

MSMS 408 : Practical 05

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⊕ Question

Use rejection sampling technique to generate random sample from a distribution with PDF

$$f(x) = 20 \cdot x(1-x)^3 \cdot I_{(0,1)}(x)$$

⊕ Algorithm

Suppose we have to generate random sample from $p(x)$, we call it our **target distribution**. We choose a **proposal distribution** $q(x)$, say.

- I. Generate $x_i \sim q(x) \forall i = 1(1)n$.
- II. Generate $u_i \sim U(0, 1) \forall i = 1(1)n$.
- III. Accept x_i if

$$u_i \leq \frac{p(x_i)}{M \cdot q(x_i)}$$

where $M > 0$ is a suitable constant so that $p(x) \leq M \cdot q(x)$ is satisfied.

Accepted samples follow the target distribution $p(x)$.

Here, we are given that $p(x) = 20 \cdot x(1-x)^3$. We take $q(x) = 1 \cdot I_{(0,1)}(x)$ i.e. $U(0, 1)$ distribution.

To find constant M recall that we need $p(x) \leq M \cdot q(x) \Rightarrow p(x) \leq M$. Notice, $p(x)$ is the PDF of a $\beta_1(2, 4)$ distribution which has mode

$$\frac{2-1}{2+4-2} = \frac{1}{4}.$$

So $p(0.25) \approx 2.11$ is a suitable choice for M .

➔ R Program

```
set.seed(22)
```

```
n <- 2000
```

```
u <- runif(n)  
x <- runif(n)
```

```
p <- function(x) 20 * x * (1-x)^3
```

```
M <- 2.11
```

```
good <- u <= p(x) / M  
accepted <- x[good]
```

```
count_accepted <- length(accepted) # or sum(good)  
count_accepted  
## [1] 929
```

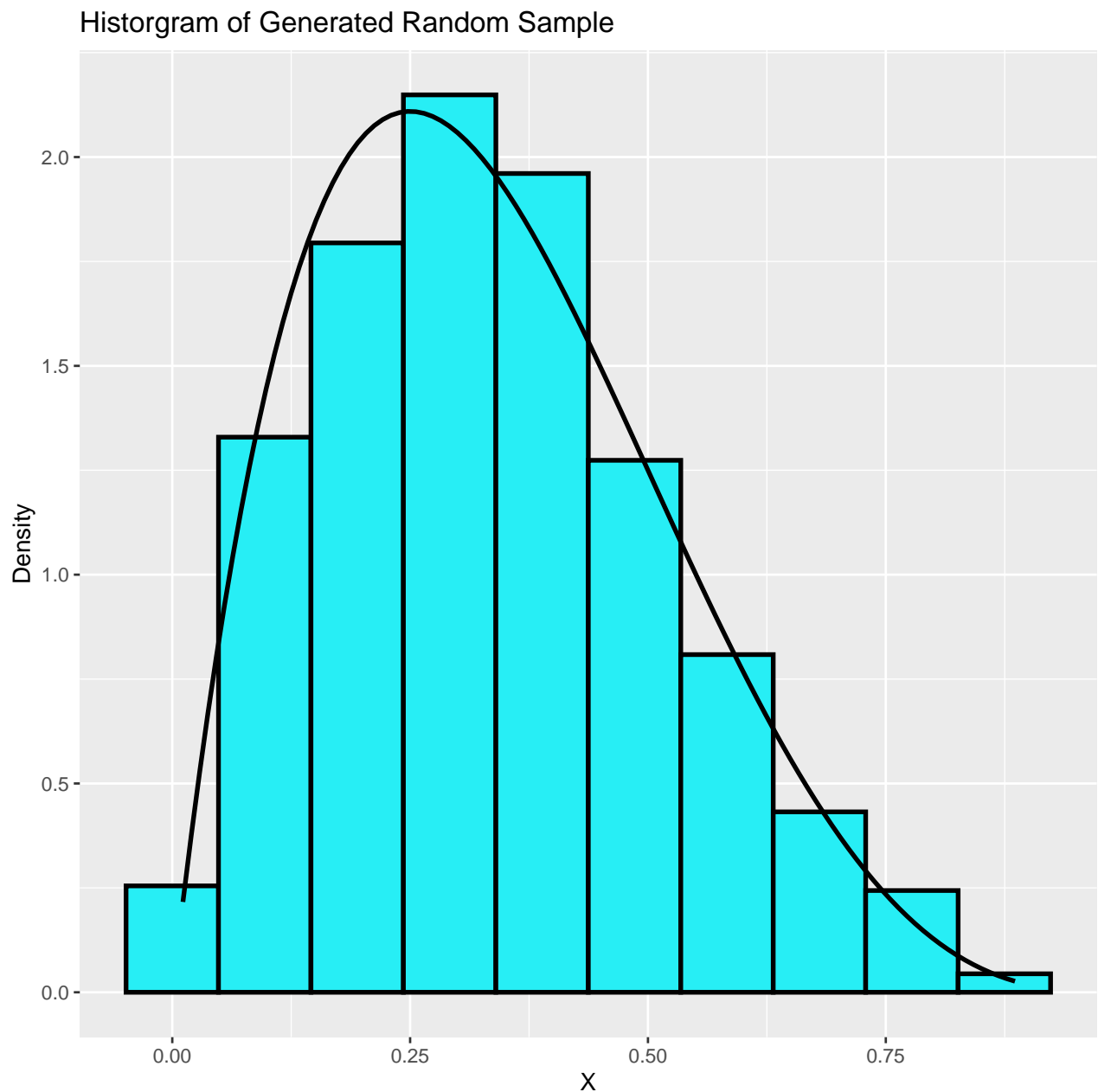
Thus we have a sample of size 929 from $p(x)$.

The **acceptance rate** was 0.4645 whereas the **theoretical acceptance rate** is 0.4739336.

```
df <- data.frame(x = x, u = u, result = ifelse(good, "accepted", "rejected"))
```

Let us have a histogram of the generated sample.

```
df %>%  
  filter(result == "accepted") %>%  
  ggplot(aes(x = x)) +  
    geom_histogram(aes(y = after_stat(density)), bins = 10,  
                  linewidth = 1, color = "black", fill = "#27EEF5") +  
    stat_function(fun = p, linewidth = 1) +  
    labs(x = "X", y = "Density",  
         title = "Histogram of Generated Random Sample")
```



➔ Conclusion

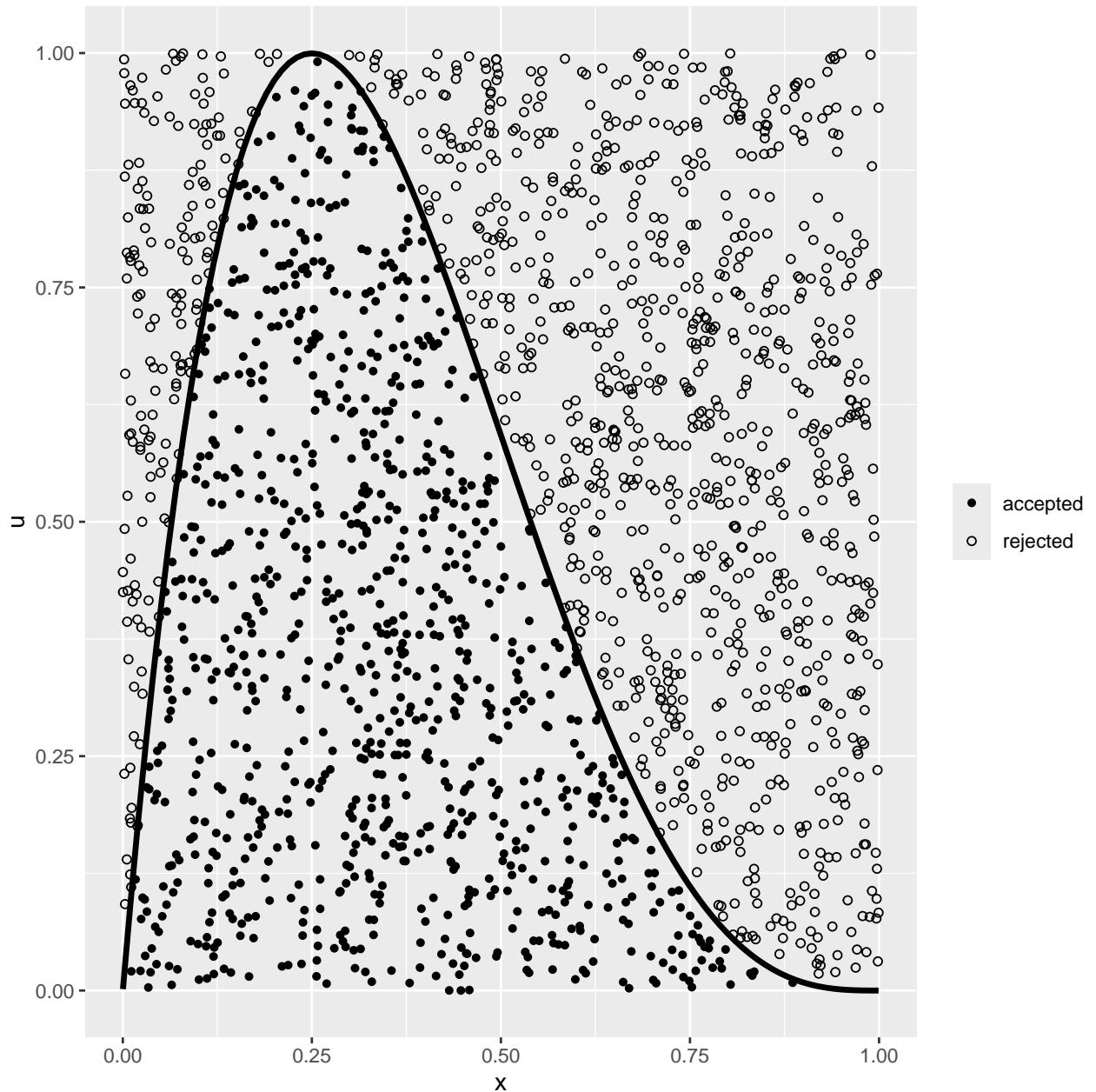



The actual density curve fits the histogram well.

Let us have a simple visualization of the rejection sampling technique.

```
p_scaled <- function(x) p(x) / M
```

```
df %>%  
  ggplot(aes(x = x, y = u, shape = result)) +  
  geom_point() +  
  scale_shape_manual(values = c("accepted" = 16,  
                                "rejected" = 1)) +  
  stat_function(fun = p_scaled, linewidth = 1.25, inherit.aes = FALSE) +  
  theme(legend.title = element_blank())
```



 The (x, u) pairs that fall under the scaled target density are accepted and rest are rejected.