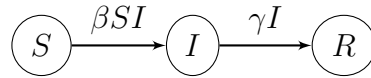
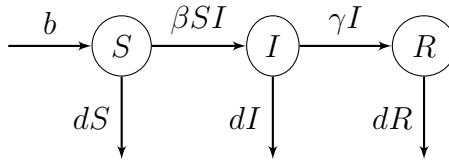

AARMS 2023 Summer School
20–30 August 2023
Metapopulations & introductions models problem set

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



and the *endemic* SIR model with demography



- (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 β_{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.