Modelling the emerging infectious diseases in wildlife
Modélisation des maladies infectieuses émergentes chez la faune sauvage
(Org: **Seyed M. Moghadas** and/et **Jingjing Xu** (York University))

MARTHA GARLICK, South Dakota Mines
Connecting Local of Movement of Mule Deer with Regional Spread of Chronic Wasting Disease

Chronic wasting disease (CWD) is an infectious, slow-developing prion disease that affects mule deer, as well as other members of the Cervidae family. Spatial models using ecological diffusion allow for aggregation of populations in desirable habitats and therefore allow an interaction between density dependent disease transmission and landscape structure. The techniques discussed in this talk can be extended to many ecological applications, such as modeling insect infestations, invasive species, and escaped genetically modified organisms, as well as other wildlife diseases.

STACEY SMITH?, The University of Ottawa
Modelling mutation in equine infectious anemia virus infection suggests a path to viral clearance with repeated vaccination

EIAV is a lentivirus similar to HIV that infects horses. Clinical and experimental studies demonstrating immune control of EIAV infection hold promise for efforts to produce an HIV vaccine. Antibody infusions have been shown to block both wild-type and mutant virus infection. We develop a mathematical model that describes the interactions between antibodies and both wild-type and mutant virus populations, in the context of continual virus mutation. The aim of this work is to determine whether repeated vaccinations through antibody infusions can reduce both the wild-type and mutant strains of the virus below 1 particle, and if so, to examine the vaccination period and number of infusions that ensure eradication. We use impulsive theory to determine the maximal vaccination intervals that would be required to reduce the wild-type and mutant virus levels below one particle per horse. We also show that seven boosts of the antibody vaccine are sufficient to eradicate both the wild-type and the mutant strains. In the case of a mutant virus infection that is given infusions of antibodies targeting wild-type virus (i.e., simulation of a heterologous infection), seven infusions were likewise sufficient to eradicate infection, based upon the data set. However, if the period between infusions was sufficiently increased, both wild-type and mutant virus would eventually persist in the form of a periodic orbit. These results suggest a route forward to design antibody-based vaccine strategies to control viruses subject to mutant escape.

JINGJING XU, York University
Spreading speed of chronic wasting disease across deer groups with overlapping home ranges

Chronic wasting disease (CWD) is a fatal disease of cervid species that continues to spread across North America and now in Europe. It poses a threat to cervid populations and the local ecological and economic communities that depend on them. Although empirical studies have shown that host home range overlap and male dispersal are important in the spread of disease, there are few mechanistic models explicitly considering those factors. We built a spatio-temporal, differential equation model for CWD spreading with restricted movement of hosts within home ranges. The model incorporates both direct and environmental transmission within and between groups as well as male dispersal. We compared the relative influence of host density, sex ratio, home range size, and male dispersal distance on the spreading speed using sensitivity analysis. We also assessed the effect of landscape heterogeneity, quantified as edge density, on the spreading speed of CWD because it jointly alters the host density and home range size. Our model binds the theoretical study of CWD spreading speed together with empirical studies on deer home ranges and sets a base for models in 2D space to evaluate management and control strategies. (Coauthored with Evelyn H. Merrill and Mark A. Lewis, University of Alberta)