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1.1 Preamble

The use of mathematical models to understand infectious disease dynamics has a very rich history in epidemiology. Kermack and McKendrick (1927) is the seminal paper that introduced the equations for the general Susceptible-Infected-Recovered model and showed how a set of restrictive assumptions lead to the standard SIR model of ordinary differential equations. During the 1930s and early 1940s stochastic theories of disease dynamics were developed by Bailey (1937) and Bartlett (1940). Bartlett (1955, 1960a) further pioneered the use of Monte Carlo simulations of epidemics with the aid of “electronic computers” (as opposed to regular human computers), while Muench (1959) proposed the “mass mix” framework for understanding age-incidence patterns. The decades to follow saw broad expansions of theories as well as a surge in real-life application of mathematics to diagnosis and control of infectious disease.

There are several excellent textbooks of mathematical epidemiology including Anderson and May (1991) and Keeling and Rohani (2008). The purpose of the current text is not to duplicate these efforts but rather use these frameworks as a starting point to discuss practical implementation and analysis. The discussion will be centered around a somewhat incoherent collection of case studies selected to explore various conceptual, mathematical, and statistical issues. The text is designed to be more of a “primer in infectious disease dynamics.”

The dynamics of infectious disease show a wide diversity of patterns. Some have locally persistent chains-of-transmission, others persist spatially in “contingent-reserve metapopulations.” Some infections are prevalent among the young, some among the old, and some are age-neutral. Typically, some diseases have little

¹ Though as reviewed by Olfelt and Henshaw (1942), the original equations leading to the Kermack model was proposed by Daniel Bernoulli in the late eighteenth century.