

MODELING FOR ZONOTIC DIARRHEAL DISEASE EPIDEMIC

Boseung Choi

Korea University Sejong Campus, Sejong, South Korea

Grzegorz A. Rempala

The Ohio State University, Columbus, USA

We introduce a statistic inference method for the household dynamics of an endemic zoonotic diarrheal disease based on the observational, cross-sectional data as often available from household health surveys. We apply the dynamic SID (susceptible-infected-diseased) model that describes the disease steady-state to such data. The model adjusts the household age-structure and environment contamination. Using the idea of the synthetic likelihood we estimate the SID transmission rate parameters using Bayesian approach via MCMC (Markov Chain Monte Carlo) methods. Our approach appears capable of genuinely capturing the complex dynamics of disease transmission across various human, animal and environmental compartments at the household level and can be possibly used in other epidemiological settings where it is desirable to fit steady state dynamics using cross-sectional data. We apply proposed method to the household survey data in Cameroon and provide the SID analysis allows for a more detailed examination of how household occurrence risk is associated with the water environment and how it is transferred across age compartments.

REFERENCE

- [1] Casper Woroszyło, Boseung Choi, Jessica Healy Profitos, Jiyoung Lee, Rebecca Garabed, Grzegorz A. Rempala, Modeling household transmission dynamics: Application to waterborne diarrheal disease in Central Africa, PLOS ONE, 13(11), 20206418 (2018)