

University of Idaho
Division of Statistics

Master's Thesis Defense

Hua Feng

**Friday, April 4, 2003
10:30 a.m.**

Albertson 203

**Estimating Population Size by Non-Invasive
Genetic Sampling with Allelic Dropout**

ABSTRACT

Recent advances in genetic technology provide a way to study populations by extracting DNA from animal hair and scats without handling animals. The non-invasive genetic sampling is playing an important role in mark-recapture studies. Despite the promise of the new molecular approach, there are several sources of error during PCR (polymerase chain reaction) amplification, and these errors can significantly bias such studies.

Mark-recapture events were simulated under a given population size, capture probability and allelic dropout rate. Population sizes were estimated by the Petersen-Lincoln estimator. The simulation study shows evidence that the allelic dropout can cause overestimation of population size.

Based on simulated data of mark-recapture model, a least squares bias correcting method was developed. Using the least squares bias correcting method adjusts the over estimated population size tending to true population size holding the allelic dropout rate in the data. The simulation results reveal that adjusted population size estimates are closer to the true population size than unadjusted estimates. Therefore, the approach is an effective adjustment.