UNIVERSITY OF RIVERSITY OF CALIFORNIA

Statistical Consulting Collaboratory

SCASA – 2005, November 5, 2005

Southern California Chapter of the American Statistical Association Fall Kick Off - Claremont, California

Abstract

In most statistical analyses the data is collected using a fixed sample size and is then analyzed using the complete dataset. In contrast, sequential sampling takes one sample at a time and analysis is performed at each step. Sampling in this way continues until sufficient information in the cumulative sample is obtained to make an appropriate decision using statistical inference methods have the potential sample at d fixed samples, one can draw conclusions during the data collection and often reach a decision using stuckly. Sequential inference methods have the potential to greatly reduce the time and costs associated with decision making processes. As a result, they are applied to a variety of different fields such as Entomology, where the average pest density number is the parameter of interest, and to the study of clinical traits.

The mathematics associated with designing and utilizing sequential procedures can be complex for practitioners, and as such can dissuade users from availing themselves of the advantages they offer. We propose to develop a software tool that facilitates an easier use of the methods, and enables a convenient platform for carrying out sequential inference. The tool implements the appropriate inference procedures associated with each design within an innovative and scalable software architecture. It also hides the complex mathematics of the designs, and provides a user-friendly interface to design a sequential sampling scheme, understand its important statistical properties, and implement the scheme on real data. This tool not only allows the user to analyze the data in real time, but also saves the data and all other text and graphical outputs for use in subsequent analyses. The software design and architecture allows for the scalability and portability across the platform of operating systems.

Background

The Basic SPRT:



Example: SPRT Negative Binomial Sampling Boundaries

The 2-SPRT



are constructed. Based on the values of the likelihood ratio, one of the following decisions is made: a) Accept H₀ if $\lambda_n \leq B$ b) Accept H₁ if $\lambda_n \geq A$ c) Continue sampling otherwise



Advanced Sequential Sampling Methods and Their Implementation Within a Portable Computing Environment

Arunava Chakravartty¹, Payal Shah¹, Carlos Rendon² Daniel R. Jeske¹, Pengyue J. Lin³, Robert Luck⁴

¹Department of Statistics, College of Natural and Agricultural Sciences, University of California, Riverside, CA 92521 ²Department of Computer Science, College of Engineering, University of California, Riverside, CA 92521 ³College of Humanities, Arts and Social Sciences, University of California, Riverside, CA 92521 ⁴Department of Entomology, University of California, Riverside, CA 92521

Methods

Sequential Bayes Procedure

We test $H_0: \mu = \mu_0$ vs $\mu = \mu_1$ where $x_k \sim f(\mu; \delta)$

 δ is a nuisance parameter We assume a discrete prior $g(\mu, \delta_i)$ for (μ, δ) , $i \in \{0, 1\}$ $j \in \{1, ..., n\}$

Step 1:

For the k^{\pm} observation x_i , we get the posterior probabilities of $\mu, \delta; i \in \{0, 1\}, j \in \{1, ..., n\}$ as

 $p(\mu_i, \delta_i \mid x_k, \dots, x_1) \propto f(x_k, \dots, x_1 \mid \mu_i, \beta_i) \times g(\mu_i, \beta_i)$

We now compute the marginal posterior probabilities of θ_i , $i \in \{0, 1\}$ as

 $p(\mu_i | x_k, ..., x_1) \propto \sum_{i=1}^{n} p(\mu_i, \delta_j | x_k, ..., x_1)$

Step 2:

 $\text{If } p(\mu_0 \mid x_k, ..., x_l) \geq \rho \text{ then accept } H_0 \text{ else if } p(\mu_l \mid x_k, ..., x_l) \geq \rho \text{ then accept } H_1$

else $g(\mu_i, \delta_j) = p(\mu_i, \delta_j | x_k, ..., x_i)$ and obtain another observation x_{k+1} and goto Step 1



OC and ASN Curves

 The term 'operating characteristic function', or better known as the OC function reports the probability of acceptance.

• The term 'average sample number function', often shortened to ASN function reports the average amount of samples required in order to make a decision.



Objectives

- Facilitate easier use of advanced sequential sampling methods
- Conceal the complex mathematics of the design and
- implementation of the methods from field practitionersDevelop a laptop software tool to implement the appropriate
- inference procedures associated with each design
- Design an evolutionary and scalable software architecture
- Provide a user-friendly interface to the features of the tool



Sequential analysis tool architecture

· User selects design protocol and model for the distribution of the data

User can examine shape and position of sampling boundaries

- User can examine the OC and ASN functions for the sampling design
- User sequentially enters the observations and can view the dynamic

sampling boundary and the estimates under the assumed model

· User can save graphs and reports to external files

Results





Three step process of choosing the design protocol and model

Sequential Bayes Procedure



 In this parameter input window, the user is required to input both the parameter values and their prior probabilities to initiate the Sequential Bayes procedure.

• The rest of the outputs are similar to the ones for the other protocols.

Window to input the prior distributions of the parameters of interest for the sequential bayes procedure

OC and ASN Curves



Screen shots of the OC and ASN curves from the tool

Sequential Data Generated Outputs



Dynamic graphs show the process of entering the sequential data, a report window keeps track of all the steps taken in the procedure and an estimation window gives current estimates of the parameters at each step of the procedure

Conclusion

- This tool serves as an interface between the theory of sequential analysis and the end user practitioner.
- The tool provides the ability to compare and contrast alternative sequential sampling designs.
- The tool hides the complicated mathematical computations to make
 the application of sequential methods easier.
- The tool works well on laptop which facilitates its use in field environments.

• Future enhancements could be made by incorporating sequential protocols used in clinical trial applications.

Research Funded by: UCR Statistical Consulting Collaboratory and UCR Department of Entomology