Estimation of Herd-Level Prevalence: Strategies for Sampling Design.

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Summary:
A two-stage sampling approach is proposed for estimation of herd-level prevalence. Herd-level test characteristics are constructed based on individual animal test characteristics, herd size, sample size and within-herd level prevalences. The distribution of within herd prevalence is modeled using intracluster correlation coefficient. A herd-level sample size formula was developed which incorporates the herd-level test characteristics and allows for consideration of alternative sampling design protocols.

Introduction:
Surveys of disease prevalence are often intended to provide information to substantiate claims of disease freedom at a regional or national level. A two-stage sampling approach has been proposed as a basis for such a purpose. Studies of the distribution of disease in a population may be concerned with estimating herd-level prevalence rather the disease detection. However, the objective of two-stage sampling typically is to estimate characteristics of the second stage units (animal-level).

Objective:
We propose the use of a herd-level sample size formula based on a common adjustment for prevalence estimates in a two-stage sampling scheme when diagnostic tests are imperfect. The formula depends on an estimate of herd-level sensitivity and specificity which in turn are dependent on a number of variables including animal-level test sensitivity and specificity, within-herd prevalence, herd size, sample size and cutpoint.

Materials and Methods:
A model was constructed to simulate two-stage sampling. Inputs into the model include herd size, animal-level sensitivity (SE) and specificity (SP), animal-level prevalence, within-herd sample size, percent of herds that are negative, and the cutpoint needed to designate a herd as positive. The model was first used to explore the affect of varying levels of intracluster correlation on herd-level sensitivity and specificity as well as herd-level positive and negative predictive values.

The model was then used to investigate a hypothetical example of two stage sampling. Specifically, the example explored the impact of a single test positive versus a variable cutpoint for declaring a herd positive on herd. Survey-level test characteristics were used to evaluate within-herd and herd-level design scenarios.

A real life two-stage sampling design example was developed for estimating herd-level prevalence of Ovine Progressive Pneumonia (OPP) in sheep. Intracluster correlation was estimated from National Animal Health Monitoring System data. Two sample design strategies were evaluated (fixed versus variable cutpoint, and varying herd-level test characteristic targets).

Results:
The Monte Carlo results indicate that at low prevalence, herd-level sensitivity increased with increasing intracluster correlation but the sensitivity was less affected at higher prevalence. Also at low prevalence many herds are being classified as positive based only on false positive test results. Positive predictive values drop sharply with increasing intracluster correlation (Figure 1).

Figure 1. The relationship between intracluster correlation coefficient and the predictive value positive (pvp) and predictive value negative (pvn) of a herd-level level test at different cutpoints for determining herd-level status (n=20).
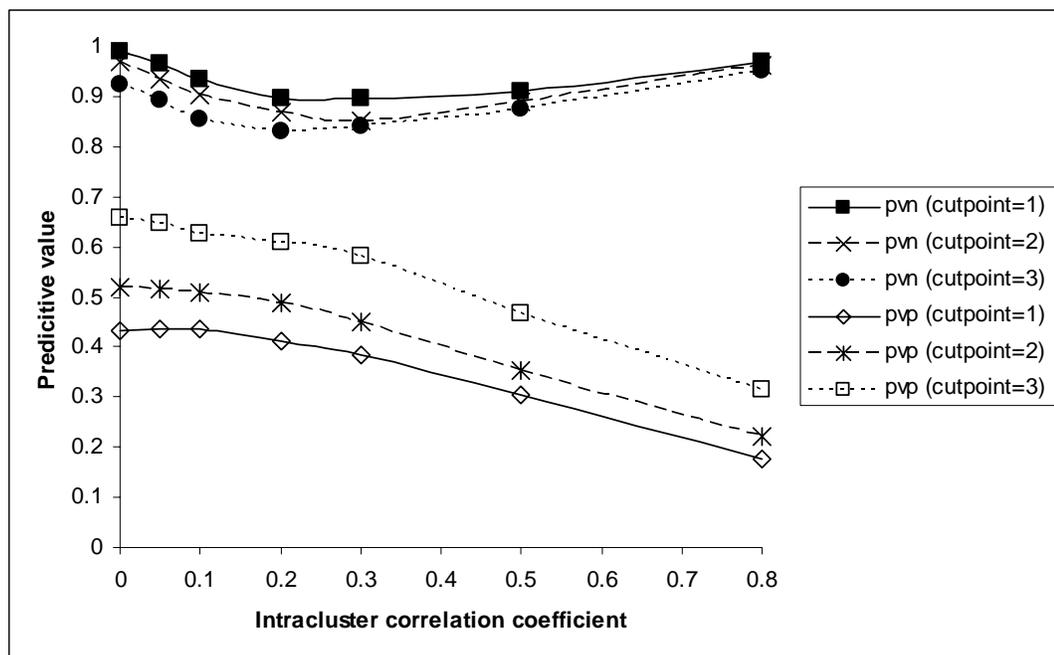
For the hypothetical example of two stage sampling, within-herd sample sizes varied by herd size and cutpoint in order to achieve herd sensitivity and specificity targets. Survey-level sensitivity and specificity were altered by changing cutpoints (Table 1).

Table 1. Survey-level sensitivity (SN_s), specificity (SP_s), positive predictive value (PPV), and negative predictive value (NPV) for herd-size categories under two herd-level design strategies, with and without a fixed cutpoint of one. (SE=98%, SP=99%, π=20%, Ψ=60%, ρ=.1)

Herd sampling strategy	SN_s	SP_s	PPV	NPV
Fixed cutpoint =1	93.4	85.8	79.4	95.7
Variable cutpoint	95.1	90.7	86.7	96.7

Fewer herds were needed using the variable cutpoint design strategy compared to the fixed cutpoint design to attain the survey-level characteristics (127 versus 150). However, the variable cutpoint design required sampling more animals than did the fixed cutpoint design (2215 versus 3390).

The two proposed OPP sampling targets yielded very different designs. In order to estimate herd-level prevalence with 95% confidence and an error bound of 10 percent using a design with herd-level specificity of 70% and a fixed cutpoint it would be necessary to visit 439 operations and sample 5105 animals. In contrast, the same confidence using a design with herd-level sensitivity of about 80% and a variable cutpoint would decrease the number of herds to 274 but increase the number of animals tested to 11982.

Conclusions:
The two stage sampling approach for estimating herd-level prevalence is a flexible methodology that allows researchers to address sampling objectives. The use of a distribution for within-herd prevalence results in a conservative estimate of herd-level test characteristics. The model allows for researchers to tradeoff between the number of herds and the number of animals sampled by manipulating herd-level test characteristics.