

# Introduction to the Bootstrap World

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*Abstract.* The bootstrap has made a fundamental impact on how we carry out statistical inference in problems without analytic solutions. This fact is illustrated with examples and comments that emphasize the parametric bootstrap and hypothesis testing.

*Key words and phrases:* Statistical inference, hypothesis testing, confidence intervals, resampling, resamples.

## 1. INTRODUCTION

What is the bootstrap? It is a general technique for estimating unknown quantities associated with statistical models. Often the bootstrap is used to find

- (1) standard errors for estimators,
- (2) confidence intervals for unknown parameters or
- (3)  $p$  values for test statistics under a null hypothesis.

Thus the bootstrap is typically used to estimate quantities associated with the sampling distribution of estimators and test statistics.

Recall that a statistical model is essentially a set of probability distributions that attempts to describe the true state of nature and the related random data available to understand that true state. The goal of statistical inference is to choose one of these probability distributions and give some notion of the uncertainty of that choice [usually by means of (1), (2) or (3) above]. In other words, we make inferences about unknown populations (represented by statistical models) from sample data. The bootstrap, first introduced by Efron in 1977, is an important tool in making such inferences, especially in complicated models.

So, we have a set of distributions  $\mathcal{P}$  and one distinguished member  $P_0$  that describes the true state of nature and the available data. Any of the above items (1)–(3) could be described as functionals  $Q(P_0)$ , and the bootstrap estimate is  $Q(\hat{P})$ , where  $\hat{P}$  is an estimate of  $P_0$ . If  $\mathcal{P}$  is indexed by a finite-dimensional parameter  $\theta$ , then the model is called *parametric* and use of  $Q(\hat{P})$  is called a parametric bootstrap. Oth-

erwise the term *nonparametric bootstrap* is typically used (even for *semiparametric* models like regression models with unknown error distribution).

This “plug-in” description is deceptively simple. The functional approach to estimating parameters like the mean  $T(F) = \int x dF(x)$  by  $T(F_n) = \bar{X} = \int x dF_n(x)$ , where  $F_n$  is the empirical distribution function, was already well known by 1977. In fact, an elegant asymptotic theory for  $T(F_n)$  was available (see Serfling, 1980, Chapters 6–8). However, when Efron introduced the bootstrap in 1977, it was a truly novel idea even if in hindsight we can describe it simply as a functional. The key theoretical difference is that the bootstrap functionals are much broader and more complicated than functionals like  $T(F) = \int x dF(x)$ . In fact, the most basic bootstrap functional is a sampling distribution itself.

I think the real reason the bootstrap was so path-breaking and has remained so popular is that Efron described it mainly in terms of creating a “bootstrap world,” where the data analyst knows everything. That is, in this parallel world the true sampling design of the data is reproduced as closely as possible and unknown aspects of the statistical model are replaced by sample estimates. In this world, the data analyst can obtain any quantity of interest by simulation. For example, if the variance of a complicated parameter estimate in this world is desired, just computer generate  $B$  replicate samples (bootstrap samples or resamples), compute the estimate for each resample and then use the sample variance of the  $B$  estimates as an approximation to the variance. As  $B$  grows large, this sample variance converges to the true variance in the bootstrap world. Of course in terms of the estimator based on the original data (the real world), this limiting sample variance is just an estimator of the true variance of the

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estimate. Thus we create a bootstrap world where anything can be computed, at least up to Monte Carlo error. Those true quantities calculated in the bootstrap world are estimates of the parallel quantities in the real world.

In effect this bootstrap world simulation approach opened up complicated statistical methods to anybody with a computer and a random number generator. Random variable calculus *can* be replaced by computing power. (I can hear groans about all the possible misuses. The same can be said about standard statistical software packages, but few people would doubt their importance.)

How important is the bootstrap resampling technique in statistical inference? First we need to separate the practical, everyday world from the research world that results in journal articles. In the everyday world, nothing can compare to the impact of statistical packages like SAS and SPSS, but as far as I can tell, SAS has only one PROC that directly uses the bootstrap (PROC MULTTEST). Splus has a general bootstrap program, but it is not automatic. Moreover, I contend that a majority of practical statistical problems are handled by analysis of variance or regression for which standard methods are usually adequate. Thus, in terms of overall usage, the percentage of analyses that use bootstrap resampling is fairly low. On the other hand, I will try to show in the examples below, that in almost any problem that is slightly nonstandard, it could be helpful to use the bootstrap. When packages that have the bootstrap are as easy to use as StatXact, then we will see a huge rise in practical usage.

In the world of journal articles, the bootstrap has had a tremendous impact. Typing “bootstrap” into the ISI Web of Science topic search resulted in 6,248 articles (and growing every day—a few weeks earlier it was 6,212). More than half of the 2000 and 2001 articles that cited Efron (1979) were from nonstatistical journals. So the bootstrap is making a large impact outside the statistics mainstream as well. Personally, I think the use of the parametric bootstrap in all kinds of analyses is going to grow in the future. In fact, I see some analogies between the parametric bootstrap in frequentist inference and Markov chain Monte Carlo methods in Bayesian analysis.

The rest of this article consists of two sections. The first section is a series of examples that I hope illustrates the ubiquity of the bootstrap; the first and second examples came directly from my own consulting. Then the final section discusses a number of issues that arise in using the bootstrap in the context of hypothesis testing.

## 2. EXAMPLES

EXAMPLE 1. A masters student in civil engineering wanted to model the relationship between watershed area and the maximum flow over a 100 year period at gauging stations on rivers in North Carolina. He had a model  $R = kA^{\eta-1}$  that related the 100 year maximum flow rate at a station ( $R$ ) to the watershed area ( $A$ ) at the station;  $k$  and  $\eta$  are unknown parameters. Taking logarithms leads to a simple linear model. He had values of  $A$  for 140 stations, but the  $R$  measurement for each station was the maximum flow during the time the station had been keeping records. These lengths of time varied between 6 and 83 years, so they really were not comparable and also were not appropriate for the maximum over 100 years.

I discovered that the student could get yearly maximums for a number of stations. The data in Table 1 are  $n = 35$  yearly maximum flow rates at one particular station. Assuming year-to-year independence for the yearly maximums, the distribution function of the maximum of 100 yearly maximums is  $P(R_{(100)} \leq t) = [F(t)]^{100}$ , where  $F(t)$  is the distribution function of a single yearly maximum. I proposed that we estimate the median, say  $t_0$ , of the distribution function  $[F(t)]^{100}$  to be used as the response variable in the regression model. Setting  $[F(t_0)]^{100} = 1/2$  implies that  $F(t_0) = (1/2)^{0.01} = 0.993$ . Thus,  $t_0$  is actually the 0.993 quantile of the yearly maximum distribution. Because the sample sizes were too small to estimate this quantile nonparametrically, I suggested that we assume a parametric model for the yearly maximum. So, for the data of Table 1, I assumed a location–scale extreme value model that had distribution function

$$F(t; \mu, \sigma) = \exp\left\{-\exp\left(-\frac{t-\mu}{\sigma}\right)\right\}.$$

I confirmed this assumption with a quantile–quantile (QQ) plot and then fit the data by maximum likelihood, obtaining  $\hat{\mu} = 4395.1$  and  $\hat{\sigma} = 1882.5$ . The estimate of the 0.993 quantile is then

$$\hat{\sigma}\{-\log[-\log(0.993)]\} + \hat{\mu} = 13729.2.$$

TABLE 1  
Yearly maximum flow rates (gallons per second) at a gauging station in North Carolina

|        |       |       |       |        |       |       |
|--------|-------|-------|-------|--------|-------|-------|
| 5,550  | 4,380 | 2,370 | 3,220 | 8,050  | 4,560 | 2,100 |
| 6,840  | 5,640 | 3,500 | 1,940 | 7,060  | 7,500 | 5,370 |
| 13,100 | 4,920 | 6,500 | 4,790 | 6,050  | 4,560 | 3,210 |
| 6,450  | 5,870 | 2,900 | 5,490 | 3,490  | 9,030 | 3,100 |
| 4,600  | 3,410 | 3,690 | 6,420 | 10,300 | 7,240 | 9,130 |

Using the inverse of the estimated Fisher information and the delta method applied to the above function, I obtained a standard error of 1375.3. The idea would be for the student to do this estimation at a number of stations and possibly use the standard errors as weights in the regression fit.

The classical tools used here are quite adequate: QQ plot, maximum likelihood and delta method. However, let us see what the bootstrap can do. I first confirmed the extreme value assumption by generating  $B = 100$  data sets of size  $n = 35$  from the fitted distribution and computed the Anderson–Darling (AD) goodness-of-fit statistic for each sample. Since 95 of these were larger than the value 0.178 for the data in Table 1, the parametric bootstrap  $p$  value is 0.95. If the  $p$  value had been fairly small, I would have taken  $B$  to be much larger. The null distribution of AD for this situation has been tabled by Stephens (1977), but the bootstrap has made tabling such distributions obsolete. In fact, the bootstrap distribution here is exact up to Monte Carlo error, because the distribution of AD does not depend on the values of the parameter. This is true for any location–scale family. I also kept track of the bootstrap parameter estimates and the estimated 0.993 quantile for each bootstrap resample. The mean of the quantile estimates was 13572.2, illustrating some negative bias of the estimate, since 13572.2 is smaller than 13729.2, the true value in the bootstrap world. The standard deviation of the quantile estimates was 1386.0, a parametric bootstrap standard error quite close to the parametric delta method value of 1375.3. Finally, I made a histogram and QQ plot of the 100 bootstrap 0.993 quantile estimates and observed that they are approximately normally distributed (suggesting that the 0.993 quantile estimate from different stations will be a statistically well-behaved response variable in the linear regression). These bootstrap analyses are modest additions to the original analysis, but they do add some insight. For some folks, just avoiding the Fisher information and delta theorem calculus is attractive.

**EXAMPLE 2.** A local Raleigh company came to me several years ago with data on two methods of detecting polychlorinated biphenyls (PCBs). They were developing a solid phase fluoroimmunoassay method that is called ELISA; the other method is referred to as GS for gold standard, because its results were accepted as truth. Figure 1 displays the data, the

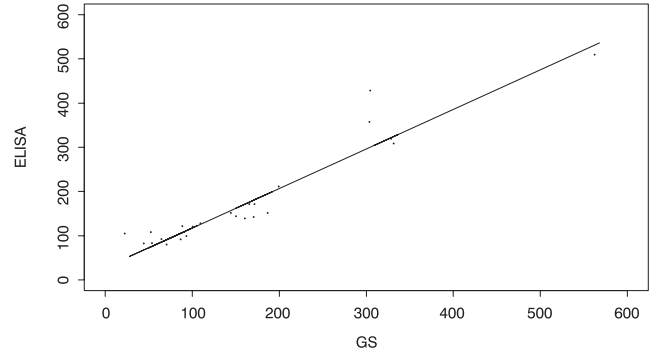


FIG. 1. Two methods for detecting PCBs overlaid with the least squares line.

$n = 24$  pairs of (GS, ELISA) values given in Table 2. The company was interested in detecting PCB levels of 200 ppb (parts per billion) or more using an “action limit” of 100 ppb for their ELISA method. That is, they planned to declare that PCBs were present whenever ELISA was greater than or equal to 100.

After some discussion, we determined that the company wanted the probability of a false negative when  $GS = 200$ ,  $P(ELISA < 100 | GS = 200)$ . In screening test terminology, this probability would be 1 minus the *sensitivity* of the test. They also were interested in the probability of a false positive (1 minus the *specificity* of the test) for different levels of GS. Since all of these calculations are similar, I will focus here on the sensitivity.

To make the problem simple, I decided to model the ELISA results as a linear function of GS with normal homogeneous errors,

$$(1) \quad ELISA = \alpha + \beta(GS) + \sigma Z,$$

where  $Z$  is a standard normal random variable.

TABLE 2  
GS and ELISA values for 24 samples

| GS  | ELISA | GS  | ELISA | GS  | ELISA |
|-----|-------|-----|-------|-----|-------|
| 76  | 81    | 150 | 152   | 115 | 129   |
| 50  | 83    | 192 | 152   | 166 | 140   |
| 59  | 84    | 171 | 172   | 205 | 212   |
| 92  | 92    | 177 | 172   | 337 | 309   |
| 70  | 93    | 28  | 106   | 334 | 320   |
| 99  | 100   | 58  | 109   | 309 | 358   |
| 176 | 143   | 106 | 121   | 310 | 429   |
| 156 | 145   | 94  | 122   | 568 | 510   |

Then

$$\begin{aligned}
 & P(\text{ELISA} < 100 \mid \text{GS} = 200) \\
 &= P(\alpha + \beta(\text{GS}) + \sigma Z < 100 \mid \text{GS} = 200) \\
 (2) \quad &= P\left(Z < \frac{100 - \alpha - \beta(200)}{\sigma}\right) \\
 &= \Phi\left(\frac{100 - \alpha - \beta(200)}{\sigma}\right),
 \end{aligned}$$

where  $\Phi$  is the standard normal distribution function.

Since  $(\alpha, \beta, \sigma)$  were unknown, I used the least squares estimates from a fit to the data in Figure 1 to substitute in (2). The estimate of (2) was 0.002, but how should the variation due to the parameter estimates be taken into account? One could use the joint asymptotic normal distribution of the least squares estimates and the delta method to get a standard error for the estimate and an approximate confidence interval, but it was much simpler to just generate 10,000 samples from the model (1) with the least squares estimates in place of  $(\alpha, \beta, \sigma)$ . This is a parametric bootstrap. The bootstrap standard error was 0.005 and the upper 95% probability bound was 0.013 using the percentile method. I worried a bit about the normality assumption, and decided to try a  $t$  distribution with 5 degrees of freedom as an alternative to the normal distribution. The probability estimate was then 0.007 with bootstrap standard error 0.009 and upper 95% probability bound of 0.023. So there is clearly some sensitivity to the normal assumption. (Actually, it appears that a Weibull distribution might be more appropriate for the errors, but I did not pursue distributional alternatives further because of time and money.) One could also worry about variance heterogeneity and other model inadequacies or use a better bootstrap confidence interval method.

The key point I want to make is how easy it was to carry out the bootstrap analysis (in Splus, actually) in comparison to the classical delta method. Moreover, I was able to check on sensitivity to the normality assumption with a very slight change in my program.

**EXAMPLE 3.** Chen, Kodell and Gaylor (1996) discussed risk assessment for increasing doses of toxic agents based on continuous responses. Their second example is a study that relates glucose levels in mice who were fed various doses of carbonyl iron. The doses were 0, 15, 35, 50 and 100 dg/kg body weight of iron per day. Descriptive statistics reveal that the variance of the glucose response variable increases with

dose. (Actually, the authors ran a Bartlett test for homogeneity of variances. In my younger days I would have argued that they should have obtained a  $p$  value from the nonparametric bootstrap since Bartlett's test is so sensitive to the normality assumption; see Boos and Brownie, 1989. Here the heterogeneity is so strong that it does not matter.) Then, assuming normality for the responses and allowing each dose group to have its own standard deviation, they used maximum likelihood to fit a quadratic mean function of dose to allow for a downturn at high doses. They then gave a bias-corrected estimate (based on Taylor expansion) of "additional risk" that is a function of the parameter estimates based on the normal distribution function. Finally, they gave three methods for obtaining confidence intervals for the quantity of interest, one of which is a nonparametric bootstrap. So, they have used the bootstrap once, but they also could have used it with Bartlett's statistic and for bias correction.

They also could have worried about the normality assumption (they did in a later article; see below), especially since their procedures rely on it fairly strongly. My colleague Charles Quesenberry gave exact procedures (Quesenberry, 1976) for testing normality in multiple samples, but I did not have the program at my fingertips. Instead, I just standardized each data value by subtracting its sample mean and dividing by its sample standard deviation. Then I pooled all 118 standardized values and computed the Anderson-Darling goodness-of-fit statistic. I obtained  $AD = 0.86$ . However, what is the accompanying  $p$  value? I generated  $B = 1000$  sets of five samples and computed this AD statistic each time, resulting in a parametric bootstrap  $p$  value = 0.022. This is not overwhelming evidence, but certainly there is some nonnormality. As in Example 1, the null distribution of AD does not depend on actual parameter values and thus the parametric bootstrap  $p$  value here is exact up to Monte Carlo error.

Continuing the story, Razzaghi and Kodell (2000) also noticed the nonnormality in these data and proposed a mixture model. The distribution function of the  $j$ th observation in the  $i$ th dose group is

$$\begin{aligned}
 & P(X_j(d_i) \leq x) \\
 &= \theta \Phi\left(\frac{x - \mu_1(d_i)}{\sigma}\right) + (1 - \theta) \Phi\left(\frac{x - \mu_2(d_i)}{\sigma}\right),
 \end{aligned}$$

where they specified the mean functions  $\mu_1(\cdot)$  and  $\mu_2(\cdot)$  to be quadratic in dose. Now the bootstrap could be used in a variety of places within this model. However, the authors used standard likelihood methods, which I agree is the simplest approach.

So, the main consideration is whether the overall model is adequate. To address this question I used the fitted model to generate parametric bootstrap samples and computed a new model adequacy statistic  $IOS_A$  (in-and-out-of-sample) each time (see Presnell and Boos, 2002, for a description of the statistic). The  $p$  value was 0.24 for  $B = 100$ , suggesting that the model is reasonable.

My conclusion from looking at these examples is that the bootstrap has potential uses in almost any problem. Whether it is used or not depends a lot on how easy it is to implement and whether there is an acceptable standard procedure available.

### 3. BOOTSTRAP SAMPLING FOR HYPOTHESIS TESTS

Since the bootstrap literature has not emphasized hypothesis testing very much, I thought it might be interesting to highlight some of the issues associated with resampling test statistics.

#### 3.1 Correct Resampling for Hypothesis Tests

An understanding of bootstrap resampling for obtaining a standard error or confidence interval does not necessarily provide intuition concerning how to resample in a hypothesis testing situation. The key point is that to get a  $p$  value, resampling must be performed under an appropriate null hypothesis, whereas for standard errors and confidence intervals, resampling is unrestricted.

To make this clear, consider the case of two independent samples  $X_1, \dots, X_m$  and  $Y_1, \dots, Y_n$ , and suppose that we are interested in the difference in population means, say  $\mu_X - \mu_Y$ . For a nonparametric bootstrap confidence interval, we merely draw independent samples from the empirical c.d.f.'s or equivalently with replacement from the sets  $\{X_1, \dots, X_m\}$  and  $\{Y_1, \dots, Y_n\}$ , respectively. Instead, consider testing  $\mu_X - \mu_Y = 0$  with a  $t$  statistic, say the pooled  $t$  statistic

$$t_p = (\bar{X} - \bar{Y}) / \sqrt{s_p^2 \left( \frac{1}{m} + \frac{1}{n} \right)},$$

where

$$s_p^2 = \frac{(m-1)s_X^2 + (n-1)s_Y^2}{m+n-2},$$

$$s_X^2 = \frac{1}{m-1} \sum_{i=1}^m (X_i - \bar{X})^2,$$

$$s_Y^2 = \frac{1}{n-1} \sum_{i=1}^n (Y_i - \bar{Y})^2.$$

The above method of resampling from each sample separately leads to a test with power approximately equal to the nominal level.

Why is that resampling method wrong? Resampling in the above fashion puts no restriction on the data and thus does not generate an approximation to the null distribution of the  $t_p$  statistic. For confidence intervals for  $\mu_X - \mu_Y$ , we do not want any restriction in the bootstrap world, but for the null distribution of  $t_p$ , we need to force the means to be equal when drawing bootstrap samples.

One way to do this is to draw both samples with replacement from the pooled set  $\{X_1, \dots, X_m, Y_1, \dots, Y_n\}$ . By doing this, in the bootstrap world we have created the null hypothesis

$$(3) \quad H_0: P(X^* \leq t) = P(Y^* \leq t) = H_N(t),$$

where  $P(X^* \leq t)$  is the distribution function of an  $X$  in the bootstrap world,  $P(Y^* \leq t)$  is the distribution function of a  $Y$  in the bootstrap world and  $H_N(t)$  is the empirical distribution function of the pooled set with  $N = m + n$ . In effect we are trying to test the real world hypothesis

$$(4) \quad H_0: F(t) = G(t),$$

where  $F$  and  $G$  are the distribution functions of the  $X$  and  $Y$  samples, respectively.

It might be worth pointing out that there is an exact permutation test available for (4), obtained by constructing all  $N!/m!n!$  partitions of  $\{X_1, \dots, X_m, Y_1, \dots, Y_n\}$  into two samples of size  $m$  and  $n$ , respectively. Then  $t_p$  is computed for each partition; the empirical distribution of these  $N!/m!n!$  values is called the permutation distribution. The statistic  $t_p$  for the original sample is then compared to this distribution to get exact tests and  $p$  values. This elegant approach was introduced by Fisher (1934); a firm theoretical foundation can be found in Hoeffding (1952).

How do permutation tests and bootstrap tests compare? Permutation tests are limited to a relatively small number of testing situations where permutations under the null hypothesis have the same distribution. For those situations, the permutation method gives exact results for any statistic. In contrast, the scope of application for bootstrap tests is huge. The resulting tests, though, are only approximately valid and depend on asymptotics for justification (except for the parametric bootstrap in special situations as mentioned in Examples 1 and 3). Bootstrapping Studentized statistics like  $t_p$  is usually much preferable to bootstrapping statistics like  $\bar{X} - \bar{Y}$  due to faster convergence of the bootstrap

distribution (see Hall, 1986b or 1992). For permutation tests, however, using different statistics often leads to the same result. For example, in the above problem, the permutation method applied to  $t_p$  and to  $\bar{X} - \bar{Y}$  yields the same test.

To further illustrate these ideas, consider a larger null hypothesis than (4),

$$(5) \quad H_0: \mu_X - \mu_Y = 0,$$

but with no other restrictions on the distributions except for finite second moments. This allows the distributions to have different variances and even totally different shapes. A suitable statistic might be Welch's  $t$ :

$$t_w = (\bar{X} - \bar{Y}) / \sqrt{\frac{s_X^2}{m} + \frac{s_Y^2}{n}}.$$

One way to create a bootstrap world with an appropriate null hypothesis is to draw the  $X$  resamples with replacement from  $\{X_1 - \bar{X}, \dots, X_m - \bar{X}\}$  and the  $Y$  resamples from  $\{Y_1 - \bar{Y}, \dots, Y_n - \bar{Y}\}$ . This forces the  $X$  and  $Y$  distributions in the bootstrap world to have mean 0. Of course, we could add the same constant to both sets of resamples and not change the results (since  $t_w$  is invariant to such additions). It is easy to show that the bootstrap distribution of  $t_w$  converges with probability 1 to a standard normal distribution, the same limiting distribution as  $t_w$  in the real world under the null distribution (5). Thus under (5), the bootstrap  $p$  value converges with probability 1 to a uniform random variable. The permutation method cannot handle (5).

Other examples of creating null hypotheses in the bootstrap world can be found in Beran and Srivastava (1985), Boos, Janssen and Veraverbeke (1989) and Davison and Hinkley (1997, Chapter 4).

### 3.2 Definition of Bootstrap $p$ Values and the "99 Rule"

Suppose that  $T_0$  is the value of a test statistic  $T$  computed for a particular sample. Then  $P(T \geq T_0 | H_0)$  is the definition of the  $p$  value in situations where large values of  $T$  support the alternative hypothesis. If the null distribution of  $T$  is a discrete uniform distribution on some values  $t_1, \dots, t_k$  (each value has probability  $1/k$ ), then the  $p$  value is just the proportion of  $t_i$ 's greater than or equal to  $T_0$ . In analogous fashion, when  $B$  resamples are made in the bootstrap world under an induced null hypothesis, define the bootstrap  $p$  value

$$p_B = \frac{\{\# \text{ of } T_i^* \geq T_0\}}{B},$$

where  $T_1^*, \dots, T_B^*$  are the values of  $T$  computed from the resamples. This is the definition I prefer and is the one given by Efron and Tibshirani (1993, page 221). I should note, however, that Davison and Hinkley (1997, pages 148 and 161) and others prefer  $(p_B + 1)/(B + 1)$ .

Consider a situation where the statistic  $T$  is continuous and a parametric bootstrap will give the exact sampling distribution as  $B$  grows large (such as in Example 1). In this case,  $T_0, T_1^*, \dots, T_B^*$  are i.i.d., all  $(B + 1)!$  orderings are equally likely and  $p_B$  has a discrete uniform distribution,

$$\begin{aligned} P(p_B = 0) &= P\left(p_B = \frac{1}{B}\right) = \left(p_B = \frac{2}{B}\right) \\ &= \dots = P(p_B = 1) = \frac{1}{B + 1}. \end{aligned}$$

Thus, the test defined by the rejection region  $p_B \leq \alpha$  has exact level  $\alpha$  if  $(B + 1)\alpha$  is an integer. For example, if  $\alpha = 0.05$ , then  $P(p_B \leq 0.05) = 5/(99 + 1) = 0.05$  if  $B = 99$ , but  $P(p_B \leq 0.05) = 6/(100 + 1) = 0.0594$  if  $B = 100$ . So, for small  $B$  one should use values like  $B = 19, 39$  or  $99$  to get standard  $\alpha$  levels. I call this the "99 rule" and note that simulation-based tests such as this are often called Monte Carlo tests (first suggested by Barnard, 1963). Hall (1986a) gave an approximate version of this result for the nonparametric bootstrap; thus the "99 rule" should be followed generally in bootstrap testing situations.

When analyzing a single data set, it is often possible to use a large  $B$  where there is very little difference between using  $B$  and  $B + 1$  ( $B = 1000$  gives a rejection rate of  $51/1001 = 0.051$ ). However, for studying the power function of a bootstrap test, two Monte Carlo loops are required (the outer one for replicate samples of the true data situation; the inner one for the bootstrap procedure) and computations can be time consuming. Thus  $B = 59, 99$  or  $199$  might be used to save time. Since the resulting power estimates are typically monotone increasing in  $B$ , one can adjust the estimates if  $B$  is taken to be small (see Boos and Zhang, 2000). Davison and Hinkley (1997, Section 4.5) use related arguments to justify the use of 99 resamples in the inner loop of a double bootstrap procedure to get adjusted bootstrap  $p$  values for a single data set.

### 3.3 Convergence of Parametric Bootstrap $p$ Values

There have been many articles on the convergence properties of nonparametric bootstrap distributions, but not as many on convergence of parametric bootstrap distributions (see Beran, 1986 and 1988 for several).

Recently, Robins, van der Vaart and Ventura (2000) gave an interesting result for the parametric bootstrap. One conclusion for bootstrap  $p$  values from their Theorem 1 is as follows. If the test statistic  $T$  is asymptotically normal ( $a(\theta), b^2(\theta)/n$ ), then under some fairly strong but general conditions, the parametric bootstrap  $p$  value is asymptotically uniform if  $a$  does not depend on  $\theta$  and asymptotically conservative otherwise. The context of the result is an article on  $p$  values for model adequacy, and the authors suggest that the conservative property is not appealing in that context. They may have a point, but I find the result comforting in terms of general usage of the bootstrap in hypothesis testing situations.

#### 4. CLOSING REMARKS

The bootstrap is a fundamental statistical tool that can be used in almost any application. Clearly, it is most useful in complex situations where asymptotic approximations are difficult to compute or just not available. As computing power continues to increase, the routine use of bootstrap resampling will continue to grow.

#### ACKNOWLEDGMENT

I wish to thank Cavell Brownie, longtime collaborator and friend, for helpful suggestions on this manuscript.

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