Sharpening the Boundaries of the Sequential Probability Ratio Test

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SHARPENING THE BOUNDARIES OF THE SEQUENTIAL PROBABILITY RATIO TEST

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By
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SHARPNING THE BOUNDARIES OF THE SEQUENTIAL PROBABILITY RATIO TEST

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# TABLE OF CONTENTS

| List of Figures                      | v        |
| List of Tables                      | vi       |
| Abstract                            | vii      |
| Chapter 1: Introduction             | 1        |
| Chapter 2: Sequential Probability Ratio Test | 3        |
| 2.1 Wald’s Sequential Probability Ratio Test | 3        |
| 2.2 Mingot’s Expansion of SPRT       | 9        |
| 2.3 Iglewicz’s Expansion of SPRT     | 9        |
| 2.4 McWilliams’ Expansion of SPRT    | 10       |
| 2.5 Ignatova, Deutsch, and Edwards’ Expansion of SPRT | 11       |
| Chapter 3: A Method for Sharpening the Boundaries | 18       |
| 3.1 Creating the Bounds             | 18       |
| 3.2 Results for the New Bounds      | 24       |
| Chapter 4: Simulation Studies       | 34       |
| 4.1 Simulation Method               | 34       |
| 4.2 Simulation Results              | 35       |
| Chapter 5: Conclusion and Future Work | 47       |
| Appendix                            | 49       |
| A.1 Boundaries for $n_T = 4$        | 49       |
| A.2 R Code                          | 60       |
|  A.2.1 check.step()                 | 60       |
|  A.2.2 create.bounds()              | 61       |
|  A.2.3 alpha.bounded()              | 64       |
|  A.2.4 errors.bounded()             | 66       |
|  A.2.5 sim.sprt()                   | 69       |
|  A.2.6 Wald.bnd()                   | 73       |
|  A.2.7 Wald.step.bnd()              | 74       |
| References                          | 75       |
LIST OF FIGURES

Figure 2.1  Full Pascal’s Triangle Example 12
Figure 2.2  Modified Pascal’s Triangle Method 13
Figure 2.3  Wald Boundary Example 17
Figure 3.1  Standard Hypothesis Test 19
Figure 4.1  Binomial $n_T = 10$ Simulation with $\pi_0 = 0.1$ and $\pi_1 = 0.7$ 42
Figure 4.2  Binomial $n_T = 10$ Simulation with $\pi_0 = 0.1$ and $\pi_1 = 0.9$ 43
Figure 4.3  Binomial $n_T = 10$ Simulation with $\pi_0 = 0.2$ and $\pi_1 = 0.8$ 44
Figure 4.4  Binomial $n_T = 10$ Simulation with $\pi_0 = 0.2$ and $\pi_1 = 0.9$ 45
Figure 4.5  Binomial $n_T = 10$ Simulation with $\pi_0 = 0.3$ and $\pi_1 = 0.9$ 46
LIST OF TABLES

Table 3.1 Possible Single Boundaries for \( n_T = 4 \) 21
Table 3.2 Total Number of Potential Boundaries for \( n_T \) 24
Table 3.3 Binomial Results for \( n_T = 10 \) 26
Table 3.4 Binomial Results for \( n_T = 20 \) 27
Table 3.5 Binomial Results for \( n_T = 30 \) 28
Table 3.6 Binomial Results for \( n_T = 40 \) 29
Table 3.7 Hypergeometric Results for \( n_T = 10 \) 30
Table 3.8 Hypergeometric Results for \( n_T = 20 \) 30
Table 3.9 Hypergeometric Results for \( n_T = 30 \) 31
Table 3.10 Hypergeometric Results for \( n_T = 40 \) 31
Table 4.1 Hypergeometric Simulation Results for \( n_T = 10 \) 36
Table 4.2 Hypergeometric Simulation Results for \( n_T = 20 \) 36
Table 4.3 Hypergeometric Simulation Results for \( n_T = 30 \) 37
Table 4.4 Hypergeometric Simulation Results for \( n_T = 40 \) 37
Table 4.5 Binomial Simulation Results for \( n_T = 10 \) 38
Table 4.6 Binomial Simulation Results for \( n_T = 20 \) 39
Table 4.7 Binomial Simulation Results for \( n_T = 30 \) 39
Table 4.8 Binomial Simulation Results for \( n_T = 40 \) 40
In this thesis, we present an introduction to Wald's Sequential Probability Ratio Test (SPRT) for binary outcomes. Previous researchers have investigated ways to modify the stopping boundaries that reduce the expected sample size for the test. In this research, we investigate ways to further improve these boundaries. For a given maximum allowable sample size, we develop a method intended to generate all possible sets of boundaries. We then find the one set of boundaries that minimizes the maximum expected sample size while still preserving the nominal error rates. Once the satisfying boundaries have been created, we present the results of simulation studies conducted on these boundaries as a means for analyzing both the expected number of observations and the amount of variability in the sample size required to make a decision in the test.
Chapter 1: Introduction

In statistical analysis we are concerned with data-driven decision making, and one avenue that we pursue to test conjectures is hypothesis testing. In hypothesis testing, we test $H_0$, the null hypothesis, versus $H_1$, the alternative hypothesis. In a standard hypothesis test, we take a sample of size $n$, and make a decision based on the entire collection of data. The sequential probability ratio test (SPRT) instead requires that each item be sampled one at a time. After each item, the researcher either makes a decision in the hypothesis test or decides to continue sampling by selecting another item. Thus, the SPRT can result in a significantly smaller sample size than a standard hypothesis test.

In practice, SPRT tends to be more efficient than standard hypothesis testing and is more cost effective in industry. For example, SPRT has been used in detecting Medicare fraud; instead of examining every case that a particular doctor turns in for Medicare to pay, the analyst looks at one case at a time and either makes a decision that the case is or is not fraudulent. From that, the investigator may be able to make a decision about the doctor without looking at all of his cases. Thus, money and time are possibly saved because the testing will likely terminate before all cases have been examined. Additionally, in quality control for industry, instead of examining an entire production line of goods, a company could find it more economical to look at one product at a time and determine whether or not the item is defective and, in turn, make a decision about the entire product line before sampling the entire group of products. Thus,
companies can increase profit by spending less time and money on testing for defects in production. They can also more quickly identify and correct production problems.

For the purpose of this thesis, we are interested in formulating a possible method that can reduce the expected number of observations necessary to make a decision in the sequential probability ratio test. Some research in this area has been conducted, but we set out to build upon and improve the methods that already exist.

In Chapter 2, we first look at the original SPRT developed by Wald and then continue by looking at expansions on SPRT by other researchers. Next, Chapter 3 will detail the process of creating new sets of boundaries as an exploration in sharpening the boundaries of the SPRT. In Chapter 4, we provide a description of simulation studies that were conducted as a way to analyze the new sets of boundaries. Finally, we summarize the research in Chapter 5 and examine some improvements that could be made in the future.
2.1 Wald’s Sequential Probability Ratio Test

In 1947, Abraham Wald published a book entitled *Sequential Analysis* [6], in which he details the process for conducting the sequential probability ratio test for quality control. We define a random variable $X$ on the items being inspected by letting $X = 1$ if the item observed is found to be defective and $X = 0$ if the item observed is non-defective. Define $f(x, \pi)$ to be the probability distribution function of the random variable $X$ where $\pi$ is the proportion of defective items in a (possibly infinite) collection of size $N$. When considering binary outcomes (defective vs. non-defective), the first $n$ successive observations of $x$ will be designated as $x_1, x_2, \ldots, x_n$, where $x_i$ indicates whether the item is found to be defective or non-defective. It is of interest to test two competing values of $\pi$. We let $H_0$ be the hypothesis that $\pi = \pi_0$ and $H_1$ be the hypothesis that $\pi = \pi_1$, where $\pi_0 < \pi_1$. Thus, $f(x, \pi_0)$ is the distribution function of $X$ when the null hypothesis is true, and $f(x, \pi_1)$ is the distribution function of $X$ when the alternative hypothesis is true. We let $y_n = \sum_{i=1}^{n} x_i$ be the total number of defective items in the $n$ sampled items. For any positive value $n$, the probability that a sample $x_1, \ldots, x_n$ is observed is determined by the likelihood functions $L(y_n, \pi_0) = \prod_{i=1}^{n} f(x_i, \pi_0)$ when $H_0$ is true and $L(y_n, \pi_1) = \prod_{i=1}^{n} f(x_i, \pi_1)$ when $H_1$ is true. The sequential probability ratio test (SPRT) for testing $H_0$ against $H_1$ is determined by the following process.
Two positive constants $A$ and $B$ are chosen such that $B < A$. At each stage of the test ($n^{th}$ trial), compute $\Lambda_n = \frac{L(y_n, \pi_1)}{L(y_n, \pi_0)}$. If $B \leq \Lambda_n \leq A$, continue the test by taking another observation. If $A < \Lambda_n$, the test is ended, and the null hypothesis is rejected. If $\Lambda_n < B$, the test is ended, and we fail to reject the null hypothesis.

For practicality in computation, $\ln(\Lambda_n)$ is often used over $\Lambda_n$ since $\ln(\Lambda_n)$ can be written as the sum of $n$ terms, i.e.

$$\ln(\Lambda_n) = \ln\left(\frac{f(x_1, \pi_1)}{f(x_1, \pi_0)}\right) + \ldots + \ln\left(\frac{f(x_n, \pi_1)}{f(x_n, \pi_0)}\right).$$

The $i^{th}$ term of the sum is denoted as $z_i$. Thus, at each stage of the test ($n^{th}$ trial) the cumulative sum $\sum_{i=1}^{n} z_i$ is computed. If $\ln(B) \leq \sum_{i=1}^{n} z_i \leq \ln(A)$, continue the test by taking more observations. If $\ln(A) < \sum_{i=1}^{n} z_i$, the test is ended, and $H_0$ is rejected. If $\sum_{i=1}^{n} z_i < \ln(B)$, the test is ended, and $H_0$ is not rejected.

Assuming that the test has not terminated prior to a given step $n$, we consider a sample $(x_1, \ldots, x_n)$. We say that the sample is of type 1 if $A < \Lambda_n$, which leads to rejection of $H_0$ at step $n$. We say that the sample is of type 2 if $\Lambda_n < B$, which leads to failing to reject $H_0$ at step $n$.

For any type 1 sample, the probability of achieving such a sample under $H_1$ is at least $A$ times as large as the probability of achieving such a sample under $H_0$, as seen by $L(y_n, \pi_1) \geq A \cdot L(y_n, \pi_0)$. Therefore, the probability that the sequential test will terminate with rejection of $H_0$ is also at least $A$ times as large under $H_1$ as it is under $H_0$. When $H_0$ is true, the probability that the test will
terminate with rejection of $H_0$ is $\alpha$. This incorrect decision is a Type I error, where $\alpha$ is the Type I error rate. When $H_1$ is true, the probability that the test will correctly terminate with rejection of $H_0$ is denoted as $1 - \beta$. Thus we obtain,

$$L(y_n, \pi_1) \geq A \cdot L(y_n, \pi_0)$$

$$1 - \beta \geq A \alpha$$

$$A \leq \frac{1 - \beta}{\alpha},$$

which determines an upper limit for $A$ to be $\frac{1 - \beta}{\alpha}$.

In a similar manner, a lower limit for $B$ can be derived. For any given type 2 sample $(x_1, \ldots, x_n)$, the probability of achieving such a sample under $H_1$ is at most $B$ times as large as the probability of achieving such a sample under $H_0$, $L(y_n, \pi_1) \leq B \cdot L(y_n, \pi_0)$. Therefore, the probability that the sequential test will terminate with failing to reject $H_0$ is also at most $B$ times as large under $H_1$ as it is under $H_0$. When $H_0$ is true, the probability that the test will correctly terminate without rejection of $H_0$ is denoted $1 - \alpha$. When $H_1$ is true, the probability that the test will incorrectly terminate with failure to reject $H_0$ is $\beta$. This incorrect decision is referred to as a Type II error, where $\beta$ is the Type II error rate. Thus we obtain,

$$L(y_n, \pi_1) \leq B \cdot L(y_n, \pi_0)$$

$$\beta \leq B(1 - \alpha)$$

$$B \geq \frac{\beta}{1 - \alpha},$$

which determines a lower limit for $B$ to be $\frac{\beta}{1 - \alpha}$. Consequently, upper limits are obtained for $\alpha$ and $\beta$ based on the above inequalities:
\[ \alpha \leq \frac{1}{A} \text{ and } \beta \leq B. \] (2.3)

We must also now consider the opposite approach in which we are not given the values of \( A \) and \( B \). Previously, we chose a given \( A \) and \( B \) and determined the Type I and Type II error rates. In practice, testing will be conducted under predetermined maximum allowable error rates (\( \alpha \) and \( \beta \)), and \( A \) and \( B \) must instead be determined. We would like to test with given strength (\( \alpha \), \( \beta \)); so, denote \( A(\alpha, \beta) \) and \( B(\alpha, \beta) \) as the values of \( A \) and \( B \) which satisfy the predetermined (\( \alpha \), \( \beta \)). From the previously mentioned inequalities, (2.1) implies

\[ A(\alpha, \beta) \leq \frac{1-\beta}{\alpha}, \text{ and (2.2) implies } B(\alpha, \beta) \geq \frac{\beta}{1-\alpha}. \]

Wald [6] proposed to set \( A = \frac{1-\beta}{\alpha} = a(\alpha, \beta) \), which is in fact greater than or equal to the exact value of \( A(\alpha, \beta) \), and \( B = \frac{\beta}{1-\alpha} = b(\alpha, \beta) \) which is less than or equal to the exact value of \( B(\alpha, \beta) \). Wald discusses the consequences that the assigned combinations of \( A \) and \( B \) have on the error rates \( \alpha \) and \( \beta \). When \( A \) is a value greater than or equal to \( A(\alpha, \beta) \) and \( B \) is equal to \( B(\alpha, \beta) \), the Type I error rate is less than the nominal \( \alpha \), but the Type II error rate is greater than \( \beta \). If \( A \) is equal to \( A(\alpha, \beta) \) and \( B \) is a value less than or equal to \( B(\alpha, \beta) \), then the Type II error rate is less than the nominal \( \beta \), but the Type I error rate is greater than \( \alpha \). If \( A \) is a value greater than \( A(\alpha, \beta) \) and \( B \) is a value less than \( B(\alpha, \beta) \), then the effect on the Type I and Type II error rates is unclear. Wald thus proposes to denote \( \alpha' \) and \( \beta' \) as the respective error rates when \( A=a(\alpha, \beta) \) and \( B=b(\alpha, \beta) \).
From above, \( \frac{\alpha'}{1-\beta'} \leq \frac{1}{a(\alpha, \beta)} = \frac{\alpha}{1-\beta} \) and \( \frac{\beta'}{1-\alpha'} \leq \frac{1}{b(\alpha, \beta)} = \frac{\beta}{1-\alpha} \). Thus, upper limits for \( \alpha' \) and \( \beta' \) can be found to be \( \alpha' \leq \frac{\alpha}{1-\beta} \) and \( \beta' \leq \frac{\beta}{1-\alpha} \). Through some arithmetic, it can be shown that \( \alpha' + \beta' \leq \alpha + \beta \). Thus, we set \( A = \frac{1-\beta}{\alpha} \) and \( B = \frac{\beta}{(1-\alpha)} \).

We now consider the case of sampling with replacement (or sampling without replacement from a population of infinite size). Since the probability of selecting a defective item is \( \pi \) for each item and observations are independent, each observation can be considered a Bernoulli trial. Thus, Wald’s boundaries can be found as follows. In the likelihood ratio \( \Lambda_n \), the binomial density can be substituted for the likelihood functions, giving

\[
\Lambda_n = \frac{L(y_n, \pi_1)}{L(y_n, \pi_0)} = \left( \frac{n}{y_n} \right)^{y_n} \left( 1 - \pi_1 \right)^{n-y_n} \left( \frac{n}{y_n} \right)^{y_n} \left( 1 - \pi_0 \right)^{n-y_n}.
\]  

(2.4)

Using the criterion \( B \leq \Lambda_n \leq A \) presented by Wald,

\[
B \leq \frac{L(y_n, \pi_1)}{L(y_n, \pi_0)} = \left( \frac{n}{y_n} \right)^{y_n} \left( 1 - \pi_1 \right)^{n-y_n} \left( \frac{n}{y_n} \right)^{y_n} \left( 1 - \pi_0 \right)^{n-y_n} \leq A.
\]

(2.5)

Notice that instead of computing this ratio at each observation, we can solve for \( y_n \) as follows:
Notice that $y_n$ is now bounded above and below by parallel lines. Thus, if the total number of defectives at the current position $n$ is between or on these lines, $y_n$ is said to fall in the “zone of indifference”. Although values of $y_n$ may occur here, sampling continues within this region, and we therefore do not refer to these results as possible outcomes of the test. We refer to $y_n$ values that are above the upper boundary line as being in the “rejection region,” for these are the outcomes that would lead to rejection of the null hypothesis. Though we never actually accept $H_0$ when values of $y_n$ are below the lower bound, instead of referring to the region as the “zone of failing to reject,” for simplicity we call it the “acceptance region;” values of $y_n$ in this region are the outcomes that would lead to failing to reject the null hypothesis.

Wald [6] has shown that the sequential probability ratio test will eventually end in a decision being made with a probability of 1, but in practice, the sequential test is truncated at a maximum allowable sample size, $n_T$. If a decision has not been made prior to reaching the $n_T$ observation, sampling stops.
with the \( n_T \) observation. Then a decision is made based on the value of \( y_{n_T} \). We say that sequential testing is a closed procedure because testing is limited to a maximum allowable size.

Research on SPRT has continued since its first introduction by Wald, and selected examples are presented in the following sections of this chapter.

### 2.2 Mingoti’s Expansion of SPRT

Researchers have also been interested in determining the effects that the choices of the hypothesized values, \( \pi_0 \) and \( \pi_1 \), have on the required sample size. Mingoti [3] discusses the sample size needed to perform Wald’s sequential probability ratio test when items are generated by a process for which the results of the inspections are correlated. It was shown that for values of \( \pi_0 \) and \( \pi_1 \) which are close together, the sample size is larger than that which are found to be necessary when using values of \( \pi_0 \) and \( \pi_1 \) that are more distant. Additionally, when considering correlation (\( \rho \)) between the results of the \( n \) observations with respect to a binary response variable, the sample size increases as the value of the correlation coefficient \( \rho \) increases. In fact, when comparing the corresponding expected sample size for when \( \rho = 0 \) to when \( 0.5 < \rho < 0.7 \), the expected sample size is three times higher; it is six times higher when \( \rho > 0.7 \).

### 2.3 Iglewicz’s Expansion of SPRT

It is most common for sequential procedures to be compared in terms of the expected sample size, which is also known as the average sample number
This type of comparison does not consider sample size variability and is often biased in favor of tests with large sample-size variability. In terms of practicality, large sample-size variability is costly because it often leads to a large number of observations being required before the process terminates. Thus, Iglewicz [1] proposes an alternative measure for the ASN, 
\[ D(\pi) = \frac{N - E(n|\pi)}{\sigma_n(\pi)} \]
where \( N \) is the number of required observations for a fixed sample size test, \( \pi \) is the true value of the parameter, \( E(n|\pi) \) is the average sample number, and \( \sigma_n(\pi) \) is sample-size standard deviation. \( D(\pi) \) is a measure of the gain obtained by using a sequential procedure in place of a fixed sample size procedure. When \( D(\pi) \) is large, the sequential test is efficient, but when \( D(\pi) \) is small, the design is not.

2.4 McWilliams’ Expansion of SPRT

Due to the lack of published research regarding truncation on the SPRT, McWilliams [4] presents two case studies that inspect the influence that the choice of truncation parameters have on test performance. He examines both the choice of the truncation sample size and the choice of the truncation rejection value \( R \). When the test reaches the truncation sample size, \( R \) identifies how many defectives are required for rejection. Through the explanation of the two case studies, both choices appear have a deep impact on test performance.

McWilliams compares the ASN under both the null hypothesis, \( \pi = \pi_0 \), and the alternative hypothesis, \( \pi = \pi_1 \), since the value of the ASN will differ depending
upon the true value of \( \pi \) in the population. Additionally, the author examines the amount of variability in required sample size and the value of the error rates. McWilliams concludes that adopting an aggressive truncation strategy results in consequences in terms of the error probabilities and the ASN. The author does not generalize his results but expresses that, from his findings, the performance of the test over various values of \( R \) needs to be considered instead of an arbitrary choice of the rejection value.

2.5 Ignatova, Deutsch, and Edwards’ Expansion of SPRT

While considering closed sequential or multistage sampling from a lot of \( N \) items, the goal is to make conclusions about the proportion of defectives, \( \pi \), in the sample. Instead of using asymptotic results, Ignatova, et. al. [2] show that exact inference about the proportion of defectives can be calculated using current statistical software.

While considering \( y_n \) to be the number of defectives at stage \( n \), a decision is made whether to continue sampling or to end testing by comparing \( y_n \) to a set of boundaries. Since, in practice, sequential testing is truncated at \( n_T \), the truncated SPRT is the sole focus for the authors. For a given outcome, \( y_n \), there are \( \binom{n}{y_n} \) sequences of \( y_n \) defectives and \((n - y_n)\) non-defectives that result in a total of \( y_n \) defectives in \( n \) trials. As an example, consider the case of \( n_T = 10 \), shown in Figure 2.1. Each number represented in Figure 2.1 represents the number of ways to get \( y_n \) (on the \( y \)-axis) defectives in \( n \) trials (on the \( x \)-axis); we
refer to this as a path-count. Thus, we can consider the number of “paths” to a specific point \((n, y_n)\) on the graph. Arbitrarily chosen upper and lower boundaries are shown as a reference, but no modifications in the path counts have been made as a result of outcomes falling outside of the boundaries. The unrestricted path-counts are found via Pascal’s triangle.

Figure 2.1: Full Pascal’s Triangle Example
The boundaries must now be taken into account to determine the actual number of paths to $y_n$. An observation occurring outside of the boundaries results in sampling to end; thus, the paths extending from that point no longer exist. Based on a modified Pascal’s triangle algorithm, [2] utilizes a path-count method to determine the various paths that lead to specific termination points, while staying within the boundaries. A visual example of the path-count method can be seen in Figure 2.2.

Figure 2.2: Modified Pascal’s Triangle Method
Note that the solid dots that appear in Figure 2.2 are outcomes for which a decision is made and sampling ends. There are indeed values of $y_n$ which exist between the lower and upper bounds, but no decision is made in the test and sampling continues. Notice that points (4,0), (6,1), (9,2), and (10,10) all occur outside of the upper and lower boundaries shown. Thus, paths extending from (4,0), (6,1), and (9,2) do not exist, and the path-count for successive points are altered. For example, the path-count to point (5,1) reduced from five in the Pascal’s triangle example (Figure 2.1) to four in the modified Pascal’s triangle method; the path-count to point (7,2) reduced from 21 to 14. Additionally, notice that some of the paths to the outcomes on the truncation boundary are also reduced. For example points (10,3) and (10,5) reduced from 120 to 62 and 252 to 242, respectively. Also, notice that not all path-counts were altered.

Ignatova, et al. consider this method for both the binomial and hypergeometric cases. They have crossed into new territory by examining the hypergeometric case, as no other authors have pursued it [2]. Now consider the case of testing without replacement from a population of a finite size $N$. Thus, Wald’s boundaries can be determined where $y_n$ is a hypergeometric random variable. Similar to what was done in the binomial case in (2.4), the hypergeometric density can be substituted for the likelihood functions, giving
\[ \Lambda_n = \frac{L(y_n, D_1)}{L(y_n, D_0)} = \frac{\binom{D_1}{y_n} \binom{N-D_1}{n-y_n}}{\binom{D_0}{y_n} \binom{N-D_0}{n-y_n}} = \frac{\binom{D_1}{y_n} \binom{N-D_1}{n-y_n}}{\binom{D_0}{y_n} \binom{N-D_0}{n-y_n}} \]

(2.7)

where \( D_0 \) is the number of defective items in the population under \( H_0 \) and \( D_1 \) is the number of defectives in the population under \( H_1 \).

Using the criterion \( B \leq \Lambda_n \leq A \) presented by Wald, we have

\[ B < \frac{\binom{D_1}{y_n} \binom{N-D_1}{n-y_n}}{\binom{D_0}{y_n} \binom{N-D_0}{n-y_n}} < A. \]

(2.8)

In the pursuit of trying to isolate \( y_n \) in (2.8), we begin trying to simplify, giving

\[ B < \frac{(D_1)(N-D_1)}{(D_0)(N-D_0)} \cdot \frac{(D_0-y_n)(N-D_0-n+y_n)}{(D_1-y_n)(N-D_1-n+y_n)} < A \]

\[ \frac{B(D_0)(N-D_0)}{(D_1)(N-D_1)} < \frac{(D_0-y_n)(N-D_0-n+y_n)}{(D_1-y_n)(N-D_1-n+y_n)} < \frac{A(D_0)(N-D_0)}{(D_1)(N-D_1)}. \]

(2.9)

Although it was attempted, isolation of \( y_n \) could not be determined at this time.

The authors created a function entitled seqbin, using the statistical software package R [5], to determine sequential acceptance sampling for binary outcomes from a population of size \( N \) while sampling with or without replacement. Based on Wald’s SPRT method, a truncation position \( n_T \) and upper and lower boundaries are given as arguments to the function. The authors determined that Wald’s boundaries can be represented as a step boundary.
because as \( n \) increases by one, the value of \( y_n \) stays the same (if that observation is non-defective) or increases by one (if that observation is defective). Sampling continues if \( y_n \) is between or on the boundaries and \( n < n_T \). Using the boundary-modified Pascal algorithm, the seqbin function detects all possible outcomes (and the number of “paths” possible to reach that outcome) where \( y_n \) is less than the lower bound or greater than the upper bound (i.e., where the test does not stop before reaching \( n_T \)) or where \( y_n \) is on the truncation boundary. Additionally, the seqbin function calculates the number of defectives sampled and calculates the probability distribution of all possible outcomes.

We now consider an example of Wald’s truncated SPRT for testing the null hypothesis that \( \pi_0 = 0.2 \) versus the alternative hypothesis that \( \pi_1 = 0.8 \), with \( n_T = 10 \), \( \alpha = 0.05 \), and \( \beta = 0.10 \). Using \( A = (1 - \beta)/\alpha \) and \( \beta/(1 - \alpha) \) as defined in section 2.1, we have \( A = 18 \), and \( B \equiv 0.1053 \). From (2.6), the lower boundary line is given by \( l_n \equiv -0.8119819 + 0.5n \), and the upper boundary line is given by \( u_n \equiv 1.0424813 + 0.5n \), indicated by the dotted lines in Figure 2.3. The blue dashed line and red line represent step-boundary representations of the Wald upper and lower boundaries, respectively. The points in Figure 2.3 are the possible outcomes; notice that points exist in both the rejection region and acceptance region. The points that occur at \( n = n_T = 10 \) represent the outcomes that occur when sampling has not ended before reaching the truncation boundary. It is necessary that each of these points be included in either the rejection region or the acceptance region since a decision needs to be made in the test.
Figure 2.3: Wald Boundary Example
Chapter 3: A Method for Sharpening the Boundaries

3.1 Creating the Bounds

Based on the work previously completed by others, the goal of this thesis is to determine if there are better boundaries available than the ones which have been currently found in [6] and [2]. We would like to consider all possible sets of boundaries that exist for a given $n_T$. We will then use certain criteria to determine which of these sets of boundaries is the “best.” We first consider the set of boundaries that are equivalent to the standard hypothesis test: the lower boundary is the line $y_n = 0$, and the upper boundary is the line $y_n = n$. In other words, the lower bound includes successive observations of all non-defective items and the upper bound includes successive observations of all defective items. Observations here are always in the zone of indifference, so the sample size will always reach the truncation value of $n_T$. This gives boundaries that form a triangle, as can be seen in Figure 3.1 for the case when $n_T = 4$. 
Starting with this set of “triangle boundaries,” we will find all possible sets of boundaries for a given \( n_T \). We then want to determine all sets of upper and lower boundaries that have both the Type I and Type II error rates bounded. Then we would like to examine under various criteria which set of boundaries is indeed the best.

For a given \( n_T \), we must first generate every possible set of boundaries. When a sample is taken at \( n = 1 \) (i.e., only the first item is sampled), either zero defective items can be observed \( (x_1 = y_1 = 0) \) or one defective item is observed \( (x_1 = y_1 = 1) \); thus, every upper and lower boundary is restricted to beginning at either \( y_1 = 0 \) or \( y_1 = 1 \). Next, it is required that the step size is non-decreasing and of at most one because as the number of observations increases by one, the value of the number of defectives \( (y_n) \) can only either stay the same or increase.
by one. Additionally, the upper and lower boundaries are created such that they can touch one another but may not cross.

To create all sets of possible boundaries, we first create all possible single boundaries. Once this has been done, we combine all possible boundaries such that we have lower and upper boundaries that do not cross. To create all of the single boundaries, we first designate the initial boundary as \((0,0,0,\ldots,0)\), a boundary of \(n_T\) zeros (i.e., all \(n_T\) sampled items are non-defective). For an index \(i\) initially set equal to zero, we add 1 to the \(n_T - i\) position in the boundary, as we keep the bounds that are non-decreasing with a step-size of at most 1. After 1 can no longer be added to the \(n_T - i\) column due to the step-size requirement, \(i\) is incremented by one, and the process continues of adding 1 to the next position to the left until the step-size requirement is no longer fulfilled, and \(i\) is again incremented. The process continues successively until the boundary that represents a sample of \(n_T\) defective items, \((1,2,3,\ldots,n_T)\), is obtained. Working backwards, we then designate that the bound begins as \((1,2,3,\ldots,n_T)\) and for an index \(i\) initially set equal to zero, we subtract 1 from the \(n_T - i\) position in the boundary as we keep the bounds that are non-decreasing with a step-size of at most 1. After 1 can no longer be subtracted from the \(n_T - i\) position due to the step-size requirement, \(i\) is incremented by one, and the process continues of subtracting 1 from the next position to the left until the step-size requirement is no longer fulfilled, and \(i\) is again incremented. The process continues until the \((0,0,0,\ldots,0)\) boundary is obtained. We then combine all bounds that have been found and delete any duplicate boundaries. Table 3.1 displays the boundaries.
generated for \( n_T = 4 \) via the above described process (before deleting duplicate boundaries).

<table>
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<tr>
<th>Building Up</th>
<th>Building Down</th>
</tr>
</thead>
<tbody>
<tr>
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<td>1 2 3 4</td>
</tr>
<tr>
<td>0 0 0 1</td>
<td>1 2 3 3</td>
</tr>
<tr>
<td>0 0 1 1</td>
<td>1 2 2 3</td>
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<td>0 0 1 2</td>
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<td>0 1 2 2</td>
<td>1 1 1 2</td>
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<tr>
<td>0 1 2 3</td>
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<tr>
<td>1 1 2 3</td>
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<td>1 2 3 4</td>
<td>0 0 0 0</td>
</tr>
</tbody>
</table>

We then combine this “master” set of boundaries into sets of lower and upper boundaries, keeping only the boundaries which do not cross one another. An R [5] function called create.bnds has been created to implement this procedure (see Appendix A.2.2). An example of all possible sets of boundaries for \( n_T = 4 \) can be found in Appendix A.1.

Once all of the possible sets of boundaries are created, we are left to determine which set of boundaries is the “best.” In practical testing, you will be given a maximum allowance for Type I and Type II error rates. Thus, we must reduce the possible set of boundaries by first determining which sets of boundaries preserve \( \alpha \), the predetermined maximum allowable Type I error rate. To determine if \( \alpha \) is preserved, each set of upper and lower \( n_T \) boundaries is considered individually. A given set of bounds is first evaluated using the seqbin
function. Using this, we then determine which of the outcomes are in the rejection region, which are in the acceptance region, and which are on the truncation boundary. Then, assuming that the null hypothesis is true ($\pi = \pi_0$), the outcomes in the rejection region, if they exist, are used to calculate $\alpha$. For each outcome in the rejection region, we consider the probability of that outcome occurring, $P((n_{out}, y_{out}))$, assuming $\pi = \pi_0$ where $n_{out}$ and $y_{out}$ denote the number of items sampled and the number of defectives, respectively, for a given outcome. $P((n_{out}, y_{out}))$ is found by taking the product of the probability mass function and the proportion of paths staying within the boundaries leading to $(n_{out}, y_{out})$, as shown by [2]. Then, $\alpha$ is calculated by taking the sum of $P((n_{out}, y_{out}))$ for each outcome in the rejection region. If no outcomes appear in the rejection region, $\alpha = 0$ initially. It is important to note that at this stage, the outcomes on the truncation boundary are not yet considered. Once $\alpha$ has initially been calculated for a given set of bounds, we determine if this initial value of $\alpha$ is indeed bounded by the pre-specified value. All sets of boundaries which preserve the given Type I error rate are retained, and the remaining sets of boundaries are eliminated. An R [5] function called alpha.bounded has been written to determine the sets of boundaries for which the Type I error rate is preserved (see Appendix A.2.3).

From the remaining sets of boundaries, we must then determine which of those sets of bounds also maintain $\beta$, the predetermined maximum allowable Type II error rate. To determine if $\beta$ is maintained, each set of upper and lower
\( \alpha \)-bounded boundaries for \( n_T \) must be considered. First, a given set of \( \alpha \)-bounded bounds is evaluated using the seqbin function. Using this, we then determine which of the outcomes are in the rejection region, which are in the acceptance region, and which are on the truncation boundary. Then, assuming that the null hypothesis is true (\( \pi = \pi_0 \)), the outcomes in the rejection region, if they exist, are used to calculate \( \alpha \) as explained above. If no outcomes appear in the rejection region, \( \alpha = 0 \) initially. Now the outcomes that occur on the truncation boundary need to be considered, and a decision in the test must be made. Beginning with the outcome on the truncation point closest to the rejection region, we add that outcome to the rejection region as long as \( \alpha \) remains bounded by our desired significance level. Each successive outcome on the truncation point is added to the rejection region until \( \alpha \) is beyond our desired bound. Thus, the remaining truncation outcomes are then added to the acceptance region. Assuming that the alternative hypothesis is true (\( \pi = \pi_1 \)), \( \beta \) is calculated using the sum of \( P(\left( n_{\text{out}}, y_{\text{out}} \right)) \) for all of the \( \left( n_{\text{out}}, y_{\text{out}} \right) \) outcomes in the acceptance region. All sets of boundaries which preserve the given Type II error rate are retained, and the remaining sets of boundaries are eliminated. An R [5] function called errors.bounded has been written to determine the sets of boundaries for which both the Type I and II error rates are preserved (see Appendix A.2.4).

Once the sets of boundaries that preserve both \( \alpha \) and \( \beta \) have been collected, we begin trying to discover which set of boundaries is the best for given values of \( n_T, \pi_0, \) and \( \pi_1 \). One way to define which set of boundaries is the
best is to identify which set of boundaries minimizes the expected number of observations required to make a decision in the hypothesis test. Since the true value of $\pi$ is unknown, we use a fine grid of 1001 $\pi$-values from 0 to 1 in steps of 0.001 to assist in determining the expected number of total observations required to make a decision in the test, denoted as $E(n)$. Using the value of $n$ at each outcome, $n_{\text{out}}$, and the probability of $n_{\text{out}}$ over all outcomes, we are able to determine the expected number of observations to be

$$E(n) = \sum_{n_{\text{out}}} n_{\text{out}} \cdot P(n_{\text{out}}).$$  \hspace{1cm} (3.1)$$

Once $E(n)$ is calculated using $\pi$ equal to each of the 1001 values, we determine the maximum expected number of observations, $\max\{E(n)\}$, for each set of $\alpha$- and $\beta$-bounded boundaries. We then determine the best set of boundaries to be that which minimizes $\max\{E(n)\}$.

### 3.2 Results for the New Bounds

The method described in section 3.1 has been conducted for $n_T = 10, 20, 30, \text{ and } 40$ in both the binomial and hypergeometric cases with all combinations of $\pi_0 = 0.1, 0.2,$ and $0.3$ and $\pi_1 = 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, \text{ and } 0.9$. The determined total number of possible sets of lower and upper boundaries (disregarding conservation of the error rates) is shown in Table 3.2.

<table>
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<tr>
<th>$n_T$</th>
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<td>10</td>
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<td>20</td>
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<tr>
<td>30</td>
<td>277,208</td>
</tr>
<tr>
<td>40</td>
<td>844,893</td>
</tr>
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</table>
In the case of the binomial distribution, for each combination of $n_T$, $\pi_0$, and $\pi_1$ the original Wald boundary has also been calculated as a comparison to determine if this new method is indeed an improvement. R [5] functions written to find the Wald boundaries can be found in Appendices A.2.6 and A.2.7. Because the likelihood ratio in the hypergeometric case cannot be simplified to have parallel upper- and lower-boundary lines as in the binomial case, determining a closed form for the Wald upper and lower boundaries has limitations as seen in (2.9). Thus, the Wald boundaries for the hypergeometric case have not been considered at the present time.

In Tables 3.3 through 3.10, the results for the “best” new boundaries appear for both the binomial and hypergeometric distributions. In the binomial case, the corresponding Wald results also appear. For each $\pi_0$ and $\pi_1$ combination that has been considered, the value of the minimized $\max\{E(n)\}$ is given along with the corresponding values of $\alpha$ and $\beta$. The combinations of $\pi_0$ and $\pi_1$ which appear as a shaded box are not possible due to the condition that $\pi_0 < \pi_1$. The combinations of $\pi_0$ and $\pi_1$ which are empty indicate that no boundaries where both $\alpha$ and $\beta$ are bounded were found.
Table 3.3: Binomial Results for $n_T = 10$

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Table 3.4: Binomial Results for $n_T = 20$

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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>0.4</td>
<td>30.1737</td>
<td>24.3469</td>
<td>22.9849</td>
<td>12.7119</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>$\alpha$</td>
<td>0.0500</td>
<td>0.0487</td>
<td>0.0268</td>
<td>0.0268</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>$\beta$</td>
<td>0.0694</td>
<td>0.0898</td>
<td>0.0919</td>
<td>0.0993</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
In Tables 3.3 through 3.10, results marked with an asterisk (*) have multiple sets of boundaries with the same $\max\{E(n)\}$ and $\beta$ value when testing $\pi_0$ vs. $\pi_1$. Thus, the result presented in the table is the set of boundaries that has the smallest value of $\alpha$.

Taking note from the results presented in Tables 3.3 through 3.10, it can be seen that for $n_T = 10$, the new boundaries found for testing $\pi_0 = 0.1$ vs. $\pi_1 = 0.7$, $\pi_0 = 0.1$ vs. $\pi_1 = 0.9$, $\pi_0 = 0.2$ vs. $\pi_1 = 0.8$, $\pi_0 = 0.2$ vs. $\pi_1 = 0.9$, and $\pi_0 = 0.3$ vs. $\pi_1 = 0.9$ all reduced the minimized $\max\{E(n)\}$ when compared to the Wald boundaries for the binomial case. For $n_T = 10$, the new boundaries found for testing $\pi_0 = 0.1$ vs. $\pi_1 = 0.7$ reduces the expected number of observations by 0.6875, which was greatest difference observed.

It was not until close to the end of conducting this research that the Wald boundaries were calculated and analyzed. Only after analyzing this summary information did we notice a discrepancy between the Wald boundaries and the new boundaries. Because we set out to determine all sets of possible boundaries for any given $n_T$, the Wald boundaries should have been included in our possible set of boundaries with both $\alpha$ and $\beta$ bounded. Thus, the new “best” boundaries should be no worse than the Wald boundaries. When analyzing the results, we should have seen that if the minimized $\max\{E(n)\}$ of the new boundaries was not smaller than the $\max\{E(n)\}$ of the Wald boundaries, then the minimized $\max\{E(n)\}$ should have at most been equal to that of the Wald boundaries.
After retracing our steps, it was discovered that although our R functions correctly reduce a given collection of lower/upper boundaries to those for which both $\alpha$ and $\beta$ are bounded, the process in which we generated all possible boundaries was not exhaustive for all $n_T$. The idea of creating all possible bounds for $n_T$ under the conditions that the lower and upper bounds must both begin at zero or one, the lower and upper bounds must have a non-decreasing step size of at most one, and the lower and upper bounds may touch one another but not cross is correct. Thus, we discovered that not all possible boundaries under the three conditions were generated using the algorithm that we created; only a subset of the possible boundaries was generated. Unfortunately, as $n_T$ grows larger, it appears that more and more boundaries were missed. When creating the method for generating all possible boundaries for $n_T$, we tested the method by hand for several small $n_T$ values and incorrectly assumed it would work for all $n_T$ values.

Since $n_T = 10$ is the smallest $n_T$ value included in this research, we were able to find new boundaries with smaller minimized $\max\{E(n)\}$ than their corresponding Wald boundaries because enough of the possible boundaries were generated. Thus, we are optimistic that this method actually would sharpen many more of the boundaries for the SPRT if all possible boundaries are generated.
Chapter 4: Simulation Studies

4.1 Simulation Method

To test the performance of the boundaries, a simulation study was performed for each set of new \( n_T \)-boundaries that minimized the \( \max\{E(n)\} \) for a specified \( \pi \) so that we could observe the value of the required sample size and the decision made in each simulation. Because we have two values being tested of the known unknown parameter \( \pi, \pi = \pi_0 \) and \( \pi = \pi_1 \), we performed each simulation study for a set of bounds under both assumptions individually, similar to what was done in [4].

For each set of lower and upper bounds which minimize the \( \max\{E(n)\} \), the rejection and acceptance regions are determined and decisions are made regarding the outcomes on the truncation boundary. When sampling from an infinite population (or sampling with replacement), sample data is created with the specified probability of success, \( \pi = \pi_0 \) or \( \pi = \pi_1 \), by using the binomial random variable generator in R with \( n_T \) trials [5]. The total number of defectives at stage \( n \) is calculated for \( 1 \leq n \leq n_T \). When sampling without replacement, a population with a specified size of 1,000 is created with the correct proportion of defective and non-defective items. From the created population we randomly sample \( n_T \) items from the population without replacement (resulting in a hypergeometric random variable), and the number of defectives at stage \( n \) is calculated for \( 1 \leq n \leq n_T \). The SPRT is then performing using this generated data and the given set of boundaries. For each simulation setting (a given value of \( \pi \),
a given set of boundaries, and a given distribution), 10,000 samples were simulated and analyzed with SPRT.

For each set of new boundaries that were determined to minimized the max\{E(n)\}, simulations were run for both \(\pi = \pi_0\) and \(\pi = \pi_1\). We also performed simulations for the boundaries where the max\{E(n)\} was within one of the minimized max\{E(n)\}. Additionally, when sampling with replacement, the Wald boundaries were also studied via simulation. Since the simulations were conducted before the results were recognized as incomplete, 53 Wald boundaries, 216 minimized max\{E(n)\} boundaries, and 1,216 boundaries with a max\{E(n)\} within one of the minimized max\{E(n)\} were analyzed. The R [5] function created for the simulation study can be found in Appendix A.2.5.

### 4.2 Simulation Results

Although we know that we do not have all possible boundaries, we also do not have the Wald boundaries with which to compare in the hypergeometric case. Thus, for each combination of \(\pi_0\) and \(\pi_1\) we present max\{E(n)\} (calculated as described in section 3.1), the simulated average required number of observations when \(\pi = \pi_0\), denoted as \(\hat{E}_0(n)\), and the simulated average required number of observations when \(\pi = \pi_1\), denoted as \(\hat{E}_1(n)\). These results can be seen in Tables 4.1 through 4.4. For max\{E(n)\} we notice that for \(\pi_0 = 0.1\), as \(\pi_1\) increases, the value of max\{E(n)\} either stays the same or decreases; this is consistent with the results found in [3]. Considering \(\pi_0 = 0.2\) and the lowest satisfying \(\pi_1\) value, max\{E(n)\} starts at a higher value than the lowest
combination of $\pi_0 = 0.1$ and $\pi_1$, but the pattern does continue that as $\pi_0$ and $\pi_1$
become more distant, the value of $\max\{E(n)\}$ either decreases or stays the same.
However, in simulation, this pattern also came very close to holding true for
$\hat{E}_0(n)$ and $\hat{E}_1(n)$. If we had increased the number of simulations, it is possible
that the pattern would have always held for $\hat{E}_0(n)$ and $\hat{E}_1(n)$.

Table 4.1: Hypergeometric Simulation Results for $n_T = 10$

<table>
<thead>
<tr>
<th>$\pi_0$</th>
<th>$\pi_1$</th>
<th>$\max{E(n)}$</th>
<th>$\hat{E}_0(n)$</th>
<th>$\hat{E}_1(n)$</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.1</td>
<td>0.6</td>
<td>5.9235</td>
<td>4.7752</td>
<td>4.6734</td>
</tr>
<tr>
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<td>0.7</td>
<td>4.3668</td>
<td>3.3625</td>
<td>3.1840</td>
</tr>
<tr>
<td></td>
<td>0.8</td>
<td>4.3668</td>
<td>3.3849</td>
<td>2.8129</td>
</tr>
<tr>
<td></td>
<td>0.9</td>
<td>3.3697</td>
<td>2.1955</td>
<td>3.0085</td>
</tr>
<tr>
<td>0.2</td>
<td>0.7</td>
<td>7.3149</td>
<td>6.2719</td>
<td>5.6530</td>
</tr>
<tr>
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<td>0.8</td>
<td>5.1550</td>
<td>3.6390</td>
<td>4.5566</td>
</tr>
<tr>
<td></td>
<td>0.9</td>
<td>3.3697</td>
<td>2.3866</td>
<td>2.9850</td>
</tr>
<tr>
<td>0.3</td>
<td>0.8</td>
<td>7.0736</td>
<td>5.5370</td>
<td>6.2295</td>
</tr>
<tr>
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<td>0.9</td>
<td>4.8052</td>
<td>2.8088</td>
<td>4.4061</td>
</tr>
</tbody>
</table>

Table 4.2: Hypergeometric Simulation Results for $n_T = 20$

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<th>$\pi_1$</th>
<th>$\max{E(n)}$</th>
<th>$\hat{E}_0(n)$</th>
<th>$\hat{E}_1(n)$</th>
</tr>
</thead>
<tbody>
<tr>
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<td>13.7763</td>
<td>12.2465</td>
<td>9.7108</td>
</tr>
<tr>
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<td>10.8738</td>
<td>9.1128</td>
<td>7.5435</td>
</tr>
<tr>
<td></td>
<td>0.6</td>
<td>9.0133</td>
<td>7.3063</td>
<td>6.2372</td>
</tr>
<tr>
<td></td>
<td>0.7</td>
<td>6.7308</td>
<td>5.1811</td>
<td>5.1907</td>
</tr>
<tr>
<td></td>
<td>0.8</td>
<td>6.7308</td>
<td>5.1525</td>
<td>4.7787</td>
</tr>
<tr>
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<td>0.9</td>
<td>2.0000</td>
<td>1.9029</td>
<td>1.9957</td>
</tr>
<tr>
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<td>13.2908</td>
<td>11.1347</td>
<td>10.8846</td>
</tr>
<tr>
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<td>10.7414</td>
<td>8.3162</td>
<td>9.1039</td>
</tr>
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<td>7.1898</td>
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</tr>
<tr>
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<td>4.5873</td>
</tr>
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<td>0.7</td>
<td>13.1629</td>
<td>11.0000</td>
<td>11.6911</td>
</tr>
<tr>
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<td>0.8</td>
<td>12.0721</td>
<td>8.3228</td>
<td>10.8826</td>
</tr>
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<td>0.9</td>
<td>7.3560</td>
<td>4.1959</td>
<td>6.7192</td>
</tr>
</tbody>
</table>
Table 4.3: Hypergeometric Simulation Results for \( n_T = 30 \)

<table>
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<tr>
<th>( \pi_0 )</th>
<th>( \pi_1 )</th>
<th>( \max{E(n)} )</th>
<th>( \hat{E}_0(n) )</th>
<th>( \hat{E}_1(n) )</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.1</td>
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</tr>
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<td>12.3564</td>
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</tr>
<tr>
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<td>11.9721</td>
<td>9.9179</td>
<td>7.8238</td>
</tr>
<tr>
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<td>6.8775</td>
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</tr>
<tr>
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<td>6.8910</td>
<td>5.9896</td>
</tr>
<tr>
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<td>0.9</td>
<td>4.0000*</td>
<td>3.1406</td>
<td>3.9953</td>
</tr>
<tr>
<td>0.2</td>
<td>0.5</td>
<td>21.7086</td>
<td>19.0467</td>
<td>17.2162</td>
</tr>
<tr>
<td></td>
<td>0.6</td>
<td>18.5264</td>
<td>15.7705</td>
<td>14.0164</td>
</tr>
<tr>
<td></td>
<td>0.7</td>
<td>14.4479</td>
<td>11.905</td>
<td>11.7568</td>
</tr>
<tr>
<td></td>
<td>0.8</td>
<td>13.0612</td>
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<td>4.7981</td>
<td>6.3865</td>
</tr>
<tr>
<td>0.3</td>
<td>0.6</td>
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<td>20.6262</td>
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<tr>
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<td>19.1758</td>
<td>16.1491</td>
<td>16.8933</td>
</tr>
<tr>
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<td>17.0431</td>
<td>11.1249</td>
<td>15.5119</td>
</tr>
<tr>
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<td>10.0671</td>
<td>5.5498</td>
<td>9.1159</td>
</tr>
</tbody>
</table>

Table 4.4: Hypergeometric Simulation Results for \( n_T = 40 \)

<table>
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<tr>
<th>( \pi_0 )</th>
<th>( \pi_1 )</th>
<th>( \max{E(n)} )</th>
<th>( \hat{E}_0(n) )</th>
<th>( \hat{E}_1(n) )</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.1</td>
<td>0.3</td>
<td>28.6847</td>
<td>25.4916</td>
<td>22.0905</td>
</tr>
<tr>
<td></td>
<td>0.4</td>
<td>22.4998</td>
<td>18.8053</td>
<td>15.9250</td>
</tr>
<tr>
<td></td>
<td>0.5</td>
<td>19.6704</td>
<td>16.1707</td>
<td>13.0795</td>
</tr>
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</tr>
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</tr>
<tr>
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<td>0.8</td>
<td>10.5957</td>
<td>8.6645</td>
<td>7.1912</td>
</tr>
<tr>
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<td>0.9</td>
<td>5.0000*</td>
<td>3.9628</td>
<td>4.9896</td>
</tr>
<tr>
<td>0.2</td>
<td>0.5</td>
<td>28.1084</td>
<td>25.0704</td>
<td>22.4594</td>
</tr>
<tr>
<td></td>
<td>0.6</td>
<td>24.4261</td>
<td>20.8494</td>
<td>18.6746</td>
</tr>
<tr>
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<td>0.7</td>
<td>18.2432</td>
<td>15.4056</td>
<td>14.3170</td>
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<tr>
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<td>16.6563</td>
<td>11.9775</td>
<td>14.7202</td>
</tr>
<tr>
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<td>6.0116</td>
<td>7.9092</td>
</tr>
<tr>
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<td>0.6</td>
<td>30.1737</td>
<td>27.0055</td>
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</tr>
<tr>
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<td>6.9240</td>
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</tbody>
</table>
In Tables 4.2 through 4.4, results marked with an asterisk (*) in the max\{E(n)\} column have multiple sets of boundaries with the same max\{E(n)\} when testing \(\pi_0\) vs. \(\pi_1\). Thus, the result presented in the table is for one such set of boundaries.

Since we had the available Wald boundaries for comparison in the binomial case, we also considered max\{E(n)\}, \(\hat{E}_0(n)\), and \(\hat{E}_1(n)\) for each combination of \(\pi_0\) and \(\pi_1\) using the Wald boundaries, as seen in Tables 4.5 through 4.8. In Tables 4.7 and 4.8, results marked with an asterisk (*) in the max\{E(n)\} column have multiple sets of boundaries with the same max\{E(n)\} when testing \(\pi_0\) vs. \(\pi_1\). Thus, the result presented in the table is for one such set of boundaries.

Table 4.5: Binomial Simulation Results for \(n_T = 10\)

<table>
<thead>
<tr>
<th>(\pi_0)</th>
<th>(\pi_1)</th>
<th>max{E(n)}</th>
<th>(\hat{E}_0(n))</th>
<th>(\hat{E}_1(n))</th>
<th>Wald max{E(n)}</th>
<th>Wald (\hat{E}_0(n))</th>
<th>Wald (\hat{E}_1(n))</th>
</tr>
</thead>
<tbody>
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<td>3.2164</td>
<td>5.0508</td>
<td>3.6937</td>
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<td>3.3536</td>
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<td>2.8029</td>
</tr>
<tr>
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<td>3.3677</td>
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<td>3.0484</td>
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<td>2.4292</td>
<td>2.4408</td>
</tr>
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<td>6.4211</td>
<td>4.7574</td>
<td>5.2695</td>
</tr>
<tr>
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</tr>
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<td>3.0185</td>
<td>3.4787</td>
<td>2.4989</td>
<td>2.5743</td>
</tr>
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<td>7.0678</td>
<td>5.5660</td>
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<td>5.9209</td>
<td>3.9921</td>
<td>4.9784</td>
</tr>
<tr>
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<td>4.8007</td>
<td>2.7889</td>
<td>4.4095</td>
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<td>3.0866</td>
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</tbody>
</table>
Table 4.6: Binomial Simulation Results for $n_T = 20$

<table>
<thead>
<tr>
<th>$\pi_0$</th>
<th>$\pi_1$</th>
<th>$\max{E(n)}$</th>
<th>$\hat{E}_0(n)$</th>
<th>$\hat{E}_1(n)$</th>
<th>Wald $\max{E(n)}$</th>
<th>Wald $\hat{E}_0(n)$</th>
<th>Wald $\hat{E}_1(n)$</th>
</tr>
</thead>
<tbody>
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<td>11.9671</td>
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</tr>
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</tr>
<tr>
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<td>3.2995</td>
<td>4.6401</td>
<td>3.9961</td>
<td>2.4436</td>
<td>2.4404</td>
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<td>4.6090</td>
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<td>2.5746</td>
</tr>
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</table>

Table 4.7: Binomial Simulation Results for $n_T = 30$

<table>
<thead>
<tr>
<th>$\pi_0$</th>
<th>$\pi_1$</th>
<th>$\max{E(n)}$</th>
<th>$\hat{E}_0(n)$</th>
<th>$\hat{E}_1(n)$</th>
<th>Wald $\max{E(n)}$</th>
<th>Wald $\hat{E}_0(n)$</th>
<th>Wald $\hat{E}_1(n)$</th>
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<tr>
<td>0.0</td>
<td>0.4</td>
<td>18.1587</td>
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<td>13.8616</td>
<td>13.5398</td>
<td>9.6654</td>
<td>9.4107</td>
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<tr>
<td>0.1</td>
<td>0.5</td>
<td>15.2001</td>
<td>12.5394</td>
<td>9.4200</td>
<td>8.8907</td>
<td>6.0493</td>
<td>5.8684</td>
</tr>
<tr>
<td>0.2</td>
<td>0.6</td>
<td>11.9479</td>
<td>9.8374</td>
<td>7.8029</td>
<td>6.1424</td>
<td>4.1344</td>
<td>4.2086</td>
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<tr>
<td>0.3</td>
<td>0.7</td>
<td>8.6750</td>
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<tr>
<td>0.1</td>
<td>0.9</td>
<td>4.0000*</td>
<td>3.2063</td>
<td>4.0035</td>
<td>4.0000</td>
<td>2.4322</td>
<td>2.4498</td>
</tr>
<tr>
<td>0.2</td>
<td>0.0</td>
<td>22.0886</td>
<td>19.1325</td>
<td>18.6147</td>
<td>15.9520</td>
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<tr>
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<td>11.7403</td>
<td>7.8916</td>
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<tr>
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<td>4.0000</td>
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<td>20.1917</td>
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We observed that the same pattern described in [3] was exhibited in the binomial case for both the new boundaries and the Wald boundaries, as it was in the hypergeometric case. After closer observation, we also found that for a few of the new boundaries, \( \hat{E}_0(n) \), and \( \hat{E}_1(n) \) were smaller than that of their Wald counterparts. These instances are highlighted in Tables 4.5 through 4.8. To be exact, \( \hat{E}_0(n) \) was found to be better on four occurrences, and \( \hat{E}_1(n) \) was found to be better on three occurrences, all occurring when \( n_T = 10 \). These instances correspond to the new boundaries that were found to be better than the Wald boundaries, described in section 3.2.

For an additional qualification of what could be considered as the best boundary, we have also considered the boundaries that in simulation minimize

<table>
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<tr>
<th>( \pi_0 )</th>
<th>( \pi_1 )</th>
<th>( \max{E(n)} )</th>
<th>( \hat{E}_0(n) )</th>
<th>( \hat{E}_1(n) )</th>
<th>Wald ( \max{E(n)} )</th>
<th>Wald ( \hat{E}_0(n) )</th>
<th>Wald ( \hat{E}_1(n) )</th>
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the variability in required sample size, similar to [1]. Since only five new sets of boundaries were found to have minimized max\{E(n)\} in comparison to the Wald boundaries, we only present further results for the five cases where an improvement was found. However, many more simulation results are available from the author.

Figures 4.1 through 4.5 detail the results for the combinations of $\pi_0$ and $\pi_1$ for which an improvement in maximum expected sample size was found (with the new boundaries labeled as “Min”). For each set of boundaries, the horizontal dotted line extends one standard deviation above and below $\hat{E}_0(n)$, which is indicated by the open circle. Similarly, the solid horizontal line extends one standard deviation above and below $\hat{E}_1(n)$, which is indicated by the open circle. Additionally, the max\{E(n)\} is presented as a solid circle. Since we also conducted simulations for the sets of boundaries whose max\{E(n)\} is within one of the minimized max\{E(n)\} value, we present results for those observations as well. These boundaries are labeled as “Min +1” in the figures, and the subscript serves as a signifying index for each considered set of boundaries for the hypotheses being tested.
In Figure 4.1, we notice that under the null hypothesis ($\pi_0 = 0.1$), based upon the simulation performed, all new boundaries considered tend to require a smaller sample size to make a decision in the test than Wald’s boundaries; however, less variation is observed in the new boundaries under the alternative hypothesis ($\pi_1 = 0.7$). To the contrary, under the alternative hypothesis, the use of Wald’s boundaries tends to require a smaller sample size than the new boundaries (except for the new “best” boundary), and the null case exhibits less
variation for the Wald boundaries. Additionally, all new $\text{max}\{E(n)\}$ (except for $\text{Min} + 1_1$) are less than $\text{max}\{E(n)\}$ for Wald.

Figure 4.2 demonstrates that although $\text{max}\{E(n)\}$ has been reduced with the new boundaries, under simulation Wald’s boundaries result in more consistency in that it has small variation under both the null ($\pi_0 = 0.1$) and alternative hypotheses ($\pi_1 = 0.9$). In simulation using the new “best” bounds and the bounds whose $\text{max}\{E(n)\}$ are within one, under the null hypothesis all but one ($\text{Min} + 1_7$) has less variation than under Wald’s simulation.

Figure 4.2: Binomial $n_T = 10$ Simulation with $\pi_0 = 0.1$ and $\pi_1 = 0.9$
Figure 4.3 shows that although $\max\{E(n)\}$ is reduced, Wald appears again to be more consistent under both the null ($\pi_0 = 0.2$) and alternative ($\pi_1 = 0.8$) hypotheses. Also, $\max\{E(n)\}$ for the new bounds is the only $\max\{E(n)\}$ value which is less than Wald’s. Figures 4.4 and 4.5 demonstrate that under the alternative hypothesis ($\pi_1 = 0.9$), much more variability is shown in the new “best” bounds than in Wald’s boundaries.

Figure 4.3: Binomial $n_T = 10$ Simulation with $\pi_0 = 0.2$ and $\pi_1 = 0.8$
Figure 4.4: Binomial $n_T = 10$ Simulation with $\pi_0 = 0.2$ and $\pi_1 = 0.9$
Figure 4.5: Binomial $n_T = 10$ Simulation with $\pi_0 = 0.3$ and $\pi_1 = 0.9$
For this thesis, we set out to determine a possible method to reduce the expected number of observations needed in a sequential probability ratio test. The goal was to generate all possible boundaries for a given value of $n_T$ that preserve a given set of error rates ($\alpha, \beta$). We conducted this research on binary data for binomial and hypergeometric random variables. In the binomial case, we were able to compare the newly created boundaries to the boundaries established by [6]. In some cases, we were able to find boundaries that reduced the expected number of observations for making a decision in the test from that which is required by the standard Wald boundaries. Although we believe that the overall method that we intended to use is correct, we discovered that there was a problem in one of the algorithms developed to implement this method. Additionally, we were able to conduct simulation studies on the boundaries to estimate $\max\{E(n)\}$ and the amount of variability of the required sample size in practice, under both the null hypothesis and the alternative hypothesis.

In the future, the first thing that needs to be determined is a correct algorithm for generating all possible boundaries for $n_T$. Although the idea of considering all possible boundaries with the conditions of beginning at zero or one, have a step size of at most one, and being allowed to touch one another but not cross is correct, the method that was used to implement it appears to be incomplete and not exhaustive. The overall method that has been developed in this research for sharpening the boundaries is hopeful, so the generation of all
possible boundaries should be a top priority. Additionally, the efficiency of the
correct R functions that have been created (alpha.bounded and errors.bounded)
needs to be improved. At this time, we were only able to consider \( n_T \) as large as
40 because some of these functions take days to run on a standard computer.
Now knowing that not even all of the possible boundaries were considered, it is
unimaginable how long it would have taken to run had an exhaustive list of
boundaries been used.

Alternative areas to explore in this research are also available. Since all
data that we have considered has been binary, we could explore testing data that
is not binary. Additionally, we could consider testing composite alternative
hypotheses \((<, >, \neq)\) as opposed to the simple alternative that was considered in
this research. Also, since little to no research has been conducted on the SPRT
in the hypergeometric case, there is much left to consider, including the Wald
boundaries. We could also take direction from [3] and explore testing in the
situation of correlated binary data.

In conclusion, we have explored the sequential probability ratio test
beginning with Wald’s first introduction of the test. We also examined
expansions on the SPRT that other authors have considered. Utilizing the
research presented in [2], we have presented and attempted to develop a
potential new method for sharpening the boundaries of the sequential probability
ratio test.
APPENDIX

A.1 Boundaries for $n_T = 4$
A.2 R Code

A.2.1 check.step()

Purpose of Function:
Check the step size of the boundaries to ensure that the step sizes are non-decreasing and are at most one.

Input:
test Boundaries which are to be tested.

Output:
flag Value of 1 indicates that the set of boundaries does not meet the step size requirement. Value of 0 indicates that the set of boundaries does meet the step size requirement.

Function:
check.step<-function(test)
{
  i<-1
  flag<-0
  while(flag==0 && i < length(test))
  {
    if((test[i+1]-test[i])>1 | (test[i+1]-test[i])<0)
      flag<-1
    i<-i+1
  }
  flag
}

A.2.2 create.bnds()

**Purpose of Function:**
Create all possible sets of lower and upper bounds (for a specified n\(_T\)) which either begin at zero or one, have steps that are non-decreasing and of size at most one, and (possibly) touch one another but do not cross.

**Input:**
n\(_T\) Value of the maximum allowable sample size.

**Output:**
List containing the following matrices, rows of which correspond to one another:
lbnd.mat Matrix of all possible lower boundaries for specified n\(_T\).
ubnd.mat Matrix of all possible upper boundaries for specified n\(_T\).

**Function:**
create.bnds<-function(nT)
{
### A matrix to hold the upper and lower bounds
bnd.mat<-matrix(0,nrow=1,ncol=nT)

### Bnd.now begins as (0,0,0,...,0)
bnd.now<-rep(0,nT)

### Designates that bnd.now is no more than (1,2,3,...,nT)
while(sum(bnd.now==(1:nT)) != nT)
{
  flag<-0
  i<-0

  while(flag==0)
  {
    bnd.new<-bnd.now
    bnd.new[nT-i]<-bnd.new[nT-i]+1 ### Adds 1 to the nT-i column

    if(check.step(bnd.new)==0)
    {  
      ### Combines bounds that are non-decreasing with step- size of at most 1
      bnd.mat<-rbind(bnd.mat,bnd.new)
      bnd.now<-bnd.new
      flag<-1
    }  # end of if(check.step(bnd.new)==0)
    i<-i+1
  }  # end of while(flag==0)
}  # end of while(sum(bnd.now==(1:nT)) != nT)

### Bnd.now begins as (1,2,3,...,nT)
bnd.now<-(1:nT)
### Designates that bnd.now is no less than (0,0,0,...,0)
while(sum(bnd.now) !=0)
{
  flag<-0
  i<-0

  while(flag==0)
  {
    bnd.new<-bnd.now
    bnd.new[nT-i]<-bnd.new[nT-i]-1    ### Subtracts 1 from the nT-i column

    if(check.step(bnd.new)==0)
    {
      ### Combines bounds that are non-decreasing with step-size of at most 1
      bnd.mat<-rbind(bnd.mat,bnd.new)
      bnd.now<-bnd.new
      flag<-1
    }  # end of if(check.step(bnd.new)==0)

    i<-i+1
  }  # end of while(flag==0)
}  # end of while(sum(bnd.now) != 0)

### Combines all bounds found by adding/subtracting 1 to column nT-i and deletes duplicates
bnd.list<-bnd.mat[!duplicated(bnd.mat),]
row.names(bnd.list)<-1:nrow(bnd.list)

lbnd.mat<-matrix(NA,ncol=nT)
ubnd.mat<-matrix(NA,ncol=nT)

for(i in 1:nrow(bnd.list))
{
  for(j in 1:nrow(bnd.list))
  {
    if(sum(bnd.list[i,]<=bnd.list[j,])==nT)
    {
      ### Creates matrix of lower bounds
      lbnd.mat<-rbind(lbnd.mat,bnd.list[i,])

      ### Creates matrix of upper bounds
      ubnd.mat<-rbind(ubnd.mat,bnd.list[j,])
    }  # end of if(sum(bnd.list[i,]<=bnd.list[j,])==nT)
  }  # end of for(j in 1:nrow(bnd.list))
}  # end of for(i in 1:nrow(bnd.list))
lbd.mat<-lbd.mat[-1,]
ubnd.mat<-ubnd.mat[-1,]

out<-list(lbd.mat, ubnd.mat)
names(out)<-c("lbd.mat","ubnd.mat")
out
}

A.2.3 alpha.bounded()

Purpose of Function:
Reduce the list of all possible sets of lower and upper bounds (for a specified n_T) such that the Type I error rate, \( \alpha \), is preserved.

Input:
- \( n_T \)  Value of the maximum allowable sample size.
- \( lbnd.mat \) Matrix of lower boundaries to be tested.
- \( ubnd.mat \) Matrix of upper boundaries to be tested.
- \( p0 \)  Value of null proportion to be tested.
- \( target.a \) Value of target Type I error rate. Default value is “0.05”.
- \( dist \) Distribution under which to test the boundaries. Default value is “binom”.

Output:
List containing the following matrices, rows of which correspond to one another:
- \( lbnds.a.bounded \) Matrix of lower boundaries which preserve \( \alpha \).
- \( ubnds.a.bounded \) Matrix of upper boundaries which preserve \( \alpha \).

Function:
```r
alpha.bounded<- function(nT,lbnd.mat,ubnd.mat,p0,target.a=0.05,dist="binom") {

  numbounded<-0
  alphabounded<-rep(NA,nrow(lbnd.mat))
  lbnds.bounded<-matrix(NA,nrow=1,ncol=nT)
  ubnds.bounded<-matrix(NA,nrow=1,ncol=nT)

  #### the following will be done for all possible bounds for n_T
  for(j in 1:nrow(lbnd.mat)) {
    #### run seqbin for current set of bounds
    lbnd.now<-lbnd.mat[j,]
    ubnd.now<-ubnd.mat[j,]
    out<-seqbin.nT(nT,lbnd.now,ubnd.now,plotit=F,dist=dist)
    outcomes<-out$outcomes
    probs<-out$probs

    trunc<-outcomes[,1]==nT
    lower<-rep(NA,nrow(outcomes))
    upper<-rep(NA,nrow(outcomes))

    #### determine which outcomes are in the rejection/acceptance regions and which are at the truncation
    for(i in 1:nrow(outcomes)) {
      
    }
  }
}
```
lower[i] <- outcomes[i, 2] < lbnd.now[outcomes[i, 1]]
upper[i] <- outcomes[i, 2] > ubnd.now[outcomes[i, 1]]
if(lower[i] == T)
  trunc[i] <- F
if(upper[i] == T)
  trunc[i] <- F
} # end of for(i in 1:nrow(outcomes))
	nowlength <- sum(lower)
  trlength <- sum(trunc)
  uplength <- sum(upper)

##### use values in rejection region (if they exist) to calculate alpha
if(uplength > 0)
  alpha <- sum(probs[nrow(outcomes):(nrow(outcomes)-uplength+1),(p0*1000+1)]) else alpha <- 0

##### determine if alpha is bounded
if(alpha > target.a)
  alphabounded[j] <- F else alphabounded[j] <- T

##### save the bounds for which alpha is bounded
if(alphabounded[j] == T)
  {  
      lbnbd.bounded <- rbind(lbnbd.bounded, lbnbd.mat[j,])  
      ubnbd.bounded <- rbind(ubnbd.bounded, ubnbd.mat[j,])  
      numbounded <- numbounded + 1
  } # end of if(alphabounded[j] == T)
} # end of for(j in 1:nrow(lbnd.mat))

##### return the list of boundaries for which alpha is bounded
out <- list(lbnbd.bounded[-1,], ubnbd.bounded[-1,])
names(out) <- c("lbnbd.a.bounded", "ubnbd.a.bounded")
out
} # end of alpha.bounded
A.2.4 errors.bounded()

**Purpose of Function:**
Reduce a list sets of lower and upper bounds (for a specified \( n_T \)) such that not only the Type I error rate, \( \alpha \), is preserved, but also the Type II error rate, \( \beta \).

**Input:**
- \( n_T \) Value of the maximum allowable sample size.
- \( \text{lbnd.mat} \) Matrix of lower boundaries to be tested.
- \( \text{ubnd.mat} \) Matrix of upper boundaries to be tested.
- \( p_0 \) Value of null proportion to be tested.
- \( p_1 \) Value of alternative proportion to be tested.
- \( \text{target.a} \) Value of target Type I error rate. Default value is “0.05”.
- \( \text{target.b} \) Value of target Type I error rate. Default value is “0.10”.
- \( \text{dist} \) Distribution under which to test the boundaries. Default value is “binom”.

**Output:**
List containing the following objects (rows of which correspond):
- \( \text{lbnds} \) Matrix of possible lower boundaries with both \( \alpha \) and \( \beta \) bounded.
- \( \text{ubnds} \) Matrix of possible upper boundaries with both \( \alpha \) and \( \beta \) bounded.
- \( \text{alphas} \) Vector containing \( \alpha \) for each set of boundaries.
- \( \text{betas} \) Vector containing \( \beta \) for each set of boundaries.
- \( \text{maxEn} \) Vector containing \( \max\{E(n)\} \) for each set of boundaries.

**Function:**
```r
errors.bounded<- function(nT,lbnd.mat,ubnd.mat,p0,p1,target.a=0.05,target.b=0.10,dist="binom")
{
    numbounded<-nrow(lbnd.mat)

    betas<-rep(NA,numbedded)
    alphas<-rep(NA,numbedded)
    bbounded<-rep(NA,numbedded)
    maxEn<-rep(NA,numbedded)

    #### the following will be done for all bounds for nT for which
    alpha is bounded
    for(j in 1:numbounded)
    {
        lbnd.now<-lbnd.mat[j,]
        ubnd.now<-ubnd.mat[j,]

        #### run seqbin for current set of bounds
        out<-seqbin.nT(nT,lbnd.now,ubnd.now,plotit=F,dist=dist)
        En<-out$outcomes[,1]%*%out$probs
        maxEn[j]<-max(En)    #### find the max\{E(n)\} for this set of
    }
}
```
boundaries

outcomes<-out$outcomes
probs<-out$probs

trunc<-outcomes[,1]==nT
lower<-rep(NA,nrow(outcomes))
upper<-rep(NA,nrow(outcomes))

##### determine which outcomes are in the rejection/acceptance
regions and which are at the truncation
for(i in 1:nrow(outcomes))
{
  lower[i]<-outcomes[i,2] < lbnd.now[outcomes[i,1]]
  upper[i]<-outcomes[i,2] > ubnd.now[outcomes[i,1]]
  if(lower[i]==T) trunc[i]<-F
  if(upper[i]==T) trunc[i]<-F
} # end of for(i in 1:nrow(outcomes))

lowlength<-sum(lower)
trlength=sum(trunc)
uplength=sum(upper)

if(uplength>0)
{
  abounded<-T
  i<-nrow(outcomes)-uplength+1
  
  ### add points on truncation to rejection region, as long
  as alpha stays bounded
  while((abounded == T) && (i > lowlength))
  {
    if(sum(probs[nrow(outcomes):i,(p0*1000+1)])
      <= target.a)
    {
      alpha<-sum(probs[nrow(outcomes):i,(p0*1000+1)])
      i<-i-1
    } else abounded<-F  # end of if
  } # end of while((abounded == T) && (i > lowlength))
} # end of if(uplength>0)

if(uplength==0)
{
  abounded<-T
  i<-nrow(outcomes)
  
  ### add points on truncation to rejection region, as long
  as alpha stays bounded
  while((abounded == T) && (i > lowlength))
  {
if(sum(probs[nrow(outcomes):i,(p0*1000+1)]) <= target.a)
{
    alpha<-sum(probs[nrow(outcomes):i,(p0*1000+1)])
    i<-i-1
} else abounded<-F  # end of
if(sum(probs[nrow(outcomes):i,(p0*1000+1)]) <= target.a)
}  # end of while((abounded == T) && (i > lowlength))
}  # end of if(uplength==0)

#### calculate beta using all point in acceptance region and
remaining truncation points
beta<-sum(probs[1:i,(p1*1000+1)])  
#### determine if beta is bounded; if yes, save results
if(beta<=target.b)
{
    bbounded[j]<-T
    betas[j]<-beta
    alphas[j]<-alpha
} else bbounded[j]<-F  # end of if(beta<=target.b)
}  # end of for(j in 1:numbounded)

#### save results for only the sets that have both alpha and beta
 bounded
if(sum(is.na(alphas))>0)
{
    lbnds.bounded.out<-lbnd.mat[-which(is.na(alphas)),]
    ubnds.bounded.out<-ubnd.mat[-which(is.na(alphas)),]
    betas.out<-betas[-which(is.na(alphas))]
    alphas.out<-alphas[-which(is.na(alphas))]
    maxEn.out<-maxEn[-which(is.na(alphas))]
}  # end of if(sum(is.na(alphas))>0)

#### save results for all sets of bounds (because alpha and beta
are bounded for all in this case)
if(sum(is.na(alphas))==0)
{
    lbnds.bounded.out<-lbnd.mat
    ubnds.bounded.out<-ubnd.mat
    betas.out<-betas
    alphas.out<-alphas
    maxEn.out<-maxEn
}  # end of if(sum(is.na(alphas))==0)

#### return results for boundaries that have both error rates
bounded
out=list(lbnds.bounded.out,ubnds.bounded.out,alphas.out,betas.out
,maxEn.out)
names(out)<-c("lbnds","ubnds","alphas","betas","maxEn")
out}  # end of errors.bounded
A.2.5 \texttt{sim.sprt()}

\textbf{Purpose of Function:}  
Conduct a specified number of simulations on a given set of boundaries to determine the decision made in the test and the required sample size for each simulation.

\textbf{Input:}  
- \texttt{nT} \hspace{1cm} \text{Value of the maximum allowable sample size.}  
- \texttt{p} \hspace{1cm} \text{Value of proportion of defectives in the population.}  
- \texttt{p0} \hspace{1cm} \text{Value of null to be tested.}  
- \texttt{lbnd} \hspace{1cm} \text{Lower boundary to be used.}  
- \texttt{ubnd} \hspace{1cm} \text{Upper boundary to be used.}  
- \texttt{sim.size} \hspace{1cm} \text{Value of the number of simulations to conduct. Default value is “10000”.}  
- \texttt{dist} \hspace{1cm} \text{Distribution under which to simulate the data. Default value is “binom”.}  
- \texttt{pop.size} \hspace{1cm} \text{Value of size of the population. Default value is “1000”. This argument is only used when dist=“hyer”.} 

\textbf{Output:}  
List containing the following objects:  
- \texttt{decision} \hspace{1cm} \text{Vector of decisions made for each run of the simulation. Value = 1 if decision was made to fail to reject the null hypothesis, and value = 0 if decision was made to reject the null hypothesis.}  
- \texttt{n.stop} \hspace{1cm} \text{Vector of the required sample size to make a decision in the test for each run of the simulation.} 

\textbf{Function:}  
\begin{verbatim}
sim.sprt<-  
  function(nT,p,p0,lbnd,ubnd,sim.size=10000,dist="binom", 
            pop.size=1000) 
  { 
    decision<-rep(NA,sim.size) ####### accept = 1; reject = 0 
    n.stop<-rep(NA,sim.size) 
    
    ### get seqbin results 
    out<-seqbin.nT(nT,lbnd,ubnd,plotit=F,dist=dist) 
    outcomes<-out$outcomes 
    probs<-out$probs 
    
    trunc<-outcomes[,1]==nT 
    lower<-rep(NA,nrow(outcomes)) 
    upper<-rep(NA,nrow(outcomes)) 
    
    ### determine which outcomes are in the rejection/acceptance regions and which are at the truncation 
    for(i in 1:nrow(outcomes))
      
  }
\end{verbatim}
\{
    lower[i]<-outcomes[i,2] < lbdn[outcomes[i,1]]
    upper[i]<-outcomes[i,2] > ubnd[outcomes[i,1]]
    if(lower[i]==T)
        trunc[i]<-F
    if(upper[i]==T)
        trunc[i]<-F
\}  # end of for(i in 1:nrow(outcomes))

lowlength<-sum(lower)
trlength=sum(trunc)
uplength=sum(upper)

### use values in rejection region (if they exist) to calculate alpha
if(uplength>0)
{  
    abounded<-T
    i<-nrow(outcomes)-uplength+1
    
    ### add points on truncation to rejection region, as long as alpha stays bounded
    while((abounded == T) && (i > lowlength))
    {
        if(sum(probs[nrow(outcomes):i,(p0*1000+1)]) <= 0.05)
        {  
            alpha<-sum(probs[nrow(outcomes):i,(p0*1000+1)])
            i<-i-1
        }  
        else abounded<-F
        # end of if(sum(probs[nrow(outcomes):i,(p0*1000+1)])
        <= target.a)
    }  # end of while((abounded == T) && (i > lowlength))
 }

if(uplength==0)
{
    abounded<-T
    i<-nrow(outcomes)
    
    ### add points on truncation to rejection region, as long as alpha stays bounded
    while((abounded == T) && (i > lowlength))
    {
        if(sum(probs[nrow(outcomes):i,(p0*1000+1)]) <= 0.05)
        {  
            alpha<-sum(probs[nrow(outcomes):i,(p0*1000+1)])
            i<-i-1
        }  
        else abounded<-F
        # end of if(sum(probs[nrow(outcomes):i,(p0*1000+1)])
        <= target.a)
    }  # end of while((abounded == T) && (i > lowlength))

if(0

{  
    abounded<-T
    i<-nrow(outcomes)
    
    ### add points on truncation to rejection region, as long as alpha stays bounded
    while((abounded == T) && (i > lowlength))
    {
        if(sum(probs[nrow(outcomes):i,(p0*1000+1)]) <= 0.05)
        {  
            alpha<-sum(probs[nrow(outcomes):i,(p0*1000+1)])
            i<-i-1
        }  
        else abounded<-F
        # end of if(sum(probs[nrow(outcomes):i,(p0*1000+1)])
        <= target.a)
    }  # end of while((abounded == T) && (i > lowlength))

70
for(j in 1:sim.size)
{
  if(dist=="binom")
  {
    ### create sample data with specified probability of success
    x<-cumsum(rbinom(nT,1,p))  ### cumsum calculates "yn"
  } # end of if(dist=="binom")
  if(dist=="hyper")
  {
    ### create a "population" with the correct proportion of defectives/nondefectives
    population<-c(rep(1,p*pop.size),rep(0,(1-p)*pop.size))
    ### randomly sample from the population without replacement (making it hypergeometric)
    x<-cumsum(sample(population,nT,replace=F))  ### cumsum calculates "yn"
  } # end of if(dist=="hyper")
}

done<-0
k<-1

### continue "sampling" until a decision is made
while(done==0 & k<nT)
{
  ### determine if in the acceptance region
  if(x[k] < lbnd[k])
  {
    done<-1
    n.stop[j]<-k
    decision[j]<-1
  } # end of if(x[k] < lbnd[k])

  ### determine if in the rejection region
  if(x[k] > ubnd[k])
  {
    done<-1
    n.stop[j]<-k
    decision[j]<-0
  } # end of if(x[k] > ubnd[k])
  k<-k+1
} # end of while(done==0 & k<nT)

### make a decision if sampling reached maximum sample size
if(is.na(n.stop[j]))
{
  n.stop[j]<-nT
}
if(x[nT]>=outcomes[i+1,2]) decision[j]<-0
if(x[nT]<outcomes[i+1,2]) decision[j]<-1
} # end of if(is.na(n.stop[j]))
} # end of for(j in 1:sim.size)

#### return decision and needed sample size for all sim.size simulations
out<-list(decision,n.stop)
names(out)<-c("decision","n.stop")
out

} # end of sim.spert
A.2.6 Wald.bnd()

**Purpose of Function:**
Calculate the Wald boundaries in the binomial case.

**Input:**
- `p0` Value of null proportion.
- `p1` Value of alternative proportion.
- `alpha` Value of maximum allowable Type I error rate, \( \alpha \). Default value is “0.05”.
- `beta` Value of maximum allowable Type II error rate, \( \beta \). Default value is “0.10”.

**Output:**
List containing the following objects:
- `l.int` Value of the intercept for the lower boundary.
- `u.int` Value of the intercept for the upper boundary.
- `slope` Value of the slope for the parallel boundaries.

**Function:**
```r
Wald.bnd<-function(p0, p1, alpha=0.05, beta=0.10)
{
  A<-(1-beta)/alpha
  B<-beta/(1-alpha)
  #### slope for the parallel boundaries
  slope<--log((1-p1)/(1-p0))/log((p1/p0)*((1-p0)/(1-p1)))
  #### intercept for lower boundary
  l.int<-log(B)/log((p1/p0)*((1-p0)/(1-p1)))
  #### intercept for upper boundary
  u.int<-log(A)/log((p1/p0)*((1-p0)/(1-p1)))
  out<-c(l.int, u.int, slope)
  names(out)<-c("l.int", "u.int", "slope")
  out
}
```
A.2.7 Wald.step.bnd()

**Purpose of Function:**
Convert the Wald boundaries to a step boundary.

**Input:**
- l.int  Value of the intercept for the lower boundary to be converted.
- u.int  Value of the intercept for the upper boundary to be converted.
- slope  Value of the slope for the parallel boundaries to be converted.
- nT     Value of the maximum allowable sample size.

**Output:**
List containing the following objects:
- lbnd   The converted Wald lower bound as a step boundary.
- ubnd   The converted Wald upper bound as a step boundary.

**Function:**
Wald.step.bnd<-function(l.int, u.int, slope,nT)
{
  n<-1:nT
  lbnd<-ceiling(l.int+slope*n)
  ubnd<-floor(u.int+slope*n)
  out<-list(lbnd,ubnd)
  names(out)<-c("lbnd", "ubnd")
  out
}

REFERENCES


