

Metapops

Relaxing the homogeneous mixing assumption

A fundamental assumption of the simple compartmental model presented in `?@sec-Compartmental_models` is that any susceptible individual is equally likely to become infected by any of the infectious individuals (at a rate proportional to the size of each compartment in the population). However, real-world populations are not uniform in their interactions (particularly on a scale like that of `?@sec-Melb_SIR`), and the assumption of homogeneous mixing can be relaxed to produce more realistic models that demonstrate heterogeneous mixing patterns.

Multi Patch ‘Metapopulation’ Model

In the simple SIR model of `?@sec-CompartmentalModels`, a single population is divided into a number of compartments, each with their own properties.

We can extend this model to instead consider a set of n populations, each with their own number of residents N_i for that make up the larger population N

$$\sum_{i=1}^n N_i = N$$

Each of these sub-populations, which will hereafter be referred to as ‘patches’, contains compartments which behave analogously to those from `?@sec-CompartmentalModels`, such that

$$S_i + I_i + R_i = N_i$$

While individuals can only transition between compartments of their respective patch (i.e. N_i is constant), patches are coupled such that susceptibles may still contract the disease by coming in to contact with infectious individuals from another patch. The coupling between two patches $i, j \in \{1, \dots, n\}$ is termed the mixing coefficient, denoted m_{ij} , and is defined as the probability

that an individual from patch i will next come into contact by an individual from patch j . As such, $0 \leq m_{ij} \leq 1$ and $\sum_j m_{ij} = 1$.

We can now define the **force of infection** in patch i that is exerted by infectious individuals from patch j , as

$$\lambda_{ij} = \beta \cdot I_j \cdot m_{i,j}$$

The total force of infection experience by patch i

$$\Lambda_i = \sum_{j=1}^n \lambda_{ij}$$

And thus describe an ODE model of patch i as

$$\begin{aligned} S'_i &= -\Lambda_i \cdot \frac{S_i}{N_i} \\ I'_i &= \Lambda_i \cdot \frac{S_i}{N_i} - \gamma I_i \\ R'_i &= \gamma I_i \end{aligned}$$

Similarly to **sec-Stochastic** SIR, we can construct a Continuous Time Markov Chain Metapopulation SIR model with a state space

$$\mathbb{S} = \{(s_1, \dots, s_i, \dots, s_n, i_1, \dots, i_i, \dots, i_n) : 0 \leq s_i, i_i; s_i + i_i < N_j\} \quad (1)$$

and transition rates

$$\begin{aligned} q_{x, x+inf_i} &= \Lambda_i \frac{S_i}{N_i} \\ q_{x, x+rec_i} &= \gamma I_i \end{aligned} \quad (2)$$

for $i, j \in \{1, \dots, n\}$, where

- $x = (s_1, \dots, s_i, \dots, s_n, i_1, \dots, i_i, \dots, i_n)$
- $\mathbf{inf}_i = \mathbf{e}_{2i} - \mathbf{e}_i$, where \mathbf{e}_i is a vector of 0s (length $2n$) with a 1 in the i^{th} position,
- $\mathbf{rec}_i = -\mathbf{e}_{2i}$

Following from [@sec-Stochastic_SIR_sim](#), we can simulate sample paths of this CTMC meta-population model using a stochastic simulation algorithm ([Algorithm 1](#)). The process outlined in [Algorithm 1](#) is similar to that of [Algorithm ??](#) with the main distinction[[^metapop2s-1](#)] being that there are now $2n$ possible events (i.e. an infection and recovery event for each patch). Each element of the state change vector \mathbf{v} now encodes both the location and type of an event

$$\mathbf{v}_i = \begin{cases} \mathbf{e}_{2i} - \mathbf{e}_i & \text{for } i \leq n \\ -\mathbf{e}_{2i}, & \text{for } i > n \end{cases}$$

The propensity vector \mathbf{a} is similarly defined using the rates from Q defined in [Equation 2](#) such that

$$a_i = \begin{cases} \frac{S_i}{N_i} \Lambda_i & \text{for } i \leq n \\ \gamma I_{n-i} & \text{for } i > n \end{cases}$$

Note that the event location and type are determined by the same random number r_1 .

Also note that at the beginning of a simulation, all patches are composed of entirely susceptible individuals. A number, I_0 , of individuals in a randomly selected patch, α , become infected before initial transition rates are computed.

$$S_i(0) = \begin{cases} N_i & \text{if } i \neq \alpha \\ N_i - E_0 & \text{if } i = \alpha \end{cases}$$

$$I_i(0) = \begin{cases} 0 & \text{if } i \neq \alpha \\ I_0 & \text{if } i = \alpha \end{cases}$$

for $i \in \{1, \dots, n\}$ where $\alpha \sim \mathcal{U}\{1, n\}$.

Example: Origin-destination Spatial Metapopulation model

Following [@moss2019](#), we will use as an example a meta-population model of the Greater Melbourne region subdivided into 40 patches according to the [@2023AustralianStatistical-Geography](#) SA3 classification system. The population of each patch along with its numeric SA identifier is given in [@sec-appendix1](#) and shown in [Figure 1](#)

Algorithm 1 Stochastic simulation of SIR Metapopulation CTMC

Input: N, I_0, β, γ, M

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1:  $t \leftarrow 0.0$  ▷ Initialise time
2: for all  $i$  do ▷ Initialise susceptibles
3:    $S_i \leftarrow N_i$ 
4: end for
5: Select  $i \sim \mathcal{U}[1, n]$ ,  $I_i \leftarrow I_0$  ▷ Seed infection
6: while  $I \geq 0$  do
7:   for all  $i \in \{1, \dots, n\}$  do
8:      $a_i \leftarrow \frac{S_i}{N_i} \cdot \sum_{j=1}^n \beta \cdot I_j \cdot M'_{j,i}$  ▷ Update Infection Rates
9:      $a_{n+i} \leftarrow \gamma I_i$  ▷ Update Recovery Rates
10:    update  $a_{net} = a_{net} + a_i + a_{n+i}$ 
11:   end for
12:   generate two random numbers  $r_1, r_2 \sim \mathcal{U}(0, 1)$ 
13:   select  $\mu$  such that  $\sum_{j=1}^{\mu} a_j \leq r_1 a_{net}$ 
14:   compute  $\tau \leftarrow \frac{1}{a_{net}} \ln(\frac{1}{r_2})$ 
15:   update  $X \leftarrow X + v_{\mu}$ 
16:   set  $t \leftarrow t + \tau$ 
17: end while
```

Origin-destination mixing matrix

The mixing matrix was developed after @moss2019 using an empirically informed origin-destination (OD) matrix derived from ‘Place of work’ data taken from the Australian Census @ABS_census2016. Rows (‘origin’) are the ‘usual residence’, and the columns (destination) are the ‘place of work’. The OD matrix

$$F = \begin{pmatrix} f_{1,1} & f_{1,2} & \cdots & f_{1,n} \\ f_{2,1} & f_{2,2} & \cdots & f_{2,n} \\ \vdots & \vdots & \ddots & \vdots \\ f_{n,1} & f_{n,2} & \cdots & f_{n,n} \end{pmatrix}$$

f_{ij} is the proportion of people who usually reside in patch i listing patch j as their place of work. This empirical method is expected to describe contact patterns *between regions*, but contact patterns *within* the region of residence are expected to result more from contact outside of a work context. Therefore, diagonal elements are set to zero.

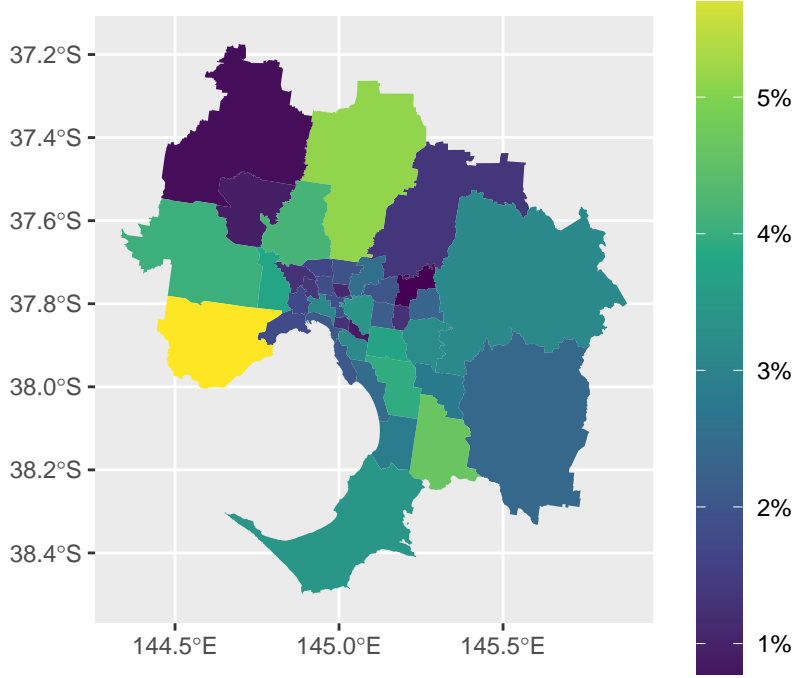


Figure 1: ?(caption)

$$f_{i,i} = 0$$

$$\sum_{j=1}^r f_{i,j} = 1 \quad \forall i \in [1..r]$$

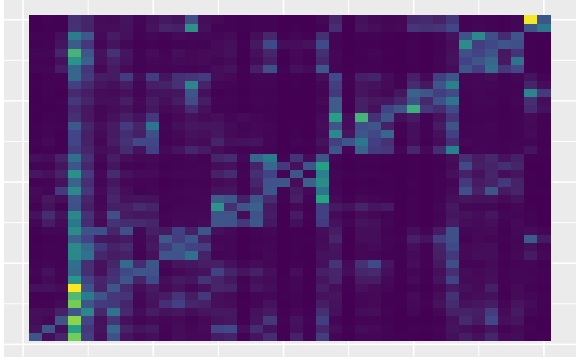
The final mixing matrix is defined using the ‘local’ mixing is given by a parameter δ^H . Diagonal elements are set to δ^H with the remaining proportion, $\delta^* = 1 - \delta_i^H$ distributed among the non-local patches equally.

$$M = \begin{pmatrix} \delta_1^H & \delta_1^* f_{1,2} & \cdots & \delta_1^* f_{1,r} \\ \delta_2^* f_{2,1} & \delta_2^H & \cdots & \delta_2^* f_{2,r} \\ \vdots & \vdots & \ddots & \vdots \\ \delta_r^* f_{r,1} & \delta_r^* f_{r,2} & \cdots & \delta_r^H \end{pmatrix}$$

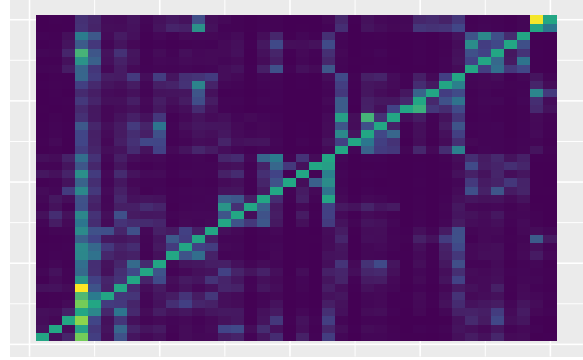
OD matrices for several values of δ^H are presented as heatmaps in ?@fig-OD_matrices

Simulation results

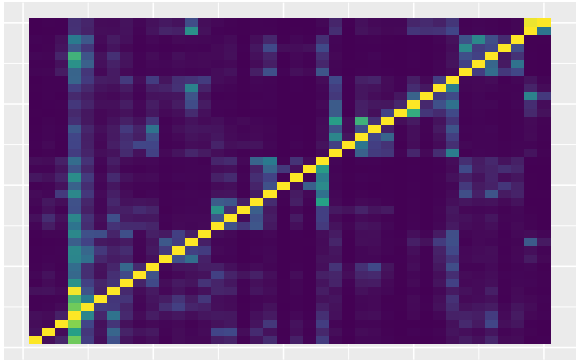
We can observe the metapopulation infection curves for our OD model for a range of R_0 and δ^H values in Figure 3, and the key infecton statistics in Figure 4



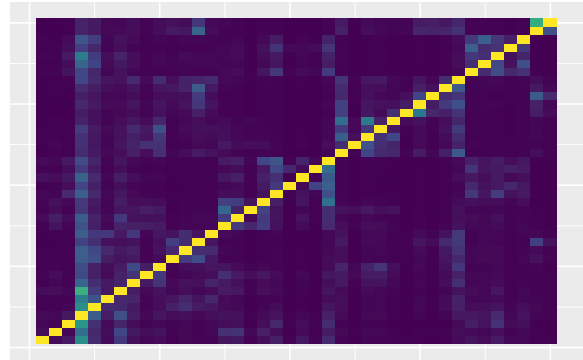
(a)



(b)



(c)



(d)

Figure 2: showing OD mixing matrices with values of $\delta^H =$ (a) 0.1, (b) 0.2, (c) 0.3, (d) 0.4

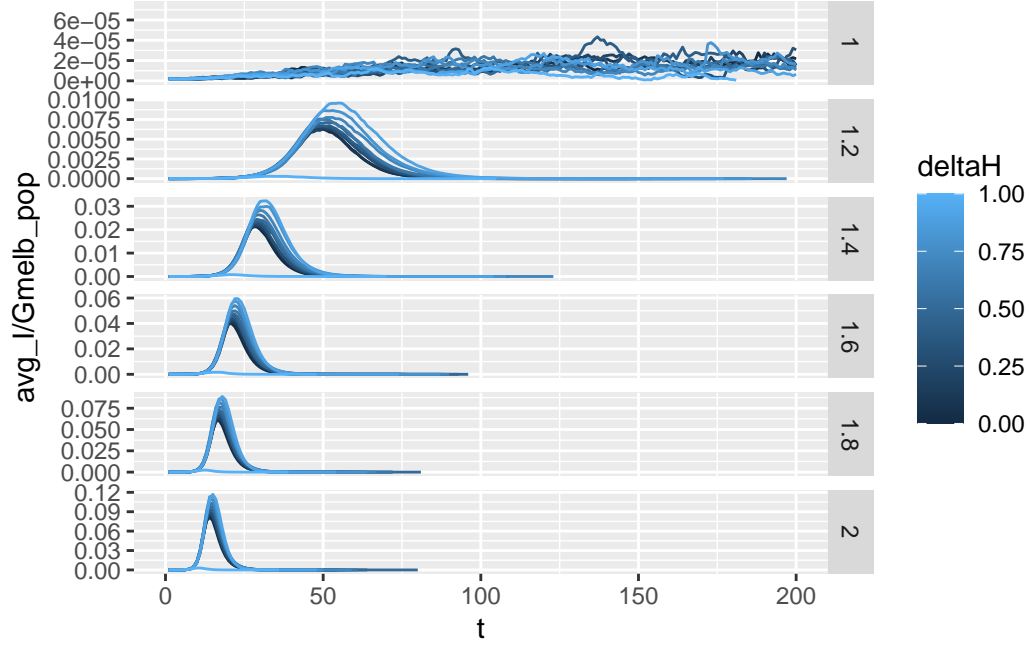


Figure 3: Average proportion of the population over time for simulations of a OD mixing metapopulation model of the melbourne metropolitan area with a range of Basic reproduction numbers (R_0), and local mixing coefficients(δ^H). Note the different y scale in each facet.

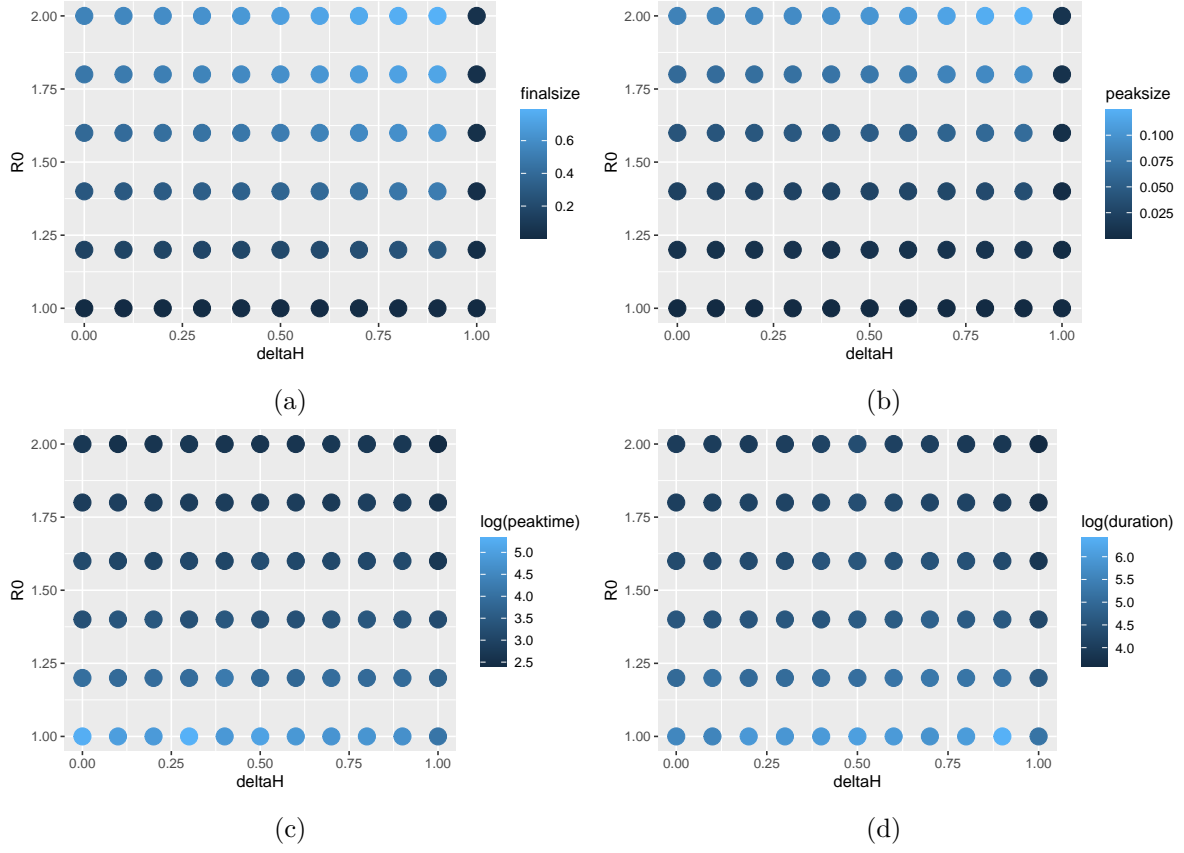


Figure 4: Final (a) and peak (b) infection numbers (as a proportion of the entire population), peak time (c) and total duration (d) of a simulated SIR metapopulation model with OD mixing matrix at different values of δ^H and R_0

However, now we can decompose these metapopulation scale outcomes into those of the underlying subpopulation. For example, [?@fig-OD_patchinf_curve_eg](#)

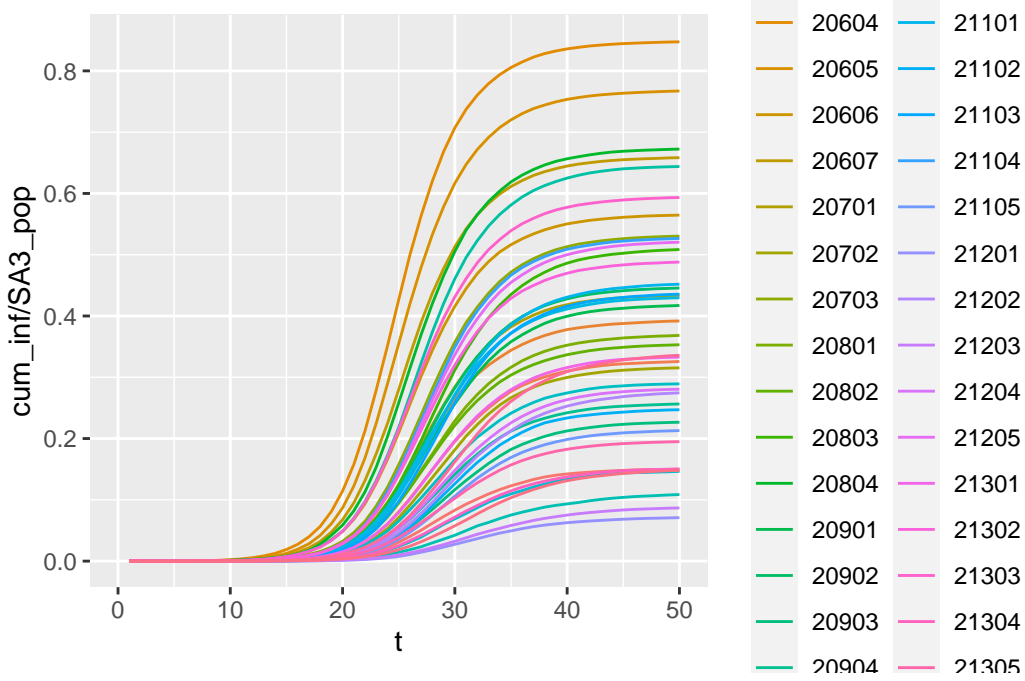


Figure 5: Cumulative infections (as a proportion of patch population) for each SA3 scale patch in the first 50 days of single simulation of an OD mixing metapopulation SIR model of the greater Melbourne region. $R_0 = 1.4$, $\delta^H = 0.5$.

And we can summarise over multiple simulations to get a better understanding of the differential influence of the local mixing parameter δ^H in each SA3 population. For example, Figure 6 shows the consistent trend toward higher peak infections with greater proportions of local mixing (higher δ^H). However, certain patches demonstrate the opposite effect - the Melbourne City patch for example has the highest peak proportion infection (of any patch) when local mixing is low. This can be explained by the relatively large number of residents from all patches working in the city (this is evident in the OD mixing matrices of Figure 2, where the city POW is identifiable as a bright column). High inter-patch mixing means that the city center has a constant supply of infectious contacts.

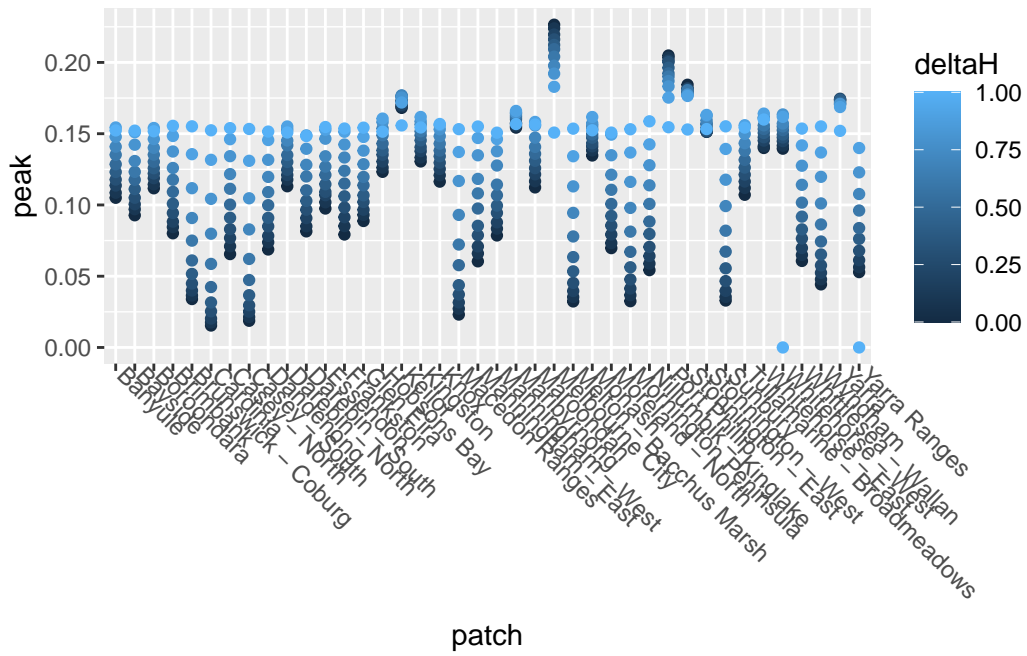


Figure 6: showing the peak proportion of infected individuals in each SA3 patch of an OD mixing metapopulation with varying contributions of local mixing(\hat{H})