

Comparison of the Count Regression Models in Evaluation of the Effects of Hazelnut Harvest Season Variations on Pulmonary Aspergillus

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Abstract

Pulmonary aspergillosis has recently emerged as a worldwide health care problem especially in patients with underlying lung disease. The objective of this study was to compare the Poisson and COM-Poisson regression models and to find the best fitted model for determining the effect of hazelnut harvest season on pulmonary aspergillosis. The data obtained from the state hospital of our city in the time period of two years, from September, 2012 to August, 2014. A retrospective study was conducted. Respiratory specimens which showed repeated isolation of *Aspergillus* were included in the study however only one of the samples was analysed. Cases were classified according to revised definitions given by European Organization for Research and Treatment of Cancer/Invasive Mycosis Study Consensus Group (EORT/MSG). Culture positive 36 patients were detected from 3457 patients. Poisson and Conway-Maxwell-Poisson (COM-Poisson) regression models were compared to determine the best fitted model for identifying the number of new pulmonary aspergillosis cases in hazelnut harvest season. To describe the best fitted model of count data, dispersion, deviance and Akaike Information Criteria (AIC) test statistics were used. Based on statistical test for dispersion, the under-dispersion was found non-significant. This results clearly indicate that Poisson regression model is more appropriate for pulmonary aspergillosis data when compared to COM-Poisson regression model. Deviance and AIC values also confirm this result. Poisson regression model and COM-Poisson regression model were compared with statistical tests. According to statistical tests Poisson regression model was found to be the best fit model for pulmonary aspergillosis data.

Keywords: AIC; Poisson regression; COM-Poisson regression; Pulmonary aspergillosis; Hazelnut harvest season.

Introduction

Pulmonary aspergillosis has recently emerged as a worldwide health care problem especially in patients with underlying lung disease. *Aspergillus* spp. is a saprophytic and pathogenic fungus with a cosmopolitan distribution. It is best known for its colonisation of tree nuts. *Aspergillus* infections can occur while hosts are still in the field, but often show no symptoms until postharvest storage and/or transport [1,2].

In Turkey on Black Sea Coast, hazelnuts are harvested annually in late August and September. During the harvest season spores of fungi disperse with the wind and many COPD and asthma patients apply to the hospital with exacerbation of the disease secondary to infection following the harvest. These exacerbations cause extensive use of broad spectrum antibiotics, immunosuppressive agents and increasing population of terminally ill patients.

In our study the data obtained from a state hospital in the time period of two years, from September, 2012 to August, 2014. A retrospective study was conducted. Demographic details, clinical and radiological findings, predisposing factors and treatments were noted down. Cases were classified as proven, probable and possible invasive Aspergillosis according to revised definitions given by European Organization for Research and Treatment of Cancer/Invasive Mycosis Study Consensus Group (EORT/MSG) [3]. According to the suggestion of this group, all culture positive patients and those fulfilling the following clinical criteria were included in the study; 1) Long term steroid therapy 2) radiological features suggestive of Aspergillosis 3) Microbiological findings. To rule out the changes of contamination respiratory specimens which showed repeated isolation of *Aspergillus* were included in the study however only one of the sample taken for analysis. To demonstrate the relationship with hazelnut farm harvest season (August and September), number of the patients were divided

into two parts according to their hospital visits whether in the nuts picking season or not. Culture positive 36 patients were detected.

All samples were identified as *Aspergillus* spp. morphologically. Patients were on steroid treatment at a minimum dose of 0.3 mg/kg/day of prednisone equivalent for more than three weeks. They had at least one radiological findings supporting the diagnosis of pulmonary aspergillosis. Despite the antifungal therapy 22.2% of the patients died. In clinical work the researcher often encounters situations where the outcome variable is numeric, but in the form of counts. Often it is a count of rare events for a certain period of time. To explore the relationship between dependent variable and some or all of the explanatory variables regression analysis are used [4]. If the dependent variable characterized by rare events count data and all the counts are positive integers Poisson distribution is the most common for fitting. The main assumption of Poisson distribution is that the mean and variance are equal (equidispersion). Unfortunately many real data do not adhere this assumption [5]. In case of violation of assumption, two-parameter generalized form of the Poisson distribution, called the Conway-Maxwell-Poisson (COM-Poisson) distribution allows for over (i.e., the variance is larger than the mean)-and under (i.e., the variance is smaller than the mean) dispersion [6].

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In this study, we compared the Poisson to COM-Poisson regression model and illustrate its usefulness by using two years period of pulmonary aspergillosis data.

Poisson regression models

Poisson regression is one of the members of the Generalized Linear Models (GLM) framework. The simplest distribution used for modeling count data is the Poisson distribution with probability density function

$$f(y; \mu) = \frac{\exp(-\mu) \mu^y}{y!} \quad (1)$$

The canonical link is $g(\mu) = \log(\mu)$ resulting in a log-linear relationship between mean and linear predictor. The variance in the Poisson model is identical to the mean, thus the dispersion is fixed at $\phi = 1$ and the variance function is $V(\mu) = \mu$. The mean Poisson regression can be assumed to follow a log link, $E(Y_i) = \mu_i = (x_i' \beta)$, where x_i denotes the vector of explanatory variables and β the vector of regression parameters. The maximum likelihood estimates can be obtained by maximizing the log likelihood.

Conway-Maxwell-Poisson (Com-Poisson) models

The Conway-Maxwell-Poisson (COM-Poisson) distribution has been re-introduced by statisticians to model count data characterized by either over- or under-dispersion [6-10]. The COM-Poisson distribution was first introduced in 1962 by Conway and Maxwell; in 2008 Guikema et al. [8] evaluated it in the context of a GLM, in the same year Bayesian approach of COM-Poisson are extended by Lord et al. [9]. Sellers and Shmueli [11] enlarged the application area by developing COM Poisson Reg code in R package program. The COM-Poisson distribution is a two-parameter generalization of the Poisson distribution that is flexible enough to describe a wide range of count data distributions [11].

The COM-Poisson probability distribution function is given by the equation:

$$f(y; \lambda, \nu) = \frac{\lambda^y}{(y!)^\nu z(\lambda, \nu)} \quad (2)$$

for a random variable Y, where $Z(\lambda, \nu) = \sum_{j=0}^{\infty} \frac{\lambda^j}{(j!)^\nu}$ and $\nu \geq 0$ is a normalizing constant; ν is considered the dispersion parameter such that $\nu > 1$ represents under-dispersion, and $\nu < 1$ over-dispersion. The COM-Poisson distribution includes three well-known distribution as special cases: Poisson ($\nu = 1$), Geometric ($\nu = 0, \lambda < 1$), and Bernoulli well-known distribution as special cases: Poisson ($\nu = 1$), Geometric ($\nu = 0, \lambda < 1$),

Taking a GLM approach, Sellers and Shmueli (2010) proposed a COM-Poisson regression model using the link function,

$$\eta(E(Y)) = \log \lambda = X' \beta = \beta_0 + \sum_{j=1}^p \beta_j X_j \quad (3)$$

Because of indirectly relationship between $(Y)'$ β , estimating β and ν via associated normal equations become complex. Using (0) and $(0) = 1$, as starting values. These equations can thus be solved via an appropriate iterative reweighted least squares procedure (or by maximizing the likelihood function directly using an optimization program) to determine the maximum likelihood estimates, $\hat{\beta}$ and $\hat{\nu}$. The associated standard errors of the estimated coefficients are derived using the Fisher Information matrix [12].

Testing for variable dispersion

In statistical analysis of count data, if the variance of the random variable is constrained to equal the mean which is called equidispersion,

the Poisson regression model is usually adequate. Because of different factors can invalidate equidispersion hypothesis in the data its implicit restriction: consequently, data often exhibit overdispersion (i.e., the variance is larger than the mean) and, occasionally they exhibit underdispersion with the mean exceeding the variance [13].

In GLM to detect over or under-dispersion simply, the researcher may look at the rule of thumb that the mean deviance, that is deviance/degree of freedom should be close to unity. Deviance theoretically allows one to determine if the fitted GLM model is significantly worse than the saturated model [14].

Sellers et al. [11] established a hypothesis testing procedure to demonstrate the need for a COM-Poisson regression model over a simple Poisson regression model by determine if significant data dispersion exists or not, in other words, they test whether ($\nu = 1$) or otherwise [9]. The test statistics,

$$C = -2 \log \Lambda = -2 \left[\log L(\hat{\beta}^{(0)}, \hat{\nu} = 1) - \log L(\hat{\beta}, \hat{\nu}) \right] \quad (4)$$

where Λ is the likelihood ratio test statistic, β_0 are the maximum likelihood estimates obtained $\hat{\beta}^{(0)}$ under $\nu = 1$ (i.e., the Poisson estimates), and $(\hat{\beta}, \hat{\nu})$, ν are the maximum likelihood estimates under the general state space for the COM-Poisson distribution with 1 degree of freedom. For small samples, the test statistic distribution can be estimated via bootstrap [11].

Akaike information criteria (AIC)

In statistical literatures, based on several likelihood measure, one can compare several models performance. One of the most regularly used measure is AIC. The AIC penalized a model with larger number of parameters, and is defined as

$$AIC = -2 \ln L + 2p \quad (5)$$

where $\ln L$ denotes the fitted log likelihood and p the number of parameters [15]. A relatively small value of AIC is preferred for the fitted model. Analyses were performed using R program. Respectively, `glm()` function from "stats" and `cmp()` function from "COMPoissonReg" package were used.

Result and Conclusion

To obtain the first overview of the dependent variable, the histogram of the observed count frequencies were employed. Figure 1 illustrates the histogram, the marginal distribution exhibits substantial variation (Figures 1 and 2).

Figure 2 presents line plot of total number of patients with positive culture. From the plot we could conclude that, especially in August and September the number of patients with positive culture were increased.

Poisson regression model was fitted to the data, regressing the number of patients with positive culture (Y) on hazelnutfarm harvest season (X) (1: Yes, 0: No); the estimated coefficients were given by $\hat{\beta}_0 = -0.1054$, $\hat{\beta}_1 = 1.6094$, then COM-Poisson regression model was fitted to determine whether equi-dispersion was a reasonable assumption. After dividing the COM-Poisson coefficients by ν dispersion parameter ($-2.1822/1.5082 = 1.4469$), the results in Table 1 indicate that the regression parameters for two models had similar estimates in terms of the coefficient magnitudes.

While the estimated dispersion parameter for Poisson regression model is 0.84, for COM-Poisson model is $\nu = 1.51$, indicating underdispersion. To determine whether the dispersion parameter is

	Classic Poisson			COM-Poisson		
	Estimated Coefficient	Standart Error	z value	Estimated Coefficient	Standart Error	z value
Intercept	-0.1054	0.2357	-0.4472	0.1437	0.4007	0.3586
Season	1.6094	0.3333	4.8287*	2.1822	0.8569	2.5466*
Dispersion parameter	0.84			1.51	[95%CI = (0.70;4.02)]	
Deviance AIC		18.478			26.988	
		68.065			69.382	

Table 1: Estimated regression models for patients with positive culture.

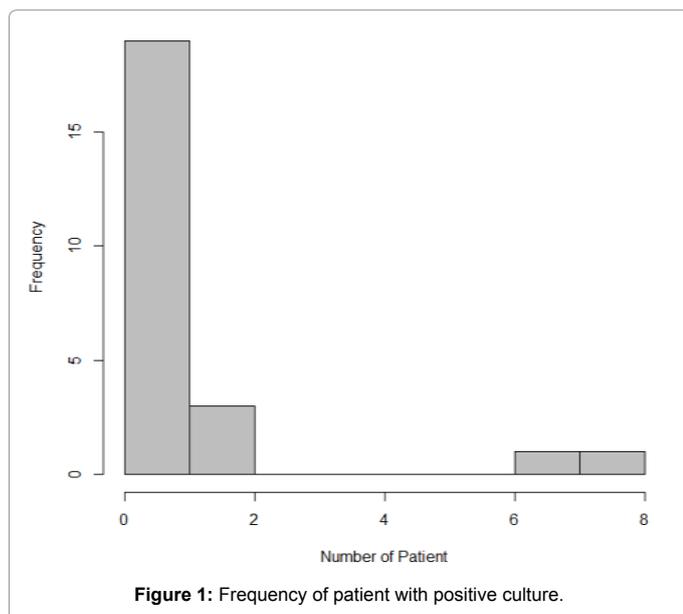


Figure 1: Frequency of patient with positive culture.

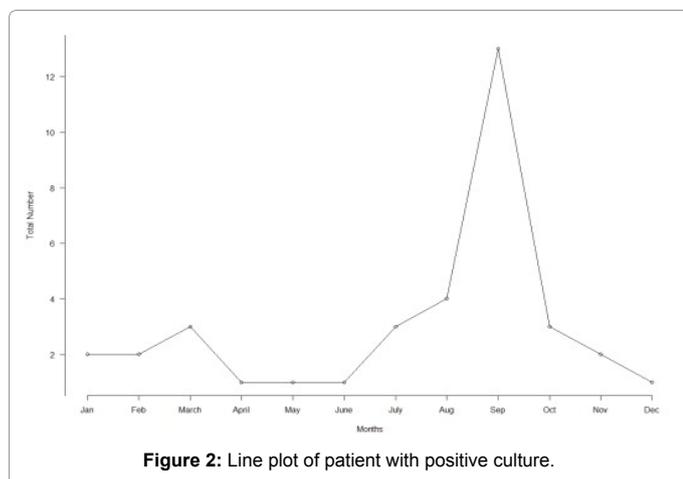


Figure 2: Line plot of patient with positive culture.

significant or not a hypothesis test which established by Sellers and Shmueli [11] was used. The p value was found 0.4085, and the 95% bootstrap confidence interval for ν include the value 1 (using 1000 samples). Indicating that, it is reasonable to assume a Poisson to model this relationship. Table 1 display estimated regression models for patients with positive culture.

According deviance and AIC, the Poisson regression model is better than the COM-Poisson regression model. In terms of model interpretation, the Poisson regression indicates that pulmonary aspergillosis is effected from hazelnut harvest season about five times more.

In this paper Poisson regression model was compared with COM-Poisson model for modeling pulmonary aspergillosis data. We revealed that under-dispersion was not statistically significant and thus it was reasonable to assume a Poisson model to investigate the effects of hazelnut harvest season on pulmonary aspergillosis.

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