

# Comparison of time series and mechanistic models of vector-borne diseases

- Vyhmeister E.<sup>a</sup>
- Provan G.<sup>a</sup>,
- Doyle B.<sup>b</sup>,
- Bourke B.<sup>b</sup>,
- Castane G.G.<sup>a</sup>,
- Reyes-Bozo L.<sup>c</sup>

## **Abstract**

Vector-borne disease models are widely used to understand the dynamics involved in virus transmission. The simplest version of the mechanistic SEIR-SEI model is the most widely used representation of the dynamics involved in vector-borne diseases. Modifications to the basic model can improve the complex dynamics' accuracy. This work evaluates the capability of different models to represent the dynamics involved in dengue virus transmission. The models include a vector life stage representation, a re-susceptibility factor, and environmental variables in a mechanistic form. Furthermore, Autoregressive Integrated Moving Average methodologies (ARIMA method) were also used for comparison. The inclusion of environmental variables and vector life cycle improves the model's accuracy for mechanistic models, but the modification's complexity can restrict its applicability. Data-driven techniques were shown to be less accurate than all the mechanistic-based models (based on all criteria adopted). © 2022

## **Author keywords**

ARIMA; Modelling; SEIR-SEI; Vector-borne diseases