Detection of some social parameters on child mortality through joint generalized linear models

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Abstract: In general demographic characteristics are positive in nature. In regression models for positive observations analysis can often be based on either the log-normal or the gamma model. Recently log-normal and gamma models are of interest in fitting data arising from quality-improvement experiments. It is known that the gamma model with the constant coefficient of variation and the log-normal model with constant variance often give similar analysis. However, in the analysis of data from quality improvement experiments neither the coefficient of variation nor the variance needs to be constant, so that the two models do not necessarily give similar results. A choice needs to be made between the gamma and the log-normal models. This article analyzes the effects of social factors in children survival times through joint generalized linear models, and many interested social parameters have been detected in its mean and variance model.

Keywords: Joint generalized linear model; Multiplicative model; Non-constant coefficient of variation; Structured dispersion; Children survival times

1. Introduction

Child mortality is an important factor of population growth and fertility of a nation. Under-five mortality rate for the world dropped from 193 per thousand births in 1960 to 86 in 1998, which corresponds to 55 percent decrease (UNICEF, 2001). In Sub-Saharan Africa, the reduction in mortality rates for children aged 5 and younger, between 1960 and 1989, was nearly 34 percent (from 261 to 173 per thousand births). For example, in Ivory Coast, the same source indicates that under-five mortality rate decreased from 300 to 150 per thousand births between 1960 and 1998. Although much progress has been made in terms of prevention and child care, under-five mortality rates in the Sub-Saharan African region remain high, compared to the mortality rate of 6 per thousands births observed in the industrialized countries in 1998 (UNICEF, 2001).

A number of studies have focused on the factors affecting children mortality (Manda, 1999; Kuate-Defo, 1992; Akoto and Tabutin, 1990; Pebley and Stupp, 1987; Martin *et al.*, 1983, among others). These researches showed that child mortality in developing countries

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was mainly associated with measurable socio-economic conditions such as nutritional status and poor living conditions. However, some unmeasured genetic, environmental and behavioral components still remain non-negligible. In effect, children belonging to the same family share certain unobserved characteristics (or heterogeneity), which may not be sufficiently described by the covariates included in the earlier standard models (Guo and Rodriguez, 1992). The ignorance of such family-level correlation may lead to biased parameters estimates. This unobserved heterogeneity, also referred to as frailty (Vaupel *et al.*, 1979), operates at three different levels, at least: child, family and community (Sastry, 1997). At the family level, children from the same parents inherit common genetic factors and usually grow up in the same household environment. Parents are also more likely to adopt similar child care behavior for all their children. Genetic factors remain the major component of the family-level frailty. However, each child has a proper susceptibility to infection, independently of his family membership (Childs *et al.*, 1992). This idiosyncratic genetic factor remains the major child-level unobserve frailty component. In addition, inside the common global family behavioral factor, parents may adopt a slightly different prenatal and neonatal attitude from one child to the next: the length of the breastfeeding period, the health care practice and the nutritional status, for example. At the community level, the random effects are more likely of behavioural and environmental nature.

During the last ten years, the unobserved heterogeneity has been intensively associated to child mortality studies: Guo and Rodriguez (1992) and Guo (1993)applied a multivariate proportional hazard model to capture the family-specific random effects on clustered data from Guatemala; a logistic model with family random effects was used to examine the frailty common to all children from same mothers in Brazil (Curtis *et al.*, 1993) and Bangladesh (Zenger, 1993), Ronsmans (1995) investigated the patterns of family-level clustering in a rural community of Senegal; Sastry (1987) also presented a hazard model with nested frailty to control for unobserved family and community effects in data from Brazil. More recently, Kuate-Defo (2001) estimated a model for hierarchically clustered data and applied it to child survival in Cameroon.

The model parameters and the distribution for the random effects were generally estimated via the Expectation-Maximization (EM) algorithm (Manda, 2001; Sastry, 1987; Curtis *et al.*, 1993; Guo and Rodriguez, 1992). The EM algorithm is an iterative method, which heavily relies on the choice of starting values. Hence, it may converge toward a local maximum instead of the global one (Sinha and Dey, 1997). To circumvent this problem, a full Bayesian approach, which uses Markov Chain Monte Carlo methods, can be used. Recently, Bayesian frailty models have been developed successfully for child survival data in Mali (Gemperli *et al.*, 2004), Minnesota (Banerfee *et all.*, 2003) and Malawi (Bolstad and Manda, 2001). Kandala *et al.* (2002) also used Bayesian approach to analyze the determinants of undernutrition in Malawi, Tanzania and Zambia. Unlike the EM algorithm,

the Bayesian approach avoids the computation of cumbersome high-dimensional integrals (Manda, 2001).

So far no author studied demographic characteristics through joint modeling of mean and variance. But in general the positive observations mainly belong to exponential family where mean and variance may have certain relation, and the variance may not be constant. Das and Lee (2008a, 2008b) examined quality improvement data with non-constant variance, and analyzed properly. In statistical literature, models are mainly focused on the mean, so that the modeling of the dispersion has often been neglected. The goal of this work is to investigate family heterogeneity in child mortality data from Bihar, through joint generalized linear models (JGNL). In this paper we propose to use the joint modeling of mean and dispersion in children survival times, and many social parameters have been detected in its mean and variance model. We rely on Indian survey data of National Family Health Survey-2(NFHS-2) in 1998-1999 from Bihar State of India. In India Bihar is one of the most poor State, and we analyze the survival times of children of that State.

2. Log-normal and gamma models with constant variance

In regression models for positive observations analysis can often be based on either the log-normal or the gamma model. There is a well known correspondence between multiplicative regression models and additive models of their logarithms. In classical linear models, it is assumed that the variance of the response (Y) is constant over the entire range of parameter values. When the variance increases with the mean we may consider a model with the constant coefficient of variation:

$$Var(Y) = \sigma^2 \mu_Y^2,$$

where σ is the coefficient of variation of Y and $\mu_Y = E(Y)$. In generalized linear models (GLMs; McCullagh and Nelder, 1989) the gamma model satisfies the mean and variance relationship above. For small σ, the variance-stabilizing transformation, $Z = \log(Y)$, has approximate moments

$$E(Z) = \log \mu_Y - \sigma^2/2 \;\; and \; Var(Z) \simeq \sigma^2.$$

If the systematic part of the model is multiplicative on the original scale, and hence additive on the log scale, then

$$Y_i = \mu_{Y_i} \epsilon_i \;\; (i = 1, 2, ..., n) \tag{1}$$

with

$$\eta_i = \log \mu_{Y_i} = x_i^t \beta = \beta_0 + x_{i1}\beta_1 + ... + x_{ip}\beta_p$$

and $\{\epsilon_i\}$ are independent identically distributed (IID) with $E(\epsilon_i) = 1$. In GLMs μ_{Y_i} is the scale parameter and $Var(\epsilon_i) = \sigma^2$ is the shape parameter. Then

$$Z_i = \log Y_i = \mu_{Z_i} + \delta_i \quad (i = 1, 2, ..., n) \tag{2}$$

with

$$\mu_{Z_i} = [\beta_0 + E\{\log(\epsilon_i)\}] + x_{i1}\beta_1 + ... + x_{ip}\beta_p$$

and $\{\delta_i = \log \epsilon_i - E\{\log(\epsilon_i)\}\}$'s are IID with $E(\delta_i) = 0$.

Conversely, if Y_i follows a log-normal distribution, i.e. $Z_i \sim N(\mu_{Z_i}, \sigma^2)$ then

$$\mu_{Y_i} = E(\exp Z_i) = \exp(\mu_{Z_i} + \sigma^2/2) \neq \exp(\mu_{Z_i}).$$

Thus, with the exception for the intercept term, the remaining parameters $\beta_1, \beta_2, ..., \beta_p$ can be estimated either from the constant coefficient of variation model (1) or linear model for the transformation of the original data to log scale (2). The intercept parameters in models (1) and (2) are not the same, but they will often be unimportant in practice: see discussion in Myers et al. (2002; page 169).

Firth (1988) gave a comparison of the efficiencies of the maximum-likelihood (ML) estimators from gamma model (the constant coefficient of variation model) when the errors are in fact log-normal with those of the log-normal model when the errors have a gamma distribution. He concluded that the ML estimators from the gamma model perform slightly better under reciprocal misspecification. For small σ^2 it is likely to be difficult to discriminate between Normal-theory linear models for $\log Y$ and gamma-theory multiplicative models for Y.

3. Multiplicative models with non-constant coefficient of variation

If σ^2 is not constant, i.e. ϵ_i is not identically distributed with a common $E(\log \epsilon_i)$, parameter estimates from one model may have no interpretation on the other model. For analysis of data from quality-improvement experiments the aim is to minimize variance using covariates while controlling mean to the target. Thus, in the analysis of the data from quality-improvement experiments, σ^2 is often not constant. For these situations, Lee and Nelder (1998, 2003) proposed to use joint GLMs (JGLMs) to allow for structured dispersions. A detailed discussion on JGLMs is given in Lee, Nelder and Pawitan (2006): see also Qua, Tan and Rybicky (200), Park and Lesperance (2003) and Das and Lee (2008a, 2008b).

Consider a JGLM for the multiplicative model (1)

$$E(Y_i) = \mu_{Y_i}, \quad and \quad Var(Y_i) = \sigma^2_{Y_i}\mu^2_{Y_i},$$

where

$$\eta_i = \log(\mu_{Y_i}) = x_i^t \beta_Y, \quad and \ \xi_i = \log(\sigma^2_{Y_i}) = g_i^t \gamma_Y, \tag{3}$$

where g_i is the row vector of the model matrix used in the dispersion model. The ML estimators for β_Y are obtained by maximizing the log-likelihood

$$\ell_g(\theta) = \sum_i \log f(y_i, \theta) \tag{4}$$

and restricted ML (REML) estimators for γ_Y are estimated by maximizing the (log) adjusted profile likelihood of Cox and Reid (1987) and Lee and Nelder (1998)

$$p_{\beta_Y}(\ell_g(\theta)) = \{\ell_g(\theta) - \{\log \det(E(-\partial \ell_g^2(\theta)/\partial \beta_Y^2)/2\pi)\}/2\}|_{\beta_Y = \hat{\beta}_\gamma}. \tag{5}$$

The whole estimation process is done iteratively by using two interconnected iterative weighted least squares (Lee *et al.*, 2006).

Consider a JGLM for the log normal model (2)

$$E(Z_i) = \mu_{Z_i}, \quad and \quad Var(Z_i) = \sigma^2_{Z_i},$$

where

$$\mu_{Z_i} = x_i^t \beta_Z, \quad and \quad \xi_i = \log(\sigma^2_{Z_i}) = g_i^t \gamma_Z. \tag{6}$$

The ML estimators for β_Z under the log-normal model are obtained by maximizing the log-likelihood

$$\ell_l(\theta) = \sum_i \{\log f(z_i, \theta) - z_i\} \tag{7}$$

and REML estimators for γ_Z are estimated by maximizing the adjusted profile likelihood

$$p_{\beta_Z}(\ell_l(\theta)) = \{\ell_l(\theta) - \{log \ det(E(-\partial \ell_l^2(\theta)/\partial \beta_Z^2)/2\pi)\}/2\}|_{\beta_Z = \hat{\beta}_\gamma}, \tag{8}$$

where $-z_i = \log|dz_i/dy_i| = -\log y_i$ is logarithm of Jacobian of the transformation.

For gamma model the Akaike information criteria (AIC) is

$$AIC = -2\ell_g(\theta) + 2p_g,$$

where p_g is the number of parameters in the gamma JGLM and for log-normal model the AIC is

$$AIC = -2\ell_l(\theta) + 2p_l,$$

where p_l is the number of parameters in the log-normal JGLM. If we are comparing models with the same number of parameters ($p_g = p_l$) then we need only compare the maximized likelihoods. To compare models with different scales of response variables (y

for the gamma model and $\log y$ for the log-normal model) we need the Jacobian term in (7).

4. Data and covariates

Description of data: The National Family Health Survey, Bihar 1998-99: India's first National Family Health Survey(NFHS-1)was conducted in 1992-93.The Ministry of Health and Family Welfare(MOHFW)subsequently designated the International Institute for Population Sciences(IIPS), Mumbai, as the nodal agency to initiate a second survey(NFHS-2),which was conducted in 1998-99.An important objective of (NFHS-2) is to provide state-level and national-level information on fertility, family planning, infant and child mortality, reproductive health, child health, nutrition of women and children, and the quality of health and family welfare services. Another important objective is to examine this information in the context of related socioeconomic and cultural factors. NFHS-2 used three types of questionnaires: the Household questionnaire, the Woman Questionnaire, the Village Questionnaire. The Woman Questionnaire collected information from ever-married women age 15-49 who were usual residents of the sample household. This questionnaire included questions relating to respondent's background, the details of births which had occurred to her during the last three years, and practice of contraception. The Child Questionnaire was designed to record details of antenatal care, details of delivery, breastfeeding, and post partum amenorrhoea, immunization and health care for the two most recent births occurred to each eligible woman during three years preceding the survey.

Description of covariates and levels:

For our study, we have used the data on place of residence, religion, caste, education of the mother and place of delivery and some anti-natal and post-natal care etc. for those children who had died. The covariates are categorised according to the following levels.

Place of residence : Urban (1) and Rural (2).

Religion : All religions except Muslim (1) and Muslim (2).

Caste : Scheduled caste and Scheduled tribe (1), Backward classes (2) and general classes (3).

Education of mother : Illiterate (1) and literate (2).

Sex of the child : Male (1) and female (2).

Birth order no. of the child : 1 for eldest and so on.

Tetanus injection befor child birth : No (1), at least one (2).

Place of delivery : At home (1) and hospital or equivalent (2).

Whether recieved BCG or not : No (1) and yes (2).

Similar categorisations for DPT1, Polio-1, DPT-2, Polio-2, DPT3, Polio-3, Measles and Polio-0.

Breast feeding : Never brestfed (1) and otherwise (2).

5. Analysis

Recently, log-normal and gamma models (Myers et al., 2002) are of interest in fitting data arising from quality-improvement experiments. In this section, we analyze the sample data (NFSH-2) of survival times of children in Bihar by using structured dispersion.

In NFSH-2 data, there are many covariates and factors which are presented in Section 4. For factors we take a constraint that the effects of the first levels in the factors are zero. That is we take the first level of each factor as the reference level by taking the estimate of the effect of the first level as zero. Suppose that α_i for $i = 1, 2, 3$ represents the main effect of A. We take $\hat{\alpha}_1 = 0$, so that $\hat{\alpha}_2 = \hat{\alpha}_2 - \hat{\alpha}_1$. For example the estimate for the effect A_2 means the effect of difference between the second and the first levels in the main effect A, i.e. $\hat{\alpha}_2 - \hat{\alpha}_1$. The selected models have the smallest Akaike information criterion (AICs) value in each class. Because AIC selects a model which minimizes the predicted squared error loss (Hastie *et al.*, 2001, p. 203), it is not necessary that *all* the selected effects are significant. We retain some insignificant effects in the model in order to respect the marginality rule, namely that when an interaction term is significant all related lower-order interactions and main effects should be included in the model (Nelder, 1994).

It was found in the exploratory data analysis stage that anti-natal and post-natal care vaccinations such as various doses of DPT, Polio, Measles etc. were not significant and hence those covariates are not included in our further analysis steps. We present the following explanations with the remaining covariates.

From Table 1, the values of AIC of Log-normal model is 490.8, while Gamma model is 532.19., so that AIC clearly choose Log-normal model. Again in the mean model of Log-normal model (in Table 1), variable birth-order and factor education of the mother are not significant, while they are significant in the mean model of Gamma model. So it is expected to obtain better model than this under Log-normal distribution. In Table 2, we have presented our final models under Log-normal (with AIC 489.5) and Gamma model (with AIC 532.19), and AIC selects the Log-normal model as the appropriate final model.

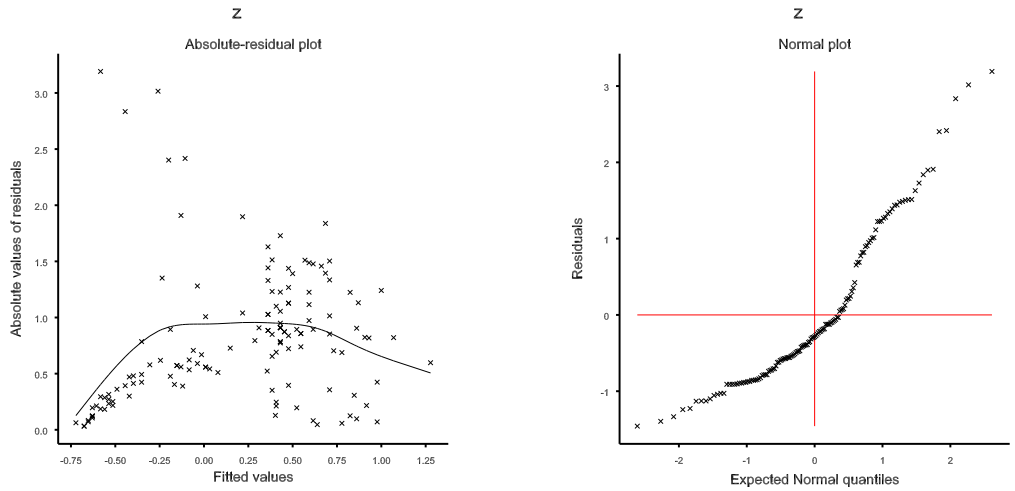
In Figure 1(a), we plot the absolute values of residuals with respect to fitted values, and in Figure 1(b), we plot the normal probability plot for the mean model in Table 2 of our final selected Log-normal model. Figure 1(a) has a flat running means which indicates that joint modeling of mean and variance (in Table 2) would be satisfactory, and also Figure 1(b) does not show any systematic departures, indicating no lack of fit of our final selected Log-normal model (in Table 2).

From Table 2, it is seen that the two factors namely place of delivery and whether breastfed or not in the dispersion model to the levels (1, 1), the variance will be reduced.

Table 1: Results for mean and dispersion models of children survival times data from log-normal and gamma fit

		log-normal model				gamma model			
	Covar.	estimate	*s.e.*	t	P-value	estimate	*s.e.*	t	P-value
Mean model	Const.	-1.31	0.37	-3.57	0.00	-1.95	0.44	-4.44	0.00
	mother's age	0.04	0.02	2.19	0.02	0.10	0.02	4.42	0.00
	birth order	-0.07	0.05	-1.32	0.19	-0.21	0.06	-3.45	0.00
	educ-literate	-0.24	0.23	-1.08	0.28	-0.58	0.25	-2.31	0.02
	delivery-Hospital	0.40	0.23	1.74	0.07	0.70	0.25	2.81	0.01
	breastfed-yes	1.04	0.17	6.04	0.00	1.47	0.18	7.96	0.00
Dispers. model	Const.	-3.04	0.78	-3.90	0.00	-2.07	0.75	-2.76	0.01
	mother's age	0.12	0.04	3.39	0.00	0.09	0.03	2.68	0.01
	birth order	-0.29	0.10	-2.99	0.01	-0.23	0.09	-2.48	0.01
	delivery-hospital	0.85	0.33	2.57	0.01	0.54	0.32	1.67	0.09
	breastfed-yes	1.43	0.30	4.81	0.00	0.77	0.30	2.59	0.01
AIC		$468.80 + 2 \times 11$				$509.19 + 2 \times 11$			

So, we do not use above two factors in the mean model to adjust the mean because it will affect the variance.



(a) (b)

Figure 1: For final Log-normal non-constant variance models (a) The Absolute residual plots with respect to fitted values and (b) Normal probability for mean of children survival times

Table 2: Final results for mean and dispersion models of children survival times data from log-normal and gamma fit

		log-normal model				gamma model			
	Covar.	estimate	*s.e.*	t	P-value	estimate	*s.e.*	t	P-value
Mean	Const.	-1.09	0.31	-3.50	0.00	-1.95	0.44	-4.44	0.00
model	mother's age	0.02	0.01	1.90	0.05	0.10	0.02	4.42	0.00
	birth order	–	–	–	–	-0.21	0.06	-3.45	0.00
	educ-literate	–	–	–	–	-0.58	0.25	-2.31	0.00
	delivery-hospital	0.48	0.23	2.11	0.03	0.70	0.25	2.81	0.00
	breastfed-yes	1.01	0.17	5.94	0.00	1.47	0.18	7.96	0.00
Dispers.	Const.	-3.09	0.80	-3.84	0.00	-2.07	0.75	-2.76	0.01
model	mother's age	0.12	0.04	3.28	0.00	0.09	0.03	2.68	0.01
	birth order	-0.29	0.10	-2.91	0.00	-0.23	0.09	-2.48	0.01
	delivery-hospital	0.91	0.33	2.78	0.01	0.54	0.32	1.67	0.09
	breastfed-yes	1.46	0.29	4.99	0.00	0.77	0.30	2.59	0.01
AIC		$471.5 + 2 \times 9$				$509.19 + 2 \times 11$			

4. Concluding remarks

When there is heterogenity in the data the log-transformation is often recommended. If σ^2 is constant, i.e. ϵ_i is identically distributed with a common $E(\log \epsilon_i)$, parameters from the log-normal and gamma models have a common interpretation. We see for the analysis of children survival times data (NFHS-2) that the simple log-transformation may not be sufficient, so that a further structured dispersion model is required. Furthermore, with structured dispersion there is no reason that the two models will give parameterizations with a common interpretation. In all tables we found that the standard error of estimates from two models are very similar, regardless of the presence of structured dispersions. However, parameter estimates can be sufficiently different as to give different conclusions. In such circumstances the AICs and model checking plots are useful in selecting a better model. As log-normal and gamma models become popular for the analysis of life-time data, further studies about the model choice are of interest. Thus, proper modeling of structured dispersion is important for the analysis of life-time data giving the optimal setting of interested parameters. From the two fitted final models (Log-normal and Gamma in Table 2) significant social parameters effecting in the children survival times can be easily determined.

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