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Preface

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Preface to theme issue 'Modelling infectious disease outbreaks in humans, animals and plants: epidemic forecasting and control'

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This preface forms part of the theme issue 'Modelling infectious disease outbreaks in humans, animals and plants: epidemic forecasting and control'. This theme issue is linked with the earlier issue 'Modelling infectious disease outbreaks in humans, animals and plants: approaches and important themes'.

1. Introduction

The twenty-first century has already seen many infectious disease outbreaks in human, animal and plant populations, including the outbreak of plague in Madagascar in 2017 [1], outbreaks of Foot and Mouth disease in countries including the United Kingdom [2,3] and Japan [4], and the outbreak of olive quick decline in Italy due to the bacterial pathogen *Xyelella fastidiosa* which was first detected in that country in 2013 [5]. In §2d of the main introductory article of this pair of theme issues [6], we describe three of the main uses of epidemiological models today, namely: (i) guiding surveillance; (ii) epidemic forecasting; and (iii) assessing the potential impacts of interventions. These analyses are increasingly carried out in real-time when outbreaks are ongoing [2,7–15].

In this theme issue, we present articles about epidemic detection, forecasting and control at different stages of an outbreak by researchers from across the complementary fields of mathematical epidemiology in human, animal and plant systems. The questions that models are used to address inevitably change throughout an outbreak, according to the needs of decision makers and/or public health teams. Questions that are considered in this theme issue include the following.

Before and early in an outbreak:

- (i) how vulnerable is the population to disease, where will the pathogen arrive and where should surveillance be focused? [16–18],
- (ii) which surveillance method should be used? [10,19],
- (iii) what is the current outbreak size, and where is the pathogen now? [20,21],
- (iv) where and how can interventions be introduced to eradicate the pathogen quickly? [22], and
- (v) which data and resources are required to allow forecasting and control to be performed effectively? [10,20,23].

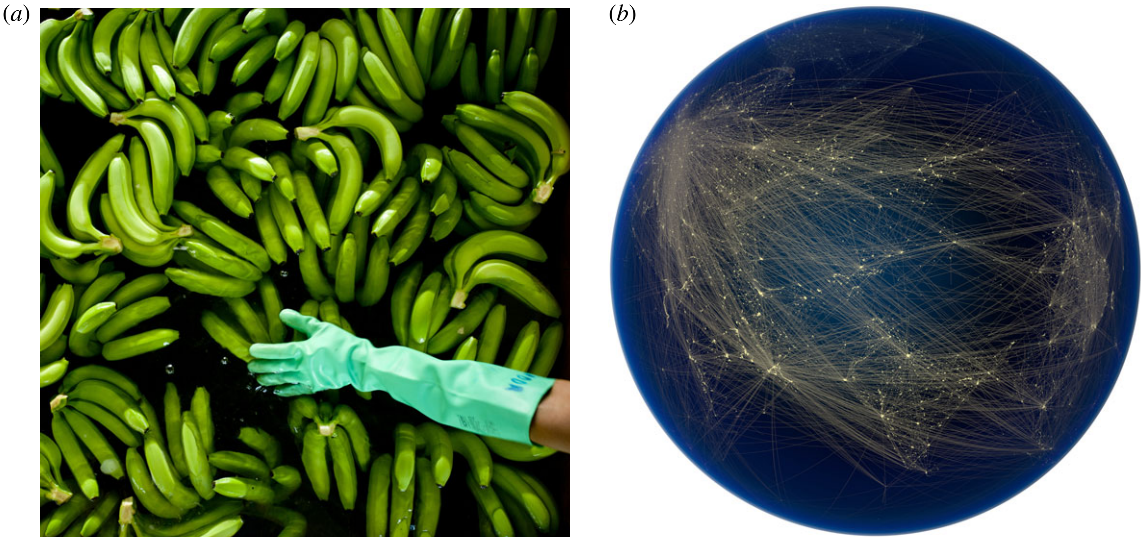

Figure 1. (*a*) Epidemiological models can be used to predict the impacts of current and proposed disease control measures in populations of humans, animals and plants. As an example of an intervention, fungicides are applied to banana plantations in Costa Rica 40–80 times per year to control Black Sigatoka disease, which has been exacerbated by climate change [26]. Here, bananas in another country—Columbia—are being washed prior to packing. Credit: David Bebber, 2017. This photograph is also the cover image of the linked theme issue 'Modelling infectious disease outbreaks in humans, animals and plants: approaches and important themes'. (*b*) Complex epidemiological models require detailed datasets for accurate parametrization. Here, a visualization of air traffic routes over Eurasia, which could be used to inform travel rates or connectivities in models of global pathogen transmission (e.g. [17,27]). Credit: Globaïa, 2011. This photograph is also the cover image of this theme issue. (Online version in colour.)

Once a major epidemic is ongoing:

(vi) how transmissible is the pathogen, by which transmission routes is it spreading, and how many cases will there be? [23–25],
(vii) how effective are current control efforts (figure 1*a*)? [28], and
(viii) which interventions should be introduced, and how should they be adapted as the epidemic continues? [18,22,24,28–30].

At the end of a major epidemic:

(ix) can the epidemic be declared over, or do hidden cases remain in the population? [20,31].

2. Requirements for outbreak modelling

In order to answer the types of questions outlined above, two important components are required. First, a model designed to answer the specific questions of interest is needed. For example, to predict the effects of interventions that are inherently spatial, such as culling all hosts within a fixed radius of known infecteds—a commonly used control for outbreaks in animal [32,33] and plant [34,35] populations—a spatially explicit epidemiological model is required. As described in the Introduction to the theme issue 'Modelling infectious disease outbreaks in humans, animals and plants: approaches and important themes' [6], a suite of modelling frameworks has been developed. For example, for representing outbreak dynamics, compartmental models that track the numbers of individuals in different infection or symptom states [36–39] or renewal equations that count the numbers of infections [40–42] can be used. For modelling disease surveillance, a number of statistical approaches have been designed [19,21,43].

Second, data relevant to the ongoing outbreak are required so that the model can be parametrized. To estimate the values of transmission parameters, temporal data are usually needed, such as time-series data describing the number of new cases in each time period (e.g. [44]). Because more data become available as an outbreak progresses, this leads to parameter estimates that change over time [45,46], and even to questions surrounding when parameters are known with sufficient certainty to allow action to be taken [45,47]. In certain scenarios, genetic data can provide information on temporal variables such as transmission rates between hosts or locations and rates of pathogen evolution [48–50]. The increasing complexity of models that are developed has led to the requirement for more data so that the models can be parametrized accurately, often including detailed datasets such as the precise locations of hosts in the landscape or travel routes and frequencies between different regions (figure 1*b*).

Data availability is extremely important. Despite well-documented instances in which crucial data were unavailable to modellers, such as during the early response to the 2014–16 Ebola epidemic [51], publically available datasets (such as those in the Project Tycho database [52]) and computing code (e.g. the code underlying the Nextstrain pathogen evolution tracker [53]) are increasingly common. Teaching tools such as the recent book by Ottar Bjørnstad [54] are introducing more mathematical modellers to epidemiological modelling. These advances are permitting the questions outlined above to be answered more accurately for pathogens in populations of humans, animals and plants.

3. Outlook

Collaboration between modellers, experimental or clinical epidemiologists and policy makers has been recommended in an attempt to build a framework that will allow outbreaks to be managed optimally [15,39,55]. However, collaboration between epidemiological modellers focused on different host types is encouraged more rarely [56]. Distinctions between different human, animal and plant populations and the pathogens that cause disease in those populations, such as the lack of adaptive immunity in plant hosts unlike in vertebrate animals [57], demand that certain research questions can only be addressed by modellers who are experts in particular systems.

However infectious disease outbreaks in humans, animals and plants also share many similarities [6]. Most of the questions addressed in this theme issue are relevant not only to particular pathogens in specific systems, but to almost all outbreaks irrespective of the type of host. As a result, we contend that increased collaboration between mathematical epidemiologists interested in infectious diseases of humans, animals and plants will lead to improved mathematical tools. Partnerships between modellers from different disciplines, combined with interaction with epidemiologists and decision makers, will permit epidemic responses to be performed most effectively.

We hope that this theme issue serves as a foundation on which to build this unified approach.

Data accessibility. This article has no associated data.

Competing interests. We have no competing interests.

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Editors' biographies

Dr Robin Thompson is a Junior Research Fellow at the University of Oxford, UK, and is the lead guest editor of this pair of theme issues. His research involves using mathematical models to represent the epidemiological or evolutionary dynamics of infectious disease outbreaks in human, animal and plant populations. This includes using statistical methods to estimate parameters associated with pathogen transmission and developing stochastic or deterministic models for generating outbreak forecasts. These forward projections can be used to predict the effects of proposed control interventions. Robin has developed models for a range of infectious diseases in human and plant populations—including Ebola virus disease, HIV, sudden oak death and citrus greening. He also recently developed a method for determining the optimal time to introduce control of an invading pathogen, with applications to diseases of livestock.

Dr Ellen Brooks-Pollock is a Lecturer at the University of Bristol, UK. She is interested in applying mathematical modelling and data science to applied questions in the control of infectious diseases. She has spent a lot of time thinking about tuberculosis (TB) in humans, bovine TB in cattle and zoonotic TB transmission from cattle to humans, but is also branching out into Hepatitis A, influenza and vaccination strategies. Ellen has spoken about bovine TB on BBC1's Countryfile and BBC Radio 4's Farming Today and sits on the Editorial board for Mathematics Today.

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