Rejection sampling algorithm.

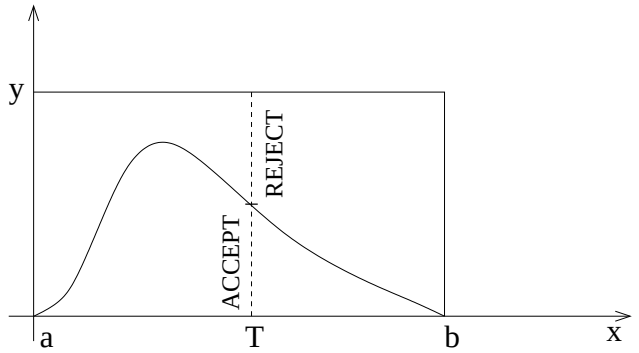
- *Step 1:* Generate T with the density m, where ***f(t) < I*** $_x$ ***m(t)=M(t), I***=const.

Sampling from ***f(x)*** distribution is hard. Sampling from distribution ***m(x)*** is easy.

- *Step 2:* Generate U, uniform on $[0, 1]$ and independent of T.

If $M(T) \times U \leq f(T)$ $\rightarrow$ accept, then set $X = T$.

Otherwise $\rightarrow$ reject, go back to step 1



Why does this work?

Let ***A*** be a subset of ***[a : b]=support(f(.))***, ***a*** and/or ***b*** may be infinite. To show that: $P(X \in A) = \int_A f(t)\,dt$, we expand the left hand side

$$P(X \in A) = P(T \in A \mid \text{Accept}) = \frac{P(T \in A \text{ and Accept})}{P(\text{Accept})}$$

Condition on $T = t$ ($I = \int_a^b M(t)dt$, since ***m(t)*** is a density and ***I*** x ***m(t)=M(t)***)

$$\begin{aligned} P(T \in A \text{ and Accept}) &= \int_a^b P(T \in A \text{ and Accept}|T = t)\, m(t)\, dt \\ &= \int_a^b P(U \le f(t)/M(t) \text{ and } t \in A) m(t)\ \ dt \\ &= \int_A \frac{f(t)}{M(t)} m(t)\, dt = \frac{1}{I}\int_A f(t)\, dt \end{aligned}$$

Similarly

$$P(\text{Accept}) = \int_a^b P(\text{Accept}|T = t) m(t)\, dt = \int_a^b \frac{f(t)}{M(t)} m(t)\, dt = \frac{1}{I}.$$

Remark : High efficiency if algorithm accepts with high probability, i.e. M close to f.

Example

Suppose we want to sample from a density whose graph is shown below.

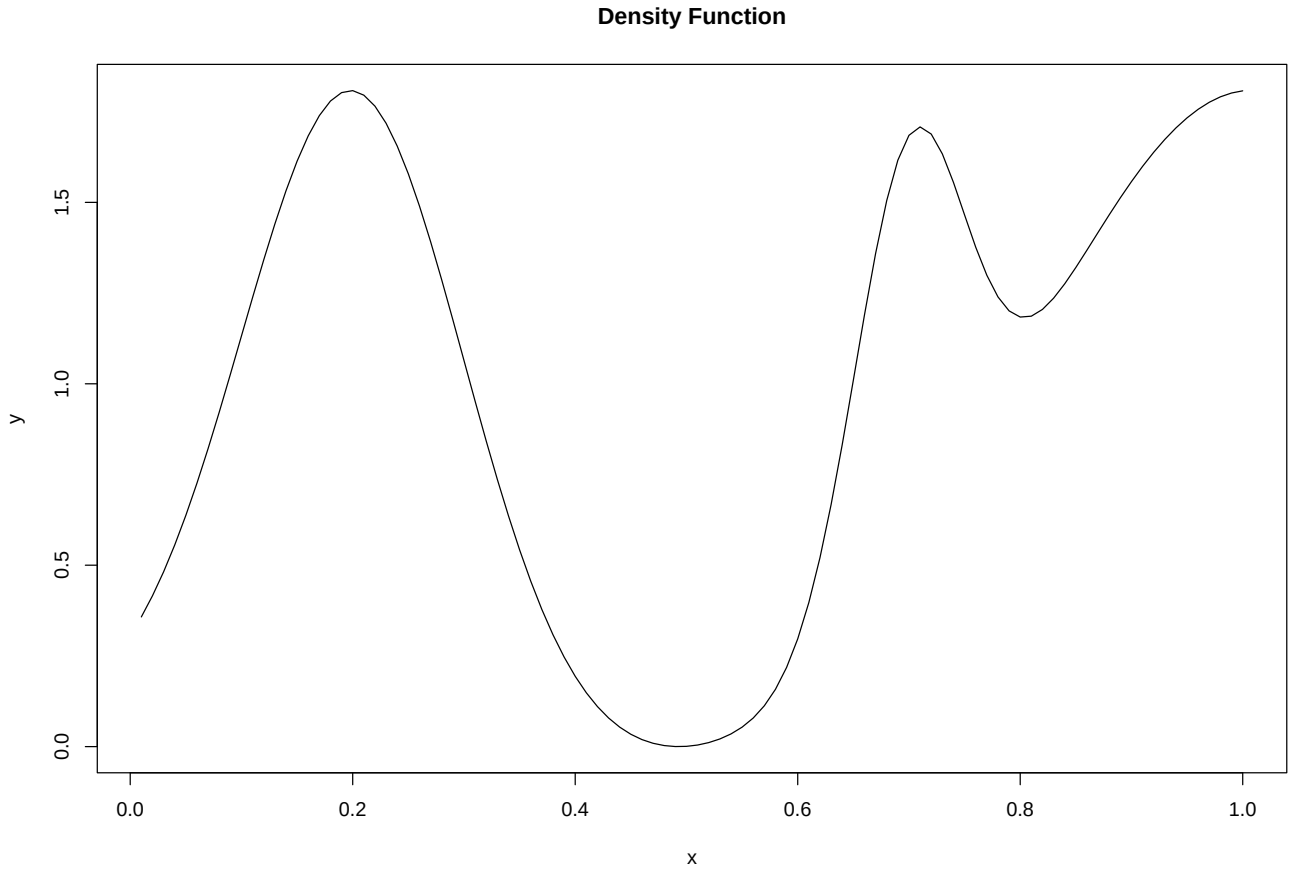


Figure 1: Density function

In this case we let $M(T)$ be the maximum of f over the interval $[0, 1]$, namely

$$M(x) = \max(f), \quad 0 \leq x \leq 1$$

so that m is the uniform density over the interval $[0, 1]$.

Implementation

```
R : Copyright 2000, The R Development Core Team
Version 1.0.1  (April 14, 2000)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type    "?license" or "?licence" for distribution details.

R is a collaborative project with many contributors.
Type    "?contributors" for a list.

Type    "demo()" for some demos, "help()" for on-line help, or
        "help.start()" for a HTML browser interface to help.
Type    "q()" to quit R.

x <- 0:100
M <- max(knownDensity(x))
```

Routine for sampling once from the density f

```
OK <- 0
while(OK<1)
  {
    # Generate T
    T <- runif(1, min = 0, max = 1)
    # Generate U
    U <- runif(1, min = 0, max = 1)
    if(M*U <= knownDensity(T))
      {
        OK <- 1
        RN <- T
      }
  }
```

This routine will sample n iid samples from the density f

```
RejectionSampling <- function(n)
  {
    RN <- NULL
    for(i in 1:n)
      {
        OK <- 0
        while(OK<1)
          {
            T <- runif(1,min = 0, max = 1)
            U <- runif(1,min = 0, max = 1)
            if(U <= knownDensity(T))
              {
                OK <- 1
                RN <- c(RN,T)
              }
          }
      }
    return(RN)      # Demo:: R-File:  R_scriptHelp.txt
  }                 # C:\Documents and Settings\ivo\Desktop\Applications\R
```

Visualization of the results

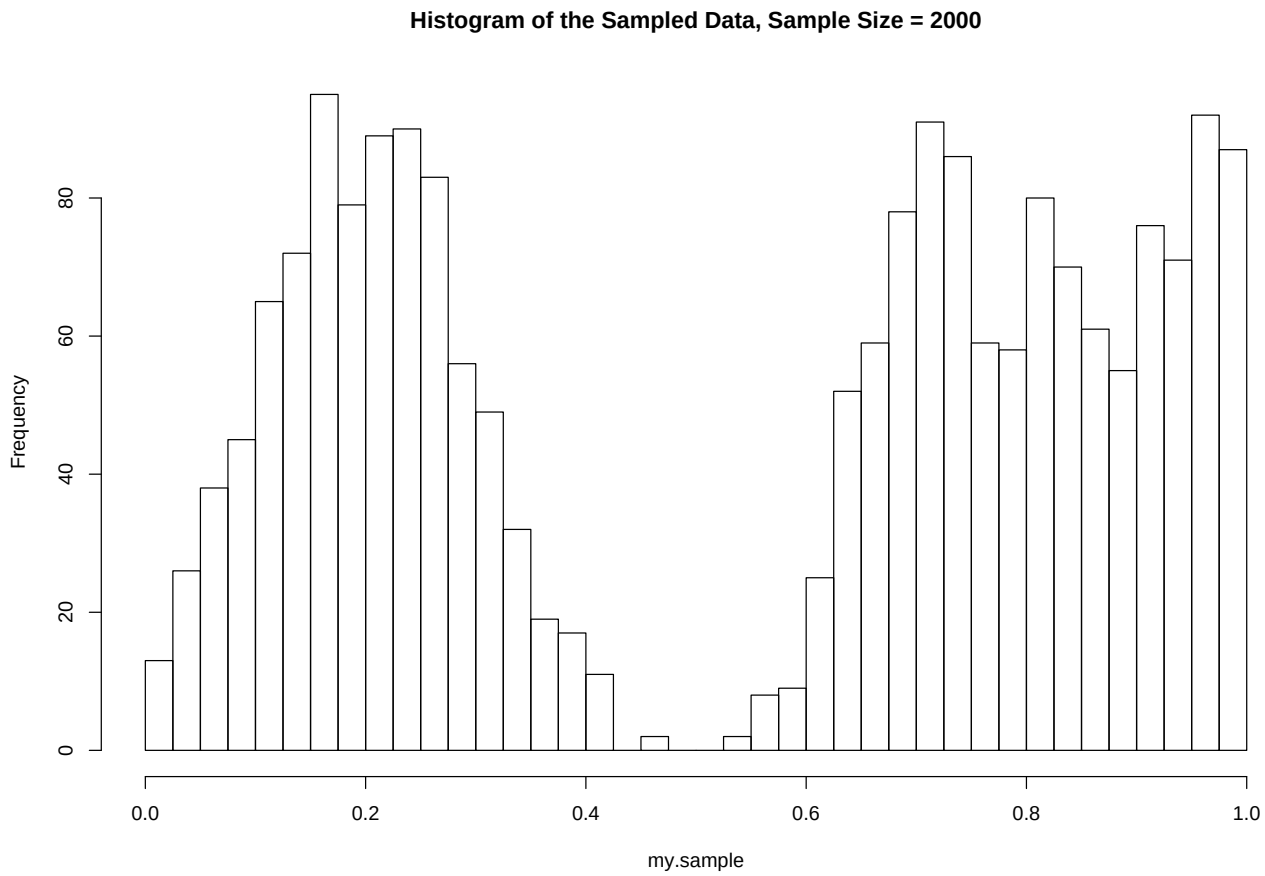


Figure 2: Histogram of the Sampled Data

```
#     1. Define a density of interest that will be approximated by "REJECTION
SAMPLING"
minRgDensity  <- 0
maxRgDensity  <- 10
maxDensityValue  <-  1
sampleSize  <-  3000

knownDensity <- function(x)
{     minRgDensity  <-  0
      maxRgDensity  <-  20
      maxDensityValue  <-  1
      return(dbeta(x, 3, 10))
}

rawDensity <- rbeta(sampleSize, 3, 10)


#     2. Rejection sampling method
RejectionSampling <- function(n)
{
      RN <- NULL
      for(i in 1:n)
      {
            OK <- 0
            while(OK<1)
            {
                  T <- runif(1,min = minRgDensity, max = maxRgDensity  )
                  U <- runif(1,min = 0, max = 1)
                  if(U*maxDensityValue  <=  knownDensity(T))
                  {
                        OK <- 1
                        RN <- c(RN,T)
                  }
            }
      }
      return(RN)
}

#     3. Generate n=sampleSize samples from the model-simulation density
(RejectionSampling)
simulatedDensity <- RejectionSampling(sampleSize)

#     4. Calculate the two histograms
histoRaw <- hist(rawDensity)
histoSimulated <- hist(simulatedDensity)

#     5. Q-Q plot raw vs simulated densities
plot( rawDensity )
plot( simulatedDensity, rawDensity )
qqplot(simulatedDensity, rawDensity )
qqline(simulatedDensity, col = 2)

#  qqplot( rawDensity, simulatedDensity);
#  abline(0,1)


#     6.  for comparison Q-Q plot of simulated Beta is quite diff from N(0,1)
```

```
#qqplot(simulatedDensity, rnorm(1:sampleSize, 0, 1))
```