Lab 5: Rejection Sampling

In this section we'll review rejection sampling.

Why We Need Different Sampling Strategies

- Remember that in Monte Carlo methods, to compute a integral numerically we need to sample from a distribution first. The pdf of this distribution can be of any form as long as it is a legal pdf.
- For some distributions, such as normal, beta, gamma and so on, we can easily do the sampling using build in functions in R.
- If not, we need to be more clever about how we generate samples. There are two common approaches for sampling from a *univariate* distribution:
  - Inversion Sampling
  - Rejection sampling

Probability Integral Transform

- Suppose that a random variable, Y has a continuous distribution for with CDF is F_Y.
- Then the random variable $U = F_Y(Y)$ has a uniform distribution
  - This is known as the "probability integral transform PIT"
- By taking the inverse of F_Y we have $F^{-1}(U) = Y$

Inversion Sampling

The inverse transform sampling method works as follows:

1. Generate a random number u from Unif$[0, 1]$
2. Find the inverse of the desired CDF, e.g. $F_Y^{-1}(u)$.
3. Compute $y = F_Y^{-1}(u)$. y is now a sample from the desired distribution.

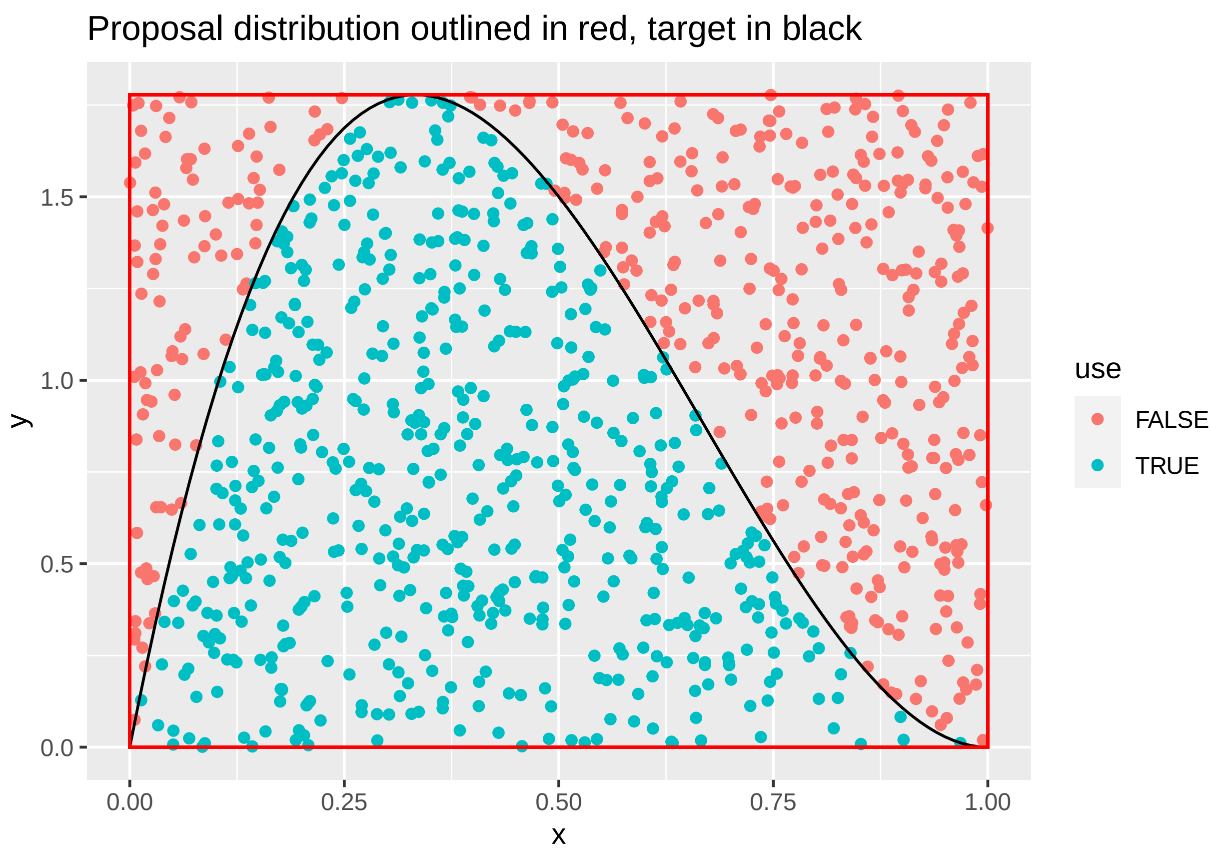
But for most cases we only know the pdf $f(x)$ instead of cdf $F(x) = \int f(x)dx$. To find cdf, we need to do another integral and we comes back to the original problem in Monte Carlo Method again: sampling to approximate the integral.

Rejection Sampling

Intuition

- A naive thought: If I fill a region that envelopes the pdf with points uniformly, then those points under the curve form a good representation of the target pdf and the corresponding x values constitute a good sample from the target distribution. A example:

```
## Warning: 'as.tibble()' was deprecated in tibble 2.0.0.
## i Please use 'as_tibble()' instead.
## i The signature and semantics have changed, see '?as_tibble'.
## This warning is displayed once every 8 hours.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
## generated.
```



The points highlighted in green have the desired distribution. We throw away the reddish samples.

- But we can't control the exact sample size n (how much points are accepted). Also it is not efficient in the tails in the above example.

A Better Algorithm to Complete the Task: Rejection Sampling Algorithm

1. Choose a proposal density, $q(\theta)$ that we can easily sample from (e.g. uniform or normal) such that:
2. Find $M = \max \frac{p(\theta|y)}{q(\theta)}$

- If $M = \infty$ then q cannot be used as a proposal distribution
- If M is finite, $Mq(\theta)$ "envelopes" $p(\theta\ y)$

3. Draw a sample, $\theta^{(s)}$ from $q(\theta)$
4. Draw a $u^{(s)} \sim \text{Unif}(0,1)$

   - If $u^{(s)} < \frac{p(\theta^{(s)}|y)}{Mq(\theta^{(s)})}$ then accept $\theta^{(s)}$ as a samples
   - Otherwise throw out $\theta^{(s)}$ and try again

- Discussion:

  – The crucial part is to find a good proposal density that can envelope our target density and make sampling efficient.
  – Uniform distribution won't work when our target distribution has a domain $(-\infty, +\infty)$
  – In the case where target distribution has a domain $(-\infty, +\infty)$, normal distribution might be a good proposal but it is not always a good choice.

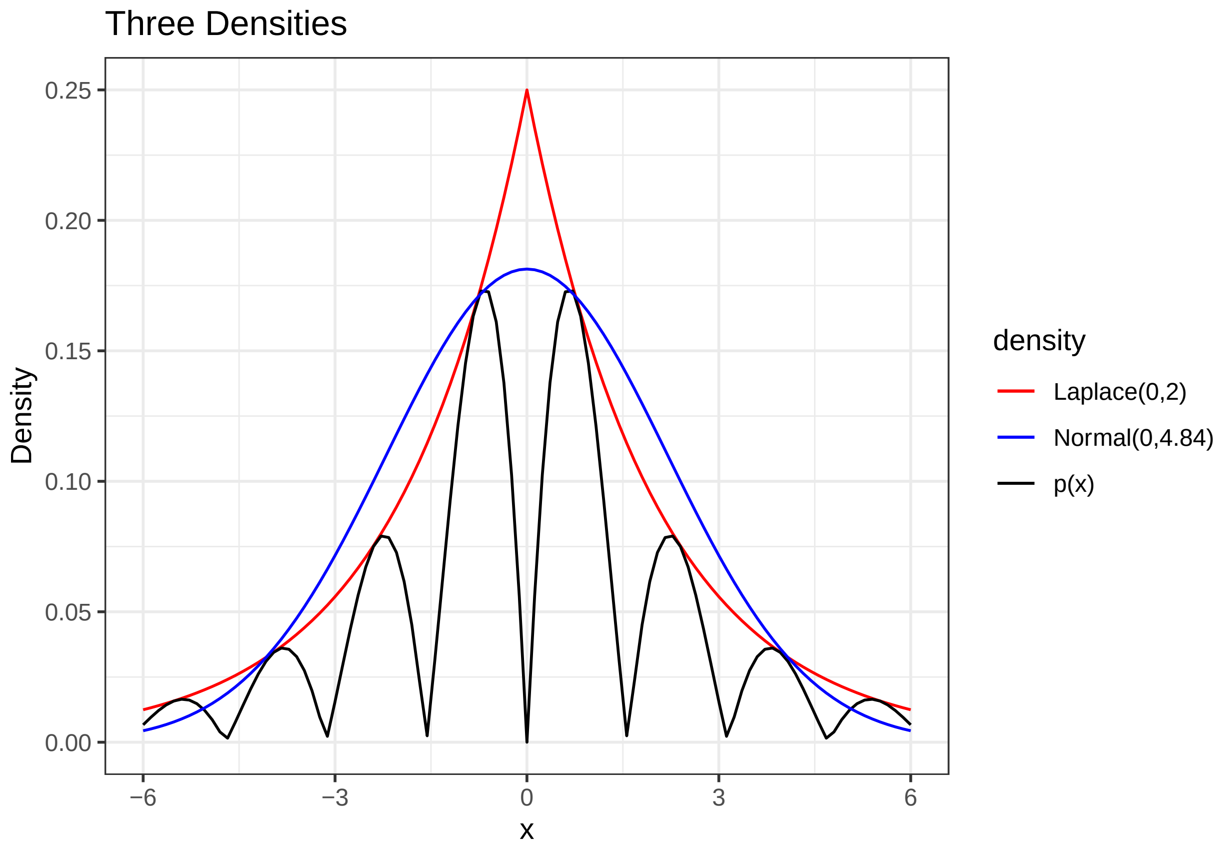
An Example on Rejection Sampling

Problem and Analysis

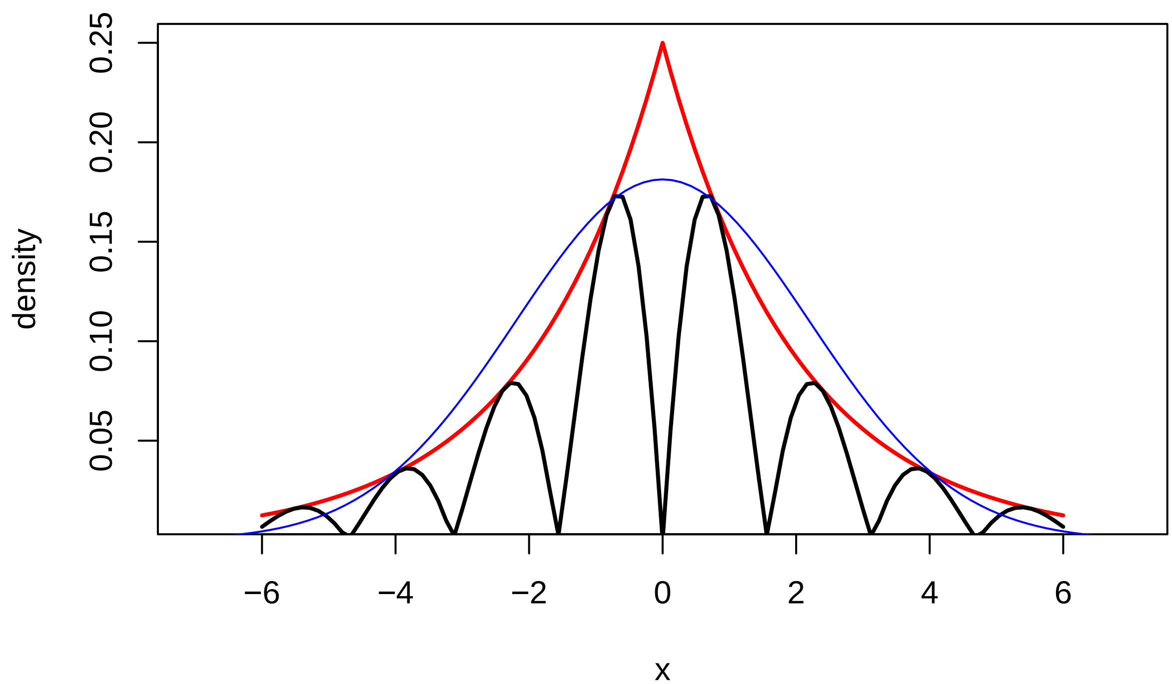
- Suppose our target density is $p(x) \propto \frac{1}{4}e^{-|x|/2}|\sin 2x|$. We can find the constant part using Laplace transformation but for now let's consider it as C. So $p(x) = C\frac{1}{4}e^{-|x|/2}|\sin 2x|$
- If we look closely we can notice that the nonperiodic part $\frac{1}{4}e^{-|x|/2}$ is the pdf of laplace distribution.
- Let's visualize the laplace density and the main part of $p(x)$: $\frac{1}{4}e^{-|x|/2}|\sin 2x|$

Two methods are introduced to draw the same plot, we recommend you using ggplot

```
#Method 1
ggplot(aes(x=x), data = data.frame(x=0) )+
  stat_function(fun = function(x) dlaplace(x, 0, 2), aes(colour = "Laplace(0,2)"))+
  stat_function(fun = function(x) dlaplace(x, 0, 2)*abs(sin(2*x)), aes(colour = "p(x)"))+
  stat_function(fun = function(x) dnorm(x, 0, 2.2), aes(colour = "Normal(0,4.84)"))+
  xlim(c(-6,6))+theme_bw()+scale_y_continuous(name = "Density")+scale_colour_manual(name="density",valu
```




```r
#Method 2
curve(dlaplace(x, 0, 2), from=-6, to=6, xlim=c(-7, 7), lwd=2, col = "red", ylab = "density")
curve(dlaplace(x, 0, 2)*abs(sin(2*x)), from=-6, to=6, xlim=c(-7, 7), lwd=2, add = TRUE)
curve(dnorm(x, 0, 2.2), add = TRUE, col = "blue")
```



The above plot shows that we can always evenlopes $p(x)$ by $Cq(x)$ where $q(x) = \frac{1}{4}e^{-|x|/2}$ is the density for Laplace(0,2). Thus Laplace(0,2) can be our proposal density

- The other potential proposal density is normal density. We want to see whether normal density can be a proper proposal distribution. As we can see from the blue line of the plot. A N(0, 4.84) density can cover the middle of our density but not the tails. That's because Laplace distribution have heavier tails than normal distribution and our target is originated from laplace distribution.
- Is it possible that if we amplify N(0, 4.84) by a constant, it will cover the target? No. Because of the heavier tail property, the amplified N(0, 4.84) will eventually goes under our target distribution

Solve the problem with Laplace(0,2)

- Follow the algorithm, our proposal density $q(x) = \frac{1}{4}e^{-|x|/2}$ is Laplace(0,2)
- Next, we should find $M = \max \frac{p(\theta|y)}{q(\theta)}$. It can be easily found to be C, the constant part of $p(x)$. If we ignore C, then M should be 1. The following code verifies this.

important code for HW

```
density_ratio<-function(x){#ratio of densities, in HW you should use the exact form of density.
  dlaplace(x, 0, 2)*abs(sin(2*x))/dlaplace(x, 0, 2)
}

M <- optimize(density_ratio, lower = -10, upper = 10, maximum = TRUE)$objective
M
```

```
## [1] 1
```

- Then we should draw sample from $q(theta)$ and then use another uniform sample to decide whether we should accept or reject the sample.

important code for HW

```r
set.seed(123)
n <- 1e6
laplace_sample<- rlaplace(n, 0, 2)
accept <- runif(n)< density_ratio(laplace_sample)/M
samples <- laplace_sample[accept]
head(accept)
```

```
## [1]  TRUE  TRUE  TRUE FALSE  TRUE FALSE
```

```r
mean(accept)
```

```
## [1] 0.62968
```

```r
var(samples)
```

```
## [1] 8.10665
```

```r
mean(samples)
```

```
## [1] -0.00868812
```

Estimated 60% quantile interval and 60% HPD(Highest Posterior Density) region To calculate HPD based on samples we need `HDInterval` package.

All the follows are important code for HW

```r
hd_region <- hdi(density(samples), allowSplit = TRUE, credMass = 0.6)
hd_region
```

```
##           begin        end
## [1,] -2.5035597 -2.0885406
## [2,] -1.2585023 -0.2209545
## [3,]  0.1940647  1.2316125
## [4,]  2.0616508  2.4766699
## attr(,"credMass")
## [1] 0.6
## attr(,"height")
## [1] 0.1067766
```

The total length HPD region is given by:

```r
sum(hd_region[,"end"]-hd_region[,"begin"])
```

```
## [1] 2.905134
```

Teh quantile interval and it's lenght is given by:

```r
quantile_interval<-quantile(samples,c(0.2,0.8))
quantile_interval
```

```
##       20%       80%
## -2.017739  2.002357
```

```r
quantile_interval[2] - quantile_interval[1]
```

```
##      80%
## 4.020097
```

```r
curve(dlaplace(x, 0, 2)*abs(sin(2*x)), from=-6, to=6, xlim=c(-7, 7))
segments(x0=hd_region[1, 1], y0=0, x1=hd_region[1, 2], y1=0, col="red", lwd=3)
segments(x0=hd_region[2, 1], y0=0, x1=hd_region[2, 2], y1=0, col="red", lwd=3)
segments(x0=hd_region[3, 1], y0=0, x1=hd_region[3, 2], y1=0, col="red", lwd=3)
segments(x0=hd_region[4, 1], y0=0, x1=hd_region[4, 2], y1=0, col="red", lwd=3)
segments(x0=quantile_interval[1], y0=0.01, x1=quantile_interval[2], y1=0.01, col="blue", lwd=3)
```