Stochastic Modelling of Measles in a Disease-Eliminated Setting in Europe

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Abstract

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1 Background

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2 Model Dynamics

2.1 SEIR Compartmental Model

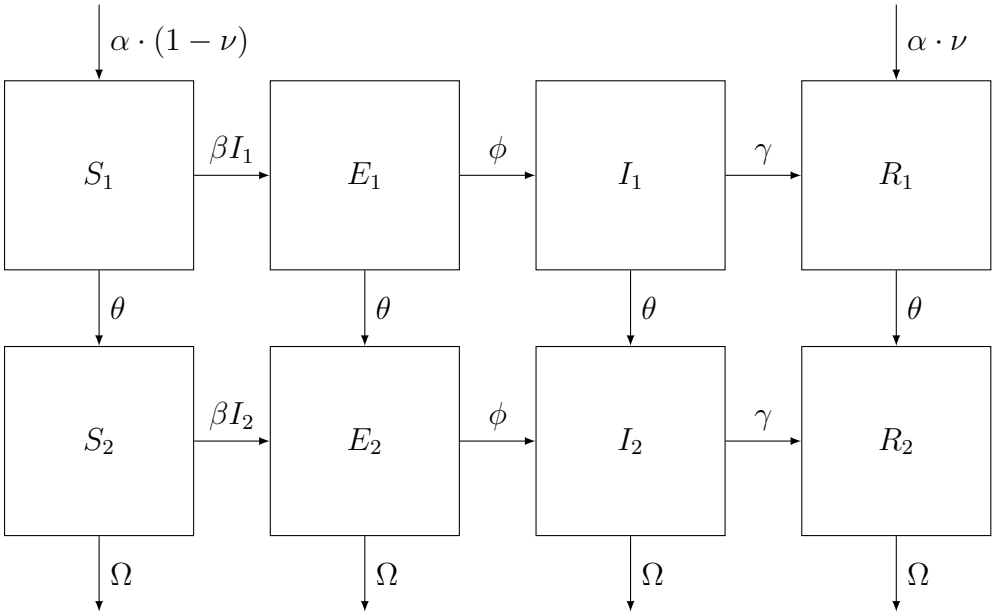

Figure 1: Age stratified SEIR Model with vital dyanmics

Where:
β_n = Rate of contact between infectious and susceptible persons
ϕ = Rate of onset of infectiousness subsequent to being infected
γ = Rate of recovery from measles from infectious period
α = Crude birth rate
ν = Effective vaccination rate at birth
Ω = Crude death rate
θ = Rate of aging from young to old compartments

To explore the infection dynamics of measles, a SEIR model was selected with two age compartments for younger and older populations. This was chosen for a few reasons. Firstly, it allows for the modelling of heterogeneous mixing within these age groups. Additionally, it allows for the model to more closely align with the seroprevalence data given, thereby reducing the number of assumptions which would need to be made to fit incoming data. Finally, the selection of two compartments over some higher dimension limits the mathematical complexity of both modeling the data as well as mapping the parameter space while also allowing for some variation in age demographics.

2.2 Model Dynamics as Deterministic ODEs

The dynamics which describe the compartmental model can be written deterministically as ordinary differential equations :

$$\frac{\mathrm{d}S_1}{\mathrm{d}t} = N\alpha\,(1-\nu) - S_1\,(\beta I_1 + \theta) \tag{1}$$

As detailed in equation 1, this is a test of model 1.

2.3 Calculating R0

We can calculate R0 by taking the leading eigenvalue of the Next Generation Matrix

2.4 Defining Model Steady-State Conditions

This section may not need to exist

2.5 The Model as a Stochastic System

Model stochasticity was accomplished through the R package, adaptivetau[2]. The deterministic differential equations are supplied as a rate function and evaluated by adaptivetau. Transistions are supplied as a vector and their rates defined by a rate function. The model is then stepped using a process called "explicit tau-leaping"[5]. This process provides an approximation of the output expected from Gillespie algorithm by maximizing the time step (called τ) between data points while minimizing the rate of change of the transition. The resulting output supplies many data points where the rate of change in a transition is high and sparse data points where the rate of change is low. This serves a dual purpose:

- To provide vastly superior performance to the Gillespie algorithm
- To introduce model stochasticity by using a random walk variable to define transition advancement

In making the model stochastic, we can now represent the standard compartmental model as a markov chain process.

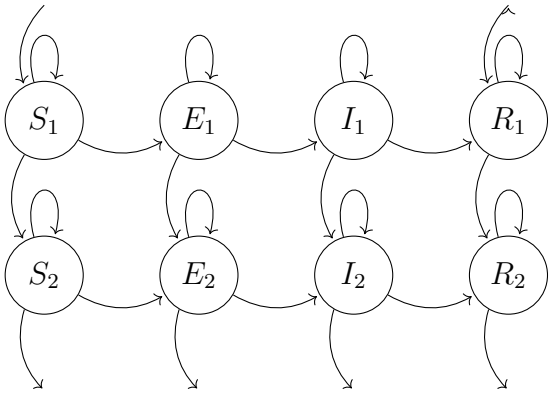

Figure 2: Markov-chain representation of the SEIR Model

This serves to highlight the possible transitions between each state per time step. The "force" of the transitions can stil be described in the same way as the comparmental SEIR Model in Figure 1. However, the probability of any transition per time step is now a function of a poisson-distributed random walk variable defined in the adaptivetau modelling function.

$$P\left(transition\right) \sim Poisson\left(R_{trans} \cdot \tau\right) \tag{2}$$

As a consequence, for sufficiently large transition rates (R_{trans}) or time steps (τ), Equation 2 can be simplified using the normal distribution:

$$P\left(transition\right) \sim N\left(R_{trans} \cdot \tau, \sqrt{R_{trans} \cdot \tau}\right) \tag{3}$$

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