

Documentation: Assignment 12

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Q 1 Generate the first 25 values of the Van der Corput sequence x_1, x_2, \dots, x_{25} using the radical inverse function $x_i := \phi_2(i)$ and list them in your report. Next, generate the first 1000 values of this sequence and plot the overlapping pairs (x_i, x_{i+1}) as a two dimensional plot. What do you observe ? Now, generate first 100 and 100000 values of this sequence and plot the sampled distributions for both the cases. Compare these plots with the sampled distributions of 100 and 100000 values generated by an LCG, by plotting the sampled distributions in two graphs side by side for both the cases. Specify the LCG that you have used.

Code : R

```
1 lcg<-function(a,x,m,count){
2   u<-c()
3   for(i in 1:count){
4     u[i]=x/m
5     x=(x*a)
6     x=x%%m
7   }
8   return(u)
9 }
10 vanDerCorput<-function(n,base){
11   sum=0
12   temp=1/base
13   while(n!=0){
14     sum=sum+(n%%base)*temp
15     n=n%%base
16     temp=temp/base
17   }
18   return(sum)
19 }
20 count<-25
21 cat("Number of sequence elements= ",count,"\n")
22 sample<-c()
23 for(i in 1:count){
24   sample[i]<-vanDerCorput(i,2)
25   cat(sample[i],"\n")
26 }
27 count<-1000
28 sample<-c()
29 sample1<-c()
```

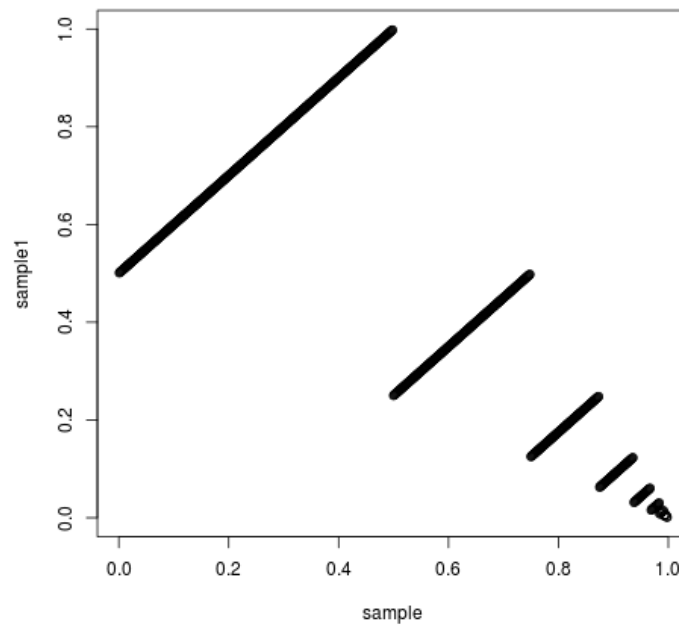
```
30 png(paste("question1_", count, ".png", sep=""))
31 for(i in 1:count){
32   sample[i] <- vanDerCorput(i, 2)
33   if(i > 1){
34     sample1[i-1] <- sample[i]
35   }
36 }
37 sample1[count] <- vanDerCorput(count+1, 2)
38 plot(sample, sample1)
39 counts <- c(100, 100000)
40 x <- -23
41 a <- -16807
42 m <- 2^31 - 1
43 for(count in counts){
44   sample <- c()
45   for(i in 1:count){
46     sample[i] <- vanDerCorput(i, 2)
47   }
48   sample1 <- lcg(a, x, m, count)
49   png(paste("question1_", toString(count), ".png", sep=""))
50   par(mfrow=c(1, 2))
51   hist(sample, main="Van Der Corput", breaks=20, col="blue", ylab="Frequency",)
52   hist(sample1, main="LCG", breaks=20, col="red", ylab="Frequency",)
53 }
```

Output:

First 25 values of Van Der Corput sequence:

0.5
0.25
0.75
0.125
0.625
0.375
0.875
0.0625
0.5625
0.3125
0.8125
0.1875
0.6875
0.4375
0.9375
0.03125
0.53125
0.28125
0.78125
0.15625
0.65625
0.40625
0.90625
0.09375
0.59375

Graph of overlapping pairs (x_i, x_{i+1}) for 1000 values:

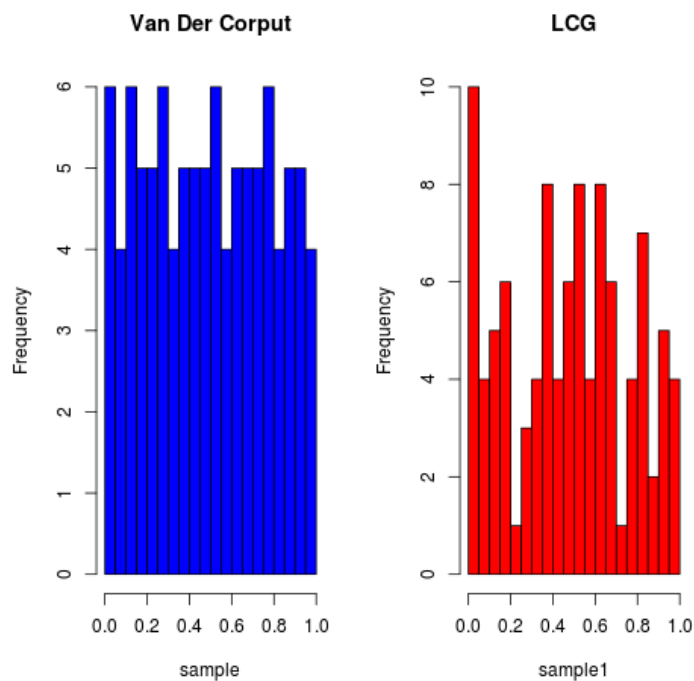


(a) $X1$

Graph:

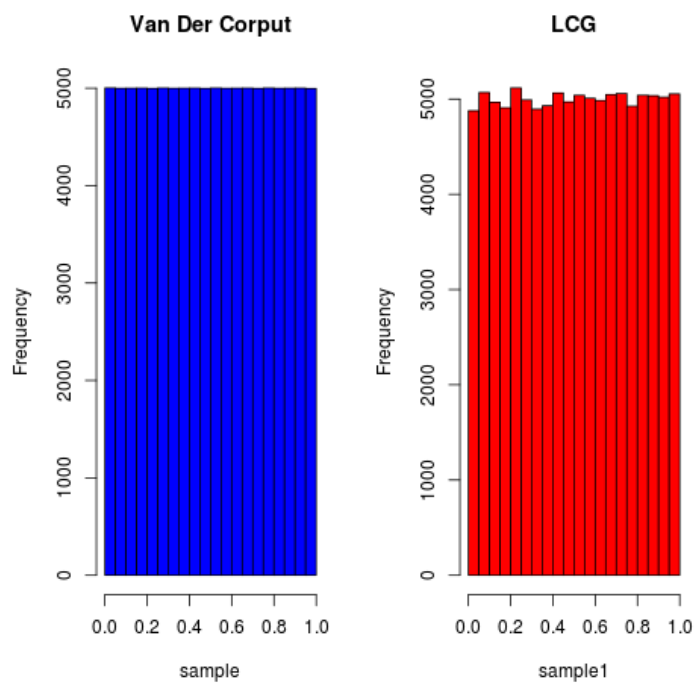
LCG used is $(ax) \bmod(m)/m$ where $a = 16807$, $x_0 = 23$ and $m = 2^{31} - 1$

Sampled Distributions for 100 values



(b) $X1$

Sampled Distributions for 100000 values



(c) $X1$

Q 2 Generate the Halton sequence $x_i = (\phi_2(i), \phi_3(i))$ (as points in R_2) and plot the first 100 and 100000 values. What are your observations? Recall that the radical inverse function is defined by

$$\phi_b(i) = \sum_{k=0}^j d_k b^{-k-1} \text{ where } i = \sum_{k=0}^j d_k b^k$$

Code : R

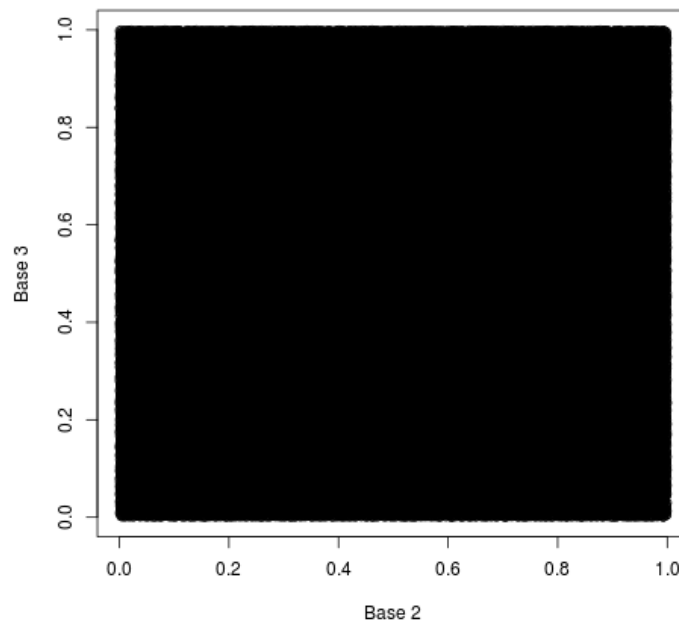
```
1 vanDerCorput<-function(n, base){
2   sum=0
3   temp=1/base
4   while(n!=0){
5     sum=sum+(n%%base)*temp
6     n=n%%base
7     temp=temp/base
8   }
9   return(sum)
10 }
11
12 counts<-c(100,100000)
13 for(count in counts){
14   sample2<-c()
15   sample3<-c()
16   for(i in 1:count){
17     sample2[i]<-vanDerCorput(i,2)
18     sample3[i]<-vanDerCorput(i,3)
19   }
20   png(paste("question2_",count,".png",sep=""))
21   plot(sample2,sample3,xlab="Base 2",ylab="Base 3")
22 }
```

Observation:

We are getting all points in range $[0,1]$ and more closer to uniform. Plus as we are generating in higher dimension i.e. 2, so we will get net variance/error less than that of numeric method.

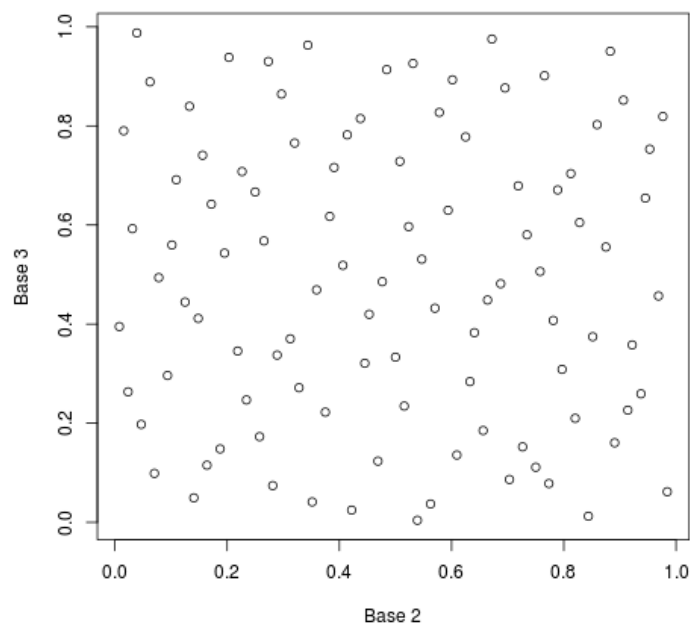
Graph:

For 100000 values



(d) $X1$

For 100 values



(e) $X1$