ABSTRACT

In this talk, I will introduce a new statistical method motivated by the need for studying the biotic and abiotic factors affecting the prevalence of plague among the great gerbils in Kazakhstan. The great gerbil populations constitute several natural foci to plague (caused by the bacteria *Yersinia pestis*) in Kazakhstan where the disease may be transmitted to humans by vectors, mainly, fleas. A long-term monitoring study of this natural plague system was undertaken from 1949-1995, for tracking the prevalence of plague in the great gerbil population. Monitoring efforts consisted primarily of trapping the great gerbils, together with their fleas, and testing both rodents and fleas for plague using a bacteriological test and a serological test. Plague is still prevalent in several Asian, African, and American countries including the USA, and is today one of the re-emerging diseases.

The major difficulty and/or novelty of this problem is that epizootics only occur if the number of secondary infections arising from a primary infection, (known as the basic reproductive ratio $R_0$), is greater than 1. This condition translates to the requirement that in host-pathogen dynamics, there is an unknown ‘threshold population abundance’ below which an infectious disease is unlikely to invade a fully susceptible host population and persist. The Threshold Logistic Regression (TLR) model incorporates this threshold condition for analyzing epidemiological time series. Maximum likelihood estimation of a TLR model and its large sample properties will be discussed. I shall illustrate the method by an analysis with the Kazakhstan monitoring data.