# Statistics 1 Unit 2: Random Number Generation


Kurt Hornik

# Outline

- Motivation
- Basics
- Inverse transform method
- Acceptance-rejection method

# Motivation

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- What are “random numbers”?
- What are good sources of random numbers?
- In particular, where do computers get random numbers from?

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# Uniform random numbers

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Technically, one uses the term *pseudorandom numbers*.

These are really perfectly deterministic, but work well enough for “real” random numbers.

# Uniform random numbers

Uniform (on the unit interval) pseudorandom numbers can be simulated using multiplicative congruential random number generators which use recursions

$$x_n = bx_{n-1} \pmod{m}, \qquad u_n = x_n/m$$

for suitable initial seed $x_0$.

Clearly,

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Clearly,

- $x = 0$ “absorbs”
- The generated sequence will be *periodic*
- The best we can get is period of $m-1$ (giving all remainders from 1 to $m-1$)

# Uniform random numbers

To illustrate:

```
R> myrng <- function(n, m, b, x) {
+     u <- numeric(n)
+     for(i in 1 : n) {
+         x <- (b * x) %% m
+         u[i] <- x / m
+     }
+     u
+ }
```

# Uniform random numbers

BnM Example 5.1:

```
R> myrng(7, 7, 3, 2)

[1] 0.8571429 0.5714286 0.7142857 0.1428571 0.4285714 0.2857143
[7] 0.8571429
```

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[1] 0.8571429 0.5714286 0.7142857 0.1428571 0.4285714 0.2857143
[7] 0.8571429
```

BnM example for bad:

```
R> myrng(5, 29241, 171, 3)

[1] 0.01754386 0.00000000 0.00000000 0.00000000 0.00000000
```

# Uniform random numbers

BnM Example 5.2:

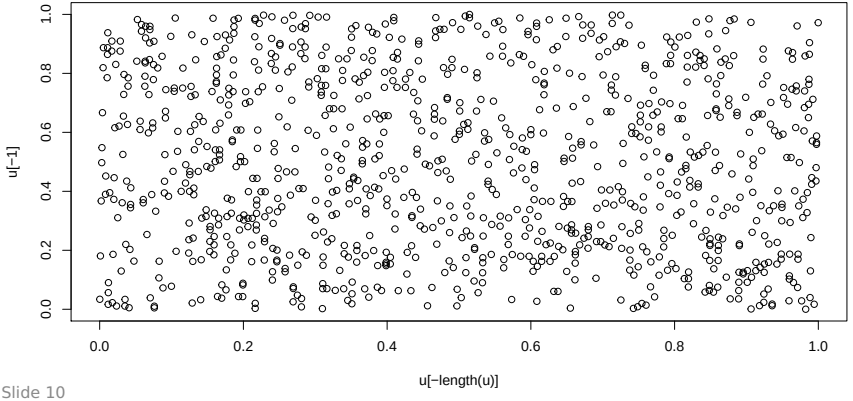
```
R> myrng(50, 30269, 171, 27218)

 [1] 0.76385080 0.61848756 0.76137302 0.19478675 0.30853348 0.75922561
 [7] 0.82757937 0.51607255 0.24840596 0.47741914 0.63867323 0.21312234
[13] 0.44391952 0.91023820 0.65073177 0.27513297 0.04773861 0.16330239
[19] 0.92470845 0.12514454 0.39971588 0.35141564 0.09207440 0.74472232
[25] 0.34751726 0.42545178 0.75225478 0.63556774 0.68208398 0.63636063
[31] 0.81766824 0.82126929 0.43704780 0.73517460 0.71485678 0.24051009
[37] 0.12722587 0.75562457 0.21180085 0.21794575 0.26872378 0.95176583
[43] 0.75195745 0.58472364 0.98774324 0.90409330 0.59995375 0.59209092
[49] 0.24754700 0.33053619
```

# Uniform random numbers

Illustrating the “randomness”:

```
R> u <- myrng(1000, 30269, 171, 27218)
R> plot(u[-length(u)], u[-1])
```



# Uniform random numbers

R has several built-in (pseudo) random number generators. E.g., method “Knuth-TAOCP-2002” uses the recursion

$$x_n = (x_{n-100} - x_{n-37}) \pmod{2^{30}}$$

which has a period around $2^{129}$.

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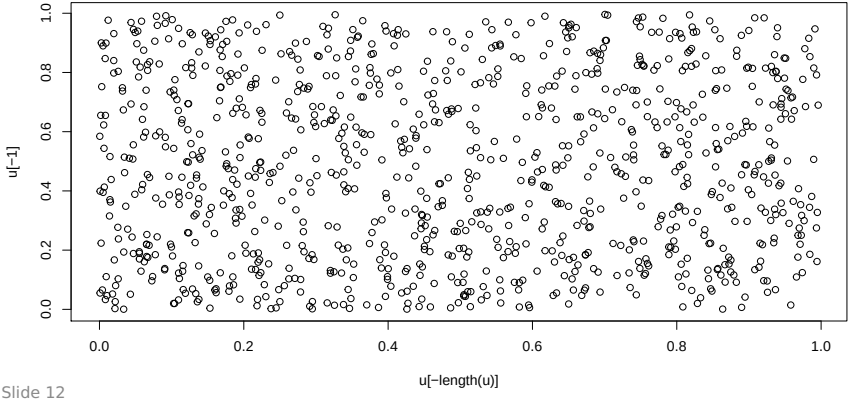
which has a period around $2^{129}$.

To get a sample of uniform (peudo) random numbers: `runif()`.

# Uniform random numbers

Illustrating the “randomness” again:

```
R> u <- runif(1000)
R> plot(u[-length(u)], u[-1])
```



# Uniform distribution

The (continuous) uniform distribution on the interval from $a$ to $b$ has density

$$f_{\text{uniform}(a,b)}(x) = \begin{cases} \frac{1}{b-a}, & a < x < b, \\ 0, & \text{otherwise.} \end{cases}$$

Often denoted by $U(a, b)$ or $U_{a,b}$ or $\mathcal{U}_{a,b}$.

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It has two parameters:

- $a$ is the minimum (inf) of its support,
- $b$ is the maximum (sup) of its support.

If $a = 0$ and $b = 1$, we have the standard uniform distribution.

# Uniform distribution

In R, the parameters are called `min` and `max`.

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For many common probability functions, R provides the above 4 functions, using the d-p-q-r naming scheme.

# Uniform distribution

The 4 functions for the uniform distribution have arguments

```
dunif(x, min = 0, max = 1, log = FALSE)
punif(q, min = 0, max = 1, lower.tail = TRUE, log.p = FALSE)
qunif(p, min = 0, max = 1, lower.tail = TRUE, log.p = FALSE)
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- `log.p = TRUE` says use/give log-probabilities (can be better numerically)

# Normal distribution

The normal distribution has density

$$\frac{1}{\sqrt{2\pi}\sigma}\exp\left(-\frac{(x-\mu)^2}{2\sigma^2}\right)$$

where $\mu$ is the mean and $\sigma^2$ the variance, and hence $\sigma$ the sd (standard deviation).

For $\mu = 0$ and $\sigma = 1$ we get the standard normal distribution.

# Normal distribution

In R,

```
dnorm(x, mean = 0, sd = 1, log = FALSE)
pnorm(q, mean = 0, sd = 1, lower.tail = TRUE, log.p = FALSE)
qnorm(p, mean = 0, sd = 1, lower.tail = TRUE, log.p = FALSE)
rnorm(n, mean = 0, sd = 1)
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Note that this uses parameters `mean` ($\mu$) and `sd` ($\sigma$) (but not the variance $\sigma^2$ as we commonly do in probability)!

Why?

# Normal distribution

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We all know:

$X$ is normal with mean $\mu$ and sd $\sigma \Leftrightarrow Z = \dfrac{X-\mu}{\sigma}$ is standard normal.

I.e.,

$$\mathbb{P}(X \leq x) = \mathbb{P}\left(Z \leq \frac{x-\mu}{\sigma}\right) = \Phi\left(\frac{x-\mu}{\sigma}\right)$$

where $\Phi$ is the CDF of the standard normal distribution.

# Normal distribution

For the densities:

$$\frac{d}{dx}\mathbb{P}(X \leq x) = \Phi'\left(\frac{x-\mu}{\sigma}\right)\frac{1}{\sigma} = \frac{1}{\sigma}\phi\left(\frac{x-\mu}{\sigma}\right)$$

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where $\phi$ is the density of the standard normal distribution.

There is nothing special about the standard normal here: whenever the numeric random variable $Z$ has CDF $F$ and density $f$, the location-scale family generated by this distribution has CDFs and densities

$$F\left(\frac{x-\mu}{\sigma}\right), \qquad \frac{1}{\sigma}f\left(\frac{x-\mu}{\sigma}\right).$$

# Rate and scale

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Somewhat confusingly, for the exponential distribution R takes the "usual" parametrization with rate parameter $\lambda$, i.e., densities

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Clearly, $\sigma = 1/\lambda$ would be the corresponding scale parameter.

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Clearly, $\sigma = 1/\lambda$ would be the corresponding scale parameter.

As a "compromise", for the gamma distribution (which includes the exponential distribution as a special case), one can use both `rate` or `scale`!

# Discrete distributions

The most common discrete distributions are

- The binomial distribution with parameters $n$ (`size`) and $p$ (`prob`), with density (probability mass function)

$$f_{\text{binomial}(n,p)}(x) = \begin{cases} \binom{n}{p} p^x (1-p)^{n-x}, & x \in \{0, \ldots, n\}, \\ 0, & \text{otherwise} \end{cases}$$

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  In R, `dbinom()` etc.
- The Poisson distribution with parameter $\lambda$, with density

$$f_{\text{Poisson}(\lambda)}(x) = \begin{cases} \frac{\lambda^x}{x!} e^{-\lambda}, & x \in 0, 1, 2, \ldots, \\ 0, & \text{otherwise} \end{cases}$$

  In R, `dpois()` etc.

# Discrete distributions

These densities are not with respect to Lebesgue measure (hence giving integrals) but with respect to counting measure on the integers (hence giving sums).

More in probability theory!

# Sampling from values

Using `sample()`, we can sample given values with or without replacement:

```
sample(x, size, replace = FALSE, prob = NULL)
```

E.g., to generate a random permutation of the numbers from 1 to 10:

```
R> sample(1 : 10, 10)
 [1]  4  1  7  8  9 10  5  3  6  2
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 [1]  4  1  7  8  9 10  5  3  6  2
```

E.g., to randomly draw 13 numbers from 1 : 7 with replacement:

```
R> sample(1 : 7, 13, replace = TRUE)
 [1] 7 5 5 5 4 2 3 7 3 1 5 6 6
```

# Simulation experiments

Once we can draw (pseudo) random numbers, we can perform simulation experiments.

E.g., we know from probability theory that if $X_1, X_2, \ldots$ are i.i.d. (independent identically distributed) $\sim F$ (with distribution function $F$), then by the law of large numbers,

$$\frac{1}{n}\sum_{i=1}^{n} g(X_i) \to \mathbb{E}(g(X)) = \int g(x)\, dF(x).$$

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We can use this to determine $\mathbb{E}(g(X))$ by *Monte Carlo simulation*: more on this next week.

# Simulation experiments

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- Generate a sample $Z_1, \ldots, Z_n$ from the distribution of $Z$.
- Investigate the *empirical distribution* of the sample, and compare it to reference distribution.

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How can we illustrate via a simulation experiment?

- Generate a sample $Z_1, \ldots, Z_n$ from the distribution of $Z$.
- Investigate the *empirical distribution* of the sample, and compare it to reference distribution.

This needs $n$ large for the approximating the underlying distribution by the empirical distribution.

# Simulation experiments

To generate a sample of size $n$ from the standardized binomial with parameters $m$ and $p$, i.e.,

$$Z_i = \frac{X_i - mp}{\sqrt{mp(1-p)}}, \qquad X_i \sim \text{binomial}(m, p),$$

we can do

```
R> simbin <- function(n, m, p) {
+     (rbinom(n, size = m, prob = p) - m * p) / sqrt(m * p * (1 - p))
+ }
```

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+     (rbinom(n, size = m, prob = p) - m * p) / sqrt(m * p * (1 - p))
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```

E.g.,

```
R> z <- simbin(1000, 200, 0.4)
```

# Simulation experiments

How can we now investigate the empirical distribution?

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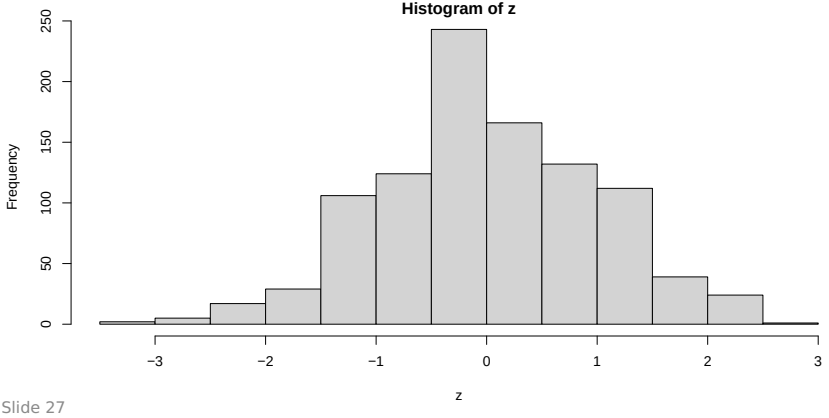
How can we now investigate the empirical distribution? Usual answer: histogram.

```
R> hist(z)
```



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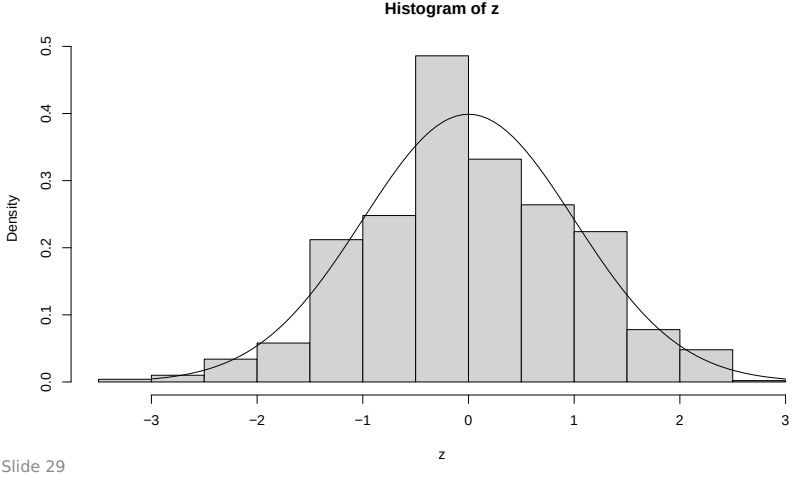
One could do so by doing the histogram on the probability scale and superimposing the density of the standard normal.

# Simulation experiments

```
R> hist(z, probability = TRUE); curve(dnorm, -3, 3, add = TRUE)
```



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If the distributions are the same modulo a location-scale transformation, the QQ plot will be close to a straight line.

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If the distributions are the same modulo a location-scale transformation, the QQ plot will be close to a straight line.

Why?

# Simulation experiments

Suppose

$$G(x) = F\left(\frac{x-\mu}{\sigma}\right), \qquad F(z_\alpha) = \alpha.$$

Then

$$G(x) = \alpha \Leftrightarrow F\left(\frac{x-\mu}{\sigma}\right) = \alpha \Leftrightarrow \frac{x-\mu}{\sigma} = z_\alpha \Leftrightarrow x = \mu + \sigma z_\alpha.$$

(As we know for the normal distribution.)

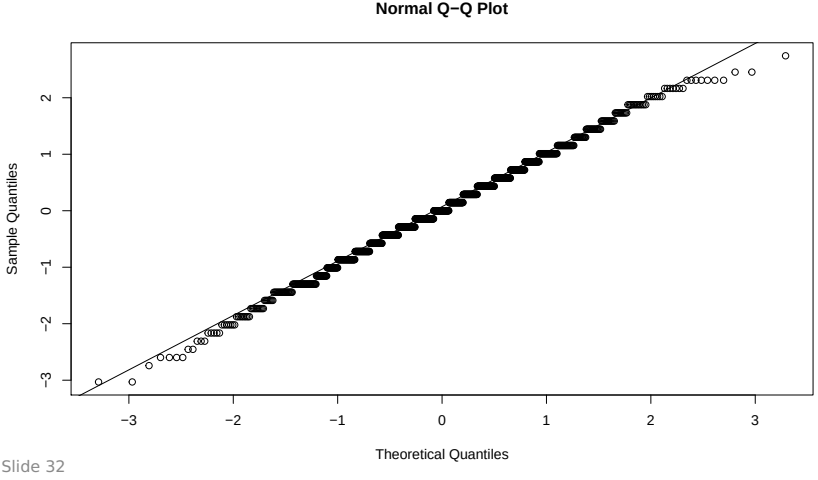
So the quantile functions $Q_F$ and $Q_G$ of $F$ and $G$ satisfy

$$Q_G(\alpha) = \mu + \sigma Q_F(\alpha)$$

and plotting $(Q_F(\alpha), Q_G(\alpha))$ gives a straight line!

# Simulation experiments

```
R> qqnorm(z); qqline(z)
```



# Simulation experiments

If we integrate the QQ plot into the simulation, we can create nice movies illustrating the CLT, i.e., how the approximation becomes better when increasing *m*:

```
R> simbin <- function(n, m, p) {
+     z <- ((rbinom(n, size = m, prob = p) - m * p) /
+           sqrt(m * p * (1 - p)))
+     qqnorm(z, ylim = c(-4, 4), main = paste("QQ-plot, m =", m))
+     qqline(z)
+ }
```

# Simulation experiments

A simple movie:

```
R> for(m in seq(1, 100, 3)) {
+     simbin(1000, m, 0.4)
+     Sys.sleep(1)
+ }
```

# Simulation experiments

Everyone knows that for large $m$, the binomial distribution can be approximated by the normal distribution.

What is much less known is that for large $\lambda$, the Poisson distribution can also be approximated by the normal distribution:

If If $X$ is Poisson with parameter $\lambda$ and

$$Z = \frac{X - \lambda}{\sqrt{\lambda}},$$

then $Z$ is approximately standard normal as $\lambda$ gets large.

# Simulation experiments

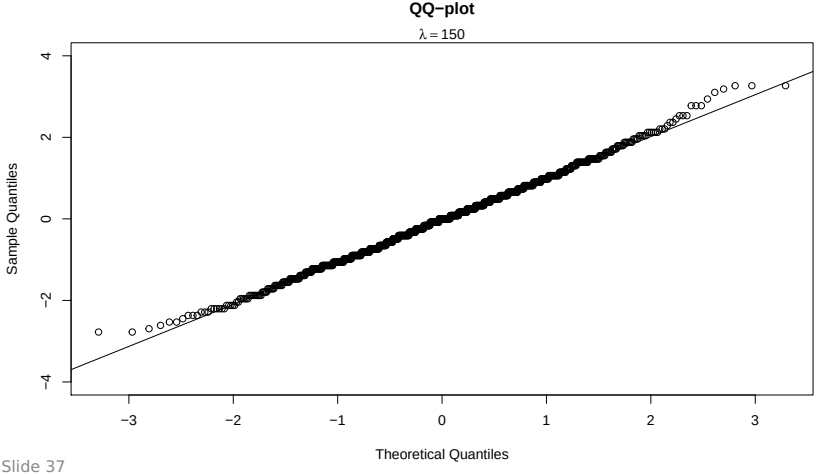
To illustrate, we can use

```
R> simpois <- function(n, lambda) {
+     z <- (rpois(n, lambda = lambda) - lambda) / sqrt(lambda)
+     qqnorm(z, ylim = c(-4, 4), main = "QQ-plot")
+     qqline(z)
+     mtext(bquote(lambda == .(lambda),), 3)
+ }
```

E.g., for $\lambda = 150$:

# Simulation experiments

```
R> simpois(1000, 150)
```



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# Introduction

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The two most important methods for sampling from a distribution are

- the inverse transform method
- the acceptance-rejection method

# Quantiles

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Ideally, if $F$ is a distribution function, then the $\alpha$-quantile $x_\alpha = F^{-1}(\alpha)$ solves

$$F(x) = \alpha.$$

However,

- The solution may not be unique ($F$ could be flat in some interval)

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However,

- The solution may not be unique ($F$ could be flat in some interval)
- The solution may not even exist!

Remember: if $F$ is a CDF, it is right-continuous with left limits!

# Quantiles

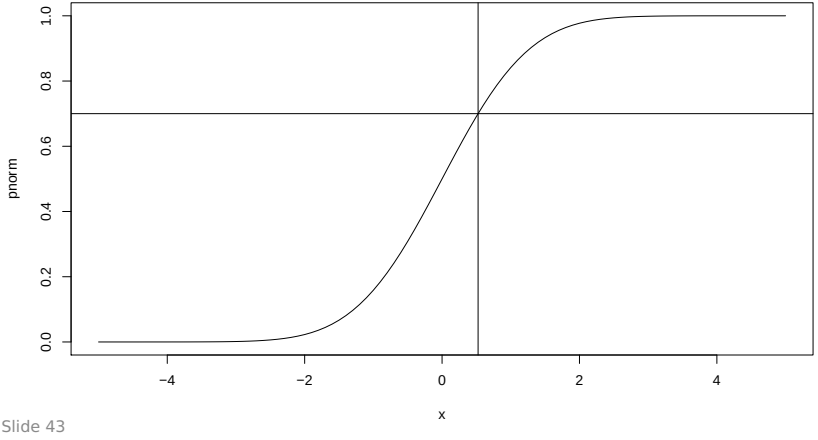
The CDF of the standard normal is continuous and increasing, so

$$\Phi(x) = \alpha$$

has a unique solution for all $0 < \alpha < 1$:

# Quantiles

```
R> p <- 0.7; plot(pnorm, -5, 5); abline(h = p); abline(v = qnorm(p))
```



# Quantiles

The binomial with parameters $m$ and $p$ has its support in $\{0, \ldots, m\}$. So the CDF has jumps at these points, and is flat otherwise.

The equation

$$\text{pbinom}(x, m, p) = \alpha$$

only has a solution for

$$\alpha \in \{\text{pbinom}(0, m, p), \text{pbinom}(1, m, p), \ldots, \text{pbinom}(m, m, p)\}.$$

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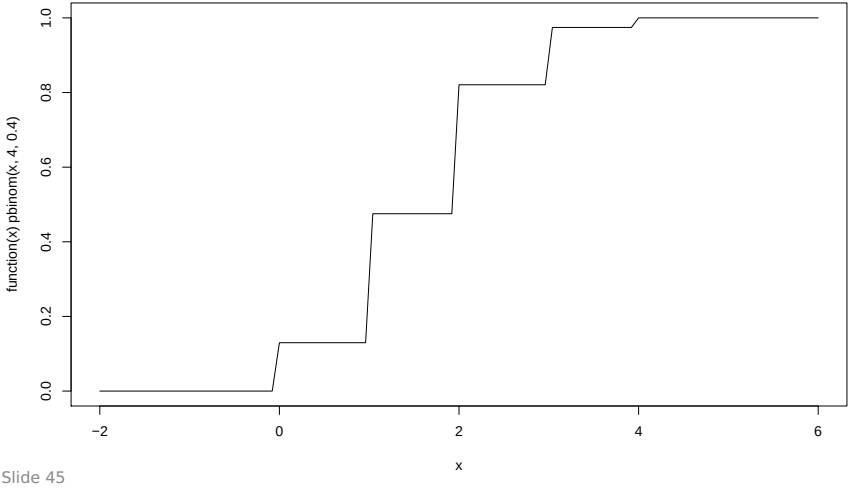
To illustrate for $m = 4$ and $p = 0.4$:

# Quantiles

```
R> plot(function(x) pbinom(x, 4, 0.4), -2, 6)
```



# Quantiles

This is actually a bit silly in context as we don’t see the jumps. Can we do better?

We can create a step function $s$ which does

$$s(x) = \begin{cases} y_0, & x < x_1, \\ y_i, & x_i < x < x_{i+1}, 1 \leq i < n, \\ y_n, & x > x_n. \end{cases}$$

(and specify whether we want right or left continuous).

# Quantiles

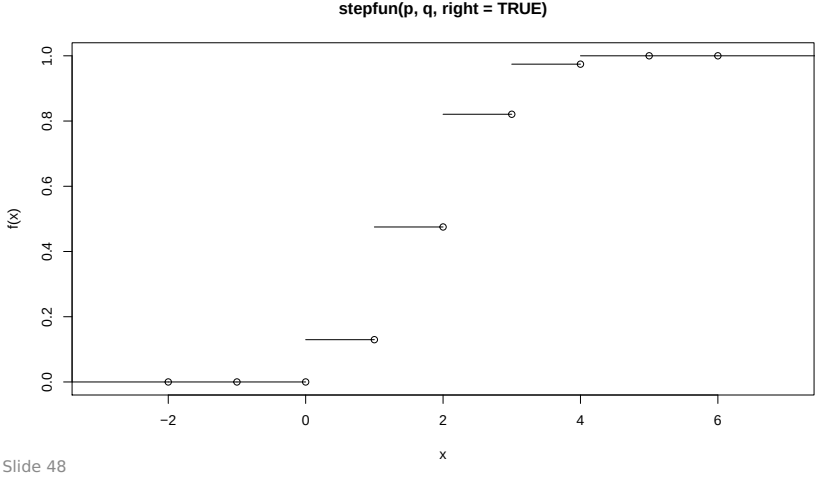
E.g.,

```
R> p <- seq(-2, 6)
R> q <- c(0, pbinom(p, size = 4, p = 0.4))
R> s <- stepfun(p, q, right = TRUE)
```

With this:

# Quantiles

```
R> plot(s, vertical = FALSE)
```



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E.g., for $\alpha = 0.7$, we see that

$$\begin{aligned} F(1) &= \text{pbinom}(1, 4, 0.4) = 0.4752 < 0.7, \\ F(2) &= \text{pbinom}(2, 4, 0.4) = 0.8208 > 0.7 \end{aligned}$$

so should we take 1 or 2? (Or perhaps the solution using the linear interpolation of $F(1)$ and $F(2)$?)

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so should we take 1 or 2? (Or perhaps the solution using the linear interpolation of $F(1)$ and $F(2)$?)

The common convention is to use the smallest $x$ such that $F(x) \geq \alpha$.

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Formally: if $F$ is a distribution function, its quantile function is defined as

$$Q_F(u) = F^{-1}(u) = \inf\{x : F(x) \geq u\}.$$

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Hence, to make the distinction clear, one sometimes writes $F^{\leftarrow}$ or (my preference) $Q_F$.

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Hence, to make the distinction clear, one sometimes writes $F^{\leftarrow}$ or (my preference) $Q_F$.

Hence in our case, the 0.7 quantile must be 2:

```
R> qbinom(0.7, 4, 0.4)

[1] 2
```

# Quantile transform method

Now let $F$ be a CDF, $Q_F$ its quantile function, and $U$ be a standard uniform random variable: $U \sim U_{0,1}$.

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I.e., the *quantile transform* $Q_F(U)$ has distribution (function) $F$!

# Quantile transform method

This nice mathematical theorem forms the basis of the *quantile transform method*:

> To draw $X \sim F$, take $X = Q_F(U)$ with $U \sim U_{0,1}$.

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> To draw $X \sim F$, take $X = Q_F(U)$ with $U \sim U_{0,1}$.

This looks nice and very general, but is useful only if we can efficiently compute the quantile function $Q_F$!

Of course, we can always use repeated bisection, but that may not be efficient enough.

# Quantile transform method: Example 1

Suppose we want to draw from the distribution with density

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$$F(x) = \int_0^x f(t)\,dt = x^3.$$

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$$F(x) = x^3 = u \Rightarrow x = Q_F(u) = u^{1/3}.$$

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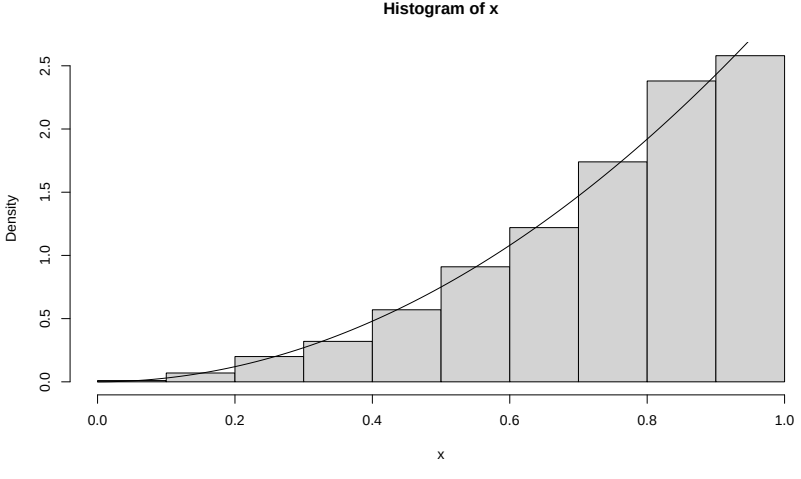
Thus, if $U$ is standard uniform, $U^{1/3} \sim F$.

# Quantile transform method: Example 1

To illustrate, generate a sample, draw its (probability) histogram, and add the true density:

```
R> n <- 1000
R> x <- runif(n) ^ (1/3)
R> hist(x, probability = TRUE)
R> y <- seq(0, 1, .01)
R> lines(y, 3 * y ^ 2)
```

# Quantile transform method: Example 1



# Quantile transform method: Example 2

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Thus, if $U$ is standard uniform, $-\log(1-U)/\lambda \sim \text{exponential}(\lambda)$.

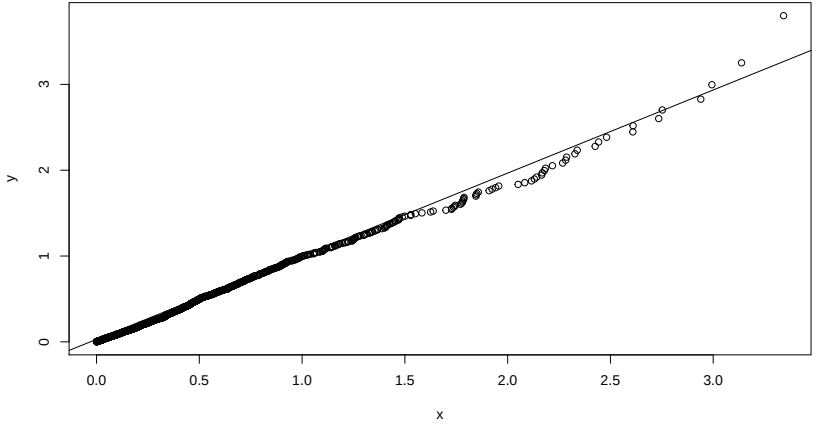
In fact, $1-U$ is standard uniform too. So we can simplify to $-\log(U)/\lambda \sim \text{exponential}(\lambda)$.

# Quantile transform method: Example 2

To illustrate, generate a sample, and do a QQ plot against the exponential distribution.

```
R> rate <- 2
R> n <- 1000
R> x <- -log(runif(n)) / rate
R> y <- qexp(ppoints(n), rate = rate)
R> qqplot(x, y)
R> qqline(x, distribution = function(p) qexp(p, rate = rate))
```

# Quantile transform method: Example 2



# Quantile transform method: Example 3

The simplest (non-trivial) discrete distribution is the Bernoulli distribution:

$$\mathbb{P}(X = 1) = p, \quad \mathbb{P}(X = 0) = q = 1 - p.$$

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$$F(x) = \begin{cases} 0, & x < 0, \\ 1 - p, & 0 \le x < 1, \\ 1 & x \ge 1. \end{cases}$$

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$$F(x) = \begin{cases} 0, & x < 0, \\ 1 - p, & 0 \le x < 1, \\ 1 & x \ge 1. \end{cases}$$

Hence the quantile function is

$$Q_F(u) = \begin{cases} 1, & u > 1 - p, \\ 0, & \text{otherwise.} \end{cases}$$

# Quantile transform method: Example 3

Thus, if $U$ is standard uniform, then $I(U > 1-p)$ has a Bernoulli distribution with parameter $p$.

But

$$U > 1-p \Leftrightarrow 1-U < p.$$

So we can simplify to $I(U < p)$.

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But

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So we can simplify to $I(U < p)$.

Which is what we would presumably have used in the first place, without knowing the quantile transform method.

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Suppose we run a Bernoulli experiment until the first success. What is the distribution of the number $X$ of failures before the first success?

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How can we use the quantile transform method to draw from the geometric distribution?

# Quantile transform method: Example 4

In general, how can we find the quantile function for a discrete distribution?

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Suppose that the support of the distribution is $x_1 < x_2 < \cdots$ (possibly countably infinite, as for the geometric of Poission).

Then

$$F(x) = F(x_i), \quad x_i \leq x < x_{i+1}.$$

Clearly,

$$F(x_{i-1}) < u \leq F(x_i) \Leftrightarrow Q_F(u) = x_i.$$

Why? $F(x_{i-1}) < u$ and $F(x_i) \geq u$, and we're looking for smallest $x$ such that $F(x) \geq u$!

# Quantile transform method: Example 4

For the geometric distribution (and $x$ a non-negative integer),

$$F(x) = \sum_{i=0}^{x} pq^i = p\frac{1-q^{x+1}}{1-q} = 1-q^{x+1}.$$

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For the quantile function, we thus get

$$\begin{aligned} Q_F(u) = x &\Leftrightarrow 1-q^x < u \leq 1-q^{x+1} \\ &\Leftrightarrow q^x > 1-u \geq q^{x+1} \\ &\Leftrightarrow x < \frac{\log(1-u)}{\log(q)} \leq x+1 \end{aligned}$$

# Quantile transform method: Example 4

Now

$$\begin{aligned} x < \xi \leq x+1 &\iff \xi - 1 \leq x < \xi \\ &\iff x = \text{ceiling}(\xi - 1) = \text{ceiling}(\xi) - 1. \end{aligned}$$

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Hence, we found:

$$Q_F(u) = \text{ceiling}\left(\frac{\log(1-u)}{\log(q)}\right) - 1.$$

And thus: if $U$ is standard uniform,

$$\text{ceiling}\left(\frac{\log(1-U)}{\log(1-p)}\right) - 1 \sim \text{geometric}(p).$$

# Outline

- Motivation
- Basics
- Inverse transform method
- Acceptance-rejection method

# Motivation

Suppose we want to sample from the distribution with density

$$f(x) = 6x(1-x), \qquad 0 < x < 1.$$

We can still easily compute

$$F(x) = \int_0^x f(t)\,dt = 6\left(\frac{t^2}{2} - \frac{t^3}{3}\right)\Bigg|_{t=0}^{x} = 3x^2 - 2x^3, \qquad 0 \le x \le 1$$

but solving $F(x) = u$ gives a cubic equation, which is not so "straightforward" to solve.

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but solving $F(x) = u$ gives a cubic equation, which is not so "straightforward" to solve.

Can we draw from $F$ without determining $Q_F$?

# Acceptance-rejection method

The acceptance-rejection method allows the following:

We want to draw $X \sim f$ and know to draw $Y \sim g$, where $f(t) \leq cg(t)$ for all $t$.

We can do this as follows: for each random variate required,

1. Draw $y$ from $g$
2. Draw $u$ from $U_{0,1}$
3. If $u < f(y)/(cg(y))$ accept and deliver $x = y$; otherwise, reject $y$ and restart.

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Why does this work?

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Why does this work? Sorry in advanced for the awful notation.

# Acceptance-rejection method

First,

$$\mathbb{P}(\text{accept}|y) = \mathbb{P}\left(U < \frac{f(y)}{cg(y)}\right) = \frac{f(y)}{cg(y)}.$$

Don't worry if $g(y) = 0$: we cannot really draw such $y$.

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Hence, using a variant of the theorem of total probability,

$$\mathbb{P}(\text{accept}) = \int \mathbb{P}(\text{accept}|y)dG(y) = \int \frac{f(y)}{cg(y)}g(y)dy = \frac{1}{c}$$

# Acceptance-rejection method

To see that $X$ has the right distribution:

$$\begin{aligned}
\mathbb{P}(X = x|\text{accept}) &= \frac{\mathbb{P}(Y = x, \text{accept})}{\mathbb{P}(\text{accept})} \\
&= \frac{\mathbb{P}(\text{accept}|x)\mathbb{P}(Y = x)}{\mathbb{P}(\text{accept})} \\
&= \frac{\frac{f(x)}{cg(x)}g(x)}{\frac{1}{c}} \\
&= f(x)
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WOW!

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$$f(t) \leq cg(t) \text{ for all } t \Rightarrow \int f(t)\,dt \leq \int cg(t)\,dt \Rightarrow 1 \leq c.$$

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As $f$ and $g$ are densities,

$$f(t) \leq cg(t) \text{ for all } t \Rightarrow \int f(t)\,dt \leq \int cg(t)\,dt \Rightarrow 1 \leq c.$$

Every try accepts with probability $p = 1/c$, so the number of rejects has a geometric distribution with parameter $p$.

On average, the number of tries needed is thus

$$1 + \mathbb{E}(\text{geometric}(p)) = 1 + \sum_{x=0}^{\infty} xpq^x = 1 + \frac{q}{p} = \frac{p+q}{p} = \frac{1}{p} = c.$$

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Now multiply by $pq$:

$$\sum_{x=0}^{\infty} x p q^x = pq \frac{1}{(1-q)^2} = \frac{q}{p}.$$

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$$f(x) = \frac{x^{\alpha-1}(1-x)^{\beta-1}}{B(\alpha,\beta)}, \qquad 0 < x < 1,$$

where

$$B(\alpha,\beta) = \frac{\Gamma(\alpha)\Gamma(\beta)}{\Gamma(\alpha+\beta)}$$

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where

$$B(\alpha,\beta) = \frac{\Gamma(\alpha)\Gamma(\beta)}{\Gamma(\alpha+\beta)}$$

is the Beta function. We see that in our case, $\alpha = \beta = 2$.

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Ok, that was too easy. Clearly, we can take the standard uniform.

# Acceptance-rejection method: Example

How can we use use acceptance-rejection to draw from $f$?

We need a density $g$ on $(0, 1)$ we know to draw from.

You get three guesses . . .

Ok, that was too easy. Clearly, we can take the standard uniform.

What about $c$? Well, for $0 < x < 1$

$$\frac{f(x)}{g(x)} = \frac{6x(1-x)}{1} = 6x(1-x) \leq 6$$

so we could take $c = 6$, and accept if

$$\frac{f(y)}{cg(y)} = \frac{6y(1-y)}{6} = y(1-y) > u.$$

# Acceptance-rejection method: Example

Let us write an acceptance-rejection sampler for $f$ which hard-wires $c = 6$ (not so good) but counts the number of tries (good).

# Acceptance-rejection method: Example

```
R> myrbeta22 <- function(n) {
+     k <- 0
+     j <- 0
+     x <- numeric(n)
+     while(k < n) {
+         u <- runif(1)
+         j <- j + 1
+         y <- runif(1)    # random variate from g
+         if(y * (1 - y) > u) {
+             k <- k + 1
+             x[k] <- y
+         }
+     }
+     list(x = x, num_of_iterations = j)
+ }
```

# Acceptance-rejection method: Example

Then to generate a sample of size $n = 1000$:

```
R> res <- myrbeta22(1000)
R> res$num_of_iterations

[1] 6063
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Of course, using $c = 6$ is really silly!

# Acceptance-rejection method: Example

We need that for $0 < x < 1$,

$$\frac{f(x)}{g(x)} = 6x(1-x) \leq c$$

and

$$\max_{0 \leq x \leq 1} 6x(1-x) = 6x(1-x)|_{x=1/2} = \frac{6}{4} = \frac{3}{2}$$

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So any $c \geq 3/2$ will work, and $c = 3/2$ is “best possible”.

Using the best possible $c$, the average number of iterations/tries would go down to

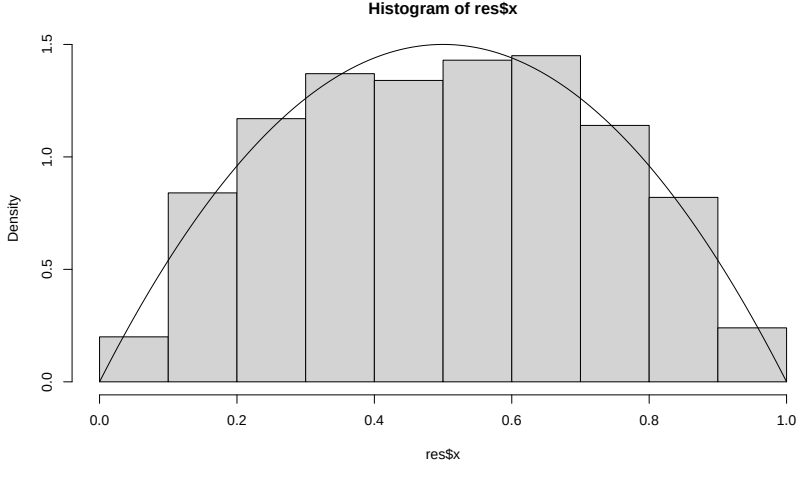
$$n \times \frac{3}{2} = 1000 \times \frac{3}{2} = 1500!$$

# Acceptance-rejection method: Example

To illustrate that our sampler “works”, first using histograms:

```
R> hist(res$x, probability = TRUE)
R> x <- seq(0, 1, by = 0.001)
R> lines(x, dbeta(x, 2, 2))
```

# Acceptance-rejection method: Example



# Acceptance-rejection method: Example

Or (better), using QQ plots:

```
R> qqplot(res$x, qbeta(x, 2, 2))
```