Pre ISVEE 10 Course
"Introduction to Bayesian Modeling and Inference Using Win BUGS"

Instructors:

Adam Branscum, University of California, Davis.
Richard Evans, Iowa State University.
Wesley Johnson, University of California, Davis.

Overview: The purpose of this course is to introduce basic biostatistical methods from the Bayesian perspective and to analyze epidemiological data using the program Win BUGS. Bayesian methods are characterized by virtue of modeling all uncertainty with probability. Each unknown parameter in a statistical model, is modeled with its own probability distribution that reflects the scientist's uncertainty about that parameter. In veterinary epidemiology, this amounts to incorporating scientific knowledge (in the form of probabilities) into a data analysis. This prior knowledge might involve knowledge of the sensitivity and specificity of a screening test or the probability of an event e.g. abortion in dairy cattle . The purpose of the data analysis might be to estimate disease prevalence, estimate the risk of abortion, or even the time to abortion. The program Win BUGS is an exceptionally versatile computing environment to obtain Bayesian inferences. Advantages of the Bayesian approach using Win BUGS are: (i) large sample sizes are not necessary for correctness of results, (ii) scientific knowledge is encouraged in the modeling and analysis, (iii) complicated models are often relatively simple and straightforward to deal with (iv) complicated parameters are virtually always easy to handle (for example, it is notoriously difficult to obtain an appropriate interval inference for the relative risk of event in a logistic regression model, or in a survival model, but they are easy to obtain in Win BUGS.

Prerequisites: The course is designed for veterinary epidemiologists who would like to be able to analyze standard types of epidemiological data using a unified method and format. All participants should have a background in probability theory and preferably experience with logistic regression and survival analysis.

Course Objectives: Those who complete the course should be able to analyze a number of basic types of epidemiological data, including simple binomial and multinomial data, one and two sample normal data, and simple versions of logistic regression data, survival data, one and two-test screening data, and data that are modeled hierarchically, as in the case of sampling multiple animals from multiple herds or sub-populations.

Class Size: dependent on the size of the computer lab 3 students per computer.

Registration Fee: $350, 50% discount for PhD. and MSc. students.

Course Program:

Thursday November 13th

Overview of the course and introductions (Evans/Johnson)
Introduction to Bayesian methods-1 (Johnson)
Introduction to Bayesian methods- 2 (Johnson)
Introduction to Win BUGS -1 (Evans) (The basics)
Hands-On WinBUGS-1 (Getting started: Class will write their own code for several simple statistical problems)
Introduction to Win BUGS –2 (Evans) (Beyond the basics)

Friday November 14th

Diagnostic Testing-1 (Introduction) (Johnson)
Hands-On WinBUGS-2 (Class will write their own code to analyze one-test, one-population screening data)
Bayesian Logistic Regression With and Without Error (Johnson)
Introduction to WinBUGS-3 (Evans) (convergence diagnostics, Gibbs Sampling, thinning, over relaxation)
Hands-on WinBUGS-3 (Class will write their own code to analyze logistic regression data, including diagnostics)

Saturday November 15th

Bayesian Parametric Survival Analysis (Branscum)
Case Study: Joint Survival and Logistic Regression Analysis: Analysis of Cow Abortion data
Hands-on Win BUGS (Analyze Simple Survival Data)
Bayesian Hierarchical Modeling (Mixed Models) (Johnson/Evans)
Hands on WinBUGS-5 (Class will analyze mixed model data)

Sunday, November 16th

Diagnostic testing-2 (Two Independent or Dependent Screening Tests) (Johnson)
Hands on WinBUGS-5 (Class will analyze two-test, two-population screening data including diagnostics)