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DISEASE PROPERTIES AFFECT ON DEATH RATES
An Extension To The SIR-Model

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Contents

1 Introduction **2**

2 Model **3**
2.1 SIR . . . 3
2.2 Travel between Cities . . . 3
2.3 SIHRD . . . 4
2.4 Quarantine . . . 5
2.5 Time periods for model validity . . . 5
2.6 Network generation . . . 6
2.6.1 Road generation . . . 6

3 Results **7**
3.1 Network results . . . 8
3.2 Landscapes . . . 9

4 Analysis **10**
4.1 Landscape for α and β . . . 10
4.2 Landscape for ξ and ϑ . . . 10
4.3 Conclusion . . . 10

1 Introduction

This study investigates how different properties of a disease affect the death rate in the population of a simulated network of cities. Considered parameters are mortality, days of incubation, transmission rate and average days of recovery.

The goal of the study is to investigate how the total deaths from a disease outbreak can be minimized by using different measurements, such as quarantines.

The approach is using an extension to the SIR model, where deceased, incubated and hospitalized are considered as their own groups. This introduced another stage of realism and delicacy to the SIR-model.

2 Model

2.1 SIR

The SIR-model is an approach to model the spread of a disease. In the model one considers three groups, those susceptible to the disease (S), the infected (I) and the recovered/immune (R).

Figure 1: Susceptibles can become infected while infected can become recovered. The two transitions are described as α and β.

Every individual belongs to one of these tree groups and can only go from susceptible to infected to recovered, as shown in fig. 1. One can argue that the rate of change for the different groups are as in eq. 1. Here N is the total population, α is the recovery rate and β is the transmission rate.

$$\frac{\mathrm{d}S}{\mathrm{d}t} = -\frac{1}{N}\beta SI \qquad \frac{\mathrm{d}I}{\mathrm{d}t} = \frac{1}{N}\beta SI - \alpha I \qquad \frac{\mathrm{d}R}{\mathrm{d}t} = \alpha I \tag{1}$$

As the considered system is closed there should be no change in the number of considered individuals. One can verify this by confirming that sum of the derivatives equals zero.

The functions $S(t)$, $I(t)$ and $R(t)$ can be estimated using a numerical approach, such as the Euler Method or a Runge-Kutta method. This requires an initial value with preferably a non-zero amount of infected individuals (otherwise the model would not be very interesting).

2.2 Travel between Cities

So far we have only considered one city. If one instead considers several cities there would be a SIR-group for each city. As people travel between the different cities a few susceptibles from one city might meet infected from another city. However, we do not take moving into account and hence should the population of each city remain constant. Let it for susceptibles be described as eq. 2 where $\omega_{n\to m}$ is the rate of travel from city n to m. R and I follow the same pattern. This contribution is then added to the derivatives discussed in subsec. 2.1.

$$\sum_m \omega_{m\to n} S_m - \omega_{n\to m} S_n \tag{2}$$

Enforcing the condition of a constant population results in

$$\frac{\omega_{m\to n}}{\omega_{n\to m}} = \frac{N_n}{N_m}. \tag{3}$$

This implies that weights cannot be symmetric in this model. However, given one of them the other is easily computed.

2.3 SIHRD

Let extend the SIR-model to include death and incubation. As in SIR there one group of susceptibles, S, capable of catching the disease and a group of recovered, R, who are immune to the strain. The infected are divided into two groups, incubation I and hospitalized H[1]; one which yet experience no symptoms and one which does. One new group is D, which are the ones who decease due to the disease. The flowchart in fig. 2 illustrate how these groups relate to each other.

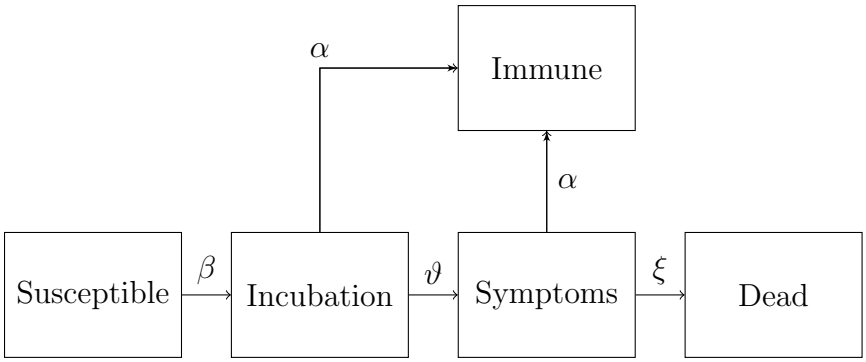


Figure 2: A chart of how the different groups relate to each other.

The new groups, as well as newly added transitions, results in a few new derivatives. We introduce the following two variables: the mortality of the disease, ξ and reverse incubation time, ϑ. Which transitions these correspond to can be seen in fig. 2.

Assume that those experiencing symptoms travel to a less extent and can thus be ignored.

$$\frac{\mathrm{d}S}{\mathrm{d}t} = -\frac{1}{N}\beta S(I+H) \tag{4}$$

$$\frac{\mathrm{d}I}{\mathrm{d}t} = \frac{1}{N}\beta S(I+H) - (\alpha+\vartheta)I \tag{5}$$

$$\frac{\mathrm{d}H}{\mathrm{d}t} = -(\xi+\alpha)H + \vartheta I \tag{6}$$

$$\frac{\mathrm{d}D}{\mathrm{d}t} = \xi H \tag{7}$$

$$\frac{\mathrm{d}R}{\mathrm{d}t} = \alpha(I+H) \tag{8}$$

One can confirm that the sum of the derivatives is zero as it should. One weak assumption used in this model is that those who experience symptoms meet as many people as those who are not experience any symptoms.

[1]Not necessarily in an hospital.

2.4 Quarantine

One efficient way of minimizing the spread of a disease is the use of quarantine. Assume when a city is set in quarantine all connections to and from it is shut down and visibly infected are screened off from the rest of the city population. In reality this is a most expensive and serious action and most only be utilized if really required. In order to create a measure of whether quarantine should be utilized or not define a threshold $\nu \in (0, 1)$.

$$\Upsilon = H\left[\max\left(\frac{H}{N} - \nu, \frac{1}{N\nu}\frac{\mathrm{d}H}{\mathrm{d}t} - \nu\right)\right]$$

H is the Heaviside step function. An more sensitive version is the following.

$$\Upsilon = H\left(\frac{H}{N} + \frac{1}{N\nu}\frac{\mathrm{d}H}{\mathrm{d}t} - \nu\right)$$

Neither of these methods for determining quarantine was implemented.

2.5 Time periods for model validity

The simulation is meant to study the disease during a few months, hence making the population changes as births and natural deaths negligible. Therefore this model is most reliable when studying shorter outbreaks, preferably less than a year.

2.6 Network generation

In order to create a network of cities a position and size of population was randomly drawn given two conditions. The point was picked from a uniform distribution and the population from a narrow Gauss distribution.

1. The distance between the picked point and all other cities must be above a certain threshold.

2. The population must belong to a defined range with a lower and upper bound.

2.6.1 Road generation

Let define a quantity labeled travel-rate between two cities as the following. The constant C was chosen to 1/5000.

$$\lambda(a,b) = C\,\frac{\text{Population } a + \text{Population } b}{\text{Distance}(a,b)}$$

Roads were drawn according to two rules.

1. For any cities a and b draw a road if $\lambda(a,b) \geq 1$.

2. Draw for each city a that is not connected a road to another city b for which $\lambda(a,b)$ is minimal.

Along each road a travel-rate $\omega(a,b)$ was calculated for each time step using the formula below. Let define a quantity labeled travel-rate between two cities as the following. N is the total population throughout the network and C is a constant chosen to 5/1000.

$$\omega(a,b) = \frac{C}{N}\,\frac{\text{Population } a}{\text{Distance}(a,b)}$$

$\omega(a,b)$ is used as $\omega_{a\leftarrow b}$ in eq. 1, 3 and 6.

3 Results

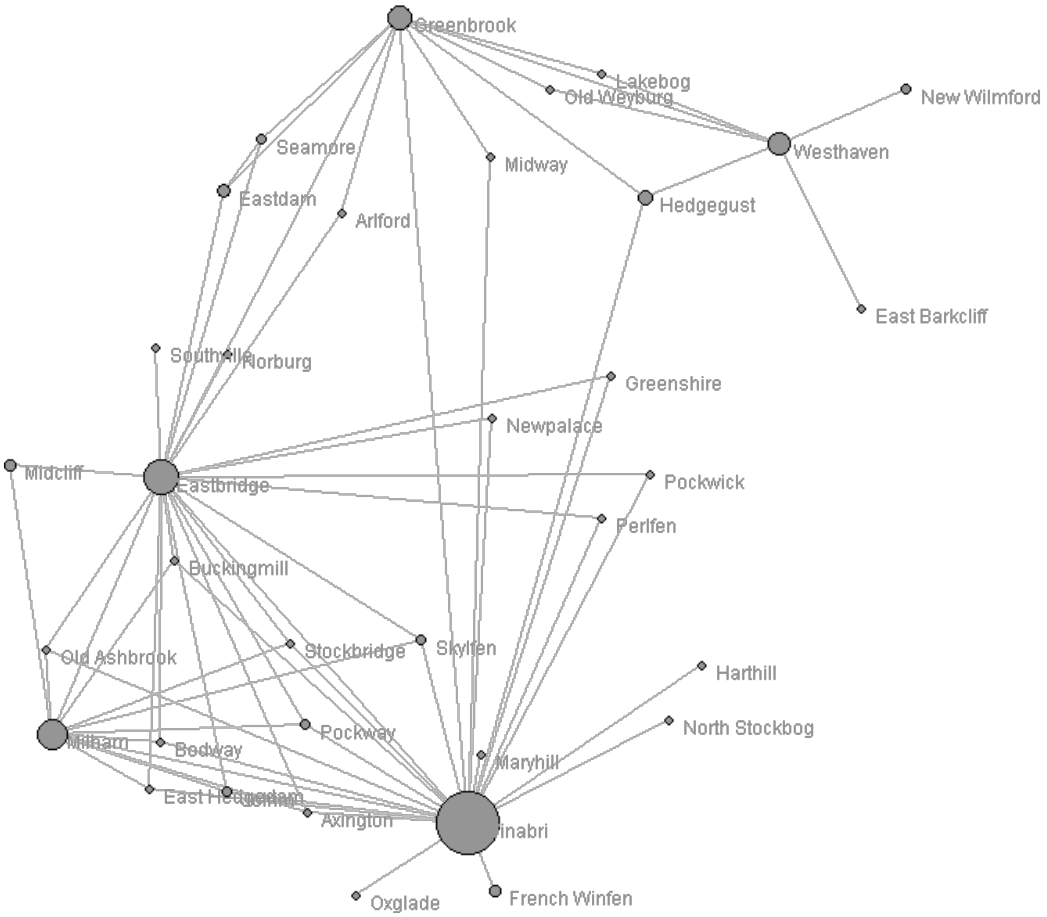


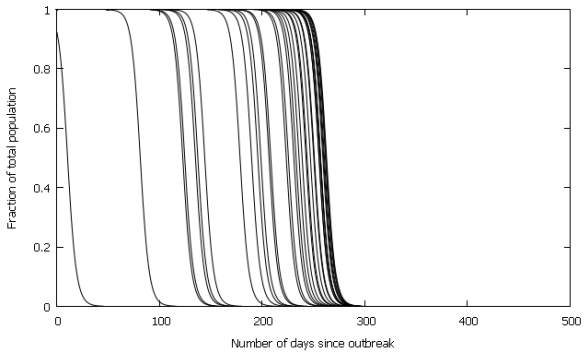
Figure 3: A map over the studied city network.

One randomly generated network consisting of 35 cities was chosen due to its interesting connection properties. The disease outbreak started in city of New Wilmford. The following parameters was used:

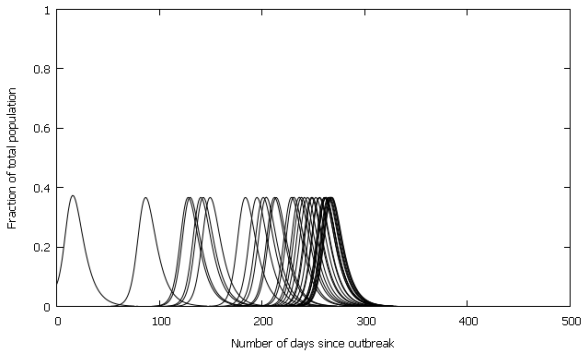
Parameter	Value
α	0.01
β	0.25
ϑ	10
ξ	0.01
Time period	50 days
Time interval	1 day

Table 1: Parameters used in 3.1.

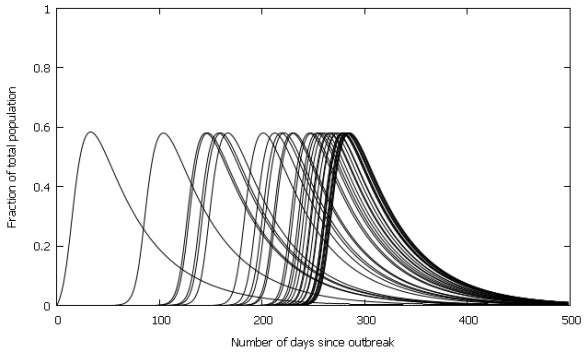
3.1 Network results



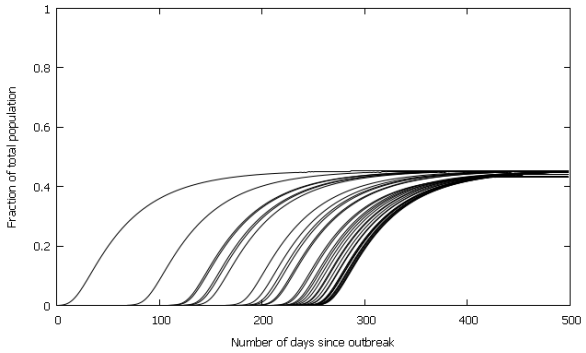
(a) Susceptible.



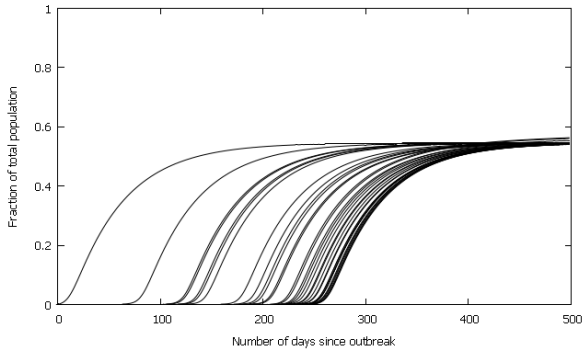
(b) Incubation.



(c) Symptoms.



(d) Dead.

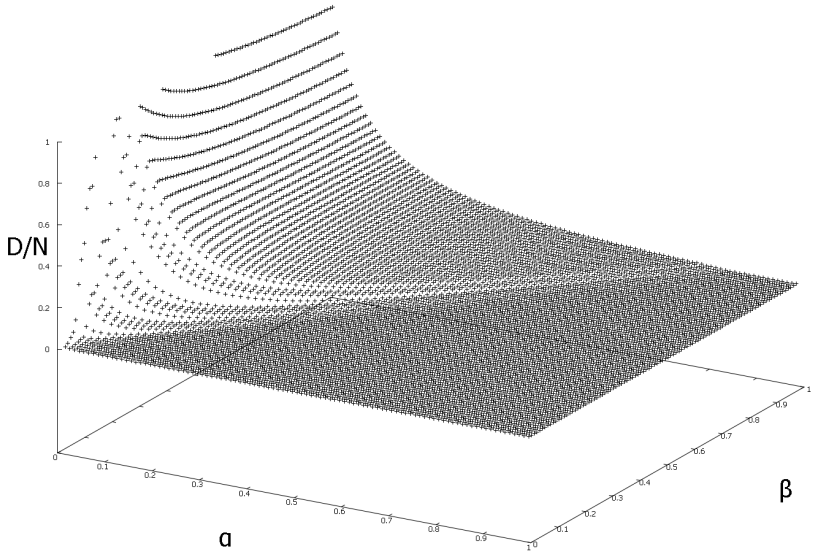


(e) Recovered.

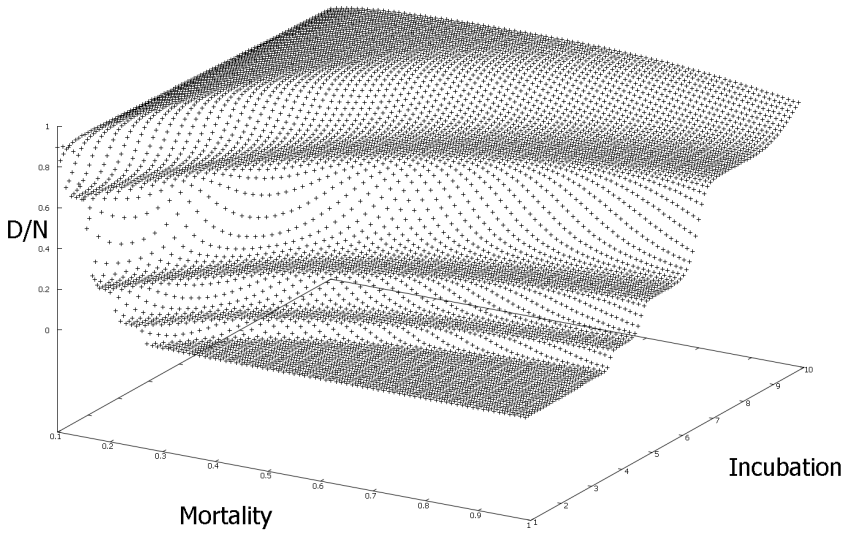
Figure 4: How each group relates to total population as a fraction. One line corresponds to a group in one city.

How each group changed at every time step was studied and is presented in the figures above. The maximum error in each fraction in the figures above is of the order 10^{-8}, calculated using eq. **??**.

3.2 Landscapes



(a) Fraction as a function of α and β. $\xi = 0.5$ and $\vartheta = 15$.



(b) Fraction as a function of mortality ξ and incubation ϑ. $\alpha = 0.01$ and $\beta = 0.25$.

Figure 5: Fraction dead of total population over the network as function of different simulation parameters.

4 Analysis

The total death rate seem to approach 45 % of the total population while recovered approach 55 %. This is not surprising since these are the only remaining groups hence should reach stability given enough time. Since all populations share the same properties the point of stability is the same in every city together with the same curve characteristics. Said points should be possible to calculate analytically given the model parameters. However no such relation have been found.

4.1 Landscape for α and β

The landscape presented in fig. 5a is flat for $\alpha > \beta$ which was to be expected since if the rate of recovery, α is greater than the rate of transmission, β, the disease will wear away. However, if $\beta > \alpha$ does $\frac{D}{N}$ seem to increase exponentially as α decreases. This implies that in this model does the transmission rate have little effect as long as the recovery rate is low. As $\alpha \to 0$ the disease will result in a mass extinction.

4.2 Landscape for ξ and ϑ

The landscape in fig. 5b implies that for long incubation times a disease will reach a certain threshold discussed in a former paragraph - given enough time. For lower incubation times there is a ladder-type of behavior where those who have lower mortality in general result in more deaths. This is due to the weak assumption made in the model that those who experience symptoms socialize to same degree as those who do not experience any symptoms. This affect the model by favoring parameters where those who experience symptoms are maximized. Redoing the model without this assumption could hence further improve the results.

The equi-surfaces in the ladder are points where $\frac{\partial D}{\partial \xi} = \frac{\partial D}{\partial \vartheta} = 0$ and are probable regions for actual diseases since a disease where any of these derivatives are non-zero are more likely to change.

4.3 Conclusion

This model suggests that diseases with a long incubation time are the most hazardous - which does seem plausible. The fact that the model favors low mortality is less realistic and probably due to a weak assumption in the model.

References

[1] Lund University, *ODE, Lecture 2, FYTN03 Computational Physics.*