

DISCRETE EPIDEMIC MODELS

FRED BRAUER^{a,b}, ZHILAN FENG^{a,c} and CARLOS CASTILLO-CHAVEZ^{a,d,e,f}

^a Mathematical, Computational Modeling Sciences Center
PO Box 871904, Arizona State University, Tempe, AZ 85287, USA

^b Department of Mathematics, University of British Columbia
Vancouver, BC V6T 1Z4, Canada

^c Department of Mathematics, Purdue University
Lafayette, IN 47907, USA

^d School of Human Evolution and Social Changes
Arizona State University, Tempe, 85287, USA

^e School of Mathematics & Statistics
Arizona State University, Tempe, 85287, USA

^f Santa Fe Institute, 1399 Hyde Park Road
Santa Fe, NM 87501, USA

Dedicated to Horst R. Thieme on the Occasion of his 60th Birthday

ABSTRACT. The mathematical theory of single outbreak epidemic models really began with the work of Kermack and Mackendrick about 8 decades ago. This gave a simple answer to the long-standing question of why epidemics would appear suddenly and then disappear just as suddenly without having infected an entire population. Therefore it seemed natural to expect that theoreticians would immediately proceed to expand this mathematical framework both because the need to handle recurrent single infectious disease outbreaks has always been a priority for public health officials and because theoreticians often try to push the limits of existing theories. However, the expansion of the theory via the inclusion of refined epidemiological classifications or through the incorporation of categories that are essential for the evaluation of intervention strategies, in the context of ongoing epidemic outbreaks, did not materialize. It was the global threat posed by SARS in 2003 that caused theoreticians to expand the Kermack-McKendrick single-outbreak framework. Most recently, efforts to connect theoretical work to data have exploded as attempts to deal with the threat of emergent and re-emergent diseases including the most recent H1N1 influenza pandemic, have marched to the forefront of our global priorities. Since data are collected and/or reported over discrete units of time, developing single outbreak models that fit collected data naturally is relevant. In this note, we introduce a discrete-epidemic framework and highlight, through our analyses, the similarities between single-outbreak comparable classical continuous-time epidemic models and the discrete-time models introduced in this note. The emphasis is on comparisons driven by expressions for the final epidemic size.

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