

# Hierarchical metapopulation models

In [?@sec-MossGmelb](#), we observed the construction of a meta-population mixing matrix from empirical origin-destination (OD) data. The patches used in the example were based on the SA3 regions of the Australian Statistical Geography Standard’s Statistical Areas (SA) classification [[@2023AustralianStatisticalGeographya](#)] (comprising 40 patches for the Greater Melbourne region in that example). In this chapter we will use the larger ASGS SA classification structure to create multiple meta population models of the same geographical region at different spatial resolutions.

## Hierarchical Structure of the SA classification

An important feature of the SA classification structure is that there are multiples scales of classification organised such that lower level SAs are nested within higher level SAs. These levels are denoted by the numbers 1-5, with special groupings for capital city areas (Figure 1, blue). For example, several SA3 regions can reside within a single SA4 region, and multiple SA4 regions are contained within the Greater Melbourne Capital City SA (GMCCSA). Moreover, each SA3 region is partitioned into a number of SA2 scale regions, which in turn are partitioned further into a number of SA1 scale regions. Figure 2 shows the borders of the 361 SA2, 40 SA3, and 9 SA4 regions of the GMCCSA.

For a specific example, the Maribyrnong SA3 region sits inside the West Melbourne SA4 region alongside Essendon SA3 [?@fig-FootscraySAexample](#). Both West Melbourne and the neighbouring Inner Melbourne SA4 (containing the city center and other SA3 regions), are part of the GSCCSA. Moreover, within Marybirnong SA3 there are six SA2 level regions (Braybrook, Footscray, Maribyrnong, Seddon - Kingsville, West Footscray - Tottenham, Yarraville), which can likewise be partitioned in to smaller SA1 level and ‘Mesh Block’ level regions Figure 1. In [?@fig-FootscraySAexample](#), we highlight the SA1-SA4 level regions containing the main Footscray CBD (SA1 code ‘21303134811’; see Figure 3).

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Note that each red-bounded area represents a higher resolution (‘lower’ SA level) than the one that encloses it.

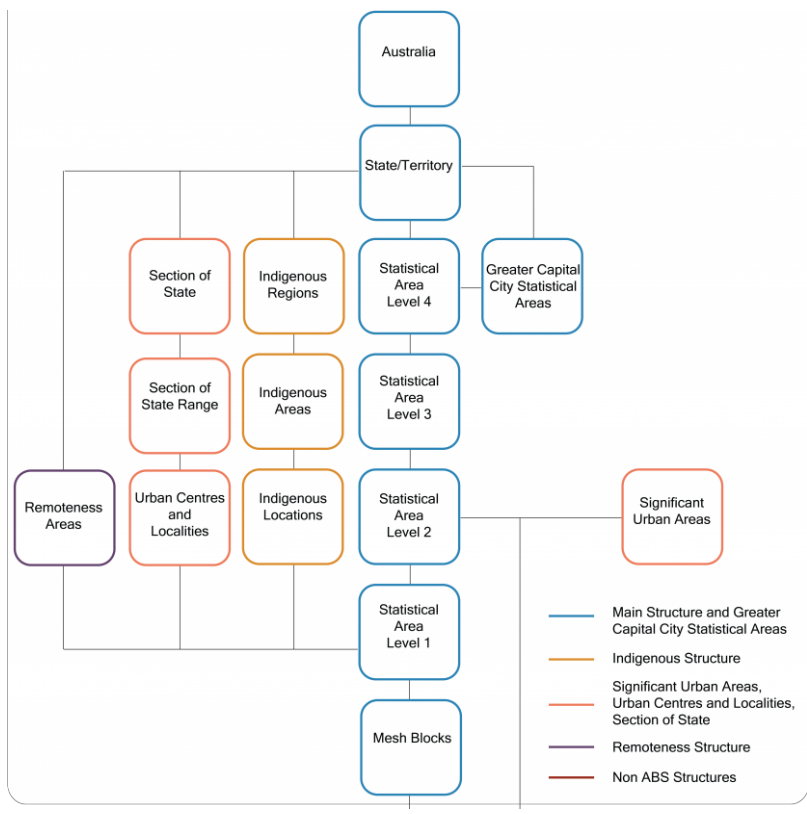


Figure 1: Structure of The Australian Statistical Geography Standard (ASGS) Statistical Areas (SA) Classification

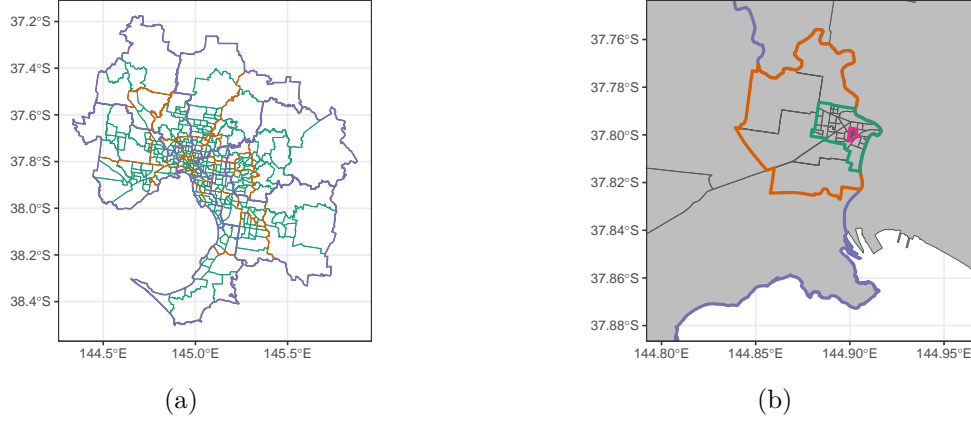


Figure 2: SA2, SA3 and SA4 borders of the Greater Melbourne Greater Capital City Statistical Area (GMGCCSA) and the the five SA3 blocks that make up the ‘Melbourne - West’ SA4 region, the six SA2 blocks that make up the Maribyrnong SA3 region, the forty SA1 regionsa that make up the ‘Footscray’ SA2 region, and the sixteen mesh blocks that make up the central Footscray ‘21303134811’ SA1 region.

Helpfully, besides a common name label, Statistical Areas are also indexed by a structured code representing their classification hierarchy. For example, SA1 regions are denoted by an 11 digit code which can be decomposed into the higher level area codes in which the region sits. Figure 3 demonstrates this for the Footscray SA1 region considered above.

S/T	SA4	SA3	SA2	SA1
2	13	03	1348	11

Figure 3: Decomposition of theFootscray SA1 region code from **21303134811** into its hierachical SA components. 2 - Victoria; 13 - West Melbourne; 03 - Maribyrnong; 1348 - Footscray.

### Comparisons between models of different scales

- Spatial Epidemic models derived from empirical data are limited by the spatial resolution of their source material.
- Comparing models at different scales has been achieved by using different model parameterisations incorporate different sources of empirical spatial information (e.g. @watts2005, @ajelli2010, @zachreson2022). However, creating equivalent models for controlled testing with different underlying model structures can be difficult.

- We can exploit the hierarchical structure of the ASGS Statistical Areas structure to create meta-population models representing the same overarching spatial structure), but with varying levels of resolution (e.g. by using SA2 scale patches instead of SA3 scale patches).
- To do this, we will parametrically define the mixing matrix  $M$ . In doing this, we will explicate two common forms of mixing described in meta-population models.

## Mixing strategies in meta-population models

How can we replicate the homogeneous mixing described for the single patch SIR presented in [?@sec-CompartmentalModels?](#) We might initially consider a construct a mixing matrix with uniform mixing across patches, i.e.

$$m_{ij} = \frac{1}{n}$$

Where  $n$  is the total number of patches. While this mixing matrix would entail homogeneous mixing in a meta-population where  $N_i = N_j, \forall i, j$ , we have seen in [?@fig-SA3Gmelb\\_popn](#), and it is shown in [?@fig-SA2Gmelb\\_popn](#), that population size is not homogeneous in the GMGCCSA metapopulation under consideration. This leads patches with a higher population to have disproportionately greater

## Proportionate mixing

To correct for heterogeneous patch populations, We can scale mixing coefficients by their patch size i.e. for two patches  $i$  and  $j$  the mixing coefficient  $\phi_{i,j}$ :

$$\phi_{ij} = N_j / N_{tot}$$

Which gives mixing matrices shown in [?@fig-GMGCC\\_PMM](#)

-total size -peak size -Duration of pop prop models with SA2 SA3 SA4 homogeneous patches - Expect equivalence

## Statistical Area Mixing structure

We can encode the hierarchical structure of the SA classification in hierarchical block matrices representing within and between SA region mixing. To do so, we specify a set of coefficients  $\xi = [\xi_1, \dots, \xi_i]$  such that  $\sum_i \xi_i = 1$ , which determine the proportion of mixing occurs at each level,  $L$ , of the spatial hierarchy (i.e. between SA2 regions, between SA3 regions, etc.) . This

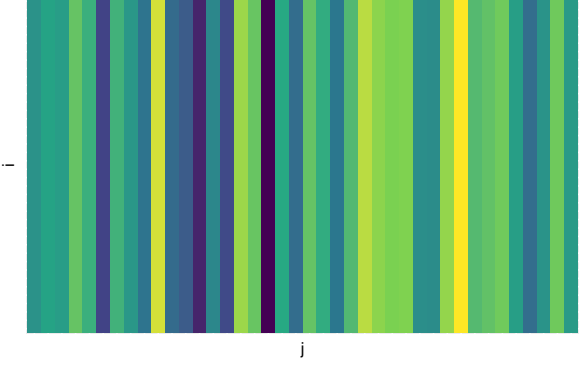


Figure 4: SA3

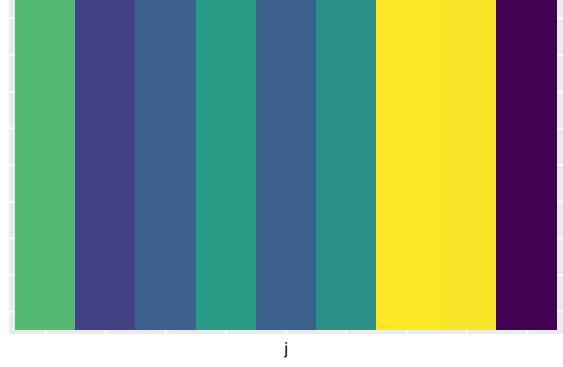


Figure 5: SA4

coefficient is distributed amongst patches occurring in the same level  $L$  region, so mixing for any two patches,  $i$  and  $j$

$$M_{ij} = \frac{\xi_L}{n^L} \quad (1)$$

where

$$j \in S_i^L \text{ \& } j \notin S_i^{L-1}$$

and  $S_i^L$  is the set of patches in the same level  $L$  region as  $i$ .

To extend the example from **?@sec-XX**, we can consider a subset of SA2 regions from the GMGCCSA (**?@fig-GMelb\_eg\_Map**, @tab-MMeg)

Docklands and West industrial are SA2 regions within the ‘Melbourne City’ SA3 region. Port Melbourne and Port Industrial are SA2 regions within the ‘Port Melbourne’ SA3 region. Footscray, Seddon-Kingsville, and Yarraville are SA2 regions within the ‘Maribyrnong’ SA3 region. Newport SA2 is within the Hobsons Bay SA3 region. Port Melbourne and Port Industrial are SA2 regions within the ‘Port Melbourne’ SA3 region. Furthermore, both ‘Melbourne city’ and ‘Port Melbourne’ are within the ‘Inner Melbourne’ SA4 region, while Maribyrnong and Hobsons Bay SA3 lie inside the ‘West Melbourne’ SA4 Region.

To model mixing between these SA2 patches (isolated from the rest of the GMGCCSA), we can construct a  $8 \times 8$  mixing matrix with  $\xi = [\frac{1}{4}, \frac{1}{4}, \frac{1}{4}, \frac{1}{4}]$  as follows:

let  $i = \text{Footscray}$ . Since Footscray is it’s own SA2 region,

$$M_{i,i} = \frac{1}{4}$$

When  $j$  is a region in Maribyrnong SA3 (alongside Footscray), like Yarraville or Seddon-Kingsville,  $M_{i,j}$  will be a proportion of  $\xi_{SA3}$ .

$$M_{i,j} = \frac{\xi_{SA3}}{P_i^{SA3} - P_i^{SA2}} = \frac{\frac{1}{4}}{3 - 1} = \frac{1}{8}$$

When  $j$  occurs outside the Maribyrnong SA3, but within the West Melbourne SA4, like Newport SA2

$$M_{i,j} = \frac{\xi_{SA4}}{P_i^{SA4} - P_i^{SA3}} = \frac{\frac{1}{4}}{4 - 3} = \frac{1}{4}$$

Finally when  $j$  is a patch outside the West Melbourne SA4, like those in the Inner Melbourne SA4

$$M_{i,j} = \frac{\xi_{SA5}}{P_i^{SA5} - P_i^{SA4}} = \frac{\frac{1}{4}}{8 - 4} = \frac{1}{16}$$

thus for the row  $M_i$ , representing the mixing of individuals from Footscray,  $\sum_j M_j = \frac{1}{4} + \frac{1}{8} + \frac{1}{8} + \frac{1}{4} + \frac{1}{16} + \frac{1}{16} + \frac{1}{16} + \frac{1}{16} = 1$ . Repeating this for all patches  $i$ , gives the mixing matrix represented in **fig-GMelb\_eg\_MixMat**

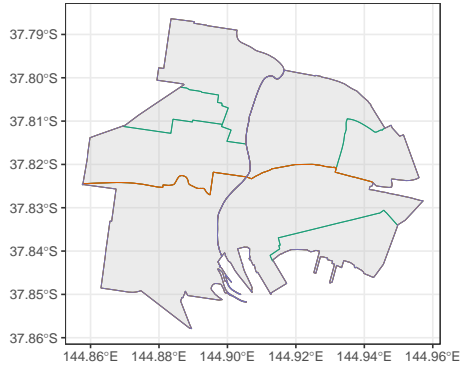


Figure 6: **?(caption)**

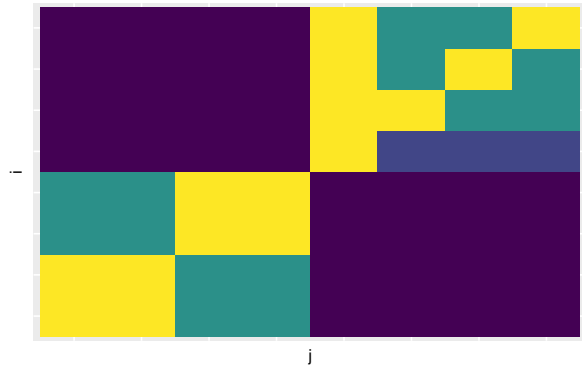


Figure 7: **?(caption)**

Applying this process to the whole GMGCCSA yields the mixing matrices presented in figure **fig-GCC\_HMM**

Hierarchical Mixing matrices for the Greater Melbourne Capital City Statistical Area (GMGCCSA) at three levels of spatial resolution.

### Population normalised SA mixmat

- in the same way as in **sec-proportionatemixing**, the SA structured mixingmatrix given in Section , Equation 1, will result in hetrogenous mixing due to the different population per patch **fig-gmelbpop**.
- Again, we can rectify this by scaling columns in the mixing matrix by the according population size. Due to the hierarchical structure we can reduce patch counts to population counts

$$M_{ij} = \frac{N_j}{N_i^L - N_i^{L-1}} \xi^L$$

if  $j \in S_i^L$  &  $j \notin S_i^{L-1}$

where  $i, j$  are patches  $S_i^L$  is the set of patches in level  $L$   $N_i$  is the population of  $i$   $N_i^L$  is the population of  $S_i^L$   $\xi^L(\delta)$  is the proportion of mixing that occurs within  $S_i^L$  but not  $S_i^{L-1}$

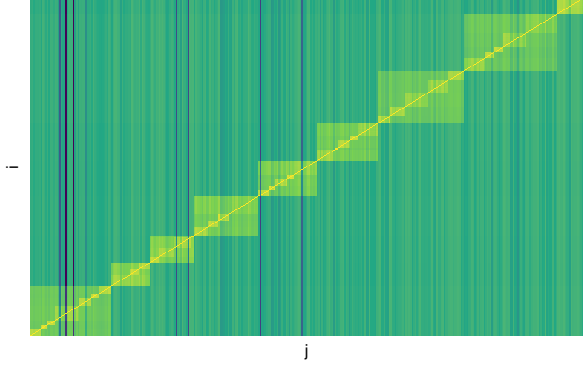


Figure 8: fig-gmelbpop\_SA1

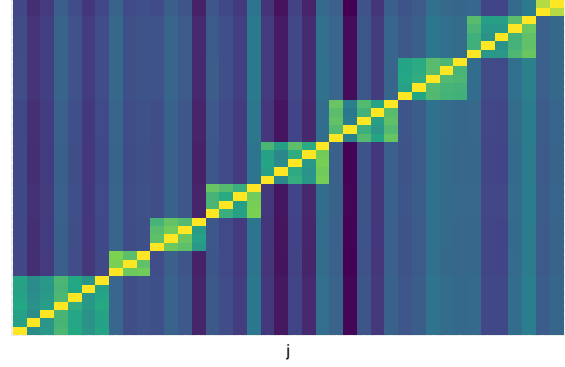


Figure 9: fig-gmelbpop\_SA2

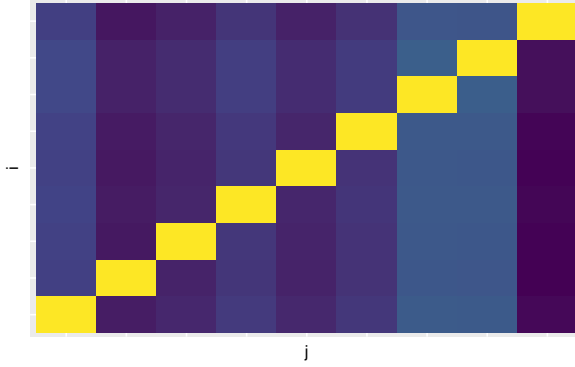
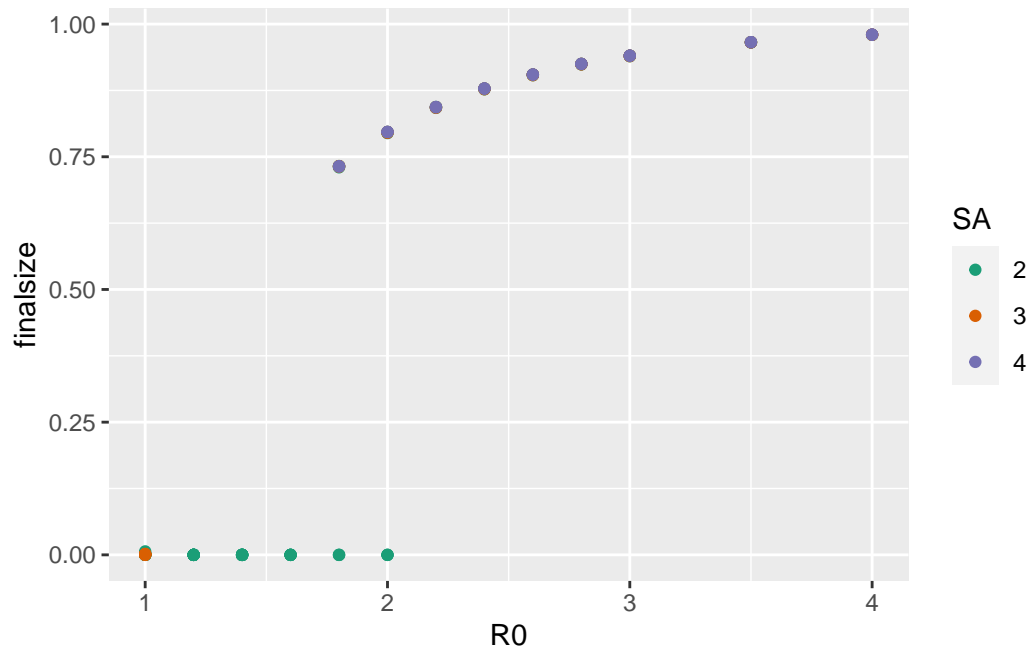


Figure 10: fig-gmelbpop\_SA3

### blending between population and hiereachy

parameter  $\mu$  ### Simulation

We can now simulate the spread of disease through the GMGCCSA using the mixing matrices presented in Section and **?@sec-HPMM**. We will use the same parameters as in **?@sec-sim**, but now with mixing determined by the population normalised mixing matrices defined above.



However, now we can decompose these metapopulation scale outcomes into those of the underlying subpopulation. For example, [fig-OD\\_patchinf\\_curve\\_eg](#)

**Note that we can also apply a similar protocol to OD mixing matrices from [sec-OD\\_](#)**



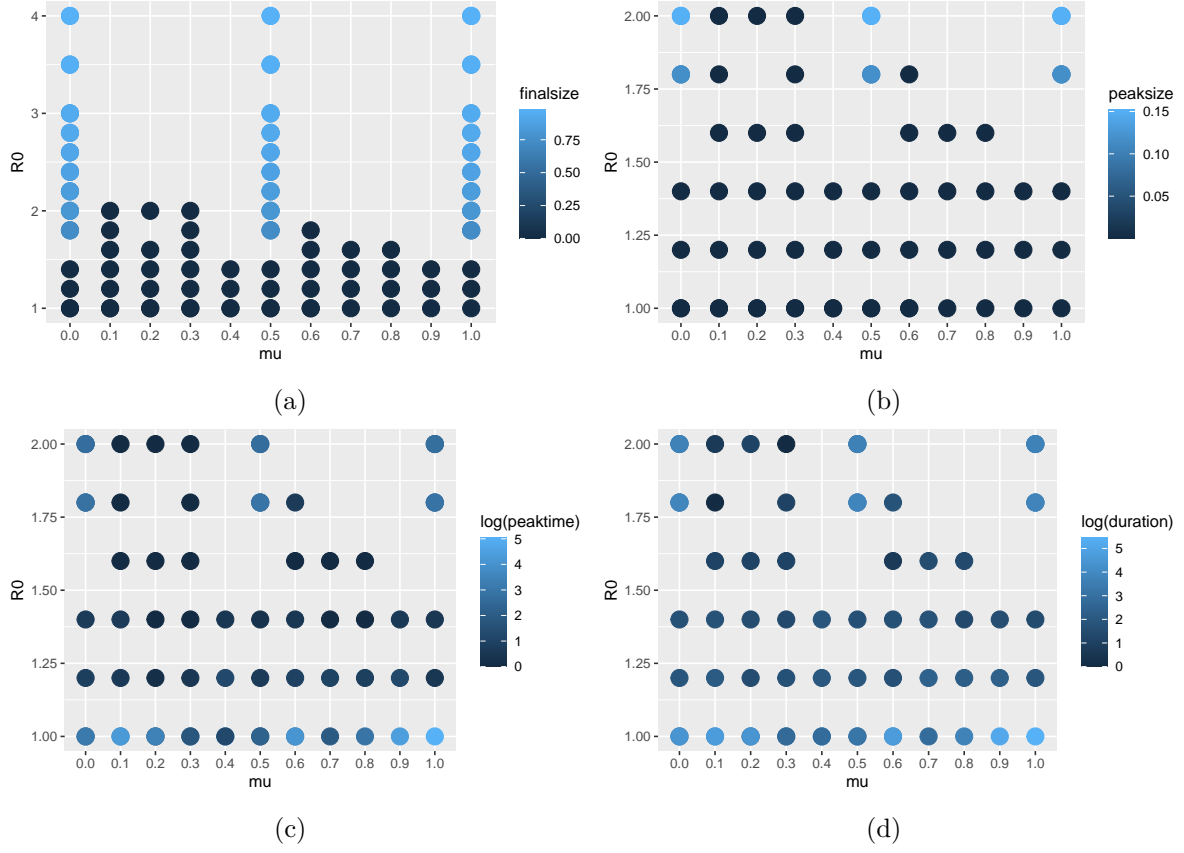


Figure 11: Final (a) and peak (b) infection numbers (as a proportion of the entire population), peak time (c) and total duration (d) of a simulated SIR metapopulation model with OD mixing matrix at different values of  $\delta^H$  and  $R_0$

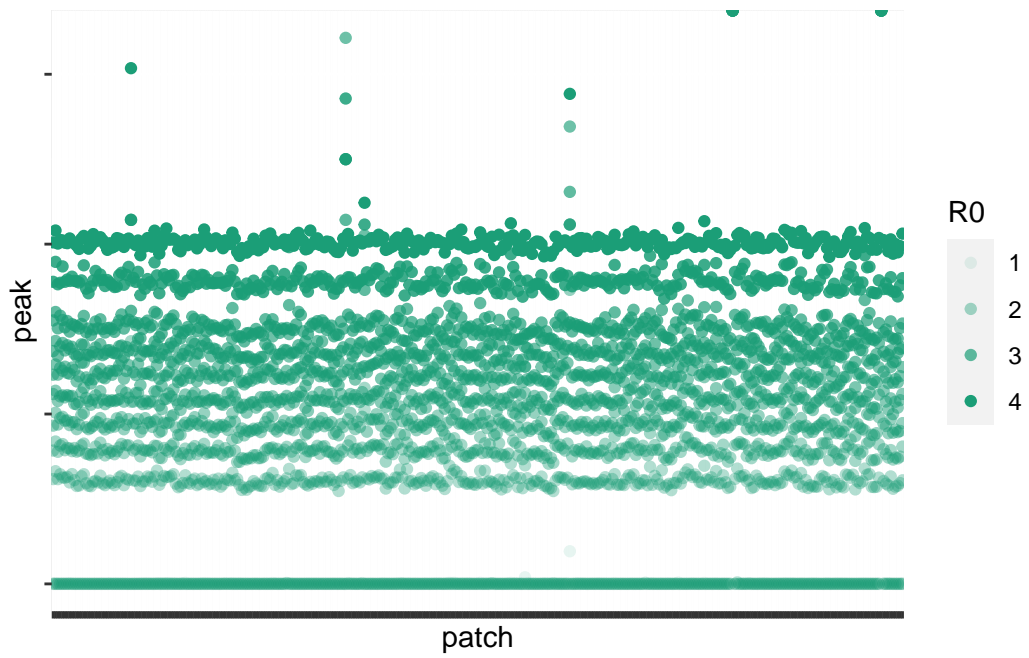


Figure 12: showing the peak proportion of infected individuals in each SA3 patch of an OD mixing metapopulation with varying contributions of local mixing( $\hat{H}$ )

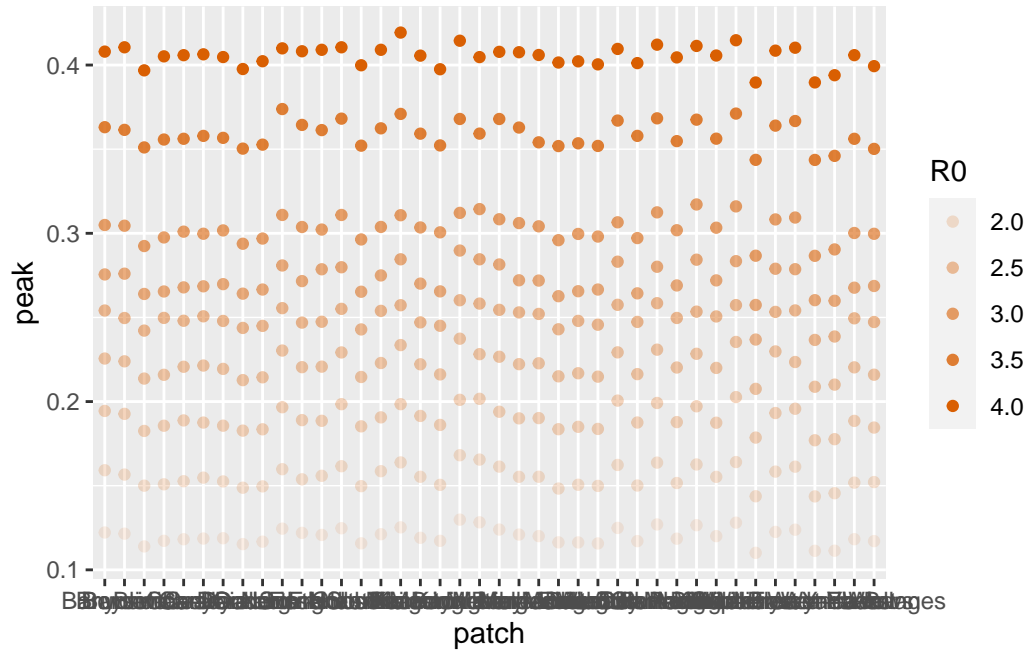


Figure 13: showing the peak proportion of infected individuals in each SA3 patch of an OD mixing metapopulation with varying contributions of local mixing( $\hat{H}$ )

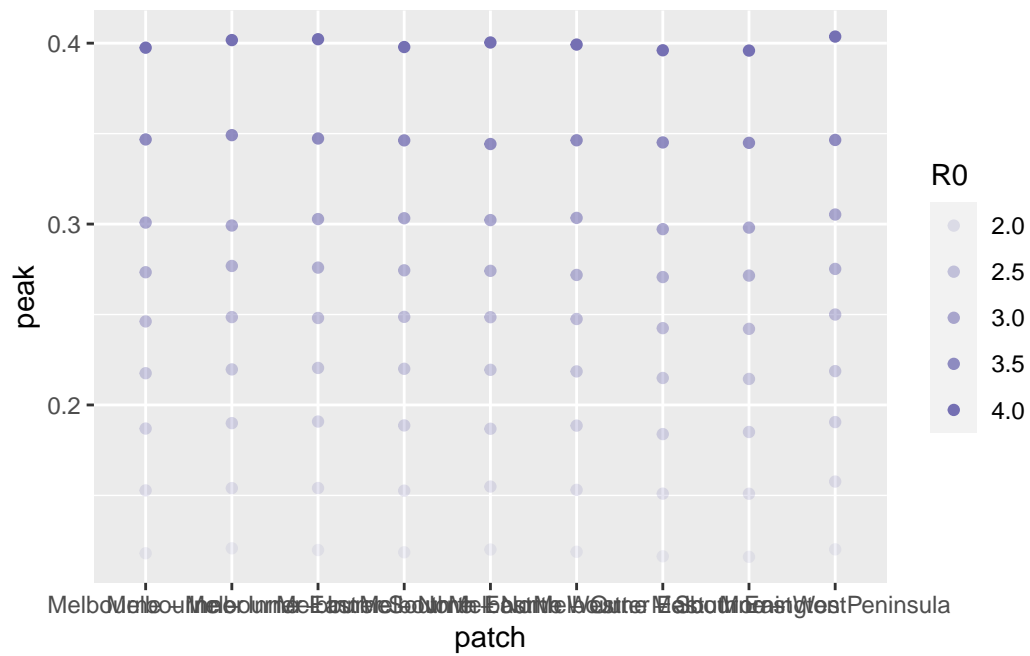


Figure 14: showing the peak proportion of infected individuals in each SA3 patch of an OD mixing metapopulation with varying contributions of local mixing( $\hat{H}$ )