Tutorial: Rejection Sampling

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Sampling

Sampling is one of the most common tasks in statistical data analysis and in particular Monte Carlo simulations.

The task of sampling is to draw samples of a random variable (r.v.), given its probability density/mass function.

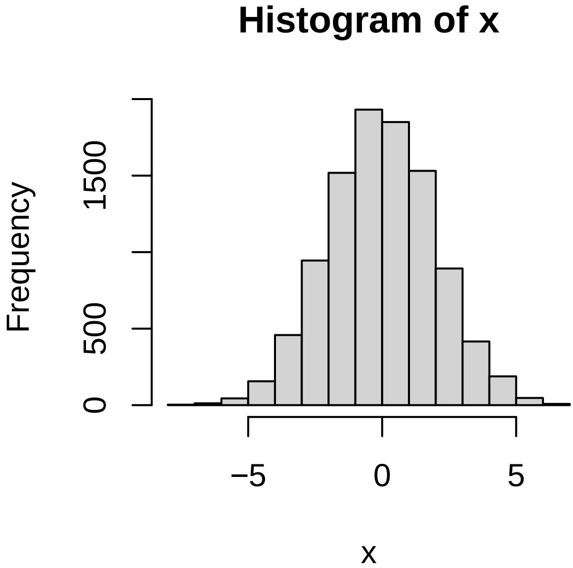
R provides lots of built-in samplers following the pattern:

```
rdistr(n, par1, par2, par3, ...)
```

which outputs a vector of n random variable from a distribution with parameters `par1`, `par2`, `par3`, ...

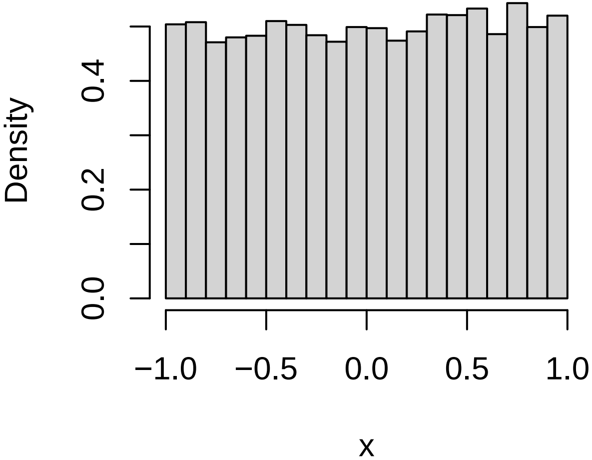
Example: sample from $N(\mu, \sigma^2)$ with $\mu = 0$ and $\sigma = 2$:

```r
x <- rnorm(n = 1e4, mean = 0, sd = 2)
hist(x)
```



Sample from $Unif(a, b)$ with $a = -1$ and $b = 1$:

```
x <- runif(n = 1e4, min = -1, max = 1)
hist(x, prob = TRUE, main = "")
```

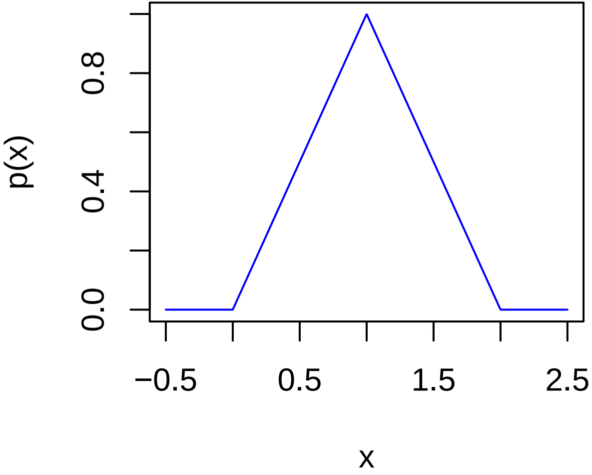


We use `prob = TRUE` to have probability densities on y-axis.

Sampling for non-standard distributions

But, how do you sample from (e.g.) a triangular distribution?

Suppose we know its p.d.f. $p(x) = 1 - |x - 1|, x \in [0\ 2]$?



Solution: Rejection Sampling

Basic idea:

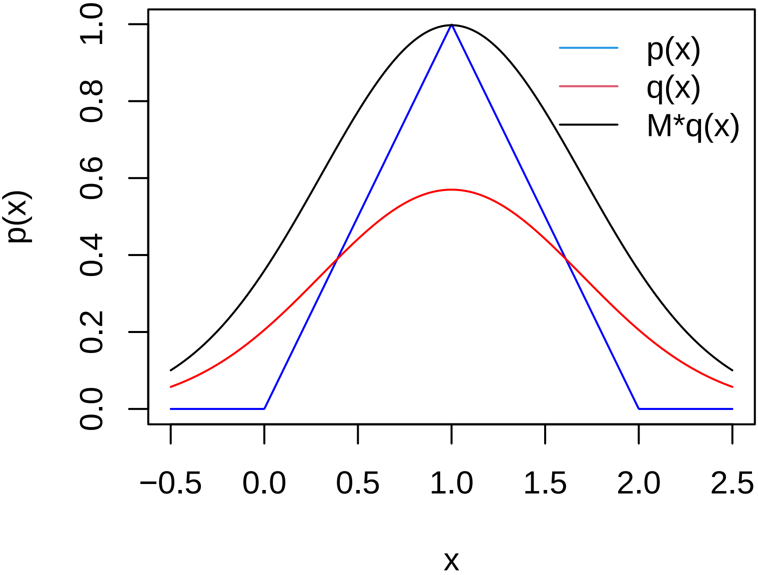
1. sample from a distribution you know how to sample from (the **proposal distribution**);
2. "adjust" that sample so it becomes a sample from the distribution of interest (the **target distribution**).

Let $p(x)$ be the p.d.f. of target and $q(x)$ be the p.d.f. of proposal.

Let $M^* > 1$ be smallest constant such that:

$$p(x) \leq M^* q(x) \text{ for any } x \text{ s.t. } p(x) > 0.$$

Sounds confusing? We just need to $Mq(x)$ to "cover" $p(x)$...



NB: you can choose $M > M^*$, but $p(x) \leq Mq(x)$ is necessary.

Algorithmic Implementation

Objective: get a sample of n_{max} independent random variables (r.v.s) from target.

Algorithm:

1. Draw a r.v. x from $q(x)$ and a uniform sample $u \sim U(0,1)$
2. If $u < \frac{p(x)}{M^* q(x)}$, accept sample x and store it.
3. If number of accepted samples so far equals to n_{max}, quit. Otherwise, go back to step 1.

Here we will use $Unif(a=0, b=2)$ as proposal distribution $q(x)$.

When accepting a sample in step 2, we need to add it to the vector of accepted samples so far.

Two ways of doing it:

```r
a <- c(1,2,3,4)


a[5] <- 5
print(a)
```

```
[1] 1 2 3 4 5
```

```r
# OR
a <- c(a, 6)
print(a)
```

```
[1] 1 2 3 4 5 6
```

Code Skeleton

```
# how many samples do we want?
n_max = 1000

p_target <- function(x){
  # TODO: the PDF of distribution, from which
  # you want to sample.
}

acc <- c() # create an empty vector
n <- 0 # how many samples have we already obtained?
M <- NA # TODO you should be able to work it out!
while(n < n_max){
 # TODO
}
hist(acc) #plot the histogram of accepted samples
```

Questions:

1. Complete the above code skeleton according to the rejection sampling algorithm.
2. What output is expected when the algorithm is implemented correctly?
3. What happens if you increase M above M^*? Is the algorithm still correct (use visualisation to assess this)? Does the code become faster or slower?
4. What happens if you decrease M below minimum required value?

Challenge: try using $N(\mu = 1, \sigma^2 = 0.5^2)$ as proposal:

- Computing optimal M^* might be hard, but you just need M big enough.
- To compute it you need to know the Gaussian p.d.f. (see `?dnorm`).
- Is this more efficient than using a uniform proposal?