



**Ahmedabad
University**

**School of Engineering and Applied Science (SEAS), Ahmedabad
University**

**B.Tech(CSE) Semester IV: Probability and Stochastic Processes
(MAT 277)**

Group No: 13

Group Members

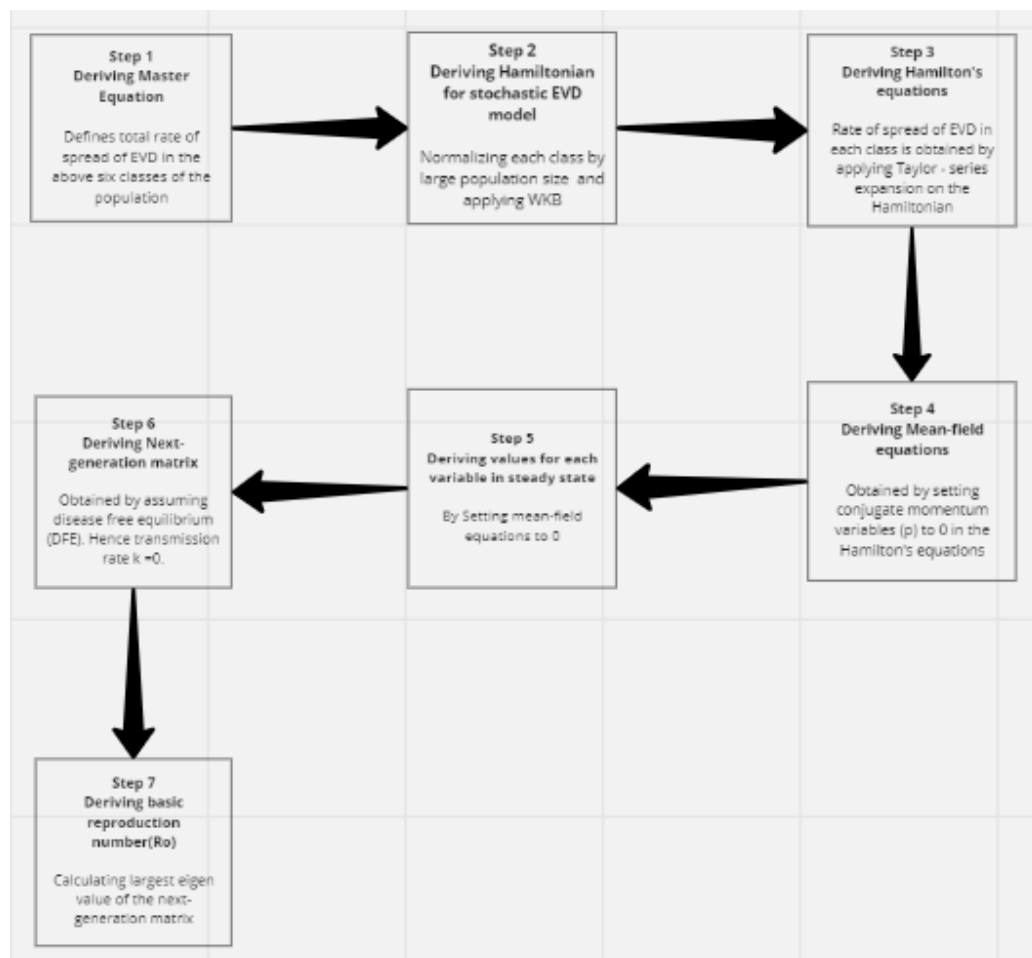
Name	Enrolment Number	Program
Shrey Patel	AU1940110	BTech in CSE
Shubham Patel	AU1940155	BTech in CSE
Vraj Kavathiya	AU1940129	BTech in CSE
Mithil Parmar	AU1940183	BTech in CSE
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Project Title:

EBOLA VIRUS STOCHASTIC MODEL

Justify how probabilistic model/PSP concept is used in your project. How uncertainty is modelled?

Total Population in this outbreak of Ebola virus here has been divided into 6 different populations classes called S(Susceptible), E(Exposed), I(Infected), R(Recovered), H(Hospitalized) and D(Deceased) and amount of population keeps flowing through these classes due to uncertain random events like getting infected from Ebola, death from Ebola, natural death, healthy birth etc. There transitions are called random events which have some certain transition rates which are used to find the total probability of that transition using total probability theorem. The model captures movement between the classes as stochastic transitions that occur at specified transition rates. Each of these transitions represents a random event that can occur in a population. If the transitions between states are short and uncorrelated then we assume the population is well mixed, the system is a Markov process and the evolution of the probability is described by a master equation. We have used the iterative action minimizing method (IAMM) to find 1500 points approximating the 12-dimensional optimal path of the stochastic EVD model, with a maximum error of 2.4487×10^{-10} using Gillespie type algorithm. We have used Monte Carlo methods for producing the possible disease trajectory which is represented by individual stochastic realizations. Below is the stochastic block diagram that has been followed:



Clearly enlist the new things done in the coding part, excluding the shared code. [If no new code is written/added/modified, then please write NA]

New Code-1 (PSP_Project/Innovation/ ExtinctionTime_EVD_COVID

/ExtinctionTime_EVD_COVID.m): Using the Gillespie type algorithm, we had generated the data for population in S(Susceptible), E(Exposed), I(Infected), R(Recovered), H(Hospitalized), and D(Deceased) classes for 1000 days for Covid and Ebola. The results for the same can be found in PSP_Project/Innovation/ ExtinctionTime_EVD_COVID/ExtinctionTime_EVD_COVID.pdf.

New Code-2 (PSP_Project/Innovation/Comparison_EVD_COVID.m): We had written code that plots the generated data and shows the extinction time of disease (infected individuals = 0) in terms of optimal path points and the number of infected individuals. From this, we can compare the real-time effect of Covid and Ebola on the infected individuals. We had also written code for comparing the rate of change in the S(Susceptible), E(Exposed), I(Infected), R(Recovered), H(Hospitalized), and D(Deceased) classes for Ebola and Covid on the optimal path to extinction with zero reservoir transmission. This will help us model the behaviour of the disease on the optimal path to extinction. The results for the same can be found running PSP_Project/Innovation/Comparison_EVD_COVID.m file.

New Code-3 (PSP_Project/Innovation/Vaccination_COVID.m): Also, we had written code to compare the effect of different vaccination rates for Covid on susceptible populations. This would allow the decision-makers and policymakers to appropriately act during the pandemic. The results for the same can be found in PSP_Project/Innovation/Vaccination_COVID.pdf.

Also, we had reproduced the figures of the article which can be found in the folder PSP_Project/EVD_Extinction and PSP_Project/Ebola.

We had generated the figures for Covid disease which can be found in the folder PSP_Project/COVID_Extinction and PSP_Project/Covid. (The parameter values for the Covid are taken from [1] in the references).

Contribution of team members:

TECHNICAL:

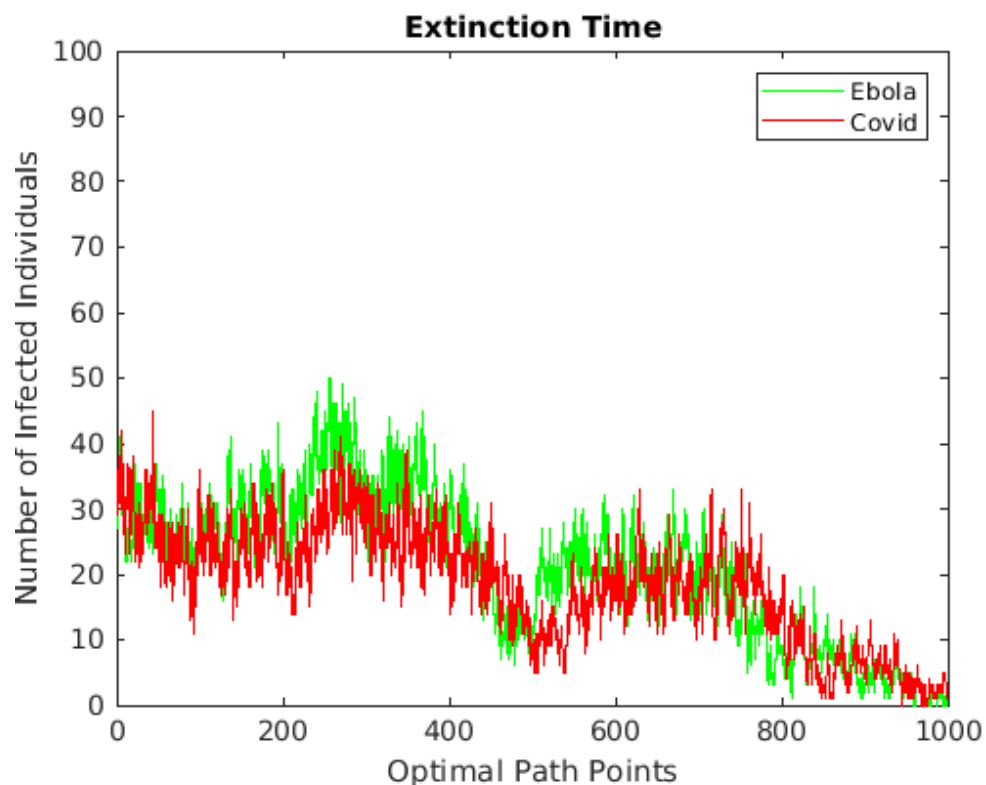
Tasks	Shrey	Shubham	Vraj	Dhruv	Mithil
Task1	Debugging errors and helped Shubham to solve them	Reproduced graphs and plots of the article	Helped Shubham in Reproduction of graphs and plots of the article	Searched for articles regarding innovation and existing code.	Helped in finding parameters of coding.
Task2	Helped in coding of Innovation	Brought a innovative idea and has done coding for it	Generated optimal path for trajectory	-	-

NON-TECHNICAL:

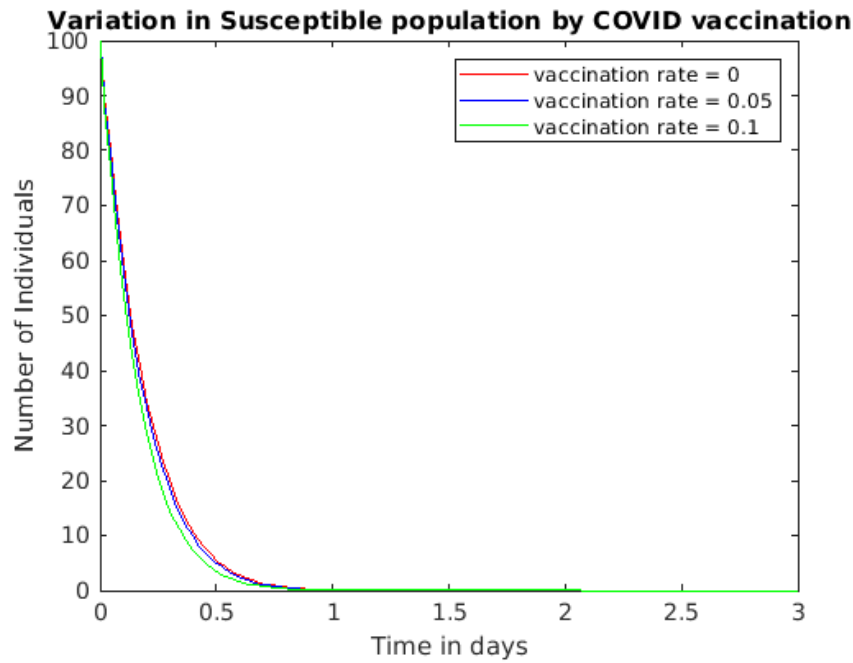
Tasks	Shrey	Shubham	Vraj	Dhruv	Mithil
Task1	Worked on Miro Board	Worked on Miro Board	Worked on Miro Board	Worked on Miro Board	Worked on Miro Board
Task2	Done modelling of SEIR model	Done modelling of SEIR model	Done modelling of SEIR model	Done modelling of SEIR model	Done modelling of SEIR model
Task3	Made the Final Report with all references and given template	Has written coding part(2 nd point) in final report	Helped Shrey in final report	Helped Shrey in final Report	Helped Shrey in making report

Any innovation done considering the society/neighbourhood problem?

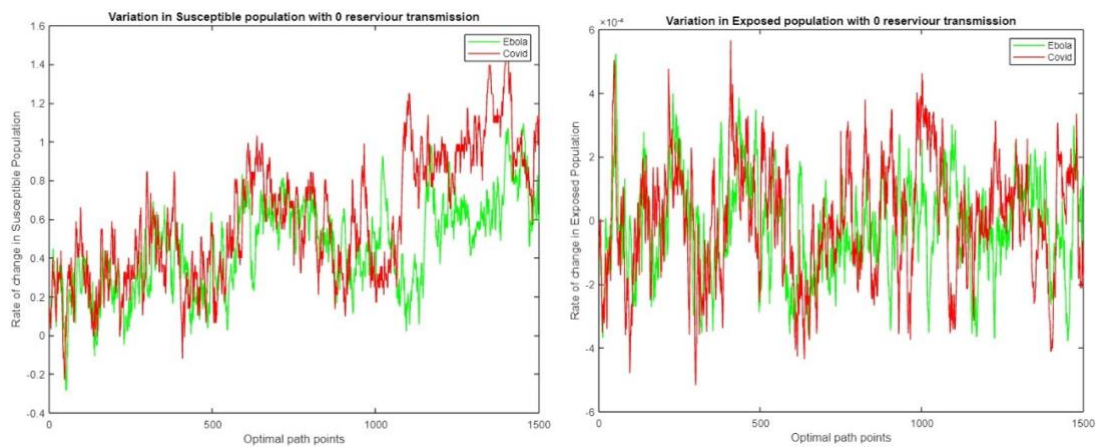
Using the Iterative action minimizing method(IAMM) algorithm (provided in the text) for finding the optimal points for the extinction we had generated the data for the six population classes S, E, I, D, H, R for both Ebola and Covid taking the population size of 5,00,000. We have compared the number of infected individuals on the optimal path to extinction for Ebola and Covid. (The parameter values for the Covid are taken from [1] in the references). This can help policymakers to model the behaviour of the disease during the optimal path and get an estimate for the highest number of infected individuals any disease can take and also the number of days it takes to eradicate the disease. Below figure shows the result for the same.

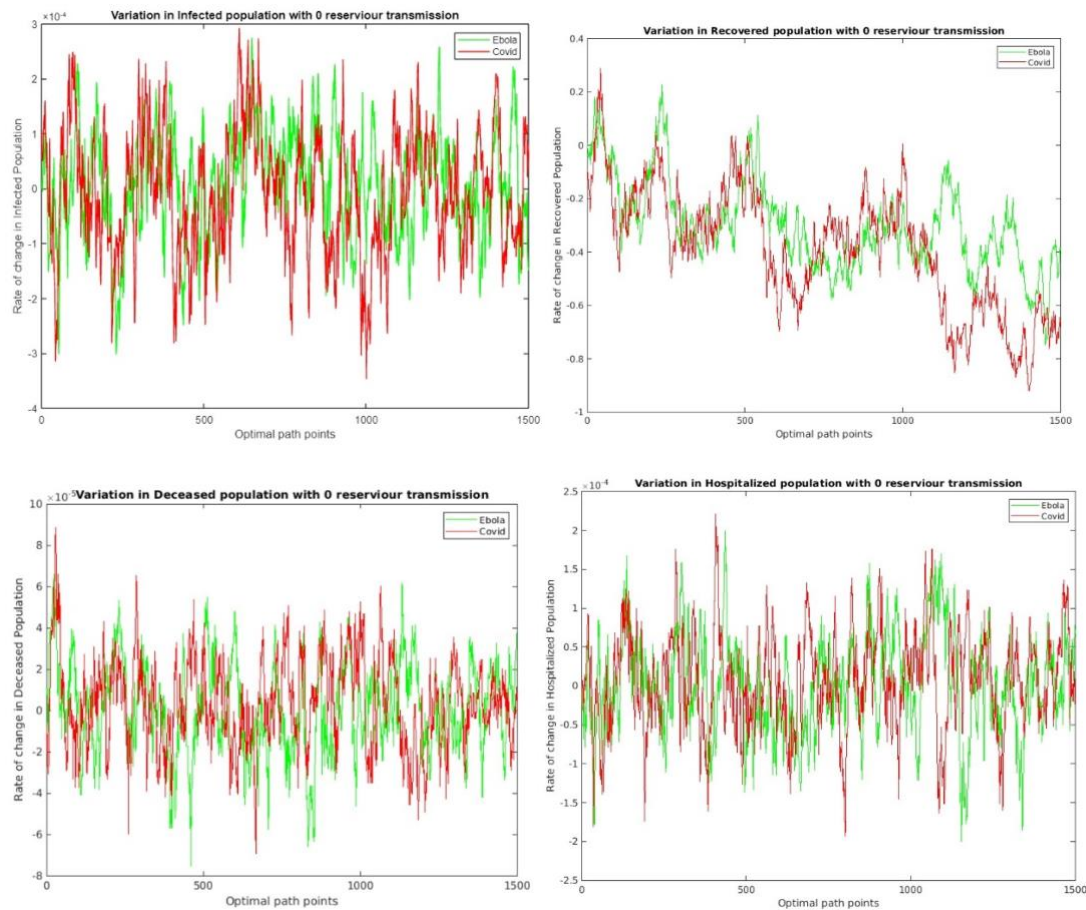


Then secondly assuming the susceptible population size of 100, and we had tried to compare the change in the Susceptible population under the Covid disease and for different rate of vaccination. (The parameter values for the Covid are taken from [1] in the references). This can help decision makers to make appropriate decision for controlling the disease and act appropriately. Below figure shows the result for the same.



Then we had compared the behaviour of Ebola and Covid on optimal path to extinction on the six population classes namely S, E, I, D, H, R. This can help to get a bird view of change in the respective population classes for respective disease. Which intuitively can help to predict the time it takes for the disease to completely eradicate. Below figure shows the result for the same.





Enumerate the inferences derived from user-centric perspective.

The best way to prevent and slow down transmission is to be well informed about the virus. A stochastic discrete-time susceptible-exposed-infectious-recovered (SEIR) model for infectious diseases like Ebola is developed with the aim of estimating parameters from daily incidence. This stochastic model simulation helps us to understand the extinction and invasion states of disease using the transition states and probabilistic calculations. In order to capture the stochastic nature of the transitions between the compartmental populations in such a model Gillespie algorithm is used. binomial distributions. If we manipulate transition events, rates and population classes by taking precautions and measures, then we can take control over extinction and invasion of the virus. The SEIR Model of Ebola virus is used to show analysis of transition states between population classes (S,E,I,R,H,D) out of total population.

Also, it can be derived from the parameters for Ebola and Covid the contact rate for infectious population, deceased population, hospitalized population, and the death rate for Covid is high compared to Ebola, the rate change in infected population is high which can be inferred from Fig. 3 (Infected). Also, as per the parameters, the recovery rate for the Covid is high compared to Ebola hence the rate of change in the recovered population for Covid is high compared to Ebola which can be verified from Fig. 3 (Recovered). Applying the equations derived in the text; **we obtained basic reproduction number for Ebola as 1.8406 and for Covid as 2.1951. So it is inferred that the reproduction rate of Covid is greater than Ebola which can be verified by the infectious rate parameter of Covid being high than Ebola.**

Often, decision makers need to know the effects of potential public policy decisions in a very short time window using limited resources this SEIR model plots help them to take decisions. We believe that this model can provide valuable insights for public health authorities who are able to predict the spread and analyse factors to give control measures and guide the government on what actions to take in public sector. Vaccination strategies can be planned looking at the stochastic model data and this model also can be helpful in future pandemic conditions as an example that has used or supported targeted vaccination of population subgroups.

BIBLIOGRAPHY:

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