

Infectious Disease Modeling Lab

Developed by Dr. Casey Cazer, DVM, PhD

This lab uses Epidemix, an infectious disease modeling app developed by EPI-Interactive, City University of Hong Kong, and the Royal Veterinary College. Epidemix can be accessed at <https://epidemix.app/>. The COVID-19 model experiment is based on the [November, 2020 Epidemix webinar](#).

Part 1: COVID-19 Model

First, we will explore the COVID-19 model to understand compartmental models. Open the “Plus” version and select the disease-specific COVID-19 model on the upper left menu.

The COVID-19 model structure and parameterization is described in detail here: https://plus.epidemix.app/pdf/Epidemix_Covid-19_Model_Summary.pdf. It is an S-E-I-R compartmental model with additional compartments to track healthcare utilization.

- S: susceptible
- E: exposed (described below as latent)
- I: infected
- R: recovered

Compartmental models track units (in this case, people) as they move between different states (compartments). The basic model assumptions include that each compartment is homogenous and that recovered individuals have lifelong immunity (i.e., they cannot become susceptible again). The movement of people between compartments is described by differential equations.

Epidemix allows you to change the model structure and parameters in the left-hand menu. Make sure you click “submit” after you make changes to see the model outputs.

Model outputs can be examined in several ways. There is an epidemic curve, showing the number of people in each compartment over time. There is an incidence curve, showing the number of people moving from the latent to the infected compartments. Finally, you can examine individual timepoints in the data table.

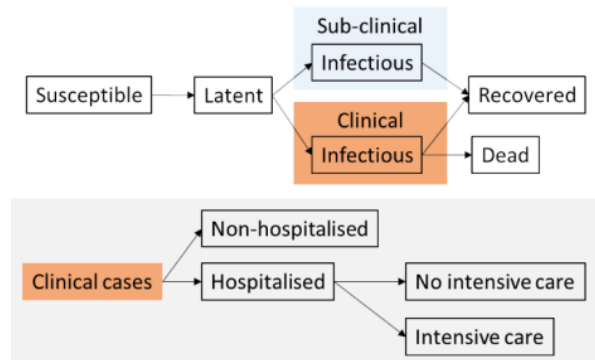
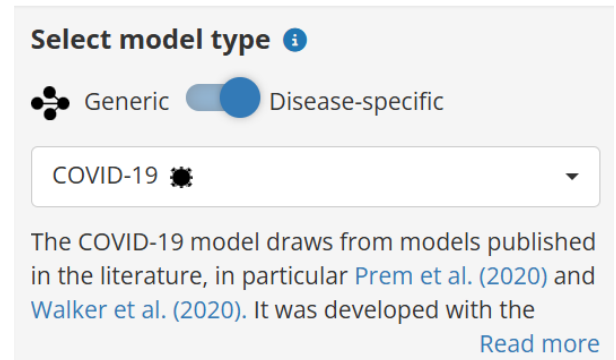


Figure: SEIR model and healthcare levels.

Experiment #1: Compartmental models typically assume that each compartment is homogenous and evenly mixed. For example, all infected individuals have the same infectiousness and all susceptible individuals have the same risk of infection. However, we know that is not the case in the real world. One type of heterogeneity is age demographics. For example, older adults are at higher risk for severe COVID-19 than young adults. In addition, contact among individuals, which is necessary for infection, likely varies by age. For example, young children in school interact more frequently with other young children than a typical adult interacts with young children.

- A) Select the United States in the “Define host population features” box. Remember to click “submit”. Explore the model results, looking at how long the epidemic lasts, how many are still susceptible when it ends, how many ICU beds are needed, and how many people die.
- B) Write a hypothesis for the impact of age-specific mixing compared to homogenous mixing on the number of susceptible and recovered individuals at the end of the epidemic.
- C) Change the model parameters to explore the effect of accounting for age demographic structure and age-specific mixing. These parameters are in the “Define host population features” box. First check yes for “age demographic structure” and then explore the model results and the Population graphs. Later check yes for “age-specific mixing”. Click “submit” after each change.
- D) What is the impact on the epidemic curve (number of susceptible, infected, recovered, and dead individuals)? Why do you think this happened?
- E) [There are approximately 80,000 ICU beds in the United States](#). What is the impact on the healthcare system (number of hospitalized and ICU beds used)?

Part II: Measles

Next, let's try building our own model.

Open the base model at <https://base.epidemix.app/>. Note that the base model does not have a "submit" button. It will update as you change the parameters.

There is currently a measles outbreak in Texas. As of [February 21, 2025](#), at least 90 people have been infected and 16 (18%) have been hospitalized. The majority of the cases are in Gaines County, which has a population of about [22,000 people](#). In Gaines County, about [82% of kindergarten children are vaccinated against measles](#).

Here is some useful information about measles.

- Measles is a highly contagious disease. [One infected person can infect between 12 to 18 other people.](#)
- Measles is transmitted via airborne transmission (aerosols and droplets in the air).
- For the purposes of this exercise, assume that there are no asymptomatic infections (in real life, asymptomatic infections are possible in previously infected individuals but rare).
- The [incubation period of measles is 8 to 12 days](#). This is the time from exposure to the measles virus to the first symptoms, which are typically fever and cough.
- The measles rash appears [3 to 5 days after the first symptoms and lasts 5 to 6 days](#).
- A person who has measles is infectious for [4 days prior to rash onset and 4 days after rash onset](#).
- In a country like the United States, where infected individuals have access to high-quality healthcare, between 1 and 3 children per 1,000 infected children will die of measles.
- The measles vaccine is very effective. For the purposes of this exercise, assume that it is 100% effective – vaccinated individuals do not get infected.
- For the purposes of this exercise, assume that individuals who are infected with measles and survive (recover), they have lifelong immunity against measles.

Experiment #2: Set up the base Deterministic Homogenous COMP (compartmental) model for Gaines County using the information above. For now, assume that the vaccination rate in Gaines County is 0 (nobody is vaccinated). You will need to calculate the latent period (the time from exposure to becoming infectious) and the number of effective contacts (when infection occurs) per person per day. Consider the number of people a person infects over the course of their infection and the duration of their infectious period.

Over a one-year period, if one person with measles enters the county, how many people are infected, how many die, what is the maximum number who would need to be hospitalized at one time, and how long does it take the epidemic to end?

Experiment #3: Add the current vaccination rate in Gaines County (82%). How does that change the epidemic?

Experiment #4: What percentage of people need to be vaccinated to prevent an epidemic?

Experiment #5: Reset your vaccination rate back to 0. Open the “Parameter Compare” tab. Use this tab to explore how variation in the number of effective contacts per day and latent period affect the results. What is the impact on the number of people infected, hospital burden, and the duration of the epidemic?

Experiment #6: Switch to the “Stochastic Homogenous COMP” model. In the stochastic compartmental model, individuals move between compartments as a random process, governed by probabilities and distributions. Set the model to run 100 simulations. Rerun Experiment #3 with the stochastic model. Use the “Investigate Variability” tab to see how randomness can influence the model results. In particular, look at variability in the “removed” group (these are people who died of infection) and the infectious symptomatic group and consider how random variation can result in wide ranges of possible outcomes in morbidity and mortality. What would you tell Gaines County public health and government leaders about what they can expect in this measles outbreak?

Experiment #7: Now integrate parameter uncertainty with random uncertainty. Rerun Experiment #5 in the stochastic model. What has a larger impact on the results of this model, parameter uncertainty or random uncertainty? Note that the parameter uncertainty tab only shows the median result for each parameter condition. You may want to change parameters in the left side bar and investigate the variability that way.

Part III: Bonus Experiment

Return to the COVID-19 model in the Plus version of Epidemix.

- A) Write a hypothesis for the difference in the epidemic curve between a country with an older population vs a younger population.
- B) Select “Uganda” with “age demographic structure” and “age-specific mixing” on in the “Define host population features” box. Click submit. Uganda has a younger population than the US (explore the Population graphs). [Uganda is estimated to have only 100 ICU beds.](#)
- C) What is the impact of a younger population on the epidemic curve and healthcare demands compared to the older US population? Why do you think this happened?