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With the development of database systems and networking technologies, Hospital Information Management Systems (HIMS) and web-based clinical or medical systems (such as the Medical Director, a generic GP clinical system) are widely used in health and clinical practices. Healthcare and medical service are more data-intensive and evidence-based since electronic health records are now used to track individuals' and communities' health information. These highlights substantially motivate and advance the emergence and the progress of health informatics research and practice. Health Informatics continues to gain interest from both academia and health industries. The significant initiatives of using information, knowledge and communication technologies in health industries ensures patient safety, improve population health and facilitate the delivery of government healthcare services. Books in the series will reflect technology's cross-disciplinary research in IT and health/medical science to assist in disease diagnoses, treatment, prediction and monitoring through the modeling, design, development, visualization, integration and management of health related information. These technologies include information systems, web technologies, data mining, image processing, user interaction and interfaces, sensors and wireless networking, and are applicable to a wide range of health-related information such as medical data, biomedical data, bioinformatics data, and public health data.

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Jiming Liu • Shang Xia

Computational Epidemiology

From Disease Transmission Modeling
to Vaccination Decision Making

 Springer

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*This book is dedicated to all the people
around the world, who came together to fight
against the novel coronavirus (COVID-19)
pandemic.*

Jiming Liu and Shang Xia

Preface

What Can We Learn from COVID-19?

To see a World in a Grain of Sand
And a Heaven in a Wild Flower
Hold Infinity in the palm of your hand
And Eternity in an hour

William Blake (1757–1827) *Auguries of Innocence*

The title of this preface may look a bit unusual for a research monograph. Nevertheless, this was indeed the kind of questions that came to our mind when we were writing it.

This book was born in a special time. As it was being written and published, the world was enduring one of its greatest challenges in decades, if not in centuries. The novel coronavirus, known as COVID-19, had rapidly spread to around 200 countries and territories in 6 continents (with only Antarctica untouched) within a few months, resulting in more than 5 million people infected and over 300,000 deaths (as of May 2020). All the people, no matter where they were and who they were, found themselves caught right amid this most unprecedented global crisis, with devastating casualties, country lockdowns, service/business shutdowns, and possible economic meltdown.

The world is truly in a state of emergency, a time of great uncertainty and anxiety.

Yet, as in the history of human civilization, we all should be hopeful that humankind will be able to learn and prevail in the end. There will be no exception this time. One of the important lessons that we can probably learn from the Mother Nature in this global fight against COVID-19 is that **only by being united as one, as humanity, working together to remove the barriers of races,**

nation-states, political ideologies, religions, and special interests, and coexisting harmoniously in an increasingly interconnected and interdependent world, can human beings be saved. This also calls upon scientists to rethink their roles and social responsibilities, to rediscover the world, and to advance sciences beyond the usual disciplinary boundaries. Under such a unique circumstance, the theme of this book becomes particularly appropriate, as it attempts to show how disciplines such as computer science, systems science, and epidemiology can converge and address some of the most pressing, socially relevant issues in eradicating diseases.

The contents presented in this book reflect part of our ongoing initiatives at Hong Kong Baptist University (HKBU), which are aimed to address several important problems in infectious disease epidemiology and to solve them in a systematic way through the developed computational models, methods, tools, and case studies. Some examples of the problems are as follows:

- How has the field of epidemiology evolved (Chap. 1)? How can data-centric technologies be incorporated? (Chaps. 1 and 7)
- How can the heterogeneous nature of disease transmission be modeled and characterized? (Chap. 2)
- How can we strategically plan and achieve disease interventions (Chap. 3)?
- How can we take into consideration the human (individual and social) aspects of decision-making in disease interventions? (Chaps. 4–6)
- How can the epidemiological challenges be best addressed from a systems perspective? (Chap. 7)
- What promises does systems epidemiology hold? What is the best way to pursue it? (Chap. 7)

Solutions to the above problems can help governments, public health policy-makers, scientists, and front-line practitioners in seeing the current and future global health challenges, such as COVID-19, from a systematic, data-driven computational modeling perspective, and hence developing the corresponding effective intervention strategies. For instance, the solutions provided in this book can help respond to the following questions in the case of COVID-19: Once a coronavirus vaccine becomes available, what will be the best (scientifically sound and yet practically acceptable) way to administer the limited supplies? Who will have the priorities? Will there be enough people to take the vaccine, so that the target coverage (herd immunity) can be achieved? How will people make their vaccination decisions?

The book is intended to serve as a reference book for researchers and practitioners in the fields of computer science and epidemiology, who may read Chaps. 1 and 7 of the book first, to gain a holistic view of the domain, prior to reading Chaps. 2–6 for further studies on the specific problems and issues involved.

Together with the provided references for the key concepts, methods, and examples being introduced, the book can readily be adopted as an introductory text for undergraduate and graduate courses in computational epidemiology as well as systems epidemiology and as training materials for practitioners and field workers,

who may study the book in the regular order of Chaps. 1–7 and then revisit Chaps. 2–6 to extend some of the topics and problems.

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Jiming Liu
Shang Xia

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Abbreviations

ACIP	Advisory Committee on Immunization Policy
AEFI	Adverse events following immunization
BPA	Basic probability assignment
CHP	Centre for Health Protection
DST	Dempster–Shafer theory
H1N1	Influenza A virus (H1N1)
H7N9	Avian influenza A virus (H7N9)
HSI	Human swine influenza
HSIVP	Human Swine Influenza Vaccination Programme
MMR	Measles–mumps–rubella
NVAC	National Vaccine Advisory Committee
SARS	Severe acute respiratory syndrome
SEIR	Susceptible–exposed–infectious–recovered
SIR	Susceptible–infectious–recovered
SIS	Susceptible–infectious–susceptible
SIT	Social impact theory
STD	Sexually transmitted disease

Notation

S	Population in susceptible compartment
I	Population in infectious compartment
R	Population in recovered compartment
N	Overall population
S_i	Susceptible subpopulation i
I_i	Infectious subpopulation i
R_i	Recovered subpopulation i
N_i	Overall subpopulation i
α	Infectivity
β	Susceptibility
λ	Infection rate
μ	Transmission rate
γ	Recovery rate
c_{ij}	Contact frequency between two subpopulations i and j
R_0	Basic reproduction number
R_t	Effective reproduction number
\mathbf{C}^H	Contact matrix for household setting
\mathbf{C}^S	Contact matrix for school setting
\mathbf{C}^W	Contact matrix for workplace setting
\mathbf{C}^G	Contact matrix for general community setting
\mathbf{C}	Contact matrix for overall social setting
Φ	Social settings (H, S, W, G)
r^H	Household contact coefficient
r^S	School contact coefficient
r^W	Workplace contact coefficient
r^G	General community contact coefficient
\mathbf{K}	Disease reproduction matrix or next-generation matrix
\mathbf{A}	Infectivity matrix, $\text{diag}(\alpha_1, \dots, \alpha_N)$
\mathbf{B}	Susceptibility matrix, $\text{diag}(\beta_1, \dots, \beta_N)$
\mathbf{S}	Susceptible population matrix, $\text{diag}(S_1, \dots, S_N)$
\mathbf{I}	Infectious population vector, $[I_1 \dots I_N]^T$

$\rho(\mathbf{K})$	Top eigenvalue of \mathbf{K}
\mathbf{x}_1	Top left eigenvector of \mathbf{K}
\mathbf{y}_1	Top right eigenvector of \mathbf{K}
N_i^{vac}	Number of vaccinated neighbors
N_i^{non}	Number of unvaccinated neighbors
w_{ij}	Social closeness between two connected individuals i and j
$\hat{\lambda}_i$	Perceived infection rate for subpopulation i
$\hat{\beta}$	Perceived susceptibility
θ	Herd immunity threshold
ζ	Cost of disease infection
ξ	Cost of vaccination
r_c	Cost ratio $r_c = \xi/\zeta$
σ_i	Vaccination decision
$\hat{\sigma}_i$	Cost-minimized choice
$\tilde{\sigma}_i$	Social opinion from connected neighbors
l_i^{vac}	Social influence for vaccination
l_i^{non}	Social influence against vaccination
Δl_i	Influence discrepancy
ν	Responsiveness to influence discrepancy in Fermi function
$P(\Delta l_i)$	Probability generated from Fermi function
r_f	Conformity rate
G	Social network, $G = \langle V, L \rangle$
V	Network nodes (individuals)
L	Network links (interactions)
Θ	Universal set of vaccination decision, {Yes, No}
ϕ	Empty set
2^Θ	Power set, $\{\phi, \{Yes\}, \{No\}, \Theta\}$
$m(\cdot)$	Basic probability assignment
$m(Yes)$	Belief value of vaccination
$m(No)$	Belief value of non-vaccination
$m(\Theta)$	Belief value of no decision (uncertainty)
m_i	Set of belief values
m'_i	Updated belief values
m_i^e	Obtained awareness about negative events
m_{dis}^e	Belief values generated by a severe disease infection
m_{vac}^e	Belief values generated by a vaccine adverse event
f	Coefficient of awareness fading
ϵ	Reporting rate of severe disease infections
κ	Reporting rate of vaccine adverse effects