MSMS 408 : Practical 06

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Question

Use rejection sampling technique to generate random sample from Gamma distribution with shape $= \frac{3}{2}$ and scale $= 1$ *i.e.*

$$f(x) = \frac{1}{\Gamma(3/2)} x^{\frac{1}{2}} e^{-x} \cdot I_{(0,\infty)}(x)$$

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 $p(x) = \frac{2}{\sqrt{\pi}} x^{\frac{1}{2}} e^{-x}$. We take $q(x) = \frac{1}{2} e^{-\frac{x}{2}} \cdot I_{(0,\infty)}(x)$ *i.e.* Exp(rate $= 1/2$) distribution.

To find constant M recall that we need $p(x) \leq M \cdot q(x) \Rightarrow \frac{p(x)}{q(x)} \leq M$.

Now, $\frac{p(x)}{q(x)} = \frac{\frac{2}{\sqrt{\pi}} x^{\frac{1}{2}} e^{-x}}{\frac{1}{2} e^{-\frac{x}{2}}} = \frac{4}{\sqrt{\pi}} x^{\frac{1}{2}} e^{-x/2} = h(x)$, say.

Maximizing $h(x)$ is equivalent to maximizing $\ln h(x) = \frac{1}{2} \ln x - \frac{x}{2}$.

$$\frac{d}{dx} \ln h(x) = 0$$
$$\Rightarrow \frac{1}{2x} - \frac{1}{2} = 0$$
$$\Rightarrow x = 1$$

So $h(1) \approx 1.369$ is a suitable choice for M.

➜ R Program

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

```r
n <- 2000
```

```r
u <- runif(n)
x <- rexp(n, rate = 1/2)
```

```r
p <- function(x) (2 / sqrt(pi)) * x^(1/2) * exp(-x)
```

```r
q <- function(x) (1/2) * exp(-x/2)
```

```r
M <- 1.369
```

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

```r
count_accepted <- length(accepted) # or sum(good)
count_accepted

## [1] 1471
```

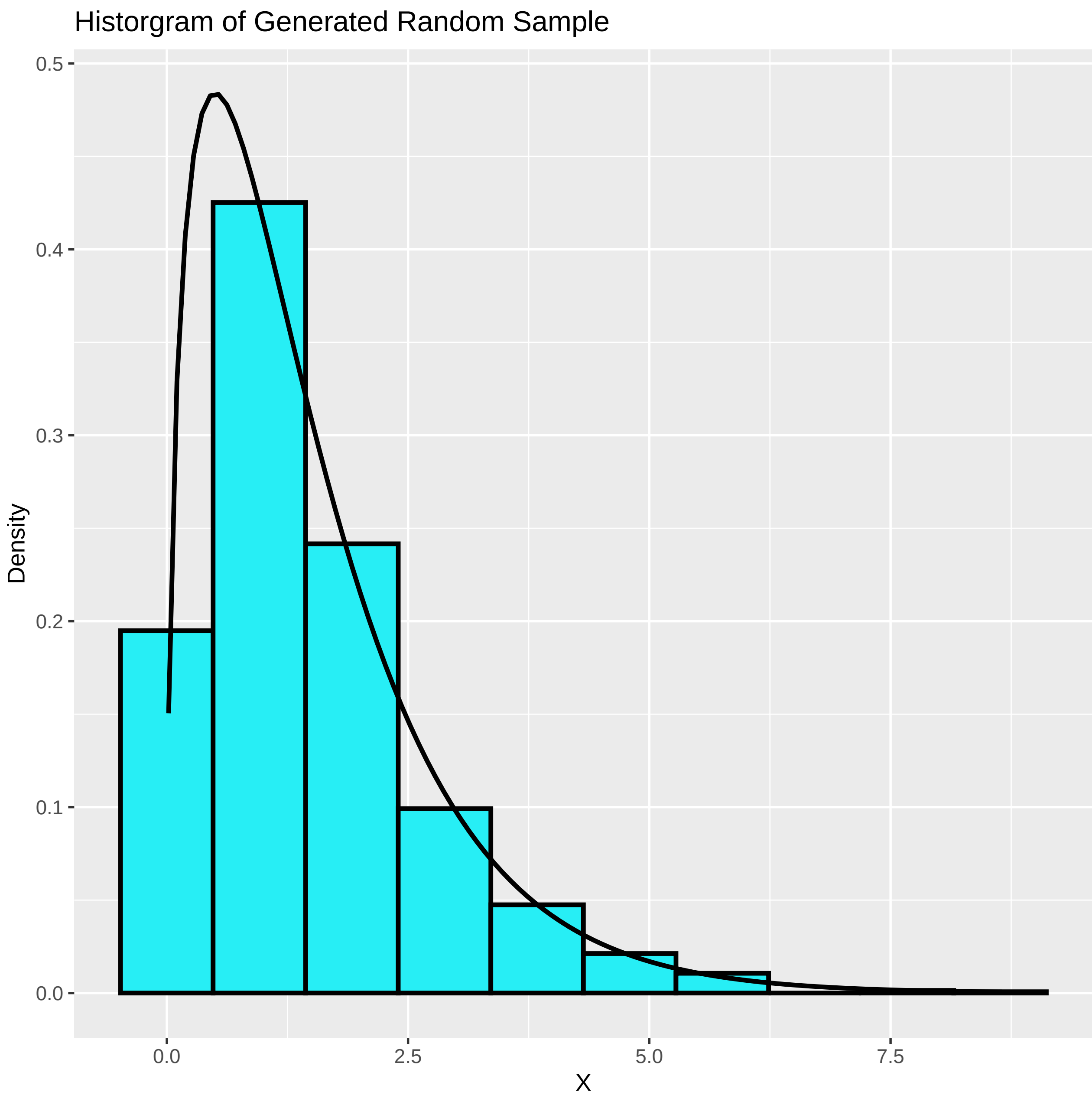
Thus we have a sample of size 1471 from $p(x)$.

The **acceptance rate** was 0.7355 whereas the **theoretical acceptance rate** is 0.7304602.

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

Let us have a histogram of the generated sample.

```r
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 = "Historgram of Generated Random Sample")
```



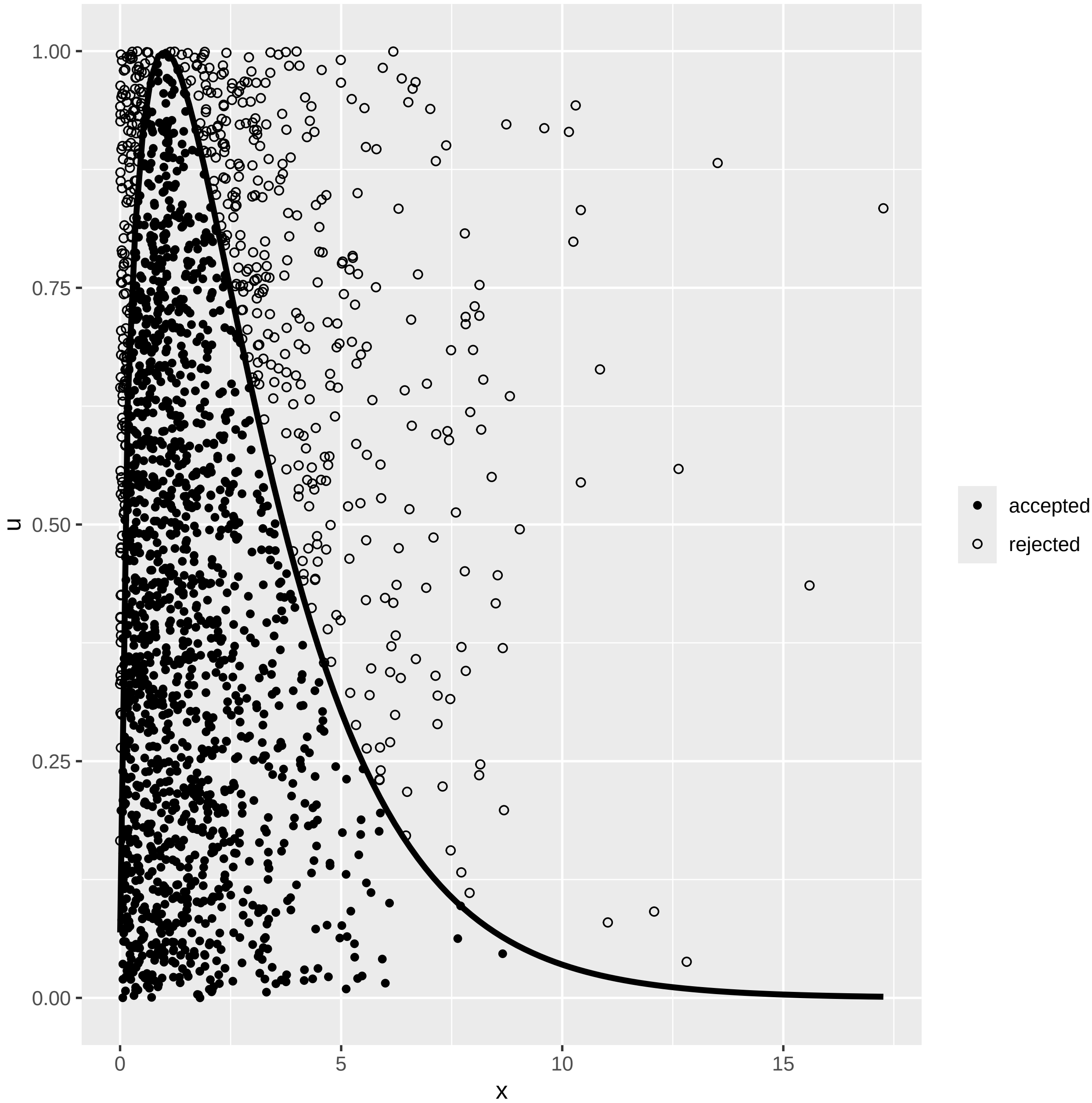
Conclusion

✎ The actual density curve fits the histogram well.

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

```
h_scaled <- function(x) p(x) / (M * q(x))
```

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



✎ The (x, u) pairs that fall under the curve are accepted and rest are rejected.