

# Can you predict how a disease will spread in a population?

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How, when and where a pathogen is transmitted between two individuals in a population is crucial in understanding and predicting how a disease will spread. New research has laid the foundation for a new generation of zoonotic disease spreading models, which could allow for more targeted prevention strategies.

By using novel complexity sciences tools the study, published in *Physical Review Letters*, outlines a predictive model of a spatial epidemic spread in a population of territorial animals.

By quantifying the instances of transmission events, the research team, Dr Luca Giuggioli, Senior Lecturer in Complexity Sciences in the Department of Engineering Mathematics and the School of Biological Sciences at the University of Bristol, and Dr David Sanders and Master's student, Sebastian Pérez-Becker, from UNAM, Mexico, have determined the propagation speed of a pathogen based on the knowledge of the demography of a species, the way animals wander and the degree of contagiousness of the disease.

As a large percentage of new and reemerging human infectious diseases are of animal origin, models that track how pathogens hop from one [animal host](#) to another will help develop more effective control measures that are capable of identifying specific individuals or class of individuals rather than ineffective and costly widespread culling procedures of an entire population.

Dr Giuggioli said: "The research findings have the potential to be applicable to various populations of territorial animals worldwide including in the UK [bovine Tb](#) in badgers, which has enormous economic implications for the cattle industry."

[Bovine tuberculosis](#) (Tb) in badgers, which affects cattle, the [farming industry](#) and has become a political issue, is an example of how the model could be used. Badgers are territorial animals and do transmit the infection by passing the [bacterial pathogen](#) to individuals in neighbouring territories, which is what the researchers have quantified in their model.

**More information:** Encounter times in overlapping domains: application to epidemic spread in a population of territorial animals, Luca Giuggioli, Sebastian Pérez-Becker and David P. Sanders, *Physical Review Letters*, published 30 January 2013.

Provided by University of Bristol

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