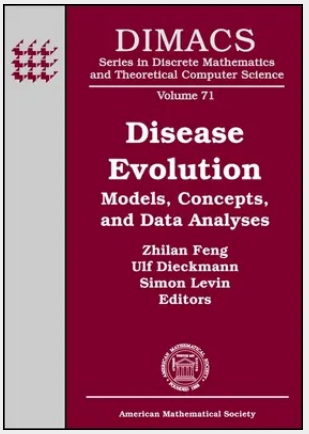
Feng / Dieckmann / Levin

# Disease Evolution

Infectious diseases are continuing to threaten humankind. While some diseases have been controlled, new diseases are constantly appearing. Others are now reappearing in forms that are resistant to drug treatments. A capacity for continual re-adaptation furnishes pathogens with the power to escape our control efforts through evolution. This makes it imperative to understand the complex selection pressures that are shaping and reshaping diseases. Modern models of evolutionary epidemiology provide powerful tools for creating, expressing, and testing such understanding. Bringing together international leaders in the field, this volume offers a panoramic tour of topical developments in understanding the mechanisms of disease evolution. The volume's first part elucidates the general concepts underlying models of disease evolution. Methodological challenges addressed include those posed by spatial structure, stochastic dynamics, disease phases and classes, single- and multi-drug resistance, the heterogeneity of host populations and tissues, and the intricate coupling of disease evolution with between-host and within-host dynamics. The book's second part shows how these methods are utilized for investigating the dynamics and evolution of specific diseases, including HIV/AIDS, tuberculosis, SARS, malaria, and human rhinovirus infections. This volume is particularly suited for introducing young scientists and established researchers with backgrounds in mathematics, computer science, or biology to the current techniques and challenges of mathematical evolutionary epidemiology.




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