

Statistics 1 Unit 3: Simulation



Kurt Hornik

- Sums and mixtures
- Stochastic processes
- Monte Carlo estimation

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$$(X|Y = i) \sim F_i.$$

I.e., conditional on $Y = i$, X has distribution function F_i .

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This is the *discrete mixture* of F_1, \dots, F_k with mixture probabilities (weights) $\theta_1 = \mathbb{P}(Y = 1), \dots, \theta_k = \mathbb{P}(Y = k)$.

The above just write the marginal distribution of X in terms of the conditional distribution of X given Y and the marginal distribution of Y .

We can do something similar in case Y has a continuous distribution with density g :

$$\mathbb{P}(X \leq x) = \int \mathbb{P}(X \leq x | Y = y) g(y) dy.$$

This write the CDF of X as a *continuous mixture* of the conditional distributions of X given Y , weighted by the marginal density of Y .

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- Then draw X from its conditional distribution given y .

Convolutions

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What is the distribution of $Z = X + Y$?

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Suppose $X \sim F$ and $Y \sim G$ are independent.

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If G has density g , we find that

$$\begin{aligned}\mathbb{P}(X + Y \leq z) &= \int \mathbb{P}(X + Y \leq z | Y = y) g(y) dy \\ &= \int \mathbb{P}(X \leq z - y | Y = y) g(y) dy \\ &= \int F(z - y) g(y) dy.\end{aligned}$$

If F has density f and everything is fine, the distribution of Z has density

$$\frac{d}{dz} \mathbb{P}(Z \leq z) = \int f(z-y)g(y)dy = \int g(z-x)f(x)dx.$$

This is the *convolution* of the densities f and g .

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In general, the CDF of Z is given by the convolution

$$\int F(z-y)dG(y) = \int G(z-x)dF(x)$$

with these integrals as explained in the probability course.

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(Well, that's what convolutions are.)

Example

Take $X_1 \sim \text{gamma}(2, 2)$ and $X_2 \sim \text{gamma}(2, 4)$ and compare the distribution of the sum to the discrete mixture with weights 1/2.

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E.g., using a sample size of $n = 1000$:

```
R> n <- 1000
R> x1 <- rgamma(n, 2, 2)
R> x2 <- rgamma(n, 2, 4)
R> ## Convolution:
R> s <- x1 + x2
R> ## Mixture:
R> u <- runif(n)
R> g <- (u > 0.5)
R> m <- g * x1 + (1 - g) * x2
```

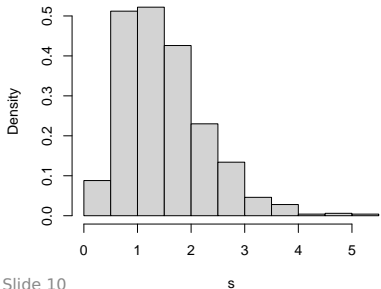
Note how the mixture is done: if $g = 0$, we take x_2 ; otherwise, x_1 .

Example

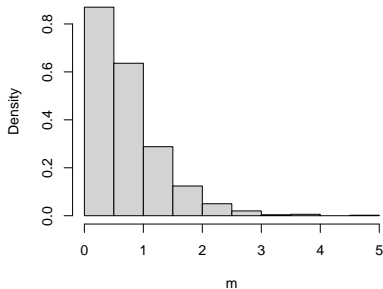
Compare:

```
R> op <- par(mfcol = c(1, 2))  
R> hist(s, probability = TRUE)  
R> hist(m, probability = TRUE)  
R> par(op)
```

Histogram of s



Histogram of m



Note 1

Note that mixtures and convolutions are two fundamentally different things!

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Mixtures are weighted sums (actually, means) of CDFs, whereas convolutions relate to the CDFs of independent sums of random variables!

Note 2

Of course, for discrete mixtures, we can always do

$$X = \sum_{i=1}^k I(Y = i)X_i, \quad X_1 \sim F_1, \dots, X_k \sim F_k$$

but that's actually not very efficient (only need to draw that from the F_i where $y = i$).

Note 2

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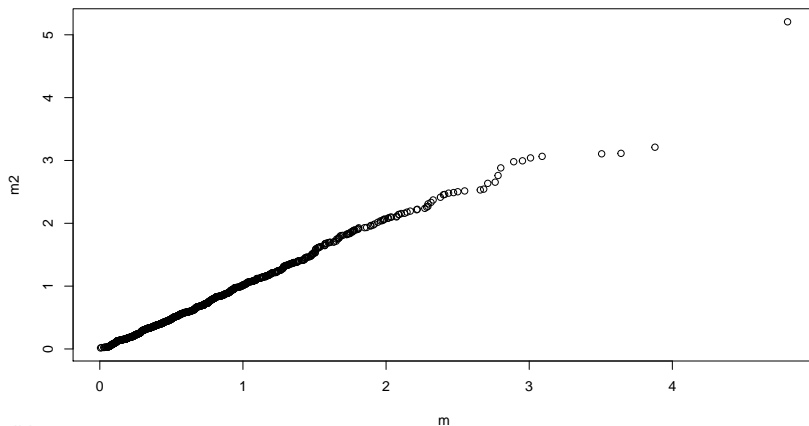
but that's actually not very efficient (only need to draw that from the F_i where $y = i$).

In R, often can conveniently use the fact the the d-p-q-r functions are vectorized. E.g., for our example:

```
R> m2 <- rgamma(n, 2, ifelse(u > 0.5, 2, 4))
```


Note 2

```
R> qqplot(m, m2)
```



Outline

- Sums and mixtures
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Of course, the most important such process is the Wiener process (Brownian motion): but that's not so easy, so will be discussed in later courses.

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Of course, the most important such process is the Wiener process (Brownian motion): but that's not so easy, so will be discussed in later courses.

Here, we discuss the (homogeneous) Poisson process (and in the homeworks, compound Poisson processes).

Renewal processes

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What is the number $N(t)$ of replacements we need to make up to time t ?

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Clearly,

$$N(t) = \begin{cases} 0, & \tau_0 \leq t < \tau_1, \\ 1, & \tau_1 \leq t < \tau_2, \\ \vdots & \vdots \\ n, & \tau_n \leq t < \tau_{n+1}, \\ \vdots & \vdots \end{cases}$$

Equivalently,

$$N(t) = \sum_n I(\tau_n \leq t)$$

($N(t)$ is the number of replacements up to t), and

$$N(t) \geq n \Leftrightarrow \tau_n \leq t$$

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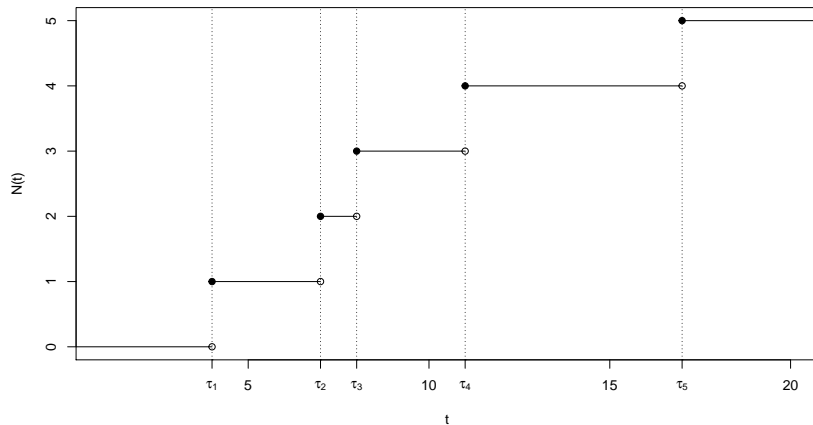
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(there were at least n replacements up to t if and only if the time of replacement n is not after t).

If the ρ_i are i.i.d., we call the discrete-time sequence $(\tau_n, n = 0, 1, \dots)$ or equivalently, the continuous-time process $(N(t), t \geq 0)$ a *renewal process*.

Renewal processes

Graphical illustration:



Renewal processes

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Write $\tau_0 = 0$, and $\rho_n = \tau_n - \tau_{n-1}$ for the time between event $n - 1$ and event n .

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Consider a sequence of events, with event n at time τ_n .

Write $\tau_0 = 0$, and $\rho_n = \tau_n - \tau_{n-1}$ for the time between event $n - 1$ and event n .

Then if the (ρ_n) are i.i.d., the $(\tau_n, n = 0, 1, \dots)$ or the equivalent (event) counting process $(N(t) = \sum_n I(\tau_n \leq t), t \geq 0)$ is a renewal process.

Poisson process

As a special case, if the (ρ_n) are i.i.d. exponentially distributed with rate parameter λ , (τ_n) or $(N(t))$ is a *Poisson process* with rate parameter λ .

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One can show: if λ is the rate parameter of the ρ_n , then

- The number of events/points in a set is Poisson with rate equal to λ times the size of the set.

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One can show: if λ is the rate parameter of the ρ_n , then

- The number of events/points in a set is Poisson with rate equal to λ times the size of the set.
- The numbers of events/points in non-overlapping sets are independent of each other.

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In particular,

$$N(t) \sim \text{Poisson}(\lambda t).$$

Simulating a Poisson process A

Suppose we want to simulate the (times of the) first n events of a Poisson process with rate λ .

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Suppose we want to simulate the (times of the) first n events of a Poisson process with rate λ .

This is easy: we need to simulate i.i.d. $\rho_i \sim \text{exponential}(\lambda)$, and then compute the cumulative sums of these:

```
R> rppA <- function(n, lambda) {  
+   cumsum(rexp(n, lambda))  
+ }  
R> (x <- rppA(20, 1.5))
```

```
[1] 0.267819  1.368932  1.630125  1.957936  2.382470  2.546440  
[7] 3.864321  4.121348  5.719247  5.822406  6.742708  6.866921  
[13] 6.978267  7.298553  7.677173  8.026610  9.159534  9.693273  
[19] 11.488227 11.865750
```

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Well, we already know that $N(t) \sim \text{Poisson}(\lambda t)$.

One can show: given $N(t) = n$, the points τ_1, \dots, τ_n are distributed as an ordered sample of size n from the uniform distribution on $[0, t]$!

Simulating a Poisson process B

Thus, we can do:

```
R> rppB <- function(t, lambda) {  
+   sort(runif(rpois(1, t * lambda), max = t))  
+ }
```

E.g.,

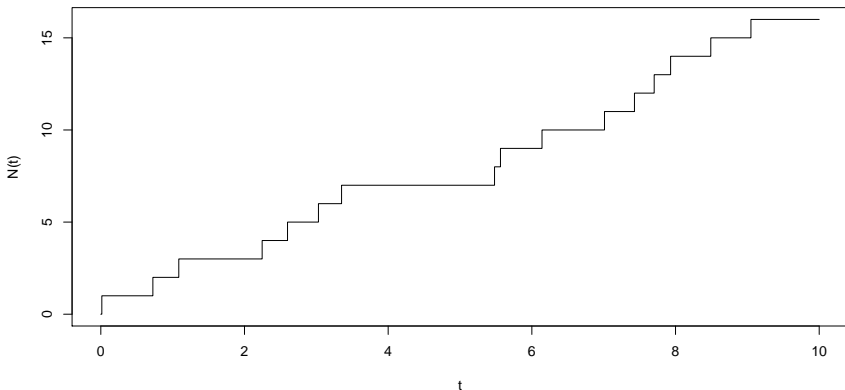
```
R> (x <- rppB(10, 1.5))
```

```
[1] 0.01409716 0.72473996 1.08543110 2.24573281 2.59902724 3.02953019  
[7] 3.35133575 5.48057882 5.56310538 6.14135012 7.01132067 7.42835590  
[13] 7.70294162 7.93157549 8.49079620 9.04964288
```


Simulating a Poisson process B

To visualize, simple variant:

```
R> plot(c(0, x, 10), c(0, seq_along(x), length(x)),  
+      type = "s", xlab = "t", ylab = "N(t)")
```



- Sums and mixtures
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Basic idea

Suppose we want to (approximately) compute an integral of the form

$$\theta = \int g(x)f(x) dx$$

where f is a density function.

Clearly, if $X \sim f$,

$$\mathbb{E}(g(X)) = \int g(x)f(x) dx = \theta$$

and we know from the Law of Large numbers that if n is large and X_1, \dots, X_n are drawn i.i.d. from f ,

$$\frac{1}{n} \sum_{i=1}^n g(X_i) \approx \mathbb{E}(g(X)) = \theta.$$

MC estimation

This suggests we could estimate θ via the following Monte Carlo method:

- Draw an i.i.d. sample x_1, \dots, x_n from f .

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This suggests we could estimate θ via the following Monte Carlo method:

- Draw an i.i.d. sample x_1, \dots, x_n from f .
- Approximate θ by

$$\hat{\theta} = \frac{1}{n} \sum_{i=1}^n g(x_i).$$

MC estimation

How well can this work?

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If X_1, \dots, X_n are i.i.d. from f ,

$$\mathbb{E}(\hat{\theta}) = \mathbb{E}\left(\frac{1}{n} \sum_{i=1}^n g(X_i)\right) = \frac{1}{n} \sum_{i=1}^n \mathbb{E}(g(X_i)) = \theta$$

and (using independence!),

$$\text{var}(\hat{\theta}) = \text{var}\left(\frac{1}{n} \sum_{i=1}^n g(X_i)\right) = \frac{1}{n^2} \sum_{i=1}^n \text{var}(g(X_i)) = \frac{\text{var}(g(X))}{n}.$$

MC estimation

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So to improve the precision by a factor of 10, we need to increase the sample size by a factor of 100!

Of course, we do not know $\text{sd}(g(X))$, but we can estimate it from the MC sample (using the sample sd). This gives the estimated precision

$$\widehat{\text{sd}}(\hat{\theta}) = \frac{\text{sd}(g(x_1), \dots, g(x_n))}{\sqrt{n}}.$$

Example 1

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via MC estimation. (Of course, we know that $\theta = 1 - e^{-1}$.)

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for some density f .

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If we take $g(x) = e^{-x}$, we get $f(x) = 1$ for $0 < x < 1$. I.e., we need to sample from the standard uniform!

Example 1

We can thus do

```
R> n <- 1234  
R> x <- runif(n)  
R> theta_hat <- mean(exp(-x))  
R> c(theta_hat, 1 - exp(-1))
```

```
[1] 0.6306469 0.6321206
```

and estimate the standard error as

```
R> sd(exp(-x)) / sqrt(n)
```

```
[1] 0.005215123
```

Example 1

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We could also write

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Now $g(x) = I_{(0,1)}(x)$ and f is the density of the standard exponential distribution!

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Which approach do you expect to work better?

Example 1

E.g.,

```
R> x <- rexp(n)
R> theta_hat <- mean(x <= 1)
R> c(theta_hat, 1 - exp(-1))
```

```
[1] 0.6345219 0.6321206
```

with an estimated standard error of

```
R> sd(x <= 1) / sqrt(n)
```

```
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This seems to be much worse!

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- For a given θ , there may be several ways to write it as $\theta = \mathbb{E}(g(X))$, $X \sim f$.
- Better MC estimates have smaller standard errors $\text{sd}(g(X))$, $X \sim f$.

Importance sampling

Equivalently, suppose we want to compute/approximate

$$\theta = \int g(x) dx.$$

For arbitrary f , we can do

$$\theta = \int \frac{g(x)}{f(x)} f(x) dx$$

and hence estimate θ via

$$\hat{\theta} = \frac{1}{n} \sum_{i=1}^n \frac{g(x_i)}{f(x_i)}, \quad x_1, \dots, x_n \text{ i.i.d. } \sim f.$$

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By suitably choosing f , we can reduce the variance/sd of the MC estimate: *importance sampling*.

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What is the best f we can find?

Need to choose f to minimize

$$\begin{aligned} \text{var}\left(\frac{g(X)}{f(X)}\right) &= \int \left(\frac{g(x)}{f(x)} - \theta\right)^2 f(x) dx \\ &= \int \left(\frac{g(x)^2}{f(x)} - 2\theta g(x) + \theta^2 f(x)\right) dx \\ &= \int \frac{g(x)^2}{f(x)} dx - \theta^2. \end{aligned}$$

Importance sampling

Write

$$I = \int |g(x)| dx, \quad g_0(x) = |g(x)|/I.$$

Then $\theta_0 = \int g_0(x) dx = 1$,

$$\int \frac{g(x)^2}{f(x)} dx = \int \frac{(g_0(x) \cdot I)^2}{f(x)} dx = I^2 \int \frac{g_0(x)^2}{f(x)} dx.$$

and from the above computation with g_0 instead of g ,

$$\int \frac{g_0(x)^2}{f(x)} dx = 1 + \int \left(\frac{g_0(x)}{f(x)} - 1 \right)^2 f(x) dx.$$

Importance sampling

Clearly,

$$\int \left(\frac{g_0(x)}{f(x)} - 1 \right)^2 f(x) dx$$

is minimal for $f = g_0$, and hence the same is true for

$$\int \frac{g(x)^2}{f(x)} dx.$$

Importance sampling

We have thus proved: optimal variance reduction in importance sample is achieved for

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(Provided of course that $\int |g(x)| dx < \infty$.)

Example 2

For $x > 0$, compute (approximate)

$$\Phi(x) = \int_{-\infty}^x \frac{1}{\sqrt{2\pi}} e^{-t^2/2} dt = \frac{\theta}{\sqrt{2\pi}} + \frac{1}{2}, \quad \theta = \int_0^x e^{-t^2/2} dt$$

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The obvious idea is using $g(t) = xe^{-t^2/2}$ and f uniform on $(0, x)$.

Alternatively, substituting $y = t/x$,

$$\theta = \int_0^x e^{-t^2/2} dt = \int_0^1 xe^{-(xy)^2/2} dy.$$

So we could also draw from the standard uniform, and use the same sample to do MC estimation for several x !

Example 2

A possible implementation of this idea:

```
R> mypnorm <- function(x, n = 10000) {  
+   u <- runif(n)  
+   p <- numeric(length(x))  
+   for(i in seq_along(x)) {  
+     g <- x[i] * exp(-(u * x[i])^2 / 2)  
+     p[i] <- mean(g) / sqrt(2 * pi) + 0.5  
+   }  
+   p  
+ }
```

Example 2

This gives e.g.

```
R> x <- seq(.1, 2.5, length.out = 10)
```

```
R> (p <- mypnorm(x))
```

```
[1] 0.5398272 0.6430338 0.7365815 0.8155038 0.8774419 0.9226071  
[7] 0.9531367 0.9721733 0.9830047 0.9884799
```

```
R> p - pnorm(x)
```

```
[1] -6.672781e-07 -3.231938e-05 -1.605042e-04 -4.360894e-04  
[5] -8.856296e-04 -1.511640e-03 -2.297791e-03 -3.215848e-03  
[9] -4.231838e-03 -5.310464e-03
```

Antithetic variables

As everyone knows,

$$\text{var}(X + Y) = \text{var}(X) + \text{var}(Y) + 2\text{cov}(X, Y)$$

So maybe we could reduce the variance of MC estimates even more if we used pairs of negatively correlated random variables from the same distribution?

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Well, yes, but how could we get such pairs?

Remember the quantile transform method $X_i = Q(U_i)$. We could also use $Y_i = Q(1 - U_i)$, and U_i and $1 - U_i$ are negatively correlated.

Maybe the same is true for X_i and Y_i ?

Antithetic variables

One can show: if $g = g(x_1, \dots, x_k)$ is monotone, then

$$g(Q(U_1), \dots, Q(U_k)), \quad g(Q(1 - U_1), \dots, Q(1 - U_k))$$

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For MC estimation: if we can draw from f via its quantile function, generate $n/2$ replicates each X_i and Y_i using the same U_{i1}, \dots, U_{ik} , and use

$$\hat{\theta} = \frac{2}{n} \sum_{i=1}^{n/2} \frac{X_i + Y_i}{2}.$$

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$$\hat{\theta} = \frac{2}{n} \sum_{i=1}^{n/2} \frac{X_i + Y_i}{2}.$$

This requires $nk/2$ instead of nk uniform variates, and reduces estimation variance by using antithetic variables.

Antithetic variables

To illustrate, continue MC estimation of $\Phi(x)$.

We had

$$\theta = \mathbb{E}_U(xe^{-(xU)^2/2}),$$

for U standard uniform.

When restricting to $x > 0$, $g(u) = xe^{-(ux)^2/2}$ is monotone.

Hence, we can use

$$X_i = xe^{-(xU_i)^2/2}, \quad Y_i = xe^{-(x(1-U_i))^2/2}.$$

Antithetic variables

We provide a function which has a flag for toggling the use of antithetic sampling

```
R> mypnorm2 <- function(x, n = 10000, antithetic = TRUE) {  
+   u <- runif(n / 2)  
+   v <- if(!antithetic) runif(n / 2) else 1 - u  
+   u <- c(u, v)  
+   p <- numeric(length(x))  
+   for(i in seq_along(x)) {  
+     g <- x[i] * exp(-(u * x[i])^2 / 2)  
+     p[i] <- mean(g) / sqrt(2 * pi) + 0.5  
+   }  
+   p  
+ }
```

and perform the following MC experiment:

Antithetic variables

```

R> x <- seq(.1, 2.5, length.out = 10)
R> Phi <- pnorm(x)
R> set.seed(123)
R> system.time(p1 <- mypnorm2(x, antithetic = FALSE))
  
```

```

    user  system elapsed
0.013   0.000   0.013
  
```

```

R> set.seed(123)
R> system.time(p2 <- mypnorm2(x))
  
```

```

    user  system elapsed
0.002   0.000   0.002
  
```

So clearly, the antithetic variant is *faster*. It is also *more precise*:

Antithetic variables

```
R> print(round(cbind(x, Delta1 = p1 - Phi, Delta2 = p2 - Phi), 5))
```

```
      x  Delta1 Delta2
[1,] 0.10000 0.00000 0e+00
[2,] 0.36667 0.00003 0e+00
[3,] 0.63333 0.00016 1e-05
[4,] 0.90000 0.00041 3e-05
[5,] 1.16667 0.00077 4e-05
[6,] 1.43333 0.00119 5e-05
[7,] 1.70000 0.00158 5e-05
[8,] 1.96667 0.00190 3e-05
[9,] 2.23333 0.00209 -2e-05
[10,] 2.50000 0.00215 -9e-05
```

Graphically:

Antithetic variables

```
R> plot(p1 - Phi, p2 - Phi)
```

