

A SEIR-SEI model calibration for the Zika virus epidemic in Brazil

Eber Dantas, Michel Tosin, Americo Cunha Jr

Universidade do Estado do Rio de Janeiro, Brazil
 NUMERICO - Nucleus of Modeling and Experimentation with Computers
 eber.paiva@uerj.br, michel.tosin@uerj.br, americo@ime.uerj.br

Keywords. Zika virus epidemic, mathematical biology, nonlinear dynamics, inverse problem, Bayesian updating

EXTENDED ABSTRACT

Introduction

The Zika virus has been reported as autochthonously transmissible in over 30 countries and has reached more than 200,000 probable cases in Brazil. Thus, the use of mathematical models for epidemics become of great importance, since they are useful tools to predict the underlying outbreak numbers and allow one to test the effectiveness of different strategies used to combat the associated diseases. In previous works (Dantas, 2017; Tosin, 2017), the authors have identified reasonable parameters and initial conditions (IC) that fit a SEIR-SEI model to epidemic data of the Brazilian outbreak, by the deterministic solution of an inverse problem. This work uses Bayesian Inference to explore the uncertainties associated to the initial number of infectious humans, an IC that lacks reference data on the literature related to the epidemic, updating the associated stochastic model with experimental data provided by the Brazilian Ministry of Health. *Posterior* probability density functions are generated assuming uniform and gamma *prior* distributions over different conditions.

Mathematical Model

Figure 1 depicts schematically the evolution of human and mosquito (vector) populations through the compartmental model, with its dynamics governed by the following nonlinear system of ordinary differential equations

$$\begin{aligned}
 dS_h/dt &= -\beta_h S_h I_v, & dE_h/dt &= \beta_h S_h I_v - \alpha_h E_h, & dI_h/dt &= \alpha_h E_h - \gamma I_h, & dR_h/dt &= \gamma I_h, \\
 dS_v/dt &= \delta - \beta_v S_v I_h/N - \delta S_v, & dE_v/dt &= \beta_v S_v I_h/N - (\alpha_v + \delta) E_v, & dI_v/dt &= \alpha_v E_v - \delta I_v, & dC/dt &= \alpha_h E_h,
 \end{aligned} \tag{1}$$

where the susceptible (S), exposed (E), infectious (I) and recovered (R) groups compartmentalize the populations at time t (h for human's groups, counted as individuals, and v for vector's, computed as a proportion of the total vector population); $C(t)$ regards the cumulative number of infectious people; $1/\alpha$ is the disease's incubation period; $1/\gamma$, the human infection period; $1/\delta$, the vector lifespan; β , the transmission rate; and N is the total human population.

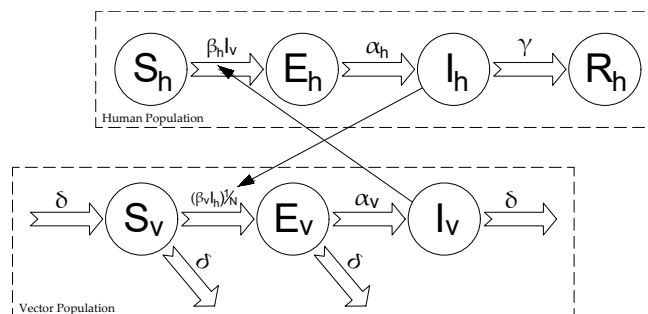


Figure 1: Schematic representation of the SEIR-SEI model for the Zika virus outbreak description.

Deterministic identification of the parameters and IC has been previously conducted (Dantas, 2017; Tosin, 2017), taking into account empirical data of the outbreak (Ministério da Saúde, 2017). Figure 2 displays one fitting of the model, achieved by solution of an inverse problem via a Trust-Region-Reflective method. The main issue of the deterministic fitting is the lack of reference data for some IC, in particular, the initial number of infectious humans (I_h^i).

Results

Equation 2 summarizes the Bayesian formalism

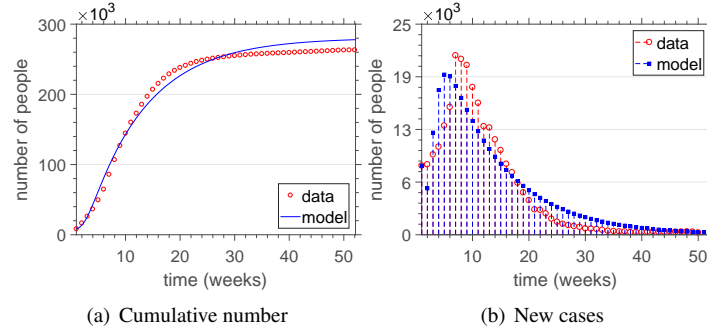


Figure 2: Outbreak data (red) and calibrated model response (blue). Cumulative number of infectious humans on the left, and the number of new infectious cases at each week on the right.

$$\pi(\text{model} \mid \text{data}) \propto \pi(\text{data} \mid \text{model}) \times \pi(\text{model}), \quad (2)$$

where, in this context, $\pi(\text{model})$ is the *prior* distribution of I_h^i , analyzed as uniform and gamma distributions; $\pi(\text{data} \mid \text{model})$ identifies the likelihood, modeled by assuming a Gaussian error on the system when comparing the empirical data with the model response of the fitting in Figure 2; and $\pi(\text{model} \mid \text{data})$ is the *posterior* distribution, the probability density function of I_h^i updated by the empirical data. Figure 3 and 4 displays the analysis results for uniform and gamma *priors*, respectively. Different supports of the uniform *prior* were used ($[0, 25,000]$, $[0, 50,000]$, $[0, 75,000]$, $[0, 100,000]$), while on the gamma distributions 4 coefficient of variation were tried (20%, 40%, 60%, 80%) with the same mean of $\mu = 10^3$. The standard deviation of the likelihood was kept the same on all cases ($\sigma = 10^4$).

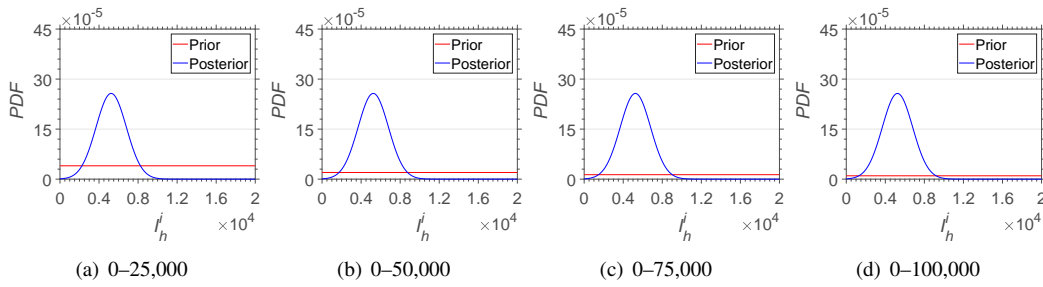


Figure 3: Uniform *priors* and *posteriors* for I_h^i .

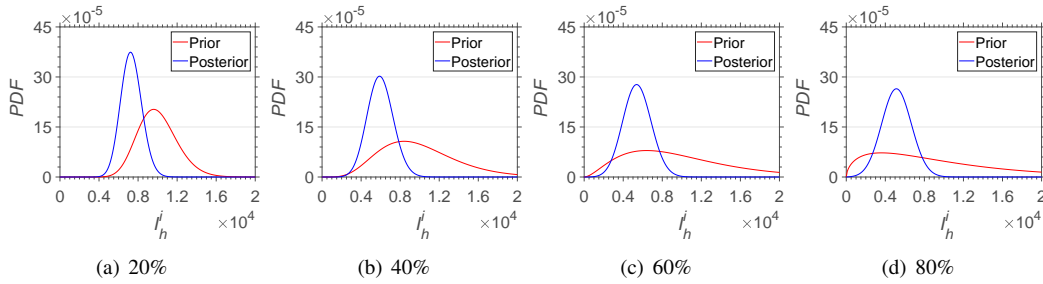


Figure 4: Gamma *priors* and *posteriors* for I_h^i .

Conclusion

Multiple updated distributions were generated for I_h^i , allowing considerations over the effect of the *priors*. In future works, the authors intend to conduct the same procedure to other IC, and implement Markov chain Monte Carlo methods to better analyze the stochastic model adjacent to the SEIR-SEI.

ACKNOWLEDGEMENTS

The authors are indebted to the Brazilian agencies CNPq, CAPES and FAPERJ for the financial support.

REFERENCES

- Dantas, E., Tosin, M. and Cunha Jr, A., 2017, ‘‘Calibration of a SEIR-SEI epidemic model to describe the Zika virus outbreak in Brazil’’, <https://hal.archives-ouvertes.fr/hal-01456776v3>
- Tosin, M., Dantas, E., and Cunha Jr, A., 2017, ‘‘Zika virus in Brazil: calibration of an epidemic model for 2016 outbreak’’, In XXXVII Congresso Nacional de Matematica Aplicada e Computacional (CNMAC 2017), Sao Jose dos Campos, Brazil.
- Ministerio da Saude, ‘‘Obtencao de numero de casos confirmados de Zika, por municipio e semana epidemiologica’’, <https://goo.gl/3Tf19j>, 2017. Accessed: 08/18/2017.