COLLOQUIUM

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Closed Sequential and Multistage Inference with Binary Response

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10:20 a.m. - 11:10 a.m.
Refreshments: 10:00 a.m.

Abstract

The talk considers closed sequential or multistage sampling, with or without replacement, from a lot of N items, where each item can be identified as defective (in error, tainted, etc.) or not. The goal is inference on the proportion π of defectives in the lot, or equivalently on the number of defectives in the lot $D = N\pi$. Until just a few years ago, inference on π was typically done approximately (even with a fixed sample size) - binomial for hypergenometric,normal or Poisson for binomial, Monte-Carlo determined boundaries and/or inference, etc. In this paper we show that exact inference on π using closed (bounded) sequential or multistage procedures with general pre-specified elimination boundaries is completely tractable and not at all inconvenient using modern statistical software. Relevant theory is provided, and functions for this purpose written in *R* (www.R-project.org) are demonstrated. Our focus is on frequentist inference, but exact Bayesian approaches are also readily available. Examples provided are (1) a sharpening of Wald's (1947) SPRT used in industrial acceptance sampling; (2) two-stage sampling for auditing Medicare healthcare providers; and (3) Risk limited sequential procedures for election audits.

Keywords: binomial; hypergeomeric; Pascal's triangle; Centers for Medicare and Medicaid Services (CMS); probe samples; risk-limited election audits; precinct sampling

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