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

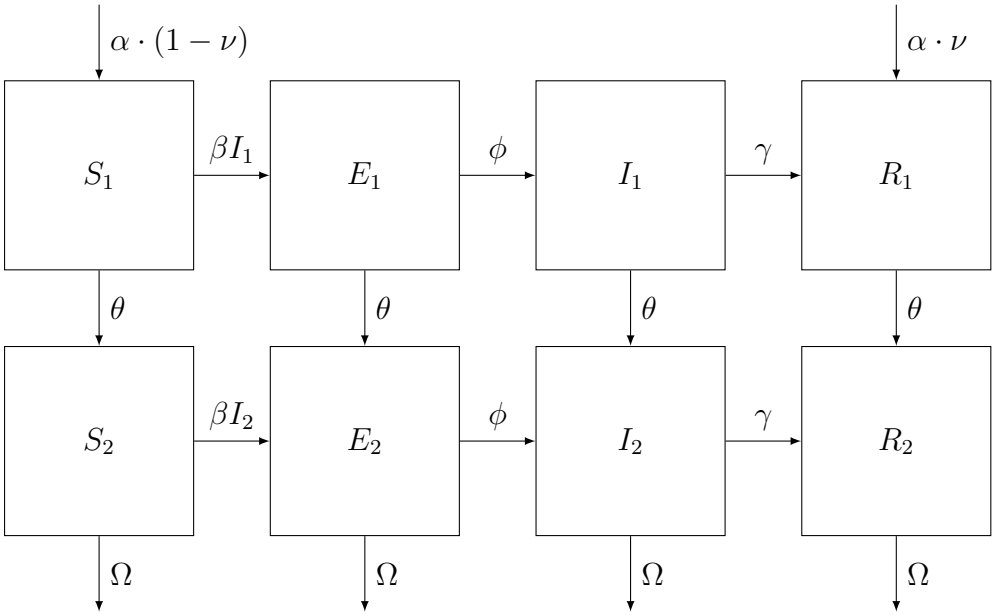

Figure 1: Age stratified SEIR Model with vital dyanmics

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 is accomplished through the R package, adaptivetau[2]. The deterministic differential equations are supplied as a rate function evaluated by adaptivetau. Each transition defined by the rate function (movement between compartments) is 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 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 (in this model, the outbreak curve) and sparse data points where the rate of change is slow. This serves a dual purpose:

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

References

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