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BOARD INVITED REVIEW: Prospects for improving management of animal disease introductions using disease-dynamic models

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ABSTRACT: Management and policy decisions are continually made to mitigate disease introductions in animal populations despite often limited surveillance data or knowledge of disease transmission processes. Science-based management is broadly recognized as leading to more effective decisions yet application of models to actively guide disease surveillance and mitigate risks remains limited. Disease-dynamic models are an efficient method of providing information for management decisions because of their ability to integrate and evaluate multiple, complex processes simultaneously while accounting for uncertainty common in animal diseases. Here we review disease introduction pathways and transmission processes crucial for informing disease management and models at the interface of domestic animals and wildlife. We describe how disease transmission models can improve disease management and present a conceptual framework for integrating disease models into the decision process using adaptive management principles. We apply our framework to a case study of African swine fever virus in wild and domestic swine to demonstrate how disease-dynamic models can improve mitigation of introduction risk. We also identify opportunities to improve the application of disease models to support decision-making to manage disease at the interface of domestic and wild animals. First, scientists must focus on objective-driven models providing practical predictions that are useful to those managing disease. In order for practical model predictions to be incorporated into disease management a recognition that modeling is a means to improve management and outcomes is important. This will be most successful when done in a cross-disciplinary environment that includes scientists and decision-makers representing wildlife and domestic animal health. Lastly, including economic principles of value-of-information and cost-benefit analysis in disease-dynamic models can facilitate more efficient management decisions and improve communication of model forecasts. Integration of disease-dynamic models into management and decision-making processes is expected to improve surveillance systems, risk mitigations, outbreak preparedness, and outbreak response activities.

Key words: adaptive management, disease, domestic, interface, transmission model, wildlife

INTRODUCTION

Diseases that can be transmitted between domestic animals and wildlife are especially challenging to manage. There are multiple possible routes of initial pathogen introduction. Some pathogens are readily transmitted from wildlife to domestic host species and vice versa, which can complicate elimination. One example is the introduction of African swine fever virus (ASFv) in 2007 from Africa into Georgia and...
subsequent spread throughout Europe and Asia causing economic losses greater than US$267 million in Russia alone (Sánchez-Cordón et al., 2018). While domestic swine were initially considered the primary species involved in the epidemic, wild boar are now recognized to have an important role in the spread and maintenance of ASFv throughout affected regions (Gallardo et al., 2015). An additional example is the recent emergence and rapid global circulation of the Goose/Guangdong (GsGD) lineage of highly pathogenic avian influenza virus (e.g., subtypes H5N1, H5N2, and H5N8) (Verhagen et al., 2015). In North America, Clade 2.3.4.4 GsGD lineage was introduced through wild bird migratory routes resulting in reassortment with local strains and a multiyear (2014 to 2015) outbreak in commercial poultry with economy-wide losses of at least US$3.3 billion (Greene, 2015; Hill et al., 2017). At least 18 independent introductions from wild birds into commercial poultry occurred (Li et al., 2018) as well as transmission from commercial poultry back into wild bird populations (Ramey et al., 2018). While management was eventually effective, it did not prevent reintroductions from wildlife species. These major economic burdens and complex ecologies illustrate the need to develop risk assessment systems that aim to better understand and predict drivers of new introductions.

Key challenges for management of pathogen introductions into domestic animals include estimates of introduction risk, surveillance of pathogens and what to do with findings, and how to apply biosecurity and other mitigation strategies to minimize introduction risks. Routes of pathogen introduction can include complicated trade networks of domestic animals and their products, as well as air travelers; both of which are frequently poorly described. Introduction can also occur via wildlife species with complex ecology and lead to spillover and spillback between domestic animals and wildlife, driven by ecological processes that are often ill-understood. Thus, understanding and predicting introduction pathways is not straightforward—quantitative models can be important tools for interpreting the outcome of multiple, complex component processes, and for assimilating uncertainty in surveillance data and ecological processes to provide information to improve management decisions (Pepin et al., 2014; Huyvaert et al., 2018; Manlove et al., 2019). Models can also be the first, most efficient method of providing information for management decisions because of their ability to assimilate and evaluate multiple, complex processes concurrently and rapidly.

A major gap in quantitative model development is to estimate pathogen introduction risks by considering disease processes in both the source and recipient host populations (Lloyd-Smith et al., 2009). This is important because changing ecology in either source or recipient host population can dramatically alter introduction risk by changing the dynamics involved in the introduction pathway. Thus, inference based solely on a single component population or on retrospective patterns could produce erroneous predictions as conditions change. A second issue is that many analytical tools remain idiosyncratic, investigating disease dynamics in local source populations. It can be difficult to extrapolate findings based on locally focused systems for disease management decisions at broader spatial scales, or policy implementation that is typically at state, regional, or national scales. Lastly, despite the prospects of analytical tools to better understand disease introduction risks and support disease management and policy-making at the wildlife–domestic animal interface, decisions often rely on expert opinion that is based on historical experiences (Joseph et al., 2013).

To address these gaps we first review introduction pathways and disease transmission in the context of ecological processes that are crucial for informing disease management and policy decisions at the interface of domestic animal production systems and wildlife. We then describe how disease transmission models can improve disease management, specifically, for decision-making in risk assessment, response planning, and surveillance design. Next we introduce a conceptual framework for improving management of introduction risks for diseases with complex ecology, focusing on how models can improve decision-making. We then apply our framework to an important case study, ASFv in wild and domestic swine, to demonstrate opportunities for informing disease preparedness and response. We conclude with a discussion of opportunities to bridge current gaps between disease research and management.

ECOLOGICAL PROCESSES GOVERNING DISEASE EMERGENCE

New introductions of a pathogen into a naïve domestic animal production system can originate by contamination from the same domestic animal
production system in another area (e.g., movement of animals within a country or transboundary) or from another host species located in the same or a different area. Introduction into a wildlife population results from similar processes. We distinguish these processes as “lateral” versus “cross-species” transfer events, respectively. Both pathways can pose a risk to a particular domestic animal population or wildlife population, and involve several different ecological and epidemiological processes (Fig. 1A) that need to be understood for determining optimal management strategies.

**Lateral Transfer**

Domestic-to-domestic animal introductions can occur by multiple different mechanisms, for example, exposure to fomites or carcasses, direct contact with domestic animals, or contact via vectors (Fig. 1A). Exposure to fomites can occur through many routes including consumption of contaminated human food waste, animal feed, or mechanical transport by humans or equipment that have come into contact with infected domestic animals. Direct contact with infected domestic animals can be another significant route of lateral transfer, which can occur by importation of infected domestic animals from other countries or from farms within the same country.

**Cross-Species Transfer**

As with lateral transfer, transmission mechanisms between host species can involve fomites, vectors, environmental persistence, or direct contact (Fig. 1B). An additional layer of complexity with cross-species transfer is that donor host (i.e., host population that the pathogen originates) ecology may be significantly different than recipient host (i.e., host population that receives the pathogen) ecology, which can impose additional constraints for establishment and ongoing spread (Pepin et al., 2010; Plowright et al., 2017). Additionally, disease dynamics in one species can greatly influence the probability of cross-species transfer and in some cases persistence of the disease in the recipient host when repeated introductions are required to maintain transmission (Lloyd-Smith et al., 2009). For example, changing prevalence of a pathogen (or virulence) in wildlife can influence the risk of transmission to domestic animals. When wildlife migrate they can also impose risk over a broader

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**Figure 1.** Conceptual cycle of ecological processes governing lateral transfer of disease and subsequent establishment and transmission among domestic and wild animal hosts (panel A). Lateral transfer can occur through various pathways into either domestic or wild animals. Transmission between domestic and wild animals can occur directly or indirectly via the environment or vectors. Panel B describes a noninclusive representation of potential processes for lateral transfer and transmission of African swine fever virus (ASFv). Transfer directly into wild suid species is thought to primarily occur through contact with contaminated swine products that are imported or carried by travelers. Transfer directly into domestic swine can occur via contaminated products or through infected domestic swine. Whether ASFv is present in either wild or domestic populations various routes of transmission (direct and indirect) can facilitate cross-species transmission (i.e., spillover or spillback). Direction of arrows indicates expected direction of transmission (i.e., source and donor populations). Dotted arrows indicate hypothesized routes of transmission that are currently less supported by available data.
Spatial area compared with a donor host species that does not move very far (Manlove et al., 2019). Furthermore, the donor host may have originally become infected by contamination from domestic animals; thus, there are often complex spillover–spillback dynamics that can involve several domestic and wild host species.

Successful Establishment and Ongoing Transmission

The average number of transmissions from a single infectious host in a completely susceptible population, referred to as $R_0$, and the per-capita rate at which susceptible individuals become infected, termed the force of infection (FOI), are useful quantities for understanding, predicting, and managing epidemiological dynamics (for an extensive review of FOI and $R_0$, see Vynnycky and White, 2010; Keeling and Rohani, 2011). Estimates of $R_0$ can be used for predicting pathogen establishment; $R_0$ values <1 predict that the pathogen will not establish and $R_0$ values >1 predict ongoing transmission. Similarly, estimates of FOI describe infection risk for susceptible individuals, and can predict epidemic severity through time. $R_0$ is determined by 3 components: 1) the probability of infection given contact between a susceptible and infectious individual, 2) the average rate of contact between susceptible and infectious individuals (where 1 and 2 together describe the “transmission rate”), and 3) the duration of infectiousness. The transmission rate as well as the current number or proportion of infectious individuals determines FOI (i.e., for density- or frequency-dependent transmission, respectively). Thus, host ecology such as demographic dynamics, movement and spatial structure, social interactions, and physiological condition, as well as pathogen characteristics are important determinants of $R_0$ and FOI because they ultimately determine transmission rates.

The Role of Ecological Processes in Ongoing Transmission

The frequency and variation of contacts among infected and susceptible hosts (i.e., contact structure) (Fig. 1B) have important consequences for transmission rates (Keeling, 1999, 2005; Bansal et al., 2007; Sah et al., 2018). Variation in contact structure affects the probability that a pathogen will become established as well as outbreak size (Lloyd-Smith et al., 2005). Contact structure can be decomposed into 2 primary components, 1) the rates that individuals contact one another and 2) who contacts who (i.e., which individuals are connected). In wild animals, contact structure can vary seasonally due to birth pulses, seasonal resource patterns, or weather-related behavior such as hibernation (i.e., dynamic rather than static contact structures in which the frequency of contacts do not change through time). Wildlife contact structure is typically heterogeneous across multiple scales due to spatial structure and movement behavior, resource distribution, and social relationships (Sah et al., 2018). In contrast, domestic animal populations can be very dense and well-mixed at the farm level but can demonstrate heterogeneity in contact at larger geographic scales due to shipment patterns, marketing of domestic animals, and seasonal production practices (Gorsich et al., 2016, 2019). These differences in contact structure between domestic animal populations and wild animals can result in very different epidemiology, even for the same pathogen. Outbreaks in well-mixed populations are typically characterized by more rapid and severe outbreaks relative to those in populations with heterogeneous contact (Keeling, 1999; Bansal et al., 2007). The interaction between individual host movement behavior, population demographics, environmental conditions, and infection-induced behavioral changes can result in significant changes in disease dynamics (White et al., 2018). Because host ecology can have such dramatic impacts on disease dynamics, understanding these components is crucial for predicting and managing disease introductions into domestic animal populations (Plowright et al., 2017).

APPLICATION OF DISEASE TRANSMISSION MODELS TO MANAGE DISEASE INTRODUCTIONS IN DOMESTIC ANIMALS

Analytical tools such as disease transmission models used to model the dynamics of infectious diseases leverage a well-established and expanding body of disease transmission theory to construct representations of epidemiological systems. Disease transmission models provide a means for understanding how multiple, nonlinear processes such as host demographic dynamics, movement, contact, and host-to-host pathogen transmission determine outbreak probability and severity in a target host species. Disease transmission theory has shown that 3 quantities determine the initial introduction and ongoing transmission dynamics in a naïve host species (recipient): prevalence in
the donor host population, contact rate between the donor and recipient hosts, and probability of infection given contact (Lloyd-Smith et al., 2009). Together, these 3 components define the introduction force of infection for a pathogen that is a direct measure of infection risk to recipient host populations. Understanding the dynamics of introduction force of infection has provided valuable insight toward risk assessment, prevention, and response planning of livestock diseases (see below), but remains an underused tool (Lloyd-Smith et al., 2009).

Applications of disease transmission ecology typically have considered disease transmission processes in either the donor or recipient host populations, because dynamics at the interface of donor host and recipient populations is complex such that even conceptual development remains in its infancy (Plowright et al., 2017). Below we describe potential applications of disease ecology for informing management of disease in domestic and wild animals.

**Risk Assessment**

Risk analysis is an often broadly used term referring to risk characterization, communication, and management, that provides support for decision-making and is frequently used in policy development (Suter, 2016). For animal disease, risk analysis is an important process used to identify and characterize potential risks posed by implementation of a specific policy or event such as importation or movement of domestic animals (Sugiura and Murray, 2011). Thus, risk analyses are foundational for the development of animal health policy (Miller et al., 2013). The application of quantitative risk assessment models to predict lateral transfer (Fig. 1A) and cross-species transfer (i.e., outbreak dynamics) (Fig. 1B) is typically conducted independently. Disease risk in a recipient population is a function of both disease dynamics in the donor population and recipient populations (see ecological processes governing disease emergence). Quantitative risk assessment models in a recipient host population can be broadly classified into 2 types: dynamical and nondynamical. Dynamical models of risk represent time-varying disease transmission processes in host populations to infer transmission parameters related to force of infection using case data in recipient host populations (e.g., Bonney et al., 2018), or to predict outbreak dynamics from data of component processes (e.g., Fournié et al., 2013). These approaches are frequently implemented in a spatially explicit context (e.g., Buhrnerkempe et al., 2014; Bonney et al., 2018) but do not have to be spatial (e.g., Pepin and VerCauteren, 2016). Nondynamical risk models correlate predictors to case data (in donor or recipient host populations) to make predictions about potential risk in the recipient host population (e.g., Belkhiria et al., 2016) or predict risk probabilistically using conditional probability and historical surveillance patterns (Faverjon et al., 2015; Fountain et al., 2018). Nondynamical risk models have dominated the literature when assessing risks of transboundary introduction by lateral transfer. They are appealing because they allow for a multitude of introduction mechanisms to be compared against each other to identify the most likely pathway of introduction and quantify overall introduction risk. They frequently use expert elicitation approaches or preexisting data sources, and are often performed in user-friendly software such as Microsoft Excel (e.g., Miller et al., 2015). These features allow for rapid quantification in emergencies or when data are limited making them readily accessible across disciplines. Also, their structure of quantifying risk pathways through a series of conditional probabilities is appealing because it allows the propagation of parameter uncertainty and forms a process-based chain of events that lead to introduction. Whether applied to transboundary or within country introduction these approaches serve as a standard approach that is repeatable and transparent providing an important link with standards of the World Organisation for Animal Health (OIE) (Murray, 2004; Sugiura and Murray, 2011). More recently, conceptualizing disease introductions through a series of conditional probabilities, such as the OIE framework, has also been proposed for examining cross-species disease transmission using dynamical models (Plowright et al., 2017).

Limitations in assessing risk using nondynamical models are that risk of lateral transfer is typically based on historical data, and many of these approaches do not consider spatiotemporal heterogeneities. Using simulations, Enright and O’Hare (2017) have emphasized the importance of temporal dynamics in accurately capturing risk. They showed that ignoring temporal dynamics in animal movement can lead to overestimation of predicted outbreak size and nonoptimal response plans. Additionally, reliance solely on historical data can be misleading as ecological conditions change. Ignoring ongoing or seasonal dynamics in the donor host population could cause erroneous predictions of risk. In contrast, dynamical models can address these limitations because they inherently incorporate temporal changes and are readily
amenable to explicit representation of space. For example, in a dynamical model, domestic animal movement networks can be represented through time (Fournié et al., 2013; Buhnerkempe et al., 2014) to examine seasonality in risk and understand how particular changes in either the donor or recipient host population affect outbreak probability or severity (Buhnerkempe et al., 2014; Sokolow et al., 2019). These types of analyses are not as powerful in nondynamical models because they do not capture how nonlinear processes interact.

Dynamical models are typically used in 2 different ways: prediction from data on parameters (Halasa et al., 2016; Merkle et al., 2018) or estimation of epidemiological parameters by fitting the model to outbreak data (Bonney et al., 2018; Hayer et al., 2018) and have rarely been used to do both. One example where both have been successfully implemented are models developed by Hobbs et al. (2015) to support adaptive management of an ongoing outbreak of brucellosis in wild bison. They used extensive historical data describing population dynamics as well as information on contact structure and disease prevalence through time. Integrating historical data with current data they developed an iterative method to evaluate the probability of success for alternative management actions as well as estimating epidemiologically important parameters such as $R_0$ and FOI along with the changes in these parameters as a result of previous and current management decisions.

In addition to quantifying risk, dynamical models allow an understanding of how different components of disease transmission affect risk metrics, which in turn allows for process-based planning of outbreak response (Pepin et al., 2014). By targeting processes that determine risk rather than consequential patterns, response plans can be robust to changes in the underlying ecology driving disease transmission. A significant challenge of dynamical modeling approaches is they are often technically complex to develop and implement, which may limit their use and interpretation across disciplines in animal health management (Manlove et al., 2016). Because of their analytical complexity, dynamical models can also be computationally and time-intensive, which has further limited their use for rapid risk assessment when new threats are perceived. Also, while nondynamical models can rely on expert opinion, dynamical models need appropriate data on a variety of processes such as animal movement, disease prevalence, and host densities (Merkle et al., 2018). Appropriately formulating the model and accounting for multiple sources of uncertainty can require significant analytical effort to explore parameter sensitivity, understand whether processes are accurately portrayed, and examine consistency in parameter estimation or prediction (see Cross et al., 2019 for data and modeling challenges). Despite these challenges dynamical models can provide the most accurate portrayal of risk across space and time because they can explicitly account for changing nonlinear processes.

**Planning Response to Outbreaks**

Dynamical models have been used to explore optimal response plans for domestic animal diseases. Buhnerkempe et al. (2014) assimilated movement data for cattle shipments within the United States and used a dynamical model to show that local movement restrictions might be more effective at controlling an introduction of foot-and-mouth disease virus relative to state or national-scale movement bans. Similarly, Roche et al. (2015) used 5 different dynamical models to evaluate the effectiveness of different vaccination strategies for foot-and-mouth disease control and found that for all models vaccination led to a significant reduction in predicted epidemic size and duration compared to the “stamping-out” strategy alone. These results emerge from consideration of the interaction of dynamic host populations and epidemiological processes through time. In nondynamical models, disease dynamics in donor host populations are not represented explicitly, which neglects assessment of response plans that aim to limit transmission in donor host populations (Ebinger et al., 2011).

In diseases that have wildlife reservoirs, where spillover–spillback dynamics can lead to disease persistence, dynamical models have shown that the ecology of both the donor and recipient host populations need to be considered for optimal control (Cowled et al., 2012), and that the optimal control strategy may involve mitigation in both the donor and recipient host populations (Ward et al., 2015). However, the type of optimal control strategies employed in donor and recipient populations may differ as a function of host ecology and viral characteristics (Manlove et al., 2019). In wild pigs, contact structure can be fragmented (Pepin et al., 2016), such that viruses causing acute infections are not sustained (Pepin and VerCauteren, 2016). Optimal control strategies in the donor population can thus differ substantially based on the combined effects of infectious period of the virus and the contact structure of the donor host (Pepin and VerCauteren, 2016), which changes both the risk...
landscape and optimal control strategies of spill-over in space and time. A similar result arises from considering landscape heterogeneity in space and time—where consideration of the contact rates in space is important for determining optimal response plans (LaHue et al., 2016).

Additionally, accounting for these heterogeneities as well as uncertainties in successful management has only recently been addressed. Hobbs et al. (2015) found that accounting for uncertainty in the ability to implement management to control an ongoing outbreak of brucellosis in wild bison, elk, and cattle after accounting transmission heterogeneities dramatically influenced the probability of achieving disease control goals. A major gap in the use of dynamical models for response planning is a lack of applying these approaches in a “learning by doing” framework—where the models are used to predict optimal strategies, then the predicted strategies are implemented, and data for assessing effectiveness are collected and used to validate and refine the models (Restif et al., 2012). Incorporating economic principles in dynamical models for evaluating alternative response strategies is a second gap that is only rarely addressed. Economic assessments using dynamical models have typically used the model predictions as inputs into economic models in post hoc analyses (Thompson et al., 2018, 2019).

**Surveillance Design**

Analytical surveillance design has overwhelmingly been based on sample size statistics (Herzog et al., 2017) or risk-based ranking approaches (Stärk et al., 2006). Because surveillance resources (before an emergency) are often limited compared with response resources (during an emergency) efficient surveillance plans are crucial. In other words, surveillance needs to be “risk-based” and favor “early detection” (Stärk et al., 2006; Comin et al., 2012). Dynamical models have potential to inform effective risk-based or early-detection surveillance plans because they can concurrently evaluate how implementation of surveillance and response approaches affect outbreak severity (Comin et al., 2012), but dynamical models remain underused (Herzog et al., 2017).

Accounting for transmission processes in a spatially explicit framework is especially useful for determining optimal surveillance strategies (i.e., who, when, where, and how much) because they can help target surveillance to species, locations, and times where transmission risk is expected to be greatest. Gonzales et al. (2014) developed a dynamical model that accounts for within-flock transmission as well as the spatial location of flocks and between flock transmission. The model predicted transmission risk across space, producing a targeted risk-based surveillance strategy that allowed for early detection of low pathogenicity avian influenza in domestic chicken flocks in Denmark. Their model allowed for a dynamic evaluation of effective sampling frequency that optimizes resource allocation, but is seldom included in conventional methods of surveillance design. Additionally, because this approach dynamically evaluates changes in seroprevalence during an outbreak, it can provide insight into changes in transmission risk factors, and evaluation of control measures such as vaccination. Similarly, in the United States, an adaptive targeted risk-based approach has been used to allocate surveillance for avian influenza in wild birds (APHIS, 2016) and pathogens of interest in feral swine (APHIS, 2017). In both cases previous surveillance data were used to determine uncertainty in risk. Surveillance resources were then reallocated annually to prioritize greatest risk areas and those with the greatest uncertainty in risk. This adaptive approach to surveillance allocation was intended to reduce uncertainty in risk predictions and improve allocation of surveillance through time.

The application of dynamical models to guide surveillance planning is relatively new. One limitation of existing approaches using dynamical models is that risk-based targeting is often done as a post hoc analysis using the predictions of disease spread or contact and movement of at-risk animals from a dynamical model (Gorsich et al., 2018). While useful, this limits the utility when risk factors important for introduction or spread of a pathogen change seasonally and from year-to-year (Walton et al., 2016). Examples of changing introduction risks are seasonal differences in domestic animal shipment, changes in demand of animal products and live animals, or changes in global movement of people among countries. The flow of people, animals, and products can change dramatically across time and space. For example, Jurado et al. (2018) found that risks associated with ASFv introduction changed seasonally and varied spatially among years due to changes in frequency of airline travel among different airports in countries with and without ASFVs. Dynamical models mechanistically represent host-pathogen ecology allowing nonlinear relationships among risk factors to be included explicitly meaning that changes in risk factors (e.g., changes in movement of airline travelers, shipment...
patterns of domestic animals, or movement of wild birds) through time can allow for time-varying allocation of surveillance effort to optimize detection in response to shifting locations of greatest risk (Leslie et al., 2014; Walton et al., 2016).

A frequent objective of disease surveillance activities at the wildlife–domestic animal interface is monitoring changes in risk to domestic animals or effectiveness of risk reduction mitigations (Morner et al., 2002; Hoinville et al., 2013). Dynamical models have frequently been used to determine the transmission of pathogens among species in multi-host disease systems (Craft et al., 2008). Despite the established theory and application to understand disease transmission among species, dynamical models have rarely been used to determine surveillance in both donor and recipient populations concurrently (Shriner et al., 2016). As cross-species transfer depends on disease dynamic conditions in both the donor and recipient populations (Lloyd-Smith et al., 2009), surveillance of only a single component could fail to distinguish differences in the magnitude of risk across space or through time. For example, analysis of a low pathogenic avian influenza outbreak found that when the network of poultry producer relationships was explicitly included, the location of the index case (i.e., location of introduction) strongly effected both outbreak probability and size (G. Gellner, United States Department of Agriculture, unpublished data). Similarly, a continental scale analysis of foot and mouth disease that explicitly accounts for spatial differences in cattle shipment and density found that the duration and size of outbreaks was dependent on which local population the index case first occurred (Buhnerkempe et al., 2014). This indicates that disease risk in the recipient population is a function of both disease dynamics in the donor and recipient populations.

When wildlife are a potential donor host species, disease-dynamical models can be used to optimize when and where to conduct surveillance in both wild and domestic animals to improve risk monitoring in wildlife and early identification of introduction events into domestic animals. Conversely, when domestic animals are the donor, the utility and effectiveness of monitoring for potential spill-over from domestic animals to wildlife can be evaluated, which has been identified as a critical need for control and eradication of chronic diseases such as bovine tuberculosis and pneumonia (Miller and Sweeney, 2013; Besser et al., 2013). Additionally, the selection of pathogens to conduct surveillance in wildlife is frequently not representative of potential risks of introduction and transmission (Miller et al., 2017). Dynamical models can be used to evaluate potential risks and consequences posed among many pathogens allowing limited surveillance resources to be allocated to those with the greatest potential risks and consequences within the populations being managed.

THE WAY FORWARD FOR INTEGRATION OF DISEASE-DYNAMIC MODELS IN MANAGEMENT

Management and policy decisions are continually made to mitigate disease introduction and transmission risks. It is broadly recognized across a diversity of domains that science-based management, sometimes referred to as data-driven management, leads to more effective decisions but is challenging because it requires making the synthesis of data more accessible and relevant to policy decisions (Gregory et al., 2012; Williams and Hooten, 2016; Dietze et al., 2018). Additionally, scientific data are less valuable to decision-makers when there is considerable uncertainty or complexity. Integration of science in decision-making is further complicated because policy decisions and science frequently have different timelines, incentives, and stakeholders, which can hamper efficient integration of science into the decision process (Funtowicz and Strand, 2007).

Synthesizing science to improve its usefulness in disease management requires monitoring data intended to understand factors and processes that drive disease introductions and ongoing transmission. Improving the understanding of disease processes that drive pathogen introduction and transmission is fundamentally essential and ultimately leads to better, more efficient policy decisions (e.g., biosecurity or response planning). Thus, prioritizing “learning” in the adaptive management cycle (Fig. 3) can be a very important part of management and the science intended to support management decisions.

Adaptive Management

Science-based disease management requires a fundamental shift from simply monitoring to surveillance—i.e., using monitoring data to predict changes in disease risk and management effectiveness, and decide/perform management actions that mitigate risks. Disease-dynamic models provide an analytical framework for both understanding and predicting disease processes in a
management context using monitoring data. The adaptive management framework then provides a method for integrating disease data using disease-dynamic models to iteratively reduce uncertainty in decision-making over time resulting in improved decisions and outcomes (Allen et al., 2011) (Fig. 3).

The adaptive management cycle is typically broken into 2 processes. First, a structured decision-making process (Fig. 3A) formalizes the definition of the problem, objectives, evaluation of decision trade-offs, and results in a current optimal management decision. The second process is characterized as learning. This process represents the management decision implementation, monitoring of the system and evaluation of progress toward management objectives and any adjustment to management decisions through time that improve progress toward objectives. In disease management applications, adaptive management is a method for integrating surveillance data and analysis of disease management iteratively through time to allow learning through disease management actions (Fig. 3B). Through formal analyses of uncertainty, disease surveillance can be guided to improve learning about the most important factors affecting risk or management effectiveness in order to optimize information for decision-making.

Adaptive management has been suggested as an approach to manage disease (Miller et al., 2013; Webb et al., 2017), allocate disease surveillance (Gonzales et al., 2014), and improve disease interventions (Merl et al., 2009; Shea et al., 2014) but has rarely been formally implemented to manage a disease system.

**ASFv as an Example**

Recently emerged as a significant threat to domestic swine production globally, ASFv is currently present in many regions of Africa, Europe, and Asia (Fig. 2A). Currently, ASFv is reportable to the OIE, and transboundary introduction into a country free of the disease can have severe economic consequences resulting from production losses, loss of export markets, and eradication programs. Species in the *Suidae* family are susceptible to infection with ASFv (Penrith and Vosloo, 2009). Infection with ASFv in most *Suidae*, particularly domestic swine, typically results in high mortality; however, once established in a population, the disease can manifest as a subacute clinical form that can be sustained in the population (Gallardo et al., 2015; Nurmoja et al., 2017; Sánchez-Cordón et al., 2018). Transmission of ASFv can be through direct contact with infected pigs, indirect contact through fomites, or through soft tick species in the genus *Ornithodoros* (Mellor et al., 1987; Penrith and Vosloo, 2009; Guinat et al., 2016). The virus is highly resistant to inactivation and can remain viable in the environment for many days and in undercooked or cured pork products for at least 4 months (Plowright et al., 1969; Farez and Morley, 1997). The high stability of ASFv in addition to multiple potential routes of transmission that include vectors, fomites, and direct transmission has made ASFv particularly difficult to control in populations and a significant concern globally (Sánchez-Cordón et al., 2018).

Introduction of ASFv into the western hemisphere could threaten food security and have a large economic impact resulting from the presence of sympatric vector species and susceptible feral and domestic swine host populations (Brown and Bevins, 2018) (Fig. 2D–F). The Americas account for 58% of total global pork exports, 83% of global imports and exports of live domestic swine, and have the third largest standing inventory of domestic swine (USDA, 2018). The predicted economic impacts resulting from an ASFv outbreak in North America are more than US$4.25 billion, with a cost-benefit ratio of ASFv prevention programs of more than US$450 billion (Rendleman and Spinelli, 1999) making ASFv a threat to the global economy (Sánchez-Cordón et al., 2018). Contaminated animal-derived products have been identified as one of the greatest risks for the entry of ASFv and other foreign animal diseases (FADs) (Mur et al., 2012). Specific to ASFv the annual probability of transboundary introduction varies through time and by pathway. Introduction via swine products carried by travelers or through importation is considered more likely than importation of infected live domestic swine (Herrera-Ibata et al., 2017; Jurado et al., 2018). If introduced into the western hemisphere the risk of establishment is expected to vary geographically by the pathway of introduction and the presence of wild and domestic swine (Herrera-Ibata et al., 2017; Jurado et al., 2018). Currently available risk estimates for transboundary introduction are complicated by multiple pathways of introduction via legal and illegal routes (e.g., illegal importation of swine products), the presence of competent soft tick vectors, and the presence of both feral and domestic swine (Sánchez-Cordón et al., 2018). Dynamical models offer a potential tool to account for the complex geographic and temporal risks resulting from the distribution of vector species, densities of feral
and domestic swine, and differing routes of lateral and cross-species transfer that are expected to vary through time.

**Adaptive Management of ASFv**

New populations continue to be invaded by ASFv through multiple pathways yet the specific pathways of greatest importance appear to vary among regions and there is uncertainty about how best to mitigate location-specific risks. The conceptual approach presented in Fig. 3 offers an opportunity to address these challenges because analyses and associated risk predictions can be continually updated using newly available data allowing allocation of surveillance resources to specific pathways, locations, or animal populations (wild or domestic) to be varied and improved through time. For example, frequently updating analyses using new data can improve allocation of surveillance effort among different pathways of lateral and cross-species transfer through time resulting in earlier detection of ASFv introduction by targeting surveillance of swine populations most likely to be exposed to contaminated materials (Figs. 1 and 2). The resulting ASFv surveillance data (e.g., Fig. 2) can then be integrated, using dynamical models, with previous monitoring data and near-term host population data (e.g., density, movement, and contact) to provide new predictions of ASFv introduction risks, spread, and consequences. This provides a method of integrating analyses assessing lateral and cross-species transfer that are typically conducted separately. Through time this dynamical modeling allows a method of synthesizing across the entire system to improve and optimize surveillance guidance (adaptive surveillance) that best mitigates changes in risk resulting in improved understanding of risks (Fig. 3B). Similarly, mitigations to reduce introduction risks such as placing limitations on...
Applying models in disease management

Importation of products most risky for ASFv or refined targeting of inspections of imported products or airline travelers from ASFv regions can be iteratively evaluated and optimized through time. Uncertainty analysis can identify which ASFv surveillance streams or surveyed populations are most critical for reducing uncertainty in predictions. Value-of-information analysis can aid in the prioritization of ASFv surveillance streams or populations (wild or domestic) to be monitored by providing a means to evaluate the “return on investment” provided by the allocation of resources in each surveillance data stream. Additionally, the sensitivity of decision-making to forecast uncertainty can be used to identify how better model predictions would improve decision trade-offs and when the model is adequate to meet decision needs (Dietze et al., 2018).

Changes in ASFv introduction risks and improved knowledge of introduction risks gained through iterative adaptive surveillance directly influence predictions of disease spread, consequences, and optimal control options. Correspondingly, ASFv control options can be improved as fundamental disease drivers in a region change (e.g., changes in density of wild and domestic swine) or

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**Figure 3.** Conceptual relationship between iterative disease predictions and adaptive decision-making. Panel A describes a generalized depiction of the adaptive management cycle that includes both structured decision-making and learning processes (Allen et al., 2011). Panel B describes a conceptual approach for integrating disease modeling into the decision-making process. Iterative prediction using disease-dynamic models (blue oval) integrates data describing risk factors to make predictions of introduction risk, spread, and associated consequences. Using these predictions optimal risk-based targeted surveillance strategies to detect introductions, risk mitigations to reduce introduction and spread, and optimal control options are determined. Surveillance guidance informs (adaptive surveillance) decisions concerning allocation of surveillance (i.e., when, where, and how much). Optimal risk mitigations and potential control options inform adaptive planning and preparedness decisions. New surveillance data are then integrated with new data describing changes in risk using the iterative prediction cycle to provide updated and improved guidance for surveillance, risk mitigations, and control options. Thus, learning has occurred and better information is available to support decision-making.
as the types, volume, and origin of imported swine products change. Predicted ASFv optimal control strategies can be used in an adaptive planning process that improves the potential alternatives considered. For ASFv this could include proactive population reduction of wild swine, which is currently being implemented in some European countries, or greater targeted removal of invasive feral swine in countries with active population control programs. Additionally, changes in predicted introduction and spread of ASFv can be used to iteratively update guidance on the predicted culling or biosecurity practices required to limit spread if introduced. This information can be used by managers to forecast resource needs and develop more accurate and useful response plans that are more dynamic rather than static.

In the event that a pathogen such as ASFv is successfully introduced, predictions of optimal disease control strategies serve as a starting point from which to begin managing an outbreak and monitoring its progress. “Learning by doing” can then be used to continually improve surveillance designs and response plans. This could be particularly important for FADs such as ASFv that may not have previously occurred in a country resulting in no prior data describing disease dynamics. For example, ASFv has not previously been introduced into North America but at least 5 experimentally competent tick vectors for ASFv occur and sympatric populations of wild and domestic swine are present (Fig. 2D–F). An additional advantage of using an iterative prediction cycle to inform decision-making is that consequences of introduction and spread can be explicitly included in models. This allows for evaluation of potential risk mitigations (either proactive or during an outbreak) to be evaluated using cost-benefit approaches, providing practical guidance based on current resources. Uncertainties can be included in the cost-benefit analysis allowing for improved understanding of which data may be needed to improve consequence assessments.

**Practical Challenges**

Our conceptual approach for integrating disease-dynamic models directly within the decision-making process using adaptive management are not without challenges. And several key challenges need to be tackled for adaptive disease management to be most successful, especially for disease systems that cross the wild–domestic animal interface.

Updating predictions and forecasts iteratively requires data that can be difficult to collect and can be labor-intensive. One of the largest challenges is the need to collect multiple types of data—data describing disease occurrence, changes in wild and domestic animal populations (occurrence and population density), changes in population contact (whether via products, humans, or directly), and changes in other epidemiologically important processes such as vector distribution and occurrence (e.g., Fig. 3B). Some of these data, such as monitoring of domestic animal populations, already have systems in place to collect and maintain data. However, disease surveillance data within wild animal populations or for common routes of disease introduction are frequently not available, or are only available at broad spatial or temporal scales that might not match the epidemiological scales of interest, or do not align with epidemiological risks (Miller et al., 2013, 2017; Cross et al., 2019). Surveillance data collection is often limited by the number of samples, spatial locations, or time frames that samples can be collected. However, the conceptual approach we present here offers a framework to rigorously address these challenges by allowing for the evaluation, comparison, and identification of those data of greatest importance for management decision trade-offs.

Additionally, the implementation of disease-dynamic models can be technically difficult and time-consuming. As a result the development and application of these approaches has more frequently been implemented in an academic environment to address specific, narrowly focused policy decisions. An opportunity to increase the application of dynamical models within the decision-making process is to focus on objective-driven models that provide practical predictions that are directly useful to those managing disease. Indeed, dynamic models have been used mechanistically for avian influenza (Malladi et al., 2012; Weaver et al., 2012; Bonney et al., 2018), brucellosis (Hobbs et al., 2015), and foot-and-mouth disease (Buhnerkempe et al., 2014; Roche et al., 2015) providing practical objective-driven predictions to support disease management decisions. Recognizing that modeling is a means to improve disease management and outcomes is important and fosters increased use of these tools. This is most successful when these approaches are implemented in a cross-disciplinary environment that includes scientists and decision-makers representing both wildlife and domestic animal health. Imbedding technical expertise within the decision-making process will likely ensure
long-term success of decision processes that use model-based support. There is an additional opportunity to integrate economic principles such as value-of-information and cost-benefit analysis into the surveillance and monitoring decision process using the framework we presented. While the adaptive management framework is often discussed with regard to improving decisions through learning it also offers opportunities to address these other challenges by continually reassessing the approaches used to support decision processes.

CONCLUSIONS

Using adaptive disease management with dynamical models can support the development of optimal surveillance systems, risk mitigations, as well as disease preparedness and response activities because this approach allows learning to occur from the most current conditions. Further it allows a method of synthesizing across and integrating analytical processes that are frequently conducted independently which can facilitate learning about the system being managed. This can be particularly important for FADs that frequently have limited data available that may or may not represent disease dynamics in recipient host populations. While ASFv was highlighted as an example, the conceptual framework described could be applied to other diseases such as classical swine fever or avian influenza. This conceptual framework does not have to be restricted to FADs and can provide significant benefit for managing endemic diseases as well. Using dynamical models within the decision-making process can foster the resilience and flexibility needed to address the uncertainty associated with disease decisions, thus improving the ability to tackle inevitable changes and surprises that arise.

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LITERATURE CITED

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