Compartmental models on networks

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Abstract

In this artice we try to figure out the realtion between the total R_0 of a country and the R_0 of the individual cities how it varies with respect to migration between the cities. We model this using SIR and SEIR not graphs with vertices as cities and edges representing the migration. We try to figure out this relationship using numerically and analytically. To proceed numerically we use simulations to create data and calculate R_0 using the relation derived here. Analytically we try to use next generation operator method to figure out the combined R_0

1 Motivation

H_1N_1 commonly called Swine Flu is a human respiratory infection caused by an influenza strain, which nearly costs 284000 lives in 2009 alone globally. In *epidemiology* each disease can be modelled using compartmental models, one such commonly used models are SIR and SEIR models. Each disease can be given a charateristic value R_0 known as basic reproductive number which represents the average number of infections an infected individual can cause over its infectious period in an uninfected population. A paper by Jesan,Menon and Sinha use the incidence data to calaculate the R_0 of swine flu in India assuming the SIR model.

We see that in the table from their paper that the R_0 of India which was calculated to be 1.45 is not the average of the R_0 of the individual cities. So here in this article we try to find out this relation between the R_0 of the cities and the total R_0.

2 Methodology followed

In order to numerically figure out the relationship between total and individual city R_0, We try to model this scenario into simple case with just two vertices having 3 or 4 compartments each and 2 edges represting the migration between the cities. We write down the differential equations for these systems, which are elaborately mentioned in the next section. We then apply Gillespie Algorithm on these equations to stochastically simulate the models. Using this data we try to figure out R_0 via the realtion between intrinsic/exponential growth rate of the infected individuals and R_0. This relation between intrinsic growth rate r and R_0 depends upon the model used, we will derive the relation between them in each case in the following sections. We will then try to see how the total R_0 of the system change from individual R_0 of the cities as the transfer rates between the cities are increased. We will try to apply the above method on SIR and SEIR(with the restriction that the infected individuals are not allowed to migrate). Analyically we will try to use next generation operator method on the system of equation to derive the total R_0 of the system in the last part of this article.

3 Modelling using SIR model

Equations
where λ is the birth rate,μ is the death rate,γ is the recovery rate and β_i is the contact rate in city i.

The above model was stochastically simulated using Gillespe algoritm. Below is the graph of one such simulation. Using this simulation we can obtain the time series of the infected individuals in each city and for the system(by adding the individual time series). We now try to figure out the relation between the intrinsic growth rate r and R_0. At initial conditions when $S_i = N_i$ and $I = 0$,

$$\frac{dI}{dt} = rI$$

integrating,

$$I(t) = ce^{rt}$$

where c is a constant. Hence to calculate r we can fit a straight line to $log(I)$ vs t at inital part and the slope of this line should give r.

3.1 Relation between r and R_0

We start by deriving **Lotka-Euler** equation and then applying epidemology to it.
Assumptions

1. There are only females in the population and can reproduce independent of males.
2. time and age are measured in years. $t = 0$ denotes the present time
3. The population displays exponential growth rate at a fixed growth rate
4. Age distribution of the population does not change with time.

- Total No. of births at time $t = \sum$ all children born to **all ages of mothers** at a particular time t.
- No. of births to mother of age a at time t = (Total number of births at time $t - a$)×(Expected No. of offsprings per year for mother of age a)

Note:(Total number of births at time $t - a$) denotes the total number of mother of age a at time t, ie these many were born.
Combining above two equations we get,

$$b(t) = \int_{a=0}^{\infty} b(t)n(a)da$$

where $b(t)$ denotes the number of birth at time t and $n(a)$ denotes the expected number of offsprings a single mother of age a will produce.
Since population is growing exponentially with a constant exponential rate r,
No. of birth at time t = (No. of births at time $t - a$)×(Exponential growth from time a)

$$b(t) = b(t - a)e^{ra}$$

From above equations we get

$$b(t) = \int_{a=0}^{\infty} b(t)e^{-ra}n(a)da \tag{1}$$

Define R as $R = \int_{a=0}^{\infty} n(a)da$ total number of offsprings a single women will produce in her lifetime.
Define $g(a)$ as $\frac{n(a)}{R}$ this will denote the probability that a female will produce an offspring at age a, which

is the PDF of the female producing the offspring over her life time. Now we relate this to epidemology by considering birth of offspring=production of new infection and age a = time since infection.
From definition of R_0, Averge No. of secondary infections produced by a single infected individual over its infectious period.

$$R_0 = \int_0^\infty n(a)da \tag{2}$$

Multiplying $eq(1)$ by $\frac{1}{b(t)R_0}$ we, get

$$\frac{1}{R} = \int_{a=0}^\infty e^{-ra} g(a)da$$

We know that Moment generating function of a probabilty distribution $g(a)$ is $M(z) = \int_0^\infty e^(za)g(a)da$ putting $z = -r$ we get the relation

$$\frac{1}{R} = M(-r) \tag{3}$$

In our case $g(a)$ is the generation interval distribution. Assuming it to be exponential with mean $1/gamma$. We find moment generating function of expoential distribution with mean λ to be $M(t) = \frac{\lambda}{\lambda - t}$. So

$$R_o = 1 + \frac{r}{\gamma} \tag{4}$$

Hence using the above relation we can find the R_0 of the system numerically.

3.2 Results

4 Modelling using SEIR model

Equations
Where σ denotes the rate of getting infectious from exposed, all other symbols denotes the same. As you can see we have restricted the migration of Infected indiciduals between the cites. So the infection can transfer between the cities only through migration of exposed individuals.
Similar analysis as SIR model was used, but the relation between r and R_0 has to be re-derived for this system.

4.1 Relation between r and R_0

In this model the generation interval distribution $g(a) = Exp(\frac{1}{\gamma}) + Exp(\frac{1}{\sigma})$, where $Exp(\lambda)$ denotes exponential distribution with mean λ.
Convolution of two expoential distribution with mean $\frac{1}{\lambda}$ and $\frac{1}{\theta}$ has the following pdf

$$f(x) = \frac{\lambda\theta}{\lambda - \theta}(e^{-\lambda x} - e^{-\theta x})$$

with MGF as

$$M(t) = \frac{\theta\lambda}{(\lambda - t)(\theta - t)}$$

. So in our case R_0 turns out to be

$$R_0 = (1 + \frac{r}{\gamma})(1 + \frac{r}{\sigma}) \tag{5}$$

Using Eq(5) instead of Eq(4) and similar analysis as SIR model gave us the following result.

5 Results

6 Theoritical derivation

6.1 The Next generation operator method

R_0 is defined as the spectral radius of the 'next generation operator'. To find the next generation operator, we need to first identify the infected and non-infected compartments. Suppose there are n compartments of which m are infected. Let $\bar{x} = (x_1, x_2, \ldots, x_n)$ where each x_i denotes the number of individuals in i^{th} compartment. Let, $F_i(x)$, denote the rate of apperance of new infections in compartment i. $V_i^-(x)$ be the rate of transfer of individuals into compartment i by all other means and $V_i^+(x)$ be the rate of transfer of individuals out of compartment i.

$$\frac{dx_i}{dt} = F_i(x) - V_i(x) = f(x_i)$$

where $V_i(x) = V_i^+(x) - V_i^-(x)$.

We then construct $\mathcal{F}$ and $\mathcal{V}$ matrices by taking the partial derivatives of the F_i with respect to x_i and similarly for $\mathcal{V}$ by taking partial derivatives of V_i. We define R_0 to be the spectral radius of the $\mathcal{F}\mathcal{V}^{-1}$.
Spectral radius of square matrix It is the largest absolute value of the matrix's eigen value.

6.2 Assumptions

1. If $\bar{x} \geq 0$, then $F_i, V_i^+, V_i^- \geq 0 \forall i$
2. If $\bar{x} = 0$, then $V_i^- = 0$
3. $F_i = 0$ if $i \geq m$
4. If $\bar{x} \in X_s$, where X_s is set of all Disease Free states. Then $F_i, V_i^+ = 0$
5. It is assumed that a disease free equilibrium exists and it is a locally asymptotically stable solution of the disease free model.Thus if x_0 denotes a disease free equilibrium of the system, then if $\mathcal{F}(x)$ is set to zero, then all eigenvalues of $Df(x_0)$ have negative real parts.

6.3 SIR model with birth and death

The following is the derivation of R_0 for SIR model with birth and death.
Equations

$$\frac{dS_1}{dt} = \lambda(S_1 + I_1 + R_1) - \mu S_1 - \beta_1 S_1 I_1 + \epsilon S_2 - \epsilon S_1$$

$$\frac{dI_1}{dt} = -\mu I_1 + \beta_1 S_1 I_1 + \epsilon I_2 - \epsilon I_1 - \gamma I_1$$

$$\frac{dR_1}{dt} = -\mu R_1 + \epsilon R_2 - \epsilon R_1 + \gamma I_1$$

Similarlly for City 2

- **For single city in isolation with no transfer rates**
  $\epsilon = 0$, $n = 3$ and $m = 1$
  F_i is the rate of apperance of infection at compartment i, It is enough to consider the I compartment, Since only I contributes for the infection.

$$\frac{dI}{dt} = \beta SI - \gamma I - \mu I$$

$$F = \beta SI, V = -\gamma I - \mu I$$

$$\frac{dF}{dI} = \beta S, \frac{dV}{dI} = -\gamma - \mu$$

at Disease Free equilibrium $S1 = N_0$ *where* N_0 *is the initial number of people*

$$\frac{dF}{dI}|_{DFE} = \beta N_0, \frac{dV}{dI}|_{DFE} = -\gamma - \mu$$

$$\mathcal{F} = \frac{dF}{dI}|_{DFE}, \mathcal{V} = \frac{dV}{dI}|_{DFE}$$

Since R_0 equals the spectral radius of $\mathcal{F}\mathcal{V}^{-1}$, We find that

$$R_0 = \frac{\beta N}{(\gamma + \mu)}$$

- **For two cities with transfer rates**
  $n = 6$ and $m = 2$ where I_1 and I_2 are the two infected compartments.

$$F_1 = \beta_1 S_1 I_1, F_2 = \beta_2 S_2 I_2$$
$$V_1 = -\gamma I_1 - \mu I_1 - \epsilon I_1 + \epsilon I2, V_2 = -\gamma I_2 - \mu I_2 - \epsilon I_2 + \epsilon I1$$

Now,

$$\mathcal{F} = \begin{bmatrix} \beta_1 N_1 & 0 \\ 0 & \beta_2 N_2 \end{bmatrix}$$

$$\mathcal{V} = \begin{bmatrix} \text{-}\gamma - \mu - \epsilon & \epsilon \\ \epsilon & \text{-}\gamma - \mu - \epsilon \end{bmatrix}$$

The Eigen values of $\mathcal{F}\mathcal{V}^{-1}$ was calculated using mathematica,

The spectral radius defined as the absolute value of the largest eigen value turns out to be

$$R_0 = \frac{X + \sqrt{X^2 - 4\beta_1\beta 2N_1N_2Y}}{2Y}$$

where $X = (\beta_1 N_1 + \beta 2N_2))(\epsilon + \mu + \gamma)$ and $Y = (2\epsilon\gamma + \gamma^2 + 2\epsilon\mu + 2\mu\gamma + \mu^2)$

6.4 SEIR Model

Equations

$$\frac{dS_1}{dt} = \lambda(S_1 + E_1 + I_1 + R_1) - \mu S_1 - \beta_1 S_1 I_1 + \epsilon S_2 - \epsilon S_1$$
$$\frac{dE_1}{dt} = -\mu E_1 + \beta_1 S_1 I_1 + \epsilon E_2 - \epsilon E_1 - \sigma E_1$$
$$\frac{dI_1}{dt} = \sigma E_1 - \gamma I_1 - \mu I_1$$
$$\frac{dR_1}{dt} = -\mu R_1 + \epsilon R_2 - \epsilon R_1 + \gamma I_1$$

Similarlly for City 2

- **For single city in isolation with no transfer rates**
  $\epsilon = 0$, $n = 4$ and $m = 2$, E_1 and I_1 are considered as infective compartments

$$F_1 = \beta_1 S_1 I_1, F_2 = 0$$

$$V_1 = -\mu E_1 - \sigma_1, V_2 = \sigma E_1 - \gamma I_1 - \mu I_1$$

Now, calculating $\mathcal{F}$ and $\mathcal{V}$ at DFE $S_1 = N_1$

$$\mathcal{F} = \begin{bmatrix} 0 & \beta_1 N_1 \\ 0 & 0 \end{bmatrix}$$

$$\mathcal{V} = \begin{bmatrix} \text{-}\sigma - \mu & 0 \\ \sigma & \text{-}\gamma - \mu \end{bmatrix}$$

The Spectral radius of $\mathcal{F}\mathcal{V}^{-1}$ was calculated using mathematica.

$$R_0 = \frac{\beta_1 N_1 \sigma}{(\gamma + \mu)(\mu + \sigma)}$$

For two cities with transfer rates
$n = 8$ and $m = 4$, E_1,I_1,E_1 and I_1 are considered as infective compartments.

$$F_1 = \beta_1 S_1 I_1, F_2 = 0$$

$$F_3 = \beta_2 S_2 I_2, F_4 = 0$$

$$V_1 = -\mu E_1 + \epsilon E_2 - \epsilon E_1 - \sigma_1, V_2 = \sigma E_1 - \gamma I_1 - \mu I_1$$

$$V_3 = -\mu E_2 + \epsilon E_1 - \epsilon E_2 - \sigma_2, V_4 = \sigma E_2 - \gamma I_2 - \mu I_2$$

Now, calculating $\mathcal{F}$ and $\mathcal{V}$ at DFE $S_1 = N_1 and S_2 = I_2$

$$\mathcal{F} = \begin{bmatrix} 0 & \beta_1 N_1 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \beta_2 N_2 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

$$\mathcal{V} = \begin{bmatrix} \text{-}\sigma - \mu - \epsilon & 0 & \epsilon & 0 \\ \sigma & \text{-}\gamma - \mu & 0 & 0 \\ \epsilon & 0 & \text{-}\sigma - \epsilon - \mu & 0 \\ 0 & 0 & \sigma & \text{-}\mu - \gamma \end{bmatrix}$$

The Spectral radius of $\mathcal{F}\mathcal{V}^{-1}$ was calculated using mathematica.

$$R_0 = \frac{X + \sqrt{X^2 - 4\beta_1 \beta 2 N_1 N_2 \sigma^2 Y}}{2(\gamma + \mu) Y}$$

where $X = (\beta_1 N_1 \sigma + \beta 2 N_2 \sigma))(\epsilon + \mu + \sigma)$ and $Y = (2\epsilon\mu + \mu^2 + 2\epsilon\sigma + 2\mu\sigma + \sigma^2)$