Kolloquium „Statistische Methoden in der empirischen Forschung"

Wann: 10. Februar 2015, 17:00 – 18:30 Uhr

Wo: Lebenswissenschaftliche Fakultät, Humboldt-Universität zu Berlin,
Hörsaal 2, 2. Etage, Invalidenstr. 42, 10115 Berlin

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Bayesian true prevalence estimation in structured populations using poor diagnostic tests

An important part of any disease control effort is knowledge of the prevalence in the population. For most animal diseases the estimation of prevalence is often hampered by lack of reliable, cheap and accurate tests, thus making prevalence estimation somewhat more challenging. For many purposes, the use of the apparent prevalence (AP, i.e. proportion of test positives) is sufficient for decision making. However, there are also situations where it is desirable to have an estimate of the true prevalence (TP) in the population (i.e. the proportion of truly infected animals, rather than test positives).

Given a diagnostic test with sensitivity (Se=Pr(T+|D+)) and specificity (Sp=Pr(T-|D-)) the association between apparent and true prevalence is given as: AP = Se*TP + (1-Sp)*(1-TP). With onset in this relationship, a series of 5 examples based on published model will be presented to illustrate the flexibility and potential of Bayesian modelling in the OpenBUGS framework.

In the first example we will estimate the true prevalence of disease in different breeds of cattle in order to see if there are differences between breeds. The second example is concerned with estimating prevalence in a population of herds, where it is possible for a herd to be free of infection. In third example we analyze data where the prevalence is adjusted for misclassification introduced by the use several different raters/tests in the population. The fourth example demonstrates how OpenBUGS can be used to integrate estimation and simulation in the same model. The final example looks into prevalence estimation with a continuous test and explores different possibilities for presenting prevalence measures.