

The population ecology of infectious diseases with pertussis as a case study

Supplementary Information

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Overview

We describe the methods used to find the seasonal transmission rates of pertussis in Thailand. The ESM is structured as follows:

1. Seasonality in Thailand
 - Time series SIR model (TSIR)
 - Susceptible reconstruction

Seasonality in Thailand

We applied the time series SIR (TSIR) framework to estimate monthly transmission parameters in Thailand (Finkenstadt *et al.*, 2000; Finkenstadt *et al.*, 2002). Here, we first describe the susceptible reconstruction which is required to provide estimates of particular parameters. Second, we describe the TSIR model.

Susceptible reconstruction

Susceptible reconstruction is used to estimate the reporting rate ρ in addition to the deviations of the number of susceptibles from the mean at each time point in our data (Z_t), both of which are required in the TSIR model.

Following the methodology of (Finkenstadt *et al.*, 2000), the number of susceptible individuals at time t is assumed to be given by unvaccinated births and susceptible individuals from the last time point minus by the number of new infections:

$$S_t = S_{t-1} + b_t(1 - p_t) - \frac{C_t}{\rho} \quad (\text{A1})$$

where C_t is the number of reported cases, ρ is the constant-valued reporting rate, S_t is the number of susceptibles, and b_t is the number of births reduced by a proportion p_t vaccinated individuals. Susceptible individuals can be written as $S_t = Z_t + \bar{S}$ where Z_t are the deviations from the mean number of susceptibles (\bar{S}) at each time.

$S_t = Z_t + \bar{S}$ is substituted into Equation A1 so that

$$Z_t = Z_{t-1} + b_t(1 - p_t) - \frac{C_t}{\rho}. \quad (\text{A2})$$

Iterating Equation A2 for an initial condition Z_0 gives us

$$Z_t = Z_0 + \sum_{i=1}^t b_i(1 - p_i) - \sum_{i=1}^t \frac{C_i}{\rho}. \quad (\text{A3})$$

This equation can be rearranged as

$$\sum_{i=1}^t b_i(1 - p_i) = \frac{1}{\rho} \sum_{i=1}^t C_i + Z_t - Z_0. \quad (\text{A4})$$

Under the assumption that all unvaccinated individuals acquire infection within their lifetime, the slope of a linear regression between the cumulative births (discounted by vaccination) and the cumulative reported cases provides the inverse of the reporting rate ($1/\rho$) and Z_t is estimated as the residuals from the regression (Finkenstadt *et al.*, 2000; Metcalf *et al.*, 2009). The resulting value of ρ is 0.0063 (or 0.63% reporting).

Time series SIR model

Susceptible individuals are given by S_t and the true number of infected individuals I_t – case reports C_t corrected for under reporting so that $I_t = C_t/\rho$ – are described by the equations:

$$E[I_t|I_{t-1}, S_{t-1}] = \lambda_t S_{t-1} = \frac{\beta_{t-1}(I_{t-1})^\alpha}{N_{t-1}} S_{t-1} \quad (\text{A5})$$

$$S_t = b_t(1 - p_t) + S_{t-1} - I_t. \quad (\text{A6})$$

Starting with I_t infected individuals and assuming independence, this is a birth-death process following the negative binomial distribution such that

$$I_t \sim NB(\lambda_t S_{t-1}, I_{t-1}) \quad (\text{A7})$$

where $\lambda_t S_{t-1}$ is the expectation and I_{t-1} is the clumping parameter. Using our estimates of I_t and replacing S_t with $\bar{S} + Z_t$ (see previous section), and given that I_t follows the negative binomial distribution, we used maximum likelihood to estimate β_t , α , and \bar{S} .

References

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