

Integrating experiments, field data, and models to understand infectious disease ecology

Research Topic Overview

In infectious disease ecology, the classical mathematical models have provided valuable insights into infectious disease spread in animal populations, but sometimes these models can not accurately represent these dynamics mathematically. Part of the reason may be that the classical mathematical models have focused on general model predictions and did not consider about mechanisms of disease transmission which mean detailed knowledge of epidemiological theory is not required to use these models. If the traditional mathematical models don't fit the data very well, we can't use these models to predict future disease spread, develop disease control strategies, and test hypotheses. Hence, we need to build new models based on assumptions, test the models by using a combination of experiments(lab, field) and observational data(lab, field), and use the best models to make forecasts. In the presentation, professor Mihaljevic gives us two examples which are Douglas-fir tussock moth nuclear polyhedrosis virus and Amphibian ranaviruses.

The traditional epidemiological model (SIR model: susceptible-infectious-removed) can be used to describe natural baculovirus epizootics, which lead to population crashes in Douglas-fir tussock moth (DFTM) populations. However, the spray works (see Figure2) in the research show that mortality in the unsprayed (control) plots the same as spray plots even though control plots had an initially undetectable level of virus infection. These findings suggest that additional considerations may be warranted in the research. Using a combination of

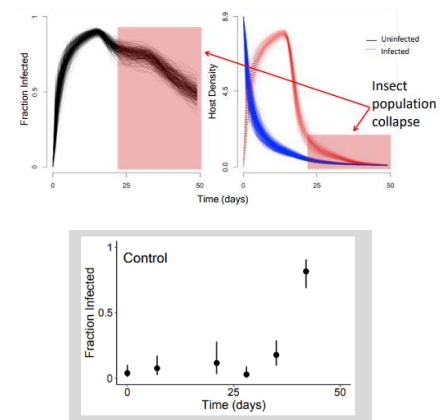


Figure2: The Spray Works

experiments, observational data, and nonlinear-fitting algorithms, we find that when host density is high, even very low initial virus densities can lead to high cumulative infection rates, which means, in some cases, baculovirus sprays may have been applied to populations that would have collapsed from natural epizootics, even without any intervention. The research illustrates that there is a new stage between S stage and I stage and shows that SEIR models can provide valuable guidance for microbial control programs (see Figure3).

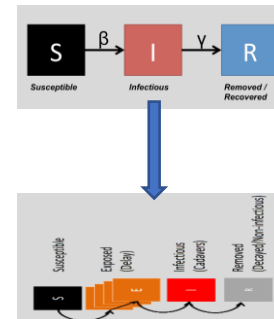


Figure3: SEIR Model

In Amphibian ranaviruses, the research uses historical data to parameterize a model of ATV transmission in Arizona tiger salamander populations. Amphibian ranaviruses grow faster at higher temperatures in cell culture, and viral shedding rate from infected animals also increases. Hence, it is necessary to analyze an effect of heat to explain data in this case. However, the historical data are insufficient to support an essential role of temperature-dependent shedding rate to explain epizootics (see Figure 5).

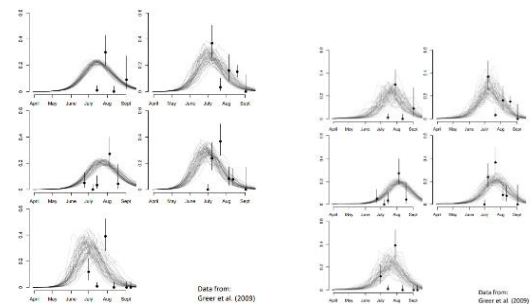


Figure5: temperature dependent model

Using the model with a temperature shedding rate, dependent the researcher fit well with the data. However, a model without this effect fits equally well, assuming a shallow initial viral concentration in the water. There are insufficient data to support a necessary role of temperature-dependent shedding rate to explain epizootics.

Research Connections

Dr. Mihaljevic's analysis and presentation are centered on the application of a complicated situation, like the traditional model do not fit data very well, or the data size is insufficient. Using an approach to uncover alternative methods to find a new model based on the traditional model will significantly enhance the capabilities of the model. Since a significant portion of my research will be focused on pair programming, understanding the interaction of the data to determine the method of pair programming could be of vital importance once movement was incorporated. More specifically, even the research filed is different, but both of us are analyzing the data and trying to find a new model based on the traditional one to fit the data which means expose the new model to make relatively minimal sacrifices for the greater good (i.e., most efficient outcome) the most useful data fitting. Expanding on the traditional model, to consider the integrity of the study (data, field, and the parameters of the research), the future, decision history, and time as factors to be seen. In essence, establishing a new model which are incentivized by using the traditional model will create a deeper, broader, and more resilient system.

Discussion

Even though I have no direct relationship to infectious disease ecology, the underlying problems in Dr. Mihaljevic's study are the same to my research.

The first problem is how could the classical mathematical models be optimized through consider more parameter in the research. In the first topic of the presentation, researchers find that additional considerations (or other settings) may be warranted in the study. Then, the professor uses a combination of experiment data, observational data, and nonlinear-fitting algorithms to conduct a new model. I don't know the exact answer about this problem. But, in my research, if the traditional model or original idea can't fit the data very well, I always go back to the experiment or algorithm to check if there is an element which could affect the research or create a new parameter which is a combination of the existed variable in the experiment.

The second problem is what combination of strategies will yield the most effective model if we can't see a classical model to be used. For instance, in amphibian ranaviruses (the second example in Dr. Mihaljevic's presentation), the research uses historical data to parameterize a model of ATV transmission in Arizona tiger salamander populations. However, the historical data are insufficient to support an essential role of temperature-dependent shedding rate to explain epizootics. In my research, if I don't have enough data, I will do more experiments to collect more data. However, sometimes, we don't have another chance to collect more data. For example, in Dr. Mihaljevic's research, professor suggests us to analyze the different parameters or conditions, such as in this example the researcher could measure the shedding rate and estimates of initial conditions (host densities and viral concentrations).

Conclusion

As discussed previously, Dr. Mihaljevic's research seeks to find a better model to fit the research data based on the classical mathematical models (if we have). As he discussed, there are some significant challenges to be addressed before this concept will become realized, and researchers can mutually benefit from being continually interconnected. Some of the obstacles are maintaining the parameter of the research and the data. The other difficulties are data size is too small to reflect the relationship between the data and conditions of the investigation.