How migration between settlements affect the effective reproduction number a disease

July 8, 2017

Introduction

The basic reproductive number R_0, is widely used in study of infectious disease (epidemiology). R_0 is defined as the mean number of individuals infected by a single infected individual during his or her infectious period, in a population which is entirely susceptible. From this, definition it is clear that if $R_0 > 1$ the disease will spread in the population in the long run and if $R_0 < 1$ the disease will be cleared from the population in long run. R_0 can also be used to calculate $p_c = 1 - \frac{1}{R_0}$ which represents the critical proportion of the population needed to become immune to stop the transmission of disease thus giving rise to herd immunity in the population. Thus estimation of R_0 of a disease is important, there are several methods to estimate R_0 of a disease some of them are disscussed in this paper. Since it is always not feasible to collect records of infection from each and every part of the world or country to estimate R_0, So one collects data for some major countries or cities and estimate R_0 of the disease. But estimation of R_0 of a single city or a village or a settelement cannot be extend to a country or vice-versa. Since, people migrate and travel at faster rates nowadays and contact structure of different cities or countries are not always the same. Here we try address how the rate of migration between settlements affect the effective R_0 of the system.

Methods

We consider two compartmental models firstly, SIR with transfer rates between the settlements.Secondly, SEIR with transfer rates between settlements with the restriction that infected individuals cannot migrate. It is a fair assumption to make since the disease can impair migration of infected people. We also assume the transfer rates from settlement 1 to 2, is same as 2 to 1.

0.1 SIR model on 2 settlements

The SIR model on two settlements is a modification of the conventional SIR model accounting for the migration between the settlements.

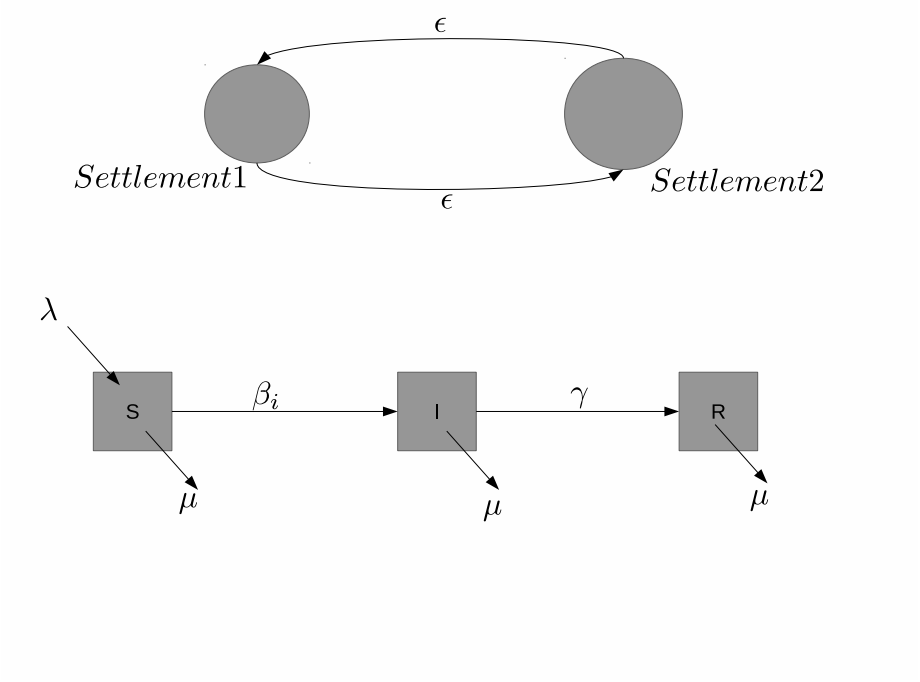


Figure 1: Each of the settlements contain this SIR compartments with ϵ as transfer rates between the settlements

$$
\begin{aligned}
\frac{dS_1}{dt} &= \lambda(S_1 + I_1 + R_1) - \mu S_1 - \beta_1 S_1 I_1 + \epsilon S_2 - \epsilon S_1 \\
\frac{dI_1}{dt} &= -\mu I_1 + \beta_1 S_1 I_1 + \epsilon I_2 - \epsilon I_1 - \gamma I_1 \\
\frac{dR_1}{dt} &= -\mu R_1 + \epsilon R_2 - \epsilon R_1 + \gamma I_1 \\
\frac{dS_2}{dt} &= \lambda(S_2 + I_2 + R_2) - \mu S_2 - \beta_2 S_2 I_2 + \epsilon S_1 - \epsilon S_2 \\
\frac{dI_2}{dt} &= -\mu I_2 + \beta_2 S_2 I_2 + \epsilon I_1 - \epsilon I_2 - \gamma I_2 \\
\frac{dR_2}{dt} &= -\mu R_2 + \epsilon R_1 - \epsilon R_2 + \gamma I_2
\end{aligned}
\tag{1}
$$

where S_i is susceptible population of settlement i,I_i is infected population of settlement i,R_i is recovered population of settlement i,β_i is transmission rate in settlement i(depends upon the contact structure of settlement i), γ is rate of recovey, μ is the death rate, λ is the birth rate and ϵ the transfer rates between the settlements.

There are several methods to estimate R_0 from Epidemiological data. In this paper, we try to calculate R_0 from intrinsic growth rate r_0. This growth

rate is the rate at which total number of infectives, I grows in a susceptible population, such that $\frac{dI}{dt} = r_0 I$.Since we need epidemiological data to calculate r_0 and subsequently R_0, Gillespie algorithm was used to stochastically simulate the model. r_0, the intrinsic growth rate is estimated in the following way, infection time series obtained from stochastic simulations were averaged over 50 iterations to remove stochastic fluctuations, selecting only simulations that lead to an epidemic outbreak in any of the settlements.

The resulting averaged time series was then used to estimate r_0 by applying regression procedure(at the initial part) to the logarithm of the number of infected cases [log(#infected)] vs., time. To quantify the quality of regression, we calculate R^2 the coefficient of determination on the regression of the time series.R^2 is a statistical measure of how close the data are to the fitted regression line. R^2 ranges from 0 to 1 with 1 indicating exponential fit of the number of infections vs., time.

We set R^2_{cutoff} (here, $R^2_{cutoff} = 0.75$) and select only the slope of the fit whose $R^2 > R^2_{cutoff}$ as an estimate of r_0 and average them over 100 iterations to calculate the standard deviation and mean of the estimated r_0, which will give us an estimate on the range of variation of the estimated r_0.

R_0 is estimated from r_0 by using the relation between R_0 and r_0 with the assumption that the generation interval distribution of the infected is exponential.

Generation interval distribution is the probability distribution of time from infection of an individual to infection of a secondary case by that individual. The realtion between R_0 and r_0 is established in *(J. Wallinga and M. Lipsitch, 2006)*

$$R_0 = \frac{1}{M(-r_0)} \tag{2}$$

where $M(z)$ is the moment generating function of the generation interval distribution. Here, assuming exponential distribution with mean $\frac{1}{\gamma}$ we find that(for the derivation see supplimentary material)

$$R_0 = 1 + \frac{r_0}{\gamma}$$

Using this relation we estimate the effective R_0 at various transfer rates(see fig).

0.2 SEIR model on 2 settlements

In this SEIR model infected individuals are restricted to migrate, which is a fair assumption to make since diseases can render an infected individual incapable of migration.

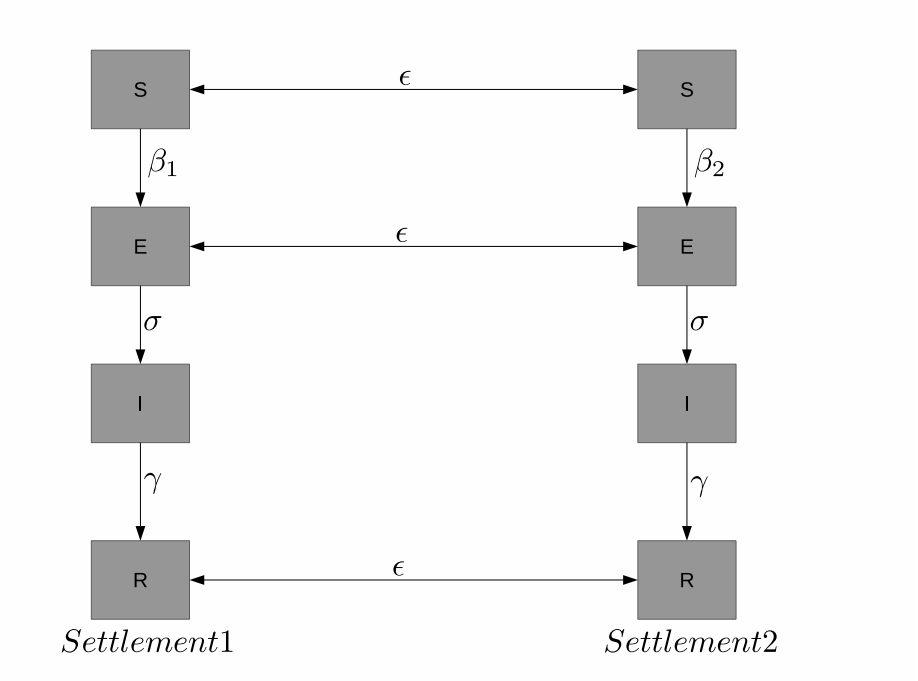


Figure 2: SEIR model

Equations

$$
\begin{aligned}
\frac{dS_1}{dt} &= \lambda(S_1 + E_1 + I_1 + R_1) - \mu S_1 - \beta_1 S_1 I_1 + \epsilon S_2 - \epsilon S_1 \\
\frac{dE_1}{dt} &= -\mu E_1 + \beta_1 S_1 I_1 + \epsilon E_2 - \epsilon E_1 - \sigma E_1 \\
\frac{dI_1}{dt} &= \sigma E_1 - \gamma I_1 - \mu I_1 \\
\frac{dR_1}{dt} &= -\mu R_1 + \epsilon R_2 - \epsilon R_1 + \gamma I_1 \\
\frac{dS_2}{dt} &= \lambda(S_2 + E_2 + I_2 + R_2) - \mu S_2 - \beta_2 S_2 I_2 + \epsilon S_1 - \epsilon S_2 \\
\frac{dE_2}{dt} &= -\mu E_2 + \beta_2 S_2 I_2 + \epsilon E_1 - \epsilon E_2 - \sigma E_2 \\
\frac{dI_2}{dt} &= \sigma E_2 - \gamma I_2 - \mu I_2 \\
\frac{dR_2}{dt} &= -\mu R_2 + \epsilon R_1 - \epsilon R_2 + \gamma I_2
\end{aligned}
\tag{3}
$$

where σ denotes the rate of becoming infected after being exposed and all other variables denote same as in SIR.

Same method of calculating R_0 from intrinsic growth rate r_0 as in SIR model was applied. Here we assume generation interval distribution as convolution of two exponential distributions with mean $\frac{1}{\sigma}$ and $\frac{1}{\gamma}$. From eq() we find the relation between r_0 and R_0 to be

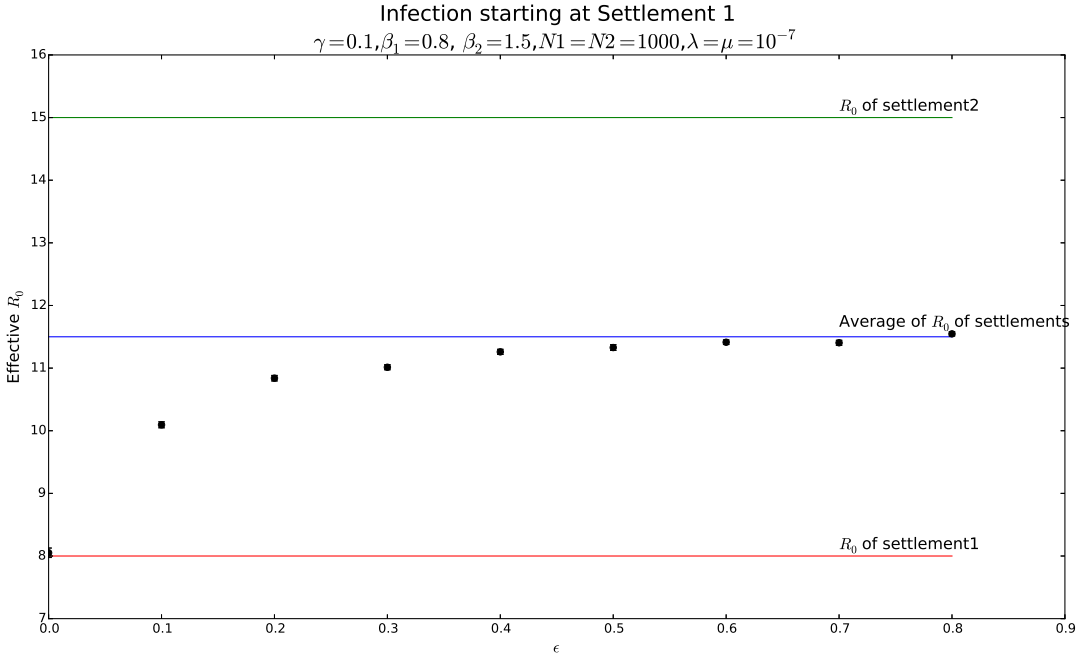
$$R_0 = (1 + \frac{r_0}{\sigma})(1 + \frac{r_0}{\gamma}) \tag{4}$$

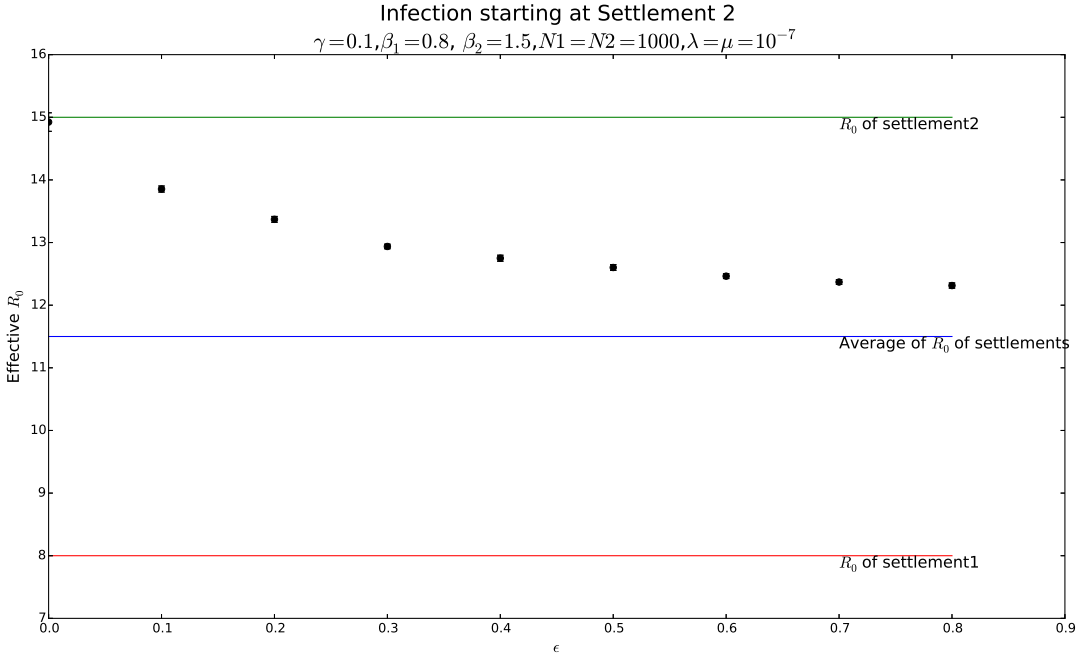
Using the above relation we estimate effective R_0 of the settlements at various transfer rates, see fig()

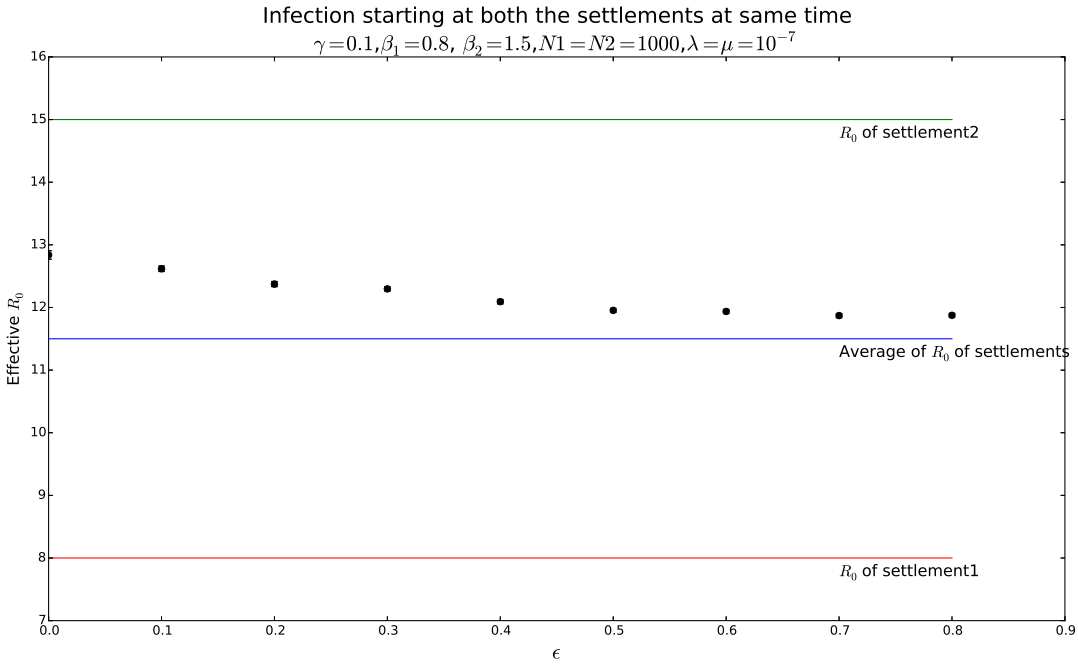
Results

0.3 SIR Model

Individual R_0 of the settlements were calculated using theoritical formula $\frac{\beta_i N_i}{\gamma}$. We observe that as transfer rates between the settlement increase the effective R_0 of the system tends toward the mean of the individual R_0 of the settlements, in all three cases irrespective of where the infection arises the effective R_0 tends towards the mean.

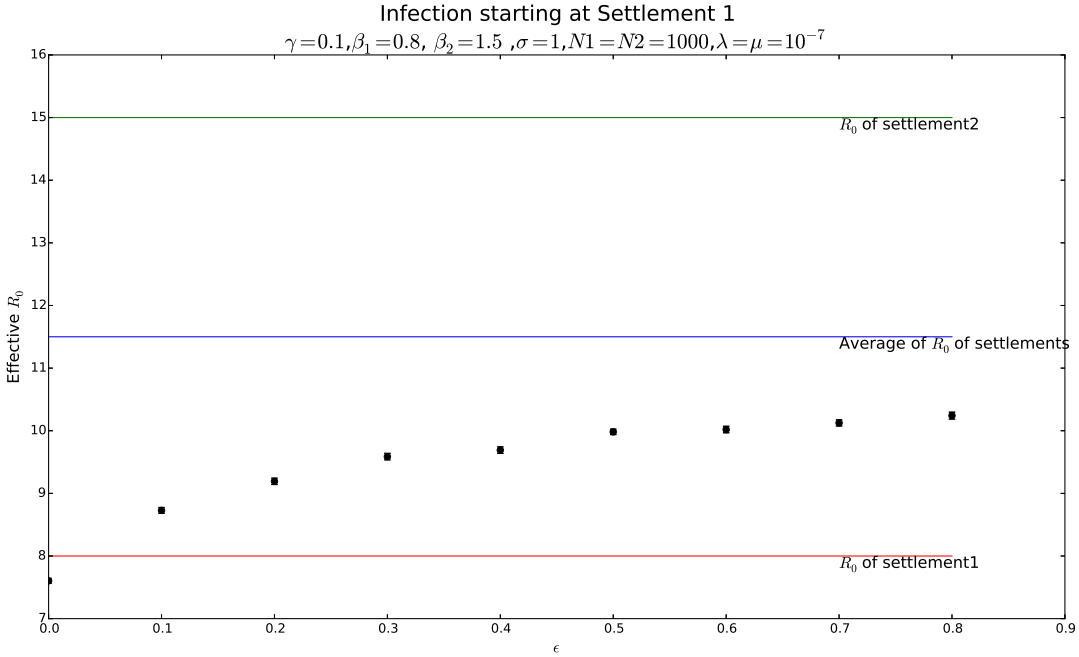

Infection starting at Settlement 1
$\gamma=0.1, \beta_1=0.8,\ \beta_2=1.5, N1=N2=1000, \lambda=\mu=10^{-7}$
R_0 of settlement2
Average of R_0 of settlements
R_0 of settlement1
Effective R_0
ϵ

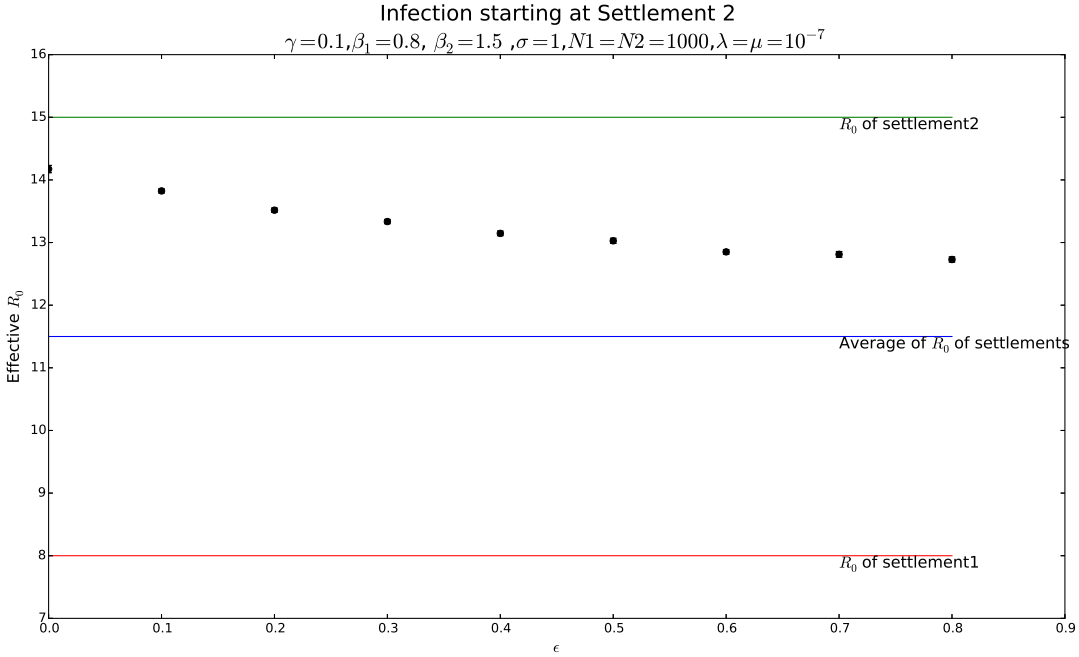

Infection starting at Settlement 2
$\gamma=0.1, \beta_1=0.8,\ \beta_2=1.5, N1=N2=1000, \lambda=\mu=10^{-7}$
R_0 of settlement2
Average of R_0 of settlements
R_0 of settlement1
Effective R_0
ϵ

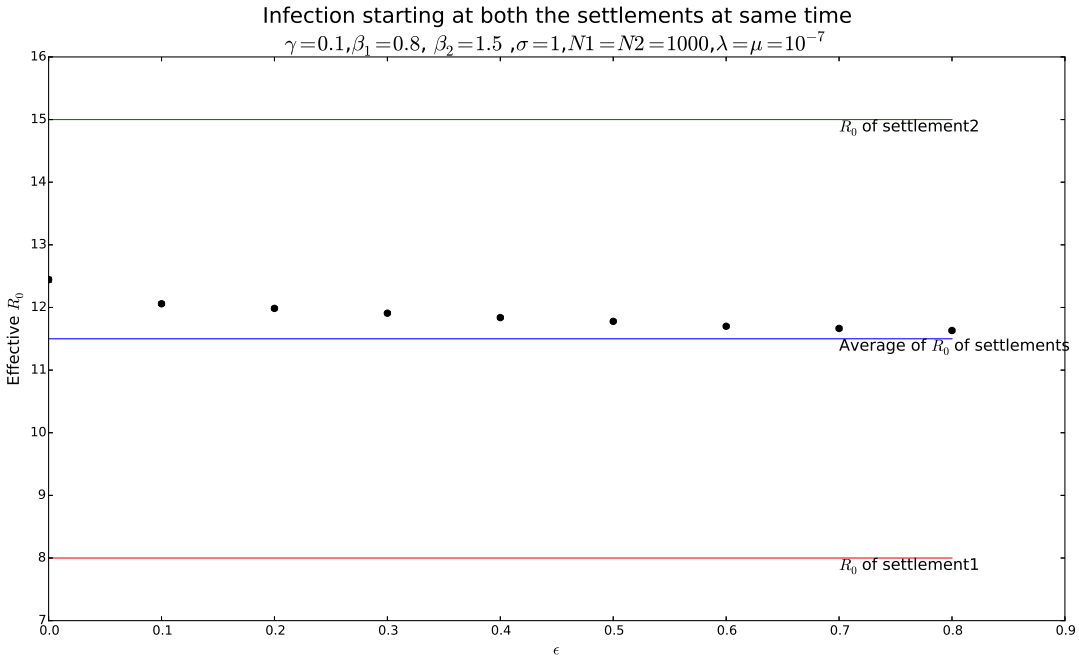


0.4 SEIR model

Individual R_0 of the settlements were calculated using theoritical formula $\frac{\beta_i N_i \sigma}{(\gamma+\mu)(\mu+\sigma)}$. We observe similar pattern as in SIR model, effective R_0 of the system converges to the mean of the individual R_0 of the settlements.


Infection starting at Settlement 1
$\gamma=0.1, \beta_1=0.8, \beta_2=1.5, \sigma=1, N1=N2=1000, \lambda=\mu=10^{-7}$
R_0 of settlement2
Average of R_0 of settlements
R_0 of settlement1
Effective R_0
ϵ


Infection starting at Settlement 2
$\gamma=0.1, \beta_1=0.8, \beta_2=1.5, \sigma=1, N1=N2=1000, \lambda=\mu=10^{-7}$
R_0 of settlement2
Average of R_0 of settlements
R_0 of settlement1
Effective R_0
ϵ



Conclusion

One may easily underestimate or overestimate the R_0 of the system, if they don't consider the rate of movement between the settlements. These rate of movements can be approximated by transport networks such as airlines,railway connectivity and other such transport modes. One can easily underestimate the R_0 if the disease first devolops in a settlement which has less contact rate β. Simillary overestimate if the disease devolopes in a settlement which has a higher contanct rate. So one should keep in mind that transport rates between settlements plays an important role in estimation of effective R_0 of a country or a system.