Epidemiology deals with “the study of the occurrence and distribution of health-related states or events in specified populations, including the study of the determinants influencing such states, and the application of this knowledge to control the health problems” [1]. As defined by MacMahon et al. [2], epidemiology is interdisciplinary by nature, concerning the sciences of etiology, genetics, biology, pharmacy, geography, ecology, as well sociology and human behavior. Epidemiological studies motivated by combating infectious diseases mainly focus on four aspects of challenges, as follows: (1) pattern analysis, by investigating the spatio-temporal distributions of the observed disease occurrences; (2) causal inference, by identifying and evaluating associated impact factors; (3) forecasting and prediction, by evaluating the dynamics of infectious diseases with reference to different scenarios; and (4) policy analytics, by exploring and conducting effective intervention measures.

Toward these ends, the pioneers in epidemiology have provided much useful knowledge to guide efforts in infectious disease control. As pointed out by Merrill [3], epidemiology has evolved from supernatural practices to research based on scientific foundations, from ad hoc reports to systematic investigations of public health events and problems, from ignorance of the causes of diseases to a scientific understanding of their hidden factors, determinants, and outcomes, and from lacking feasible means for solving public health problems to having effective approaches to disease intervention.

Developmental milestones in infectious disease epidemiology can be dated back to the work of Hippocrates (460–377 BC), who examined the influence of environments and attempted to explain how diseases transmit and cause infection in a group of host individuals [3]. Other early studies include the work of John Graunt (1620–1674), who described disease mortality rates by applying statistical and census methods [4], and Thomas Sydenham (1624–1689), who studied disease distribution patterns, moving from an observational to an analytical perspective [5]. In the nineteenth century, John Snow (1813–1858) traced the sources of disease
outbreaks (e.g., cholera in Soho, London, in 1854) and thereafter pointed out the associations of disease outbreaks with social and natural environments [6]. To more formally describe the dynamics of disease transmission, Ross (in 1911) and MacDonald (in 1957) developed a set of mathematical equations and proposed a threshold indicator, named the basic reproduction number, to quantitatively characterize the extent of disease transmission [7].

1.1 Methodological Paradigms

Various methodologies have been developed to address a wide range of challenges in infectious disease control and prevention, and these methods have been applied in epidemiological studies in the past several decades. As stated by Zadoks [8], based on the observation of disease occurrences, descriptive methods, such as clustering and hot spot analysis, have been used to analyze the patterns of infectious diseases in terms of their temporal, spatial, and demographic distributions in a population, i.e., to answer the questions of when, where, and who. Statistical methods, such as regression or Bayesian inference, can be used to further explore the causal relationships between disease occurrence and the possible impact factors, i.e., to answer the questions of why and how. Predictive methods, such as mathematical modeling or computer-based simulation, have been developed to forecast the dynamics of infectious diseases during an epidemic, and identify the most suitable indicators for representing such a dynamic process. Based on these, prescriptive methods, such as optimization, or scenario and sensitivity analyses, can be used by public health authorities to decide how to implement the most effective intervention strategies, such as the allocation of pharmaceutical resources (e.g., vaccines and antivirals) and social distancing (e.g., segregation and school closures).

Infectious disease epidemiology has undergone a number of methodological paradigm shifts throughout its development, as highlighted in Fig. 1.1. The typical methods mentioned in the preceding paragraph, i.e., descriptive, predictive, and prescriptive methods, correspond to three of those paradigms (the fourth is introduced in the next subsection and discussed in detail in the final chapter of this book). These three paradigms are (1) empirical investigation, (2) theoretical modeling, and (3) computational modeling. Accordingly, we refer to the epidemiological methodologies based on these paradigms as (1) empirical epidemiology, (2) theoretical epidemiology, and (3) computational epidemiology, respectively.

• Empirical Methods

The paradigm of empirical observation and investigation is well suited to the early stage of epidemiological studies. As mentioned by Rothman et al. [9], it typically involves (1) collecting observational data about disease transmission, i.e., when, where, and who, and associated impact factors, e.g., the characteristics of disease pathogens and host individuals at the microscopic scale, and of etiological and meteorological environments at the macroscopic scale; (2) qualitatively describing or quantitatively analyzing observational data to establish associative
1.1 Methodological Paradigms

Research paradigms in epidemiology

| Empirical | Theoretical | Computational | Systems |
|-----------|-------------|---------------|---------|
| Observational description | Mathematical modeling | Computer-based simulations | Problem-driven, data-intensive modeling |

Fig. 1.1 Major methodological paradigms in infectious disease epidemiology

or causal relationships between impact factors and disease transmission; and (3) conducting further experiments or field investigations to test epidemiological hypotheses, usually relating the proposed causes to the observed effects, the findings of which may serve as the foundation for planning and implementing disease intervention.

- **Theoretical Methods**
  The theoretical paradigm in epidemiological studies involves the use of mathematical tools, and is focused on generalizing and characterizing the processes of disease transmission and their interrelationships with various impact factors [10]. Mathematical equations or models are typically constructed to quantitatively describe the dynamics of disease transmission and estimate possible outcomes. By evaluating different conditions under which the models reach convergent, stable, or equilibrium states, public health authorities can potentially make long-term projections and informed decisions on disease intervention. Theoretical epidemiology sometimes draws on certain assumptions and simplifications about the real processes of disease transmission. Meanwhile, it may also require mathematical operations to derive model constructs of the behaviors of various diseases, and use these to infer the disease dynamics and the corresponding intervention measures.

- **Computational Methods**
  With the developments in artificial intelligence, machine learning, data analytics, data mining, and geographic science and information systems, the computational paradigm has rapidly emerged in epidemiological studies. Computational methods are aimed to better characterize and understand the real processes of disease
transmission, by modeling and analyzing the patterns of transmission and quantitatively evaluating the potential outcomes of disease intervention [11]. Primary computational tools that are used comprise computational modeling, simulation, prediction, and optimization, as well as data analytics and visualization, to make the results accessible to public health authorities and epidemiologists. This has further expanded the scope and capabilities of epidemiology for analyzing and predicting the dynamics of disease transmission and the effects of disease intervention in a given population. In addition, public health authorities are now able to more effectively conduct scenario analysis, which facilitates their strategic decision-making.

1.2 Recent Developments

The above-mentioned methods have been in vogue for several decades and have been used to make great contributions to our understanding and ability to combat infectious diseases. However, there remain a number of challenges. As schematically illustrated in Fig. 1.2, these challenges come from emerging and re-emerging infectious diseases, which are significantly correlated with multiple impact factors and their interacting effects, such as genetic mutation of disease pathogens/parasites [12], human socio-economic and behavioral changes [13], and environmental and ecological conditions [14, 15].

![Fig. 1.2 Some interacting components (in circles) and their associated impact factors that can affect the transmission of infectious diseases](image-url)
Now we examine influenza as an example. It has been shown that a wide range of factors are involved in the dynamic processes of these outbreaks [16], which may include the following: (1) pathogenic factors, such as viral genetic recombination and the expression of pathogens; (2) host factors, such as the immunity of people at different ages; (3) social and behavioral factors, such as people’s movement or travel activities; and (4) policy factors, such as disease intervention measures. Furthermore, these factors closely interact with each other. For instance, disease pathogens are carried by humans as they travel, which accelerates the recombination of different types of viruses. However, the implementation of disease intervention, e.g., school closures, changes people’s contact behaviors, effectively cutting off the route of disease transmission.

This highlights how various factors can interrelate and interact at various scales. Crucially, the coupling and interactive relationships among those impact factors can determine the intrinsic (yet possibly hidden) spatial, temporal, and social mechanisms of disease transmission. These mechanisms can involve systemic characteristics, such as feedback, saturation, bifurcation, and chaos, thus posing new challenges for comprehensive epidemiological investigations [17].

Effective intervention measures rely on biomedical understanding of disease pathogens/parasites, descriptive studies of spatio-temporal patterns of disease occurrences, and causal analysis of impact factors. In addition, predictive explorations of the trends of disease transmission, i.e., the mechanistic interactions among the components of the transmission process, are also key to understanding and combating infectious diseases. For example, an early warning system for an emerging infectious disease, like COVID-19, requires knowledge about the possible geographic routes of disease transmission, such as human air-travel networks [18]. The prevention of zoonotic and vector-borne diseases, like COVID-19 and malaria, requires both environmental and ecological changes of animal/vector species to be addressed [19], as well as human migrant and mobile behaviors [20]. Furthermore, the effectiveness of disease intervention measures depends on the efficacy of resource allocation, compliance of targeted host populations, and responsive feedback to environmental modifications.

In addition to the above-mentioned challenges, epidemiological studies also face new opportunities in the present and future data-centric era, enabled by the confluence of data from various sources and the development of modeling and analytical tools in data science [21]. For example, a global disease surveillance system connects the health agencies of its member countries and partners at different levels, via local, regional, national, and international organizations [22]. This surveillance system can be used for managing and sharing historical records and reports on when and where specific people have been infected by certain kinds of diseases.

Other data sources are also helpful for analyzing and modeling potential disease transmission. For example, remote sensing data from satellites can readily be utilized for mapping the meteorological and ecological conditions of local or global environments [23, 24].
Another important source of data is Internet-based media, which can serve as an informative channel for revealing individuals’ health-related behaviors and opinions. For example, Google Flu Trends was earlier used to assess the transmission of influenza virus [25], and the use of Internet search data was demonstrated to be effective in predicting dengue fever [26].

In view of these challenges and opportunities, it is imperative that new methodologies and paradigms are developed that offer novel perspectives and methods for comprehensive investigation of disease dynamics and associated impact factors, thus expanding our capabilities to understand, predict, control, and prevent the transmission of infectious diseases.

1.3 Infectious Diseases and Vaccination

Faced with the threat of infectious diseases, implementing timely and effective disease intervention measures is critical for preventing mortality and debilitating morbidity, and reducing the socio-economic losses. Various types of intervention measures have been widely studied and adopted for these purposes. For example, immediate isolation/quarantine can prevent transmission during an influenza-like epidemic [27, 28]. The mass prophylactic use of antiviral drugs can reduce the vulnerability of susceptible individuals exposed to infectious diseases [29]. Interventions by social distancing (e.g., school closures and workplace shutdowns) can lower the frequency of contacts among the host population and, hence, reduce the probability of transmitting diseases between susceptible and infectious individuals [30, 31].

Besides the above-mentioned intervention measures, vaccination has been regarded as one of the most effective methods for preventing infectious diseases, due to the effect of vaccine-induced herd immunity (i.e., immunizing a certain portion of the host population provides indirect protection for the unimmunized individuals [32]). That is to say, to prevent a potential outbreak, the vaccination coverage in a host population needs to be above a critical level for inducing the effect of herd immunity, known as herd immunity threshold. In practice, it remains a continual challenge for public health authorities to achieve such a threshold of vaccination coverage for preventing disease outbreaks.

The task is challenging due to a series of reasons. For one thing, although significant progress has been made over the years in vaccine development, the capacity for providing adequate and timely vaccine doses remains a concern, especially when encountering emerging infectious diseases, e.g., 2009 influenza A (H1N1) [33]. Supply restrictions can arise due to many factors, including the time needed for finalizing vaccine compositions, to respond to the constantly evolution of new disease strains [34], the limited capacity for vaccine manufacturing and logistics [35], and the difficulties in access to and uptake of vaccines due to poor delivery infrastructures and economic constraints, especially in developing countries [36]. In such situations, public health authorities in charge of vaccination
programs face the question of how to allocate a finite number of available vaccine doses to most effectively prevent disease transmission. For example, the World Health Organization (WHO) has strongly suggested that each country should respond to a possible shortage of vaccine supplies by deciding in advance which groups should have access [37].

Furthermore, the public acceptance of a vaccination program will crucially affect the actual level of vaccine uptake: any loss of confidence in vaccine safety and efficacy will lead to huge gaps between the level of public vaccination willingness and the level needed to contain disease transmission. Historically, societies have experienced several events of vaccine refusal, e.g., the pertussis vaccine scare in the 1970s [38], the decline of measles-mumps-rubella (MMR) vaccine uptake in the 1990s [39, 40], and the rise and popularity of anti-vaccination movements [41, 42]. The rejection of vaccination and the subsequent decline of vaccine uptake have brought about outbreaks of certain vaccine-preventable diseases that were thought to no longer be threats to humankind [43, 44].

In view of this, an in-depth understanding of individuals’ voluntary vaccination compliance is urgently required. It has been found that public acceptance of vaccination, which amounts to individuals’ decisions on whether or not to take vaccines, are affected by a mixture of cultural, behavioral, and socio-economic factors. For example, the public may have doubts about vaccine safety and efficacy due to scare stories around the adverse effects of vaccination [45, 46]. Or, behaving in their own self-interest, individuals may be inclined not to get vaccinated if enough other people have been vaccinated [47, 48]. The affordability and convenient accessibility of new vaccines are also of importance for individuals considering vaccination, especially in developing countries [49, 50].

Furthermore, the rapid emergence of online social media, e.g., Facebook and Twitter, allows opinions, whether for or against vaccination, to spread broadly and immediately among the population [51]. Therefore, social influences play an increasingly important role in individuals’ vaccination decisions. In this regard, an individual’s decision on whether or not to vaccinate himself/herself is no longer a personal affair, but will affect the decisions of others, and collectively determine the final coverage of a vaccination program.

Clearly, there exists an urgent need for more systematic studies of vaccination at both population and individual levels, and thereby improve the efficacy of vaccination programs for preventing the outbreak of infectious diseases.

### 1.4 Objectives and Tasks

In this book, we examine the dynamics of disease transmission in a host population, in which individuals’ contact relationships are inferred from the socio-demographic data. Based on such a description of disease transmission, we address the problem of vaccine allocation by developing a novel prioritization method that targets certain subpopulations to most effectively reduce disease transmission. Furthermore, to
investigate individuals’ acceptance of vaccination, we present decision models to characterize individuals’ voluntary vaccination and evaluate the impact of social influences and individuals’ subjective perception on the effectiveness of disease intervention by vaccination.

1.4.1 Modeling Infectious Disease Dynamics

As aforementioned, the dynamics of disease transmission depend on many disease- and host population-related factors. To characterize the heterogeneity of a host population, we need to consider its age structure, and then construct a compartmental model to describe disease dynamics with respect to individuals’ age-specific variations, i.e., the heterogeneity in terms of age-specific infectivity and susceptibility, as well as cross-age contact relationships, as in the case of COVID-19 transmission [52].

For the purpose of demonstration in this book, we consider the real-world scenario of the 2009 Hong Kong H1N1 influenza epidemic, and calibrate our demonstration parameters with reference to the epidemiological characteristics of influenza A (H1N1). As detailed information about the actual contacts among age-specific subpopulations is often unavailable, we exploit a computational method to infer the contact relationships in terms of individuals’ cross-age contact frequencies from the census data in Hong Kong. Specifically, we represent individuals’ actual contacts as cross-age contact frequencies within four specific social settings, i.e., school, household, workplace, and general community. We then estimate the overall contacts that account for disease transmission by incorporating four setting-specific contact frequency matrices, which are weighted with the coefficients corresponding to the proportions of individuals’ contacts within the considered social settings.

To computationally evaluate our model, we carry out a series of simulation-based experiments to examine its predicted disease dynamics. That is, we validate our epidemic model by comparing the model predictions with the real-world observations, in terms of the daily new infection cases and the age-specific attack rates, i.e., the proportion of infected individuals in each subpopulation. In essence, we reproduce the dynamics of disease transmission based on the heterogeneity of the age-structured host population. The results, as we describe later, can serve as the basis for further discussions on vaccine allocation methods and on individuals’ voluntary vaccination.

1.4.2 Modeling Vaccine Allocation Strategies

The heterogeneity of the host population means that the disease-preventing effects of vaccination in individuals of different ages can vary markedly. An immediately related practical question is how to allocate a finite number of vaccine doses to
most effectively reduce disease transmission; crucially, this requires knowledge of the effectiveness of this intervention. In this book, we focus on developing a problem-solving method for answering this question. Specifically, we develop a computational method for identifying the relative priority of each subpopulation, by evaluating the effectiveness of age-specific vaccination in reducing disease transmission. We examine the effects of disease intervention on containing disease transmission by measuring the reproduction number corresponding to the age-specific heterogeneity of a host population. By doing so, we identify subpopulations whose vaccination will lead to the greatest reduction in disease transmission, by considering the marginal effects of reducing the reproduction number in cases of age-specific vaccine allocation. Unlike the existing optimization-based methods, this proposed vaccine allocation method has the following distinct characteristics:

- The method utilizes prior knowledge about individuals’ age-specific susceptibility and infectivity, real-time disease prevalence in each subpopulation, and the basic patterns of individuals’ cross-age contact frequencies within each social setting. Moreover, it does not rely on detailed information about individuals’ actual contacts, nor the potential changes in these contacts in response to disease transmission, which would be difficult to rapidly and accurately determine in practice.
- The method is designed to most effectively reduce disease transmission by allocating a finite number of vaccine doses to certain target subpopulations. The identified vaccination priorities can be adaptively regulated based on the dynamics of disease transmission, i.e., the number of vaccine doses suggested to be allocated to each subpopulation can be dynamically adjusted according to the latest progress of disease transmission and vaccine supply.
- The method incorporates the effects of other disease intervention measures being implemented simultaneously with vaccination, e.g., individuals’ contact reduction. Therefore, in the situation of integrated disease intervention, the method can provide more accurate and effective solutions for vaccine allocation.

We apply above-mentioned method to the real-world scenario of the 2009 Hong Kong H1N1 influenza epidemic to identify the relative priorities of subpopulations for disease intervention in Hong Kong. The results show that this method of prioritizing age-specific subpopulations for vaccine allocation and social settings for contact reduction can readily improve the effectiveness of disease transmission-containing efforts.

1.4.3 Modeling Vaccination Decision-Making

In a voluntary vaccination program, individuals’ decisions on whether or not to uptake vaccine crucially affect the level of vaccination coverage and, thus, the effectiveness of disease intervention. In this regard, modeling and evaluating individuals’
vaccination decision-making would provide useful information for public health authorities on how to improve the effectiveness of vaccination programs [53].

Researchers have typically utilized payoff-based approaches to characterize individuals’ vaccination decision-making with respect to the perceived risks and benefits of vaccination. Moving beyond that, we consider the fact that whether an individual does or does not get vaccinated is also influenced by the decisions of others, i.e., social influences. We thus view individuals’ voluntary vaccination as an integrated decision-making process that incorporates both a cost analysis of vaccination and the impact of social influences.

Our integrated decision model is an improvement over the existing models, and has several interesting features, as follows:

- We model an individual’s vaccination decision-making as an integrated process that balances his/her self-initiated cost minimization and the social influences of others’ decisions. Moreover, this model introduces a parameter, called the conformity rate, to modulate individuals’ tendency toward two decision-making mechanisms: an individual will adopt his/her own cost-minimized decision, or the social opinion of his/her interconnected neighbors.

- Based on the existing studies in which the social influences on the process of opinion formation have been addressed, we further consider the heterogeneity of individuals’ social relationships, i.e., how individuals are socially interconnected. Computationally, we model and characterize the effect of networked social influences on individuals’ vaccination decisions based on Social Impact Theory (SIT).

- Based on this new model, we examine the effects of social influences on individuals’ decisions and on the effectiveness of disease intervention (vaccination coverage), with respect to three determinants: (1) the relative costs of vaccination and infection; (2) individuals’ conformity to social influences, i.e., conformity rate; and (3) individuals’ initial level of vaccination willingness.

We parameterize the integrated decision model based on the real-world scenario of the 2009 Hong Kong H1N1 influenza epidemic, and perform a series of simulation-based experiments to infer the coverage of voluntary vaccination programs as a result of individuals’ decision-making. The results indicate that individuals’ vaccination decision-making can be affected by both the associated costs and their conformity to social influences. Thus, it becomes necessary for public health authorities to estimate the level of individuals’ acceptance of vaccination prior to the start of a voluntary vaccination program, as well as to rapidly assess and enhance the effectiveness of their adopted vaccination policies, e.g., providing certain financial subsidies to reduce the cost of vaccination.
1.4.4 Modeling Subjective Perception

It has long been observed that the spread of awareness about an epidemic via social media can affect individuals’ opinions and behaviors concerning an epidemic. In the case of an emerging infectious disease, it can be difficult for individuals to become informed about the disease and/or a newly developed vaccine prior to their decision-making. In such a case, the spread of awareness about disease severity and vaccine safety could affect individuals’ subjective perception about vaccination and, hence, substantially affect their decisions [54].

To gain a better understanding of individuals’ voluntary vaccination, we develop a belief-based decision model to evaluate the effect of the spread of awareness on individuals’ decision-making and on the effectiveness of disease intervention. Compared with the existing studies on modeling individual-level vaccination decision-making, this belief-based model has the following unique properties:

- Unlike existing decision models that represent decision-making as a binary problem, we consider the role of uncertainty in individuals’ vaccination decision-making. Specifically, the situation in which an individual has made no firm decision can be considered as a state of “yet to decide”, due to uncertainty. In this regard, we introduce three belief variables to characterize the possible decision response from an individual, namely that he/she will accept or reject the vaccine, or has not yet decided.
- We further consider the fact that individuals’ decisions depend on their subjective perception about whether or not vaccination is acceptable. Moreover, awareness of disease severity and vaccine safety can spread from person to person—akin to a disease itself—and will substantially affect their subjective perception of vaccination.
- To model the spread of awareness, we utilize various real-world online social networks to characterize the structure of individuals’ social relationships. Thereafter, we further extend Dempster-Shafer Theory (DST) to computationally model the propagation and evolution of individuals’ beliefs, as well as their decision-making, having incorporated the awareness obtained from their socially interconnected neighbors.

We investigate the effect of the spread of awareness on individuals’ vaccination decision-making with respect to three considered impact factors, based on a series of simulations of the 2009 Hong Kong H1N1 influenza epidemic. First, the reporting rates of severe infection and adverse effects of vaccination are used to represent the frequencies of these topics, which tend to draw public attention. Next, we consider the coefficient of awareness fading, a parameter used to quantify the information flows among individuals. Finally, we examine the effect of disease reproduction number, which corresponds to the severity of an epidemic.

The simulation results show that the reporting rates will determine the number of vaccinated individuals and the time at which they receive vaccination. A higher fading coefficient will significantly reduce individuals’ vaccination willingness.
A larger value of disease reproduction number will enhance the proportion of vaccinated individuals, although this cannot compensate for the growth of the infected population size resulting from a more severe disease outbreak.

1.5 Summary

In this book, we develop a computational modeling approach to evaluate and guide the implementation of different intervention measures for controlling infectious diseases. We focus on the following topics in the remaining chapters:

In Chap. 2, we provide a general description of the concepts and related computational models and tools for characterizing disease transmission dynamics in a heterogeneous host population. Specifically, we introduce the concepts of compartmental modeling for describing disease transmission in an age-structured host population. Then, we present a computational method for inferring the cross-age contact patterns of the population. Finally, we parameterize and validate the epidemic model with a real-world epidemic scenario, which serves as the basis for our further discussions on vaccine allocation and individuals’ voluntary vaccination.

In Chap. 3, we develop a prioritization method for identifying target subpopulations for vaccine allocation that would enable us to most effectively reduce disease transmission. We walk through a series of simulation-based experiments that evaluate the performance of such a vaccine allocation method in improving the effectiveness of disease intervention.

In Chap. 4, we examine vaccination decision-making from the perspective of individuals. In particular, we show how to model individuals’ decision-making processes in response to a voluntary vaccination program. We use computational modeling to perform a game-theoretic analysis of the costs and benefits of vaccination with respect to individuals’ social relationships. Then, we experimentally examine the level of vaccination coverage, based on this game-theoretic model, through a series of simulations of voluntary vaccination.

In Chap. 5, we introduce an extended decision model that additionally addresses the effect of social influences on an individual’s decision whether to undergo voluntary vaccination. In the extended decision model, we utilize the SIT to further characterize social influences with respect to individuals’ social relationships. We evaluate the effect of social influences by computing the level of vaccination coverage through a series of simulations of voluntary vaccination based on such an integrated decision model.

In Chap. 6, we present a more complete investigation of voluntary vaccination by modeling and examining the effect of the spread of awareness on vaccination decision-making. In doing so, we develop a belief-based decision model, in which individuals’ decisions are affected by their subjective perception of vaccination. In this model, we utilize and extend DST to characterize individuals’ belief updates and changes in vaccination decisions accordingly. We evaluate the effect of the spread of
awareness by carrying out simulation-based experiments to examine the time course of vaccine administration and disease transmission.

In Chap. 7, we offer a fresh outlook on the latest methodological paradigm in infectious disease epidemiology, which is known as systems epidemiology. Specifically, we introduce the fundamental ingredients of systems thinking, which are essential for viewing and addressing complex epidemiological questions holistically. We then provide detailed systems modeling principles and practical steps that can be followed in future systems epidemiological studies.

Finally, under “References” section, we provide a detailed list of references for further reading and research.