

Preface

The intent of this monograph is to introduce graduate students to branching process applications of populations and epidemics. Deterministic models of populations and epidemics are well known in the scientific literature and they provide useful information on the dynamics when population and epidemic sizes are large. However, when sizes are not large, stochastic models and theory are required, for example, to estimate the probability of extinction. The stochastic theory of branching processes has a long history and can be used as a tool in understanding extinction in many situations. In the mid 19th century, Galton and Watson introduced branching processes to explain the extinction of family names. Whittle applied the theory in 1955 to an SIR epidemic to estimate the probability of a major outbreak. In this brief monograph, a summary is presented of single-type and multi-type branching process theory. This theory is used to estimate the probability of ultimate extinction in some classic population and epidemic models such as SEIR epidemic and logistic growth, and some new applications of species invasions and spatial spread of disease. Some MatLaB programs of stochastic simulations are provided in the Appendix, and some references are given to additional applications of branching processes to populations and epidemics.

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