**Infectious Disease Modeling in the Time of COVID**

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**Presenters:**

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**Learning objectives:**

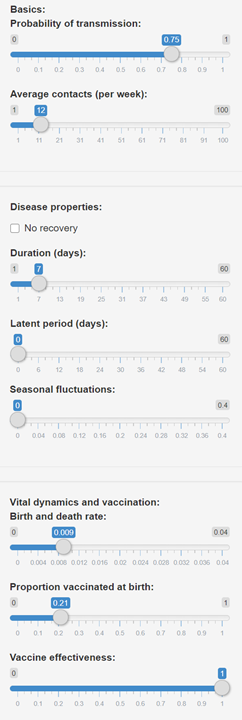
* Understand the concepts of mathematical modelling of infectious diseases, including importance and source of parameters
* Utilize epidemiological data to inform infectious disease modeling parameters
* Understand how dynamics of COVID-19 in the US relate to the biological and behavioral processes that spread the virus

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| **Recap of Prof. Buckee’s Presentation: Compartmental models in epidemiology**  S-I-R models are compartmental models used to define simplified infectious disease dynamics. In these models, the population is divided between **S**usceptibles, **I**nfected, and **R**ecovered, and transition from one compartment to the other based on parameters which define the transmission dynamics. There are many variations of this model. One variation of the compartment model we will discuss in the exercise is the S-E-I-R model, where a susceptible individual is assumed to be infected but not yet infectious for some time (***E****xposed),* before becoming infectious*.* This period between exposed and infectious is called the **latent period**.  Summary of the compartments:  **S**: Number of **S**usceptible individuals. If in contact with an infectious person, a susceptible becomes either *exposed* or *infected* depending on the model, and transitions into the corresponding compartment.  **E**: Number of **E**xposed individuals. Exposed individuals have been infected but are not yet infectious. Once infectious, they transition into the *Infectious* compartment.  **I**: Number of **I**nfectious individuals. Infectious individuals can infect the susceptible population.  **R**: Number of **R**ecovered individuals. These individuals have recovered from the infection, and cannot be infected again (they are immune). |

**Note:** The resource shared in today’s activity has many parameters and much more information than we will be able to address with you in the short time we have. Questions in *italics* will not be covered today, but have been included in case you would like to further your understanding and learn more.

Use the SIR module developed by Mathew Kiang, available at<https://mkiang.shinyapps.io/DiseaseDynamics/> to model infectious diseases.

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| ***Basics***   * **Probability of transmission:** the probability that an infectious person will infect a susceptible person at any one contact. * **Average contacts (per week):** the number of people an infected person will run into.   ***Disease properties***   * **No recovery:** when checked, if somebody becomes infected, they will be infectious forever—never recovering. * **Duration (days):** how long an infected person remains infected. This determines 1) how many days a person can infect susceptible hosts and 2) how long it takes before recovering. * **Latent period (days):** the time between being infected and being infectious (at which point they are neither susceptible nor infected, but are “exposed”). * **Seasonal fluctuations:** a function that emulates seasonal fluctuations in contact rates.   ***Vital dynamics and vaccination***   * **Birth and death rate:** in this model, kept equal to each other at 0. Adjusting it will make below options appear * **Proportion vaccinated at birth**: assumes vaccination occurs immediately at birth (therefore, this is the proportion of new births who never enter a susceptible stage). * **Vaccine effectiveness:** probability of a vaccine actually working. |

The parameters on the page are described below—note that certain parameters are only shown when they are applicable (Eg. “Proportion vaccinated at birth” will only be shown if the “Birth and death rate” are adjusted to over 0).

*Copied from:* [*https://mathewkiang.com/2013/12/20/shiny-desolve-interactive-ode-models/*](https://mathewkiang.com/2013/12/20/shiny-desolve-interactive-ode-models/)

When in breakout rooms, pick one person to share their screen and manipulate the website parameters. Other group members will read the instructions and provide guidance. You have 15 minutes to explore **Part I A and B** in your breakout room. Please be mindful of the time. **After Part I A and B, we will return to the main room for discussion before proceeding to Part II. Select a group representative to share your results.**

**Part I - A Understanding the general behavior of the model:**

1. Start the activity without adjusting any of the parameters. This is a S*usceptible-Infected-Recovered (S-I-R)* model, where infected people recover after some time and become immune.
   1. What is the impact of the probability of transmission on the disease dynamics outcome?
   2. What is the impact of the average number of contacts on the disease dynamics outcome?
   3. What is the impact of the duration of the infection on the disease dynamics outcome?
2. ***Go to Part I - B on the next page first. If time allows, feel free to come back and dig deeper with these additional models:***
3. *What changes when assuming no recovery? Check the “No recovery” box in the Disease Properties section. This is a Susceptible-Infected (SI) model.*
4. *What changes by adding a Latent period? (Make sure “No recovery” is unchecked). This is a Susceptible-Exposed-Infected-Recovered (S-E-I-R) model, with the* ***E****xposed population defined as the fraction of people who got infected, but are not yet infectious.*

**Part I - B Example with specific disease parameters:**

1. Simulate two disease-like outbreaks. What parameters do you have to change? Describe the impact of changing each of these parameters on the outbreak trajectory.

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|  | Probability of transmission | Duration | Latent period |
| Influenza | 0.18 | 3 | 2 |
| COVID-19 | 0.5 | 14 | 2 |

1. One measure taken during the Covid-19 pandemic is physical distancing, or lockdown, both of which aim to reduce the average number of contacts. Let’s take the COVID-19-like parameters, and change the average contact rate to lower or higher values. What happens if you change the average contacts?
2. ***If time allows, feel free to consider this case study on measles:***

*In the case of measles, an effective prevention measure is vaccination of young children. Let’s take the measles-like parameters and an average contact rate of 25, and look at the effect of vaccination. Set the Birth and death rate to 0.013. Adding birth and death rates result in a dynamic population, with newborns entering the population as Susceptibles. The proportion of vaccinated children then determines how many of the newborns are immunized and thus protected, or remain susceptible to the infection. Change the Time scale to Years and increase the Time max to 100. Check both boxes in the Plot settings to show the infectious curve only, and the infections past initial outbreak.You will see that without any vaccination (Proportion vaccinated at birth = 0) over the years there are recurrent outbreaks and the population is never disease-free (ie the curve for the infected population never reaches 0). Given the parameters we defined in this model, can you tell what should be the minimum proportion of vaccinated children at birth to avoid any future outbreaks after the initial peak?*

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|  | Probability of transmission | Duration | Latent period |
| Measles | 0.9 | 7 | 7 |

**After Part I A and B, we will return to the main room for discussion before proceeding to Part II. Select a group representative to share your results.**

When in breakout rooms, pick one person to share their screen and generate the graphs. You have 10 minutes to explore **Part II A and B** in your breakout room. Please be mindful of the time. **After Part II A and B, we will return to the main room for discussion. Select a group representative to share your results.**

**Part II - A Graphing real COVID-19 data**

Download files for Part II from the Life Sciences Outreach Program website at <https://lifesciencesoutreach.fas.harvard.edu/lecture-1-100820>

COVID-19 cases and deaths data in files:

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| [covid19-statistics\_MAcounties.xlsx](https://lifesciencesoutreach.fas.harvard.edu/files/lifesciencesoutreach/files/covid19-statistics_macounties.xlsx) | Massachusetts counties[[1]](#footnote-1) |
| [covid19-statistics\_USstates.xlsx](http://covid19-statistics_usstates.xlsx) | US states and territories1 |
| [covid19-statistics\_USA.xlsx](https://lifesciencesoutreach.fas.harvard.edu/files/lifesciencesoutreach/files/covid19-statistics_usa.xlsx) | US as a whole1 |
| [covid19-statistics\_China.xlsx](https://lifesciencesoutreach.fas.harvard.edu/files/lifesciencesoutreach/files/covid19-statistics_china.xlsx) | China[[2]](#footnote-2) |
| [covid19-statistics\_Italy.xlsx](https://lifesciencesoutreach.fas.harvard.edu/files/lifesciencesoutreach/files/covid19-statistics_italy.xlsx) | Italy2 |
| [covid19-statistics\_Southkorea.xlsx](https://lifesciencesoutreach.fas.harvard.edu/files/lifesciencesoutreach/files/covid19-statistics_southkorea.xlsx) | South Korea2 |

Feel free to graph the variables in whatever way is most convenient for you. If you would like graphing assistance, we have provided instructions:

* How to make graphs using [Microsoft Excel](https://docs.google.com/document/d/1N8Uwt9rJnPjlNzK8rHXmvdwjiRc-ITn_wK_04smK7S8/edit?usp=sharing)
* How to make graphs using [Google Sheets](https://docs.google.com/document/d/1JVUow9nFtyvoqpvFBIkFUa61SjO9Agg98EmkwCvgtFQ/edit?usp=sharing)

You may take screenshots of the graphs to share and paste in your worksheet below.

Plot COVID-19 new cases, cumulative cases, and deaths counts on three separate graphs for two geographic regions as follows:

**Breakout room 1:** Norfolk county and Suffolk county

**Breakout room 2:** Massachusetts and Florida

**Breakout room 3:** USA and China

**Breakout room 4:** USA and Italy

**Breakout room 5:** USA and South Korea

**Breakout room 6:** Massachusetts and USA

1. Norfolk county
2. Suffolk county
3. Massachusetts
4. Florida
5. USA
6. China
7. Italy
8. South Korea

**Part II - B Analyzing the differences between models and real data**

1. Why does the “real world” data look different to the SIR models? In addition to the uncertainties around parameter values, what factors can influence the dynamics, which were not accounted for in the models?
2. What do you think are the reasons for the observed decrease in the COVID-19 case counts?
3. Discuss how changing the scale from national to county level, changes the disease dynamics observed.

More information on case counts and deaths in the US and by state can be found here:

<https://www.nytimes.com/interactive/2020/us/coronavirus-us-cases.html>

More information on case counts and deaths in the the world by country can be found here:

<https://qap.ecdc.europa.eu/public/extensions/COVID-19/COVID-19.html#global-overview-tab>

**Updated datasets for your classroom or personal use:**

If you are interested in downloading and reformatting publicly available COVID-19 datasets like the ones used today, utilize our tutorial:

<https://docs.google.com/document/d/1de5mFTujUf9graP3uSMYOcK8in5_1vv6WAx_mV4ZlCo/edit?usp=sharing>

Data is updated daily.

1. downloaded from https://github.com/nytimes/covid-19-data [↑](#footnote-ref-1)
2. downloaded form ECDC https://www.ecdc.europa.eu/en/publications-data/download-todays-data-geographic-distribution-covid-19-cases-worldwide [↑](#footnote-ref-2)