Stochastic Multistrain Dengue model

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Multi-strain dynamics

In this paper we propose a stochastic 4-serotype SIR model with cross-immunity to describe multi-strain Dengue dynamics. The model permits up to 4 dengue infections with reduced susceptibility after the first Dengue episode due to cross immunity. Immunity to each serotype is considered complete and permanent. Figure 1 depicts all possible states and state-transitions included in the model.

Let S be individuals susceptible to all 4 types of dengue, I_i infectious with Dengue type i and R_i individuals recovered from Dengue type i. Infectious individuals already on their secondary and later Dengue infections are represented by multiple indices. For example, $I_{[23]1}$ is an individual which has had Dengues type 2 and 3 in the past – and therefore is immune to them – and is currently transmitting Dengue 1. The index outside the bracket denotes current infection. Recovered individuals indices denote their immunity, so for instance R_{123} is an individual which is immune to Dengue types 1, 2 and 3, but not to 4. Let $I_{*i} = \sum I_{[...]i}$ with [...] representing exposure history of the infected individual which can vary from 0 to 3 in length. All individuals are born to the S state and birth and death rates are equal.

The possible state-transitions and their propensities are listed in table 1.

The model is implemented as a continuous time Markov jump process. Let

$$\overrightarrow{X}(t) = [S(t), I_1(t), I_2(t), \dots, R_{1234}(t)]$$

be the state of the system at the time t. The system is written as a forward Kolmogorov differential equation, which in matrix form looks like

$$\frac{dP_X(t)}{dt} = QP_X(t) \tag{1}$$

Where $P_X(t)$ is the matrix of transition probabilities (given in table 1) and Q is the generator matrix, whose non-zero values are also given in table 1 (in the state change column). The full formula and matrices are ommitted due to their large sizes.

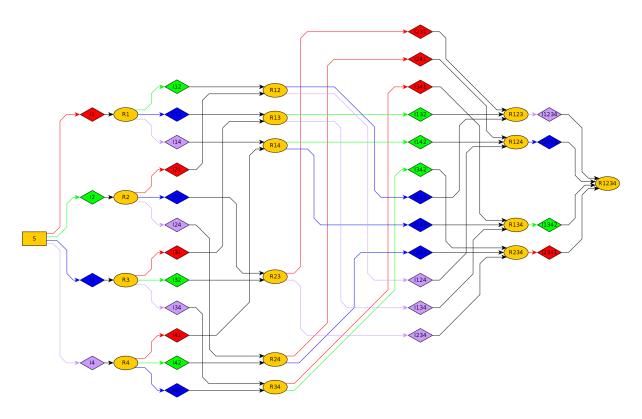


Figure 1: Block diagram detailing the stochastic model. Infected individuals with different Dengue viruses are represented by different colors. Infections are also represented by colored arrows matching the virus type.

Table 1: State-transitions and probabilities: $P(\Delta X(t)|X(t))$. The transitions are summarized below. Fully expanded, the system contemplates 64 possible state transitions, as can be verified in figure 1. † : $P(\cdot)$ is the sum of the probabilities of all possible state changing transitions.

Transition	Probability	State Change	Description
$S \to I_i$	$\beta SI_{*i}\Delta t$	$\Delta S(t) = -1, \ \Delta I_i(t) = 1$	Primary infection
$I_i \to R_i$	$\sigma I_i \Delta t$	$\Delta I_i(t) = -1, \Delta R_i(t) = 1$	Primary recovery
$R_i \to I_{[i]j}$	$\beta \delta R_i I_{*j} \Delta t$	$\Delta R_i(t) = -1, \Delta I_{[i]j}(t) = 1$	Secondary infection
$I_{[i j} \to R_{ij}$	$\sigma I_{[i]j}\Delta t$	$\Delta I_{[i]j}(t) = -1, \Delta R_{ij}(t) = 1$	Secondary recovery
$R_{ij} \to I_{[ij]k}$	$\beta \delta R_{ij} I_{*k} \Delta t$	$\Delta R_{ij}(t) = -1, \Delta I_{[ij]k}(t) = 1$	Tertiary infection
$I_{[ij]k} o R_{ijk}$	$\sigma I_{[ij]k}\Delta t$	$\Delta I_{[ij]k}(t) = -1, \Delta R_{ijk}(t) = 1$	Tertiary recovery
$R_{ijk} \to I_{[ijk]l}$	$\beta \delta R_{ijk} I_{*l} \Delta t$	$\Delta R_{ijk}(t) = -1, \Delta I_{[ijk]l}(t) = 1$	Quaternary infection
$I_{[ijk]l} o R_{ijkl}$	$\sigma I_{[ijk]l}\Delta t$	$\Delta I_{[ijk]l}(t) = -1, \ \Delta R_{ijkl}(t) = 1$	Quaternary recovery
$\rightarrow S$	$\mu N \Delta t$	$\Delta S = 1$	Birth
$All \rightarrow$	$\mu N \Delta t$	$\Delta S = \Delta I_* = \Delta R_* = -1$	Death
No transition	$1 - P(\cdot)^{\dagger}$	No change	_

Expected Change and Covariance Matrix

It is useful to calculate the expected change and the covariance matrix for the changes $\Delta X = [\Delta S, \Delta I_1, \Delta I_2, \dots, \Delta R_{1234}]^T$. Thus from the probabilities of table 1,

$$E(\Delta X) = \sum_{X} p_i \Delta X_i = \begin{pmatrix} \beta S I_{*i} \Delta t \\ \beta S I_{*i} \Delta t \\ \beta S I_{*i} \Delta t \end{pmatrix} \Delta t$$
 (2)

References