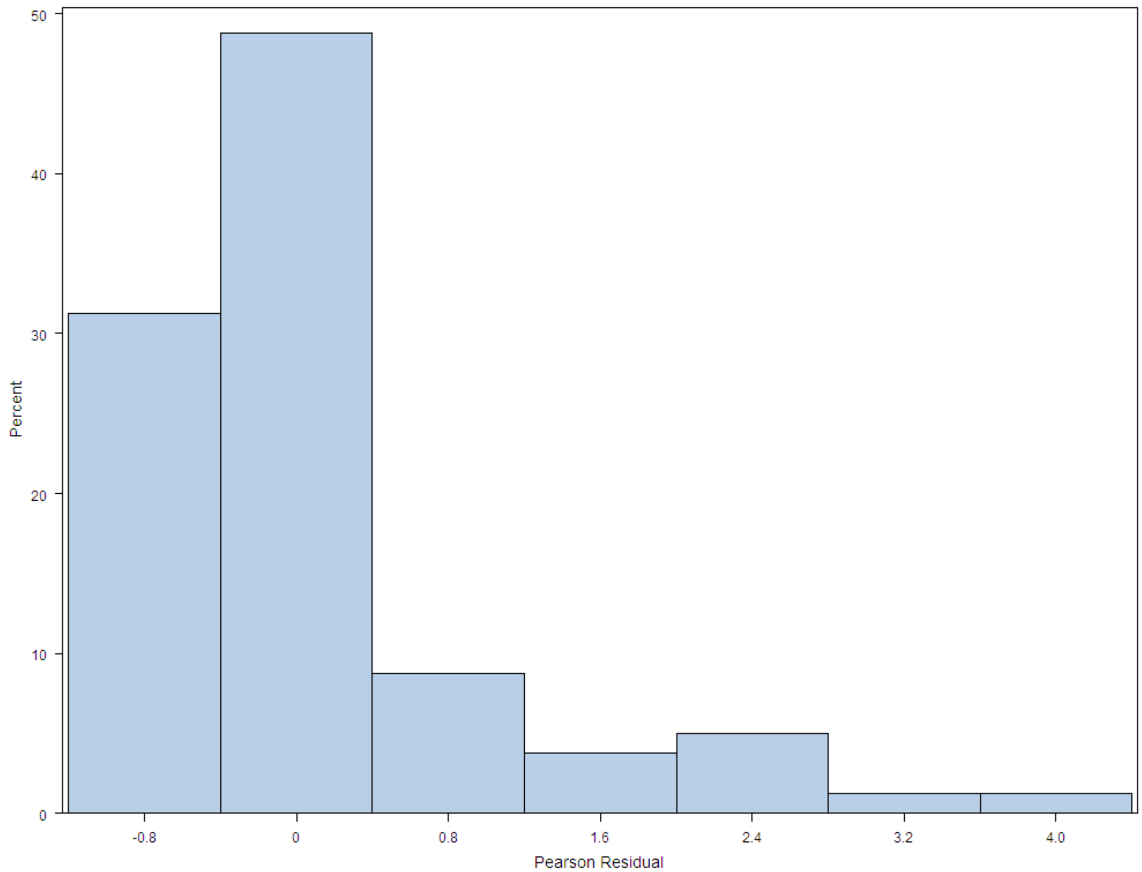


Figure E.6.6.2 Histogram of the Pearson residuals



E.6.7 September 2006 Model 7 Residual Plots

Figure E.6.7.1 Histogram of the raw residuals

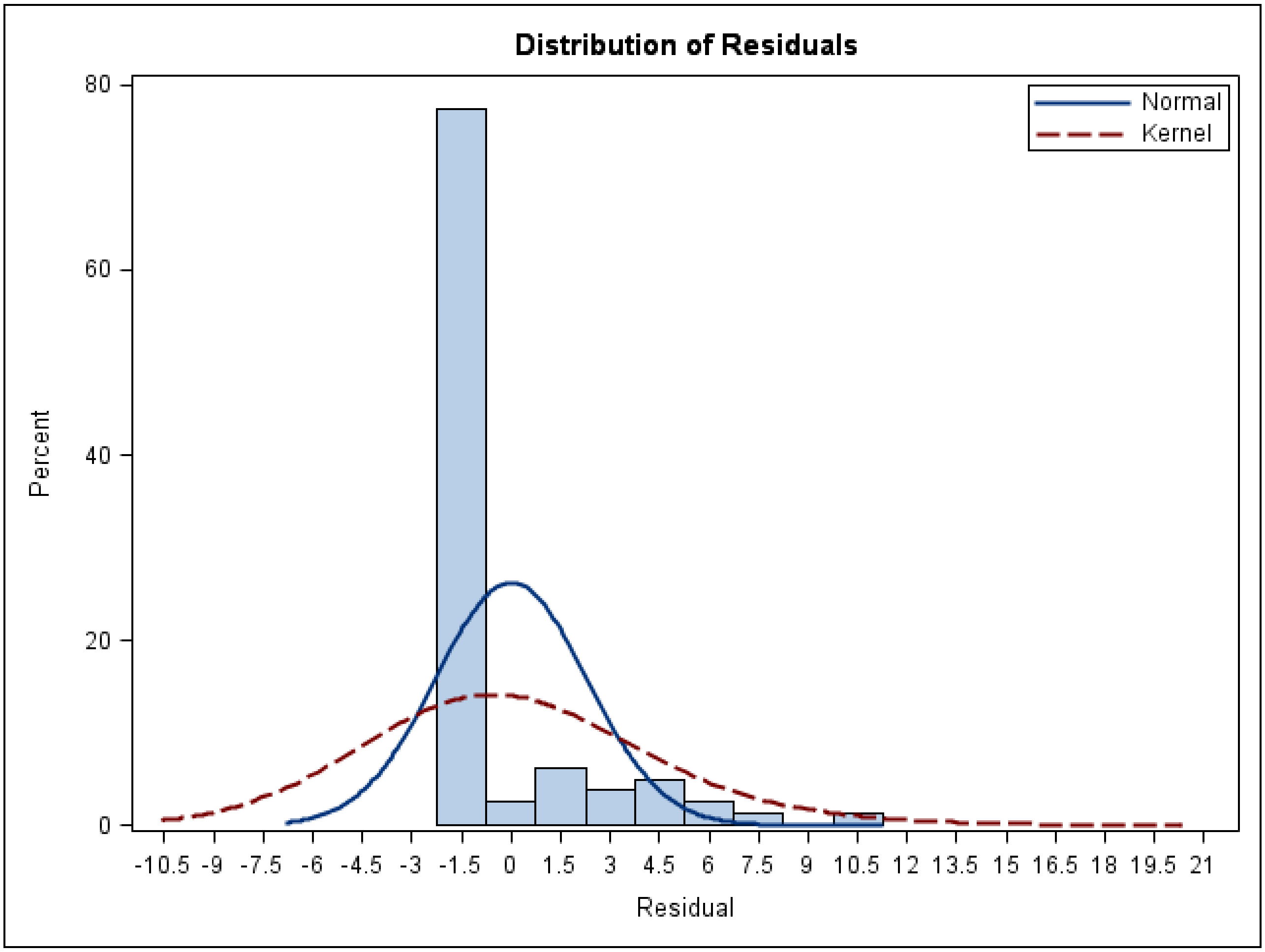


Figure E.6.7.2 Normal quantile plot of the raw residuals

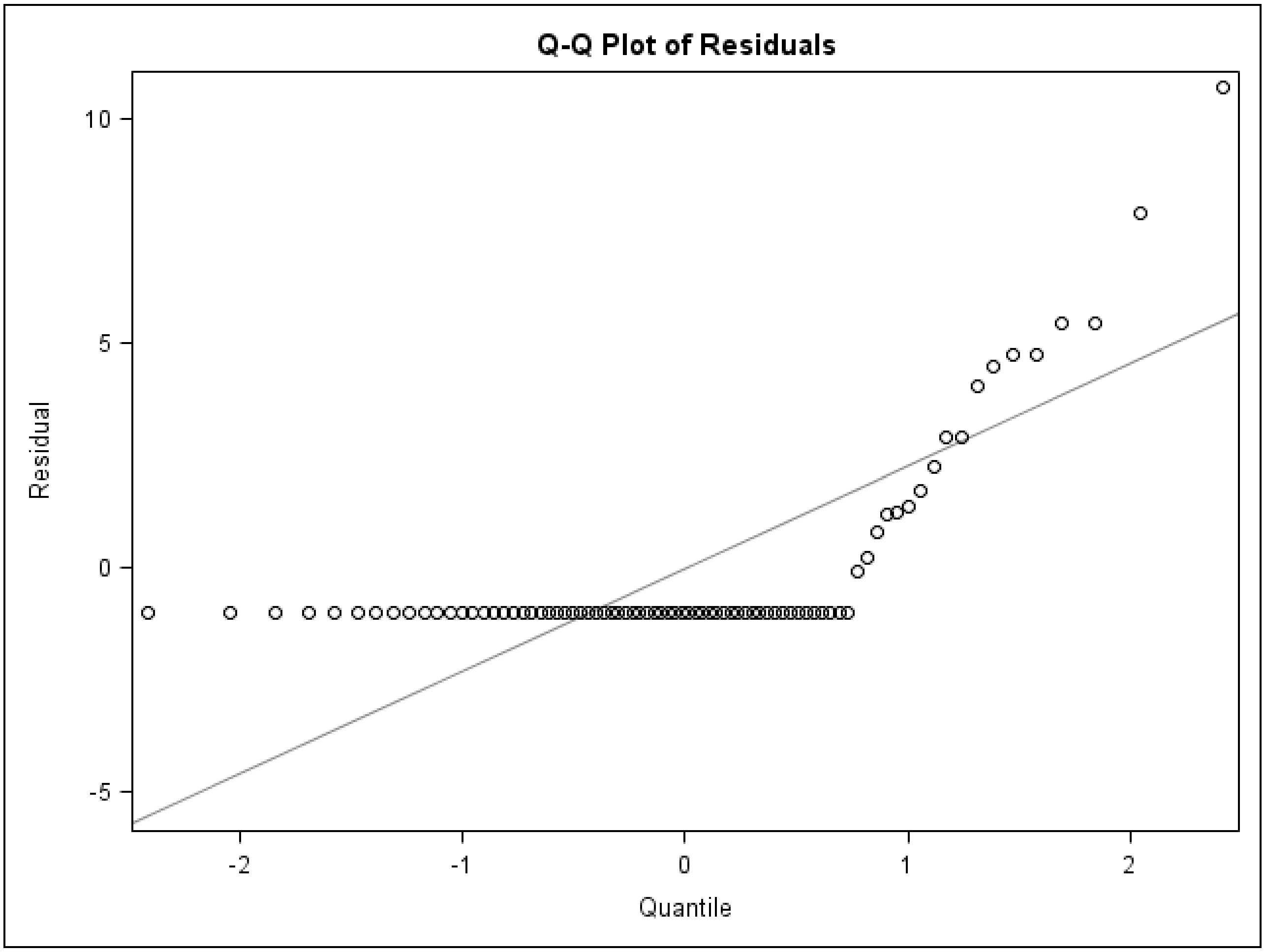


Figure E.6.7.3 Histogram of the Studentized residuals

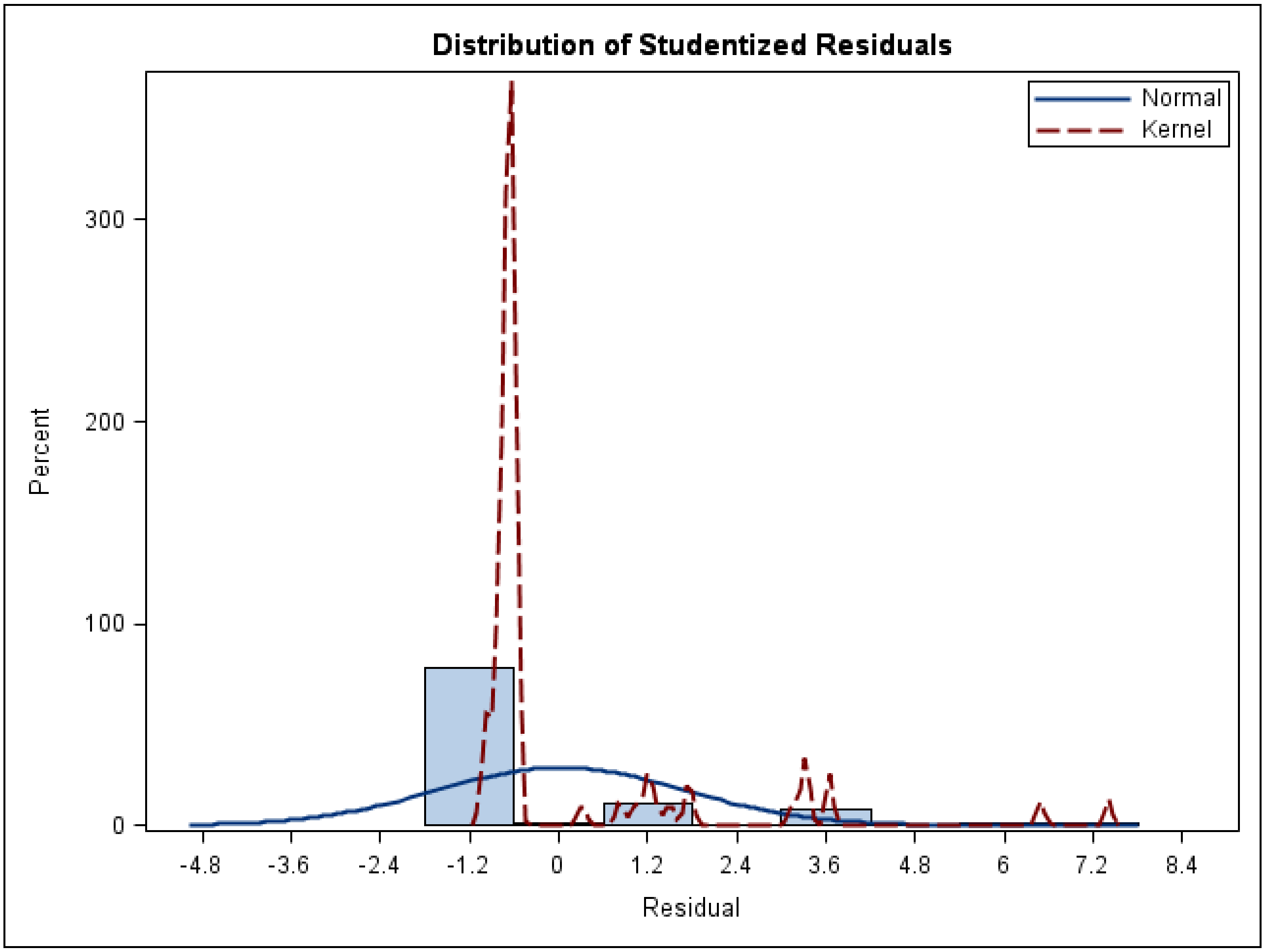


Figure E.6.7.4 Normal quantile plot of the Studentized residuals

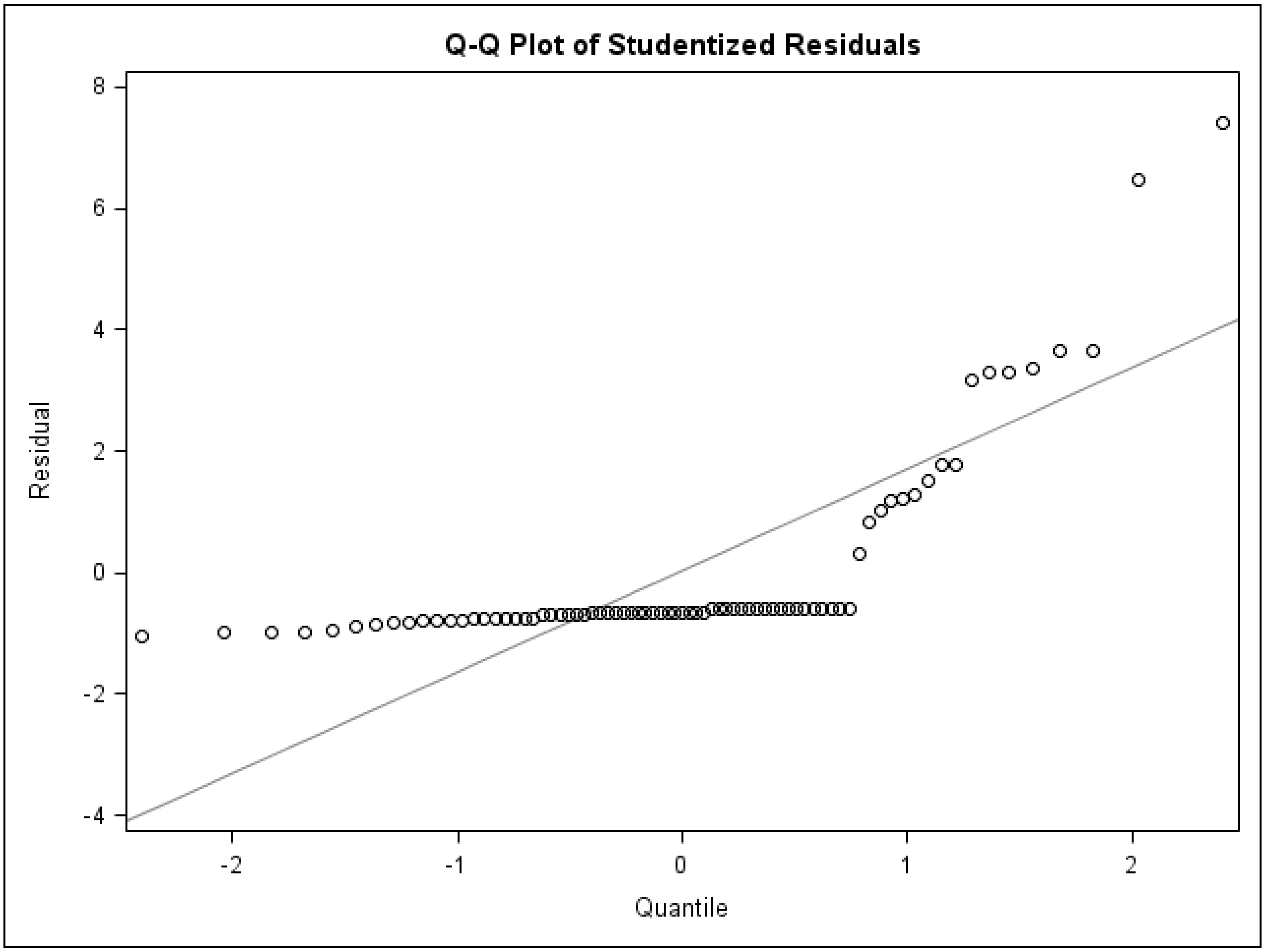


Figure E.6.7.5 Histogram of the Pearson residuals

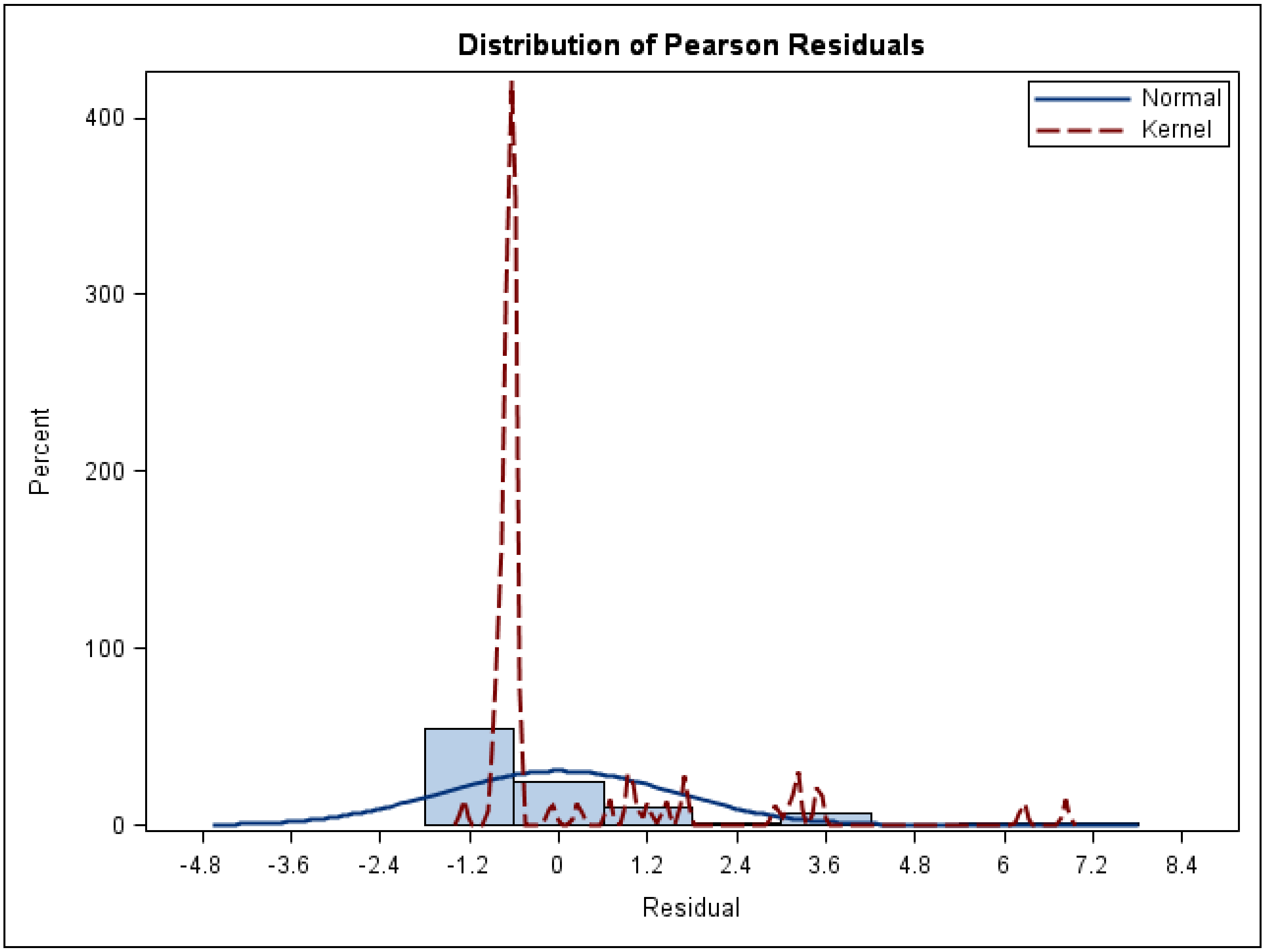
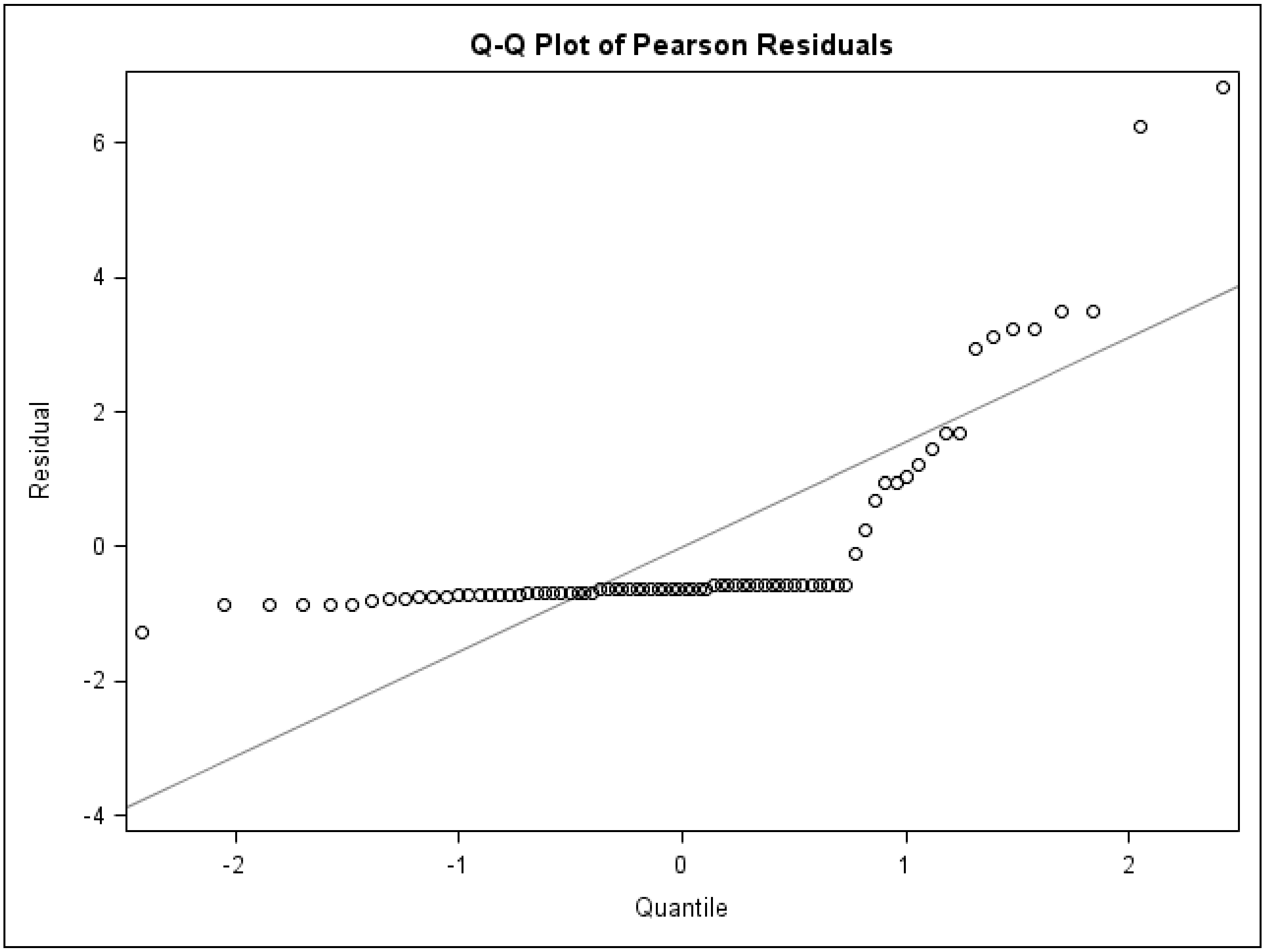
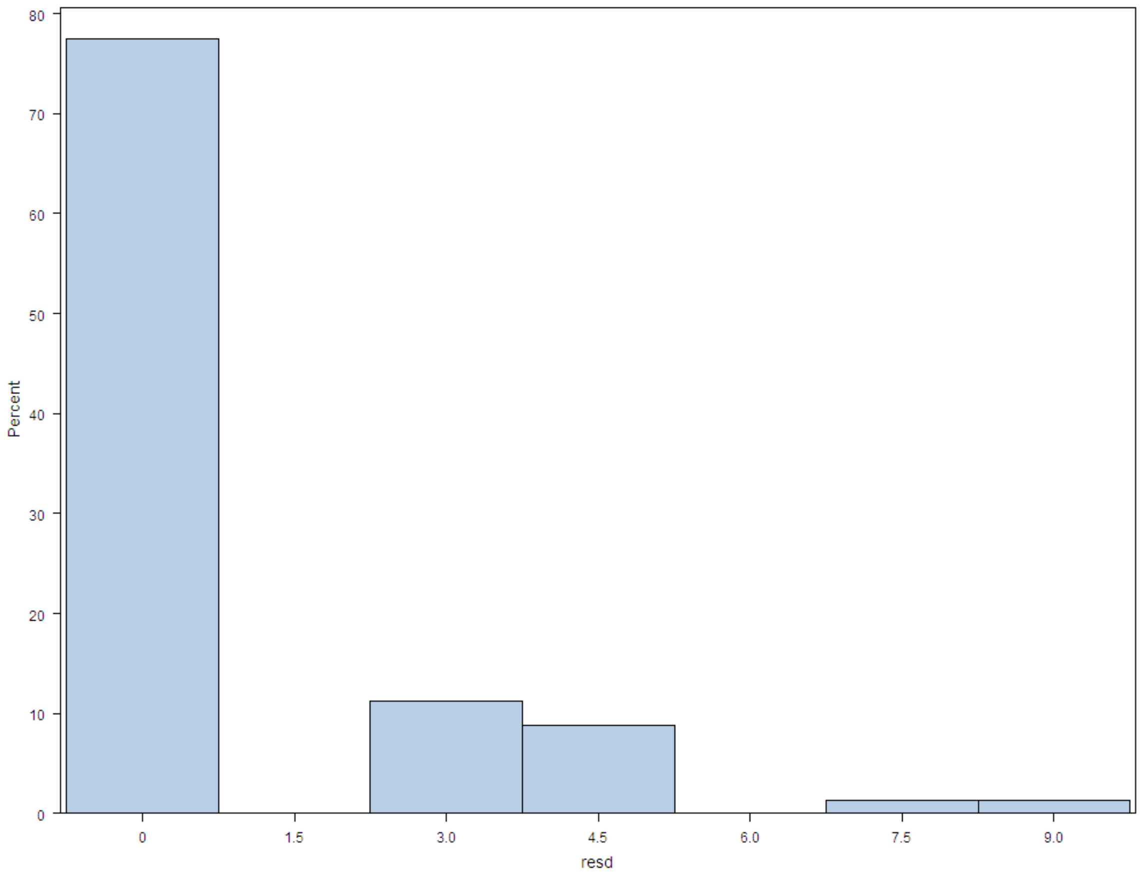


Figure E.6.7.6 Normal quantile plot of the Pearson residuals



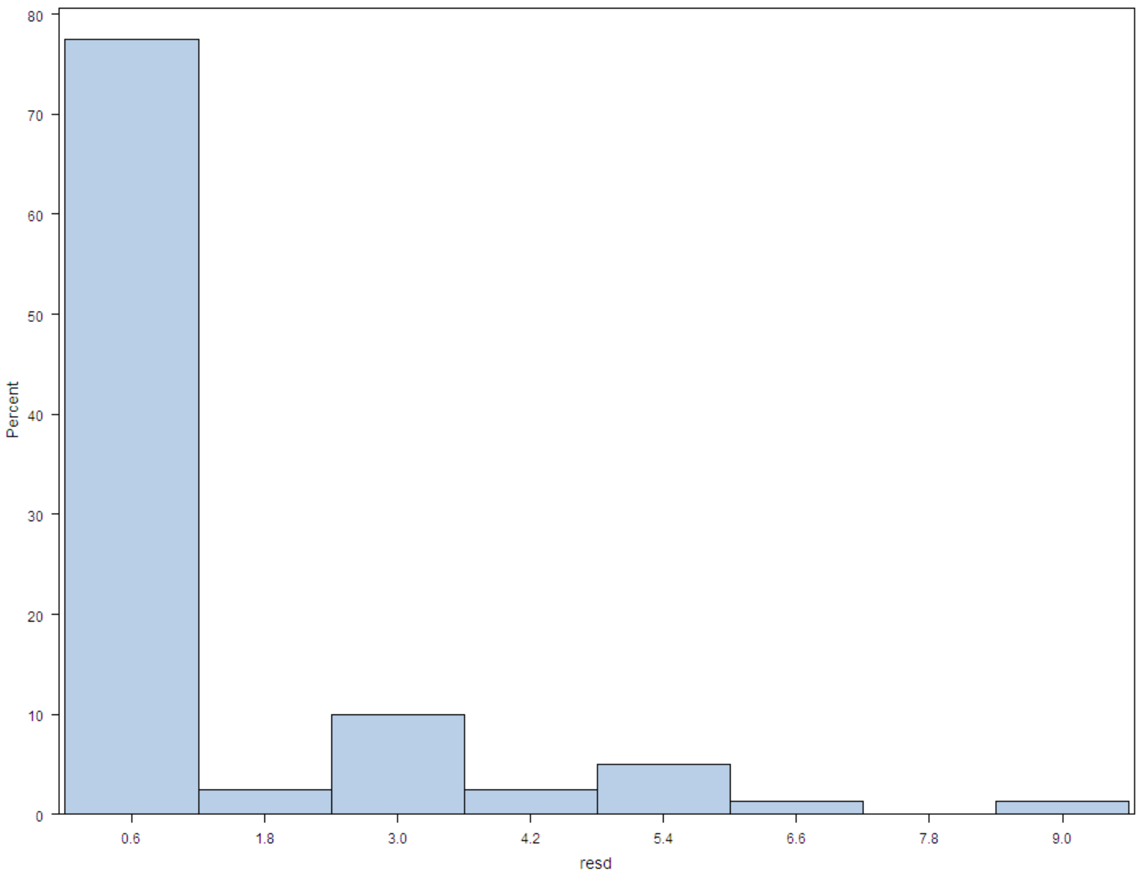
E.6.8 September 2006 Model 8 Residual Plots

Figure E.6.8.1 Histogram of the raw residuals



E.6.9 September 2006 Model 9 Residual Plots

Figure E.6.9.1 Histogram of the raw residuals



Appendix F - Mean and variance calculation for the Poisson hurdle distribution

Suppose

$$\Pr(Y = 0) = \pi$$

and

$$\Pr\{Y \sim truncatedPoisson(\lambda)\} = 1 - \pi$$

then

$$\Pr(Y = j) = \begin{cases} \pi & j = 0 \\ \dfrac{(1-\pi)(\lambda^j)\exp(-\lambda)}{j![1-\exp(-\lambda)]} & j = 1,2,3,\ldots \end{cases}$$

where $\Pr(Y = j)$ is the probability Y is equal to j, $0 < \pi < 1$ is the probability of observing at least one count given that there is at least one count, and $\lambda > 0$ is the parameter of the truncated Poisson distribution, given by Grogger and Carson (1991), which describes how many counts are observed (Welsh et al., 1996) is called a Poisson hurdle distribution.

Equation F.1 - Mean

$$E[Y] = \sum_{i=0}^{\infty} j \cdot \Pr(Y = j) = 0 \cdot \pi + \sum_{i=1}^{\infty} \frac{j \cdot (1-\pi)(\lambda^j)\exp(-\lambda)}{j![1-\exp(-\lambda)]} = \frac{(1-\pi)\exp(-\lambda)}{[1-\exp(-\lambda)]}\left[\sum_{i=1}^{\infty} \frac{j \cdot (\lambda^j)}{j!}\right]$$

$$= \frac{(1-\pi)\exp(-\lambda)}{[1-\exp(-\lambda)]}\left[\sum_{i=1}^{\infty} \frac{j \cdot (\lambda^j)}{j!} + \frac{0 \cdot \lambda^0}{0!} - \frac{0 \cdot \lambda^0}{0!}\right] = \frac{(1-\pi)\exp(-\lambda)}{[1-\exp(-\lambda)]}\left[\sum_{i=0}^{\infty} \frac{j \cdot (\lambda^j)}{j!}\right]$$

$$= \frac{(1-\pi)\exp(-\lambda)}{[1-\exp(-\lambda)]}\lambda\exp(\lambda) = \frac{\lambda(1-\pi)}{[1-\exp(-\lambda)]} = \mu$$

Equation F.2 - Variance

$$Var[Y] = E[Y^2] - E[Y]^2$$

so

$$E[Y]^2 = \left[\frac{\lambda(1-\pi)}{[1-\exp(-\lambda)]}\right]^2 = \frac{\lambda^2(1-\pi)^2}{[1-\exp(-\lambda)]^2} = \mu^2$$

and

$$E[Y^2] = \sum_{i=0}^{\infty} j^2 \cdot \Pr(Y = j) = 0^2\pi + \sum_{i=1}^{\infty} \frac{j^2 \cdot (1-\pi)(\lambda^j)\exp(-\lambda)}{j![1-\exp(-\lambda)]} = \frac{(1-\pi)\exp(-\lambda)}{1-\exp(-\lambda)} \sum_{i=1}^{\infty} \frac{j^2 \cdot (\lambda^j)}{j!}$$

$$= \frac{(1-\pi)\exp(-\lambda)}{1-\exp(-\lambda)}\left[\sum_{i=1}^{\infty} \frac{j^2 \cdot (\lambda^j)}{j!} + \frac{0^2 \cdot (0^j)}{0!} - \frac{0^2 \cdot (0^j)}{0!}\right] = \frac{(1-\pi)\exp(-\lambda)}{1-\exp(-\lambda)}\left[\sum_{i=0}^{\infty} \frac{j^2 \cdot (\lambda^j)}{j!}\right]$$

$$= \frac{(1-\pi)\exp(-\lambda)}{1-\exp(-\lambda)}(\lambda+\lambda^2)\exp(\lambda) = \frac{(1-\pi)(\lambda+\lambda^2)}{1-\exp(-\lambda)} = \frac{\lambda(1-\pi)}{1-\exp(-\lambda)} + \lambda\frac{\lambda(1-\pi)}{1-\exp(-\lambda)} = \mu + \lambda\mu$$

so

$$Var[Y] = [\mu + \lambda\mu] - \mu^2 = \mu(1+\lambda) - \mu^2 .$$

Appendix G - Predicted values

Appendix G is made up of tables consisting of the actual RKN counts side by side with the predicted mean counts based on the fitted model from each of the eight studied models (Model 9 predicted counts were excluded).

Table G.1 – Predicted values for the May 2005 data

	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6	Model 7	Model 8
rkn	PrdCount	PrdCount	PrdCount	PrdCount	PrdCount	PrdCount	PrdCount	PrdCount
1	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
3	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
7	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
3	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
0	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
1	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
0	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
11	5.667	5.646	5.667	5.667	5.667	5.667	5.510	5.667
4	5.667	5.646	5.667	5.667	5.667	5.667	5.510	5.667
4	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
2	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
9	2.151	2.137	2.121	2.121	2.121	2.750	1.395	3.531
2	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
0	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
0	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
1	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
7	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
0	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
1	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
1	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
2	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
2	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
2	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
4	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
1	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
0	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
2	1.701	2.387	1.685	1.685	1.685	2.000	1.934	2.440
4	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
0	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
0	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207

0	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
0	1.197	1.386	1.258	1.258	1.258	0.000	0.873	68.904
1	2.151	2.137	2.121	2.121	2.121	2.750	1.395	3.531
4	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
0	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
2	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
2	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
3	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
1	2.151	2.137	2.121	2.121	2.121	2.750	1.395	3.531
2	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
0	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
9	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
1	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
3	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
2	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
2	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
0	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
5	3.803	4.330	3.742	3.742	3.742	5.000	4.436	5.000
2	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
5	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
4	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
1	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
1	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
0	2.151	2.137	2.121	2.121	2.121	2.750	1.395	3.531
2	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
2	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
2	1.701	2.387	1.685	1.685	1.685	2.000	1.934	2.440
4	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
0	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
4	1.701	2.387	1.685	1.685	1.685	2.000	1.934	2.440
1	3.394	3.840	3.517	3.517	3.517	1.000	3.208	1.000
0	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
0	1.701	2.387	1.685	1.685	1.685	2.000	1.934	2.440
1	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
0	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
1	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
4	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
1	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
1	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
4	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
1	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207

0	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
1	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
2	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
0	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
1	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
0	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
1	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
2	1.821	2.310	1.822	1.822	1.822	1.803	1.858	2.207
2	5.667	5.646	5.667	5.667	5.667	5.667	5.510	5.667

Table G.2 – Predicted values for the July 2005 data

	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6	Model 7	Model 8
rkn	PrdCount	PrdCount	PrdCount	PrdCount	PrdCount	PrdCount	PrdCount	PrdCount
0	0.494	1.639	0.521	0.521	0.521	0.541	0.534	0.701
0	0.521	1.685	0.524	0.524	0.524	0.549	0.535	0.645
1	0.521	1.685	0.524	0.524	0.524	0.549	0.535	0.645
0	0.521	1.685	0.524	0.524	0.524	0.549	0.535	0.645
1	0.494	1.639	0.521	0.521	0.521	0.541	0.534	0.701
3	1.449	4.259	1.519	1.519	1.519	1.588	1.509	1.927
0	1.090	2.974	1.076	1.076	1.076	0.919	1.069	1.533
0	0.896	2.450	0.848	0.848	0.848	0.751	0.850	1.144
0	1.161	3.193	1.117	1.117	1.117	1.133	1.112	1.413
1	1.252	3.496	1.236	1.236	1.236	1.257	1.229	1.568
0	1.309	3.702	1.378	1.378	1.378	1.005	1.341	1.925
0	0.942	2.566	0.867	0.867	0.867	0.885	0.870	1.089
1	1.059	2.885	1.032	1.032	1.032	1.158	1.033	1.522
0	0.356	1.428	0.429	0.429	0.429	0.454	0.440	0.523
1	1.077	2.936	1.035	1.035	1.035	0.961	1.030	1.350
1	1.161	3.193	1.117	1.117	1.117	1.133	1.112	1.413
1	1.425	4.157	1.360	1.360	1.360	1.590	1.365	1.666
0	1.386	3.999	1.349	1.349	1.349	0.955	1.333	1.663
2	1.346	3.840	1.355	1.355	1.355	1.472	1.292	1.740
4	0.815	2.258	0.745	0.745	0.745	0.766	0.751	0.931
0	0.494	1.639	0.521	0.521	0.521	0.541	0.534	0.701
0	1.383	3.985	1.455	1.455	1.455	2.067	1.405	2.017
0	0.722	2.058	0.679	0.679	0.679	0.682	0.687	0.880
0	0.423	1.526	0.472	0.472	0.472	0.500	0.485	0.606
0	0.897	2.452	0.853	0.853	0.853	0.876	0.861	1.234
0	1.490	4.438	1.574	1.574	1.574	1.671	1.566	1.992

0	0.641	1.898	0.623	0.623	0.623	0.619	0.634	0.840
1	0.641	1.898	0.623	0.623	0.623	0.619	0.634	0.840
0	1.196	3.308	1.202	1.202	1.202	1.526	1.193	1.786
1	0.966	2.628	0.921	0.921	0.921	1.071	0.930	1.373
0	1.186	3.275	1.190	1.190	1.190	0.864	1.175	1.593
1	1.161	3.193	1.117	1.117	1.117	1.133	1.112	1.413
2	1.041	2.832	0.995	0.995	0.995	1.237	1.006	1.523
0	0.896	2.450	0.848	0.848	0.848	0.751	0.850	1.144
0	1.357	3.886	1.440	1.440	1.440	0.663	1.403	1.917
0	0.775	2.170	0.733	0.733	0.733	0.690	0.740	0.988
2	0.423	1.526	0.472	0.472	0.472	0.500	0.485	0.606
1	0.708	2.031	0.679	0.679	0.679	0.683	0.691	0.953
3	1.345	3.838	1.405	1.405	1.405	2.041	1.374	2.038
3	0.674	1.963	0.630	0.630	0.630	0.653	0.639	0.782
0	1.077	2.936	1.035	1.035	1.035	0.961	1.030	1.350
3	1.325	3.762	1.343	1.343	1.343	1.769	1.338	2.056
0	0.494	1.639	0.521	0.521	0.521	0.541	0.534	0.701
0	0.708	2.031	0.679	0.679	0.679	0.683	0.691	0.953
2	1.685	5.392	1.666	1.666	1.666	1.612	1.637	2.281
1	0.896	2.450	0.848	0.848	0.848	0.751	0.850	1.144
2	0.571	1.771	0.574	0.574	0.574	0.608	0.590	0.807
0	0.423	1.526	0.472	0.472	0.472	0.500	0.485	0.606
0	0.674	1.963	0.630	0.630	0.630	0.653	0.639	0.782
1	0.356	1.428	0.429	0.429	0.429	0.454	0.440	0.523
0	0.423	1.526	0.472	0.472	0.472	0.500	0.485	0.606
0	0.521	1.685	0.524	0.524	0.524	0.549	0.535	0.645
1	0.674	1.963	0.630	0.630	0.630	0.653	0.639	0.782
0	1.605	4.976	1.589	1.589	1.589	1.013	1.651	2.660
0	0.415	1.515	0.365	0.365	0.365	0.120	0.353	0.338
1	1.539	4.658	1.586	1.586	1.586	1.786	1.594	1.982
2	1.132	3.102	1.129	1.129	1.129	0.787	1.116	1.556
0	0.356	1.428	0.429	0.429	0.429	0.454	0.440	0.523
1	0.494	1.639	0.521	0.521	0.521	0.541	0.534	0.701
3	1.535	4.640	1.609	1.609	1.609	1.773	1.609	2.020
5	1.337	3.806	1.409	1.409	1.409	1.513	1.370	1.987
4	1.509	4.521	1.468	1.468	1.468	1.726	1.491	1.808
0	1.396	4.038	1.442	1.442	1.442	1.488	1.431	1.831
3	1.058	2.880	0.992	0.992	0.992	1.008	0.991	1.251
0	1.330	3.781	1.346	1.346	1.346	1.376	1.337	1.709
2	1.252	3.496	1.236	1.236	1.236	1.257	1.229	1.568
1	1.396	4.038	1.442	1.442	1.442	1.488	1.431	1.831

2	1.270	3.559	1.318	1.318	1.318	0.736	1.291	1.789
1	0.896	2.450	0.848	0.848	0.848	0.751	0.850	1.144
0	0.853	2.346	0.795	0.795	0.795	0.776	0.799	1.033
1	0.494	1.639	0.521	0.521	0.521	0.541	0.534	0.701
0	0.356	1.428	0.429	0.429	0.429	0.454	0.440	0.523
2	1.330	3.781	1.346	1.346	1.346	1.376	1.337	1.709
0	0.674	1.963	0.630	0.630	0.630	0.653	0.639	0.782
1	0.521	1.685	0.524	0.524	0.524	0.549	0.535	0.645
2	0.971	2.641	0.915	0.915	0.915	0.870	0.914	1.191
3	0.896	2.450	0.848	0.848	0.848	0.751	0.850	1.144
0	1.045	2.843	1.019	1.019	1.019	0.792	1.013	1.414
0	0.423	1.526	0.472	0.472	0.472	0.500	0.485	0.606
1	1.396	4.038	1.442	1.442	1.442	1.488	1.431	1.831

Table G.3 – Predicted values for the September 2005 data

	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6	Model 7	Model 8
rkn	PrdCount	PrdCount	PrdCount	PrdCount	PrdCount	PrdCount	PrdCount	PrdCount
0	0.859	2.362	0.845	0.845	0.845	0.618	0.623	0.994
0	0.575	1.777	0.556	0.556	0.556	0.613	0.603	1.033
1	0.482	1.620	0.509	0.509	0.509	0.552	0.670	0.768
0	0.575	1.777	0.556	0.556	0.556	0.613	0.603	1.033
0	0.575	1.777	0.556	0.556	0.556	0.613	0.603	1.033
0	1.139	3.123	1.138	1.138	1.138	1.118	0.635	2.501
0	0.575	1.777	0.556	0.556	0.556	0.613	0.603	1.033
0	0.859	2.362	0.845	0.845	0.845	0.618	0.623	0.994
1	0.566	1.761	0.558	0.558	0.558	0.518	0.823	0.720
0	0.742	2.101	0.668	0.668	0.668	0.644	0.910	0.909
0	0.575	1.777	0.556	0.556	0.556	0.613	0.603	1.033
0	0.859	2.362	0.845	0.845	0.845	0.618	0.623	0.994
0	0.482	1.620	0.509	0.509	0.509	0.552	0.670	0.768
0	0.479	1.615	0.510	0.510	0.510	0.499	0.743	0.681
1	0.575	1.777	0.556	0.556	0.556	0.613	0.603	1.033
2	0.482	1.620	0.509	0.509	0.509	0.552	0.670	0.768
9	1.488	4.426	1.621	1.621	1.621	0.881	0.570	5.946
1	0.880	2.410	0.873	0.873	0.873	0.828	0.707	1.255
0	0.728	2.072	0.740	0.740	0.740	0.454	0.693	0.663
0	0.479	1.615	0.510	0.510	0.510	0.499	0.743	0.681
0	0.741	2.097	0.733	0.733	0.733	0.366	1.065	0.467
0	0.566	1.761	0.558	0.558	0.558	0.518	0.823	0.720

0	1.419	4.132	1.448	1.448	1.448	0.923	1.143	1.241
1	0.575	1.777	0.556	0.556	0.556	0.613	0.603	1.033
1	0.874	2.395	0.849	0.849	0.849	0.397	0.940	0.568
1	1.209	3.351	1.144	1.144	1.144	0.759	1.294	0.822
0	0.479	1.615	0.510	0.510	0.510	0.499	0.743	0.681
0	0.482	1.620	0.509	0.509	0.509	0.552	0.670	0.768
2	0.636	1.889	0.614	0.614	0.614	1.589	0.878	2.085
0	0.464	1.590	0.418	0.418	0.418	6.260	1.075	11.249
2	0.479	1.615	0.510	0.510	0.510	0.499	0.743	0.681
1	0.479	1.615	0.510	0.510	0.510	0.499	0.743	0.681
0	1.139	3.123	1.138	1.138	1.138	1.118	0.635	2.501
2	1.080	2.945	1.053	1.053	1.053	0.692	0.560	1.777
2	0.566	1.761	0.558	0.558	0.558	0.518	0.823	0.720
1	1.364	3.912	1.246	1.246	1.246	1.581	1.107	2.462
2	0.479	1.615	0.510	0.510	0.510	0.499	0.743	0.681
1	0.742	2.101	0.668	0.668	0.668	0.644	0.910	0.909
0	0.482	1.620	0.509	0.509	0.509	0.552	0.670	0.768
0	0.736	2.087	0.742	0.742	0.742	0.343	0.851	0.501
0	1.320	3.745	1.247	1.247	1.247	1.979	0.708	12.249
0	0.566	1.761	0.558	0.558	0.558	0.518	0.823	0.720
0	2.009	7.453	2.065	2.065	2.065	1.120	0.774	489.931
0	0.575	1.777	0.556	0.556	0.556	0.613	0.603	1.033
1	0.859	2.362	0.845	0.845	0.845	0.618	0.623	0.994
0	1.080	2.945	1.053	1.053	1.053	0.692	0.560	1.777
2	0.575	1.777	0.556	0.556	0.556	0.613	0.603	1.033
1	0.566	1.761	0.558	0.558	0.558	0.518	0.823	0.720
0	0.728	2.072	0.740	0.740	0.740	0.454	0.693	0.663
0	0.482	1.620	0.509	0.509	0.509	0.552	0.670	0.768
0	0.479	1.615	0.510	0.510	0.510	0.499	0.743	0.681
0	0.575	1.777	0.556	0.556	0.556	0.613	0.603	1.033
0	0.859	2.362	0.845	0.845	0.845	0.618	0.623	0.994
0	0.728	2.072	0.740	0.740	0.740	0.454	0.693	0.663
0	0.566	1.761	0.558	0.558	0.558	0.518	0.823	0.720
0	1.080	2.945	1.053	1.053	1.053	0.692	0.560	1.777
1	0.482	1.620	0.509	0.509	0.509	0.552	0.670	0.768
0	0.687	1.988	0.709	0.709	0.709	0.361	0.768	0.528
0	0.859	2.362	0.845	0.845	0.845	0.618	0.623	0.994
1	0.482	1.620	0.509	0.509	0.509	0.552	0.670	0.768
2	1.008	2.741	0.873	0.873	0.873	0.954	1.005	1.369
1	0.631	1.879	0.670	0.670	0.670	0.389	0.870	0.538
1	0.482	1.620	0.509	0.509	0.509	0.552	0.670	0.768

0	1.809	6.107	1.945	1.945	1.945	2.436	1.218	5.281
3	0.575	1.777	0.556	0.556	0.556	0.613	0.603	1.033
0	1.364	3.912	1.246	1.246	1.246	1.581	1.107	2.462
3	0.933	2.543	0.837	0.837	0.837	2.326	0.789	4.627
2	0.711	2.035	0.732	0.732	0.732	0.536	0.785	0.752
6	1.809	6.107	1.945	1.945	1.945	2.436	1.218	5.281
1	0.631	1.879	0.670	0.670	0.670	0.389	0.870	0.538
0	0.482	1.620	0.509	0.509	0.509	0.552	0.670	0.768
0	0.575	1.777	0.556	0.556	0.556	0.613	0.603	1.033
1	0.575	1.777	0.556	0.556	0.556	0.613	0.603	1.033
1	0.482	1.620	0.509	0.509	0.509	0.552	0.670	0.768
0	0.575	1.777	0.556	0.556	0.556	0.613	0.603	1.033
0	1.080	2.945	1.053	1.053	1.053	0.692	0.560	1.777
0	0.479	1.615	0.510	0.510	0.510	0.499	0.743	0.681
0	0.482	1.620	0.509	0.509	0.509	0.552	0.670	0.768
1	0.310	1.364	0.431	0.431	0.431	0.641	1.081	0.720
1	0.482	1.620	0.509	0.509	0.509	0.552	0.670	0.768

Table G.4 – Predicted values for the May 2006 data

	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6	Model 7	Model 8
rkn	PrdCount	PrdCount	PrdCount	PrdCount	PrdCount	PrdCount	PrdCount	PrdCount
0	0.000	0.000	0.000	0.000	0.000	0.019	0.000	0.000
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
1	1.000	0.693	1.000	1.000	1.000	0.996	1.379	1.000
2	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
6	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
5	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165

0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
3	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
3	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
1	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
1	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
1	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
1	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
3	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
1	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
1	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.000	0.000	0.000	0.000	0.000	0.019	0.000	0.000
1	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
1	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
2	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
1	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
2	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
1	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165

1	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
1	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
1	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
1	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
1	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
1	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
1	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
3	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
1	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
1	2.000	1.040	2.000	2.000	2.000	1.987	2.302	2.000
0	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
2	0.653	0.349	0.653	0.653	0.653	0.653	0.640	1.165
3	2.000	1.040	2.000	2.000	2.000	1.987	2.302	2.000

Table G.5 – Predicted values for the July 2006 data

	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6	Model 7	Model 8
rkn	PrdCount	PrdCount	PrdCount	PrdCount	PrdCount	PrdCount	PrdCount	PrdCount
0	0.554	1.741	0.547	0.547	0.547	0.492	0.513	0.804
0	0.608	1.836	0.611	0.611	0.611	0.656	0.584	0.885
1	0.554	1.741	0.547	0.547	0.547	0.492	0.513	0.804
0	0.608	1.836	0.611	0.611	0.611	0.656	0.584	0.885
0	0.576	1.778	0.581	0.581	0.581	0.530	0.607	0.821
0	0.497	1.643	0.482	0.482	0.482	0.401	0.434	0.724
0	0.534	1.705	0.532	0.532	0.532	0.442	0.548	0.762
5	0.608	1.836	0.611	0.611	0.611	0.656	0.584	0.885
0	0.497	1.643	0.482	0.482	0.482	0.401	0.434	0.724
1	0.368	1.445	0.359	0.359	0.359	0.340	0.279	0.569
0	0.631	1.880	0.583	0.583	0.583	0.372	0.645	0.707
0	0.435	1.544	0.419	0.419	0.419	0.355	0.354	0.645
1	0.613	1.846	0.625	0.625	0.625	0.686	0.647	0.877
1	0.594	1.811	0.587	0.587	0.587	0.605	0.643	0.777

0	0.554	1.741	0.547	0.547	0.547	0.492	0.513	0.804
0	0.613	1.846	0.625	0.625	0.625	0.686	0.647	0.877
0	0.576	1.779	0.551	0.551	0.551	0.499	0.578	0.723
0	0.368	1.445	0.359	0.359	0.359	0.340	0.279	0.569
0	0.591	1.806	0.608	0.608	0.608	0.632	0.746	0.807
1	0.608	1.836	0.611	0.611	0.611	0.656	0.584	0.885
0	0.608	1.836	0.611	0.611	0.611	0.656	0.584	0.885
1	0.591	1.806	0.604	0.604	0.604	0.608	0.681	0.826
0	0.608	1.836	0.611	0.611	0.611	0.656	0.584	0.885
1	0.608	1.836	0.611	0.611	0.611	0.656	0.584	0.885
0	0.576	1.778	0.581	0.581	0.581	0.530	0.607	0.821
0	0.565	1.760	0.575	0.575	0.575	0.545	0.656	0.790
1	0.608	1.836	0.611	0.611	0.611	0.656	0.584	0.885
1	0.554	1.741	0.547	0.547	0.547	0.492	0.513	0.804
1	0.591	1.806	0.604	0.604	0.604	0.608	0.681	0.826
2	0.608	1.836	0.611	0.611	0.611	0.656	0.584	0.885
0	0.497	1.643	0.482	0.482	0.482	0.401	0.434	0.724
0	0.608	1.836	0.611	0.611	0.611	0.656	0.584	0.885
1	0.608	1.836	0.611	0.611	0.611	0.656	0.584	0.885
0	0.534	1.705	0.532	0.532	0.532	0.442	0.548	0.762
2	0.591	1.806	0.608	0.608	0.608	0.632	0.746	0.807
0	0.606	1.833	0.613	0.613	0.613	0.698	0.679	0.822
0	0.613	1.846	0.625	0.625	0.625	0.686	0.647	0.877
2	0.591	1.806	0.604	0.604	0.604	0.608	0.681	0.826
0	0.438	1.549	0.428	0.428	0.428	0.375	0.400	0.637
0	0.576	1.778	0.581	0.581	0.581	0.530	0.607	0.821
0	0.554	1.741	0.547	0.547	0.547	0.492	0.513	0.804
0	0.435	1.544	0.419	0.419	0.419	0.355	0.354	0.645
0	0.608	1.836	0.611	0.611	0.611	0.656	0.584	0.885
0	0.554	1.741	0.547	0.547	0.547	0.492	0.513	0.804
1	0.420	1.521	0.410	0.410	0.410	0.588	0.392	0.600
0	0.497	1.643	0.482	0.482	0.482	0.401	0.434	0.724
1	0.608	1.836	0.611	0.611	0.611	0.656	0.584	0.885
0	0.608	1.836	0.611	0.611	0.611	0.656	0.584	0.885
2	0.554	1.741	0.547	0.547	0.547	0.492	0.513	0.804
0	0.576	1.778	0.581	0.581	0.581	0.530	0.607	0.821
1	0.554	1.741	0.547	0.547	0.547	0.492	0.513	0.804
0	0.608	1.836	0.611	0.611	0.611	0.656	0.584	0.885
0	0.608	1.836	0.611	0.611	0.611	0.656	0.584	0.885
1	0.613	1.846	0.625	0.625	0.625	0.686	0.647	0.877
0	0.565	1.760	0.575	0.575	0.575	0.545	0.656	0.790

1	0.667	1.948	0.691	0.691	0.691	0.674	0.963	0.836
0	0.488	1.629	0.481	0.481	0.481	0.394	0.477	0.700
3	0.298	1.347	0.304	0.304	0.304	0.352	0.211	0.497
2	0.497	1.643	0.482	0.482	0.482	0.401	0.434	0.724
1	0.576	1.778	0.581	0.581	0.581	0.530	0.607	0.821
0	0.497	1.643	0.482	0.482	0.482	0.401	0.434	0.724
0	0.554	1.741	0.547	0.547	0.547	0.492	0.513	0.804
0	0.554	1.741	0.547	0.547	0.547	0.492	0.513	0.804
0	0.554	1.741	0.547	0.547	0.547	0.492	0.513	0.804
0	0.534	1.705	0.532	0.532	0.532	0.442	0.548	0.762
0	0.608	1.836	0.611	0.611	0.611	0.656	0.584	0.885
0	0.223	1.250	0.253	0.253	0.253	0.394	0.154	0.430
0	0.383	1.467	0.376	0.376	0.376	0.380	0.324	0.574
0	0.507	1.660	0.471	0.471	0.471	7.078	0.449	0.649
1	0.576	1.779	0.551	0.551	0.551	0.499	0.578	0.723
1	0.535	1.708	0.539	0.539	0.539	0.519	0.610	0.749
3	0.608	1.836	0.611	0.611	0.611	0.656	0.584	0.885
0	0.554	1.741	0.547	0.547	0.547	0.492	0.513	0.804
0	0.613	1.845	0.626	0.626	0.626	0.729	0.681	0.855
0	0.435	1.544	0.419	0.419	0.419	0.355	0.354	0.645
0	0.144	1.155	0.208	0.208	0.208	0.475	0.109	0.369
1	0.554	1.741	0.547	0.547	0.547	0.492	0.513	0.804
0	0.576	1.778	0.581	0.581	0.581	0.530	0.607	0.821
2	0.613	1.845	0.637	0.637	0.637	0.744	0.851	0.816
1	0.935	2.547	0.956	0.956	0.956	1.058	1.125	0.987

Table G.6 – Predicted values for the September 2006 data

	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6	Model 7	Model 8
rkn	PrdCount	PrdCount	PrdCount	PrdCount	PrdCount	PrdCount	PrdCount	PrdCount
0	0.243	1.275	0.252	0.252	0.252	0.235	0.256	0.742
0	0.306	1.358	0.312	0.312	0.312	0.340	0.307	0.875
0	0.243	1.275	0.252	0.252	0.252	0.235	0.256	0.742
0	0.344	1.410	0.332	0.332	0.332	0.301	0.310	1.155
0	0.381	1.464	0.393	0.393	0.393	0.280	0.349	1.353
0	0.243	1.275	0.252	0.252	0.252	0.235	0.256	0.742
0	0.282	1.326	0.302	0.302	0.302	0.395	0.421	0.627
1	0.454	1.575	0.465	0.465	0.465	0.414	0.444	1.423
0	0.243	1.275	0.252	0.252	0.252	0.235	0.256	0.742
0	0.243	1.275	0.252	0.252	0.252	0.235	0.256	0.742

0	0.344	1.410	0.332	0.332	0.332	0.301	0.310	1.155
0	0.439	1.552	0.411	0.411	0.411	0.534	0.398	1.044
0	0.344	1.410	0.332	0.332	0.332	0.301	0.310	1.155
5	0.665	1.945	0.657	0.657	0.657	0.824	0.560	1.918
0	0.344	1.410	0.332	0.332	0.332	0.301	0.310	1.155
1	0.337	1.401	0.345	0.345	0.345	0.538	0.453	0.732
0	0.243	1.275	0.252	0.252	0.252	0.235	0.256	0.742
0	0.488	1.629	0.493	0.493	0.493	0.415	0.425	1.602
0	0.606	1.832	0.591	0.591	0.591	0.588	0.550	1.692
1	0.642	1.901	0.574	0.574	0.574	0.520	0.557	1.259
0	0.373	1.452	0.389	0.389	0.389	0.440	0.388	1.211
1	0.306	1.358	0.312	0.312	0.312	0.340	0.307	0.875
0	0.243	1.275	0.252	0.252	0.252	0.235	0.256	0.742
0	0.439	1.552	0.411	0.411	0.411	0.534	0.398	1.044
0	0.381	1.464	0.393	0.393	0.393	0.280	0.349	1.353
1	0.913	2.491	0.928	0.928	0.928	1.188	0.798	2.322
0	0.439	1.552	0.411	0.411	0.411	0.534	0.398	1.044
0	0.243	1.275	0.252	0.252	0.252	0.235	0.256	0.742
0	0.642	1.901	0.574	0.574	0.574	0.520	0.557	1.259
0	0.243	1.275	0.252	0.252	0.252	0.235	0.256	0.742
0	0.344	1.410	0.332	0.332	0.332	0.301	0.310	1.155
0	0.243	1.275	0.252	0.252	0.252	0.235	0.256	0.742
2	0.439	1.552	0.411	0.411	0.411	0.534	0.398	1.044
0	0.243	1.275	0.252	0.252	0.252	0.235	0.256	0.742
0	0.381	1.464	0.393	0.393	0.393	0.280	0.349	1.353
1	0.243	1.275	0.252	0.252	0.252	0.235	0.256	0.742
2	1.666	5.289	1.617	1.617	1.617	1.782	2.124	1.866
0	0.344	1.410	0.332	0.332	0.332	0.301	0.310	1.155
0	0.243	1.275	0.252	0.252	0.252	0.235	0.256	0.742
0	0.373	1.452	0.389	0.389	0.389	0.440	0.388	1.211
0	0.361	1.435	0.344	0.344	0.344	0.538	0.366	1.041
1	0.296	1.345	0.281	0.281	0.281	0.202	0.422	0.543
0	0.454	1.575	0.465	0.465	0.465	0.414	0.444	1.423
2	0.381	1.464	0.393	0.393	0.393	0.280	0.349	1.353
0	0.344	1.410	0.332	0.332	0.332	0.301	0.310	1.155
1	0.243	1.275	0.252	0.252	0.252	0.235	0.256	0.742
2	0.344	1.410	0.332	0.332	0.332	0.301	0.310	1.155
0	0.243	1.275	0.252	0.252	0.252	0.235	0.256	0.742
0	0.243	1.275	0.252	0.252	0.252	0.235	0.256	0.742
0	0.306	1.358	0.312	0.312	0.312	0.340	0.307	0.875
0	0.381	1.464	0.393	0.393	0.393	0.280	0.349	1.353

0	0.243	1.275	0.252	0.252	0.252	0.235	0.256	0.742
0	0.243	1.275	0.252	0.252	0.252	0.235	0.256	0.742
0	0.381	1.464	0.393	0.393	0.393	0.280	0.349	1.353
0	0.361	1.435	0.344	0.344	0.344	0.538	0.366	1.041
0	0.344	1.410	0.332	0.332	0.332	0.301	0.310	1.155
0	0.243	1.275	0.252	0.252	0.252	0.235	0.256	0.742
0	1.230	3.422	1.389	1.389	1.389	0.922	1.229	2.842
0	0.373	1.452	0.389	0.389	0.389	0.440	0.388	1.211
0	0.344	1.410	0.332	0.332	0.332	0.301	0.310	1.155
0	0.454	1.575	0.465	0.465	0.465	0.414	0.444	1.423
3	0.243	1.275	0.252	0.252	0.252	0.235	0.256	0.742
0	0.306	1.358	0.312	0.312	0.312	0.340	0.307	0.875
2	0.381	1.464	0.393	0.393	0.393	0.280	0.349	1.353
0	0.381	1.464	0.393	0.393	0.393	0.280	0.349	1.353
0	0.606	1.832	0.591	0.591	0.591	0.588	0.550	1.692
0	0.148	1.160	0.180	0.180	0.180	0.020	0.476	0.164
0	0.344	1.410	0.332	0.332	0.332	0.301	0.310	1.155
0	0.373	1.452	0.389	0.389	0.389	0.440	0.388	1.211
2	0.344	1.410	0.332	0.332	0.332	0.301	0.310	1.155
0	0.243	1.275	0.252	0.252	0.252	0.235	0.256	0.742
0	0.296	1.345	0.281	0.281	0.281	0.202	0.422	0.543
0	0.361	1.435	0.344	0.344	0.344	0.538	0.366	1.041
0	0.665	1.945	0.657	0.657	0.657	0.824	0.560	1.918
1	0.361	1.435	0.344	0.344	0.344	0.538	0.366	1.041
2	0.361	1.435	0.344	0.344	0.344	0.538	0.366	1.041
0	0.606	1.832	0.591	0.591	0.591	0.588	0.550	1.692
0	0.344	1.410	0.332	0.332	0.332	0.301	0.310	1.155
0	0.306	1.358	0.312	0.312	0.312	0.340	0.307	0.875
0	0.344	1.410	0.332	0.332	0.332	0.301	0.310	1.155