Advanced Process Dynamics
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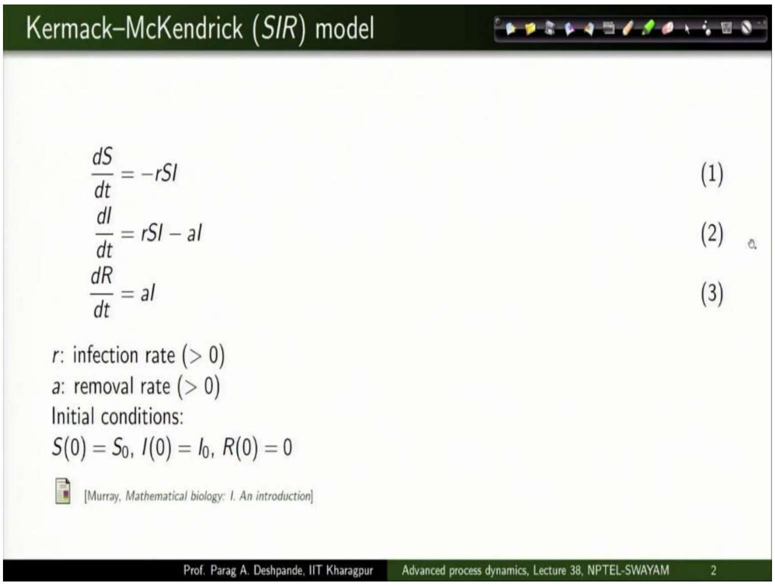
Lecture 38
Analysis of infectious disease dynamics continued…



Kermack–McKendrick (*SIR*) model

$$\frac{dS}{dt} = -rSI \quad (1)$$

$$\frac{dI}{dt} = rSI - aI \quad (2)$$

$$\frac{dR}{dt} = aI \quad (3)$$

r: infection rate (> 0)
a: removal rate (> 0)
Initial conditions:
$S(0) = S_0$, $I(0) = I_0$, $R(0) = 0$

[Murray, Mathematical biology: I. An introduction]

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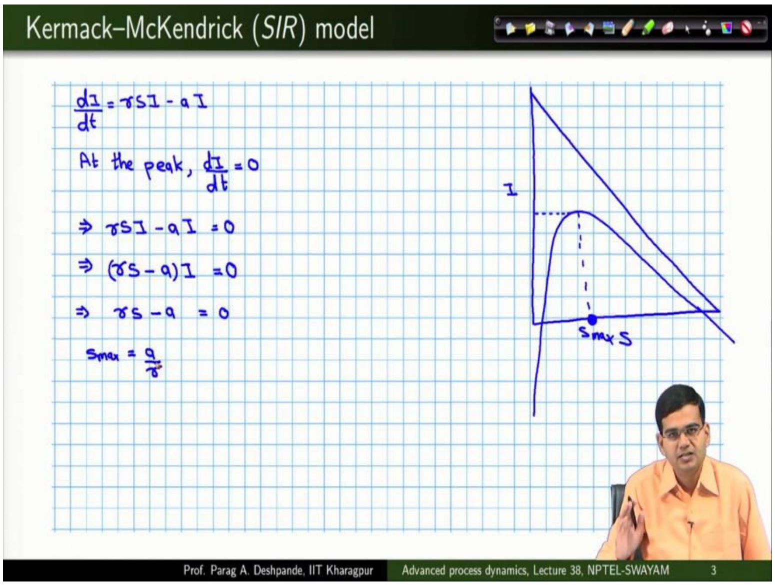

Kermack–McKendrick (*SIR*) model

$\frac{dI}{dt} = rSI - aI$

At the peak, $\frac{dI}{dt} = 0$

$\Rightarrow rSI - aI = 0$

$\Rightarrow (rS - a)I = 0$

$\Rightarrow rS - a = 0$

$S_{max} = \frac{a}{r}$

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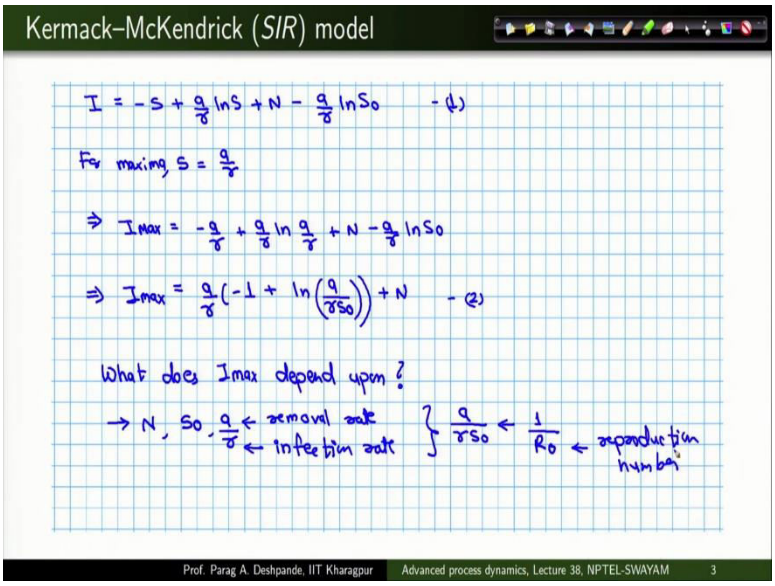


Kermack–McKendrick (*SIR*) model

$$I = -S + \frac{a}{\gamma}\ln S + N - \frac{a}{\gamma}\ln S_0 \quad -(1)$$

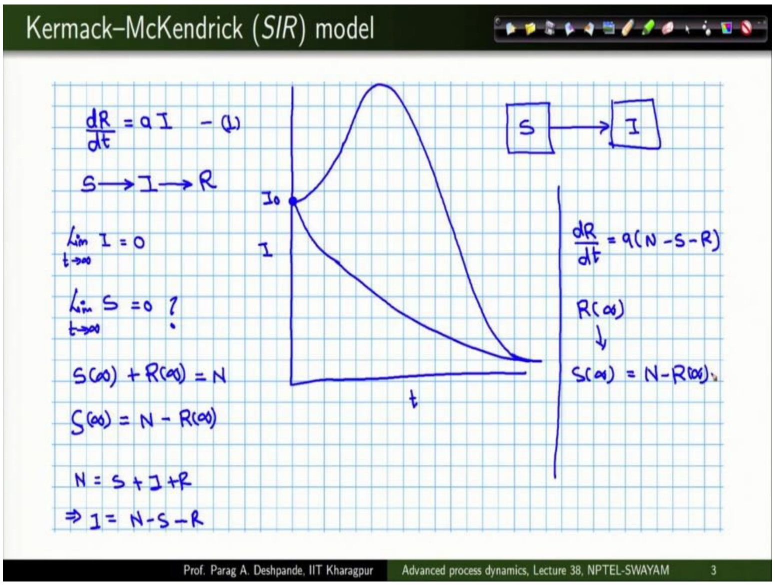
For maxima, $S = \frac{a}{\gamma}$

$$\Rightarrow I_{max} = -\frac{a}{\gamma} + \frac{a}{\gamma}\ln\frac{a}{\gamma} + N - \frac{a}{\gamma}\ln S_0$$

$$\Rightarrow I_{max} = \frac{a}{\gamma}\left(-1 + \ln\left(\frac{a}{\gamma S_0}\right)\right) + N \quad -(2)$$

What does I_{max} depend upon?

$\rightarrow N$, S_0, $\frac{a}{\gamma}$ ← removal rate / ← infection rate $\Big\}$ $\frac{a}{\gamma S_0} \leftarrow \frac{1}{R_0} \leftarrow$ reproduction number



Kermack–McKendrick (*SIR*) model

$$\frac{dR}{dt} = aI \quad -(1)$$

$$S \rightarrow I \rightarrow R$$

$$\lim_{t\to\infty} I = 0$$

$$\lim_{t\to\infty} S = 0 \; ?$$

$$S(\infty) + R(\infty) = N$$

$$S(\infty) = N - R(\infty)$$

$$N = S + I + R$$

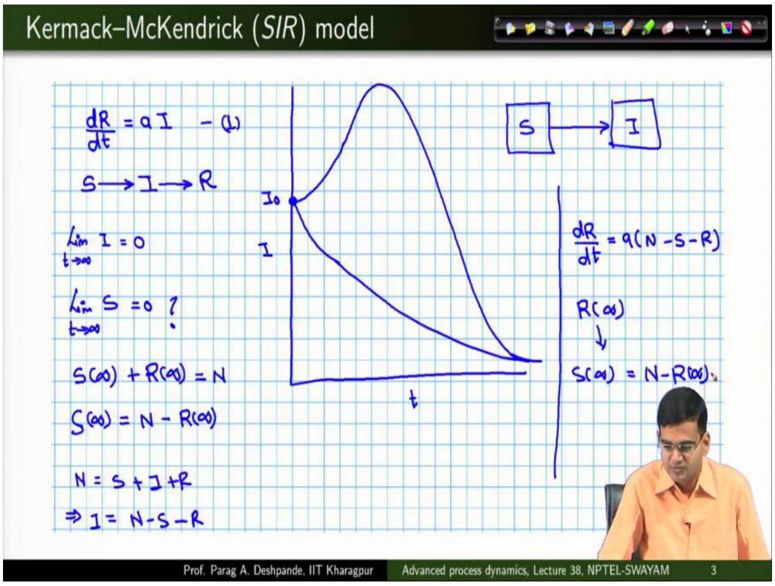
$$\Rightarrow I = N - S - R$$

$$\frac{dR}{dt} = a(N - S - R)$$

$$R(\infty)$$

$$\downarrow$$

$$S(\infty) = N - R(\infty)$$



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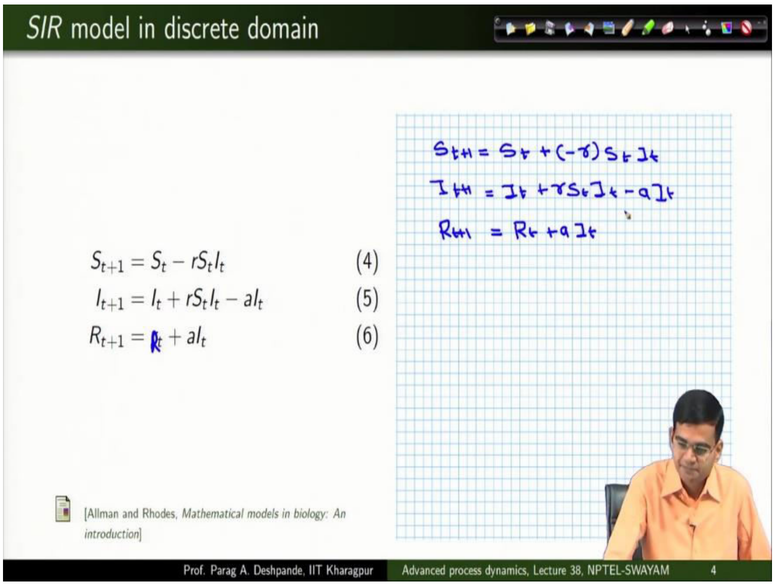


SIR model in discrete domain

$$S_{t+1} = S_t + (-r) S_t I_t$$

$$I_{t+1} = I_t + r S_t I_t - a I_t$$

$$R_{t+1} = R_t + a I_t$$

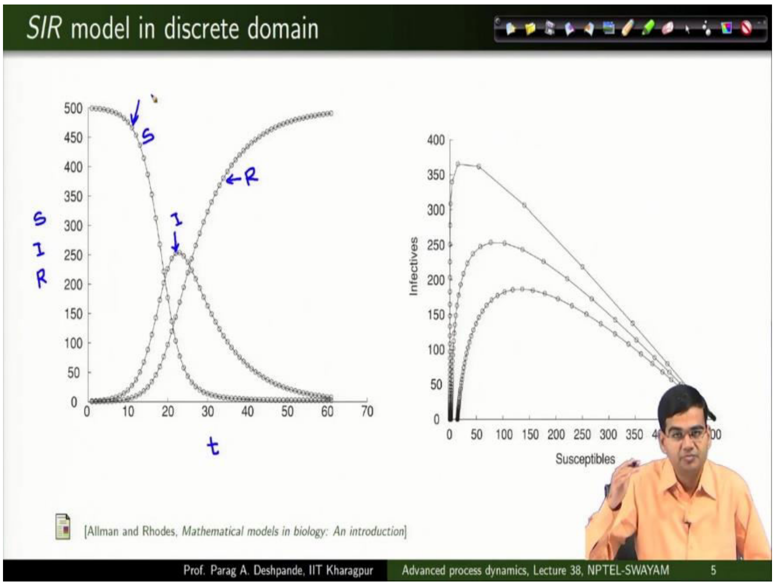
$$S_{t+1} = S_t - rS_tI_t \quad (4)$$

$$I_{t+1} = I_t + rS_tI_t - aI_t \quad (5)$$

$$R_{t+1} = R_t + aI_t \quad (6)$$

[Allman and Rhodes, *Mathematical models in biology: An introduction*]

Prof. Parag A. Deshpande, IIT Kharagpur | Advanced process dynamics, Lecture 38, NPTEL-SWAYAM | 4



SIR model in discrete domain

[Allman and Rhodes, *Mathematical models in biology: An introduction*]

Prof. Parag A. Deshpande, IIT Kharagpur | Advanced process dynamics, Lecture 38, NPTEL-SWAYAM | 5

Welcome back. Let us continue our discussion on SIR model for infectious disease dynamics. We will have a quick look into the model.

(Refer Slide Time: 00:34)

The model is in front of you, a third order system d S, given by $\frac{dS}{dt} = -rSI,$ and $\frac{dI}{dt} = rSI - aI,$ where r is the infection rate, always positive, a is the removal rate always positive, S_0 the initial number of susceptible members of the population, I_0 the initial members of the populations which have been introduced as infected ones and the initial condition for removed ones was S_0.

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Now, in the last lecture, we had a look into the behavior of I-S projection of our phase portrait and we saw how we can use the a / r ratio and the initial susceptible population to make a prediction of whether or not pandemic would prevail. Now, let us do a further analysis to see whether we can answer some more questions.

So, in the last lecture, we saw that under certain conditions, you can have the maxima in the projection which means that the number of infections would rise with time, reach a peak, that is what we are referring as peak, all of these days and then the wave starts declining. Can we make an estimation about the number of members which would get infected when the peak reaches. Let us see this.

So, I have $\frac{dI}{dt} = rSI - aI$, this was the model equation for I and when you have a maxima for the function I = I(t), then the derivative should become 0. So therefore, at the peak the $\frac{dI}{dt} = 0$, from where I can write $rSI - aI = 0$ which means $(rS – a) I = 0$. Now, I cannot be 0 because, if you do not introduce any, if you do not have any infected members, further infection cannot spread. So, therefore, I can write $rS - a = 0$.

Now, this gives me a condition for the value of S the susceptible population at which you will get a maxima, which means if you remember the I-S projection then we had a system like this we had a phase, line like this. So, this is S max. S max does not mean that S is max. S max means the max corresponding to I max. So therefore, S max would be equal to a upon r. So, when the population of the susceptibles becomes equal to a by r you get the peak.

So, now it is not very difficult to see how to make a prediction on when you will reach the maxima. So, you will reach maxima when the population of susceptibles in your system becomes equal to a upon r. That is the condition. So, whenever this condition is satisfied, you will reach the maxima in number of infected persons. So, now, if this is the case can we determine the number of infected persons in the peak, I max.

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So, in the previous lecture, we wrote an expression for I in terms of S. So, I so, let me see the expression for I, $I = - S + \frac{a}{r} lnS + N - \frac{a}{r} lnS_0$. This is what we derived in the last lecture. So, for maxima, I have $S = a / r$ from where I can write $I_{max} = - \frac{a}{r} + \frac{a}{r} ln \frac{a}{r} + N - \frac{a}{r} ln S_0$.

So, can I do some rearrangements. so, let me write this as $\frac{a}{r}$ $(- 1 + ln \frac{a}{rS_0}) + N = I_{max}$. So, now, the question is that what does, so, let me write the question, what does I_{max} depend upon? The answer would be, it depends upon N from equation number 2.

Does this make sense? Obviously, it makes sense because, if you have smaller population the number of infections which it might reach at maxima would be smaller. Countries which have very large population, the corresponding number, corresponding N is large and the number of infected persons at maxima will also be large. Intuitively this is correct.

It depends upon S_0, susceptibles. Now, the question is that if you have a population in which everyone is susceptible versus a population in which the number of susceptibles is smaller, which population is more likely to have higher number of infectives? Obviously, the ones in which there are more number of susceptible, quite simply.

It also depends upon a / r. a is the removal rate, r is the infection rate, and in fact what you have done is you have clubbed this in a r S_0 which is what, which is 1 / R_0, reproduction number. So, this is an interesting observation. So, if I have $Imax$ which is given as a / r multiplied by 1 minus 1 plus ln 1 upon the reproduction ratio plus N.

So, now, the question is what good can come out of this equation. This is a very important and interesting equation because this simply says that if I know my total population, if I know my population of susceptibles in the beginning and very safely, it can be approximated during the early stages of the pandemic as to be equal to the number, the population itself. And if I know the reproduction ratio in the beginning, then I already know how much of the population is going to be infected at the peak of the pandemic, I already know that.

The only thing which is unknown this whole business, the population would be known. So, S_0 can be approximated, what is to be determined with accuracy is a / r. So, if you can know from the initial data, the infection rate and the removal rate, then during the beginning of the pandemic itself, you can know or you can have an estimate of the number of infected persons which would the number which it would reach when you reach the maxima of your peak, interesting.

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Now, finally, we are also had an expression which is given as $\frac{dR}{dt} = aI$. Now, what happens when the pandemic where S, time t tends to infinity, when you are at the far end of your pandemic, you would like to have some more information. So, now, I have my flow scheme as $S \rightarrow I \rightarrow R$.

And this is very similar to the reaction scheme which we saw in one of our previous lectures as $a \rightarrow b \rightarrow c$. So, what is the ultimate fate of S and I and R, this is what we want to know. From $a \rightarrow b \rightarrow c$ analysis, we already have a fairly good idea about this. So, I saw that if I write the evolution of I with time with some I_0, then I have 2 options.

I may go here positive gradient depending upon S_0, $r / a > 0$, I can have this option negative gradient for the same quantity, reproduction number to be less than 1. So, in either case, this is only the initial population and we saw the S-I projection and we know that there are cases where your I goes asymptotically to 0, and even the cases where infections rise, you have a peak and then again the infections go to 0. So, therefore, limit t tends to infinity I is equal to 0.

You will not be left with any infected persons as time t tends to infinity. Why would this happen? Well this may happen because there are no susceptibles, everyone has got infected and those who have got infected, they have either been recovered or in worst case, the population has gone to extinction, everyone is dead. So therefore, eventually I will go to 0.

What about S? Is it guaranteed that every single person in the population will become infected. So therefore when you have a compartment S and from this compartment you go to I, the fate of I is that it must go to 0. But what about S? Will it always go to 0? So, limit t tends to infinity S is equal to 0, this is the question.

And we know at least by today's experience that this is, this may not be the case. It is not, there is no guarantee that every single person in the compartment S will be infected. It is a bulimics population S alright, but you still have the parameter R and therefore, R gives you, it gives you a qualitative idea of whether the fraction of, in discrete time domain, the fraction of persons would which would get infected. We will come to the discrete time model in a few moments, but that is basically what the significance of R is.

So, therefore, we would like to know the total population which would get infected or in other words, the population which would not get infected, which would remain susceptible, but which have not got the infection. And that can be established by the fact that S_∞, S at infinity plus, R_∞, total recovered population is equal to N.

$S_\infty + R_\infty = N$, or in other words $S_\infty = N - R_\infty$. So, therefore, if you know R_∞, then you can simply subtract R_∞ from N and that will give you the population S_∞, which means the susceptible population at infinity. In other words, this is the population which has not contracted the disease.

And this can be obtained by this equation, N = S - N = S + I + R which means R = N - S - I from where I can write dR/dt is equal to, sorry let me do one small change. I can write this as I and this as R. So, this is I. This is R. So, dR/dt = aN - S - R.

So, now you have an equation which is in front of you, and now you would need to solve this equation. So, if you know the time evolution of S, you can know, you can substitute that here. You can solve for R, and from here you can solve for R_∞ from where you can get $S_\infty = N - R_\infty$. This is one of the approaches to determine this.

Now, we have been following all of these methods in which you try to solve the equations analytically, turned out to be a little difficult. It was not impossible, but turned out to be a little difficult. You may want to solve this these equations numerically and that proves to be much easier task than solving them analytically.

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So, let us see what can be the strategy. I have $\frac{dS}{dt} = -rSI$, $\frac{dI}{dt} = rSI - aI$, and $\frac{dR}{dt} = aI$. So, how would I solve this numerically? Let me adopt Euler method. So, when I am solving this numerically, it is basically the algorithm is evolving the system in time. So, therefore I will have the vector S, I, R and this would be the steps in which my discretized algorithm would evolve the system, and this signifies time, n would signify the time.

So, following the Euler method what is the algorithm? I will have S at the step n + 1 is equal to S at the step n + Δt. And what is Δt, this is Δt, multiplied by the definition of the derivative which comes from the equation minus rS_nI_n. Similarly, I will have $I_{n+1} = I_{n+\Delta t}\, r\, S_n\, I_n - aI_n$.

And finally, capital $R_{n+1} = R_{n+\Delta t}\, a\, I_n$. This method will give you the evolution of the system in time, but how would you start, evolution means if you know the value at a given instant of time and discretize time like this, the method to go to the next step is in front of you. But how will you determine the first step. First step is very simple, you know S_0, you know, I_0, you know R_0.

So, therefore, if you know *R* and *a* and you have set delta t, if you know *R* and *a* and you have set delta t, then the value of S at first instant of time would be simply what S_0, which is known to you plus Δt, when you have set it minus r is known, S_0I_0. So, this is known to you. So, therefore, what will happen to S_2, you will determine S_1 and you will plug it here.

So, $S_{1 +\Delta t} - rSI_1$ and so on. So, in this way, in this manner, you can evolve your system. There is a larger theory which goes on analyzing the complexity of solutions, the error analysis convergence and so on when you adopt a numerical method like Euler technique versus an analytical method. We will not go into those details in this particular course. I encourage you to look into those aspects before you solve this problem numerically. But this is basically the algorithm.

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Now, we saw previously that one may model a problem in continuous time domain or it is possible to model it in discrete time domain and especially, for population dynamics. Now, we saw that how one particular approach may be similar or different from the other approach. The SIR model which we discussed till now was analyzed in continuous domain.

Can we do this in discrete domain as well? So, what we have here in front of us are the model equations in which you have SIR model in discrete time domain. So, what, how do you do this, you do this like this that you have, you define the population S, I and R at given instant of time.

And as I mentioned during the population dynamics in the previous lectures, it is not very difficult to see that the next population is going to be dependent upon the current population as we also find Euler technique. So, the next population is going to be the dependent on the current population.

And therefore, one of the methods can be to model the system like this that S at time t plus 1 will be equal to S at time t plus some quantity plus. Plus or minus depending upon whether the population in that particular section, that particular compartment is increasing or decreasing, but that can be taken care by the sign itself. Plus or minus some quantity. Now, that quantity should be in correspondence with the time rate of change.

And we saw in the previous case that the time rate of change is given for S as multiplication of S and I. So multiplication of S at that instant of time and multiplication of I at that instant of time. But, as we saw previously, you cannot simply take this, because there can be a fraction of the population only, which would satisfy this condition of binary fission. For example, if you remember our previous case.

So, therefore, you must multiply it with a constant. And the constant here in this case is r. So, therefore, here in this case you have minus rS_tI_t. this is the analysis, this is the model equation discrete domain. Similarly, following the same logic which we did in the previous continuous domain analysis, I can write $I_{t+1} = I_t$, the population of the current incident plus the influx contribution from the influx.

So, S_t, I_t, and the contribution from the out flux, $-aI_t$ and finally, for R_{t+1}, in an analogous manner, I can write this as R_t. So, this should be capital R, $R_t + a\,I_t$. This is the discrete time model. So, if you have again this method is very similar to the Euler's solution technique by the way, if you see there is an extra Δt.

And that delta t is now absorbed in minus r here or other constants here. So, now, if I have this model and if I try to determine the time evolution, I should in principle get the same time evolution as what you get in continuous time domain model. So, if you look at the text reference which has been given here.

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I have borrowed two results from them the figure on the left hand side gives you the evolution of S, evolution of I, evolution of R in time. And it is not very difficult to see that this continuously decreasing curve would be your S, this is your S. We saw in the previous analysis that is a peak in the number of infective, so, this is I and this is the recovered persons.

So, you will in fact have a match between what you saw in the continuous domain versus what you saw here. Similarly, we saw the SI projection, and you have the same projection here, you have the peaks. All these three cases and so, you basically see that the pandemic prevails when the infections go up, reach a maxima, have a peak and they come down.

So, now, whether you do this analysis in discrete time domain or continuous time domain, the characteristic remain unchanged, what you will basically see is that there is a infection rate, there is a removal rate, there is an initial population and depending upon these values, you can expect that if you introduce certain members which are infected, whether the pandemic would increase with time or decrease with, whether the pandemic would occur or not, or the infections will simply die down with time.

And what also we saw very interestingly is that it is possible to make predictions about the epidemic or pandemic, I am using epidemic and pandemic interchangeably because in today's scenario, the way we have interactions in different geographical locations in the world, every epidemic is very likely to be converted to a pandemic.

So, now, we can say that, we can simply use just the term pandemic. So, we also saw that it is possible to make predictions about the evolution of the pandemic during the beginning of the pandemic itself, by knowing the principles of dynamical systems. And we are also seeing we are also witnessing that there are a lot of models which have come up which make predictions about the evolution of the pandemic.

We see many of them to be really very successful. The SIR model, which we saw is the first and the very preliminary model, the models now have become much more sophisticated, but even a simple model is more or less, simple as SIR model, actually gives us a very good idea about the future projection.

Now, the last point which is worth discussing here is that what is the importance of modeling, why should we bother about modeling? Why so many groups in the world doing this modeling? And when do they fail? Why do they fail? Is there a specific physics behind them, which makes them bound to work or makes them bound to fail?

We saw that there are very simple parameters, which in the beginning itself would tell you whether the pandemic would, I mean, whether the infections would grow with time or not, but all of those dependent upon the parameters a, r and S_0. a is the removal rate, S was the infection rate.

So, during the beginning of the pandemic itself, if you have an access to good quality data, accurate data such that you will be able to make correct measurements of the removal and infection rate, then you may expect the model predictions also to be correct. Now, this is important, and that is why it is important to have the correct accurate collection of data because if your data itself is not accurate, the information that you are coming to you is not what is going on in reality in the population.

Then you would probably make a wrong prediction because the data available to you was wrong and therefore, correspondingly the parameters that you drew out of the data were wrong and obviously, the predictions would be wrong. One particular situation happens which is worth paying attention is that many times we make a projection that pandemic would happen there would be a peak, but the peak does not come.

What should we infer from this? Should it be considered as a failure or it is something else? Well, one should pay attention to the motivation behind developing these models. The motivation behind developing these models is to prepare ourselves to combat such situations. So, therefore, if one is projecting a wave, then the government as well as people have the responsibility to take actions such that the wave can be avoided.

So, therefore, if a projection is made and the wave does not come, that in fact is the success of the entire modeling business because you were doing this modeling precisely to avoid occurrence of this wave. Yes, but if you predict the wave not to occur and a wave comes, then that particular scenario is in fact the failure of modeling.

And the failure of modeling may not necessarily because of the failure of the modeling procedure but there can be several processes, several reasons report responsible behind that. The reasons may be physical that the model assumptions are not correct, the modeling process is not correct. The mathematical procedure is not correct. One of the reasons can as well be the inaccurate availability of data.

But in any case, a knowledge of dynamical system can actually help us bring about these wonderful results, which can help us and the society cope up with future evolution of the pandemic. We will take another example of physical systems in the next lecture. Till then, goodbye.