

2022년 2학기

# Computational Statistics

## HW#8

222STG10

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## Problem

6.3 Consider finding  $\sigma^2 = E\{X^2\}$  when  $X$  has the density that is proportional to  $q(x) = \exp\{-|x|^3/3\}$ .

a. Estimate  $\sigma^2$  using importance sampling with standardized weights.

$$\mu = \int h(\mathbf{x})f(\mathbf{x}) d\mathbf{x} = \int h(\mathbf{x}) \frac{f(\mathbf{x})}{g(\mathbf{x})} g(\mathbf{x}) d\mathbf{x}$$

$$\mu = \frac{\int h(\mathbf{x})f(\mathbf{x}) d\mathbf{x}}{\int f(\mathbf{x}) d\mathbf{x}} = \frac{\int h(\mathbf{x})[f(\mathbf{x})/g(\mathbf{x})]g(\mathbf{x}) d\mathbf{x}}{\int [f(\mathbf{x})/g(\mathbf{x})]g(\mathbf{x}) d\mathbf{x}},$$

$\sigma^2 = E\{X^2\}$ ,  $q(x) = \exp\{-|x|^3/3\}$ 일 때, importance sampling with standardized weights 을 이용해  $\sigma^2$  를 추정한 결과는 **0.818262** 이다.

b. Repeat the estimation using rejection sampling.

1. Sample  $Y \sim g$ .
2. Sample  $U \sim \text{Unif}(0, 1)$ .
3. Reject  $Y$  if  $U > f(Y)/e(Y)$ . In this case, do not record the value of  $Y$  as an element in the target random sample. Instead, return to step 1.
4. Otherwise, keep the value of  $Y$ . Set  $X = Y$ , and consider  $X$  to be an element of the target random sample. Return to step 1 until you have accumulated a sample of the desired size.

rejection sampling 을 이용해  $\sigma^2$  를 추정한 값은 **0.8989728** 이다.

# of total iteration	# of acceptance	# of rejection	acceptance ratio
1012	1000	12	0.9881423

c. Philippe and Robert describe an alternative to importance-weighted averaging that employs a Riemann sum strategy with random nodes [506, 507]. When draws  $X_1, \dots, X_n$  originate from  $f$ , an estimator of  $E\{h(X)\}$  is

$$\sum_{i=1}^{n-1} (X_{[i+1]} - X_{[i]})h(X_{[i]})f(X_{[i]}), \quad (6.86)$$

where  $X[1] \leq \dots \leq X[n]$  is the ordered sample associated with  $X_1, \dots, X_n$ . This estimator has faster convergence than the simple Monte Carlo estimator. When  $f = cq$  and the normalization constant  $c$  is not known, then

$$\frac{\sum_{i=1}^{n-1} (X_{[i+1]} - X_{[i]})h(X_{[i]})q(X_{[i]})}{\sum_{i=1}^{n-1} (X_{[i+1]} - X_{[i]})q(X_{[i]})} \quad (6.87)$$

estimates  $E\{h(X)\}$ , noting that the denominator estimates  $1/c$ . Use this strategy to estimate  $\sigma^2$ , applying it post hoc to the output obtained in part (b).

Philippe and Robert의 방법을 이용해  $\sigma^2$ 를 추정한 값은 **0.7808458**로 (b)보다 작은 값을 갖는다.

d. Carry out a replicated simulation experiment to compare the performance of the two estimators in parts (b) and (c). Discuss your results.

	min.	1st Qu.	median.	mean.	3rd Qu.	max.	sd..
<b>rejection sampling</b>	0.7691	0.8626	0.8848	0.8866	0.9093	1.0067	0.03530781
<b>Philippe &amp; Robert</b>	0.7544	0.7703	0.7727	0.7727	0.7752	0.8039	0.004125182

rejection sampling 과 Philippe and Robert 을 1000 번 반복했을 때, rejection sampling 의 sd 는 **0.03530781**, Philippe and Robert 의 sd 는 **0.004125182** 로 훨씬 작은 값으로 추정된다.

## Code appendix

```
# 6.3
# a
q <- function(x) exp(-abs(x)^3/3)
x <- seq(-4, 4, by=0.01)
qx <- q(x)
IS <- function(n) {
  x <- rnorm(n)
  est <- sum(x^2*q(x)/dnorm(x))/sum(q(x)/dnorm(x))
  return(est)
}
IS(1000)

# b
rs <- function(n, print=TRUE) { # n: sample 개수
  niter <- 0
  reject_num <- 0
  accept_num <- 0
  samples <- c()

  while (accept_num < n) {
    z <- rnorm(1) # proposal density
    u <- runif(1) # sample for rejection
    t <- q(z)/dnorm(z)
    if (u > t) {
      reject_num <- reject_num + 1
    }
    else {
      samples <- append(samples, z)
      accept_num <- accept_num + 1
    }
    niter <- niter+1
  }
  if (print == TRUE) {
    cat(
      "# of total iteration:", niter, "\n",
      "# of acceptance:", accept_num, "\t", "# of rejection:", reject_num, "\n",
      "acceptance ratio:", accept_num/niter, "\n")
  }
  return(samples)
}
```

```

}

rsdata <- rs(1000)
mean(rsdata^2)

# c
prmethod <- function(x) {
  x <- sort(x)
  n <- c()
  d <- c()
  for (i in 1:length(x)-1) {
    n <- append(n, (x[i+1]-x[i])*x[i]^2*q(x[i]))
    d <- append(d, (x[i+1]-x[i])*q(x[i]))
  }
  return(sum(n)/sum(d))
}
prmethod(rsdata)

# d
result <- data.frame(n = 1:1000, rs=rep(1, 1000), pr=rep(1, 1000))
for (i in 1:nrow(result)) {
  samples <- rs(1000, print=FALSE)
  result[i, 2] <- mean(samples^2)
  result[i, 3] <- prmethod(samples)
}
sd(result$rs)
sd(result$pr)
summary(result$rs)
summary(result$pr)

```