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**Linda J. S. Allen\*** ([linda.j.allen@ttu.edu](mailto:linda.j.allen@ttu.edu)), Department of Mathematics and Statistics, Texas Tech University, Lubbock, TX 79409-1042. *Probability of Disease Outbreaks in Multi-Species, Multi-Patch Models with Applications to Zoonotic Diseases*. Preliminary report.

Approximately 75% of human infectious diseases originate from an animal reservoir, many caused by viruses such as SARS coronavirus, avian influenza viruses, rabies virus, West Nile virus and hantaviruses. Human diseases originating from a nonhuman animal reservoir are referred to as zoonoses and the transmission of infection from an animal reservoir to another species is referred to as a spillover infection. In this presentation, deterministic and stochastic multi-patch models developed for the study of hantavirus in reservoir and spillover populations are used to study the probability of a disease outbreak. A continuous-time Markov chain model approximates the infection dynamics near the disease-free state. Theory from multi-type branching process is then used to estimate the probability of a disease outbreak. Numerical results show the importance of location and population densities to the probability of a disease outbreak. (Received February 10, 2014)