A SPATIALLY INTEGRATED DISEASE RISK ASSESSMENT MODEL FOR WILDLIFE/LIVESTOCK INTERACTIONS IN THE NGORONGORO CONSERVATION AREA OF TANZANIA

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Introduction
In this paper we use a mixture of long-term ecological data and computer (mathematical models) to examine the epidemiology of MCF in the Ngorongoro Conservation Area of Tanzania, East Africa. The paper emphasizes how a risk based biased mixing disease model (1) can be incorporated into a spatial ecology model, SAVANNA, (Cougenhour, PI). SAVANNA is primarily used for wildlife/domestic herbivore population studies in various ecologies throughout the world. For this study (CSU – CRSP – USAID) wildebeest population and migration patterns have been compiled for SAVANNA, (2), as well as Maasai pastoralist cattle movement patterns.

Recently reported data on the annual removal of livestock from short grass plains, during the east Africa wet season, to intermediate and highland areas in the avoidance of exposure to MCF virus secreted from 2 – 4 month old wildebeest calves (3) confirms the use of proximity as an avoidance method in reducing the spread of MCF from wildebeest to Maasai cattle. Rweyemamu, (4) discuss how MCF is spread mostly through nasal secretions onto grass and grazing areas of the NCA and Sarengetti, and Rossiter P.B.(5), has found that the MCF virus survives in the environment for as little as 3 hours under the ultraviolet rays of the sun. These facts make the MCF model a point of contact model where cattle exposure to the virus occur as the likelihood that different species occupy the same spatial area within a short period of time. All epidemiology and disease models track the progress of disease over time. It is only with recent advances in time step delineation of spatial data through computer simulation that models can be used to show epidemiology curves and infection maps that represent both where and when disease in a target population is likely to occur.

Materials and Methods
Population density maps are input to the model as raster maps gridded to 5 square kilometer cells. Maps are generated from the SAVANNA ecology model (Cougenhour, Boone). The Spatially Integrated Disease Risk Assessment Model (SIDRAM) is written in FORTRAN
and reads two population density maps from SAVANNA, one for cattle movements and one for wildebeest. Each pixel, or 5 square kilometer cell, has a value of the number of animal species that occupy the area. Many parameters and species population models make up the individual maps, which represent one week of time. For ease of computation it was decided that maps would be displayed as monthly intervals of the first week in the month as the time step.

Map figure 1. Raster data of 5 square kilometer pixels, SAVANNA determines the population density for cattle for the first week of each month.

Population density maps for the wildebeest are determined through literature and wildlife models for forage availability during wet and dry seasons. (Map Figures 1 & 2).

Map figure 2. Raster data of 5 square kilometer pixels, SAVANNA determines the population density for wildebeest for the first week of each month.

Results
The SIDRAM FORTRAN program performs an intersection of the wildebeest distribution map and the Maasai cattle distribution map for each pixel. Output maps of the intersection
of these two population maps, where pixels with large enough populations of both species to warrant infection within the weekly time step, can be shown to fit a normal curve, and represent at least one animal to be infected within the time step. (Map Figure 3.).

Map figure 3. The final outcome map represents those 5 square kilometer pixels where the spread of MCF is likely to infect at least one animal in the target population for the time step. These areas represent the best fit in both time and space for determining disease spread given the input parameters.

References