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Parameter Sensitivity Analysis of a Infectious Disease Model and Identifying Dominant Transmission Pathways

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Parameter Sensitivity Analysis of a Infectious Disease Model and Identifying Dominant Transmission Pathways

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Abstract

Emerging infectious diseases are a threat to biodiversity and fungal pathogens have caused rapid declines in amphibian populations around the globe (McCraw and Gurr, 2012). Gray et al (2015) identifies *Batrachochytrium salamandrivorans* (Bsal) as an emerging fungal pathogen that caused rapid die-offs of naïve salamanders in Europe and predicts North America will soon experience similar devastation if no policy actions are taken and the pathogen emerges. Epidemic dynamics of infectious diseases with multiple routes of transmission are complex. Mathematical models can be used to determine invasion potential and identify which transmission pathway is dominant, can ultimately help identify appropriate intervention strategies. We developed compartmental host-pathogen models to examine transmission dynamics of an emerging fungal pathogen on an amphibian population. Multiple stages of infection are incorporated into the model, allowing disease-induced mortality and zoospore shedding rates to increase as the disease progresses. Parameter sensitivity analysis using the Latin Hypercube Sampling (LHS) with the Partial Rank Correlation Coefficient (PRCC), calculations of the basic reproductive number, and numerical simulations shed insight into pathogen dynamics.

References

Gray MJ, Lewis JP, Nanjappa P, Klocke B, Pasmans F, Martel A, Stephen C, Olea GP, Smith SA, Sacerdote-Velat A, et al (2015) Batrachochytrium salamandrivorans: the north american response and a call for action. PLoS pathogens 11(12):e1005,251

McCraw S, Gurr S (2012) Emerging fungal threats to animal, plant and ecosystem health. Nature 484(7393):186,194Frank

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