EXPLORING THE ENVIRONMENTAL CONNECTION BETWEEN CATTLE AND HUMAN EHEC CASES

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Exploring the environmental connection between cattle and human EHEC cases

BACKGROUND

EHEC is an important zoonotic infection commonly caused by VTEC O157. Cattle is a reservoir for VTEC O157 and a better understanding of the transmission route from cattle to human could potentially improve public health.



- One challenge we have encountered in this study is how to share data between veterinary and public health agencies. Therefore, we have been exploring how to proceed and prepare the analysis in case we get the real dataset.
- In this work, we present a synthetic case study of how such an analysis could be performed.

DATA PROCESSING

EHEC in Human based on public data on county level

between 2008-2013 (aggregated by administrative units)

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VTEC in Environment

Stochastic SISE VTEC O157 model



 v_i : age dependent indirect transmission rate φ_i : environmental infectious pressure

The left figure shows the proportion of 1000 simulated

trajectories that each holding had at least one infected animal. The right figure shows a comparison of individual cattle VTEC O157 status from samples collected at abattoirs 2011– 2012, where the circles represent the origin of each sampled animal.

Widgren, Stefan, et al. "Spatiotemporal modelling of verotoxigenic Escherichia coli O157 in cattle in Sweden: exploring options for control." Veterinary research 49.1 (2018): 78.

RELATIONSHIP BETWEEN CATTLE AND HUMAN EHEC CASES



DISCUSSION AND FUTURE WORK

By using synthetic data instead of real EHEC case data, we were able to explore possible analysis methods for the research question.



Synthetic EHEC case density (left) and cattle farm density (right) have a spatially similar pattern.

Environmental infectious pressure (φ) of the farms near EHEC cases is much higher than the φ of the farms more than 5 km away from the cases.

With actual data, we will be able to carry out case-control analysis in the future to explore whether the distance between a case and the neighboring farms affects the presence of the pathogen.

Next step:

- Additional factors: population density, environmental factors
- Multivariate time-series model and case-control analysis

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