Supplementary Materials: Modeling the 2013 Zika outbreak in French Polynesia: Intervention Strategies

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1. Basic Reproduction Number

The basic reproduction number \( R_0 \) for a disease is defined as the average number of new cases of an infection caused by one infected individual during their infectious period in a completely susceptible population [1]. The basic reproduction number for multi category compartmental models can be calculated using the Next Generation Matrix (NGM) [2]. The next generation matrix, \( K \), introduced in [3] relates the numbers of newly infected individuals in the various categories in consecutive generations [4]. The element \( K_{ij} \) of the matrix \( K \) represents the number of new cases in state \( i \) caused by a new born individual in state \( j \). A generation is defined by number of individuals infected by the previous generation. Figure S1 shows a basic example for the next generation matrix and its use in the calculation of \( R_0 \).

**Calculation of \( R_0 \) using \( K \):**

If the infection is introduced by a vector, then the initial generation vector, \( Q_0 = [1 \ 0]^T \). The future generations of infection can be calculated as:

\[
Q_i = K_i Q_0 = [0 \ 10]^T
\]

\[
Q_i = K^K_i Q_0 = [20 \ 0]^T
\]

\[\vdots\]

\[
Q_i = K^n_i Q_0
\]

No vectors are infected in the first generation \( Q_0 \), because there are no infected humans in the previous generation. The infections alternate between vectors and humans in each generation, therefore in order to calculate \( R_0 \), the operator \( K \) is applied to the initial generation \( n \) times (\( n \) tends to infinity) and the value is averaged across all these generations by calculating the infinite norm of the matrix \( K \).

**Construction of NGM**

The process of constructing the NGM for a heterogeneous epidemiological system is described in detail in [2]. The steps involve:

1. Linearize the infected subsystem to get the Jacobian matrix, \( J \).
2. Decompose the Jacobian matrix into \( T \) and \( \Sigma \), where \( T \) is the transmission part and \( \Sigma \) is the transition matrix, such that \( J = T + \Sigma \). \( T \) represents the birth of new infections and \( \Sigma \) represents all other transitions (recovery, mortality etc). \( T_{ij} \) is the rate at which individuals in state \( i \) give rise to individuals in state \( j \) and \( -\Sigma_{ji}^{-1} \) represents the time an individual in state \( j \) will spend in state \( i \) in their future life.
3. Compute \( K \) as \(-T\Sigma^{-1}\)

**Calculation of Reproduction Number**

\( K \) can be viewed as an iterative linear operator which when applied to the current generation results in the infections in the new generation. In case of vector-borne diseases or other diseases
\[ \begin{align*}
\frac{\partial E_H}{\partial t} &= \beta V_H I_V - \alpha H E_H \\
\frac{\partial I_H}{\partial t} &= \alpha H E_H - \gamma I_H \\
\frac{\partial E_V}{\partial t} &= \beta V_H N_V I_H - (\mu_A h + \rho_A h) E_V - \alpha V E_V \\
\frac{\partial I_V}{\partial t} &= \alpha V E_V - (\mu_A h + \rho_A h) I_V
\end{align*} \] (1)

The infected subsystem involving heterogeneous populations, infections in one kind of population happen in alternate generations. Figure S1 exemplifies this phenomenon. If \( \phi_i \) denotes the \( i^{th} \) infection generation then,

\[ \begin{align*}
\phi_1 &= K \phi_0 \\
\phi_n &= K^n \phi_0
\end{align*} \]

Then, the basic reproduction number \( R_0 \) for the infection is defined as \( \frac{1}{n^{th}} \) power of the growth of \( K \) in \( n \) generations (geometric mean across \( n \) generations) as \( n \) grows to infinity, \( R_0 = \lim_{n \to \infty} (||K^n||)^{\frac{1}{n}} \) which is also equal to its spectral radius or its largest eigenvalue\( [4] \).

For the transmission system defined by equations 1 and equation 2, the infected subsystem consists of 4 categories \( \{E_H, I_H, E_V, I_V\} \). Since \( R_0 \) is calculated when the entire population is susceptible, \( \therefore S_H = N_H \) and \( S_V = N_V \) which leads to linear system of ODEs:

\[ T = \begin{bmatrix}
0 & 0 & 0 & \beta V_H \\
0 & 0 & 0 & 0 \\
0 & \beta V_H N_V & 0 & 0 \\
0 & 0 & 0 & 0
\end{bmatrix} \]

\[ \Sigma = \begin{bmatrix}
-\alpha_H & 0 & 0 & 0 \\
\alpha_H & -\gamma & 0 & 0 \\
0 & 0 & -(\mu_A h + \rho_A h + \alpha_V) & 0 \\
0 & 0 & \alpha_V & -(\mu_A h + \rho_A h)
\end{bmatrix} \]

\[ -\Sigma^{-1} = \begin{bmatrix}
\frac{1}{\alpha_H} & 0 & 0 & 0 \\
\frac{1}{\alpha_H} & 1 & 0 & 0 \\
\frac{1}{\alpha_V} & 0 & 1 & 0 \\
\frac{1}{\alpha_V} & \frac{1}{\alpha_V} & \frac{1}{\alpha_V} & 1
\end{bmatrix} \]

The transmission matrix(\( T \)) and the transition matrix (\( \Sigma \)) for the system

\( R_0 \) is calculated as the largest eigenvalue of the matrix \( K = -T \Sigma^{-1} \). Estimates for the basic reproduction number \( R_0 \) ranged from 1.56-2.95 (95% CI: 2.0767-2.2026).

References