SEIR Instructor Notes

**Epidemic Modeling:**

Biological settings are often very complicated, making it a common practice in biological modeling to use models designed for very general settings rather than for specific ones. Students of mathematical epidemiology generally study generic models, while researchers in mathematical epidemiology often create much more complicated models designed for the specific features of the target disease. This module uses the SEIR model, which is slightly more complicated than the more common SIR model, but serves as a starting point for development of a model for COVID-19.

**The Model:**

The SEIR model has four classes: Susceptible, Exposed (latent)[[1]](#footnote-1), Infectious, and Removed. It includes three processes: a transmission process changes susceptible individuals into latent ones, an incubation process changes latent individuals into infectious ones, and a removal process changes infectious individuals into individuals who can no longer infect others. As conceived, the Removed class includes deceased individuals as well as recovered ones. This is a bookkeeping device to keep the population constant when doing a short term epidemic scenario.

**The Implementation:**

The model is coded in Matlab and R. Programming is difficult for many students, but our programs are designed so that only a small number of lines need to be changed by students. One difference is in the graphing instructions. Students will need to be able to make minimal changes to run the different experiments provided as part of the model. R does not have sophisticated built-in routines for determining axis limits, legend locations, and the like. It may be necessary to modify some of the plot commands to improve the appearance of the graphs. Most of the work for students is in interpreting the results of the experiments.

**Using Models:**

To paraphrase a quotation from Albert Einstein: “Nobody believes a model except the person who created it; everybody believes data except the person who collected it.” In reality, both are very useful, but must be used cautiously.

Models are not a mathematical expression of reality. They are a mathematical representation of a caricature of reality. They are based on assumptions that are taken from general principles we believe apply to the given setting. Features of the real-world setting can be oversimplified or neglected altogether. The SEIR model makes some simplifying assumptions that sacrifice a small amount of realism for the purpose of helping scientists describe and explain the phenomena they see in real disease scenarios.

Data comes from measurements, which can be very accurate in physics and astronomy but are often inaccurate in medicine and biology. Even things that are seemingly easy to measure, like the fraction of hospitalized patients who die of a particular disease, can be difficult to determine accurately. For this reason, we cannot use the SEIR model to obtain accurate quantitative predictions of a real disease scenario, such as the COVID-19 pandemic. Important properties are only known approximately for even the most studied diseases, such as smallpox.

These cautions do not mean that models are useless. The SEIR model makes many qualitative predictions that have been borne out in studies of many actual diseases. Those who study it gain a significant level of intuition about the population dynamics of infectious disease—intuition that can help us make sense of competing claims we hear from different news sources.

**Calculation of *k*:**

The parameter *k* is the ratio of the initial size of class E to the initial size of class I. This quantity is defined by three assumptions about the early phase, right before the scenarios start: (1) E and I are growing at the same rate (if , then also We also assume and that there is no isolation of infectives. With these assumptions, the change in *E* is

Similarly, the change in *I* is

Subtracting *k* times the second equation from the first equation eliminates and leaves *I* as a non-zero common factor that can be removed. Rearranging yields the quadratic equation

This equation has one positive root, which is given in the document ‘P2-2 SEIR Student Notes’.

**Using the P2 Module:**

This module gives instructors a box of tools to use in guiding their students to explore the behavior of epidemic diseases. It includes an introductory Powerpoint presentation (P2-1), a student notes document (P2-2), a suite of 4 programs (P2-3), a set of instructions for using the programs (P2-4), and a document with questions for students to address using the completed spreadsheet and targeted modifications (P2-5). An answer key (P2-6) is available on request (write Glenn Ledder at gledder.unl.edu). Feel free to write to Professor Ledder with any questions, comments, or recommendations.

1. “Exposed” is a misleading term, since it actually refers to individuals who have already caught the disease but are not yet contagious. “Latent” is a more accurate term. [↑](#footnote-ref-1)