## AARMS 2023 Summer School 20–30 August 2023

## Metapopulations & introductions models problem set

## [10] 1. Consider the Kermack-McKendrick SIR epidemic model

$$\begin{array}{c|c}
S & \beta SI \\
\hline
& I \\
\end{array}$$

and the *endemic* SIR model with demography

$$\begin{array}{c|c}
 & b \\
\hline
 & S \\
\hline
 & dS \\
\hline
 & dI \\
\hline
 & dR \\
\hline
\end{array}$$

(a) Write simple,  $|\mathcal{P}|$ -metapopulation models based on each model, using explicit movement as well as implicit coupling. The latter means that coupling is *not* through the movement of individuals between locations, but through the incidence function, i.e., mass action incidence in patch p takes the form

$$S_p\left(\sum_{q\in\mathcal{P}}\beta_{qp}I_q\right),\,$$

with  $\beta_{qp}$  the contact parameter ("influence") of infectious individuals in patch q on susceptible individuals in patch p.

- (b) From now on, consider only the two models with explicit movement. Compute the DFE (beware in the case of the epidemic model) and  $\mathcal{R}_0$ .
- (c) In the endemic case, it is easy to compute the endemic equilibrium in the single population case, by writing the equation for the dynamics of I(t) as

$$I' = (\beta S - (\gamma + d)) I.$$

Does this work in the metapopulation case? Why/why not?

- (d) Modifying the code I gave in the CODE directory, write code to simulate both systems.
- (e) Write code to simulate both systems as continuous-time Markov chains in a two-patch situation.
- (f) (Bonus) Write code to simulate the models as CTMC in the case of an arbitrary number of patches.
- (g) Investigate introductions in the two-patch context, by using the capacity of ssa in GillespieSSA2 to return events.