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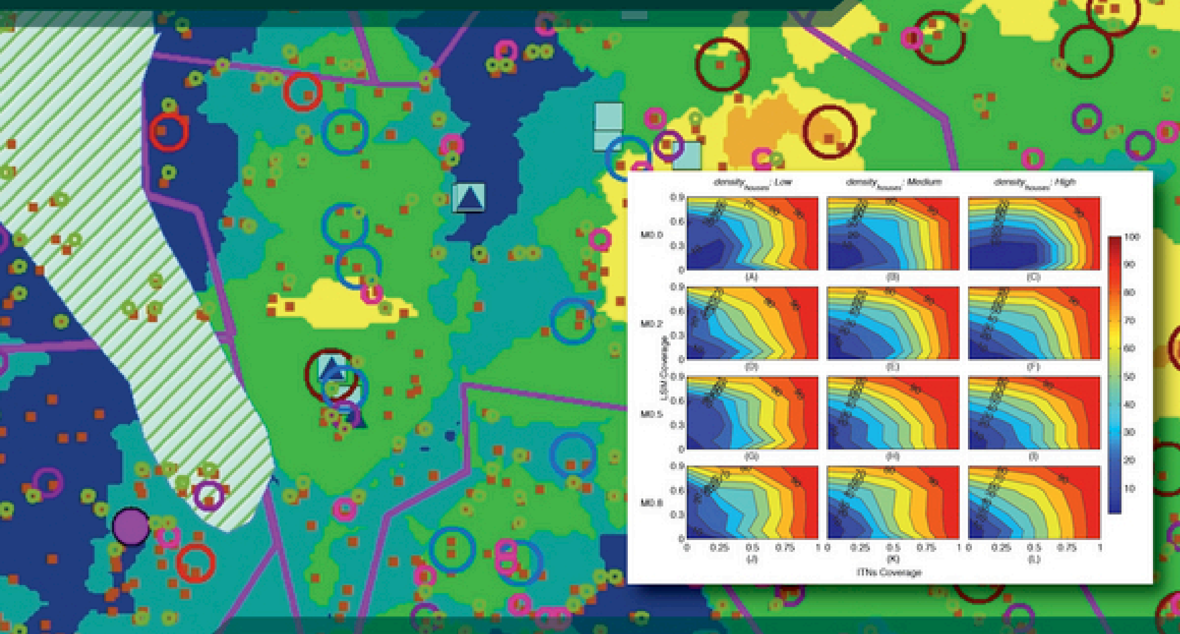

Spatial Agent-Based Simulation Modeling in Public Health

Design, Implementation, and Applications for Malaria Epidemiology

S. M. Niaz Arifin, Gregory R. Madey, and Frank H. Collins

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SPATIAL AGENT-BASED SIMULATION MODELING IN PUBLIC HEALTH

Wiley Series in Modeling and Simulation

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Design, Implementation, and Applications for Malaria Epidemiology

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To my parents:

Engineer S. M. Golam Mostofa

B.Sc. Engg. (Civil), FIE (B), PGD (CS)
My Father and Guide

Professor Parvin Akhter Jahan

M.A. (Economics), B.A. (Honors)
My Mother and Best Friend

and my wife:
Rumana Reaz Arifin

B.S., M.S.
My Soulmate

and my sister:
Mafruhatul Jannat

Ph.D., M.S., B.S.
We Grew up Together

— S. M. Niaz Arifin

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PREFACE

In today's scientifi world, *computational science* is considered the *third pillar* of scientifi inquiry, along with the two traditional pillars of theory and experimentation. Although science is still carried out as an ongoing interplay between theory and experimentation, the increased scale and complexity of both have compelled computational science to be an integral aspect of almost every type of scientifi research.

Typically, computational science uses computer simulations (to construct computational models) and quantitative analysis techniques in order to analyze and solve scientifi problems. In particular, *modeling & simulation* (*M&S*) techniques are being increasingly used to model complex systems, which in general exhibit complex properties such as heterogeneity, dynamic interactions, emergence, learning, and adaptation. With the ever-widening availability of computing resources, the increasing pool of human computational experts and due to its unconstrained applicability across academic discipline boundaries, the importance of M&S continues to grow at a remarkable rate.

Agent-based modeling and simulation (*ABMS*) is a class of M&S techniques for simulating the actions and interactions of autonomous agents with a view to assessing their effects on the simulated system as a whole. Having its roots from the investigation of complex systems, complex adaptive systems, artificia intelligence, and computer science, ABMS combines elements of game theory, complex systems, emergence, computational sociology, multiagent systems, and evolutionary programming. The suite of models developed using ABMS, known as *agent-based models* (*ABMs*), have applications in diverse real-world problems and have become increasingly popular as a modeling approach in almost all branches of science and engineering.

In public health research, epidemics and infectious disease dynamics modeling can be termed as a *signature success* of ABMS. Uses of M&S in public health include synthesizing knowledge from disparate disciplines, fillin the gaps in existing knowledge, conducting cost-benefi trade-off studies, and generating hypotheses. As such, an increasing number of U.S. universities are incorporating systems science and M&S into their curricula and research programs through the schools of public health and other health-related academic departments.

A major objective of this book is to present a practical and useful introduction to the important facets of a sufficientl complex M&S project that largely involved the evolution of a complex ABM. The ABM was developed by experts from multiple academic disciplines. Thus, major portions of the contents of this book materialized as a result of interdisciplinary, collaborative research efforts concerning ABMS (from Computer Science and Engineering) and malaria epidemiology (from Biological Sciences) at the University of Notre Dame [547].

Malaria is one of the oldest and deadliest infectious diseases in humans, and the control of malaria represents one of the greatest public health challenges of the twenty-firs century. According to the latest estimates (released in December 2014), the World Health Organization (WHO) reported about 198 million cases of malaria in 2013 and an estimated 584,000 deaths, with half of the world's population (about 3.3 billion) being at risk [567]. Human malaria is transmitted only by female mosquitoes of the genus *Anopheles*, which are regarded as the primary vectors for transmission.

The ABMs presented in this book were developed by following a conceptual, biological core model of *Anopheles gambiae* (*An. gambiae* for short) for malaria epidemiology. The notion of this core model plays a central role in the long development process of multiple versions of the ABMs, as well as in conducting such crucial steps as model verification validation, and replication. Evolution of the core model has been guided by relevant biological features concerning *An. gambiae*, which were iteratively refine and incrementally added to the existing pool of model features. Subsequently, the ABMs were updated to reflec the changes.

OUTLINE OF CHAPTERS

Chapter 1 of this book introduces the reader to its major components, presents a brief introduction to malaria and ABMs, and lists our specifi contributions. Chapters 2 and 3 present general introductions to malaria and ABMs. Their purpose is to collectively serve as a concise background for readers who are less familiar with the disease and its epidemiological aspects, and why ABMs are particularly useful in modeling diseases like malaria.

Chapter 4 thoroughly describes the biological core model of *An. gambiae*. After definin some relevant terms of interest, it addresses several important features of the mosquito life cycle, including development in different life-cycle stages, aquatic habitats, oviposition, vector senescence, and density- and age-dependent mortality rates. It also discusses some of the key features, characteristics, and limitations of the core model.

Chapter 5 discusses the design and implementation of a simplified fi ed version of the ABM. Since the ABM is developed in the *Java* object-oriented programming