

Bootstrap (Part 4)

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Stanford University, Spring 2016, Stats 205

Overview

- ▶ So far:
 - ▶ Nonparametric bootstrap on the rows (e.g. regression, PCA with random rows and columns)
 - ▶ Nonparametric bootstrap on the residuals (e.g. regression)
 - ▶ Parametric bootstrap (e.g. PCA with fixed rows and columns)
 - ▶ Studentized bootstrap
- ▶ Today:
 - ▶ Bias-Corrected-accelerated (BCa) bootstrap
 - ▶ From BCa to ABC

Motivation

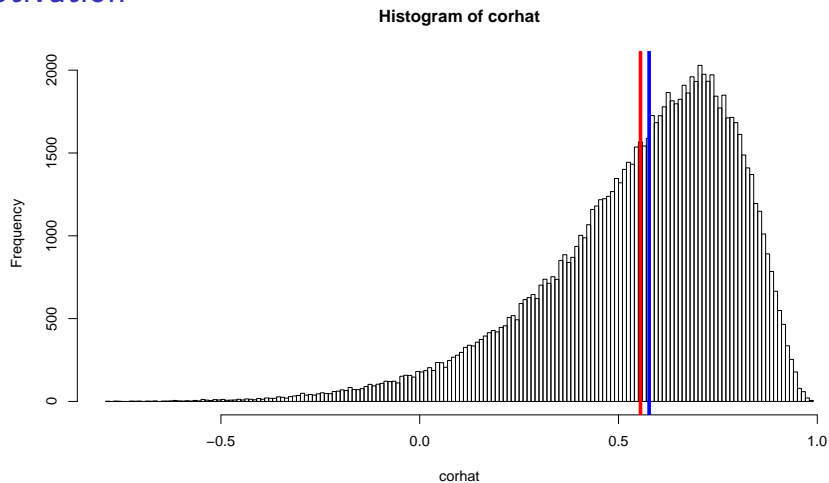
- ▶ Correlation coefficient of bivariate normal with $\rho = 0.577$

```
sigma = matrix(nrow = 2,ncol = 2)
diag(sigma) = 1
rho = 0.577
sigma[1,2] = sigma[2,1] = rho
sigma
```

```
##      [,1] [,2]
## [1,] 1.000 0.577
## [2,] 0.577 1.000
```

- ▶ Distribution of sample correlation coefficient ($n = 10$)
- ▶ Compare: Percentile, Studentized, and Bias-Corrected-Accelerated (BCa) bootstrap

Motivation

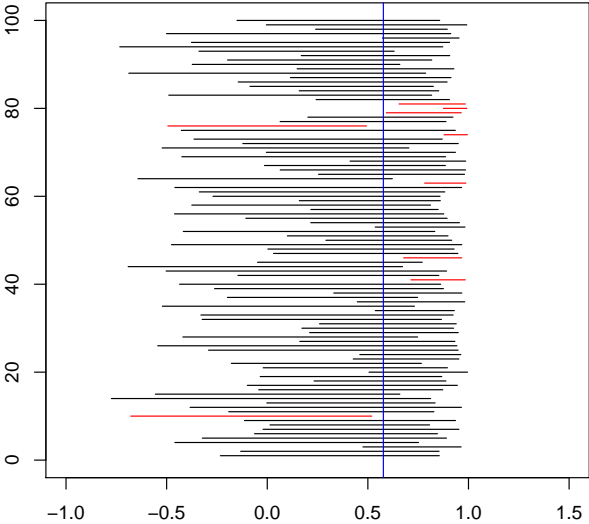


```
bias = rho - mean(corhat); bias
```

```
## [1] 0.0217078
```

Motivation

Percentile Bootstrap

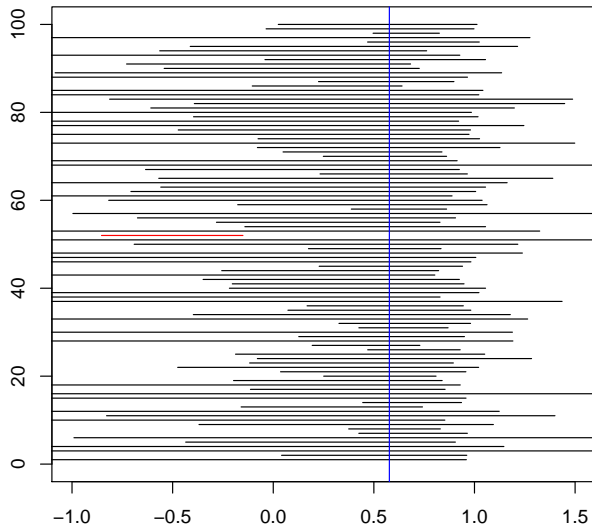


Motivation

- ▶ Studentized bootstrap with variance stabilization fails due to numerical problems

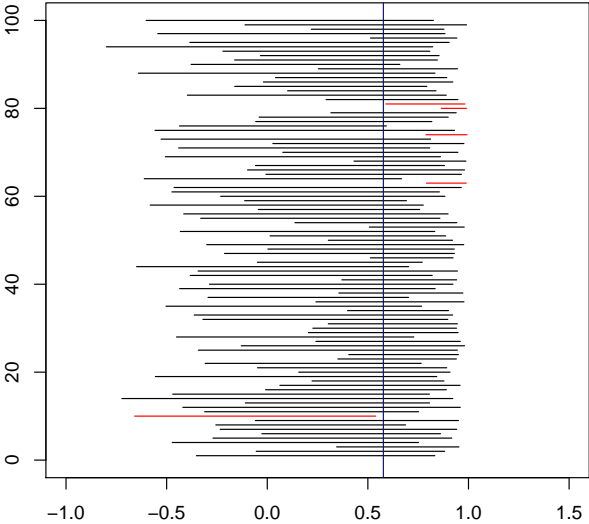
Motivation

Studentized Bootstrap Without Variance Stabilization



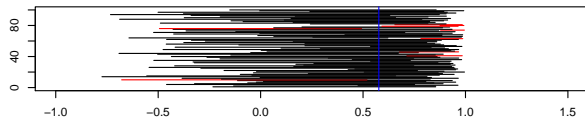
Motivation

BCa Bootstrap

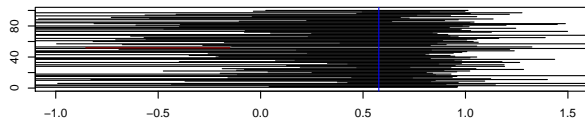


Motivation

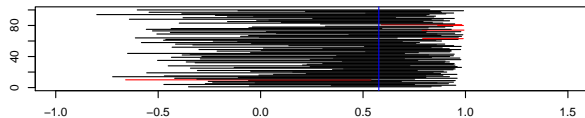
Percentile Bootstrap



Studentized Bootstrap Without Variance Stabilization



BCa Bootstrap



BCa Bootstrap

- ▶ The bias-corrected bootstrap is similar to the percentile bootstrap
- ▶ Recall the percentile bootstrap:
- ▶ Take bootstrap samples

$$\hat{\theta}^{*1}, \dots, \hat{\theta}^{*B}$$

- ▶ Order them

$$\hat{\theta}^{(*1)}, \dots, \hat{\theta}^{(*B)}$$

- ▶ Define interval as

$$(\hat{\theta}^{(*B\alpha)}, \hat{\theta}^{(*B(1-\alpha))})$$

(assuming that $B\alpha$ and $B(1 - \alpha)$ are integers)

BCa Bootstrap

- ▶ Assume that there is an monotone increasing transformation g such that

$$\phi = g(\theta) \quad \text{and} \quad \hat{\phi} = g(\hat{\theta})$$

- ▶ The BCa bootstrap is based on this model

$$\frac{\hat{\phi} - \phi}{\sigma_{\phi}} \sim N(-z_0, 1) \quad \text{with} \quad \sigma_{\phi} = 1 + a\phi$$

- ▶ Which is a generalization of the usual normal approximation

$$\frac{\hat{\theta} - \theta}{\sigma} \sim N(0, 1)$$

BCa Bootstrap

- ▶ \hat{z}_0 is the bias estimate
- ▶ \hat{z}_0 measures discrepancy between the median of $\hat{\theta}^*$ and $\hat{\theta}$
- ▶ It is estimated with

$$\hat{z}_0 = \Phi^{-1} \left(\frac{\#\{\hat{\theta}^{*b} < \hat{\theta}\}}{B} \right)$$

- ▶ We obtain $\hat{z}_0 = 0$ if half of the $\hat{\theta}^{*b}$ values are less than or equal to $\hat{\theta}$

BCa Bootstrap

- ▶ $\hat{\alpha}$ is the skewness estimate
- ▶ $\hat{\alpha}$ measures the rate of change of the standard error of $\hat{\theta}$ with respect to the true parameter θ
- ▶ It is estimated using the Jackknife
 - ▶ Delete i th observation in original sample denote new sample by $\hat{\theta}_{(i)}$ and estimate

$$\hat{\theta}_{(\cdot)} = \sum_{i=1}^n \frac{\hat{\theta}_{(i)}}{n}$$

- ▶ Then

$$\hat{\alpha} = \frac{\sum_{i=1}^n (\hat{\theta}_{(\cdot)} - \hat{\theta}_{(i)})^3}{6 \{ \sum_{i=1}^n (\hat{\theta}_{(\cdot)} - \hat{\theta}_{(i)})^2 \}^{3/2}}$$

BCa Bootstrap

- ▶ The bias-corrected version makes two additional corrections to the percentile version
- ▶ By redefining lower α_1 and upper α_2 levels as

$$\alpha_1 = \Phi \left(\hat{z}_0 + \frac{\hat{z}_0 + z^{(\alpha)}}{1 - \hat{a}(\hat{z}_0 + z^{(\alpha)})} \right) \quad \alpha_2 = \Phi \left(\hat{z}_0 + \frac{\hat{z}_0 + z^{(1-\alpha)}}{1 - \hat{a}(\hat{z}_0 + z^{(1-\alpha)})} \right)$$

with $z^{(\alpha)}$ being the 100α percentile of standard normal and Φ normal CDF

- ▶ When \hat{a} and \hat{z}_0 are equal to zero then $\alpha_1 = \alpha$ and $\alpha_2 = 1 - \alpha$
- ▶ The interval is then given by

$$(\hat{\theta}^{(*B\alpha_1)}, \hat{\theta}^{(*B\alpha_2)})$$

(assuming that $B\alpha_1$ and $B\alpha_2$ are integers)

BCa Bootstrap

- ▶ Same asymptotic accuracy as the studentized bootstrap
- ▶ Can handle out of range problem as well
- ▶ Efron (1987) for detailed justification of this model

BCa Bootstrap in R

```
library(bootstrap)
xdata = matrix(rnorm(30),ncol=2); n = 15
theta = function(x,xdata) {
  cor(xdata[x,1],xdata[x,2])
}
results = bcanon(1:n,100,theta,xdata,
                alpha=c(0.025, 0.975))
results$confpoints
```

```
##      alpha bca point
## [1,] 0.025  -0.39659
## [2,] 0.975   0.69326
```

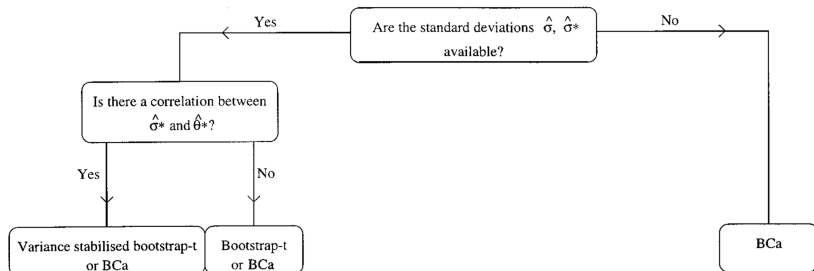

Properties of Different Bootstrap Methods

	Standard	Percentile	Studentized*	BCa
Asymptotic Accuracy	$O(\sqrt{n})$	$O(\sqrt{n})$	$O(1/n)$	$O(1/n)$
Range-Preserving	No	Yes	No	Yes
Transformation-Invariant	No	Yes	No	Yes
Bias-Correcting	No	No	No	Yes
Skewness-Correcting	No	Yes	Yes	Yes
$\hat{\sigma}, \hat{\sigma}^*$ required	No	No	Yes	No
Analytic constant or variance stabilizing transformation required	No	No	Yes	Yes

* with variance stabilization

Properties of Different Bootstrap Methods

For nonparametric bootstrap:



Source: Carpenter and Bithell (2000)

Many More Topics

- ▶ Using the bootstrap for better confidence in model selection (Efron 2014)
- ▶ Using the jackknife and the infinitesimal jackknife for confidence intervals in random forests prediction or classification (Wager, Hastie, and Efron 2014)

Approximate Bayesian Computation (ABC)

- ▶ Goal: We wish to sample from the posterior distribution $p(\theta|D)$ given data D

$$p(\theta|D) = \frac{p(D|\theta)p(\theta)}{p(D)}$$

- ▶ Setting:
 - ▶ The likelihood $p(D|\theta)$ is hard to evaluate or expensive to compute (e.g. missing normalizing constant)
 - ▶ Easy to sample from likelihood $p(D|\theta)$
 - ▶ Easy to sample from prior $p(\theta)$
- ▶ Examples:
 - ▶ Population genetics (latent variables)
 - ▶ Ecology, epidemiology, systems biology (models based on differential equations)

Approximate Bayesian Computation (ABC)

- ▶ Sampling algorithm (with data $D = \{y_1, \dots, y_n\}$):

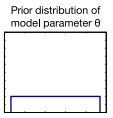
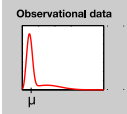
1. Sample $\theta_i \sim p(\theta)$
2. Sample $x_i \sim p(x|\theta_i)$
3. Reject θ_i if

$$x_i \neq y_j \text{ for } j = 1, \dots, n$$

- ▶ ABC sampling (define statistics μ , distance ρ , and tolerance ϵ):

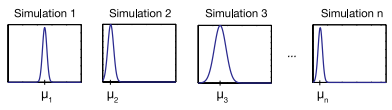
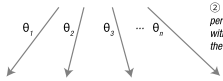
1. Sample $\theta_i \sim p(\theta)$
2. Sample $\hat{D}_i = \{x_1, \dots, x_k\} \sim p(x|\theta_i)$
3. Reject θ_i if

$$\rho(\mu(\hat{D}_i), \mu(D)) > \epsilon$$



① Compute summary statistic μ from observational data

② Given a certain model, perform n simulations, each with a parameter drawn from the prior distribution



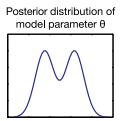
③ Compute summary statistic μ_i for each simulation

$$\rho(\mu_i, \mu) \stackrel{?}{\leq} \epsilon$$



④ Based on a distance $\rho(\cdot, \cdot)$ and a tolerance ϵ , decide for each simulation whether its summary statistic is sufficiently close to that of the observed data.

⑤ Approximate the posterior distribution of θ from the distribution of parameter values θ_i associated with accepted simulations.



References

- ▶ Efron (1987). Better Bootstrap Confidence Intervals
- ▶ Hall (1992). The Bootstrap and Edgeworth Expansion
- ▶ Efron and Tibshirani (1994). An Introduction to the Bootstrap
- ▶ Carpenter and Bithell (2000). Bootstrap Confidence Intervals: When, Which, What? A Practical Guide for Medical Statisticians
- ▶ Marin, Pudlo, Robert, and Ryder (2012). Approximate Bayesian Computational Methods
- ▶ Efron (2014). Estimation and Accuracy after Model Selection
- ▶ Wager, Hastie, and Efron (2014). Confidence Intervals for Random Forests: The Jackknife and the Infinitesimal Jackknife