Score Tests for Poisson Variation Against General Alternatives[*]

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Abstract

Variations from Poisson and binomial variation are a common concern when modeling count data. Tests for overdispersion are often based on unrealistically specific alternatives, such as the negative binomial or beta-binomial distributions, or are not model based and therefore lack power. Convincing methods for detecting and modeling underdispersion are not generally available. We use extended Poisson process models, in which an arbitrary count distribution can be represented as the realization of a pure birth process. Under and overdispersion relative to the Poisson or binomial distributions can be represented in terms of the slope and curvature of the unobserved birth rate sequence. We give a new saddlepoint approximation for birth processes which is exact in the neighborhood of the Poisson, negative binomial and binomial models. This allows us to compute score tests for the goodness of fit of standard models against very general alternatives.

Keywords: score test, saddlepoint approximation, birth process, Poisson distribution, negative binomial distribution, binomial distribution.

1 Introduction

Non-Poisson variation is a common problem when modeling count data. The particular problem of overdispersion has received the majority of the attention in the literature. However underdispersion and skewness relative to the Poisson distribution are also common and need to be detected for accurate modeling and for interpreting the process at hand.

The negative binomial distribution is a particularly popular alternative to the Poisson when overdispersion is the primary concern. Several authors, including Collings and Margolin (1985), Lee (1986), Cameron and Trivedi (1986) and Dean and Lawless (1989), have derived the likelihood score test of Poisson variation against a negative binomial alternative. These authors used the method of Cox (1983) and Chesher (1984) to show that the score test with negative binomial alternative is also a score test against other mixed Poisson alternatives. The mixed Poisson models have in common a variance function of the form

$$\mathrm{var}(Y_i|\mathbf{x}_i) = \mu_i + \gamma\mu_i^2$$

where $\mathbf{x}_i$ is a covariate vector and $\mu_i = E(Y_i|\mathbf{x}_i)$. The score test with negative binomial alternative is therefore locally optimal against deviations from Poisson variation with this sort of variance function.

In order to construct tests of Poisson variation against more general alternatives it is necessary to have a convenient representation for possible alternatives. In this paper we use the birth rate sequence of an unobserved birth process to represent an arbitrary count distribution, the distribution arising as the number of births after unit time (Faddy, 1997). In terms of the birth rates, Poisson variation corresponds to a constant sequence while the negative binomial distribution corresponds to a linear increasing sequence. A linear decreasing birth rate sequence corresponds to the binomial distribution. We compute the score test for linear trend in the birth rates and show that this test is identical to the test with negative binomial alternative. It follows that this test can be used to detect underdispersion in the direction of the binomial distribution as well as overdispersion in the direction of the negative binomial distribution.

We derive a second score test corresponding to quadratic departures from Poisson variation. This test supplements the linear test and is sensitive to skewness relative to the Poisson distribution. The two score tests together provide a practical approximation to the score test of Poisson variation against a very general class of alternative distributions.

In order to compute the score tests, we use a new saddlepoint approximation to the count probabilities of

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[*] Smyth, G. K., and Podlich, H. M. (2000). Score tests for Poisson variation against general alternatives. *Computing Science and Statistics*, 32, 97-103.

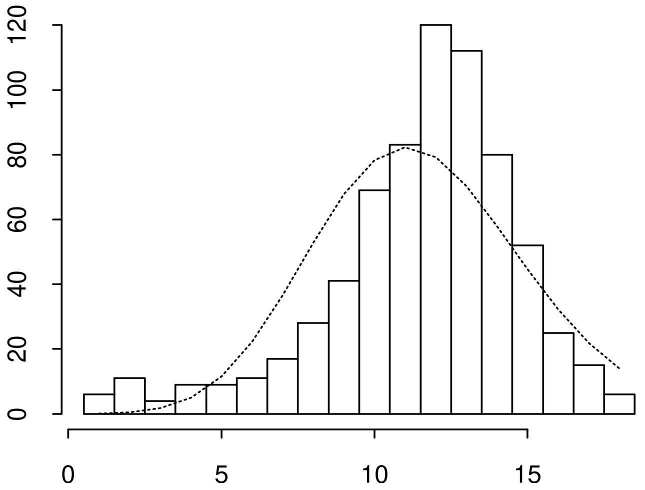

Figure 1: Frequency distribution of fetal implants in mice utero with fitted Poisson distribution overlaid.

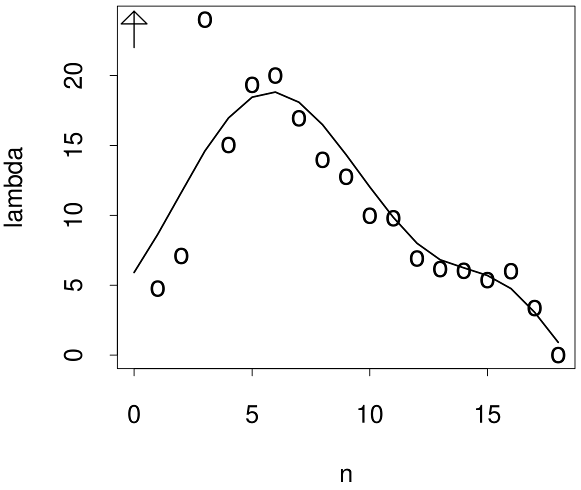

Figure 2: Fetal implants in mice: empirical birth rate profile and smoothed rate profile.

a birth process. The new approximation is more accurate than the classic saddlepoint approximation due to Daniels (1982) and has the characteristic that it is exact in the neighborhood of the Poisson, binomial and negative binomial distributions. The means that score tests for Poisson variation computed from the saddlepoint approximation are exact likelihood score tests.

The distribution of the score test with negative binomial alternative is known to converge to normality quite slowly. In small or moderate sized samples the test statistic has a distribution which is both right skew and heavy tailed. We find that the second score test with quadratic alternative is less skew in distribution than the first but more heavy tailed. In this paper we modify both score test statistics using the leverages of the fitted Poisson model to account for uncertainty in estimating the model parameters and so that they converge to normality more rapidly. We compute approximate 3rd and 4th cumulants for the test statistics and incorporate these into an Edgeworth expansion (Barndorff-Nielsen and Cox, 1989) to approximate the significance levels of the test statistics.

2 Birth Process Representation of Count Distributions

Consider a general birth process with birth rates $\lambda_n \geq 0$, $n = 0, 1, 2, \ldots$. Let $y(t)$ be the number of births after time t. Then $y(t)$ is an extended Poisson process for which the arrival rate depends on the number of arrivals so far. Let $p_n(t)$ be the probability function for $y(t)$. The extended Poisson process can be defined by

$$\begin{aligned} P\left(y(t+\delta t) = n \,|\, y(t) = n\right) &= 1 - \lambda_n \delta t + o(\delta t) \\ P\left(y(t+\delta t) = n+1 \,|\, y(t) = n\right) &= \lambda_n \delta t + o(\delta t). \end{aligned}$$

Write $p_n = p_n(1)$ for the count distribution arising after unit time.

Any birth rate sequence λ_n, $n \geq 0$, gives rise to a unique count distribution p_n. It can also be shown that for any count distribution p_n, $n = 0, 1, 2, \ldots$, there is a corresponding birth rate sequence λ_n, $n = 0, 1, 2, \ldots$, allowing λ_n to be infinite if $p_n = 0$. For example Figure 1 shows a histogram of the number of fetal implants found in the utero of pregnant mice and Figure 2 shows the birth rates corresponding to the observed relative frequencies. (Data courtesy of Ron Bosch of the Harvard School of Public Health.) The upward pointing arrow in Figure 2 indicates an infinite value. In this case $\lambda_0 = \infty$ because there were no mice with zero implants.

The λ_n are uniquely determined by the p_n for all n within the support of p_n. It follows that sequences λ_n provide a representation for the class of count distributions on the non-negative integers. This representation has advantages over the probability representation in that the λ_n are not constrained to add to one and in that, as we will see, linearity in the λ_n corresponds to well-known standard distributions. In general it makes sense to consider smooth sequences for the λ_n such as splines or low order polynomials. Figure 2 also shows the birth rates for the fetal implants in mice smoothed using a technique described in Podlich et al (1999) and Figure 3 gives the probability function corresponding to the smoothed birth rates.

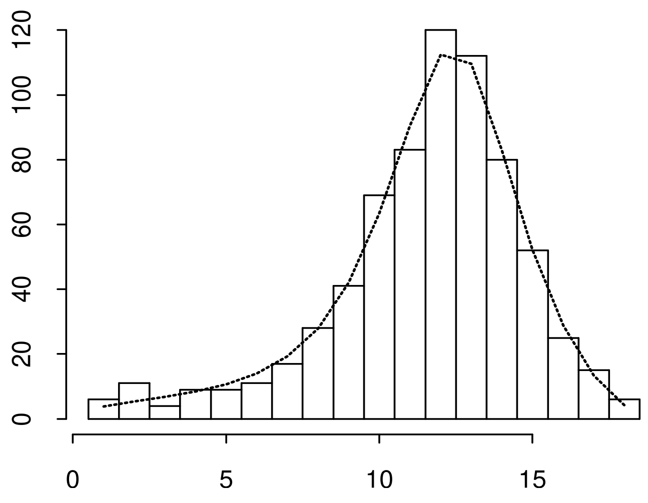

Figure 3: Fetal implants in mice: the solid line gives the probabilities obtained from the smoothed rate profile.

A constant sequence $\lambda_n = \lambda$ corresponds to the Poisson distribution with mean λ. A linear increasing sequence gives rise to a negative binomial distribution. Specifically if $\lambda_n = a(b+n)$ then $y(t) \sim \text{Neg Bin}(b, 1-e^{-a})$. A linear decreasing sequence, intersecting the λ-axis at a positive integer, give rise to a binomial distribution. Ball (1995) showed that any monotonic increasing sequence corresponds to a distribution which is overdispersed relative to the Poisson and any monotonic decreasing sequence to a distribution which is underdispersed relative to the Poisson. In general, increasing slope corresponds to increasing variance for a given mean, while convex or concave curvature corresponds to right or left skewness relative to the linear sequence with the same mean and variance.

Figure 4 illustrates some birth rate sequences corresponding to standard distributional types. Horizontal and increasing lines correspond to the Poisson and negative binomial distributions respectively. The lowest curve is underdispersed relative to the Poisson but is more right skew than the binomial with the same mean and variance. The first curve above the horizontal is overdispersed relative to the Poisson but is less right skew than the negative binomial with the same mean and variance. The top curve will represent a proper distribution provided it is asymptotically linear. It will be more right skew than the negative binomial with the same mean and variance.

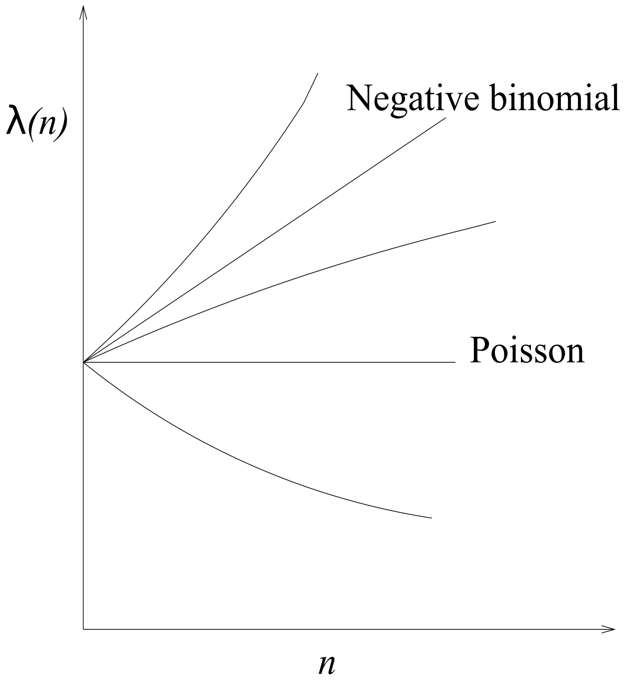

Figure 4: Classification of count distributions based on their birth rate sequences.

3 Regression Models for Count Data

We suppose independent observations $y_1, \ldots, y_N$, where each y_i is a non-negative integer, and where the means μ_i are a function of covariate vectors $\mathbf{x}_i$ and a vector of regression coefficients $\boldsymbol{\beta}$.

Consider the distribution of an arbitrary y with mean μ. We assume that the distribution of y is described by the birth rate sequence

$$\lambda_n = \gamma_0\{1 + h(n)\}$$

where $h(n)$ is some function of n and γ_0 is determined by the constraint that the mean of the distribution is μ. We assume that $h(n)$ is common to all observations but that μ (and hence γ_0) varies depending on the covariates and the regression coefficients $\boldsymbol{\beta}$.

The function $h(n)$ determines the shape of the response distribution. In particular the slope of $h(n)$ determines the dispersion of the y_i relative to the Poisson distribution while the curvature of $h(n)$ determines skewness and higher order properties of the distribution.
Example 1. Poisson. If $h(n) = 0$ for all n then y has a Poisson distribution with mean μ and $\gamma_0 = \mu$.
Example 2. Negative binomial. If $h(n) = \gamma_1 n$ with $\gamma_1 >$

0 then y has a negative binomial distribution with

$$E(y) = \mu = \frac{1}{\gamma_1}\left(e^{\gamma_0\gamma_1} - 1\right)$$

and

$$\text{var}(y) = \mu + \gamma_1\mu^2.$$

It follows that

$$\gamma_0 = \frac{1}{\gamma_1}\log(1 + \gamma_1\mu).$$

Note that $\gamma_0 \to \mu$ as $\gamma_1 \to 0$.

Example 3. Binomial. If $h(n) = -n/m$ with m a positive integer then y has a binomial distribution on $0, \ldots, m$. In this case

$$\text{var}(y) = \mu - \mu^2/m$$

and

$$\gamma_0 = -m\log(1 - \mu/m).$$

Example 4. Concave overdispersion and convex underdispersion. Suppose that $h(n) = n^\alpha$. If $0 < \alpha < 1$ then the distribution of y is intermediate between Poisson and negative binomial. The distribution has variance and all higher cumulants greater than its mean but has third and higher cumulants smaller than the negative binomial with the same mean and variance. If $-1 < \alpha < 0$ then the distribution of y is intermediate between Poisson and binomial. The distribution has variance and higher cumulants smaller than its mean but has third and higher cumulants greater than the binomial with the same mean and variance.

Example 4. Unimodal birth rate sequences. If $h(n)$ has a single maxima, i.e., is monotonic increasing for $n < m$ and monotonic decreasing for $n > m$ for some m, then the distribution of y is left skew relative to Poisson and to the negative binomial or binomial with the same mean and variance. The distribution may be over or underdispersed relative to Poisson. If $h(n)$ has a single minima then the distribution is right skew relative to the distributions with linear sequences.

Example 5. Mixed Poisson models. Consider the count distribution arising from a mixing distribution on the Poisson mean. The mixture distribution is overdispersed relative to Poisson and the corresponding sequence $h(n)$ is monotonic increasing. If the mixing distribution is gamma then the mixture is negative binomial and the corresponding $h(n)$ is linear increasing. Numerical experiments confirm that if the mixing distribution is less right skew than the gamma then $h(n)$ is concave increasing, and if the mixing distribution is more right skew than the gamma then $h(n)$ is convex increasing.

4 Locally Exact Saddlepoint Approximation

Consider a pure birth process with birth rates $\lambda_0, \lambda_1, \lambda_2, \ldots$. The following saddlepoint approximation is used for the probability distribution of the birth distribution after unit time:

$$p_n \approx \frac{e^{-a}}{n!} g(b)^n \prod_{i=0}^{n}(a + bi) \tag{1}$$

where

$$g(b) = \begin{cases} 1 & b = 0 \\ (1 - e^{-b})/b & b \neq 0 \end{cases}$$

where a and $b \geq 0$ satisfy

$$\sum_{i=0}^{n} \frac{1}{a + bi} = 1$$

and

$$\sum_{i=0}^{n} \frac{1}{(a + bi)^2} = \sum_{i=0}^{n} \frac{1}{(\lambda_i - \tilde{\theta})^2}$$

and $\tilde{\theta}$ satisfies

$$\sum_{i=0}^{n} \frac{1}{\lambda_i - \tilde{\theta}} = 1.$$

In practice we compute

$$g(b) = \begin{cases} 1 - b/2 + b^2/6 & \text{if } b < 10^{-5} \\ (1 - e^{-b})/b & \text{if } b \geq 10^{-5} \end{cases}$$

The approximation (1) becomes exact as the λ_i approach a linear sequence or can be sorted into a linear sequence. In particular the approximation becomes exact as the count distribution approaches Poisson, negative binomial or binomial. See Smyth and Podlich (1999) for a derivation of (1).

5 Score Tests for non-Poisson Variation

We now construct a 2-df score test for non-Poisson variation. We assume a quadratic polynomial model for the birth rate sequence,

$$h(n) = \gamma_1 n + \gamma_2 n^2 \tag{2}$$

over the range $0, \ldots, \max(y_i)$. This provides a 2-df approximation to the birth rate sequence for a wide range of distributions. Here $\gamma_1 = \gamma_2 = 0$ corresponds to the Poisson distribution; $\gamma_1 > 0$ represents overdispersion relative to the Poisson distribution in the direction of the negative binomial distribution; $\gamma_1 < 0$ represents underdispersion relative to the Poisson distribution in the direction of the binomial distribution; $\gamma_2 \neq 0$ represents more general departures from the Poisson distribution. In particular $\gamma_2 > 0$ is associated with distributions which are more right skew than the Poisson distribution and $\gamma_2 < 0$ is associated with distributions which are less right skew than the Poisson. Note that the sequence $h(n)$ with $\gamma_0 > 0$ would represent in an improper distribution if extended to $n \to \infty$ but we need to approximate the true birth rate sequence only up to $\max(y_i)$ for modeling the data at hand. Similarly $\gamma_2 < 0$ would result in a distribution with finite support if extended to n large enough that $h(n) \leq 0$; we need only that $h(n) > 0$ for $n = \max(y_i) - 1$.

We construct the score test of $\gamma_1 = \gamma_2 = 0$ which requires derivatives of p_y with respect to the γ_j. Calculation of these derivatives is complicated by the indirect definitions of a, b, $\tilde{\theta}$ and γ_0 in the expression for p_y. However the simple form (2) makes it possible to obtain closed form expressions for the derivatives when evaluating at $\gamma_1 = \gamma_2 = 0$.

After considerable calculation we obtain

$$U_1 = \left.\frac{\partial \log p_y}{\partial \gamma_1}\right|_{\gamma_1=\gamma_2=0} = \frac{(y-\mu)^2}{2} - \frac{y}{2}$$

and

$$U_2 = \left.\frac{\partial \log p_y}{\partial \gamma_2}\right|_{\gamma_1=\gamma_2=0} =$$

$$\frac{(y-1)y(2y-1)}{6} - \frac{\mu y(2y+1)}{6} - \left(\frac{\mu^2}{3} + \frac{\mu}{2}\right)(y-\mu).$$

The fact that the saddlepoint approximation is exact at the Poisson limit ensures that these derivatives hold all the properties of score statistics such as $E(U_1) = E(U_2) = 0$ when $y \sim \text{Poisson}(\mu)$.

These score statistics are correlated so we further compute the orthogonal quadratic statistic

$$U_{2.1} = U_2 - U_1 \text{cov}(U_1, U_2)/\text{var}(U_1).$$

Write

$$m_r = (y-\mu)^r - \mu, \quad r = 1,2,3$$

for the first three mean corrected moments. Note that $E(m_r) = 0$. We have

$$U_1 = m_2/2 - m_1/2$$

and

$$U_{2.1} = m_3/3 - m_2 + (2/3 - \mu)m_1.$$

Now

$$\text{var}(U_1) = \mu^2/2$$

and

$$\text{var}(U_{2.1}) = 2\mu^3/3$$

so standardized test statistics are

$$T_1 = \frac{\sum_{i=1}^N \hat{m}_{i,2} - \hat{m}_{i,1}}{\left(2\sum_{i=1}^N \hat{\mu}_i^2\right)^{1/2}}$$

and

$$T_2 = \frac{\sum_{i=1}^N \hat{m}_{i,3}/3 - \hat{m}_{i,2} + (2/3 - \hat{\mu}_i)\hat{m}_{i,1}}{\left\{(2/3)\sum_{i=1}^N \hat{\mu}_i^3\right\}^{1/2}}.$$

T_1 is well known as the score statistic for testing Poisson variation against a negative binomial alternative. Here it appears as the score statistic for testing for non-zero slope in the birth rate representation of the response distribution. This shows that T_1 is appropriate also for testing for underdispersion as represented by the binomial distribution. T_2 is a new statistic involving the third corrected moment of the distribution.

6 Adjusting for Estimation of the Mean

The fact that the μ_i must be estimated from the data means that the corrected moments $\hat{m}_2$ and $\hat{m}_3$ will have expectations less than zero. Dean and Lawless (1989) give an adjusted version of T_1 in which a leverage term is added to the numerator. We prefer to divide the $\hat{m}_r$ by an appropriate leverage factor because this adjusts the higher moments of $\hat{m}_r$ as well as the mean.

We assume a link-linear mean model as for a Poisson generalized linear model,

$$g(\mu_i) = \mathbf{x}_i^T \boldsymbol{\beta}$$

Let h_i be the leverages from the Poisson regression model, the diagonal elements of the hat matrix

$$H = W^{1/2}X(X^TWX)^{-1}X^TW^{1/2}$$

where X is the design matrix with rows $\mathbf{x}_i^T$ and W is the diagonal matrix of working weights for the Poisson regression. Then

$$E\left\{(y_i - \hat{\mu}_i)^2\right\} = (1-h_i)\mu_i + O(n^{-3/2}).$$

We define adjusted corrected moments

$$\hat{m}_{i,r}^a = \left(\frac{y_i - \hat{\mu}_i}{\sqrt{1-h_i}}\right)^r - \hat{\mu}_i, \quad r = 1,2,3$$

and adjusted statistics

$$T_1^a = \frac{\sum_{i=1}^N \hat{m}_{i,2}^a - \hat{m}_{i,1}^a}{\left(2\sum_{i=1}^N \hat{\mu}_i^2\right)^{1/2}}$$

and

$$T_2^a = \frac{\sum_{i=1}^N \hat{m}_{i,3}^a/3 - \hat{m}_{i,2}^a + (2/3 - \hat{\mu}_i)\hat{m}_{i,1}^a}{\left\{(2/3)\sum_{i=1}^N \hat{\mu}_i^3\right\}^{1/2}}.$$

We find that the moments of the adjusted statistics match the nominal moments computed assuming true means much more closely that do those of T_1 and T_2.

7 Edgeworth Expansions

Let T be the observed value for T_1^a or T_2^a. The statistics T_1^a or T_2^a are asymptotically standard normal so the quantile for the observed value is approximately $\Phi(T)$ where $\Phi()$ is the standard normal cumulative distribution.

A higher order approximation to the quantiles can be obtained from an Edgeworth expansion. The third and 4th cumulants for U_1 and $U_{2.1}$ can be computed using $y \sim$ Poisson(μ) to be as follows

	U_1	$U_{2.1}$
κ_3	$\frac{\mu^2}{2} + \mu^3$	$\frac{4\mu^3}{3} + 8\mu^4$
κ_4	$\frac{\mu^2}{2} + 9\mu^3 + 3\mu^4$	$\frac{8\mu^3}{3} + 136\mu^4 + 332\mu^5 + 40\mu^6$

We estimate the 3rd and 4th standardized cumulants to be

$$\rho_{31} = \frac{\sum_{i=1}^N \hat{\mu}_i^2/2 + \hat{\mu}_i^3}{\left(\sum_{i=1}^N \hat{\mu}_i^2/2\right)^{3/2}}$$

and

$$\rho_{41} = \frac{\sum_{i=1}^N \hat{\mu}_i^2/2 + 9\hat{\mu}_i^3 + 3\hat{\mu}_i^4}{\left(\sum_{i=1}^N \hat{\mu}_i^2/2\right)^2}$$

for T_1^a and

$$\rho_{32} = \frac{\sum_{i=1}^N 4\hat{\mu}_i^3/3 + 8\hat{\mu}_i^4}{\left(\sum_{i=1}^N \hat{\mu}_i^2/2\right)^{3/2}}$$

and

$$\rho_{42} = \frac{\sum_{i=1}^N 8\hat{\mu}_i^3/3 + 136\hat{\mu}_i^4 + 332\hat{\mu}_i^5 + 40\hat{\mu}_i^6}{\left(\sum_{i=1}^N \hat{\mu}_i^2/2\right)^2}$$

for T_2^a. Finally we estimate the quantiles as

$$\Phi(T) - \phi(T)\left\{\frac{\rho_{3j}H_2(T)}{6} + \frac{\rho_{4j}H_3(T)}{24} + \frac{\rho_{3j}^2 H_5(T)}{72}\right\}$$

where $j = 1, 2$, $\phi()$ is the standard normal density function and $H_2()$, $H_3()$ and $H_5()$ are the Hermite polynomials of orders 2, 3 and 5 (Barndorff-Nielsen and Cox, 1989).

Test	Lower	Upper
T_1^a	0.0076	0.0436
T_2^a	0.0294	0.0272
${T_1^a}^2 + {T_2^a}^2$	0.0000	0.0638
T_1^a Edg	0.0290	0.0262
T_2^a Edg	0.1180	0.1270
Pearson	0.0316	0.0186
Deviance	0.0290	0.0218

Table 1: Upper and lower tail rejection rates for simulated Poisson data. The nominal upper and lower rates are 0.025 except for ${T_1^a}^2 + {T_2^a}^2$ for which the upper rate is 0.05 and the lower zero.

8 Simulations

5000 data sets were simulated in order the check the null distributions of the test statistics. Data sets were of size $N = 50$ and were generated to be Poisson distributed with means

$$\mu_i = \exp(\beta_0 + \beta_1 x_i)$$

where the x_i were equally spaced between 2 and 5 and $\beta_0 = 0$ and $\beta_1 = 1$. Estimated values for β_0 and β_1 were obtained from Poisson regression for each data set.

Results are given in Table 1. The first two rows of the table give the proportion of cases for which T_1^a and T_2^a exceeded 1.96 (upper tail) or fell below -1.96 (lower tail). These give the size of the tests treating T_1^a and T_2^a as standard normal. The 3rd row gives the proportion of cases for which ${T_1^a}^2 + {T_2^a}^2$ exceeded the upper 0.05 values of the chisquared distribution on 2 df. The lower tail rate is by definition zero in this case. The 4th and 5th rows give rejection rates based on P-values computed from the Edgeworth expansion using 3rd and 4th moments for T_1^a and T_2^a. The last two rows give the rejection rates for the Pearson goodness of fit statistic and the residual deviance, treating each as chisquare on 48 df.

We see that T_1^a is rather right skew but is well corrected by the Edgeworth expansion. The Edgeworth expansion for T_2^a is not successful, but T_2^a holds its nominal size well as a standard normal statistic. All the other statistics hold their nominal size well although the Pearson statistic is somewhat skew to the left.

9 Data Example

We return to the distribution of fetal implants in mice. The Pearson goodness of fit statistic is 598.6 on 697 df while the residual deviance is 715.8 on 697 df. The Pearson statistic suggests some evidence of underdispersion while the deviance statistic does not. Recalling that the Pearson statistic is somewhat left skew, it is not clear from these statistics whether the data can be treated as Poisson or not.

On computing the score statistics we find $T_1^a = -2.64$ confirming that the distribution is underdispersed. More striking though is $T_2^a = -10.2$ showing that the distribution is strongly left skew relative to the Poisson. The two-sided P-values for T_1^a and T_2^a computed from the Edgeworth expansion here are 0.0057 and 7×10^{-22} respectively.

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