A Framework for Modeling Emerging Diseases to Inform Management

Technical Appendix

Application of framework to hypothetical scenario.

Scenario: Salamander chytridiomycosis, caused by a fungal pathogen, *Batrachochytrium salamandrivorans*, is detected from an unusual die-off occurrence in a U.S. Fish and Wildlife Refuge Complex in the Mid-Atlantic region of the United States. Park staff and visitors detected several dead and dying newts near a pond that is a popular fishing location. Currently, only one pond has been identified as containing infected eastern newts (*Notophthalmus viridescens*). At this time, a dozen specimens have been collected and all have tested positive for the fungus. The true population size of newts in the pond is unknown. There are at least three other potential breeding areas within 1 km of the infected pond.

Pathogenicity: The fungus has been shown to cause high rates of mortality in susceptible salamander species and in particular newts (online Technical Appendix Table 3) (*1*).

Environmental niche: The temperature and humidity niche of *B. salamandrivorans* is predicted to include large areas of the Mid-Atlantic (*2*,*3*).

Taxonomic breadth of hosts: Most fungal diseases are taxa specific; therefore, the risk for spread of the disease to other taxa (mammals or birds) is likely low (*4*).

Transmission pathway: Direct contact has been shown to be an effective transmission pathway for the fungus (*1*), but indirect transmission is possible with fungal spores potentially being carried by water, on fomites, and by other organisms (*4*).

Social behavior/connectivity: In general, eastern newts live in metapopulations (i.e., small populations connected to the larger population through occasional dispersal events) (*5*). Gill et al. identified two movement periods in eastern newts: a movement to breeding ponds in spring and migration periods to terrestrial habitat in the fall (*5*). Though the literature on newt movements is sparse, Regosin et al. determined that fewer than 20% of the population traveled

more than 100 m from breeding ponds (*6*). However, Roe and Grayson found that efts (i.e., juvenile stages of newts) moved up to 50 m a night indicating the potential for longer distance movements (*7*). Finally, contact during breeding season (March–August) is increased for species with aggregate breeding behaviors (e.g., spotted salamanders) but may be reduced during other times of the year.

Technical Appendix Table 1. Examples from the literature describing the use of different modeling frameworks to describe disease processes

Model type	Examples	Software
Occupancy	chytrid fungus in amphibians (*8*) flea species presence on prairie dogs (*9*) parasites in birds (*10*) chytrid fungus in amphibians (*11*) disease dynamics in metapopulations (*12*) whirling disease in fish (*13*) insects and palm trees (*14*)	Unmarked: https://cran.r-project.org/web/packages/unmarked/index.html Presence: http://www.mbr-pwrc.usgs.gov/software/presence.html MARK: http://warnercnr.colostate.edu/~gwhite/mark/mark.htm
Compartmental	brucellosis in bison (*15*) chronic wasting disease in deer (*16*) macroparasites and wildlife (*17*) bacterial infections and possums (*18*) harvest effects on wildlife disease (*19*) West Nile virus and birds (*20*) control strategies and swine flu (*21*) dengue and mosquitoes (*22*)	EpiModel: http://www.epimodel.org/ Outbreak Tools: https://cran.r-project.org/web/packages/OutbreakTools/index.html simecol:https://cran.r-project.org/web/packages/simecol/index.html Any ordinary differential equation solver: Matlab, Simulink, Excel, deSolve in R
Diffusion	rabies in foxes (*23*) foot and mouth disease in pigs (*24*) rabies in raccoons (*25*) pathogens and bumblebees (*26*) plague traveling waves (*27*) chronic wasting disease (*28*)	spate: https://cran.r-project.org/web/packages/spate/index.html simecol: https://cran.r-project.org/web/packages/simecol/index.html
Agent-based	parasite transmission in monkeys (*29*) rabies in foxes (*30*) swine fever in wild boar (*31*) territoriality and sociality of wolves (*32*) foot and mouth outbreak in cattle (*33*)	NetLogo: http://ccl.northwestern.edu/netlogo/ or RNetlogo: http://rnetlogo.r-forge.r-project.org/ Ecolab: http://ecolab.sourceforge.net/ Flame: http://www.flame.ac.uk/ Pandora: http://www.bsc.es/computer-applications/pandora-hpc-agent-based-modelling-framework Simecol: https://cran.r-project.org/web/packages/simecol/index.html

Technical Appendix Table 2. Detailed description of parameter estimates associated with each characteristic, and techniques associated with the estimation of those parameters

Key parameters	Specific parameters	Techniques
Pathogenicity	Survival and reproduction of diseased and nondiseased hosts Occupancy of patches Population density in areas with and without disease	Mark-recapture of diseased and uninfected hosts Visual counts of diseased and uninfected hosts Presence/nondetection of hosts in areas with and without disease
Environmental niche	Relationship of pathogen growth, virulence, and survival with environmental conditions such as temperature and humidity	Laboratory studies to determine pathogen response to environmental conditions. Presence/nondetection of pathogen in field surveys: environmental DNA
Taxonomic breadth of hosts	Pathogenicity for multiple hosts	Challenge experiments in the laboratory Field surveys to detect exposure or pathogen in multiple hosts Passive or active surveillance for pathogen presence, exposure, and related morbidity
Transmission pathways	Rate of transmission (if any) host to host, environment to host, vector to host, etc. Rates at which contacts result in host to host disease transmission	Laboratory experiments fulfilling Koch's postulates Field surveys to identify reservoirs and vectors Models to replicate observed dynamics Genetic studies of the pathogen Comparative genetics of potential hosts and vectors to pathogens

Key parameters	Specific parameters	Techniques
Social behavior/contact networks	Contact rates: rates at which individual species contact members of their own social group and other social groups, rates at which infectious animals move	Identification of host genetic structure or nonlethal microbes in hosts Mark recapture: spatially-explicit and multistate Telemetry Proximity collars Observational studies Spatial patterns of nonlethal microbes in hosts

Technical Appendix Table 3. Identification of key parameters for *Batrachochytrium salamandrivorans*, an emerging disease of salamanders*

Key parameters	Description	Estimates
Pathogenicity Environmental niche	Disease is highly pathogenic for susceptible species (*1*). Current models indicate conditions for *B. salamandrivorans* exist throughout the Eastern seaboard (*2,3*).	Mortality 0.90–1.00 Probability environmental niche includes local populations = 1 Probability niche includes all of species range 0.90–1.00
Taxonomic breadth of hosts	Current information indicates the probability is low that species outside of salamanders are affected.	1% chance of infecting other taxa
Social behavior/connectivity	Spatial structure: salamanders in this area live in small isolated ponds (metapopulations). Movement patterns: salamander mobility is relatively limited (unlikely to travel more than a few hundred meters). Juveniles are the dispersing class and may travel farther. Social behavior: salamanders in ponds live in close proximity to one another during the breeding season.	Probability of contact with infected host within the same pond is high (0.75–1.00). Probability of contact with an infected host from another pond is likely a function of distance. Ponds connected by riparian areas facilitate movements.
Transmission pathways	There is much uncertainty surrounding transmission pathways. Direct contact can pass fungal spores between hosts, it is also possible that fungal spores can be passed from an individual to the environment or other organisms and then to other individuals. Possibly spores can be carried on fomites.	Probability host-to-host contact leads to an infection is high (0.80–1.00). Probability host infection can occur from environment is low (0–0.10).

*Ideally parameter estimates would represent the best guess estimates of multiple experts.

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