

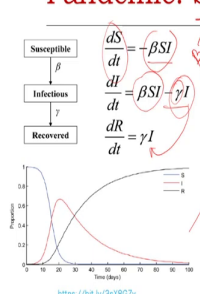
Social Network Analysis
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Chapter - 10
Lecture - 04


Let us start with another application right. So far we have looked at you know mostly the cyber security related issues sock puppets, collusion black markets so on. So, in this lecture we will focus on a very hot topic right a how to you know how to model the COVID-19 pandemic spread ok.

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Modelling the Spread of COVID-19 Pandemic: SIR Model Revisited



The diagram shows the SIR model with three compartments: Susceptible, Infectious, and Recovered. Transitions are labeled with parameters: β for infection, γ for recovery, and μ for death. The differential equations are: $\frac{dS}{dt} = -\beta SI$, $\frac{dI}{dt} = \beta SI - \gamma I - \mu I$, and $\frac{dR}{dt} = \gamma I$. A graph below shows the population dynamics over time, with S (Susceptible) decreasing, I (Infectious) peaking, and R (Recovered) increasing.



- Propagation through three stages
 - Susceptible: people who can become infected
 - Infectious: people who are infected and are capable of spreading others in contact
 - Recovered: people who have recovered or become immune to the infection
- Governed by two parameters
 - Birth rate (β): controls probability with which an infected node attacks its neighbors
 - Death rate (γ): controls the probability with which an infected node recovers from the contagion



So, last two and half years I mean I really do not need to you know motivate you why this is an important problem statement. In fact, the pandemic is pandemic is not yet over. So, last 2 years, two and half years we have seen many such models you know 1000s of such models, which basically you know can mimic the way COVID-19 spreads.

Now, COVID-19 you know pandemic is not you know similar to you know the one that we have discussed. So, far for example, Ebola spread for example, right so, but nevertheless people actually started with an existing with existing methods to see whether those methods are really useful for COVID-19 and then people basically improvised their models in different ways, ok.

So, a quick recap of what we have discussed in the diffusion cascade chapter. We have discussed SIR model susceptible infected recovery model, where with probability β susceptible population moved to infected populations right. And this is called the birth rate of the virus; whereas, with some probability γ and infected people and infected person actually moves to the recovery state right.

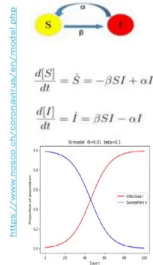
So, and if after recovery if there is no further chance of getting infected again. So, that the process ends here in some cases we have seen that even after recovery say think of a normal cold right. Cold and cough like symptom, where even after recovery there is you may end up being a susceptible user right. So, there are two important parameters β and γ . In fact, we also have seen the way we write the differential equation the rate of change of susceptible user is minus βSI , where β is the birth rate.

Now, every infected user every infected user infects a susceptible user with probability β right. So, every susceptible user is will be infected right with this one β into I , I is the fraction of infected users. And since there are s number of susceptible is fraction of susceptible users this would be the rate of change of susceptible user population, and this is negative.

Why? Because the population decreases with the same amount right, the same amount will increase the same amount contribute to the increase of the infected user right, and this is plus. But here with certain probability γ infected users again move to recovery state therefore, this is minus and the same amount contributes to the rate of change of recovery user ok. And we have seen this kind of curves in the previous lectures.

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Modelling the Spread of COVID-19 Pandemic: SIS Model Revisited



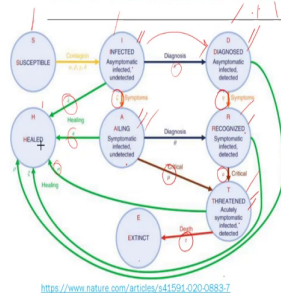
- Apt for modelling infectious diseases that can recur rapidly
- A recovered individual immediately becomes susceptible again
- Governed by two parameters
 - Birth rate (β): controls probability with which an infected node attacks its neighbors
 - Death rate (α): controls the probability with which an infected node recovers from the contagion, and becomes susceptible again



In fact, we have also seen bit simpler model, which was SIS model susceptible infected susceptible the cold one that I mentioned viral flu or cold one right. So, from susceptible you can move to infected with certain probability alpha and from infected you can further move to susceptible with some probability ok.

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Modelling the Spread of COVID-19 Pandemic: SIDARTHE Model



- Proposed by Giordano et al. in 2020, based on data collected in Italy
- Susceptible population can contact COVID-19 from four sources
 - infected (α)
 - diagnosed (β)
 - ailing (γ)
 - recognized (δ), with usually $\alpha > \gamma > \beta, \delta$
- Two more parameters in connection with detection
 - detection of asymptomatic infected individuals (ϵ)
 - detection of symptomatic infected individuals (θ)
 - Usually $\theta > \epsilon$
 - Dependent on testing strategies adopted



So, the model that I am going to discuss here this is one of the; one of the lot of models that have been proposed so far right. And this model was named as you know S I D A R T H E ok. So, there are the these names are corresponding to different states you have S, which is

susceptible you have I, which is infected then there is D, which is diagnosis right then A, which is ailing R, which is recognized I will discuss all these states T, which is threatened right H, which is healed then E, which is extinct ok.

So, susceptible population is basically the population which are prone right prone to this virus infection, which can which are vulnerable in that sense. Infected populations are those which are asymptomatic, but infected; infect asymptomatic infected, but undetected the dangerous population; undetected, but asymptomatic infected.

D diagnosed asymptomatic infected, but detected they those are safe populations because since they are detected the other undetected that the other susceptible populations would basically try to avoid those populations. Then we have A which is ailing symptomatic infected symptomatic infected undetected right. They have symptoms right, but undetected so far and then we have recognized symptomatic infected detected right. Then we have T state which is threatened right.

So, it is these kind of populations basically suffer from major Covid problems and it may lead to even death right. So, from threatened state we can move to extinct; extinct means end of life and we also have population which is healed H right. So, lots of parameters lots of states lots of parameters. So, from susceptible state we can move to infected state right, we have different probabilities we have alpha beta and gamma right.

Alpha is the infected probability beta is the diagnosed probability, ailing is the you know illness probability, and delta is the recognized probability right, with all these four probabilities susceptible populations would decrease right. You see here alpha is greater than all the other parameters. Why? Because alpha corresponds to the infected probability; so, infected states infected state is a state which is the most dangerous as I mentioned because here you know patients are asymptomatic, but they are undetected.

So, with high probability they would infect others they would basically you know attract susceptible population to infected population. And then diagnose and ailing these two probabilities are the least because if and also recognized because if things have already been recognized already been diagnosed identified then, people will basically avoid those populations right therefore, it is less right.

We have few other parameters we have you know with epsilon yeah. So, this epsilon theta these are also connected to detection right. So, this epsilon basically says that this epsilon governs the detection of asymptomatic infected individuals. This is basically transition from infected to diagnosed, this one right. Similarly we have theta, which basically you know moves population from ailing to recognized right; symptomatic undetected to symptomatic detected.

So, you see here you may want to give more weightage to theta right, because since this is symptomatic. So, there is very high chance that this would be detected; whereas, in case of this one epsilon since asymptomatic there is very high chance that this would be detected, there will be low. I mean less chance compared to theta that it will be detected therefore, you want to give more weightage to theta than epsilon ok.

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Modelling the Spread of COVID-19 Pandemic: SIDARTHE Model



- Asymptomatic individuals can transit to the symptomatic stage
 - when they have been tested positive (ϵ)
 - or, when they are not even tested positive (ζ)
- Individuals grow life-threatening symptoms irrespective of the detection of their infection
 - transition from ailing to threatened state (μ)
 - transition from recognized to threatened state (ν)
- Mortality rate after showing life threatening symptoms (τ)
- Rate at which individuals recover from all the infected states
 - from infected state (λ)
 - from ailing state (κ)
 - from threatened state (ρ)
 - from recognized state (ψ)
 - from diagnosed state (ϕ)



Then we have two other parameters right. So, from asymptomatic individuals right asymptomatic individuals can transit to symptomatic stage right. So, you see here in this figure right this one and this one right. Asymptomatic to symptomatic, infected to ailing, and diagnosed to recognized, right.

You may again want to control the parameters depending upon the actual real values. Individuals grow life-threatening symptoms irrespective of the detection of their infection: We have two parameters one is this one right; another is this one. From illness from ailing

you can move to life-threatening stage from recognized also you can move to the life-threatening stage right, ok.


Then from life threatening stage you can move to death stage with certain probability tau right. And then from all the states infected ailing life threatening right diagnosed you can directly go to the healing healed stage, and that is the that is the good news right. So, with certain probabilities you can actually move to the healed stage. So, these are as you see a lots of parameters, right.


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Modelling the Spread of COVID-19 Pandemic: SIDARTHE Model

□ Rate of change of population at different states can be defined as,

$\frac{dS}{dt} = -S(\alpha I + \beta D + \gamma A + \delta R)$	$\frac{dR}{dt} = \eta D + \theta A - (\nu + \psi)R$
$\frac{dI}{dt} = S(\alpha I + \beta D + \gamma A + \delta R) - (\epsilon + \zeta + \lambda)I$	$\frac{dT}{dt} = \mu A + \nu R - (\sigma + \tau)T$
$\frac{dD}{dt} = \epsilon I - (\eta + \rho)D$	$\frac{dH}{dt} = \lambda I + \rho D + \kappa A + \psi R + \sigma T$
$\frac{dA}{dt} = \zeta I - (\theta + \mu + \kappa)A$	$\frac{dE}{dt} = \tau T$





And we will use the same kind of differential equations that we use for SIR SIS models, again I am not go into details very straightforward you can easily look at it by you know by keeping track of the state changes. And you see that rate of change of susceptible user right rate of change of infected user death, ailing right, recovered and threatening, healed and exist extinct right.

So, if you check these parameters I mean if you solve this problem differential equations integrate it over times you can basically draw curves t and then you change of S change of I right change of D and so on. So, what you can do? You can take time t say 0 to t for tuning your parameters right, and from t to delta t you can predict ok the rate of change of these populations.

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Modelling the Spread of COVID-19 Pandemic: Other Models



- Gatto et al. in 2020 devised a modification of the SEIR epidemic model
 - It incorporates spatial characteristics, linking 107 provinces of Italy
 - They termed their model as SEPIA
 - Compartments in their model: Susceptible (S), Exposed (E), Presymptomatic (P), Infected with heavy symptoms (I), Asymptomatic/mildly symptomatic (A), Hospitalized (H), Quarantined at home (Q), Recovered (R), and Dead (D) individuals
- Liu et al. in 2020 devised a model that they designated as the SEIRU model
 - The model took into consideration the latency period of COVID-19 before which an infected person is capable of transmitting the infection
- Weitz et al. in 2020 introduced the concept of shield immunity on top of the SIR epidemic model



In fact, as I mentioned there are many other models that have been proposed. For example, you know this model Gatto et al 2020. So, they use this SEIR model we discussed earlier right, but they incorporated some sort of; some sort of spatial characteristics. Meaning the geographical locations right the other you know the other properties of this geography and so on so forth the population density and so on and so forth.

Then there was another model which was basically SEIRU model right, which took into consideration the latency period ok. In fact, there was another model which considered the hard immunity the one that mentioned earlier the shield immunity right. And that concept was you know incorporated into the SIR model for better prediction of the growth of the you know infection infectious people and recovered people.

So, I am not going with the details of this literature this again takes a whole you know semester long course if I start speaking about COVID-19 spread, but you see how you know simple ideas of network science you know are useful to in fact, model the deadly COVID-19 virus ok. So, that is about the you know modeling the spread of COVID-19.

The next lecture we will discuss another application, which is the recommendation system and I will basically tell you how bipartite network communities you know some sort of deep learning for graphs model that we discussed in the last lecture will be useful for better recommendation of products right movies to users right. And to a generic general public right, in a broader sense ok, with this we stop here. And we will meet next day.

Thanks.