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A Bayesian analysis for the bivariate geometric distribution in the presence of covariates and censored data

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Abstract

In this paper, we introduce a Bayesian analysis for bivariate geometric distributions applied to lifetime data in the presence of covariates and censored data using Markov Chain Monte Carlo (MCMC) methods. We show that the use of a discrete bivariate geometric distribution could bring us some computational advantages when compared to standard existing bivariate exponential lifetime distributions introduced in the literature assuming continuous lifetime data as for example, the exponential Block and Basu bivariate distribution. Posterior summaries of interest are obtained using the popular OpenBUGS software. A numerical illustration is introduced considering a medical data set related to the recurrence times of infection for kidney patients.

Keywords: *Bivariate geometric distribution, Lifetime data, Bayesian analysis, MCMC methods, Covariates, Censored lifetimes.*

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1. Introduction

Lifetime data is very common in medical and engineering applications associated to the survival times of patients or components. Usually, the lifetime denoted by X is assumed to be a continuous random variable with a specified parametrical distribution as for example, an exponential, a Weibull, a log-normal or a gamma distribution (see for example [13]). In some cases we could have more than one lifetime related to each unit. As a special situation, we have two lifetimes X_1 and X_2 associated to each unit, where it is important to model the possible existing dependence between the lifetimes X_1 and X_2 . This occurs for example in medical studies considering the failure times of paired organs like kidney, lungs, eyes, ears, dental implants among many others. Assuming continuous bivariate random variables we could consider different parametrical distributions to analyze bivariate lifetime data introduced in the literature [3, 11, 12, 18, 20, 21].

Due to the fact that censoring is a key aspect of survival analysis, many works recently introduced in the literature have been related to the analysis of the bivariate lifetime distributions in the presence of right censoring, which most of them are in respect to the Marshall-Olkin bivariate distribution and Block and Basu distribution, (see for example, [5, 7, 10, 17, 20]). Despite the fact that discrete measuring of the lifetime values is so common in both medical and engineering experiments, we could see only few studies in this regard in the literature, (see for example [6, 9, 22]); however a bivariate discrete lifetime distribution in the presence of censoring may be of interest to discuss.

In applications, usually we have the presence of censoring data and covariates associated to each unit. In this situation, we could have some computational difficulties to get standard classical inferences for the parameters of these models, as for example, using maximum likelihood approach. In this way, the use of Bayesian methods is becoming very popular in the statistical analysis of bivariate lifetime models (see for example, [1, 19]).

An alternative for the use of a continuous bivariate lifetime distribution, it is to assume that the lifetimes X_1 and X_2 are discrete random variables assuming any positive integer that is, we round the lifetimes given with decimal part to an integer. In this way, [2] introduced a general multivariate geometric distribution which showed that it leads in a natural way to the Marshall-Olkin multivariate exponential distribution. [16] studied the characterizations of the bivariate exponential and geometric distributions. The bivariate geometric distribution proposed by [2] has joint probability mass function (*pmf*) given by,

$$P(X_1, X_2) = \begin{cases} P_1(x_1, x_2) = \theta_1 \theta_2 (1 - \theta_1 - \theta_2)^{x_1-1} (1 - \theta_2)^{x_2-x_1-1}, & x_1 < x_2 \\ 0 & x_1 = x_2 \\ P_2(x_1, x_2) = \theta_1 \theta_2 (1 - \theta_1 - \theta_2)^{x_2-1} (1 - \theta_1)^{x_1-x_2-1}, & x_1 > x_2, \end{cases} \quad (1)$$

where the marginal probability mass function for X_1 and X_2 are standard geometric distributions starting at one, given respectively by,

$$p(x_1) = (1 - \theta_1)^{x_1-1} \theta_1, x_1 = 1, 2, 3, \dots,$$

and,

$$p(x_2) = (1 - \theta_2)^{x_2-1} \theta_2, x_2 = 1, 2, 3, \dots,$$

with means, variances, covariance and correlation given respectively, by

$$\mu_1 = E(X_1) = \frac{1}{\theta_1}, \mu_2 = E(X_2) = \frac{1}{\theta_2},$$

$$\sigma_1^2 = Var(X_1) = \frac{1 - \theta_1}{\theta_1^2}, \sigma_2^2 = Var(X_2) = \frac{1 - \theta_2}{\theta_2^2},$$

$$Cov(X_1, X_2) = \frac{-1}{1 - r},$$

$$\rho_{12} = Corr(X_1, X_2) = -\frac{\theta_1 \theta_2}{(1 - r) \left[(1 - \theta_1)(1 - \theta_2) \right]^{0.5}},$$

where, $r = 1 - \theta_1 - \theta_2$.

From (1), we observe that this bivariate discrete model assumes that $P(X_1 = X_2) = 0$, but in applications we could have this probability very small, but different of zero, a restrictive property of the model. In some cases, however, like studying the time of blindness of eyes or infection of kidneys, this probability practically is zero. In such cases the proposed model will be more fit to the data rather than the models with positive probability of $X_1 = X_2$. In medical or engineering applications, we usually consider a discretization of continuous data and we should choose an appropriate scale to use in our data. For example, if we have continuous observations 5.2 and 5.3 we could use 52 and 53 (multiplying by 10) in place of using the scale rounding up the two values equal to 5. Other characteristic of this distribution, is the negative covariance structure that is linked to the genesis of the distribution (see Arnold, 1975).

In this paper, we explore the use of a bivariate geometric distribution to analyze bivariate lifetime data, in the presence of censoring. This paper is organized as follows: in section 2, we consider the bivariate lifetime variables under the right censoring scheme and we drive the likelihood; in section 3, we introduce a Bayesian analysis in the presence of censored data; in section 4, we consider a numerical illustration considering the analysis of recurrence times of infection for kidney patients; finally in section 5, we introduce some concluding remarks.

2. Preliminaries

Let $(X_{11}, X_{21}), \dots, (X_{1n}, X_{2n})$ be a random sample of size n from an ordinary bivariate geometric (OBG) distribution with joint (pmf) in (1). Suppose that either X_1 or X_2 can be censored at Y_1 or Y_2 , respectively and that censoring is independent of the lifetimes. Let us subdivide the n observations into four classes:

C_1 : $X_{1i} < Y_{1i}$ and $X_{2i} < Y_{2i}$, thus both x_{1i} or x_{2i} are the real lifetimes;

C_2 : $X_{1i} < Y_{1i}$ and $Y_{2i} < X_{2i}$, that is, we observe x_{1i} and y_{2i} ;

C_3 : $Y_{1i} < X_{1i}$ and $X_{2i} < Y_{2i}$, we observe y_{1i} and x_{2i} ;

C_4 : $Y_{1i} < X_{1i}$ and $Y_{2i} < X_{2i}$, we observe y_{1i} and y_{2i} ;

Suppose $I_1 = \{i \in C_1 \mid x_{1i} < x_{2i}\}$, $I_2 = \{i \in C_1 \mid x_{2i} < x_{1i}\}$, $I_3 = \{i \in C_2 \mid x_{1i} < x_{2i}\}$, $I_4 = \{i \in C_2 \mid x_{2i} < x_{1i}\}$, $I_5 = \{i \in C_3 \mid x_{1i} < x_{2i}\}$, $I_6 = \{i \in C_3 \mid x_{2i} < x_{1i}\}$, $I_7 = \{i \in C_4 \mid x_{1i} < x_{2i}\}$, $I_8 = \{i \in C_4 \mid x_{2i} < x_{1i}\}$

Now based on the aforementioned definitions, the likelihood function of the actual observed data considering bivariate right censored lifetimes in this model is given by,

$$\begin{aligned} & \prod_{i \in I_6} \left(\sum_{x_{1i}=y_{1i}+1}^{\infty} P_2(x_{1i}, x_{2i}) \right) \prod_{i \in I_7} \left(\sum_{x_{1i}=y_{1i}+1}^{\infty} \sum_{x_{2i}=y_{2i}+1}^{\infty} P_1(x_{1i}, x_{2i}) \right) \\ & \prod_{i \in I_8} \left(\sum_{x_{1i}=y_{1i}+1}^{\infty} \sum_{x_{2i}=y_{2i}+1}^{\infty} P_2(x_{1i}, x_{2i}) \right) \\ & \prod_{i \in I_6} \left(\sum_{x_{1i}=y_{1i}+1}^{\infty} P_2(x_{1i}, x_{2i}) \right) \prod_{i \in I_7} \left(\sum_{x_{1i}=y_{1i}+1}^{\infty} \sum_{x_{2i}=y_{2i}+1}^{\infty} P_1(x_{1i}, x_{2i}) \right) \\ & \prod_{i \in I_8} \left(\sum_{x_{1i}=y_{1i}+1}^{\infty} \sum_{x_{2i}=y_{2i}+1}^{\infty} P_2(x_{1i}, x_{2i}) \right) \end{aligned}$$

where,

$$\begin{aligned}
\sum_{x_{2i}=y_{2i}+1}^{\infty} P_1(x_{1i}, x_{2i}) &= \theta_1(1-\theta_1-\theta_2)^{x_{1i}-1}(1-\theta_2)^{y_{2i}-x_{1i}-1}, \\
\sum_{x_{2i}=y_{2i}+1}^{\infty} P_2(x_{1i}, x_{2i}) &= \theta_1(1-\theta_1-\theta_2)^{y_{2i}}(1-\theta_1)^{x_{1i}-y_{2i}-1}, \\
\sum_{x_{1i}=y_{1i}+1}^{\infty} P_1(x_{1i}, x_{2i}) &= \theta_2(1-\theta_2)^{x_{2i}-y_{1i}-1}(1-\theta_1-\theta_2)^{y_{1i}}, \\
\sum_{x_{1i}=y_{1i}+1}^{\infty} P_2(x_{1i}, x_{2i}) &= \theta_2(1-\theta_1)^{y_{1i}-x_{2i}}(1-\theta_1-\theta_2)^{x_{2i}-1},
\end{aligned}$$

and

$$\sum_{x_{1i}=y_{1i}+1}^{\infty} \sum_{x_{2i}=y_{2i}+1}^{\infty} P_2(x_{1i}, x_{2i}) = (1-\theta_1)^{y_{1i}-y_{2i}}(1-\theta_1-\theta_2)^{y_{2i}}.$$

We can summarize the likelihood function as follow:

$$L(\theta_1, \theta_2) = \theta_1^{m_1} \theta_2^{m_2} (1-\theta_1)^{z_1} (1-\theta_2)^{z_2} (1-\theta_1-\theta_2)^{z_{12}}, \quad (2)$$

where, $n_i = |I_i|$, $i = 1, \dots, 8$, be the cardinal number of the set I_i , $m_1 = n_1 + n_2 + n_3 + n_4$, $m_2 = n_1 + n_2 + n_5 + n_6$, $z_{12} = \sum_{i \in I_1 \cup I_3} x_{1i} + \sum_{i \in I_2 \cup I_6} x_{2i} + \sum_{i \in I_5 \cup I_7} y_{1i} + \sum_{i \in I_4 \cup I_8} y_{2i}$, $z_1 = \sum_{i \in I_2 \cup I_4} x_{1i} - \sum_{i \in I_2 \cup I_6} x_{2i} + \sum_{i \in I_6 \cup I_8} y_{1i} - \sum_{i \in I_4 \cup I_8} y_{2i}$ and $z_2 = \sum_{i \in I_1} x_{2i} - \sum_{i \in I_1 \cup I_3} x_{1i} + \sum_{i \in I_3 \cup I_5 \cup I_7} y_{2i} - \sum_{i \in I_5 \cup I_7} y_{1i}$.

3. A Bayesian Analysis in the Presence of Covariates and Censored Observations

In this section we consider the Bayes estimators of θ_1 , θ_2 and the survival functions under the Squared error loss (SEL) function. In this way, we are able to obtain the closed form estimators for all parameters. Suppose that (θ_1, θ_2) has the following prior density:

$$\pi(\theta_1, \theta_2) \propto \theta_1^{\alpha_1-1} \theta_2^{\alpha_2-1} (1-\theta_1-\theta_2)^{\alpha_3-1}, \quad \theta_1 + \theta_2 < 1, \quad (3)$$

which is a conjugate prior, denoted by $Dir_2(\alpha_0, \alpha_1, \alpha_2)$, i.e., the Dirichlet distribution with parameters α_0 , α_1 and α_2 . Combining the likelihood

function (2) with the prior (3), the joint posterior density function of θ_1 and θ_2 can be written as

$$\pi(\theta_1, \theta_2 | x, y) \propto \theta_1^{m_1 + \alpha_1 - 1} \theta_2^{m_2 + \alpha_2 - 1} (1 - \theta_1)^{z_1} (1 - \theta_2)^{z_2} (1 - \theta_1 - \theta_2)^{z_{12} + \alpha_0 - 1}. \quad (4)$$

Using the result,

$$(1 - \theta_i)^{z_i} = \sum_{r=0}^{\infty} \binom{z_i}{r} \theta_i^r, i = 1, 2,$$

we can rewrite (4) as:

$$\pi(\theta_1, \theta_2 | x, y) = \frac{1}{D_1} \sum_{r=0}^{\infty} \sum_{k=0}^{\infty} (-1)^{r+k} \binom{z_1}{r} \binom{z_2}{k} \theta_1^{m_1 + \alpha_1 + r - 1} \theta_2^{m_2 + \alpha_2 + k - 1} (1 - \theta_1 - \theta_2)^{z_{12} + \alpha_0 - 1}, \quad (5)$$

where,

$$D_1 = \sum_{r=0}^{\infty} \sum_{k=0}^{\infty} \frac{(-1)^{r+k} \binom{z_1}{r} \binom{z_2}{k} \Gamma(m_1 + m_2 + \alpha_0 + \alpha_1 + \alpha_2 + z_{12} + r + k)}{\Gamma(m_1 + \alpha_1 + r) \Gamma(m_2 + \alpha_2 + k) \Gamma(z_{12} + \alpha_0)}.$$

Now, the Bayes estimators for θ_1 , θ_2 and the marginal survival functions of X_1 and X_2 , under the SEL function are obtained, respectively as follow:

$$E(\theta_1 | x, y) = \begin{cases} \frac{m_1 + \alpha_1}{m_1 + m_2 + \alpha_0 + \alpha_1 + \alpha_2 + z_{12}} & \text{if } z_1 = z_2 = 0 \\ \frac{\sum_{r=0}^{\infty} \sum_{k=0}^{\infty} (-1)^{r+k} \binom{z_1}{r} \binom{z_2}{k} \frac{\Gamma(m_1 + \alpha_1 + r + 1) \Gamma(m_2 + \alpha_2 + k)}{\Gamma(m_1 + m_2 + \alpha_0 + \alpha_1 + \alpha_2 + z_{12} + r + k + 1)}}{\sum_{r=0}^{\infty} \sum_{k=0}^{\infty} (-1)^{r+k} \binom{z_1}{r} \binom{z_2}{k} \frac{\Gamma(m_1 + \alpha_1 + r) \Gamma(m_2 + \alpha_2 + k)}{\Gamma(m_1 + m_2 + \alpha_0 + \alpha_1 + \alpha_2 + z_{12} + r + k)}} & \text{if } z_1, z_2 \neq 0, \end{cases} \quad (6)$$

$$E(\theta_2 | x, y) = \begin{cases} \frac{m_1 + \alpha_1}{m_1 + m_2 + \alpha_0 + \alpha_1 + \alpha_2 + z_{12}} & \text{if } z_1 = z_2 = 0 \\ \frac{\sum_{r=0}^{\infty} \sum_{k=0}^{\infty} (-1)^{r+k} \binom{z_1}{r} \binom{z_2}{k} \frac{\Gamma(m_1 + \alpha_1 + r) \Gamma(m_2 + \alpha_2 + k + 1)}{\Gamma(m_1 + m_2 + \alpha_0 + \alpha_1 + \alpha_2 + z_{12} + r + k + 1)}}{\sum_{r=0}^{\infty} \sum_{k=0}^{\infty} (-1)^{r+k} \binom{z_1}{r} \binom{z_2}{k} \frac{\Gamma(m_1 + \alpha_1 + r) \Gamma(m_2 + \alpha_2 + k)}{\Gamma(m_1 + m_2 + \alpha_0 + \alpha_1 + \alpha_2 + z_{12} + r + k)}} & \text{if } z_1, z_2 \neq 0, \end{cases} \quad (7)$$

$$E\left((1-\theta_1)^t \mid x, y\right) = \begin{cases} \sum_{h=0}^t (-1)^h \binom{t}{h} \frac{\Gamma(m_1 + \alpha_1 + h) \Gamma(m_2 + \alpha_2)}{\Gamma(m_1 + m_2 + \alpha_0 + \alpha_1 + \alpha_2 + z_{12} + h)} & \text{if } z_1 = z_2 = 0 \\ \frac{\sum_{h=0}^t \sum_{r=0}^{\infty} \sum_{k=0}^{\infty} (-1)^{r+k+h} \binom{z_1}{r} \binom{z_2}{k} \binom{t}{h} \frac{\Gamma(m_1 + \alpha_1 + r + h) \Gamma(m_2 + \alpha_2 + k)}{\Gamma(m_1 + m_2 + \alpha_0 + \alpha_1 + \alpha_2 + z_{12} + r + k + h)}}{\sum_{r=0}^{\infty} \sum_{k=0}^{\infty} (-1)^{r+k} \binom{z_1}{r} \binom{z_2}{k} \frac{\Gamma(m_1 + \alpha_1 + r) \Gamma(m_2 + \alpha_2 + k)}{\Gamma(m_1 + m_2 + \alpha_0 + \alpha_1 + \alpha_2 + z_{12} + r + k)}} & \text{if } z_1, z_2 \neq 0, \end{cases} \quad (8)$$

and,

$$E\left((1-\theta_2)^t \mid x, y\right) = \begin{cases} \sum_{h=0}^t (-1)^h \binom{t}{h} \frac{\Gamma(m_1 + \alpha_1) \Gamma(m_2 + \alpha_2 + h)}{\Gamma(m_1 + m_2 + \alpha_0 + \alpha_1 + \alpha_2 + z_{12} + h)} & \text{if } z_1 = z_2 = 0 \\ \frac{\sum_{h=0}^t \sum_{r=0}^{\infty} \sum_{k=0}^{\infty} (-1)^{r+k+h} \binom{z_1}{r} \binom{z_2}{k} \binom{t}{h} \frac{\Gamma(m_1 + \alpha_1 + r) \Gamma(m_2 + \alpha_2 + k + h)}{\Gamma(m_1 + m_2 + \alpha_0 + \alpha_1 + \alpha_2 + z_{12} + r + k + h)}}{\sum_{r=0}^{\infty} \sum_{k=0}^{\infty} (-1)^{r+k} \binom{z_1}{r} \binom{z_2}{k} \frac{\Gamma(m_1 + \alpha_1 + r) \Gamma(m_2 + \alpha_2 + k)}{\Gamma(m_1 + m_2 + \alpha_0 + \alpha_1 + \alpha_2 + z_{12} + r + k)}} & \text{if } z_1, z_2 \neq 0, \end{cases} \quad (9)$$

where t is a positive real number and

$$\binom{t}{i} = \begin{cases} \frac{t(t-1)\dots(t-i+1)}{i!} & i = 1, 2, \dots \\ 1 & i = 0. \end{cases}$$

Using the above exact expressions we could have some computational difficulties to obtain the Bayesian estimates in applications. As an alternative to find accurate posterior summaries of interest, we could use MCMC methods (see for example [4,8]). To this end, we write the log-likelihood function in a setting which it is easier to apply in existing available MCMC softwares used to get the posterior summaries of interesting, like the OpenBugs software.

$$\begin{aligned} l(\theta_1, \theta_2) &= \sum_{i=1}^n v_i \delta_{1i} \delta_{2i} \log P_1(x_{1i}, x_{2i}) + \sum_{i=1}^n (1-v_i) \delta_{1i} \delta_{2i} \log P_2(x_{1i}, x_{2i}) \\ &+ \sum_{i=1}^n v_i \delta_{1i} (1-\delta_{2i}) \log \left(\sum_{x_{2i}=y_{2i}+1}^{\infty} P_1(x_{1i}, x_{2i}) \right) \\ &+ \sum_{i=1}^n (1-v_i) \delta_{1i} (1-\delta_{2i}) \log \left(\sum_{x_{2i}=y_{2i}+1}^{\infty} P_2(x_{1i}, x_{2i}) \right) \\ &+ \sum_{i=1}^n v_i (1-\delta_{1i}) \delta_{2i} \log \left(\sum_{x_{1i}=y_{1i}+1}^{\infty} P_1(x_{1i}, x_{2i}) \right) \\ &+ \sum_{i=1}^n (1-v_i) (1-\delta_{1i}) \delta_{2i} \log \left(\sum_{x_{1i}=y_{1i}+1}^{\infty} P_2(x_{1i}, x_{2i}) \right) \end{aligned}$$

$$\begin{aligned}
& + \sum_{i=1}^n v_i (1 - \delta_{1i}) (1 - \delta_{2i}) \log \left(\sum_{x_{1i}=y_{1i}+1}^{\infty} \sum_{x_{2i}=y_{2i}+1}^{\infty} P_1(x_{1i}, x_{2i}) \right) \\
& + \sum_{i=1}^n (1 - v_i) (1 - \delta_{1i}) (1 - \delta_{2i}) \log \left(\sum_{x_{1i}=y_{1i}+1}^{\infty} \sum_{x_{2i}=y_{2i}+1}^{\infty} P_2(x_{1i}, x_{2i}) \right), \quad (10)
\end{aligned}$$

where δ_{1i} , δ_{2i} and v_i are indicator variables, given by, $\delta_{ji} = 1$ if X_{ji} is an observed lifetime; $\delta_{ji} = 0$ if X_{ji} is a censored observation, for $j = 1, 2$; $i = 1, 2, \dots, n$, and $v_i = 1$ if $x_{1i} < x_{2i}$ and $v_i = 0$ if $x_{1i} \geq x_{2i}$.

In the presence of a covariate vector $u = (u_1, u_2, \dots, u_p)$ associated to each bivariate lifetime (X_1, X_2) , we could assume the following logistic regression models:

$$\begin{aligned}
\theta_{1i} &= \frac{\exp \{\beta'_1 u_i\}}{1 + \exp \{\beta'_1 u_i\}}, \\
\theta_{2i} &= \frac{\exp \{\beta'_2 u_i\}}{1 + \exp \{\beta'_2 u_i\}}, \quad (11)
\end{aligned}$$

where, $\beta'_j = (\beta_{j1}, \beta_{j2}, \dots, \beta_{jp})$, $j = 1, 2$, is the regression parameter vector and $u_i = (u_{1i}, u_{2i}, \dots, u_{pi})$, $i = 1, \dots, n$.

For a Bayesian analysis of the model, we assume normal prior distributions for the regression parameters, that is:

$$\beta_{kl} \sim N(0, \sigma_{kl}^2),$$

where $k = 1, 2$ and $l = 1, 2, \dots, p$. We also assume prior independence among the regression parameters and that the hyperparameter σ_{kl}^2 is known.

4. An application considering the recurrence times of infection for kidney patients

In this section, we present as a numerical illustration of our proposed methodology, the analysis of a bivariate lifetime data set introduced by [15] assuming the bivariate geometric distribution. This data set is related to kidney infection where the recurrence of infection of 38 kidney patients, using portable dialysis machines, are recorded. Infections may occur at the location of insertion of the catheter. The time recorded, called infection time, is either the survival time (in days) of the patient until an infection occurred and the catheter had to be removed, or the censored time, where the catheter was removed by others reasons. The catheter is reinserted after

Table 1
Recurrence times of infections in 38 kidney patients.

Patient	First time	Second time	Censoring first time	Censoring second time	Sex
1	8	16	1	1	1
2	23	13	1	0	2
3	22	28	1	1	1
4	447	318	1	1	2
5	30	12	1	1	1
6	24	245	1	1	2
7	7	9	1	1	1
8	511	30	1	1	2
9	53	196	1	1	2
10	15	154	1	1	1
11	7	333	1	1	2
12	141	8	1	0	2
13	96	38	1	1	2
14	149	70	0	0	2
15	536	25	1	0	2
16	17	4	1	0	1
17	185	117	1	1	2
18	292	114	1	1	2
19	22	159	0	0	2
20	15	108	1	0	2
21	152	562	1	1	1
22	402	24	1	0	2
23	13	66	1	1	2
24	39	46	1	0	2
25	12	40	1	1	1
26	113	201	0	1	2
27	132	156	1	1	2
28	34	30	1	1	2
29	2	25	1	1	1
30	130	26	1	1	2
31	27	58	1	1	2
32	5	43	0	1	2
33	152	30	1	1	2
34	190	5	1	0	2
35	119	8	1	1	2
36	54	16	0	0	2
37	6	78	0	1	2
38	63	8	1	0	1

Censoring (0); infection occurrence (1); male (1); female (2).

some time and the second infection time is again observed or censored (data set in Table 1).

In the statistical analysis of the recurrence times of infections (see data set in Table 1), let us assume the bivariate geometric distribution with density (1) assuming discrete times. As a first analysis, we do not consider the presence of the covariate Sex. Let us denote this model as “model 1”. For a Bayesian analysis of “model 1”, let us assume a Dirichlet prior distribution (3) for θ_1 and θ_2 with hyperparameter values $\alpha_1 = \alpha_2 = \alpha_3 = 1$.

Bayesian estimators for the parameters of the model were obtained from simulated samples of the joint posterior distribution of interest using the OpenBUGS software (Spiegelhalter et al, 2003). In the simulation approach, we discarded the first 10,000 simulated Gibbs samples (“burn-in-samples”) to eliminate the effect of the initial values for the parameters of the model. Choosing every 50th simulated Gibbs sample, we obtained a final sample of size 1,000 to get the posterior summaries of interest. Convergence of the Gibbs sampling algorithm was monitored using existing methods as time series plots for the simulated samples.

The posterior means, the posterior standard-deviations and 95% credible intervals for the parameters θ_1 , θ_2 and r are given in Table 2. We also have in Table 2, the posterior summaries for the means, standard-deviations and for the correlation coefficient (see (1)) for the lifetimes X_1 and X_2 .

To have some idea of the fit of the proposed model, we could compare sample means and sample standard-deviations based on the

Table 2
Posterior summaries “model 1”.

Parameter	Mean	S.D.	95% Credible interval
μ_1	133.4	23.95	(96.28; 186.9)
μ_2	131.7	27.97	(89.44; 201.8)
r	0.9844	0.002079	(0.9802; 0.9883)
σ_1	132.9	23.95	(95.78; 186.4)
σ_2	131.2	27.97	(88.93; 201.3)
θ_1	0.007728	0.00133	(0.005389; 0.0104)
θ_2	0.007918	0.001607	(0.004963; 0.01119)
ρ_{12}	-0.003873	0.0526	(-0.00493; -0.002902)

uncensored observations with the Bayesian estimators obtained from the simulated Gibbs samples. In this way, we have the sample means and sample standard deviations for the first (32 uncensored observations) and second times (26 uncensored observations) given by: sample mean for first infection = 121.80; sample mean for second infection = 113.50; standard deviation for first infection = 153.30 and standard deviation for second infection = 131.40. Comparing these values with the obtained results of Table 2 (Monte Carlo estimates for the posterior means and 95% credible intervals for μ_1 , μ_2 , σ_1 and σ_2), we have an indication of good fit of the geometric distribution with density (1) for the recurrence times of infection for kidney patients introduced in Table 1.

In the presence of the covariate Sex, we assume the logistic regression model (11) introduced in Section 2 for the parameters θ_1 , θ_2 , σ_1 and σ_2 , that is

$$\text{logit}(\theta_{1i}) = \beta_{10} + \beta_{11} \text{Sex}_i$$

$$\text{logit}(\theta_{2i}) = \beta_{20} + \beta_{21} \text{Sex}_i,$$

where $i = 1, 2, \dots, 18$; $\text{logit}(z) = \log[z/(1 - z)]$, $\text{Sex}_i = 1$ (male) and $\text{Sex}_i = 0$ (female). Let us denote this model as “model 2”. Observe that $r_i = \theta_{1i} - \theta_{2i}$.

Assuming normal prior distributions $N(0, 10)$, for the regression parameters β_{j0} , $j = 1, 2$, and normal prior distributions $N(0, 1)$ for the regression parameters β_{j1} , $j = 1, 2$, where $N(a, b^2)$ denotes a normal distribution with mean equals to a and variance equals to b^2 , and also using the OpenBUGS software considering a burn-in-sample of size 10,000 and taking every 50th sample, after this burn-in-sample period, we have in Table 3, the posterior summaries of interest for “model 2”, obtained using a final Gibbs samples of size 1,000.

Table 3
Posterior summaries “model 2”.

Parameter	Mean	S.D.	95% Credible interval
β_{10}	-5.126	0.2069	(-5.55; -4.73)
β_{11}	1.441	0.3765	(0.69; 2.154)
β_{20}	-4.951	0.2331	(-5.423; -4.509)
β_{21}	0.2064	0.3892	(-0.639; 0.9607)

From the results of Table 3, we observe that zero is included in the 95% credible interval for β_{21} but not for β_{11} , that is, the lifetime X_2 is not affected by the covariate Sex, but X_1 is affected by the covariate Sex.

It is interesting to observe that the data set introduced by [15] related to the recurrence times of infection of 38 kidney patients also have other four covariates besides the covariate sex: age, presence of disease type GN, presence of disease type AN, presence of disease type PKD, where GN, AN and PKD are short forms of Glomerulo Neptirits, acute Neptirits and Polyciatic kidney disease.

In the presence of all five covariates, we assume the logistic regression model (11) introduced in Section 2 for the parameters θ_1 and θ_2 , that is,

$$\text{logit}(\theta_{1i}) = \beta_{10} + \beta_{11} \text{Sex}_i + \beta_{12} \text{Age}_i + \beta_{13} \text{GN}_i + \beta_{14} \text{AN}_i + \beta_{15} \text{PKD}_i$$

$$\text{logit}(\theta_{2i}) = \beta_{20} + \beta_{21} \text{Sex}_i + \beta_{22} \text{Age}_i + \beta_{23} \text{GN}_i + \beta_{24} \text{AN}_i + \beta_{25} \text{PKD}_i.$$

Let us denote this model as “model 3”. Using some prior information based on a preliminary analysis considering independent lifetimes (use of empirical Bayesian methods), we assume the following priors for the regression parameters: $\beta_{10} \sim N(-1.4, 1)$, $\beta_{11} \sim N(-2.1, 1)$, $\beta_{12} \sim N(0.008, 10)$, $\beta_{13} \sim N(0.22, 1)$, $\beta_{14} \sim N(0.76, 1)$, $\beta_{15} \sim N(-1.3, 1)$, $\beta_{20} \sim N(-3.2, 1)$, $\beta_{21} \sim N(-0.9, 1)$, $\beta_{22} \sim N(0.002, 10)$, $\beta_{23} \sim N(-0.98, 1)$, $\beta_{24} \sim N(-0.044, 10)$, $\beta_{25} \sim N(-1.34, 1)$. This choice of informative priors improves the convergence of the Gibbs sampling algorithm using the OpenBUGS software. Using the OpenBUGS software also considering a “burn-in-sample” of size 10,000 and generating a final Gibbs sample of size 1,000 taking every 50th sample, we have in Table 4, the posterior summaries of interest.

From the results of Table 4, we observe that,

(a) Lifetime X_1

Covariates Sex and disease type PKD are significative (zero is not included in the 95% credible intervals $(-2.854; -1.664)$ for β_{11} and $(-2.551; -0.1825)$ for β_{15}) all other covariates are not significative (zero is included in the 95% credible intervals for the regression parameters β_{12} , β_{13} and β_{14}).

(b) Lifetime X_2

Covariates Sex and disease type PKD are significative (zero is not included in the 95% credible intervals $(-1.719; -0.2097)$ for β_{21} and $(-2.504; -0.3823)$ for β_{25}) all other covariates are not significative (zero is included in the 95% credible intervals for the regression parameters β_{22} , β_{23} and β_{24}).

Table 4
Posterior summaries “model 3”.

Parameter	Mean	S.D.	95% Credible interval
β_{10}	-1.235	0.6043	(-2.421; -0.1361)
β_{11}	-2.244	0.3118	(-2.854; -1.664)
β_{12}	0.007145	0.01228	(-0.01694; 0.0315)
β_{13}	0.2813	0.4349	(-0.5533; 1.105)
β_{14}	0.8213	0.4522	(-0.07333; 1.675)
β_{15}	-1.358	0.6021	(-2.551; -0.1825)
β_{20}	-3.134	0.7639	(-4.581; -1.758)
β_{21}	-0.9501	0.3828	(-1.719; -0.2097)
β_{22}	0.002388	0.01263	(-0.02311; 0.02737)
β_{23}	-0.2642	0.4617	(-1.184; 0.5899)
β_{24}	0.02223	0.27	(-0.4982; 0.5527)
β_{25}	-1.442	0.5549	(-2.504; -0.3823)

As a comparison for the three proposed models, we could use a Bayesian discrimination criterion, as for example, the DIC (Deviance Information Criterion) introduced by [23], (see the appendix) and given automatically by the OpenBUGS software. Assuming “model 1”, that is, the bivariate geometric distribution not considering the presence of covariates, we have a Monte Carlo estimate for DIC given by the value 685.9; assuming “model 2”, that is, the bivariate geometric distribution in the presence of only the covariate sex, the DIC value is given by 675.8 and assuming “model 3”, that is, the bivariate geometric distribution in the presence of the covariates sex, age, presence of disease type GN, presence of disease type AN, presence of disease type PKD the DIC value is given by 668.2. This is, “model 3” gives better fit for the recurrence times of infection for kidney patients introduced by [15] (smaller value for DIC).

Observe that similar results were obtained by [19] assuming a bivariate exponential Block and Basu distribution for continuous lifetimes in the case considering only the covariate Sex. Some advantages of the bivariate geometric distribution: better convergence of Gibbs sampling algorithm even considering more non-informative prior distributions.

5. Concluding remarks

The use of a discrete bivariate geometric distribution could be a new and good alternative for the analysis of bivariate lifetime data, especially under a Bayesian approach and using MCMC methods. Usually, in medical applications, we have the presence of censored data and the presence of one or more covariates, a situation that could bring us great difficulties to get the usual classical inferences for the parameters of the model like the convergence in the iterative numerical algorithm used to get the maximum likelihood estimators for the parameters of the model. It is also important to point out that these classical inference procedures are based on asymptotical normality of maximum likelihood estimators (see for example, Lawless, 1982). This could be a problem when we have small data sizes or the presence of a large proportion of censored data, two situations very common in medical studies. Also it is important to point out that the use of available Bayesian software like the OpenBUGS software, only requires the specification of the distribution for the data and prior distributions for the parameters of the model, giving us a great simplification to obtain posterior summaries of interest, as it was observed in the application considering a medical data introduced in section 3. These results could be of great interest for applications in medical and engineering studies.

Appendix. Deviance Information Criterion (DIC)

The Deviance Information Criterion (DIC) is a criterion specially useful for selection models under the Bayesian approach where samples of the posterior distribution for the parameters of the model are obtained using MCMC methods.

The deviance is defined by,

$$D(\theta) = -2\log L(\theta) + c,$$

where θ is a vector of unknown parameters of the model, $L(\theta)$ is the likelihood function of the model and c is a constant that does not need to be known when the comparison between models is made.

The DIC criterion defined by [23] is given by,

$$DIC = D(\hat{\theta}) + 2n_D$$

where $D(\hat{\theta})$ is the deviance evaluated at the posterior mean $\hat{\theta} = E(\theta | \text{data})$ and n_D is the effective number of parameters of the model given by

$n_D = \bar{D} - D(\hat{\theta})$, where $\bar{D} = E(D(\theta) | data)$ is the posterior deviance measuring the quality of the data fit for the model. Smaller values of DIC indicates better models. Note that these values could be negative.

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