

Systems Science Methods in Public Health: Dynamics, Networks, and Agents

Douglas A. Luke¹ and Katherine A. Stamatakis²

¹George Warren Brown School of Social Work, ²School of Medicine,
Washington University, St. Louis, Missouri 63112; email: dluke@wustl.edu,
stamatakisk@wudosis.wustl.edu

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Abstract

Complex systems abound in public health. Complex systems are made up of heterogeneous elements that interact with one another, have emergent properties that are not explained by understanding the individual elements of the system, persist over time, and adapt to changing circumstances. Public health is starting to use results from systems science studies to shape practice and policy, for example in preparing for global pandemics. However, systems science study designs and analytic methods remain underutilized and are not widely featured in public health curricula or training. In this review we present an argument for the utility of systems science methods in public health, introduce three important systems science methods (system dynamics, network analysis, and agent-based modeling), and provide three case studies in which these methods have been used to answer important public health science questions in the areas of infectious disease, tobacco control, and obesity.

INTRODUCTION

In 2006 the United States established the Biomedical Advanced Research and Development Authority (BARDA), partly in response to the threat of a global H5N1 pandemic as well as the 9/11 terrorist attacks. Part of BARDA's mission is to help prepare the national plan to address the threat of emerging infectious diseases such as pandemic influenza. As part of this planning, BARDA has utilized the most current public health science to make decisions and recommendations about aspects of pandemic planning such as stockpiling and distribution of vaccines, the timing and targeting of vaccines, and the most effective use of nonmedical interventions such as social distancing (i.e., quarantines) (38). The science base for these recommendations relies to a great extent on new types of methods for simulating and modeling complex systems (56). This is a historical moment for public health science. Government, business leaders, and other stakeholders are already using public health systems science to guide national pandemic strategy, which highlights the utility and impact of these methods. However, systems science methods remain underutilized and are not featured prominently in public health curricula or training (137). The purpose of this review is to present an argument for the utility of systems science methods in public health, to introduce three important and relevant systems science methods (system dynamics, network analysis, and agent-based modeling), and to illustrate these methods through three case studies in which these methods have been used to answer important public health science questions in the areas of infectious disease, tobacco control, and obesity.

THE NEED FOR NEW METHODS TO STUDY COMPLEX PUBLIC HEALTH SYSTEMS

What Are Complex Systems?

Complex systems abound in public health. In fact, most of the interesting processes in nature,

society, and the economy derive from complex systems (2, 123). So what is a complex system? Wanting to avoid semantic distractions, Gallagher & Appenzeller (55) introduce a special issue of *Science* by stating that a complex system is "one whose properties are not fully explained by an understanding of its component parts" (p. 79). Although formal definitions may vary, there is broad acceptance that complex systems have the following properties (101, 108):

- They are made up of a large number of heterogeneous elements.
- These elements interact with each other.
- The interactions produce an emergent effect that is different from the effects of the individual elements.
- This effect persists over time and adapts to changing circumstances.

Consider the example of the national vaccine system, which according to the above criteria is clearly a complex system (133). It is made up of heterogeneous components (individuals, health clinics, public health agencies, pharmaceutical companies), which interact with each other and are organized at different levels. Certain properties of this system such as herd immunity emerge from the interactions of its various components. The vaccination system has existed over a long time period, but it does respond to changing circumstances. For example, vaccination rates across the United States have started decreasing, partially in response to media coverage of the autism-vaccination debate in the general media (129). Because the interesting behavior of systems is emergent, it is necessary to study a system as a whole, rather than to decompose it and study its individual parts (2). This implies that traditional study designs and analytic tools will not suffice to explore complex public health systems.

The Argument from Study Design

In 1968, sociologist Allen Barton stated that (16)

For the last thirty years, empirical social research has been dominated by the sample survey. But as usually practiced, using random sampling of individuals, the survey is a sociological meatgrinder, tearing the individual from his social context and guaranteeing that nobody in the study interacts with anyone else in it. . . . If our aim is to understand people's behavior rather than simply to record it, we want to know about primary groups, neighborhoods, organizations, social circles, and communities; about interaction, communication, role expectations, and social control. (p. 1)

This is as true now for public health as it was a generation ago. Public health science is dominated by randomized control trial (RCT) and epidemiologic risk factor study designs (59, 132). Social psychologist Joseph McGrath provided a framework for understanding the complementary strengths and weaknesses of various types of study designs that can be used to illustrate why traditional RCT and risk factor designs are inappropriate for studying complex public health systems (**Figure 1**) (100). Essentially, RCTs and other types of quasi-experimental designs are concerned predominantly with internal validity and the ability to measure intervention effects precisely. However, this precision sacrifices external validity and the ability to measure and understand contextual and ecological effects. Systems science study designs (such as computer simulation modeling and network observation studies) appear on the opposite side of McGrath's figure from experimental designs; thus, these types of studies may sacrifice measurement precision, but they gain external validity and the ability to assess the influence of context on behavior.

Two particular aspects of traditional study designs severely limit their appropriateness for complex systems. First, RCTs and risk-factor studies gain their precision partly through randomization for group assignment and/or sample selection. This randomization ensures that study participants are not typically drawn from naturally existing social or organizational

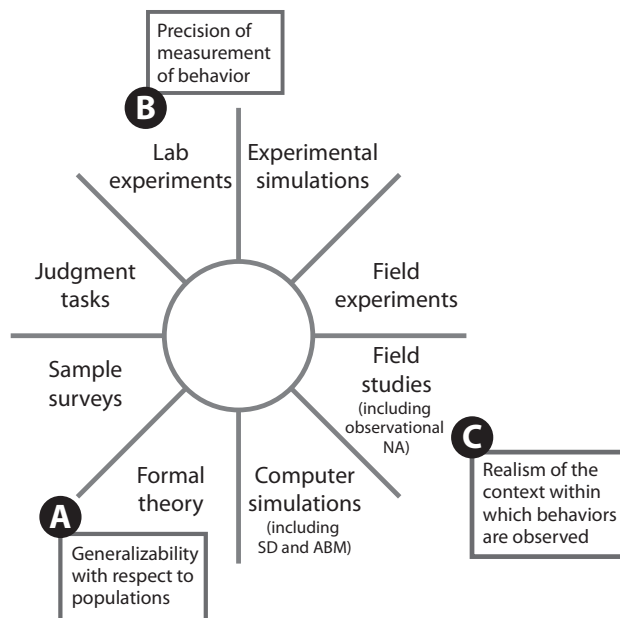


Figure 1

Complementary strengths and weaknesses of various study designs, based on McGrath's 3-Horned Dilemma (100). Abbreviations: SD, system dynamics; ABM, agent-based modeling; NA, network analysis.

systems. Not only are the behavioral effects of these social systems excluded, but study participants are not allowed to interact with one another as they typically would (132). (In fact, we often label this type of interaction as contamination and consider it a study flaw.) Second, experimental and risk-factor studies (e.g., case-control studies) are designed primarily to identify the existence or size of a specific effect or relationship, not the mechanism of the effect (sometimes called the black-box problem) (72). As Meehl (102) has pointed out, rejecting a null hypothesis of no effect is a very low epistemological bar, and the social and health sciences are better served by proposing richer predictions based on more sophisticated models of causal mechanisms. Thus, if we are to study complex public health systems, we need to use study designs and methods that allow for interactions among elements of the complex system and that are able to study, identify, and characterize the mechanisms that drive the behavior of the system (54).

Systems science: an interdisciplinary field of science focusing on complex natural and social systems

The Argument from Analysis

There is a similar mismatch between the characteristics and assumptions of traditional data analysis approaches in public health and the characteristics of the data and models that derive from complex systems. Stated most concisely, the types of statistical analyses that we use most often in public health are inappropriate for studying complex systems. Even more sophisticated analytic techniques, such as structural equation modeling and latent class analysis, which are designed to test more complicated relationships, break down in the presence of all-too-common feedback loops, threshold effects, and other types of nonlinearity. Critiques of statistical modeling are not new, but a common theme of these discussions is that statistical models are most useful when they are connected to strong study designs and appropriate data and match the structure of the theoretical predictions (52, 91).

Table 1 summarizes several reasons why the study of complex systems requires new data analysis techniques. Whereas traditional statistical modeling often assumes linear relationships where changes in dependent variables are proportional to changes in independent variables, complex systems are characterized by nonlinearity, threshold events, and chaotic behavior (118). Traditional modeling often assumes normality of variables or residuals; not only are normal distributions poor depictions of reality (105), but complex systems are more often characterized by power laws that lead to

scale-free distributions (108, 145). Complex systems are characterized by heterogeneous actors: They require representativeness in the sampling sense (43), and computational models of complex systems can also include actors of fundamentally different types (e.g., people, businesses, and products). Although some linear modeling approaches such as random effects models can be applied to multiple levels of analysis, most traditional statistical models are limited to a single level. Complex systems, on the other hand, are often multilevel (14). Although statistical analysis can of course be applied to longitudinal data, in public health these data are typically discretely longitudinal—snapshots taken at well-separated points in time. A fundamental property of complex systems is that they are dynamic, and some of the existing computational modeling tools (especially agent-based modeling, see below) allow for tracking systems as they change in real time (43). Although statistical modeling can be used to assess relationships among objects [e.g., cluster analysis (117)], it more often focuses on correlational relationships between variables. Modeling complex systems, on the other hand, typically focuses on the interactions of the actors within the system. Finally, traditional statistical modeling is inherently reductionist, focusing on individual parameter estimates, specific individual interactions, or individual links in the causal chain. Methods for studying complex systems are, by their very nature, holistic, examining whole systems or

Table 1 Comparison of traditional and complex system analytic assumptions

Domain	Traditional analytic techniques assumptions	Complex systems assumptions
Functional form	Linearity	Nonlinearity
Common distributions	Normality	Nonnormality
Characteristics of actors	Homogeneity	Heterogeneity
Level of analysis	Single level	Multiple levels
Temporality	Static or discretely longitudinal	Dynamic, with feedback
Fundamental relationships	Among variables	Interaction of actors
Perspective	Reductionist	Holistic

models of systems to help identify the complex mechanisms by which they operate (96).

Three Key Methods for Studying Complex Systems

The preceding discussion makes it clear that traditional study design and analytic methods commonly used in public health sciences are not appropriate for studying complex systems. The remainder of this review focuses on three methodological approaches commonly used to study these types of systems: system dynamics (SD), network analysis (NA), and agent-based modeling (ABM). Although there is some overlap, these three methods each approach the study of complex systems in different ways. **Table 2** presents the aspects of complex systems that each method is particularly suited to address. For example, ABM and NA are both more suited for describing how the individual actors in a system interact with one another compared with SD [see also Osgood (113)].

SD, NA, and ABM all have rich, multidisciplinary conceptual and technical histories, have benefited from recent developments in computational and modeling advances, and have been used to study complex systems of many types. Not all studies of complex systems in public health use these methods, but many do. However, despite the importance of these methods for studying complex public health systems, they do not have a prominent place in public health training and education. There are important exceptions, such as the annual National

Institutes of Health (NIH)-sponsored Institute on Systems Science and Health, which provides training in these three specific methods (<http://issh.aed.org/>).

SURVEY OF COMPLEX SYSTEMS METHODS

System Dynamics

System dynamics (SD) is based on the premise that complex behaviors of a system (e.g., population prevalence of an infection) result from the interplay of feedback loops, stocks, and flows that all occur within the bounded endogenous system (121, 130). The method arose originally in management science (50) from the recognition of the need to explicitly model nonlinear processes that are characteristic of complex phenomena such as policy resistance, the law of unintended consequences, and the often counterintuitive behavior of social systems (131). Computer simulations are used to track accumulations of stocks (e.g., people, currency, disease counts), which are determined by flows (e.g., rate of occurrence), feedback loops (causal loops with either balancing or reinforcing effects), and time delays.

The focus of SD is on building models to represent the dynamic complexity of aggregate, often high-level phenomena such as new product adoption in organizations or predator-prey relationships over time. Simulation results allow for the examination of the system behavior, which may take on various patterns [e.g., exponential growth, oscillation,

System dynamics

(SD): uses informal and formal models with computer simulation to uncover and understand endogenous sources of complex system behavior

Network analysis

(NA): the measurement and the analysis of relationships and flows among actors, including people, organizations, and other information processing entities

Agent-based modeling (ABM):

uses computer simulations to examine how elements of a system (agents) behave as a function of their interactions with each other and their environment

Table 2 Primary strengths of each system science method

System property	System dynamics	Network analysis	Agent-based modeling
Model breadth	X		
Feedback loops	X		X
Dynamic systems in real time	X		X
Interactions of individual actors		X	X
Interactions between multiple levels	X		X
Complex relational structures		X	
Heterogeneous actors	X	X	X

s-shaped growth, collapse (130)] and be compared with hypothesized or expected system behaviors (i.e., reference modes). SD models have been used to provide useful illustrative models, even absent of strong empirical data, to demonstrate relative impacts of various policies or intervention strategies, particularly when feedback loops may be used to explain patterns of nonlinearity or unintended consequences [e.g., the chronic disease-prevention model in Homer & Hirsch (68)]. Compared with other types of complex system models, SD models tend to have broader boundaries (i.e., include a larger number of relevant explanatory variables) and be more amenable to including variables for which strong empirical data may not be available (68, 115). In the SD field, there is a strong emphasis on group model building (142), where models are developed in a participatory process between modeler and practitioners or end users. Thus, the process of developing, testing, and refining an SD model is ideally both iterative and participatory.

With a typical focus on aggregate characteristics and broad boundaries, SD modeling has lent itself to an array of public health applications. It has been used to model potential public health outcomes in cases where it is not feasible to test various intervention strategies on real populations, particularly where interventions may involve factors far upstream from health outcomes (64, 67, 74). Models to guide practice in clinical preventive care (127), to plan for disasters (65), and to set more realistic public health benchmarks (107) provide other examples of the practical utility of SD models in public health. An interesting area for further exploration is its utility in examining strategies to address populations with overlapping epidemics, or “syndemics” (106).

Network Analysis

Network analysis (NA) is a research method and scientific paradigm that focuses on the relationships among sets of actors. The actors can be any type of entity that can have a relationship or tie with other entities: persons, animals,

organizations, countries, Web sites, documents, and even genes. Of the three methods considered in this review, NA has the longest history: The roots of NA can be traced back to a number of different disciplines, including mathematics (especially graph theory and topology), anthropology (kinship systems), and sociology (social ties and structure) (53). However, what we now recognize as modern NA was established in the early 1930s with Jacob Moreno’s invention of the sociogram, a graph that depicts the structure of interpersonal relations in a group (109). With the availability of efficient computer algorithms, the development of specialized NA software, and the “discovery” of NA by modern physicists and mathematicians (23), interest in NA has exploded. The new science of networks is being used in almost every area of science (15) to study important questions such as the robustness of terrorist networks (119), the structure of the Internet (13, 25), the functioning of the brain (17), political divisions of modern society (39), and the complex interactions of genes and human disease systems (90).

Perhaps because of its longer history, and the ability to analyze real-world data quickly, NA has a wider variety of applications and analytic approaches compared with SD and ABM [see Wasserman & Faust (144), Brandes & Erlebach (22)]. Despite the analytic variety, almost all NA makes use of one or more of three different analytic modes: network visualization, network description, and statistical modeling of networks. One of the attractions of NA is the ability to examine a given network visually, especially if it is small-to medium-sized. **Figure 2**, for example, shows the first HIV transmission network with Patient 0 highlighted (8) and documents both the contagion structure and possible transmission mechanism. Network description makes up the bulk of NA and can be flexibly used to address a wide variety of scientific questions. **Figure 3** highlights this diversity. Working down each column in the figure, basic NA can focus on the location of individual actors in the network, the structure of local connections

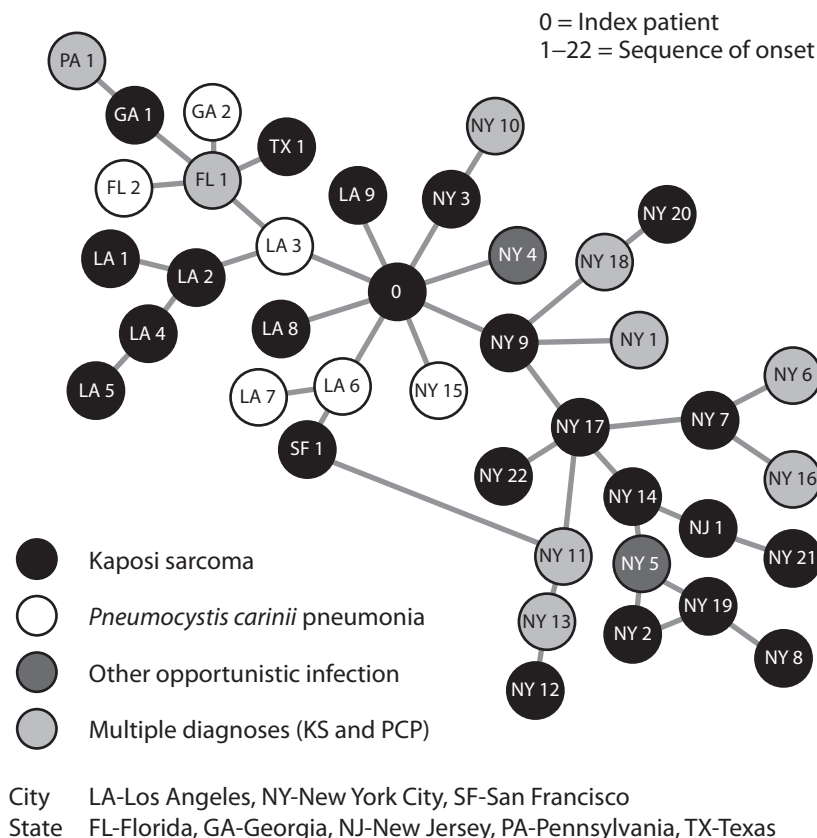


Figure 2

Sexual and disease status network of 40 men with HIV/AIDS (8).

and network subgroups, or the entire network. More advanced NA can examine multiple networks, the relationships among multiple types of network ties, multilevel networks, or how networks change over time. Finally, relatively new developments in statistical network theory are allowing, for the first time, the building and testing of statistical models and hypotheses of network processes and structures (57).

Over the past two decades, NA has become more widely used in public health, especially in the following five areas (92): disease transmission, social support and social capital, network influences on health behavior, public health service and organizational networks, and the social structure of information diffusion. Three

examples illustrate how the use of network methods has helped facilitate a greater move toward network and systems theories in public health. First, it was during the early years of the HIV epidemic [followed by work on severe acute respiratory syndrome (SARS) and other infectious diseases] that epidemiologists started to employ network analytic methods as a new way to chart the spread of a disease and to plan how to counter disease outbreaks (104, 124). This moved the fundamental S-I-R (susceptible—infectious—recovered) disease model away from a pure population-level model by incorporating local social network information into the basic model (76). The second example is in the area of information diffusion.

Early empirical work on Rogers' diffusion of innovations theory emphasized the temporal aspects of the diffusion rate over time and the identification of distinctive types of people or organizations involved with diffusion (e.g., opinion leaders) (36). It was not until Valente focused on the network aspects of diffusion of innovations, for example by studying network threshold effects on diffusion patterns (138), that diffusion studies started incorporating more relational and structural aspects of communication systems (63, 99). Finally, a recent series of studies by Christakis and Fowler (30, 31, 51) have collectively suggested that a wide variety of health behaviors and functioning (including smoking, obesity, and happiness) are "socially contagious" and directly shaped by social networks. The methods and conclusions of some of these studies have been challenged (34, 95), but the visibility of this work has helped to highlight the continuing importance of NA methods in modern public health science.

Agent-Based Modeling

Agent-based modeling (ABM) uses computer simulation to study complex systems from the ground up by examining how individual elements of a system (agents) behave as a function of individual properties, their environment, and their interactions with each other. Through these behaviors, emergent properties of the overall system are revealed. Compared with SD, this results in a form of decentralized modeling where there is no formalized definition of global system behavior (i.e., no differential equations that drive the high-level processes of the system) (21). ABM is the youngest of these three systems science methods, although its conceptual roots trace back to important twentieth-century discoveries in mathematics, philosophy, and computer science, including Von Neumann's invention of cellular automata and John Conway's Game of Life (108). One of the first influential agent-based models that clearly demonstrated how the behavior of complex systems could be described using only simple agent-level rules was Reynolds'

Table 3 Core properties that collectively underlie most agent-based models

Properties	Definition
Heterogeneous	Agents are allowed to differ from one another on important characteristics
Spatial	Agents are located in some explicitly defined space
Interactive	Agents can interact locally with one another and their environments
Bounded rationality	Agents are assumed to have imperfect knowledge
Dynamic	Models are recursive, are allowed to change nonlinearly, and exhibit nonequilibrium

simulation of flocking birds (120). Reynolds' "boids" model used only three simple bird-level rules: (a) separation (do not get too close to any other bird), (b) alignment (match the speed and direction of nearby birds), and (c) cohesion (head for the center of mass of nearby birds). The result of the simulation using these rules was "the graceful dance-like movement of the flock whose hypnotic rhythm is clearly patterned yet also highly nonlinear" (97, p. 144). ABM has been employed in a great number of disciplines but has been particularly useful to describe emergent properties of organizational, social, and cultural systems in anthropology, sociology, political science, business, and economics (9, 11, 66). More generally, ABM has been particularly useful for modeling emergent phenomena such as contagion flows, markets, organizational behavior, and diffusion (20), all of which are relevant in public health research.

ABM employs computer simulations that start with characteristics and rules about individual agents and then generates dynamic histories that reveal overall system properties and behavior. **Table 3** lists the most important characteristics of agents and agent-based models that collectively distinguish this approach from other modeling approaches such as SD (42). Although specialized software packages and libraries for agent-based models exist

(e.g., RePast), much of the academic ABM projects are based on handwritten software that utilizes object-oriented programming techniques (116). Given the dynamic nature of agent-based models, one of the important attractions of these simulations is the visual nature of the modeling environment. Many ABM simulation environments allow researchers to view the system behavior in real time (see the RePast user interface: <http://repast.sourceforge.net/>; AnyLogic: <http://www.xjtek.com/anylogic/>; or NetLogo: <http://ccl.northwestern.edu/netlogo/>). The development of ABM methods has been extremely rapid. Exciting recent developments include the integration of geographic information systems and social network information into agent-based models (10, 37) and the ability to use extremely large sets of agents in the simulations, including synthetic populations of entire communities or nations (24).

The signature success of agent-based modeling in public health is in the study of epidemics and infectious disease dynamics. Agent-based models have been used to study disease transmission at multiple scales, from individual communities to global pandemics (44). Agent-based models of epidemics have helped move epidemiology beyond the traditional S-I-R model and have demonstrated the importance of examining the role of social networks, transportation systems, local geography, and diverse behavioral responses to changing contexts on the spread of disease (45, 46, 148). Agent-based models have also started to be used to study chronic disease and health behavior, including drinking (58) and smoking (10), as well as complex public health and health care systems (75, 128). Conceptually, these models have been useful in suggesting possible mechanisms by which contexts (e.g., neighborhoods, communities, residential environments) influence health and health behavior (7). Finally, much like SD, ABM promises to provide powerful simulation laboratories where different types of public health interventions, programs, and policies can be tested when more traditional outcome studies are not possible (83).

THREE CASE STUDIES

As the above methods review suggests, SD, NA, and ABM have been used in a wide variety of public health research situations. In this section, we present three short case studies that highlight how these systems science methods have been used in particular public health research programs to answer critical scientific and policy questions that would be difficult, if not impossible, to answer using more traditional research designs and analytic tools.

Infectious Disease

The study of infectious disease has been the earliest and most important testing ground for systems science methods in public health. Scientists have long understood that the course of disease transmission in a population is the result of the complex interplay between biology, environment, and society (5). Systems science methods have been critical in moving theories of disease transmission from simplistic temporal models that assume random mixing to sophisticated models, which recognize the importance of geography, social connections, travel patterns, and nonrational behavior (78, 114). Collaborative modeling networks, such as MIDAS (Models of Infectious Disease Agent Study) (see <https://www.epimodels.org/midas/home.do>), offer an example of the types of shared investigative efforts that can approach infectious disease models from various angles to advance innovations in methodological development and utility of the models.

The importance of social ties in infectious disease underlies the relevance of methods able to capture the complexities of social interactions. HIV transmission provides an illustrative example, spreading through a heterogeneous set of contact types, including sexual and intravenous drug use (77), and determined largely by interactions between the structure of social networks and their interaction with population-level characteristics (125). Specific characteristics of network structure that are predictive of infection can lead to improved understanding of transmission processes, as illustrated by

the work of Rothenberg and colleagues, who identified relevant “microstructures” in syphilis transmission (126), and Christley et al. (33), who identified measures of network structure that are predictive of novel infections in a previously uninfected population. Christakis & Fowler (32) utilize a novel approach to studying friend networks and flu spread based on previous knowledge of the centrality of individuals in a social network who are randomly selected as friends of initial contacts. Described as the “friendship paradox” (your friends have more friends than you do), they show that this faster way of sampling and assessing social networks may be useful in improving response time to a broad array of infections.

Applications of SD in infectious disease range from early studies that emphasized describing dynamics of the spread of disease to recent work more strongly oriented toward testing potential impacts of infectious disease control strategies. Early examples of SD in infectious disease as applied to the AIDS epidemic focused on describing the dynamics of the disease transmission process and characteristics of the HIV virus, such as incubation period (70, 122). Models have offered particularly powerful results when data exist to provide a test of model validity. A classic example of the use of SD in studying the dynamic of unintended consequences is provided by Homer and colleagues (69), who developed and tested a model to study the development of antibiotic resistance in pneumonia using existing population-based data from various countries. Vickers & Osgood (143) employed SD modeling to test various assumptions for the rebound in chlamydia rates and used surveillance data to choose the most parsimonious model whose behavior mirrored that of the surveillance data, which pointed to increased testing and not to any real increases in occurrence as the reason behind the uptick in chlamydia rates. Thompson (135) helped frame the debate about polio programs oriented toward long-term eradication versus short-term controls, clarifying the economic costs and benefits for policy makers. The usefulness of broad model boundaries in SD is illustrated

by studies of overlapping epidemics. The co-occurrence of HIV and multidrug-resistant tuberculosis provides a strong example of this overlap, with the accompanying complex menu of potential policy options with which public health decision makers struggle to address various treatment and control approaches in affected populations (6, 81).

Agent-based (and hybrid system dynamic/agent-based) modeling is currently at the forefront of the modern science of infectious disease (44), with its ability to address the complex interplay between individual behavior and social connections on a large scale. Results from the MIDAS modeling network provide some good examples of the multiple ways of testing agent-based models in simulating outcomes of potential infectious disease policy and practice decisions. Lee et al. (84) modeled vaccination allocation policies in the face of an H1N1 epidemic to examine priority recommendations around high-risk individuals versus highly-infective children when vaccines are in short supply and to draw comparisons among outcomes such as attack rate, hospitalizations, and overall cost. Members of the same group (82) identified problems with school-closing strategies for controlling influenza outbreaks and found that short closures were counterproductive and that only longer closures would provide the needed lag time for implementation of long-term effective vaccination programs. Another study (83) utilized the influenza models to examine the impact of strategies for workplace H1N1 vaccination and found that those programs aimed at larger firms were more efficient and effective than were those that were spread across a larger number of smaller workplaces.

Studies of infectious disease continue to be at the forefront of the development of combined approaches that join elements across system methods to model the interaction between individual agent behavior with social networks (28, 46, 79) and with SD of epidemics (45).

Tobacco Control

Tobacco control is at once the biggest challenge for public health (tobacco use is still the

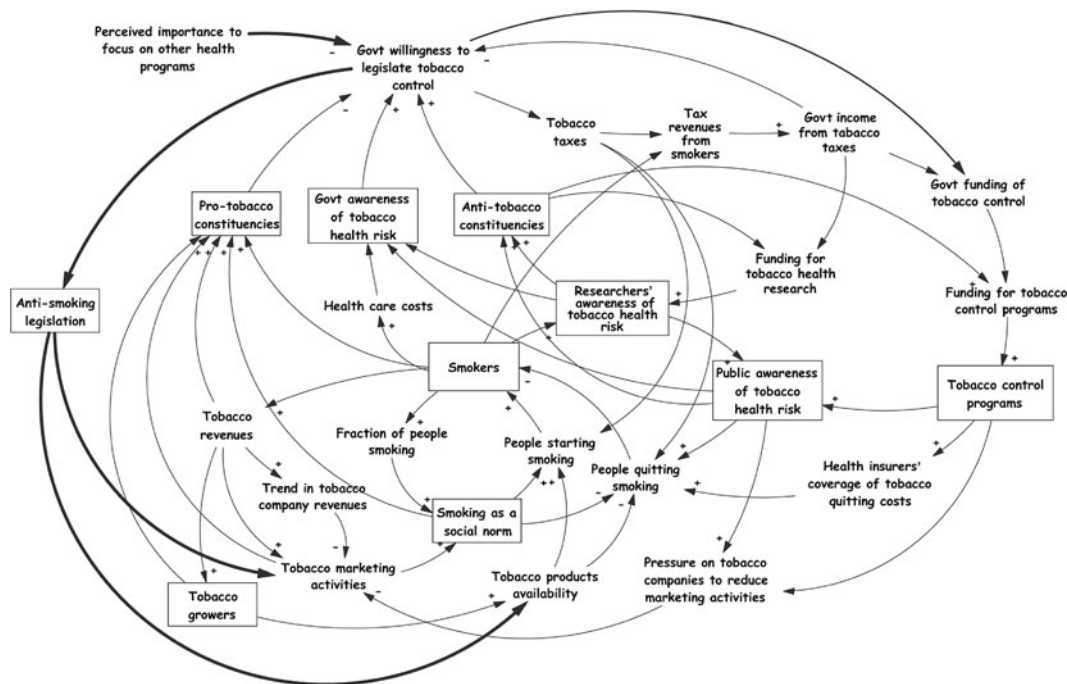


Figure 4

ISIS System Dynamics Model for Tobacco Control (112).

leading preventable cause of death in much of the world) and one of its biggest success stories (26). Starting in the mid-twentieth century, epidemiologists and clinical scientists identified the links in the causal chain between tobacco use and death and disability (mainly via cancer and heart disease) using fairly traditional research methods. However, scientists are now realizing that systems science methods may be critical tools for understanding the complex factors shaping tobacco use and addiction at the individual level and, similarly, for understanding the complex interactions of the various organizational actors in the tobacco-control public health system (98). Tobacco-control science reaches from cells to society and is clearly a classic example of a complex system: It has interacting, heterogeneous actors, and the system as a whole adapts and changes over time. This is reflected in **Figure 4**, which is a causal map for an SD model for tobacco control, developed as part of the National Cancer Institute's Initiative

on the Study and Implementation of Systems (ISIS) (112). This causal map illustrates some of the complex feedback loops (more than 1,900) that exist between the various actors, including individual smokers, tobacco growers, government regulators, public health scientists, and the tobacco industry. Similarly, public health scientists are increasingly aware that changes in tobacco control and tobacco use are likely to have complicated and sometimes unintended consequences in the larger health, economic, and political systems, including changes in health care costs, worker displacement and employment, philanthropy, state and local budgets, and health disparities (18).

SD and NA have both been used more widely in tobacco-control science compared with ABM (68). Dynamic systems simulations and modeling have been particularly useful for forecasting population-level trends, such as smoking initiation and prevalence. For example, dynamic modeling work done by Mendez

& Warner (103) has charted U.S. smoking initiation and cessation rates over time to determine the likelihood of achieving Healthy People goals of 10% smoking prevalence by 2025. These dynamic models have suggested that under a variety of conditions, smoking rates will decline over time, but achieving a 10% prevalence rate is unlikely (73). SD has also been used to explore the additive and interactive effects of multiple policies and interventions on smoking rates. This is a particularly attractive use of SD, given that in the real world single policies are never implemented in isolation. The most well-known example of this approach is the SimSmoke models of Levy and colleagues (86, 87), which have been used to explore the potential effects of tobacco-control policies on smoking in the United States and other countries. Similar dynamic systems approaches have been used to explore tobacco-control educational programs (134) and governmental investment in cessation services (136). The cumulative lesson learned from these dynamic modeling studies is that multiple, evidence-based policies need to be implemented in a comprehensive strategy to continue to lower smoking rates (88).

Although high-level, aggregate models (as found in many SD models) have been useful for forecasting long-term population-level trends, they are, by their very nature, less useful in identifying important mechanisms or relational structures that drive tobacco use. NA has proven to be more successful in this regard and has been used primarily to address two broad sets of tobacco-control questions: how social networks influence individual tobacco use and how community, state, national, and international tobacco-control systems are structured. Although it has long been known that there are strong peer and family influences on smoking behavior, NA can be used to identify which types of ties and network structures are most associated with smoking. Ennett & Bauman (41) were among the first to do this, showing that adolescents who were most isolated from their peers were most likely to smoke. Subsequent network studies have ex-

panded on this basic effect, showing the buffering effects of friendship groups (4) and the interaction of network ties with school environments (3). Current network studies of smoking are starting to establish more specific causal mechanisms: For example, Lakon and colleagues (80) suggest that networks influence smoking by structuring flows of emotional support.

NA has also been frequently used to describe and explore the complex structures of tobacco-control systems from state level to global. Harris, Luke, and colleagues (62) analyzed the contact and collaboration networks of eight state tobacco-control programs to identify a common star-shaped pattern of connections between the lead agency and four other types of organizational partners. At the national level, NA has been used to map the structure of tobacco-control leadership across agencies in the Department of Health and Human Services (85) and to develop models of collaboration among five national tobacco-control networks (93). At the international level, Wipfli and colleagues (146) used NA to show that engagement with an online network of international tobacco-control advocates was positively associated with the likelihood of formal adoption of the Framework Convention on Tobacco Control.

At this time, agent-based modeling has not been applied to tobacco-control research in any comprehensive way, although ABM has been used to study other addictive behaviors (58, 60). The ABM group at the Brookings Institution has started developing agent-based models of smoking behavior and policies (10), but these methods have yet to be widely adopted by tobacco-control scientists. This is expected to change, however, because agent-based models are ideal approaches for studying the effects of different policies when traditional experimental designs are not possible. For example, agent-based models could be built to test the dynamic effects of tobacco retailer density reduction through distinct policy approaches such as attrition, increased licensing fees, or buffer zones around schools (94).

Obesity

Like tobacco control, obesity is a growing global public health challenge. In the past two decades alone, there has been an increase in weight in the United States such that more than two-thirds of the population is now overweight or obese (48). Causal factors in obesity range from individual metabolic components to society at large, resulting in causal models that describe the various levels and sectors of society that offer potential points of public health intervention (e.g., policy, built environment, social networks) (71). Complex systems models offer a set of analytical methods that can account for this complexity (61) and build on previous simulation studies (89) to further develop models that examine the interplay between cells, individuals, and society. Large-scale, team modeling efforts now exist, such as COMNet, CompMod, and Foresight (see <http://nccor.org/envision/index.html>), that have constructed models to simulate the complex web of causation in obesity prevention. [See Vandenbroeck et al. (141) for an impressive example of the complex systems map of obesity.] These models can be further utilized to examine the impact of interventions applied as various inputs and modifications to the models.

Social NA is perhaps the best-known systems method approach in obesity and offers an illustrative example of more broadly applicable considerations in interpreting social NA results. In their influential paper, Christakis & Fowler (30) describe the spread of obesity through social networks. The authors investigated a large network of individuals in a population-based cohort of adults over a period of 32 years, and they found that subjects', or "egos," weight gain was a function of weight gain in persons to whom they were socially connected, or "alters." However, Cohen-Cole & Fletcher (35) challenge these findings and suggest that if a more comprehensive set of contextual factors are taken into account, it is the shared environment that drives social network patterns in obesity, though they concede that the evidence for tightly woven network

ties in obesity still suggests the usefulness of intervention approaches aimed at social networks. Other NA work on the spread of obesity in adolescent social networks (49, 139) further underscores the applicability of this analytical approach. Greater understanding of the types and directionality of friendship and other social and even geographic (19, 27) ties can improve efforts to develop more effective intervention approaches based on specific network targets, social norms, and broad-population versus high-risk group strategies (12), despite some of the challenges in attributing causality between network structures and obesity (35, 40).

Agent-based and SD models have also been employed in obesity research to examine the impact of dynamic interactions among multiple causal components. Recent work in ABM has explored the dynamics of determinants of walking behaviors and neighborhood versus environmental determinants of socioeconomic status (SES) differentials in obesity. Auchincloss and colleagues (7) used ABM simulations to explore income differentials in nutrition as a function of both food prices and preference, and they discuss the utility of computational models in developing a stronger set of evidence on which to base public health policy, particularly where strong empirical data are not available. Yang et al. (149) used ABM to study the role of the social and built environments on SES differentials in walking behavior, incorporating feedback mechanisms such that, for example, individual walking behavior is enforced as the number of other walkers increases. A subset of the SD literature on obesity is focused on individual weight-loss models (1, 47, 111). However, large-scale, multigroup modeling initiatives, such as the CompMod and COMNet modeling networks of the Envision project in the National Collaborative on Childhood Obesity Research (see <http://nccor.org/envision/index.html>), are supporting broader model boundaries that represent higher-level societal sectors that are likely to play a meaningful role in designing better interventions with population-level impact.

Taken as a whole, although the literature is still relatively young, these studies have helped shift the paradigms of etiology and intervention in obesity, and perhaps chronic disease in general, to include mechanisms akin to communicable disease. Although much of the current emphasis is rightly placed on the built environment, the social environment may be another important driver in creating opportunities for weight loss and healthy weight maintenance.

MOVING FORWARD WITH SYSTEMS SCIENCE METHODS IN PUBLIC HEALTH

In early 2000, Stephen Hawking said, “I think the next century will be the century of complexity” (29, p. 29A). As we have suggested in this review, public health is well on its way to fulfilling this prediction by using an array of systems science methods to study complex public health problems.

Complex system methods challenge traditional study-design and data-analysis approaches in public health research. The picture that emerges from reviewing existing work is that system methods are inherently translational, with real-world applications often explicit in the models. With a greater push for translational research in complex, real-world settings (147), we expect a growing demand for methods that account for complexity. The field of complex system methods appears to

be moving toward greater integration among the systems science methods to account for the interaction between social networks, broad system boundaries, and individual behavior to improve the utility of models for policy and practice decision-making that span multiple levels of influence (113).

Despite the promise of systems science methods for public health, these models remain underutilized and lack visibility (137, 140). Although a number of institutions and settings around the country do train and support system scientists (e.g., University of Michigan’s Center for the Study of Complex Systems, the Santa Fe Institute, NIH’s Institute on Systems Science and Health), schools of public health are only now starting to think about developing their own curriculum and degree programs. Although a brief review of course offerings in the top 20 schools of public health in the United States found that about half offered at least one course that addressed a complex system method, it is not clear that such coursework is well integrated into the methods curricula. Moss (110, p. 1) suggests that computational modeling and system science is a “third way” that moves beyond traditional quantitative and qualitative research design dichotomies. If this is so, then we need to start producing more public health scientists who are comfortable and skilled using concepts and tools that focus on dynamics, agents, and networks and ensure that the public is aware of the benefits of this approach to public health science.

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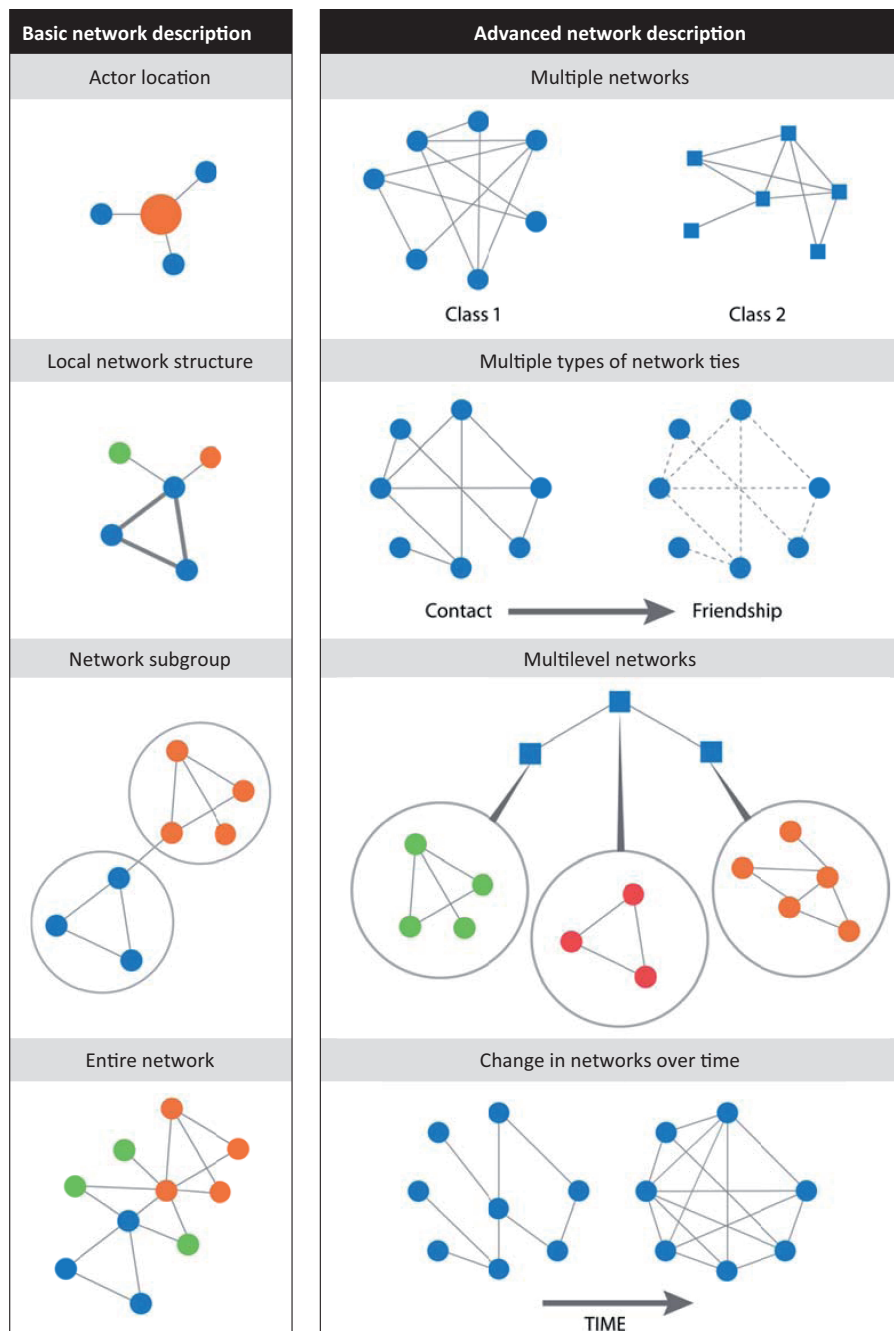


Figure 3

Analysis approaches for basic and advanced network analysis.



Contents

Symposium: Comparative Approaches to Reducing Health Disparities

Health Disparities Research in Global Perspective: New Insights and New Directions <i>Shiriki Kumanyika</i>	1
Health Inequalities: Trends, Progress, and Policy <i>Sara N. Bleich, Marian P. Jarlenski, Caryn N. Bell, and Thomas A. LaVeist</i>	7
Conceptual Approaches to the Study of Health Disparities <i>Ana V. Diez Roux</i>	41
How Society Shapes the Health Gradient: Work-Related Health Inequalities in a Comparative Perspective <i>Christopher B. McLeod, Peter A. Hall, Arjumand Siddiqi, and Clyde Hertzman</i>	59
Disparities in Infant Mortality and Effective, Equitable Care: Are Infants Suffering from Benign Neglect? <i>Diane L. Rowley and Vijaya Hogan</i>	75
Clinical Care and Health Disparities <i>B. Starfield, J. Gervas, and D. Mangin</i>	89

Epidemiology and Biostatistics

A Review of Spatial Methods in Epidemiology, 2000–2010 <i>Amy H. Auchincloss, Samson Y. Gebreab, Christina Mair, and Ana V. Diez Roux</i> ...	107
Early Intervention to Reduce the Global Health and Economic Burden of Major Depression in Older Adults <i>Charles F. Reynolds III, Pim Cuijpers, Vikram Patel, Alex Cohen, Amit Dias, Neerja Chowdhary, Olivia I. Okereke, Mary Amanda Dew, Stewart J. Anderson, Sati Mazumdar, Frank Lotrich, and Steven M. Albert</i>	123
Preventability of Cancer: The Relative Contributions of Biologic and Social and Physical Environmental Determinants of Cancer Mortality <i>Graham A. Colditz and Esther K. Wei</i>	137

The Hurrier I Go the Behinder I Get: The Deteriorating International Ranking of U.S. Health Status <i>Stephen Bezrucbka</i>	157
---	-----

Unintentional Injuries: Magnitude, Prevention, and Control <i>Sarah Stewart de Ramirez, Adnan A. Hyder, Hadley K. Herbert, and Kent Stevens</i>	175
--	-----

Environmental and Occupational Health

Community-Based Approaches to Controlling Childhood Asthma <i>Noreen M. Clark</i>	193
--	-----

Future Challenges to Protecting Public Health from Drinking-Water Contaminants <i>Eileen A. Murphy, Gloria B. Post, Brian T. Buckley, Robert L. Lippincott, and Mark G. Robson</i>	209
--	-----

Speed Limits, Enforcement, and Health Consequences <i>Rune Elvik</i>	225
---	-----

Toward a Systems Approach to Enteric Pathogen Transmission: From Individual Independence to Community Interdependence <i>Joseph N.S. Eisenberg, James Trostle, Reed J.D. Sorensen, and Katherine F. Shields</i>	239
---	-----

Public Health Practice

Advertising of Prescription-Only Medicines to the Public: Does Evidence of Benefit Counterbalance Harm? <i>Barbara Mintzes</i>	259
--	-----

Economic Evaluation of Pharmaco- and Behavioral Therapies for Smoking Cessation: A Critical and Systematic Review of Empirical Research <i>Jennifer Prah Ruger and Christina M. Lazar</i>	279
--	-----

Policies for Healthier Communities: Historical, Legal, and Practical Elements of the Obesity Prevention Movement <i>Samantha K. Graff, Manel Kappagoda, Heather M. Wooten, Angela K. McGowan, and Marice Ashe</i>	307
---	-----

Public Health and the Epidemic of Incarceration <i>Dora M. Dumont, Brad Brockmann, Samuel Dickman, Nicole Alexander, and Josiah D. Rich</i>	325
--	-----

Quitlines and Nicotine Replacement for Smoking Cessation: Do We Need to Change Policy? <i>John P. Pierce, Sharon E. Cummins, Martha M. White, Aimee Humphrey, and Karen Messer</i>	341
Systems Science Methods in Public Health: Dynamics, Networks, and Agents <i>Douglas A. Luke and Katherine A. Stamatakis</i>	357
Health Inequalities: Trends, Progress, and Policy <i>Sara N. Bleich, Marian P. Jarlenski, Caryn N. Bell, and Thomas A. LaVeist</i>	7

Social Environment and Behavior

Health Disparities Research in Global Perspective: New Insights and New Directions <i>Shiriki Kumanyika</i>	1
Health Inequalities: Trends, Progress, and Policy <i>Sara N. Bleich, Marian P. Jarlenski, Caryn N. Bell, and Thomas A. LaVeist</i>	7
Conceptual Approaches to the Study of Health Disparities <i>Ana V. Diez Roux</i>	41
How Society Shapes the Health Gradient: Work-Related Health Inequalities in a Comparative Perspective <i>Christopher B. McLeod, Peter A. Hall, Arjumand Siddiqi, and Clyde Hertzman</i>	59
Disparities in Infant Mortality and Effective, Equitable Care: Are Infants Suffering from Benign Neglect? <i>Diane L. Rowley and Vijaya Hogan</i>	75
Suicide Mortality in the United States: The Importance of Attending to Method in Understanding Population-Level Disparities in the Burden of Suicide <i>Matthew Miller, Deborah Azrael, and Catherine Barber</i>	393

Health Services

From Small Area Variations to Accountable Care Organizations: How Health Services Research Can Inform Policy <i>Harold S. Luft</i>	377
Suicide Mortality in the United States: The Importance of Attending to Method in Understanding Population-Level Disparities in the Burden of Suicide <i>Matthew Miller, Deborah Azrael, and Catherine Barber</i>	393

The Medicalization of Chronic Disease and Costs <i>Kenneth E. Thorpe and Meredith Philyaw</i>	409
The Methods of Comparative Effectiveness Research <i>Harold C. Sox and Steven N. Goodman</i>	425
Clinical Care and Health Disparities <i>B. Starfield, J. G�rvas, and D. Mangin</i>	89

Indexes

Cumulative Index of Contributing Authors, Volumes 24–33	447
Cumulative Index of Chapter Titles, Volumes 24–33	452

Errata

An online log of corrections to *Annual Review of Public Health* articles may be found at <http://publhealth.annualreviews.org/>