

ST509 Computational Statistics

Lecture 13: Bootstrap & Parallel Computing

Seung Jun Shin

Department of Statistics
Korea University

E-mail: `sjshin@korea.ac.kr`



Jackknife I

- ▶ Suppose $\hat{\theta}$ is an estimator based on an iid sample Y_1, \dots, Y_n .
- ▶ Let $\hat{\theta}_{[i]}$ denote the “leave-1-out” estimator obtaining by computing $\hat{\theta}$ with Y_i deleted from the sample.
- ▶ Jackknife pseudo-values are defined by

$$\hat{\theta}_{ps,i} = n\hat{\theta} - (n-1)\hat{\theta}_{[i]}$$

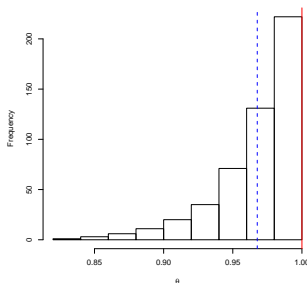
- ▶ Bias-adjusted jackknife estimator is

$$\hat{\theta}_J = \frac{1}{n} \sum_{i=1}^n \hat{\theta}_{ps,i} = \hat{\theta} - (n-1)(\bar{\theta}_1 - \hat{\theta})$$

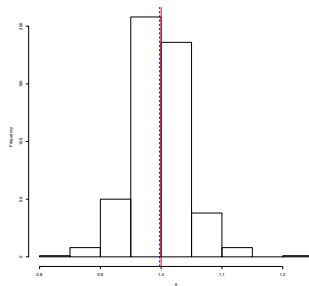
where $\bar{\theta}_1 = \frac{1}{n} \sum_{i=1}^n \hat{\theta}_{[i]}$

Jackknife II

- Illustration of the bias corrected version of the sample maximum $\hat{\theta}$ for $U_i \stackrel{iid}{\sim} (0, 1)$. (i.e. $\theta = 1$)



(a) $\hat{\theta} = U_{(n)}$



(b) Bias-Corrected $\hat{\theta}, \hat{\theta}_J$

Figure: Histogram of variance estimator for 500 independent repetitions.

Jackknife III

- ▶ The **jackknife variance estimator** for $\hat{\theta}$ is given by

$$\begin{aligned}\hat{V}_J &= \frac{(n-1)^2}{n} \frac{1}{n-1} \sum_{i=1}^n \left(\hat{\theta}_{[i]} - \bar{\theta}_1 \right)^2 \\ &= \frac{1}{n(n-1)} \sum_{i=1}^n \left(\hat{\theta}_{ps,i} - \hat{\theta}_J \right)^2\end{aligned}$$

- ex.** For $\hat{\theta} = \bar{Y}_n$, jackknife variance estimator \hat{V}_J of $\hat{\theta}$ is s_{n-1}^2/n , which is identical to usual variance estimator of \bar{X}_n .

Bootstrap I

- ▶ **Bootstrap** is a general technique for estimating unknown quantities associated with sampling distribution of estimators such as
 - ▶ Standard errors
 - ▶ Confidence intervals
 - ▶ p-values

Bootstrap II

- ▶ Suppose F is the true population distribution.
- ▶ We estimate the functional of F based on the the sample X_1, \dots, X_n .

Ex Population expectation μ

$$\mu = E(X) = \int x f(x) dx \left(= \int x dF(x) \right)$$

can be estimated by the sample average \bar{X}_n :

$$\hat{\mu} = \bar{X}_n = \sum_{i=1}^n X_i \cdot \frac{1}{n} \left(= \int x dF_n(x) \right)$$

where $F_n(x)$ denotes the empirical distribution of (X_1, \dots, X_n) ,

$$F_n(x) = \frac{1}{n} \sum_{i=1}^n \mathbb{1}\{x \leq X_i\}$$

Bootstrap III

- Underlying fundamentals of this idea is

$$F_n(x) \rightarrow F(x)$$

- Uncertainty/Randomness comes from

$$F_n(x) - F(x)$$

- Uncertainty quantification is not trivial since we only have single $F_n(x)$ for unknown $F(x)$.

Bootstrap IV

- ▶ Given a set of sample X_1, \dots, X_n , a bootstrap sample denoted by X_1^*, \dots, X_n^* is a **random drawing samples with replacement** from X_1, \dots, X_n .
- ▶ The idea of bootstrap is

$$F_n^*(x) \text{ vs } F_n(x) \quad \approx \quad F_n(x) \text{ vs } F(x)$$

where $F_n^*(x)$ denotes the empirical distribution of the bootstrap samples.

- ▶ We think the RHS as “real world” and the LHS as “bootstrap world”
- ▶ In the bootstrap world, we know both $F_n^*(x)$ and $F_n(x)$, and can obtain as many bootstrap samples as we want.

Illustration of Bootstrap method I

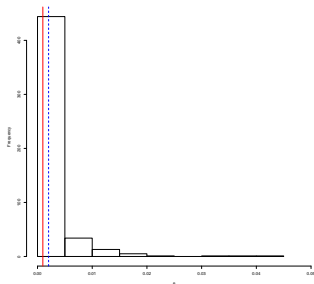
- ▶ Suppose we like to estimate θ from an iid sample X_1, \dots, X_n by $\hat{\theta}$.
- ▶ **Bootstrap estimator of the variance** of $\hat{\theta}$ can be obtained as follows.
 1. Generate a bootstrap sample $X_1^{*,b}, \dots, X_n^{*,b}$ (i.e., random drawing from X_1, \dots, X_n with replacement).
 2. Compute estimator of θ based on the bootstrap sample X_1^*, \dots, X_n^* , denoted by $\hat{\theta}^*$.
 3. Repeat Step 1-2 many, say B times. Then the bootstrap variance estimator is

$$\widehat{\text{Var}}_b(\hat{\theta}) = \frac{1}{B-1}(\hat{\theta}_b^* - \hat{\theta})^2.$$

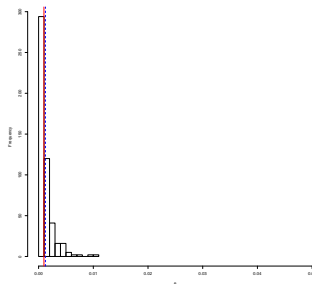
- ▶ The idea is very general and can be applied to any estimator $\hat{\theta}$.

Illustration of Bootstrap method II

- Comparison of variance estimator for sample maximum $\hat{\theta}$ for $U_i \stackrel{iid}{\sim} (0, 1)$. (i.e. $\theta = 1$)



(a) Jackknife



(b) Bootstrap

Figure: Histogram of variance estimator for 500 independent repetitions: Monte Carlo MSE is .00903 for the jackknife estimator and .00108 for the bootstrap estimator.

Illustration of Bootstrap method III

- ▶ The simplest way to construct the **confidence interval** of $\hat{\theta}$ is to just take the empirical $\alpha/2$ and $(1 - \alpha/2)$ percentile (or quantile) from the bootstrap values $\theta_1^*, \dots, \theta_B^*$.
- ▶ **Percentile CI** can be obtained as follows:
 1. Generate a bootstrap sample $X_1^{*,b}, \dots, X_n^{*,b}$ (i.e., random drawing from X_1, \dots, X_n with replacement).
 2. Compute estimator of θ based on the bootstrap sample X_1^*, \dots, X_n^* , denoted by $\hat{\theta}^*$.
 3. Repeat Step 1-2 many, say B times. Then the bootstrap percentile CI is

$$[q_b^*(\alpha/2), q_b^*(1 - \alpha/2)]$$

where $q_b^*(\alpha)$ denotes the α th sample quantile of $\hat{\theta}_1, \dots, \hat{\theta}_B$.

Illustration of Bootstrap method IV

- ▶ Another early proposal is the **reflected percentile interval** obtained as follows:

$$\left\{ \theta : q_b^*(\alpha/2) - \hat{\theta} \leq \hat{\theta} - \theta \leq q_b^*(1 - \alpha/2) - \hat{\theta} \right\}$$

- ▶ The bootstrap- t interval (or percentile- t interval) is based on the empirical distribution of

$$t^* = \frac{\hat{\theta}^* - \hat{\theta}}{\hat{\sigma}^*}.$$

That is,

$$\left\{ \theta : r_b^*(\alpha/2) \leq \frac{\hat{\theta} - \theta}{\hat{\sigma}} \leq r_b^*(1 - \alpha/2) \right\}$$

where $r_b^*(\alpha)$ denotes the α th sample quantile of t_1^*, \dots, t_B^* , and $\hat{\sigma}$ denotes some estimate of the standard deviation of $\hat{\theta}$.

Illustration of Bootstrap method V

- ▶ Fancier alternatives include
 - ▶ Bias-Corrected percentile interval (BC)
 - ▶ Bias-Corrected, accelerated interval (BC_a)
 - ▶ Double Bootstrap (Calibrated Percentile) Interval.

Illustration of Bootstrap method VI

- ▶ Using bootstrap, one can conduct **hypothesis test**.
- ▶ Suppose T_0 is the value of a test statistic T computed from an iid sample, X_1, \dots, X_n .
- ▶ The bootstrap p-value is defined as

$$p_b = \frac{1}{B} \sum_{b=1}^B \mathbb{1}\{T_b^* \geq T_0\}$$

where T_b^* is the statistic obtained from the b th bootstrap sample, $X_{1,b}^*, \dots, X_{n,b}^*, b = 1, \dots, B$. under an induced null hypothesis.

Illustration of Bootstrap method VII

```
> # two-sample mean comparison
> n <- 50; B <- 500
> mu1 <- 0; mu2 <- 1
>
> x <- rnorm(n, mu1, 2)
> y <- rnorm(n, mu2, 4)
>
> pv <- 1 - pnorm((mean(y) - mean(x)) / sqrt(4/n + 16/n)) # true.p.value
>
> # bootstrap p.value
> pool <- c(x, y)
> count <- 0
> t <- mean(y) - mean(x)
> t.bt <- NULL
> for (b in 1:B) {
+   id.bt <- sample(2 * n, replace = T)
+   x.bt <- pool[id.bt[1:n]]
+   y.bt <- pool[-id.bt[1:n]]
+   t.bt[b] <- mean(y.bt) - mean(x.bt)
+ }
> pv.bt <- mean(t.bt >= t)
>
> print(pv)
[1] 0.02245315
> print(pv.bt)
[1] 0.03
```

Illustration of Bootstrap method VIII

```
> # one-sample mean comparison
> B <- 500
> n <- 20
>
> mu <- 1
> mu0 <- 0 # null value
> sigma <- 4
> x <- rnorm(n, mu, sigma)
> pv <- 1 - pnorm(sqrt(n) * (mean(x) - mu0)/sigma) # true p.value
>
> # bootstrap p.value
> x.tilde <- x - mean(x) + mu0          # observed values under H0
> t <- sqrt(n) * (mean(x) - mu0)/sd(x)
> t.bt <- NULL
> for (b in 1:B) {
+   id.bt <- sample(n, replace = T)
+   x.bt <- x.tilde[id.bt]
+   t.bt[b] <- sqrt(n) * (mean(x.bt) - mu0)/sd(x.bt)
+ }
>
> pv.bt <- mean(t.bt >= t)
>
> pv
[1] 0.1279085
> pv.bt
[1] 0.1
```


Parallel Computing in R I

- ▶ MC / Bootstrap/ CV are often computationally intensive due to repeated computations.
- ▶ However, repetitions are independent and hence can be readily parallelized. (i.e., distribute different jobs to multi-cores)
- ▶ There are two popular packages in R for parallel computing.
 - ▶ `parallel`
 - ▶ `foreach`

Parallel Computing in R II

- Simulated example: Simple logistic regression with $n = 1000$.

```
> n <- 1000
> B <- 200
>
> ....
>
> # function for bootstrap samples
> fx <- function(b) {
+   set.seed(b)
+   id.bt <- sample(n, replace = T)
+   y.bt <- y[id.bt]
+   x.bt <- x[id.bt]
+   coef(glm(y.bt ~ x.bt, family = "binomial"))
+ }
>
> # bootstrap samples
> # for (not parallelized)
> tic1 <- Sys.time()
> beta.bt1 <- matrix(0, B, 2)
> for (b in 1:B) {
+   beta.bt1[b,] <- fx(b)
+ }
> toc1 <- Sys.time()
> print(toc1 - tic1)
Time difference of 0.5886581 secs
```

Parallel Computing in R III

- `mclapply()` function in `parallel` package

```
> # parallel package
> library(parallel)
> n.cores <- detectCores()
> n.cores
[1] 12
>
> tic2 <- Sys.time()
> beta.bt2 <- mclapply(1:B, fx, mc.cores = n.cores)
> toc2 <- Sys.time()
> print(toc2 - tic2)
Time difference of 0.186506 secs
```

Parallel Computing in R IV

- **foreach()** function **foreach** package

```
> # foreach package
> library(foreach)
> library(doParallel)
> registerDoParallel(n.cores) # set cores
> tic3 <- Sys.time()
> beta.bt3 <- foreach (b=1:B) %dopar% {
+       fx(b)
+ }
> toc3 <- Sys.time()
> print(toc3 - tic3)
Time difference of 0.2491791 secs
```