**What is the critical community size for foot-and-mouth disease?**

Foot-and-mouth disease (FMD), caused by foot-and-mouth disease virus (FMDV), is one of the most important livestock diseases in the world and outbreaks can impose huge social and economic costs. Despite reputedly being one of the most infectious diseases of animals, FMDV remains endemic in many areas, including Africa and Asia. In other regions, such as South America, widespread vaccination is used to control FMDV, but countries still experience occasional outbreaks. This raises the important question of how FMDV is able to persist in the cattle population in the longer term. For other diseases, notably measles, this has been shown to depend on the size of the host population, with a threshold population size, often termed the critical community size (CCS), required for the disease to persist in the population.

This project will investigate the CCS for FMDV using a stochastic model for the spread of the disease in cattle. More specifically, the approach will be to simulate the dynamics of FMDV infection in a metapopulation (i.e. where the cattle population is subdivided into a number of linked patches) and explore how the population size, number of patches and transmission rates interact to influence whether or not the virus can persist in the population. The student will be expected to:

1. implement the model in an appropriate computer language;
2. obtain estimates for model parameters from the published literature on FMDV;
3. use the model to explore the relationship between population size and transmission on the persistence of FMDV; and
4. compare the model predictions for the CCS for FMDV with the size of cattle populations.

The results of the project will be of interest to epidemiologists and to those involved in plans to control FMD.

There are a number of ways in which the project could be developed further as a PhD project.

* There are seven serotypes of foot-and-mouth disease, with infection with one serotype providing a degree of cross-protection against subsequent infection with another serotype. What are the patterns of multi-strain dynamics in a metapopulation? What is the impact on the persistence of FMDV of multiple serotypes and cross-protection?
* Vaccination often limits, or even prevents, the appearance of clinical signs of disease without preventing transmission. What level of surveillance would be needed to detect circulation of FMDV in a vaccinated population in absence of disease?
* Many wildlife species can be infected by FMDV, with some species acting as a reservoir (notably, African buffalo). What impact does such a wildlife reservoir have on the persistence of FMDV?