
Modeling the interface between livestock,
people, wildlife, and vectors: The results
from three consultative reports

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Outline

- ▶ Brief overview of *NAADSM*
- ▶ Our motivation, the request, and their findings
 - ▶ Public health/human dissemination models
 - ▶ Wildlife models
 - ▶ Vector-borne models
- ▶ Next steps

About *NAADSM*

NAADSM is a computer program designed to simulate the spread and control of **foreign animal diseases** in a population of **susceptible herds/flocks**. Among the goals of the *NAADSM* project are the following:

- ▶ To produce a practical, user-friendly modeling application suitable for the study of disease spread in the absence of an actual outbreak;
- ▶ To offer a tool for the assessment and evaluation of proposed disease control strategies and preparedness planning purposes;
- ▶ To provide support for researchers who will incorporate disease modeling in their work;
- ▶ To offer outreach and training in the use of disease models in general and of *NAADSM* in particular to the scientific and veterinary medical communities in North America and abroad.



Consultative report: Public health/human dissemination models

Our Motivation

- ▶ H1N1, etc
 - ▶ When H1N1 was discovered in humans in Mexico and later when swine were possibly infected from a human source in Canada, thoughts about our abilities to model cross-species transmission started.
 - ▶ We wondered whether it made sense to link human and animal disease spread models in order to better mimic the zoonotic spread of disease.

The Request

- ▶ **Task: Develop a consultative report for public health/human dissemination models**
 - ▶ Conduct a literature review designed to gather information about the availability, accessibility, capabilities, and appropriateness of various public health/human dissemination models.
 - ▶ Develop a justified recommendation, based on the research conducted, regarding which of the public health/human dissemination models are most appropriate to layer with *NAADSM* in order to better mimic the zoonotic spread of disease agents and consequently capture the public health component of disease spread.

Understanding Disease Transmission Patterns Host Species Barrier and the Implications for Simulation Modeling

Marian Talbert, Mo Salman, and Ashley Hill

June 22, 2010

1 Introduction

With the ever-increasing connectedness of distant human populations and the omnipresent threat of animal diseases spreading to humans, there is a growing interest on determining the threat that is posed due to our associations with animals, including livestock, and how we can minimize the resulting risks. Indeed according to Cleveland, zoonotic diseases account for nearly two thirds of all human infectious diseases [6]. This group of diseases represents over 800 pathogens with a vast spectrum of disease manifestations, transmission patterns, hosts dynamics, life cycles, and abilities to evolve. Here the biological events that lead to transmission of disease between animals and humans are discussed with the aim of identifying disease transmission patterns that can realistically be represented by a linkage between human and animal disease spread models. Due to key concerns related to human health, special consideration will be given to influenza A viruses and we will begin with a brief review of this disease and its agents.

2 Influenza A background

Influenza A is a virus affecting several host species with some subtypes affecting both humans and other animals. Influenza viruses discussed in this document refer only to type A influenza and not to the other types, such as influenza B and C, that are primarily diseases of humans and have not been

Consultative report on modeling zoonotic diseases

Developed by
representatives from the
Animal Population Health
Institute at Colorado State
University

- Marian Talbert
- Mo Salman
- Ashley Hill

Aim of the study

- ▶ “Biological events that lead to transmission of disease between animals and humans were examined with the aim of identifying disease transmission patterns that can realistically be represented by a linkage between human and animal disease spread models.” (*Talbert et al 2010*)

Brief summary of conclusions

- ▶ “The events associated with **disease transmission across the species barrier** are not simple and their impact from a modeling perspective should not be taken for granted.”
(Talbert et al 2010)
- ▶ “Review of the literature on zoonotic livestock diseases has **not revealed any obvious contenders** for representation using a linkage of human and animal disease spread models.” *(Talbert et al 2010)*

Consultative report: Wildlife-livestock disease transmission models

Our Motivation

- ▶ Pseudorabies, foot-and-mouth disease, etc.
 - ▶ Wildlife can play an important role in the spread and control
 - ▶ Explore existing modeling capabilities that could be readily applied to better understand the potential disease impacts that arise as a result of the domestic-livestock interface

The Request

- ▶ **Task: Develop a consultative report on modeling the wildlife/livestock interface**
 - ▶ Conduct a literature review designed to gather information about the availability, accessibility, capabilities, and appropriateness of various wildlife disease spread models.
 - ▶ Develop a justified recommendation, based on the research conducted, regarding which of the wildlife disease spread models are most appropriate to layer with *NAADSM* in order to better mimic the wildlife-livestock interface and consequently capture the wildlife component of disease spread.

Consultative Report

Wildlife-Livestock Disease Transmission Models: Literature Review and Subject Matter Expert Consultation

Karin Hamilton, Jeff Bender

I. Introduction

The North American Animal Disease Spread Model (NAADSM) is a stochastic, spatial, state-transition simulation model that was created to simulate the spread and control of highly contagious diseases in a susceptible population of animals. The user of the model inputs disease and population parameters such as “cattle” versus “swine” versus “poultry” or “aerosol” versus “indirect contact” versus “direct contact spread” etc. Control measures, including the cost of those measures, can also be included – such as vaccination, culling or depopulation. However, the model does not currently have the capabilities of assessing or projecting disease spread from wildlife to livestock.

Wildlife play an important role as reservoirs, making control of numerous diseases such as pseudorabies and foot and mouth disease difficult. Because of commonalities such as habitat overlap, biological similarities with respect to their ability to share organisms, similar feeding behaviors, etc., wildlife can both infect and become infected by captive livestock. For example, deer in the United States are known to be infected with tuberculosis and can serve as a reservoir for re-infection for livestock populations. Modeling the spread of disease exclusively in livestock is unrealistic when wildlife can be infected and serve as maintenance reservoirs of potential pathogens.

It is difficult to document disease transmission in wildlife populations let alone between wildlife and livestock. First, wildlife, by nature are wild and free ranging so it is difficult to capture, collect samples and ultimately control disease spread in these species. Also because of their free ranging nature, the best population counts are only estimates. These populations wander across designated jurisdictional and political borders. Another factor is that many of the diagnostic tests and vaccines available for livestock have not been validated in the wildlife species.

With expansion of human habitations, there are more opportunities for human-wildlife interactions. One example is deer eating food put out for cattle on farms, which results in an increased contact between deer and livestock. Another example is people putting out food in their yards for wildlife such as deer or birds, which allows for increased contact between people, domestic animals, and wildlife. When modeling diseases, wildlife rarely can be treated as a typical “livestock herd” since wildlife interactions and movement patterns are different. For example, they may live in a solitary manner in one season or group into herds during breeding season.

Because of the exchange of diseases between wildlife and livestock, it is important to explore modeling capability to better understand potential disease impacts. The

Consultative Report on modeling the wildlife-livestock interface

Developed by representatives at the Center for Animal Health and Food Safety at the University of Minnesota

- Karin Hamilton
- Jeff Bender

Aim of the study

- ▶ “A literature review was performed to identify and evaluate current models exploring disease transmission at the wildlife-livestock interface. The models that were found were then evaluated relative to their modeling capability and adaptability to *NAADSM*.” (*Hamilton et al 2010*)

Brief summary of conclusions

- ▶ **Geographic or cellular-automata models** can incorporate both wildlife and livestock disease transition states and the explicit considerations of space and time. Further this type of model is capable of examining ... control measures.” (*Hamilton et al 2010*)
- ▶ Based on the research presented, it is **unclear** which of the wildlife disease spread models are most appropriate to layer with *NAADSM* or whether it would be best to develop a separate model to serve as a companion to *NAADSM*.

Consultative report: Vector-borne disease transmission models

Our motivation

- ▶ Rift Valley Fever, etc.
 - ▶ Explore existing modeling capabilities that could be readily applied to better understand the potential disease impacts that arise as a result of the involvement of vectors
 - ▶ The ability to model vector-borne diseases would help to expand the types of questions we are able to help answer

The Request

- ▶ **Task: Develop a consultative report on modeling vector-borne diseases**
 - ▶ Conduct a literature review designed to gather information about the availability, accessibility, capabilities, and appropriateness of various vector-borne transmission models.
 - ▶ Develop a justified recommendation, based on the research conducted, regarding which of the vector-borne models are most appropriate to layer with *NAADSM* in order to better mimic the vector-borne component of disease spread.

Vector-Borne Disease Transmission Models: Literature Review and Subject Matter
Expert Consultation

Tim Boyer, Mac Farnham, Molly Emerick, Jeff Bender

I. Introduction

Vector-borne diseases (VBD) are those which use an intermediate host to transmit disease from an infectious host to a susceptible host. The vast majority of vectors are biting arthropod insects and the majority of VBD are viral. Vector-borne diseases can have complicated transmission cycles often involving multiple-hosts species some of which may be amplifying reservoirs while others are incidental or dead-end hosts. VBD may involve multiple vector species with their own population dynamics that are sensitive to environmental factors. Issues like these make it difficult to sort out all of the factors that drive VBD transmission creating the need to use models to predict outcomes and the understand transmission dynamics of VBD systems.

State-transition disease models are one of the primary tools used by scientists, medical, and veterinary professionals to study disease transmission and epidemics in populations. These models classify members of a population by their disease states such as susceptible, infectious, or recovered (SIR models) and mathematically describe how individuals move among these states. The North American Animal Disease Spread Model (NAADSM) is a spatially explicit, stochastic, state-transition model which is maintained through a collaborative effort involving the USDA Center for Epidemiology and Animal Health (CEAH), the Animal Population Health Institute (APHI) at Colorado State University, the University of Guelph Department of Computer and Information Science, the Canadian Food Inspection Agency, and the Ontario Ministry of Agriculture, Food, and Rural Affairs. The NAADSM was originally developed to evaluate the

Consultative report on modeling vector-borne diseases

Developed by
representatives at the
School of Public Health and
the Center for Animal
Health and Food Safety at
the University of Minnesota

- Tim Boyer
- Mac Farnham
- Molly Emerick
- Jeff Bender

Aim of the study

- ▶ “This consultative report comprises the primary objective of the government-university cooperative agreement: to conduct a review of the literature on VBD models and modeling expertise. The literature review was designed to gather information about the availability, accessibility, capabilities of various vector-borne disease spread models and their appropriateness for incorporation into the *NAADSM*.” (*Boyer et al 2010*)

Brief summary of conclusions

- ▶ “The best approach to building a flexible VBD model may be to create a separate model independent of the *NAADSM* using an agent-based approach. This would permit users to model multiple hosts, permit dispersal of wildlife hosts, and dispersal of either individual vectors or metapopulations of vectors. The agent based approach would also permit incorporation of landscape and climate...” (*Boyer et al 2010*)
- ▶ The *NAADSM* is a powerful, flexible, and accessible tool for modeling directly transmitted disease. Development of a separate VBD model as a companion to the *NAADSM* is the best approach to preserving the current function of the *NAADSM* while expanding the modeling capabilities offered by the *NAADSM* core development team” (*Boyer et al 2010*)

Next Steps

- ▶ Allow our collaborators to finalize their consultative reports
- ▶ Share products with the *NAADSM* development team for consideration
- ▶ Identify, more specifically, the questions of interest and expand our network of partners to leverage the expertise already existing in the modeling community