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Count time series with excess zeros: A Bayesian perspective using zero-adjusted distributions

Séries temporais de contagem com excesso de zeros: Uma perspectiva Bayesiana utilizando distribuições zero-ajustadas

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Abstract

Models for count data which are temporally correlated have been studied using many conditional distributions, such as the Poisson distribution, and the insertion of different dependence structures. Nonetheless, excess of zeros and over dispersion may be observed during the counting process and need to be considered when modelling and choosing a conditional distribution. In this paper, we propose models for counting time series using zero-adjusted distributions by inserting a dependence structure following the ARMA(p, q) process on a Bayesian framework. We perform a simulation study using the proposed Bayesian analysis and analyse the monthly time series of the number of deaths due to dengue haemorrhagic fever (ICD-A91) in Brazil.

Keywords: ARMA(p, q) process; count data; metropolis-hastings.

Resumo

Modelos para dados de contagem temporalmente correlacionados têm sido estudados utilizando diversas distribuições condicionais, como a Poisson, e com a inserção de diferentes estruturas de dependência. No entanto, os fenômenos de contagem podem apresentar características como excesso de zeros e alta dispersão, que devem ser levadas em consideração durante a modelagem e escolha de uma distribuição condicional. Este trabalho tem como objetivo estudar modelos para séries de contagem utilizando três distribuições condicionais zero-ajustadas com estruturas de dependência na forma ARMA(p, q), em uma perspectiva via inferência Bayesiana. De forma geral, foi realizado um breve estudo de simulação a partir da análise Bayesiana proposta e a série temporal do número de óbitos em decorrência de febre hemorrágica causada pelo vírus da dengue (CID-A91) no Brasil foi analisada.

Palavras-chave: processo ARMA(p, q); dados de contagem; metropolis-hastings.

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Introduction

Count data are used and analysed in areas such as economy, epidemiology, public health and many other applied areas (HASHIM; HASHIM; SHIKER, 2021; ZUO *et al*., 2021). The modelling of these types of data are commonly based on Generalized Linear Models (GLMs) introduced by Nelder and Wedderburn (1972), with a certain predominance of Poisson regression (GONÇALVES; BARRETO-SOUZA, 2020).

However, the assumption of equidispersion arising from the Poisson distribution is rarely satisfied (HILBE, 2014). This is because over dispersion is commonly observed in count data (BARRETO-SOUZA, 2017), resulting from extra population heterogeneity, the omission of important explanatory variables, the presence of atypical observations (PAYNE *et al*., 2017) and an excess of zeros (BARRETO-SOUZA, 2017); high dispersion needs to be handled during modelling because it can lead to inferential problems (PAYNE *et al*., 2017).

Regression models based on mixed Poisson distributions have become attractive for treating over dispersion by inserting a latent random effect into the mean of the Poisson distribution (BARRETO-SOUZA, 2017). Models with Negative binomial and Poisson inverse Gaussian distributions are examples of this approach (BARRETO-SOUZA, 2017; HILBE, 2014).

Excess zeros can still be observed in the applied areas (FENG, 2021), such as in disease monitoring, use of health services and number of daily deaths from certain causes (HASHIM; HASHIM; SHIKER, 2021; TAWIAH; IDDRISU; ASOSEGA, 2021; YANG; ZAMBA; CAVANAUGH, 2013), a fact that should not be ignored, since it can negatively impact the inference, for example, generating spurious relationships (ALQAWBA; DIAWARA; CHAGANTY, 2019; YANG; ZAMBA; CAVANAUGH, 2013).

For modelling count time series, Benjamin, Rigby and Stasinopoulos (2003) proposed the Generalized Autoregressive Moving Average - GARMA(p, q) - class, based on the GLM theory, inserting a dependence structure following the ARMA(p, q) process, which has been used in models with Poisson, Binomial and Negative binomial distributions.

The literature on counting time series considering excess zeros is still sparse (YANG; ZAMBA; CAVANAUGH, 2013) but is a topic of recent interest in statistics (ALQAWBA; DIAWARA; CHAGANTY, 2019). Yang, Zamba and Cavanaugh (2013), Alqawba, Diawara and Chaganty (2019), Ghahramani and White (2020), Tawiah, Iddrisu and Asosega (2021) are examples of studies that have modelled count time series with many zeros.

In the study by Yang, Zamba and Cavanaugh (2013), the zero-inflated Poisson (ZIP) distribution was used by incorporating lags of the response variable in the linear predictor to handle the temporal correlation in syphilis data. The Poisson, Negative binomial and Conway-Maxwell-Poisson distributions were adopted by Alqawba, Diawara and Chaganty (2019), who supposed that the errors of the regression follow a stationary ARMA(p, q) process.

Ghahramani and White (2020) studied the ZIP and zero-inflated Negative binomial (ZINB) models and developed a distribution-free approach when modelling the time series of syphilis cases. Tawiah, Iddrisu and Asosega (2021) analysed the COVID-19 mortality series using the ZIP and ZINB distributions with the ARMA(1, 0) dependence structure.

In this paper, we aim to study models for counting time series with excess zeros using Poisson, Negative binomial and Poisson inverse Gaussian zero-adjusted distributions, which are alternatives to zero-inflated distributions. We adopt the Bayesian approach, as in the study by Andrade, Andrade and Ehlers (2015), when modelling series using the GARMA(p, q) class.

Initially, we present the concept of zero-adjusted distributions and define models with the insertion of the ARMA(p, q) dependence structure. Then, we perform a simulation based on the proposed Bayesian analysis and analyse the time series of mortality due to dengue haemorrhagic fever (ICD-A91), according to the 10th revision of the International Classification of Diseases (ICD-10) (WORLD HEALTH ORGANIZATION, 2004). We also present some final remarks and suggestions for future work.

Background on zero-adjusted and zero-inflated distributions

When dealing with data with a high proportion of zeros, zero-inflated and zero-altered distributions, also referred to as hurdle and adjusted distributions, are used for modelling and inference (FENG, 2021; HASHIM; HASHIM; SHIKER, 2021). According to Feng (2021), there is a conceptual and parameter interpretation difference when considering zero-inflated or hurdle regression.

In zero-inflated models, which were proposed by Lambert (1992), it is assumed that the zeros come from two processes. The first process is composed of situations with structural zeros, and the second is composed of random zeros, which are modelled by a count distribution such as the Poisson distribution (FENG, 2021; HASHIM; HASHIM; SHIKER, 2021). According to Feng (2021), the structure of a zero-inflated model is given by:

$$P(Y=y_i \mid \boldsymbol{\theta}) = \begin{cases} \nu + (1-\nu)p(y_i=0 \mid \boldsymbol{\theta}), & y_i = 0, \\ (1-\nu)p(y_i \mid \boldsymbol{\theta}), & y_i > 0, \end{cases}$$

which is formed by a degenerated distribution at zero and a nontruncated count distribution, namely, $p(y_i \mid \boldsymbol{\theta})$, with parameter vector $\boldsymbol{\theta}$, where $\nu \in (0,1)$ is the probability of structural zeros.

In a hurdle, a binomial model governs the binary event when the response takes a zero or a positive value (MULLAHY, 1986). If the event is positive, the barrier is crossed, and the process is modelled by a conditional distribution that is truncated at zero (MULLAHY, 1986). According to Feng (2021), the general structure of a hurdle model is given by:

$$P(Y=y_i \mid \boldsymbol{\theta}) = \begin{cases} \nu, & y_i = 0, \\ (1-\nu)\dfrac{p(y_i \mid \boldsymbol{\theta})}{1-p(y_i=0 \mid \boldsymbol{\theta})}, & y_i > 0, \end{cases} \tag{1}$$

where ν is the probability of y_i being zero, $p(y_i \mid \boldsymbol{\theta})$ is the probability function of a count distribution and $\boldsymbol{\theta}$ is the parameter vector of $p(y_i \mid \boldsymbol{\theta})$.

In equation (1), the first structure fits the occurrence of zeros with probability ν, and the other is responsible for modelling when zeros do not occur. Note that in a hurdle, the zeros are not differentiated. In fact, events that result in zero are seen as coming from a structural source (ZUUR *et al*., 2009).

There are several possibilities to specify the conditional distribution of the positive values and the binary event in a hurdle (MULLAHY, 1986). One of them is to consider that a binary event is modelled by a binomial distribution and the positive values follow a Poisson distribution, resulting in the zero-adjusted Poisson (ZAP) model (HASHIM; HASHIM; SHIKER, 2021).

Additional topics, such as the analysis and specification of the linear predictor in zero-inflated or hurdle models, can be seen in Zuur *et al*. (2009) and Zuo *et al*. (2021). For the analysis of count time series using zero-altered models, we define the linear predictor inserting a dependence structure below.

Zero-altered models for count time series

Suppose Y is an equally spaced time series indexed at time t, $t = \{1,\ldots,n\}$. Define $\mathscr{F}_{t-1}$ as the set of previous information until $t-1$, which is given by $\mathscr{F}_{t-1} = \{y_1, y_2, \ldots, y_{t-1}, \mu_1, \mu_2, \ldots, \mu_{t-1}, \boldsymbol{x}_1, \boldsymbol{x}_2, \ldots, \boldsymbol{x}_{t-1}\}$, where $\boldsymbol{x}_t$ is the parameter vector that contains r explanatory variables, $\boldsymbol{x}_t = (\boldsymbol{x}_{t1}, \ldots, \boldsymbol{x}_{tr})^\top$, under restriction that $r < n$. Additionally, suppose $\boldsymbol{\beta} = (\beta_1, \beta_2, \ldots, \beta_r)^\top$ is the coefficient vector related to $\boldsymbol{x}_t$.

Let $\boldsymbol{\Phi}_p(B) = 1 - \phi_1 B^1 - \ldots - \phi_p B^p$ and $\boldsymbol{\Theta}_q(B) = 1 - \theta_1 B^1 - \ldots - \theta_q B^q$ be the autoregressive and moving average polynomials of orders p and q, respectively. Additionally, let $\boldsymbol{\Phi}_P(B^s) = 1 - \Phi_1 B^{s1} - \ldots - \Phi_P B^{sP}$ and $\boldsymbol{\Theta}_Q(B^s) = 1 - \Theta_1 B^{s1} - \ldots - \Theta_Q B^{sQ}$ be the seasonal autoregressive and seasonal moving average polynomials with orders P and Q, where B is the backshift operator, $B^d y_t = y_{t-d}$, and s is the length of the period.

In summary, we denote $\boldsymbol{\Phi} = (\phi_1, \ldots, \phi_p; \Phi_1, \ldots, \Phi_P)^\top$ as the set of autoregressive parameters and $\boldsymbol{\Theta} = (\theta_1, \ldots, \theta_q; \Theta_1, \ldots, \Theta_Q)^\top$ as the set of moving average parameters that compose the dependence structure.

Zero-adjusted Poisson distribution

Supposing that $y_t \mid \mathscr{F}_{t-1}$ follows a zero-adjusted Poisson distribution ZAP(μ_t, ν), $p(y_t \mid \mathscr{F}_{t-1})$ can be expressed as:

$$p(y_t \mid \mathscr{F}_{t-1}) = \nu \mathrm{I}_{(y_t=0)} + \left[\frac{1-\nu}{1-e^{-\mu_t}}\right] e^{-\mu_t} \mu_t^{y_t} \frac{1}{y_t!} \mathrm{I}_{(y_t>0)}, \tag{2}$$

when $y_t \in \mathbb{N}$, $\Omega = \{\mu_t, \nu \mid \mu_t > 0, 0 < \nu < 1\}$.

In equation (2), $\mathrm{I}_{(\cdot)}$ represents the indicator function, and ν is the exact probability of the series being zero at time t. Given the truncation of the distribution at zero, μ_t is the conditional expectation in the situation where $y_t > 0$ (RIGBY *et al*., 2019).

The conditional mean and variance of the ZAP(μ_t, ν) distribution are given by $\mathrm{E}(y_t \mid \mathscr{F}_{t-1}) = \dfrac{(1-\nu)\mu_t}{1-e^{-\mu_t}}$ and $\mathrm{V}(y_t \mid \mathscr{F}_{t-1}) = \dfrac{(1-\nu)\mu_t}{1-e^{-\mu_t}}\left[1 + \mu_t - \dfrac{(1-\nu)\mu_t}{1-e^{-\mu_t}}\right]$, respectively (RIGBY *et al*., 2019).

$\mathrm{E}(y_t \mid \mathscr{F}_{t-1})$ can be seen as a weighting of μ_t by $\dfrac{1-\nu}{1-e^{-\mu_t}}$, which is the ratio of the complementary exact probability that $y_t = 0$ and the probability that $y_t > 0$ from a Poisson distribution with a mean of μ_t.

Considering the logarithm link function, ensuring that $\mu_t \subseteq \Omega$, the linear predictor based on the GARMA(p, q) class written using the B operator is given by equation (3):

$$\begin{aligned}\log(\mu_t) = {} & \boldsymbol{\Phi}_p(B)\boldsymbol{\Phi}_P(B^s)\left[\boldsymbol{x}_t^\top\boldsymbol{\beta} - \log(y_t)\right] \\ & - \boldsymbol{\Theta}_q(B)\boldsymbol{\Theta}_Q(B^s)\left[\log(y_t) - \log(\mu_t)\right] \\ & + \log\left(\frac{y_t^2}{\mu_t}\right). \end{aligned} \tag{3}$$

It is necessary to consider a threshold (c) that guarantees the existence of the link function at zero. A possibility is to replace y_{t-j} by $y^*_{t-j} = \max(y_{t-j}, c)$, $c \in (0,1)$.

Denoting $\mathrm{L}(\boldsymbol{\beta}, \boldsymbol{\Phi}, \boldsymbol{\Theta}, \nu \mid Y)$ as the approximated likelihood function of the ZAP(μ_t, ν) model conditioned to $m = \max(p, q, sP, sQ)$ observations, we have:

$$L(\boldsymbol{\beta}, \boldsymbol{\Phi}, \boldsymbol{\Theta}, \nu \mid Y) \approx \prod_{t=m+1}^{n} p(y_t \mid \mathscr{F}_{t-1}). \tag{4}$$

Given the conditioning of the likelihood function to the first m terms, we consider that the first terms of the error are zero, as described in the studies of Benjamin, Rigby and Stasinopoulos (2003), Rocha and Cribari-Neto (2009).

In the situation where $y_t > 0$, the process is assumed to be equidispersed and modelled by a Poisson distribution, i.e., $\mathrm{E}(y_t \mid \mathscr{F}_{t-1}) = \mathrm{V}(y_t \mid \mathscr{F}_{t-1}) = \mu_t$. The following models are over dispersion alternatives.

Zero-adjusted Negative binomial distribution

We assume that $y_t \mid \mathscr{F}_{t-1}$ follows a zero-adjusted Negative binomial distribution ZANBI(μ_t, σ, ν), with a conditional density given by:

$$\begin{aligned} p(y_t \mid \mathscr{F}_{t-1}) = {} & \nu \mathrm{I}_{(y_t=0)} + \frac{(1-\nu)\mu_t}{[1-(1+\mu_t\sigma)^{\frac{-1}{\sigma}}]} \\ & \times \frac{\Gamma(y_t + \frac{1}{\sigma})}{\Gamma(\frac{1}{\sigma})\Gamma(y_t+1)} \left(\frac{\sigma\mu_t}{1+\sigma\mu_t}\right)^{y_t} \\ & \times \left(\frac{1}{1+\sigma\mu_t}\right)^{\frac{1}{\sigma}} \mathrm{I}_{(y_t>0)}, \end{aligned} \tag{5}$$

$\Omega = \{\mu_t, \sigma, \nu \mid \mu_t, \sigma > 0, 0 < \nu < 1\}$ for $y_t \in \mathbb{N}$.

The conditional mean and variance are given by $\mathrm{E}(y_t \mid \mathscr{F}_{t-1}) = \frac{(1-\nu)\mu_t}{\left[1-(1+\mu_t\sigma)^{\frac{-1}{\sigma}}\right]}$ and $\mathrm{V}(y_t \mid \mathscr{F}_{t-1}) = \frac{(1-\nu)\mu_t}{\left[1-(1+\mu_t\sigma)^{\frac{-1}{\sigma}}\right]}\left[1+\mu_t\left(1+\sigma-\frac{(1-\nu)}{\left[1-(1+\mu_t\sigma)^{\frac{-1}{\sigma}}\right]}\right)\right]$, respectively, where ν is the exact probability of the series being equal to zero. The μ_t and σ parameters are the mean and dispersion of the process in the situation where $y_t > 0$, respectively (RIGBY *et al.*, 2019).

We adopt the same structure in the linear predictor described by equation (3). However, the approximate likelihood function is written according to equation (6).

$$L(\boldsymbol{\beta}, \boldsymbol{\Phi}, \boldsymbol{\Theta}, \nu, \sigma \mid Y) \approx \prod_{t=m+1}^{n} p(y_t \mid \mathscr{F}_{t-1}). \tag{6}$$

The assumptions that the first m error terms are zero follow as detailed in the ZAP(μ_t, ν) model. Generally, the process is governed by a truncation at zero and a Negative binomial distribution with a mean of μ_t and dispersion of σ in the condition where $y_t > 0$.

Zero-adjusted Poisson inverse Gaussian distribution

Assuming that $y_t \mid \mathscr{F}_{t-1}$ follows a zero-adjusted Poisson inverse Gaussian distribution, ZAPIG(μ_t, σ, ν), the conditional density function, is given by equation (7):

$$\begin{aligned} p(y_t \mid \mathscr{F}_{t-1}) = {} & \nu \mathrm{I}_{(y_t=0)} \\ & + \frac{1-\nu}{1-e^{\frac{1}{\sigma}-\alpha}} \left(\frac{2\alpha}{\pi}\right)^{\frac{1}{2}} \mu_t^{y_t} e^{\frac{1}{\sigma}} \left(K_{y_t-\frac{1}{2}}(\alpha)\right) \\ & \times \frac{1}{(\alpha\sigma)^{y_t} y_t!} \mathrm{I}_{(y_t>0)}, \end{aligned} \tag{7}$$

$\Omega = \{\mu_t, \sigma, \nu \mid \mu_t, \sigma > 0, 0 < \nu < 1\}$ for $y_t \in \mathbb{N}$.

In equation (7), $\alpha^2 = \frac{1}{\sigma^2} + \frac{2\mu_t}{\sigma}$ and $K_\lambda(T) = \frac{1}{2}\int_0^\infty x^{(\lambda-1)} \exp\left\{-\frac{T}{2}(x+x^{-1})\right\} dx$, where $K(\cdot)$ is the modified Bessel function of the third kind[1]. The conditional mean and variance are $\mathrm{E}(y_t \mid \mathscr{F}_{t-1}) = \frac{(1-\nu)\mu_t}{1-e^{\frac{1}{\sigma}-\alpha}}$ and $\mathrm{V}(y_t \mid \mathscr{F}_{t-1}) = \left[\frac{(1-\nu)\mu_t}{1-e^{\frac{1}{\sigma}-\alpha}}\right]\left[1+\mu_t\left(1+\sigma-\frac{1-\nu}{1-e^{\frac{1}{\sigma}-\alpha}}\right)\right]$, respectively.

It is important to note that ν is the exact probability of the series being zero, and it is $p(y_t = 0 \mid \mathscr{F}_{t-1}) = \nu, \forall t$, as well as in the ZAP($\mu_t$, ν) and ZANBI(μ_t, σ, ν) models. The μ_t and σ parameters are related to the mean and dispersion of the series in the situation where $y_t > 0$ (RIGBY *et al.*, 2019).

We also considered the linear predictor shown in equation (3), ensuring that $\mu_t \subseteq \Omega$. The approximated likelihood function is analogous to equation (6) and the assumptions that the first m error terms are zero follow as detailed in the ZAP(μ_t, ν) model.

[1] Modified Bessel functions are particular forms of Bessel functions, which are solutions of the Bessel equation, being related to the Poisson process and applied in the analysis of spherical distributions (KORENEV, 2002; ROBERT, 1990). For details, see Korenev (2002).

Bayesian analysis

We consider $\boldsymbol{\theta} = (\boldsymbol{\beta}, \boldsymbol{\Phi}, \boldsymbol{\Theta}, \nu)^\top$ in the zero-adjusted Poisson model and $\boldsymbol{\theta} = (\boldsymbol{\beta}, \boldsymbol{\Phi}, \boldsymbol{\Theta}, \nu, \sigma)^\top$ in the zero-adjusted Negative binomial and zero-adjusted Poisson inverse Gaussian models. In this way, the resulting posterior, namely, $\pi(\boldsymbol{\theta} \mid Y)$, is proportional to $\mathrm{L}(\boldsymbol{\theta} \mid Y) \times \pi_0(\boldsymbol{\theta})$, where $\mathrm{L}(\boldsymbol{\theta} \mid Y)$ is the approximated likelihood function and $\pi_0(\boldsymbol{\theta})$ is the joint prior of $\boldsymbol{\theta}$.

We consider noninformative priors for $\boldsymbol{\theta}$ in all models. For the parameters associated with the explanatory variables, each component of $\boldsymbol{\beta}$ is normally distributed. It is given as:

$$p(\beta_j) \propto \exp\left[-\frac{1}{2}\left(\frac{\beta_j - \mu_j}{\tau_j}\right)^2\right],$$

where $\beta_j \in (-\infty, \infty)$, $j = \{1, \ldots, r\}$, and the hyperparameters are $\mu_j = 0$ and $\tau_j = 100$. The same structure of priors used for $\boldsymbol{\beta}$ is adopted for $\boldsymbol{\Phi}$ and $\boldsymbol{\Theta}$.

For the parameter ν, we consider a uniform distribution on the interval (0, 1), and for the models that contain a dispersion parameter, we use a Gamma(a, s) distribution with hyperparameters $a = 1$ and $s = 100^{-1}$, with the following density:

$$p(\sigma) = \frac{\sigma^{a-1}}{s^a \Gamma(a)} \exp\left(-\frac{\sigma}{s}\right), \quad \sigma > 0.$$

Given the algebraic complexity to obtain closed forms of $\pi(\boldsymbol{\theta} \mid Y)$, the inference can be performed using Markov chain Monte Carlo (MCMC) methods, such as the Metropolis-Hastings (MH) algorithm for drawing from the joint posterior of each model (ANDRADE; ANDRADE; EHLERS, 2015).

Predictive density

To make forecasts of Y over a horizon h, it is necessary to define the predictive distribution, which is the distribution of y_{t+h} conditioning to all parameters and previous observations that compose the set $\mathscr{F}_{t-1}$ (BROEMELING, 2019; SÁFADI; MORETTIN, 2003).

Combining the joint posterior $\pi(\boldsymbol{\theta} \mid Y)$ with the density of the new observation, $p(y_{t+h} \mid \boldsymbol{\theta}, \mathscr{F}_{t+h-1})$, the predictive density is given by:

$$p(y_{t+h} \mid \mathscr{F}_{t+h-1}) = \int_{\boldsymbol{\theta} \in \Omega} p(y_{t+h} \mid \boldsymbol{\theta}, \mathscr{F}_{t+h-1}) \pi(\boldsymbol{\theta} \mid Y) d\boldsymbol{\theta}.$$

There is no closed form in the considered models. Nonetheless, we can perform a Monte Carlo approximation of the predictive, drawing $\mathscr{N}$ samples from $\boldsymbol{\theta}^i$, $i = \{1, \ldots, \mathscr{N}\}$, as follows:

$$p(y_{t+h} \mid \mathscr{F}_{t+h-1}) \approx \frac{1}{\mathscr{N}} \sum_{i=1}^{\mathscr{N}} p(y_{t+h} \mid \boldsymbol{\theta}^i, \mathscr{F}_{t+h-1}).$$

Then, the expected value of y_{t+h} is given by the following expression:

$$E(y_{t+h}) = \int_{y_{t+h} \in \Omega} y_{t+h} p(y_{t+h} \mid \mathscr{F}_{t+h-1}) dy_{t+h}.$$

The approximation of the expected value is performed using the conditional mean, $\mathrm{E}(y_t \mid \mathscr{F}_{t-1})$, of each distribution. For the zero-adjusted Poisson model:

$$\widehat{y}_{t+h} \approx \frac{1}{\mathscr{N}} \sum_{i=1}^{\mathscr{N}} \frac{(1 - \boldsymbol{\theta}_4^i)\mu_{t+h}(\boldsymbol{\theta}_1^i, \boldsymbol{\theta}_2^i, \boldsymbol{\theta}_3^i, \mathscr{F}_{t+h-1})}{1 - e^{-\mu_{t+h}(\boldsymbol{\theta}_1^i, \boldsymbol{\theta}_2^i, \boldsymbol{\theta}_3^i, \mathscr{F}_{t+h-1})}}.$$

Similarly, for the zero-adjusted Negative binomial model:

$$\widehat{y}_{t+h} \approx \frac{1}{\mathscr{N}} \sum_{i=1}^{\mathscr{N}} \frac{(1 - \boldsymbol{\theta}_4^i)\mu_{t+h}(\boldsymbol{\theta}_1^i, \boldsymbol{\theta}_2^i, \boldsymbol{\theta}_3^i, \mathscr{F}_{t+h-1})}{\left\{1 - \left[1 + \mu_{t+h}(\boldsymbol{\theta}_1^i, \boldsymbol{\theta}_2^i, \boldsymbol{\theta}_3^i, \mathscr{F}_{t+h-1})\boldsymbol{\theta}_5^i\right]^{\frac{-1}{\boldsymbol{\theta}_5^i}}\right\}}.$$

Considering the zero-adjusted Poisson inverse Gaussian model, we have:

$$\widehat{y}_{t+h} \approx \frac{1}{\mathscr{N}} \sum_{i=1}^{\mathscr{N}} \frac{(1 - \boldsymbol{\theta}_4^i)\mu_{t+h}(\boldsymbol{\theta}_1^i, \boldsymbol{\theta}_2^i, \boldsymbol{\theta}_3^i, \mathscr{F}_{t+h-1})}{\left[1 - e^{\left(\frac{1}{\boldsymbol{\theta}_5^i} - \alpha\right)}\right]}.$$

A simulation study

We carry out a simulation study considering the ZAP-AR(1), ZANBI-AR(1) and ZAPIG-AR(1) models, which are expressed as follows:

$$\begin{aligned} y_t \mid \mathscr{F}_{t-1} &\sim \mathrm{ZAP}\{\mu_t, \nu\} \\ y_t \mid \mathscr{F}_{t-1} &\sim \mathrm{ZANBI}\{\mu_t, \nu, \sigma\} \\ y_t \mid \mathscr{F}_{t-1} &\sim \mathrm{ZAPIG}\{\mu_t, \nu, \sigma\}, \end{aligned}$$

where $\log(\mu_t) = (1 - \phi_1 B^1)[\boldsymbol{x}_t^\top \boldsymbol{\beta} - \log(y_t)] + \log(y_t)$. We evaluate the scenarios presented in Table 1, with $\boldsymbol{\beta} = (\beta_1)^\top$ and $\boldsymbol{x}_t = (\boldsymbol{x}_{t1})^\top$, where $\boldsymbol{x}_{t1} = (1, 1, \ldots, 1)^\top$. We establish time series with 10% and 40% of counts equal to zero and correlations of 0.30 and -0.80. For models with dispersion parameter, we fix σ at 0.10.

Table 1 – Parameter settings for the ZAP-AR(1), ZANBI-AR(1) and ZAPIG-AR(1) models.

Scenario	n	β_1	ϕ_1	ν	σ
I	100	2.00	0.30	{0.10; 0.40}	0.10
II	100	2.00	-0.80	{0.10; 0.40}	0.10

Source: The authors.

We used the MH algorithm for drawing from the joint posterior, which is described in the appendix, with the *MHadaptive* package from Chivers (2015), and each model was replicated w = 1,000 times. The pseudorandom series were generated with the *gamlss.dist* package from Stasinopoulos and Rigby (2020) using the inverse transformed method. The burn-in, thinness and number of samples needed to obtain convergence to the stationary distribution were defined in a pilot study.

We formally verified the convergence in each replicated model using the *HW* (HEIDELBERGER; WELCH, 1983), *G* (GEWEKE, 1991) and the dependence factor (I) (RAFTERY; LEWIS, 1992) diagnoses. For the *HW*, we fixed α = 5%; the absolute value of G was compared with the quantile $Z_{1-\frac{\alpha}{2}}$, and we checked if $I \to 1$. By meeting these specifications, the process was considered convergent.

Simulation results

Table 2 displays the simulation results of the first scenario, where ϕ_1 = 0.30. We observed that there was an increase in the standard deviation of the parameter β_1 with an increase in the proportion of zeros (ν). The greatest increase in the standard deviation was related to the intercept of the ZAP-AR(1) model, which increased by 85.93% in the case where $\nu = 0.40$.

According to the scenario displayed in Table 2, we verified that the mean and mode estimates of ν remain identical up to the third decimal place. However, there was a reduction in the CB and CE metrics of ν when the proportion of zeros increased.

For models with dispersion parameter, better results were obtained using the estimates based on the mode compared with those using the posterior mean. We also observed an increase in the standard deviation of σ when increasing ν, mainly in the ZAPIG-AR(1) model, where some details about the settings of the MH algorithm are available in the Appendix, presented in the *Additional Simulation Results*. Also, in the appendix, the simulation results of the second scenario are displayed and the MH settings are available. Similar results were obtained in the second scenario when compared to the first scenario, mainly when evaluating the dispersion parameter estimates based on the posterior mode in the ZANBI-AR(1) and ZAPIG-AR(1) models. The results of the evaluated scenarios indicated good inference properties, which can be verified in the CB and CE metrics. All the CE values are approximately one, and great acceptance rates were obtained using the MH algorithm.

Application: mortality from dengue haemorrhagic fever

We analysed the monthly mortality series due to dengue haemorrhagic fever (ICD-A91) of children under nine years old in Brazil. Our data were provided by Brasil ([2022]) and covered the period from January 2013 to July 2020. The behaviour of the data over time is shown in Figure 1(a), and the respective bar graph is presented in Figure 1(b).

In the studied period, 136 deaths were reported, resulting in an average of 1.53 deaths per month, with a median equal to one. The proportion of months without occurrence of deaths was 33.71%, estimated by $\hat{p} = \frac{30}{89}$, where 89 is the number of months. Considering the test for excess zeros proposed by Broek (1995), based on the Poisson distribution, the data were zero inflated (p-value < 0.001). The same result was found using the *check_zeroinflation(·)* function from Lüdecke *et al*. (2021).

To model the series, we considered the models presented in equation (8), with $\boldsymbol{\beta} = \beta_1$ and $\boldsymbol{x}_t^\top = (\boldsymbol{x}_{t1})^\top$, $\boldsymbol{x}_{t1} = (1, 1, \ldots, 1)^\top$. We used the MH algorithm with a burn-in period of 1,000 and thin = 15, resulting in a final sample of 10,000.

$$\begin{aligned} y_t \mid \mathscr{F}_{t-1} &\sim \text{ZAP}\{\mu_t, \nu\} \\ y_t \mid \mathscr{F}_{t-1} &\sim \text{ZANBI}\{\mu_t, \nu, \sigma\} \\ y_t \mid \mathscr{F}_{t-1} &\sim \text{ZAPIG}\{\mu_t, \nu, \sigma\}, \end{aligned} \tag{8}$$

where $\log(\mu_t) = (1 - \phi_1 B^1)(1 - \Phi_1 B^{12})[\beta_1 - \log(y_t)] + \log(y_t)$.

Table 3 lists the estimation results for the models expressed in equation (8), including the credibility intervals and the deviance information criterion (DIC). The Φ_1 and β_1 parameters were removed from the ZANBI(μ_t, σ, ν) model because they were not significant. The same situation occurred with the β_1 parameter of the ZAPIG(μ_t, σ, ν). We also presented the dependence factor to evaluate the convergence of the chains.

The *Box-Pierce* (BOX; PIERCE, 1970) test indicated that the residuals of the models presented in Table 3 are noncorrelated, with p-values of 0.89, 0.11 and 0.90 for ZAP-SAR(1)$(1)_{12}$, ZANBI-AR(1) and ZAPIG-SAR(1)$(1)_{12}$, respectively, evaluated up to lag 20.

The lowest DIC was obtained using the ZAP-SAR(1)$(1)_{12}$ model, and the process can be written according to the following scheme:

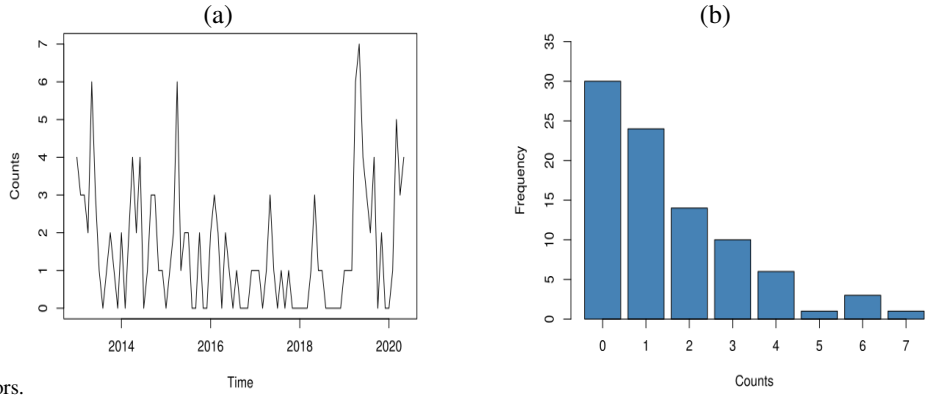
$$\begin{aligned} y_t \mid \mathscr{F}_{t-1} \sim \text{ZAP}\big\{&\log(\mu_t) = (1 - 0.381B^1)(1 - 0.253B^{12}) \\ &\times [1.062 - \log(y_t)] + \log(y_t), \nu = 0.400\big\}. \end{aligned}$$

Table 2 – Simulation results according to the first scenario, considering w = 1,000 replicates of each model.

Model	n	Parameter	Real	Mean	Mode	SD	CB	CE
ZAP-AR(1)	100	β_1	2.000	1.998	1.995	0.064	0.025	1.000
		ϕ_1	0.300	0.308	0.305	0.053	0.140	1.012
		ν	0.100	0.108	0.101	0.029	0.236	1.035
	100	β_1	2.000	2.004	1.996	0.119	0.046	1.000
		ϕ_1	0.300	0.306	0.304	0.045	0.117	1.007
		ν	0.400	0.404	0.402	0.049	0.096	1.003
ZANBI-AR(1)	100	β_1	2.000	2.004	1.997	0.090	0.036	1.000
		ϕ_1	0.300	0.313	0.309	0.057	0.154	1.024
		ν	0.100	0.108	0.101	0.029	0.236	1.038
		σ	0.100	0.124	0.108	0.047	0.404	1.117
	100	β_1	2.000	2.022	2.002	0.151	0.060	1.010
		ϕ_1	0.300	0.313	0.309	0.050	0.136	1.031
		ν	0.400	0.395	0.393	0.047	0.095	1.005
		σ	0.100	0.165	0.119	0.072	0.730	1.356
ZAPIG-AR(1)	100	β_1	2.000	2.006	1.997	0.088	0.035	1.002
		ϕ_1	0.300	0.312	0.308	0.063	0.169	1.017
		ν	0.100	0.107	0.100	0.029	0.233	1.027
		σ	0.100	0.127	0.108	0.050	0.433	1.135
	100	β_1	2.000	2.035	2.003	0.158	0.065	1.024
		ϕ_1	0.300	0.311	0.306	0.054	0.145	1.021
		ν	0.400	0.398	0.396	0.047	0.093	1.021
		σ	0.100	0.182	0.126	0.095	0.879	1.319

Source: The authors.

Figure 1 – Data over time: (a) monthly number of deaths of individuals under nine years of age due to A91 in Brazil; (b) bar graph of the data presented in (a).



Source: The authors.

The estimate of ν indicates that the probability of nonoccurrence of any death of individuals aged 0 to 9 years due to A91 in a given month t is 40.00% and varies between 28.60% and 52.10% according to the credibility interval. When considering 1 - ν, the exact probability of at least one death is 60.00%.

The average number of deaths in a given month t, conditioned to $y_t > 0$, can be estimated using the parameter μ_t, i.e., $\log(\mu_t) = (1 - 0.381B^1)(1 - 0.253B^{12})[1.062 - \log(y_t)] + \log(y_t)$.

In Figure 2, we show the forecasts for June and July 2020, where the grey areas represent the regions of high density at the 95% credibility level. The estimates point to 2.05 deaths in June and 1.63 in July. Compared with the real values of three and one death in June and July, respectively, the best forecast was for the month of July. Figure 2(c) also displays the fitted values and the forecasts for June and July 2020, with the 95% credibility intervals.

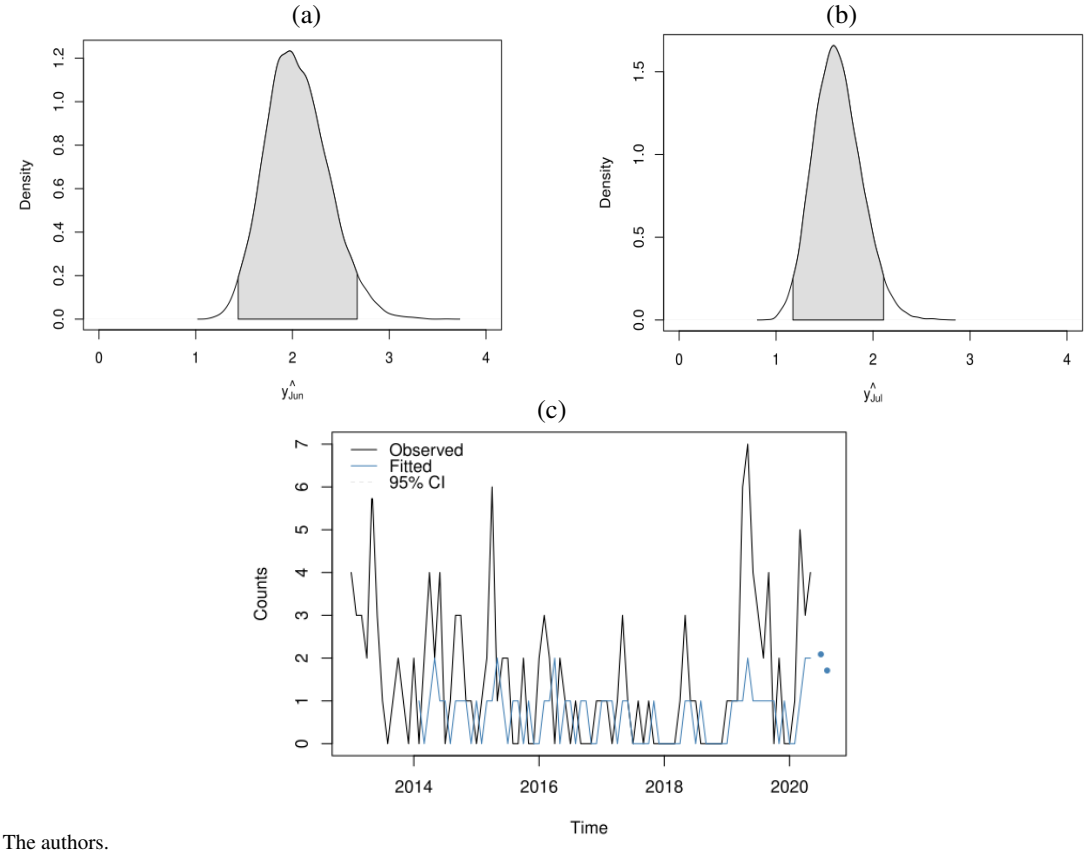
Based on the predictive density, the probability $P(\hat{y}_{Jun} = 3 \mid \mathscr{F}_{t-1})$ is 13.47%, with $CI_{95\%} = (10.50\%; 16.60\%)$. For July, $P(\hat{y}_{Jul} = 1 \mid \mathscr{F}_{t-1})$ is 13.76%, with $CI_{95\%} = (7.00\%; 20.60\%)$. In terms of accuracy, a mean absolute percent error (MAPE) equal to 47.33% was obtained using the ZAP-SAR(1)$(1)_{12}$ model.

Table 3 – Parameter estimates for the models defined in equation (8) and fit to the dengue data (A91) for children under nine years old.

Model	Parameter	Mean	SD	HPD (95%)		I	DIC
				L_l	L_u		
ZAP-SAR(1)$(1)_{12}$	β_1	1.062	0.330	0.420	1.726	1.350	569.030
	ϕ_1	0.381	0.139	0.124	0.663	1.100	
	Φ_1	0.253	0.120	0.019	0.483	1.090	
	ν	0.400	0.060	0.286	0.521	1.050	
ZANBI-AR(1)	ϕ_1	0.478	0.143	0.193	0.753	1.080	725.954
	ν	0.345	0.050	0.245	0.439	1.030	
	σ	0.957	0.433	0.248	1.825	1.010	
ZAPIG-SAR(1)$(1)_{12}$	ϕ_1	0.446	0.173	0.121	0.800	1.170	613.481
	Φ_1	0.372	0.175	0.035	0.718	1.100	
	ν	0.372	0.054	0.266	0.476	1.050	
	σ	0.784	0.524	0.019	1.775	0.976	

Source: The authors.

Figure 2 – Density of the expected number of deaths due to A91: (a) June; (b) July; (c) fitted values according to the ZAP-SAR(1)$(1)_{12}$ model.



Source: The authors.

In Table 4, we show the probability of extreme values, such as 8, 10 and 12, which is a form of analysis that allows evaluating periods of outbreak and increase in the number of deaths (YANG; ZAMBA; CAVANAUGH, 2013). According to these results, the probability that the number of deaths is greater than or equal to 12 is 0.018% in June and 0.001% in July 2020.

Table 4 – Probabilities of occurrence of atypical counts in the months of June and July 2020 based on the predictive density.

Month	$P(\hat{y}_t \geq 8 \mid \cdot)$	$P(\hat{y}_t \geq 10 \mid \cdot)$	$P(\hat{y}_t \geq 12 \mid \cdot)$
June	0.014	0.001	<0.001
July	0.003	<0.001	<0.001

Source: The authors.

Conclusions

In this work, the Poisson, Negative binomial and, Poisson inverse Gaussian zero-adjusted distributions were studied for modelling count time series. A Bayesian analysis was adopted, and its performance was evaluated using a simulation study.

When analysing mortality due to dengue haemorrhagic fever in Brazil, we verified the usefulness of the zero-adjusted distributions, which allow considering characteristics such as the excess of zeros and estimating the exact probabilities that the process assumes the zero value at a given instant of time.

These contributions allow the analysis of time series, such as the number of disease cases in populations, monitoring and predicting periods and probabilities of outbreaks over time, as discussed in Yang, Zamba and Cavanaugh (2013) and Sathish, Mukhopadhyay and Tiwari (2021).

Suggestions for future work are the study of higher ARMA(p, q) orders, the increase in the proportion of zeros and the implementation and comparison of other algorithms for drawing from the joint posterior, such as Hamiltonian Monte Carlo (HMC) algorithm (DUANE *et al.*, 1987).

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Appendices

Joint posteriors of the simulated models

This appendix presents the joint posterior of the simulated models. Considering the ZAP-AR(1) model, we have:

$$\pi(\boldsymbol{\theta} \mid Y) \propto \prod_{t=m+1}^{n} \left\{ \nu \mathrm{I}_{(y_t=0)} + \left[\frac{1-\nu}{1-e^{-\nu}} \right] \frac{e^{-\mu_t} \mu_t^{y_t}}{y_t!} \mathrm{I}_{(y_t>0)} \right\} \times \exp\left\{ -\frac{(\beta_1^2+\phi_1^2)}{200} \right\},$$

where $\mu_t = \exp\{[1-\phi_1 B^1][\beta_1 - \log(y_t)] + \log(y_t)\}$.

For the ZANBI-AR(1) model, we have:

$$\pi(\boldsymbol{\theta} \mid Y) \propto \prod_{t=m+1}^{n} \left\{ \nu \mathrm{I}_{(y_t=0)} + \frac{(1-\nu)\mu_t}{[1-(1+\mu_t\sigma)^{\frac{-1}{\sigma}}]} \times \frac{\Gamma(y_t+\frac{1}{\sigma})}{\Gamma(\frac{1}{\sigma})\Gamma(y_t+1)} \left(\frac{\sigma\mu_t}{1+\sigma\mu_t} \right)^{y_t} \left(\frac{1}{1+\sigma\mu_t} \right)^{\frac{1}{\sigma}} \times \mathrm{I}_{(y_t>0)} \right\} \left\{ \exp\left[-\frac{(\beta_1^2+\phi_1^2)}{200} - \frac{\sigma}{s} \right] \frac{\sigma^{a-1}}{s^a \Gamma(a)} \right\},$$

where $\mu_t = \exp\{[1-\phi_1 B^1][\beta_1 - \log(y_t)] + \log(y_t)\}$.

For the ZAPIG-AR(1) model, we have:

$$\pi(\boldsymbol{\theta} \mid Y) \propto \prod_{t=m+1}^{n} \left\{ \nu \mathrm{I}_{(y_t=0)} + \left[\frac{1-\nu}{1-e^{\frac{1}{\sigma}-\alpha}} \right] \times \left(\frac{2\alpha}{\pi} \right)^{\frac{1}{2}} \mu_t^{y_t} e^{\frac{1}{\sigma}} \left(K_{y_t-\frac{1}{2}}(\alpha) \right) \frac{1}{(\alpha\sigma)^{y_t} y_t!} \mathrm{I}_{(y_t>0)} \right\} \times \left\{ \exp\left[-\frac{(\beta_1^2+\phi_1^2)}{200} - \frac{\sigma}{s} \right] \frac{\sigma^{a-1}}{s^a \Gamma(a)} \right\},$$

where $\mu_t = \exp\{[1-\phi_1 B^1][\beta_1 - \log(y_t)] + \log(y_t)\}$.

Joint posterior distributions applied to the dengue data

Considering the time series, the joint posterior of the ZAP-SAR(1)$(1)_{12}$ model is given by:

$$\pi(\boldsymbol{\theta} \mid Y) \propto \prod_{t=m+1}^{n} \left\{ \nu \mathrm{I}_{(y_t=0)} + \left[\frac{1-\nu}{1-e^{-\nu}} \right] \frac{e^{-\mu_t} \mu_t^{y_t}}{y_t!} \mathrm{I}_{(y_t>0)} \right\} \times \exp\left\{ -\frac{(\beta_1^2+\phi_1^2+\Phi_1^2)}{200} \right\},$$

where $\mu_t = \exp\{[1-\phi_1 B^1][1-\Phi_1 B^{12}][\beta_1 - \log(y_t)] + \log(y_t)\}$. Considering the ZANBI-AR(1) model, we have:

$$\pi(\boldsymbol{\theta} \mid Y) \propto \prod_{t=m+1}^{n} \left\{ \nu \mathrm{I}_{(y_t=0)} + \frac{(1-\nu)\mu_t}{[1-(1+\mu_t\sigma)^{\frac{-1}{\sigma}}]} \times \frac{\Gamma(y_t+\frac{1}{\sigma})}{\Gamma(\frac{1}{\sigma})\Gamma(y_t+1)} \left(\frac{\sigma\mu_t}{1+\sigma\mu_t} \right)^{y_t} \left(\frac{1}{1+\sigma\mu_t} \right)^{\frac{1}{\sigma}} \times \mathrm{I}_{(y_t>0)} \right\} \left\{ \exp\left[-\frac{\phi_1^2}{200} - \frac{\sigma}{s} \right] \frac{\sigma^{a-1}}{s^a \Gamma(a)} \right\},$$

where $\mu_t = \exp\{[1-\phi_1 B^1][-\log(y_t)] + \log(y_t)\}$. For the ZAPIG-SAR(1)$(1)_{12}$ model, we have:

$$\pi(\boldsymbol{\theta} \mid Y) \propto \prod_{t=m+1}^{n} \left\{ \nu \mathrm{I}_{(y_t=0)} + \left[\frac{1-\nu}{1-e^{\frac{1}{\sigma}-\alpha}} \right] \times \left(\frac{2\alpha}{\pi} \right)^{\frac{1}{2}} \mu_t^{y_t} e^{\frac{1}{\sigma}} \left(K_{y_t-\frac{1}{2}}(\alpha) \right) \frac{1}{(\alpha\sigma)^{y_t} y_t!} \mathrm{I}_{(y_t>0)} \right\} \times \left\{ \exp\left[-\frac{(\phi_1^2+\Phi_1^2)}{200} - \frac{\sigma}{s} \right] \frac{\sigma^{a-1}}{s^a \Gamma(a)} \right\},$$

being $\mu_t = \exp\{[1-\phi_1 B^1][1-\Phi_1 B^{12}][-\log(y_t)] + \log(y_t)\}$.

Additional simulation results

Table 5 displays the simulation results for the second scenario. In Tables 6 and 7, we present the settings of the MH algorithm and the convergence analysis.

Table 5 – Second scenario simulation results based on w = 1,000 replicated models.

Model	n	Parameter	Real	Mean	Mode	SD	CB	CE
ZAP-AR(1)	100	β_1	2.000	2.000	2.000	0.024	0.010	1.000
		ϕ_1	-0.800	-0.800	-0.800	0.012	0.012	1.000
		ν	0.100	0.108	0.101	0.029	0.234	1.035
	100	β_1	2.000	1.999	1.998	0.042	0.017	1.000
		ϕ_1	-0.800	-0.801	-0.801	0.018	0.018	1.001
		ν	0.400	0.400	0.398	0.048	0.096	1.000
ZANBI-AR(1)	100	β_1	2.000	1.997	1.997	0.035	0.014	1.003
		ϕ_1	-0.800	-0.802	-0.801	0.029	0.029	1.002
		ν	0.100	0.110	0.103	0.030	0.251	1.081
		σ	0.100	0.113	0.102	0.032	0.267	1.052
	100	β_1	2.000	1.992	1.991	0.069	0.027	1.007
		ϕ_1	-0.800	-0.805	-0.803	0.034	0.033	1.008
		ν	0.400	0.403	0.402	0.046	0.092	1.002
		σ	0.100	0.113	0.101	0.030	0.251	1.098
ZAPIG-AR(1)	100	β_1	2.000	1.997	1.996	0.036	0.014	1.003
		ϕ_1	-0.800	-0.804	-0.803	0.029	0.029	1.008
		ν	0.100	0.108	0.101	0.029	0.234	1.037
		σ	0.100	0.113	0.100	0.032	0.269	1.077
	100	β_1	2.000	1.997	1.996	0.067	0.026	1.001
		ϕ_1	-0.800	-0.804	-0.802	0.034	0.033	1.006
		ν	0.400	0.402	0.400	0.048	0.095	1.000
		σ	0.100	0.116	0.102	0.032	0.274	1.115

Source: The authors.

Table 6 – Settings used in MH and convergence analysis for the first scenario, where $\overline{AC}$ is the probability acceptance, $\overline{I}$ is the mean of the dependence factor, $\overline{G}$ is the mean of the absolute value of G, and $\overline{HW}$ is the mean of the p-value of HW test.

Model	n	Samples	Burn-in	Thin	$\overline{AC}$	$\boldsymbol{\theta}$	$\overline{I}$	$\overline{G}$	$\overline{HW}$
ZAP-AR(1)	100	5,000	1,000	7	0.48	β_1	1.24	0.00	0.50
						ϕ_1	1.21	0.05	0.51
						ν	1.13	0.03	0.51
	100	5,000	1,000	8	0.45	β_1	1.22	0.02	0.50
						ϕ_1	1.23	0.02	0.50
						ν	1.22	0.05	0.49
ZANBI-AR(1)	100	5,000	1,000	11	0.36	β_1	1.20	0.04	0.49
						ϕ_1	1.19	0.04	0.47
						ν	1.10	0.07	0.49
						σ	1.08	0.04	0.50
	100	6,000	1,000	11	0.34	β_1	1.25	0.06	0.51
						ϕ_1	1.25	0.06	0.50
						ν	1.24	0.06	0.49
						σ	1.12	0.07	0.50
ZAPIG-AR(1)	100	5,000	1,000	11	0.36	β_1	1.21	0.08	0.50
						ϕ_1	1.20	0.10	0.49
						ν	1.12	0.13	0.48
						σ	1.09	0.10	0.48
	100	5,000	1,000	11	0.34	β_1	1.21	0.05	0.50
						ϕ_1	1.26	0.10	0.50
						ν	1.24	0.00	0.48
						σ	1.13	0.04	0.51

Source: The authors.

Table 7 – Settings used in MH and convergence analysis for the second scenario, where $\overline{AC}$ is the probability acceptance, $\overline{I}$ is the mean of the dependence factor, $\overline{G}$ is the mean of the absolute value of G, and $\overline{HW}$ is the mean of the p-value of HW test.

Model	n	Samples	Burn-in	Thin	$\overline{AC}$	$\boldsymbol{\theta}$	$\overline{I}$	$\overline{G}$	$\overline{HW}$
ZAP-AR(1)	100	5,000	1,000	8	0.45	β_1	1.25	0.08	0.50
						ϕ_1	1.25	0.07	0.50
						ν	1.13	0.14	0.49
	100	5,000	1,000	8	0.45	β_1	1.24	0.13	0.49
						ϕ_1	1.26	0.13	0.49
						ν	1.22	0.14	0.49
ZANBI-AR(1)	100	5,000	1,000	9	0.36	β_1	1.26	0.06	0.51
						ϕ_1	1.30	0.08	0.50
						ν	1.15	0.08	0.49
						σ	1.12	0.06	0.50
	100	5,000	1,000	10	0.36	β_1	1.22	0.00	0.48
						ϕ_1	1.25	0.00	0.49
						ν	1.20	0.03	0.49
						σ	1.08	0.13	0.51
ZAPIG-AR(1)	100	6,000	1,000	12	0.35	β_1	1.16	0.06	0.50
						ϕ_1	1.20	0.01	0.50
						ν	1.07	0.09	0.50
						σ	1.05	0.14	0.51
	100	6,000	1,000	12	0.35	β_1	1.17	0.07	0.49
						ϕ_1	1.20	0.05	0.50
						ν	1.15	0.06	0.48
						σ	1.05	0.16	0.50

Source: The authors.

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