Exact Probability Method for Sample Size Calculation in Single-Sample Rate Comparison (Single-Group Target Value Method) and R Language Implementation

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Abstract

Sample size calculation for single-sample rate comparison (single-group target value method) commonly employs the normal approximation method, occasionally with corresponding data transformations such as arcsine square root transformation, while the exact probability method typically necessitates commercial statistical software for iterative search or programming implementation. This study utilizes the free R software to programmatically implement sample size calculation via the exact probability method for single-sample rate comparison, and accounts for the non-monotonic relationship between test power and sample size inherent in exact probability method computations, providing direct calculation results and enabling graphical visualization of the power-sample size relationship, thereby aiming to facilitate the effective conduct of such research.

Full Text

Exact Probability Sample Size Calculation for Single Proportion Comparison (Performance Goal) with R Language

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Abstract

The common method for sample size calculation in single proportion comparison (performance goal) is the normal asymptotic approach, sometimes with corresponding data transformations such as the squared arcsine transformation. Exact probability methods, however, typically require commercial statistical

software or custom programming. This paper demonstrates how to implement exact probability sample size calculation for single proportion comparison using the free R software. Considering the non-monotonic increasing relationship between power and sample size in exact probability calculations, we provide not only direct computational results but also intuitive graphical demonstrations of the relationship between power and sample size, hoping to facilitate the effective conduct of such studies.

Key words: performance goal; single proportion comparison; sample size calculation; exact probability; R language

The performance goal (PG) approach is increasingly used in current clinical trial designs. For categorical data, the single-group performance goal method is essentially a single proportion comparison. Common sample size calculation methods include the normal approximation method and the square root arcsine transformation method. However, implementing exact probability calculations remains somewhat cumbersome. Researchers in China have previously used SAS [1, 2] or Stata [3] for programming calculations, with some considering the non-monotonic relationship between power and sample size in exact probability methods [2, 4]. This paper introduces the implementation of exact probability sample size calculation for single proportion comparison using R language (version 3.4.0).

Principles and R Programming

The basic idea of the exact probability method for single proportion comparison is to calculate power based on the cumulative binomial distribution. Referencing calculation formulas from the literature [1], we developed the following R program:

First, we create the function `exactpow` to calculate power:

```
exactpow<-function(side,alpha,p0,p1,n){
  if(side==1&p1>p0){
    while (1-pbinom(k,n,p0)<=alpha){  # pbinom is an R function that calculates binomial pro
      k=k-1
    }
    power=1-pbinom(k+1,n,p1)
  }
  if(side==1&p1<p0){
    while (pbinom(k,n,p0)<=alpha){
      k=k+1
    }
    power=pbinom(k-1,n,p1)
  }
  if(side==2){
    k1<-0
    while (pbinom(k1,n,p0)<=alpha/2){
```

```
      k1=k1+1
    }
    k2<-n
    while (1-(pbinom(k2,n,p0))<=alpha/2){
      k2=k2-1
    }
    power=pbinom(k1-1,n,p1)+1-pbinom(k2+1,n,p1)
  }
  return(power)
}
```

Then, based on the power function, we create the function `exactn` to determine sample size:

```
exactn<-function(side,alpha,beta,p0,p1,i){
  power<-1
  while (power>1-beta){
    power<-exactpow(side,alpha,p0,p1,i)
    i=i-1
  }
  return(i+2)
}
```

Note that in sample size calculation for single proportion comparison, the test power increases in a sawtooth pattern with increasing sample size [2, 4]. The programming approach here starts from a relatively large sample size (for example, i = 2000) and searches downward until the power falls below the target value (e.g., 0.8), then returns to the previous value, which is the required sample size.

Example 1

This example comes from the literature [1]. To verify the efficacy of a combined therapy for liver cancer, a clinical trial is designed. Based on previous research, the 5-year survival rate for liver cancer is 50%. Researchers expect the new combined therapy to increase the 5-year survival rate to 60%. The required sample size is estimated using a two-sided test with 80% power and an alpha level of 0.05. The original article used nQuery software, manually trying different values in the sample size row until achieving power of at least 80%, resulting in a final sample size of 208 cases. The article also used SAS programming, inputting n=207 and n=208 separately, obtaining powers of 0.79110 and 0.81396, respectively.

Using R language:

```
> exactn(side=2,alpha=0.05,beta=0.2,p0=0.5,p1=0.6,i=2000)
[1] 210
```

The result is 210, slightly different from the original article. We calculated the power for sample sizes of 207, 208, 209, and 210:

```
> exactpow(side=2,alpha=0.05,p0=0.5,p1=0.6,n=207)
[1] 0.791098
> exactpow(side=2,alpha=0.05,p0=0.5,p1=0.6,n=208)
[1] 0.8139611
> exactpow(side=2,alpha=0.05,p0=0.5,p1=0.6,n=209)
[1] 0.7979761
> exactpow(side=2,alpha=0.05,p0=0.5,p1=0.6,n=210)
[1] 0.8202484
```

The powers for sample sizes 207 and 208 match the SAS results exactly. However, when sample size increases to 209, power drops below 0.8, and only at sample size 210 does power rise above 0.8 again. Verification using PASS (version 11) and G*Power (version 3.1) software yields consistent results, suggesting that manual search methods are prone to error. We further used R to create a plot showing that power first reaches 0.8 at sample size 199, while sample sizes of 210 and above maintain power above 0.8 (Figure 1 [Figure 1: see original paper]).

```
j<-1;x<-c(0);y<-c(0)
for (i in c(188:222)){
  x[j]<-i
  y[j]<-exactpow(2,0.05,0.5,0.6,i)
  j<-j+1
}
plot(x,y,type="l",xlab="Sample Size",ylab="Power")
abline(h=0.8,lty=3)
abline(v=210,lty=3)
```

Figure 1 Sample size versus power

Example 2

Consider another example where the expected rate is lower than the target value. With α=0.05, known population rate π_0=0.07, expected population rate π_1=0.03, two-sided test, and 80% power, the original article used SAS programming and, considering the non-monotonic nature of power, obtained a final sample size of 277 [2]. Using R language:

```
> exactn(2,0.05,0.2,0.07,0.03,2000)
[1] 277
```

Discussion

This paper introduces the implementation of exact probability sample size calculation for single proportion comparison using R language. This method accounts

for the non-monotonic relationship between power and sample size in exact probability calculations, provides direct computational results, and can graphically display the relationship between power and sample size. All calculations have been verified using PASS and G*Power software.

Researchers in China have previously used SAS [1, 2] or Stata [3] for programming, with some considering the non-monotonic relationship between power and sample size [2, 4]. Our method is consistent with these approaches in terms of exact probability calculation, but differs in search strategy: we start from a large sample size and search downward until power falls below the target value, then return to the previous value as the required sample size. This approach results in more concise programming, though it may involve larger computational loads—a minor concern for modern computers.

The literature describes manual search methods using sample size calculation software like nQuery, which are error-prone [1]. PASS and G*Power software can more conveniently identify appropriate sample sizes through plotting. Our R programming approach directly provides the required sample size, and R is free software with broader applicability.

We hope this work will facilitate the effective conduct of such studies in China.

References

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Note: Figure translations are in progress. See original paper for figures.