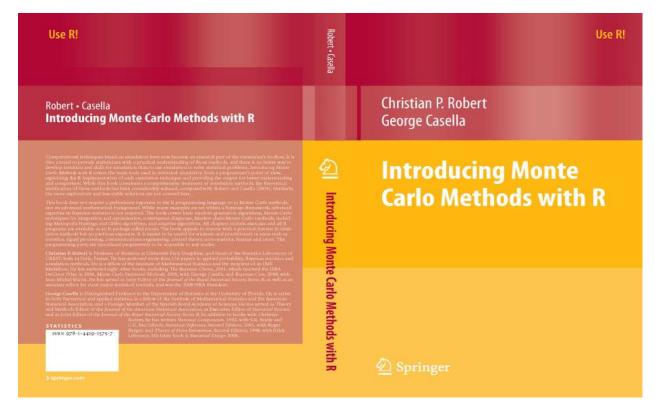
Introducing Monte Carlo Methods with R

Christian P. Robert Université Paris Dauphine xian@ceremade.dauphine.fr George Casella
University of Florida
casella@ufl.edu

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- Introducing Monte Carlo Methods with R, 2009, Springer-Verlag
- Data and R programs for the course available at http://www.stat.ufl.edu/casella/IntroMonte/



Chapter 1: Basic R Programming

"You're missing the big picture," he told her. "A good album should be more than the sum of its parts."

Ian Rankin
Exit Music

This Chapter

- ► We introduce the programming language R
- ▶ Input and output, data structures, and basic programming commands
- ► The material is both crucial and unavoidably sketchy

Basic R Programming Introduction

- ► This is a quick introduction to R
- ▶ There are entire books devoted to R
 - ▶ R Reference Card
 - ▷ available at http://cran.r-project.org/doc/contrib/Short-refcard.pdf
- ► Take Heart!
 - ▶ The syntax of R is simple and logical
 - ▶ The best, and in a sense the only, way to learn R is through trial-and-error
- ► Embedded help commands help() and help.search()
 - ▷ help.start() opens a Web browser linked to the local manual pages

Basic R Programming Why R?

- ► There exist other languages, most (all?) of them faster than R, like Matlab, and even free, like C or Python.
- ► The language combines a sufficiently high power (for an interpreted language) with a very clear syntax both for statistical computation and graphics.
- ▶ R is a flexible language that is *object-oriented* and thus allows the manipulation of complex data structures in a condensed and efficient manner.
- ► Its graphical abilities are also remarkable
 - ▶ Possible interfacing with LaTeXusing the package Sweave.

Basic R Programming Why R ?

- ▶ R offers the additional advantages of being a free and open-source system
 - \triangleright There is even an R newsletter, R-News
 - ▶ Numerous (free) Web-based tutorials and user's manuals
- ▶ It runs on all platforms: Mac, Windows, Linux and Unix
- ► R provides a powerful *interface*
 - Can integrate programs written in other languages
 - ⊳ Such as C, C++, Fortran, Perl, Python, and Java.
- ▶ It is increasingly common to see people who develop new methodology simultaneously producing an R package
- ► Can interface with WinBugs

Basic R Programming Getting started

- ► Type 'demo()' for some demos; demo(image) and demo(graphics)
- ▶ 'help()' for on-line help, or 'help.start()' for an HTML browser interface to help.
- ightharpoonup Type 'q()' to quit R.
- ► Additional packages can be loaded via the library command, as in
 - > library(combinat) # combinatorics utilities
 - > library(datasets) # The R Datasets Package
 - ▶ There exist hundreds of packages available on the Web.
 - > install.package("mcsm")
- ► A library call is required each time R is launched

Basic R Programming R objects

- ▶ R distinguishes between several types of *objects*
 - > scalar, vector, matrix, time series, data frames, functions, or graphics.
 - ⊳ An R object is mostly characterized by a *mode*
 - > The different modes are
 - null (empty object),
 - logical (TRUE or FALSE),
 - numeric (such as 3, 0.14159, or 2+sqrt(3)),
 - complex, (such as 3-2i or complex(1,4,-2)), and
 - character (such as "Blue", "binomial", "male", or "y=a+bx"),
- ▶ The R function **str** applied to any R object will show its structure.

Basic R Programming Interpreted

- ▶ R operates on those types as a regular function would operate on a scalar
- ightharpoonup R is interpreted \Rightarrow Slow
- ► Avoid loops in favor of matrix mainpulations

Basic R Programming – The vector class

> a=c(5,5.6,1,4,-5)	build the object a containing a numeric vector of dimension 5 with elements 5, 5.6, 1, 4, -5
> a[1]	display the first element of a
> b=a[2:4]	build the numeric vector b of dimension 3
> d=a[c(1,3,5)]	with elements 5.6, 1, 4 build the numeric vector d of dimension 3
> 2*a	with elements 5, 1, -5 multiply each element of a by 2
> b%%3	and display the result provides each element of b modulo 3

Basic R Programming More vector class

> e=3/d build the numeric vector e of dimension 3

and elements 3/5, 3, -3/5

> log(d*e) multiply the vectors d and e term by term

and transform each term into its natural logarithm

> sum(d) calculate the sum of d

> length(d) display the length of d

Basic R Programming Even more **vector** class

> t(d) > t(d)*e	transpose d, the result is a row vector elementwise product between two vectors
> t(d)%*%e	with identical lengths matrix product between two vectors
> g=c(sqrt(2),log(10))	with identical lengths build the numeric vector g of dimension 2
> e[d==5]	and elements $\sqrt{2}$, $\log(10)$ build the subvector of e that contains the
> a[-3]	components e[i] such that d[i]=5 create the subvector of a that contains
> is.vector(d)	all components of a but the third. display the logical expression TRUE if
	a vector and FALSE else

Basic R Programming Comments on the **vector** class

- ► The ability to apply scalar functions to vectors: Major Advantage of R.
 - \triangleright > lgamma(c(3,5,7))
 - \triangleright returns the vector with components (log $\Gamma(3)$, log $\Gamma(5)$, log $\Gamma(7)$).
- ► Functions that are specially designed for vectors include

sample, permn, order, sort, and rank

- ▶ All manipulate the order in which the components of the vector occur.
- ▶ permn is part of the combinat library
- ▶ The components of a vector can also be identified by names.
 - > For a vector x, names(x) is a vector of characters of the same length as x

Basic R Programming The matrix, array, and factor classes

- ▶ The matrix class provides the R representation of matrices.
- ► A typical entry is
 - > x=matrix(vec,nrow=n,ncol=p)
 - \triangleright Creates an $n \times p$ matrix whose elements are of the dimension np vector **vec**
- ► Some manipulations on matrices
 - ▶ The standard matrix product is denoted by **%*****%**,
 - ⊳ while * represents the term-by-term product.
 - ▶ diag gives the vector of the diagonal elements of a matrix
 - > crossprod replaces the product t(x)%*%y on either vectors or matrices > crossprod(x,y) more efficient
 - > apply is easy to use for functions operating on matrices by row or column

Basic R Programming Some matrix commands

```
> x1=matrix(1:20,nrow=5)
                                         build the numeric matrix x1 of dimension
                                         5 \times 4 with first row 1, 6, 11, 16
                                         build the numeric matrix x2 of dimension
> x2=matrix(1:20,nrow=5,byrow=T)
                                         5 \times 4 with first row 1, 2, 3, 4
> a=x1%*%t(x2)
                                         matrix product
> c = x1 * x2
                                         term-by-term product between x1 and x2
> dim(x1)
                                         display the dimensions of x1
                                         select the second column of b
> b[,2]
> b[c(3,4),]
                                         select the third and fourth rows of b
> b[-2,]
                                         delete the second row of b
> rbind(x1,x2)
                                         vertical merging of x1 and x2rbind(*)rbind
> cbind(x1,x2)
                                         horizontal merging of x1 and x2rbind(*)rbind
                                         calculate the sum of each row of x1
> apply(x1,1,sum)
                                         turn the vector 1:10 into a 10 \times 1 matrix
> as.matrix(1:10)
```

▶ Lots of other commands that we will see throughout the course

Basic R Programming The list and data.frame classes The Last One

- ► A list is a collection of arbitrary objects known as its *components*
 - > li=list(num=1:5,y="color",a=T) create a list with three arguments
- ► The last class we briefly mention is the data frame
 - ▶ A list whose elements are possibly made of differing modes and attributes
 - ⊳ But have the same length

```
> v1=sample(1:12,30,rep=T) simulate 30 independent uniform {1,2,...,12}
> v2=sample(LETTERS[1:10],30,rep=T) simulate 30 independent uniform {a,b,...,j}
> v3=runif(30) simulate 30 independent uniform [0,1]
> v4=rnorm(30) simulate 30 independent uniform [0,1]
> v4=rnorm(30) simulate 30 independent uniform [0,1]
```

► R code

Probability distributions in ${\tt R}$

ightharpoonup R , or the web, has about all probability distributions

► Prefixes: p, d,q, r

Distribution	Core	Parameters	Default Values
Beta	beta	shape1, shape2	
Binomial	binom	size, prob	
Cauchy	cauchy	location, scale	0, 1
Chi-square	chisq	df	
Exponential	exp	1/mean	1
F	f	df1, df2	
Gamma	gamma	shape,1/scale	NA, 1
Geometric	geom	prob	
Hypergeometric	hyper	m, n, k	
Log-normal	lnorm	mean, sd	0, 1
Logistic	logis	location, scale	0, 1
Normal	norm	mean, sd	0, 1
Poisson	pois	lambda	
Student	t	df	
Uniform	unif	min, max	0, 1
Weibull	weibull	shape	

Basic and not-so-basic statistics t-test

► Testing equality of two means

```
> x=rnorm(25) #produces a N(0,1) sample of size 25
> t.test(x)
```

One Sample t-test

```
data: x
t = -0.8168, df = 24, p-value = 0.4220
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
  -0.4915103   0.2127705
sample estimates:
  mean of x
-0.1393699
```

Basic and not-so-basic statistics Correlation

► Correlation

```
> attach(faithful) #resident dataset
```

> cor.test(faithful[,1],faithful[,2])

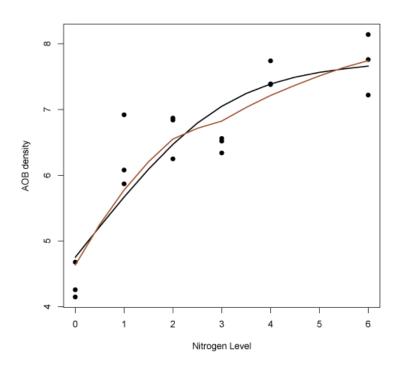
Pearson's product-moment correlation

```
data: faithful[, 1] and faithful[, 2]
t = 34.089, df = 270, p-value < 2.2e-16
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
    0.8756964 0.9210652
sample estimates:
    cor
0.9008112</pre>
```

► R code

Basic and not-so-basic statistics Splines

- \blacktriangleright Nonparametric regression with **loess** function or using natural splines
- ► Relationship between nitrogen level in soil and abundance of a bacteria AOB



- ► Natural spline fit (dark)

 > With ns=2 (linear model)
- ► Loess fit (brown) with span=1.25
- ► R code

Basic and not-so-basic statistics Generalized Linear Models

► Fitting a binomial (logistic) glm to the probability of suffering from diabetes for a woman within the Pima Indian population

```
> glm(formula = type ~ bmi + age, family = "binomial", data = Pima.tr)
```

Deviance Residuals:

```
10 Median
                           3Q
   Min
                                   Max
-1.7935 -0.8368 -0.5033 1.0211
                                2.2531
```

Coefficients:

```
Estimate Std. Error z value Pr(>|z|)
(Intercept) -6.49870 1.17459 -5.533 3.15e-08 ***
         bmi
         age
Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' '1
(Dispersion parameter for binomial family taken to be 1)
  Null deviance: 256.41 on 199 degrees of freedom
Residual deviance: 215.93 on 197 degrees of freedom
AIC: 221.93
```

Number of Fisher Scoring iterations: 4

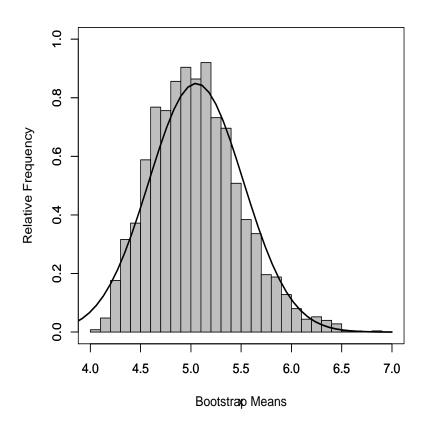
Basic and not-so-basic statistics Generalized Linear Models – Comments

- ► Concluding with the significance both of the body mass index bmi and the age
- ▶ Other generalized linear models can be defined by using a different family value
 - > glm(y ~x, family=quasi(var="mu^2", link="log"))
 - ▶ Quasi-Likelihood also
- ► Many many other procedures
 - ▶ Time series, anova,...
- ▶ One last one

Basic and not-so-basic statistics Bootstrap

- ▶ The bootstrap procedure uses the empirical distribution as a substitute for the true distribution to construct variance estimates and confidence intervals.
 - \triangleright A sample X_1, \ldots, X_n is resampled with replacement
 - \triangleright The empirical distribution has a finite but large support made of n^n points
- \blacktriangleright For example, with data y, we can create a bootstrap sample y^* using the code
 - > ystar=sample(y,replace=T)
 - ▶ For each resample, we can calculate a mean, variance, etc

Basic and not-so-basic statistics Simple illustration of bootstrap



- ► A histogram of 2500 bootstrap means
- ► Along with the normal approximation
- ► Bootstrap shows some skewness
- ► R code

Basic and not-so-basic statistics Bootstrapping Regression

- ► The bootstrap is not a panacea
 - ▶ Not always clear which quantity should be bootstrapped
 - ▶ In regression, bootstrapping the residuals is preferred
- ► Linear regression

$$Y_{ij} = \alpha + \beta x_i + \varepsilon_{ij},$$

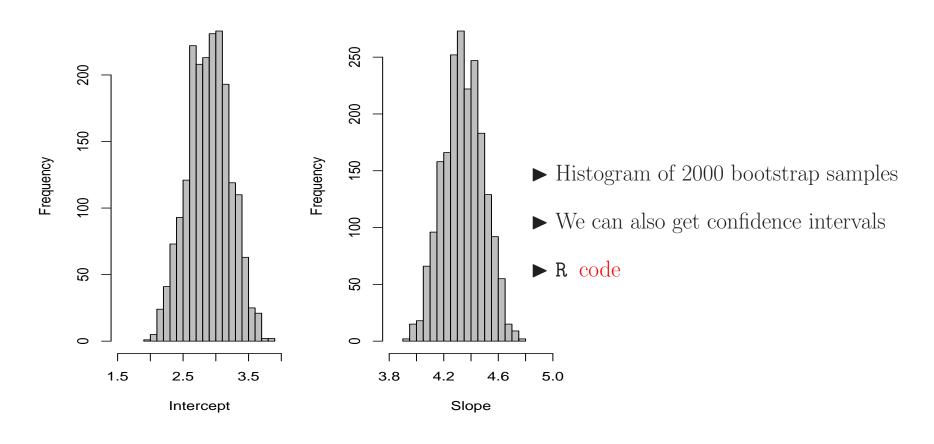
 α and β are the unknown intercept and slope, ε_{ij} are the iid normal errors

▶ The residuals from the least squares fit are given by

$$\hat{\varepsilon}_{ij} = y_{ij} - \hat{\alpha} - \hat{\beta}x_i,$$

- ▶ We bootstrap the residuals
- \triangleright Produce a new sample $(\hat{\varepsilon}_{ij}^*)_{ij}$ by resampling from the $\hat{\varepsilon}_{ij}$'s
- \triangleright The bootstrap samples are then $y_{ij}^* = y_{ij} + \hat{\varepsilon}_{ij}^*$

Basic and not-so-basic statistics Bootstrapping Regression – 2



Basic R Programming Some Other Stuff

- ► Graphical facilities
 - ⊳ Can do a lot; see plot and par
- ► Writing new R functions
 - \triangleright h=function(x)(sin(x)^2+cos(x)^3)^(3/2)
 - ▶ We will do this a lot
- ► Input and output in R
 - ▷ write.table, read.table, scan
- ▶ Don't forget the mcsm package

Chapter 2: Random Variable Generation

"It has long been an axiom of mine that the little things are infinitely the most important."

Arthur Conan Doyle

A Case of Identity

This Chapter

- ► We present practical techniques that can produce random variables
- ► From both standard and nonstandard distributions
- ► First: Transformation methods
- ► Next: Indirect Methods Accept—Reject

Introduction

- ► Monte Carlo methods rely on
 - ▶ The possibility of producing a supposedly endless flow of random variables
 - > For well-known or new distributions.
- ► Such a simulation is, in turn,
 - \triangleright Based on the production of uniform random variables on the interval (0,1).
- ▶ We are not concerned with the details of producing uniform random variables
- ▶ We assume the existence of such a sequence

Introduction Using the R Generators

R has a large number of functions that will generate the standard random variables

- > rgamma(3,2.5,4.5) produces three independent generations from a $\mathcal{G}(5/2,9/2)$ distribution
- ► It is therefore,
 - ➤ Counter-productive
 - ▶ Inefficient
 - ▶ And even dangerous,
- ➤ To generate from those standard distributions
- ► If it is built into R , use it
- ▶ But....we will practice on these.
- ▶ The principles are essential to deal with distributions that are not built into R.

Uniform Simulation

- ▶ The uniform generator in R is the function runif
- ▶ The only required entry is the number of values to be generated.
- ► The other optional parameters are min and max, with R code
- > runif(100, min=2, max=5)

will produce 100 random variables $\mathcal{U}(2,5)$.

Uniform Simulation Checking the Generator

- ▶ A quick check on the properties of this uniform generator is to
- \triangleright Look at a histogram of the X_i 's,
- \triangleright Plot the pairs (X_i, X_{i+1})
- ▶ Look at the estimate autocorrelation function
- ► Look at the R code

```
> Nsim=10^4 #:
> x=runif(Nsim)
```

> x1=x[-Nsim]

> x2=x[-1]

> par(mfrow=c(1,3))

> hist(x)

> plot(x1,x2)

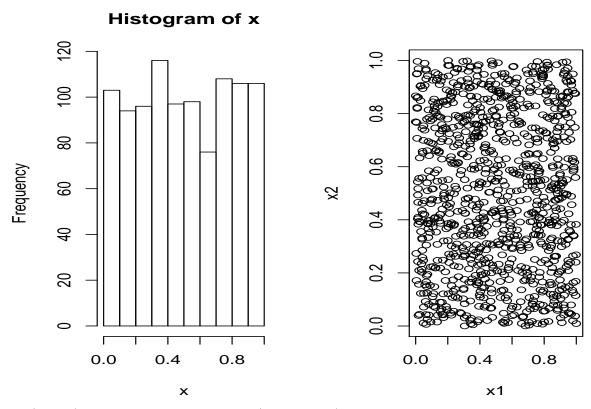
> acf(x)

#number of random numbers

#vectors to plot

#adjacent pairs

Uniform Simulation Plots from the Generator



▶ Histogram (*left*), pairwise plot (*center*), and estimated autocorrelation function (*right*) of a sequence of 10^4 uniform random numbers generated by runif.

Uniform Simulation Some Comments

- ▶ Remember: runif does not involve randomness per se.
- ▶ It is a deterministic sequence based on a random starting point.
- ► The R function set.seed can produce the same sequence.

```
> set.seed(1)
> runif(5)
[1] 0.2655087 0.3721239 0.5728534 0.9082078 0.2016819
> set.seed(1)
```

- > runif(5)
- [1] 0.2655087 0.3721239 0.5728534 0.9082078 0.2016819
- > set.seed(2)
- > runif(5)
- [1] 0.0693609 0.8177752 0.9426217 0.2693818 0.1693481
- ► Setting the seed determines all the subsequent values

The Inverse Transform

- ► The Probability Integral Transform
 - ▶ Allows us to transform a uniform into any random variable
- \blacktriangleright For example, if X has density f and cdf F, then we have the relation

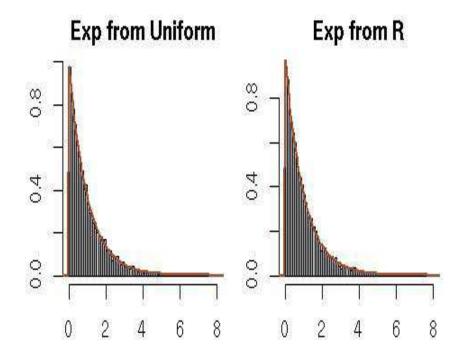
$$F(x) = \int_{-\infty}^{x} f(t) \, \mathrm{d}t,$$

and we set U = F(X) and solve for X

- ► Example 2.1
- \triangleright If $X \sim \mathcal{E}xp(1)$, then $F(x) = 1 e^{-x}$
- \triangleright Solving for x in $u = 1 e^{-x}$ gives $x = -\log(1 u)$

Generating Exponentials

```
> Nsim=10^4  #number of random variables
> U=runif(Nsim)
> X=-log(U)  #transforms of uniforms
> Y=rexp(Nsim)  #exponentials from R
> par(mfrow=c(1,2))  #plots
> hist(X,freq=F,main="Exp from Uniform")
> hist(Y,freq=F,main="Exp from R")
```



- ► Histograms of exponential random variables
 - \triangleright Inverse transform (right)
 - ▷ R command rexp (left)
 - $\triangleright \mathcal{E}xp(1)$ density on top

Generating Other Random Variables From Uniforms

- ▶ This method is useful for other probability distributions
 - > Ones obtained as a transformation of uniform random variables

- ► Logistic pdf: $f(x) = \frac{1}{\beta} \frac{e^{-(x-\mu)/\beta}}{[1+e^{-(x-\mu)/\beta}]^2}$, cdf: $F(x) = \frac{1}{1+e^{-(x-\mu)/\beta}}$.
- ► Cauchy pdf: $f(x) = \frac{1}{\pi\sigma} \frac{1}{1 + \left(\frac{x-\mu}{\sigma}\right)^2}$, cdf: $F(x) = \frac{1}{2} + \frac{1}{\pi} \arctan((x-\mu)/\sigma)$.

General Transformation Methods

- \blacktriangleright When a density f is linked in a relatively simple way
 - ▶ To another distribution easy to simulate
 - \triangleright This relationship can be use to construct an algorithm to simulate from f
- ▶ If the X_i 's are iid $\mathcal{E}xp(1)$ random variables,
 - > Three standard distributions can be derived as

$$Y = 2 \sum_{j=1}^{\nu} X_{j} \sim \chi_{2\nu}^{2}, \quad \nu \in \mathbb{N}^{*},$$

$$Y = \beta \sum_{j=1}^{a} X_{j} \sim \mathcal{G}(a, \beta), \quad a \in \mathbb{N}^{*},$$

$$Y = \frac{\sum_{j=1}^{a} X_{j}}{\sum_{j=1}^{a+b} X_{j}} \sim \mathcal{B}e(a, b), \quad a, b \in \mathbb{N}^{*},$$

where $\mathbb{N}^* = \{1, 2, \ldots\}.$

General Transformation Methods χ_6^2 Random Variables

▶ For example, to generate χ_6^2 random variables, we could use the R code

```
> U=runif(3*10^4)
> U=matrix(data=U,nrow=3) #matrix for sums
> X=-log(U) #uniform to exponential
> X=2* apply(X,2,sum) #sum up to get chi squares
```

- ▶ Not nearly as efficient as calling rchisq, as can be checked by the R code
- > system.time(test1());system.time(test2())
 user system elapsed
 0.104 0.000 0.107
 user system elapsed
 0.004 0.000 0.004
- ▶ test1 corresponds to the R code above
- ▶ test2 corresponds to X=rchisq(10^4,df=6)

General Transformation Methods Comments

- ▶ These transformations are quite simple and will be used in our illustrations.
- ► However, there are limits to their usefulness,
- ▶ No odd degrees of freedom
- ▶ No normals
- ▶ For any specific distribution, efficient algorithms have been developed.
- ▶ Thus, if R has a distribution built in, it is almost always worth using

General Transformation Methods A Normal Generator

- ▶ Box–Muller algorithm two normals from two uniforms
- ▶ If U_1 and U_2 are iid $\mathcal{U}_{[0,1]}$
- ▶ The variables X_1 and X_2

$$X_1 = \sqrt{-2\log(U_1)} \cos(2\pi U_2), \qquad X_2 = \sqrt{-2\log(U_1)} \sin(2\pi U_2),$$

- \blacktriangleright Are iid $\mathcal{N}(0,1)$ by virtue of a change of variable argument.
- ▶ The Box–Muller algorithm is exact, not a crude CLT-based approximation
- ightharpoonup Note that this is not the generator implemented in R
 - ▶ It uses the probability inverse transform
 - ▶ With a very accurate representation of the normal cdf

General Transformation Methods Multivariate Normals

- ► Can simulate a multivariate normal variable using univariate normals
 - \triangleright Cholesky decomposition of $\Sigma = AA'$

$$\triangleright Y \sim \mathcal{N}_p(0, I) \Rightarrow AY \sim \mathcal{N}_p(0, \Sigma)$$

- ► There is an R package that replicates those steps, called rmnorm
- ▶ In the mnormt library
- > Can also calculate the probability of hypercubes with the function sadmvn
- > sadmvn(low=c(1,2,3),upp=c(10,11,12),mean=rep(0,3),var=B)
- [1] 9.012408e-05
- attr(,"error")
- [1] 1.729111e-08
- ▶ B is a positive-definite matrix
- ➤ This is quite useful since the analytic derivation of this probability is almost always impossible.

Discrete Distributions

- ➤ To generate discrete random variables we have an "all-purpose" algorithm.
- ▶ Based on the inverse transform principle
- ▶ To generate $X \sim P_{\theta}$, where P_{θ} is supported by the integers,
 - ▶ We can calculate—the probabilities
 - ▶ Once for all, assuming we can store them

$$p_0 = P_{\theta}(X \le 0), \quad p_1 = P_{\theta}(X \le 1), \quad p_2 = P_{\theta}(X \le 2), \quad \dots,$$

 \triangleright And then generate $U \sim \mathcal{U}_{[0,1]}$ and take

$$X = k \text{ if } p_{k-1} < U < p_k.$$

Discrete Distributions Binomial

 \blacktriangleright Example To generate $X \sim \mathcal{B}in(10, .3)$

▶ The probability values are obtained by pbinom(k,10,.3)

$$p_0 = 0.028, \quad p_1 = 0.149, \quad p_2 = 0.382, \dots, p_{10} = 1,$$

 \triangleright And to generate $X \sim \mathcal{P}(7)$, take

$$p_0 = 0.0009, \quad p_1 = 0.0073, \quad p_2 = 0.0296, \dots,$$

- \triangleright Stopping the sequence when it reaches 1 with a given number of decimals. \triangleright For instance, $p_{20} = 0.999985$.
- ► Check the R code

Discrete Distributions Comments

- ► Specific algorithms are usually more efficient
- ▶ Improvement can come from a judicious choice of the probabilities first computed.
- ▶ For example, if we want to generate from a Poisson with $\lambda = 100$
 - ▶ The algorithm above is woefully inefficient
 - \triangleright We expect most of our observations to be in the interval $\lambda \pm 3\sqrt{\lambda}$
 - \triangleright For $\lambda = 100$ this interval is (70, 130)
 - ▶ Thus, starting at 0 is quite wasteful
- ► A first remedy is to "ignore" what is outside of a highly likely interval
 - ▷ In the current example P(X < 70) + P(X > 130) = 0.00268.

Discrete Distributions Poisson R Code

- ▶ R code that can be used to generate Poisson random variables for large values of lambda.
- ▶ The sequence t contains the integer values in the range around the mean.

```
> Nsim=10^4; lambda=100
> spread=3*sqrt(lambda)
> t=round(seq(max(0,lambda-spread),lambda+spread,1))
> prob=ppois(t, lambda)
> X=rep(0,Nsim)
> for (i in 1:Nsim){
+ u=runif(1)
+ X[i]=t[1]+sum(prob<u)-1 }</pre>
```

ightharpoonup The last line of the program checks to see what interval the uniform random variable fell in and assigns the correct Poisson value to X.

Discrete Distributions Comments

- ► Another remedy is to start the cumulative probabilities at the mode of the discrete distribution
- ▶ Then explore neighboring values until the cumulative probability is almost 1.

- ► Specific algorithms exist for almost any distribution and are often quite fast.
- ► So, if R has it, use it.
- ▶ But R does not handle every distribution that we will need,

Mixture Representations

- \blacktriangleright It is sometimes the case that a probability distribution can be naturally represented as a *mixture distribution*
- ► That is, we can write it in the form

$$f(x) = \int_{\mathcal{Y}} g(x|y)p(y) dy$$
 or $f(x) = \sum_{i \in \mathcal{Y}} p_i f_i(x)$,

▶ The mixing distribution can be continuous or discrete.

- \blacktriangleright To generate a random variable X using such a representation,
 - \triangleright we can first generate a variable Y from the mixing distribution
 - \triangleright Then generate X from the selected conditional distribution

Mixture Representations Generating the Mixture

► Continuous

$$f(x) = \int_{\mathcal{Y}} g(x|y)p(y) dy \Rightarrow y \sim p(y) \text{ and } X \sim f(x|y), \text{ then } X \sim f(x)$$

▶ Discrete

$$f(x) = \sum_{i \in \mathcal{Y}} p_i f_i(x) \Rightarrow i \sim p_i \text{ and } X \sim f_i(x), \text{ then } X \sim f(x)$$

► Discrete Normal Mixture R code

$$\triangleright p_1 * N(\mu_1, \sigma_1) + p_2 * N(\mu_2, \sigma_2) + p_3 * N(\mu_3, \sigma_3)$$

Mixture Representations Continuous Mixtures

 \triangleright Student's t density with ν degrees of freedom

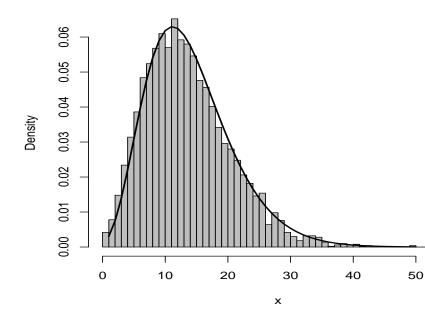
$$X|y \sim \mathcal{N}(0, \nu/y)$$
 and $Y \sim \chi_{\nu}^2$.

- \triangleright Generate from a χ^2_{ν} then from the corresponding normal distribution
- ▷ Obviously, using rt is slightly more efficient

▶ If X is negative binomial $X \sim \mathcal{N}eg(n, p)$

$$\triangleright X|y \sim \mathcal{P}(y)$$
 and $Y \sim \mathcal{G}(n,\beta)$,

▷ R code generates from this mixture



Accept–Reject Methods Introduction

- ▶ There are many distributions where transform methods fail
- ► For these cases, we must turn to *indirect* methods
 - ▶ We generate a candidate random variable
 - ▶ Only accept it subject to passing a test
- ► This class of methods is extremely powerful.
 - ▶ It will allow us to simulate from virtually any distribution.
- ► Accept-Reject Methods
 - \triangleright Only require the functional form of the density f of interest
 - $\triangleright f = \text{target}, g = \text{candidate}$
- \blacktriangleright Where it is simpler to simulate random variables from g

Accept-Reject Methods Accept-Reject Algorithm

- \blacktriangleright The only constraints we impose on this candidate density g
 - $\triangleright f$ and g have compatible supports (i.e., g(x) > 0 when f(x) > 0).
 - \triangleright There is a constant M with $f(x)/g(x) \leq M$ for all x.
- $ightharpoonup X \sim f$ can be simulated as follows.
 - \triangleright Generate $Y \sim g$ and, independently, generate $U \sim \mathcal{U}_{[0,1]}$.
 - \triangleright If $U \leq \frac{1}{M} \frac{f(Y)}{g(Y)}$, set X = Y.
 - \triangleright If the inequality is not satisfied, we then discard Y and U and start again.
- ▶ Note that $M = \sup_x \frac{f(x)}{g(x)}$
- ▶ $P(\text{Accept}) = \frac{1}{M}$, Expected Waiting Time = M

Accept-Reject Algorithm R Implementation

Succinctly, the Accept–Reject Algorithm is

Accept-Reject Method

```
1. Generate Y\sim g, U\sim \mathcal{U}_{[0,1]};
2. Accept X=Y if U\leq f(Y)/Mg(Y);
3. Return to 1 otherwise.
```

ightharpoonup R implementation: If randg generates from g

```
> u=runif(1)*M
> y=randg(1)
> while (u>f(y)/g(y))
{
    u=runif(1)*M
    y=randg(1)
    }
```

ightharpoonup Produces a single generation y from f

Accept—Reject Algorithm Normals from Double Exponentials

- $ightharpoonup \operatorname{Candidate} Y \sim \frac{1}{2} \exp(-|y|)$
- ► Target $X \sim \frac{1}{\sqrt{2\pi}} \exp(-x^2/2)$

$$\frac{\frac{1}{\sqrt{2\pi}}\exp(-y^2/2)}{\frac{1}{2}\exp(-|y|)} \le \frac{2}{\sqrt{2\pi}}\exp(1/2)$$

 \triangleright Maximum at y = 1

- ightharpoonup Accept Y if $U \le \exp(-.5Y^2 + |Y| .5)$
- ► Look at R code

Accept-Reject Algorithm Theory

- ► Why does this method work?
- ► A straightforward probability calculation shows

$$P(Y \le x | \text{Accept}) = P(Y \le x | U \le f(Y) / \{Mg(Y)\}) = P(X \le x)$$

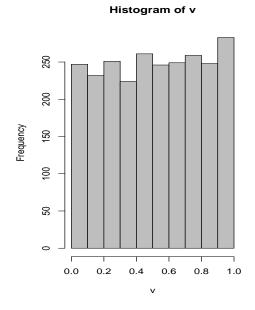
 \triangleright Simulating from g, the output of this algorithm is exactly distributed from f.

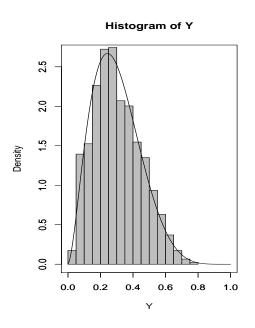
4

- ► The Accept—Reject method is applicable in any dimension
- \blacktriangleright As long as g is a density over the same space as f.
- \blacktriangleright Only need to know f/g up to a constant
- ightharpoonup Only need an upper bound on M

Accept-Reject Algorithm Betas from Uniforms

- Generate $X \sim \text{beta}(a, b)$.
- ullet No direct method if a and b are not integers.
- Use a uniform candidate
- For a = 2.7 and b = 6.3

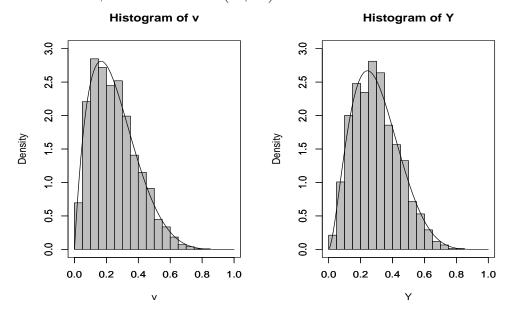




► Acceptance Rate =37%

Accept–Reject Algorithm Betas from Betas

- Generate $X \sim \text{beta}(a, b)$.
- ullet No direct method if a and b are not integers.
- Use a beta candidate
- For a = 2.7 and b = 6.3, $Y \sim \text{beta}(2, 6)$



► Acceptance Rate =60%

Accept-Reject Algorithm Betas from Betas-Details

- ▶ Beta density $\propto x^a(1-x)^b$
- ightharpoonup Can generate if a and b integers
- ▶ If not, use candidate with a_1 and b_1 integers

$$\frac{y^{a}(1-y)^{b}}{y^{a_{1}}(1-y)^{b_{1}}} \text{ maximized at } y = \frac{a-a_{1}}{a-a_{1}+b-b_{1}}$$

 \triangleright Need $a_1 < a$ and $b_1 < b$

- ► Efficiency ↑ as the candidate gets closer to the target
- ► Look at R code

Accept-Reject Algorithm Comments

4 Some key properties of the Accept-Reject algorithm::

- 1. Only the ratio f/M is needed
 - ▷ So the algorithm does not depend on the normalizing constant.
- 2. The bound $f \leq Mg$ need not be tight
 - \triangleright Accept-Reject is valid, but less efficient, if M is replaced with a larger constant.
- 3. The probability of acceptance is 1/M
 - \triangleright So M should be as small as possible for a given computational effort.

Chapter 3: Monte Carlo Integration

"Every time I think I know what's going on, suddenly there's another layer of complications. I just want this damn thing solved."

John Scalzi
The Last Colony

This Chapter

- ► This chapter introduces the major concepts of Monte Carlo methods
- ► The validity of Monte Carlo approximations relies on the Law of Large Numbers
- ▶ The versatility of the representation of an integral as an expectation

Monte Carlo Integration Introduction

▶ We will be concerned with evaluating integrals of the form

$$\int_{\mathcal{X}} h(x) f(x) dx,$$

- $\triangleright f$ is a density
- \triangleright We can produce an almost infinite number of random variables from f
- ► We apply probabilistic results

 - ▷ Central Limit Theorem
- ► The Alternative Deterministic Numerical Integration
 - \triangleright R functions area and integrate
 - ▷ OK in low (one) dimensions
 - ▶ Usually needs some knowledge of the function

Classical Monte Carlo Integration The Monte Carlo Method

► The generic problem: Evaluate

$$\mathbb{E}_f[h(X)] = \int_{\mathcal{X}} h(x) f(x) dx,$$

 $\triangleright X$ takes its values in \mathcal{X}

- ► The Monte Carlo Method
 - \triangleright Generate a sample (X_1, \ldots, X_n) from the density f
 - > Approximate the integral with

$$\overline{h}_n = \frac{1}{n} \sum_{j=1}^n h(x_j) ,$$

Classical Monte Carlo Integration Validating the Monte Carlo Method

► The Convergence

$$\overline{h}_n = \frac{1}{n} \sum_{j=1}^n h(x_j) \to \int_{\mathcal{X}} h(x) f(x) dx = \mathbb{E}_f[h(X)]$$

▶ Is valid by the Strong Law of Large Numbers

▶ When $h^2(X)$ has a finite expectation under f,

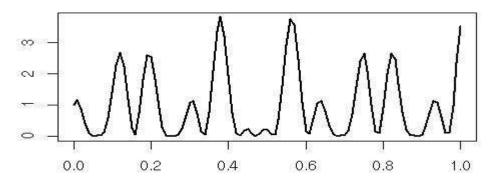
$$\frac{\overline{h}_n - \mathbb{E}_f[h(X)]}{\sqrt{v_n}} \to \mathcal{N}(0, 1)$$

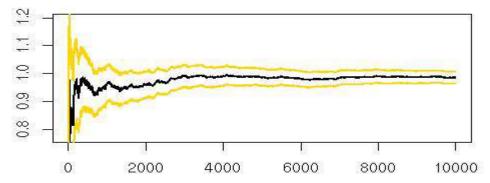
> Follows from the Central Limit Theorem

$$\triangleright v_n = \frac{1}{n^2} \sum_{j=1}^n [h(x_j) - \overline{h}_n]^2.$$

Classical Monte Carlo Integration A First Example

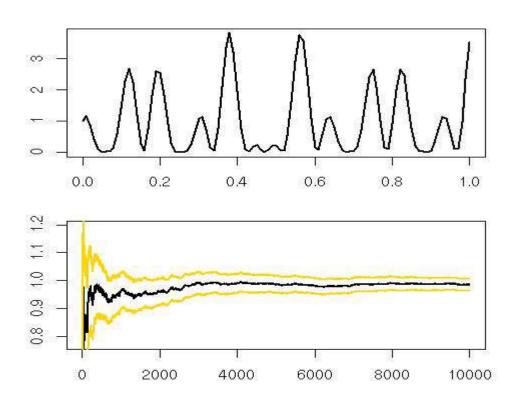
► Look at the function





- $h(x) = [\cos(50x) + \sin(20x)]^2$
- ► Monitoring Convergence
- ► R code

Classical Monte Carlo Integration A Caution



► The confidence band produced in this figure is not a 95% confidence band in the classical sense

▶ They are Confidence Intervals were you to stop at a chosen number of iterations

Classical Monte Carlo Integration Comments

4

- ▶ The evaluation of the Monte Carlo error is a bonus
- lacktriangle It assumes that v_n is a proper estimate of the variance of \overline{h}_n
- ightharpoonup If v_n does not converge, converges too slowly, a CLT may not apply

Classical Monte Carlo Integration Another Example

► Normal Probability

$$\hat{\Phi}(t) = \frac{1}{n} \sum_{i=1}^{n} \mathbb{I}_{x_i \le t} \to \Phi(t) = \int_{-\infty}^{t} \frac{1}{\sqrt{2\pi}} e^{-y^2/2} dy$$

- \triangleright The exact variance $\Phi(t)[1-\Phi(t)]/n$
- \triangleright Conservative: Var $\approx 1/4n$
- > For a precision of four decimals
 - \triangleright Want $2 \times \sqrt{1/4n} \le 10^{-4}$ simulations
 - ightharpoonup Take $n = (10^4)^2 = 10^8$
- ➤ This method breaks for tail probabilities

Importance Sampling Introduction

▶ Importance sampling is based on an alternative formulation of the SLLN

$$\mathbb{E}_f[h(X)] = \int_{\mathcal{X}} h(x) \frac{f(x)}{g(x)} g(x) dx = \mathbb{E}_g \left[\frac{h(X)f(X)}{g(X)} \right] ;$$

 $\triangleright f$ is the target density

 $\triangleright g$ is the candidate density

▶ Sound Familiar?

Importance Sampling Introduction

▶ Importance sampling is based on an alternative formulation of the SLLN

$$\mathbb{E}_f[h(X)] = \int_{\mathcal{X}} h(x) \frac{f(x)}{g(x)} g(x) dx = \mathbb{E}_g \left[\frac{h(X)f(X)}{g(X)} \right] ;$$

 $\triangleright f$ is the target density

 $\triangleright g$ is the candidate density

⊳ Sound Familiar? – Just like Accept–Reject

► So

$$\frac{1}{n} \sum_{j=1}^{n} \frac{f(X_j)}{g(X_j)} h(X_j) \to \mathbb{E}_f[h(X)]$$

► As long as

$$\triangleright \operatorname{Var}(h(X)f(X)/g(X)) < \infty$$

$$\triangleright \operatorname{supp}(g) \supset \operatorname{supp}(h \times f)$$

Importance Sampling Revisiting Normal Tail Probabilities

- ▶ $Z \sim \mathcal{N}(0,1)$ and we are interested in the probability P(Z > 4.5)
- ▶ > pnorm(-4.5,log=T)
 [1] -12.59242
- ► Simulating $Z^{(i)} \sim \mathcal{N}(0,1)$ only produces a hit once in about 3 million iterations!

 > Very rare event for the normal
 - ▶ Not-so-rare for a distribution sitting out there!
- ▶ Take $g = \mathcal{E}xp(1)$ truncated at 4.5:

$$g(y) = \frac{e^{-y}}{\int_{4.5}^{\infty} e^{-x} dx} = e^{-(y-4.5)},$$

► The IS estimator is

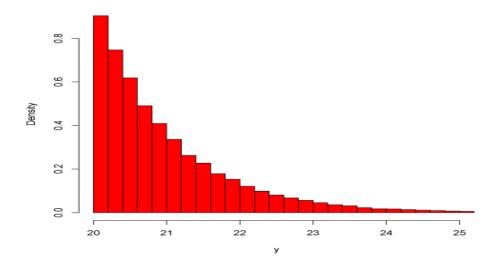
$$\frac{1}{n} \sum_{i=1}^{n} \frac{f(Y^{(i)})}{g(Y^{(i)})} = \frac{1}{n} \sum_{i=1}^{n} \frac{e^{-Y_i^2/2 + Y_i - 4.5}}{\sqrt{2\pi}}$$
 R code

Importance Sampling Normal Tail Variables

- \blacktriangleright The Importance sampler does not give us a sample \Rightarrow Can use Accept–Reject
- ▶ Sample $Z \sim \mathcal{N}(0,1)$, $Z > a \Rightarrow$ Use Exponential Candidate

$$\frac{\frac{1}{\sqrt{2\pi}}\exp(-.5x^2)}{\exp(-(x-a))} = \frac{1}{\sqrt{2\pi}}\exp(-.5x^2 + x + a) \le \frac{1}{\sqrt{2\pi}}\exp(-.5a^{*2} + a^* + a)$$

 \triangleright Where $a^* = max\{a, 1\}$



- ightharpoonup Normals > 20
- ► The Twilight Zone
- ► R code

Importance Sampling Comments

4 Importance sampling has little restriction on the choice of the candidate

- ightharpoonup g can be chosen from distributions that are easy to simulate
 - > Or efficient in the approximation of the integral.
- \blacktriangleright Moreover, the same sample (generated from g) can be used repeatedly
 - \triangleright Not only for different functions h but also for different densities f.

Importance Sampling Easy Model - Difficult Distribution

Example: Beta posterior importance approximation

 \blacktriangleright Have an observation x from a beta $\mathcal{B}(\alpha,\beta)$ distribution,

$$x \sim \frac{\Gamma(\alpha + \beta)}{\Gamma(\alpha)\Gamma(\beta)} x^{\alpha - 1} (1 - x)^{\beta - 1} \mathbb{I}_{[0, 1]}(x)$$

▶ There exists a family of conjugate priors on (α, β) of the form

$$\pi(\alpha,\beta) \propto \left\{ \frac{\Gamma(\alpha+\beta)}{\Gamma(\alpha)\Gamma(\beta)} \right\}^{\lambda} x_0^{\alpha} y_0^{\beta},$$

where λ, x_0, y_0 are hyperparameters,

► The posterior is then equal to

$$\pi(\alpha, \beta | x) \propto \left\{ \frac{\Gamma(\alpha + \beta)}{\Gamma(\alpha)\Gamma(\beta)} \right\}^{\lambda+1} [xx_0]^{\alpha} [(1-x)y_0]^{\beta}.$$

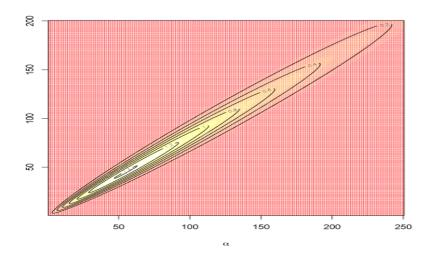
Importance Sampling Easy Model - Difficult Distribution -2

► The posterior distribution is intractable

$$\pi(\alpha, \beta | x) \propto \left\{ \frac{\Gamma(\alpha + \beta)}{\Gamma(\alpha)\Gamma(\beta)} \right\}^{\lambda+1} [xx_0]^{\alpha} [(1-x)y_0]^{\beta}.$$

- ▶ Difficult to deal with the gamma functions
- \triangleright Simulating directly from $\pi(\alpha, \beta|x)$ is impossible.

► What candidate to use?



- ► Contour Plot
- ► Suggest a candidate?
- ► R code

Importance Sampling Easy Model - Difficult Distribution - 3

- ightharpoonup Try a Bivariate Student's T (or Normal)
- ► Trial and error

 \triangleright Student's $\mathcal{T}(3,\mu,\Sigma)$ distribution with $\mu=(50,45)$ and

$$\Sigma = \begin{pmatrix} 220 & 190 \\ 190 & 180 \end{pmatrix}$$

▶ Produce a reasonable fit

⊳ R code

▶ Note that we are using the fact that

$$X \sim f(x) \Rightarrow \Sigma^{1/2}X + \mu \sim f\left((x - \mu)'\Sigma^{-1}(x - \mu)\right)$$

Importance Sampling Easy Model - Difficult Distribution - Posterior Means

 \blacktriangleright The posterior mean of α is

$$\int \int \alpha \pi(\alpha, \beta | x) d\alpha d\beta = \int \int \left[\alpha \frac{\pi(\alpha, \beta | x)}{g(\alpha, \beta)} \right] g(\alpha, \beta) d\alpha d\beta \approx \frac{1}{M} \sum_{i=1}^{M} \alpha_i \frac{\pi(\alpha_i, \beta_i | x)}{g(\alpha_i, \beta_i)}$$

where

 \blacktriangleright Note that $\pi(\alpha, \beta|x)$ is not normalized, so we have to calculate

$$\frac{\int \int \alpha \pi(\alpha, \beta | x) d\alpha d\beta}{\int \int \pi(\alpha, \beta | x) d\alpha d\beta} \approx \frac{\sum_{i=1}^{M} \alpha_i \frac{\pi(\alpha_i, \beta_i | x)}{g(\alpha_i, \beta_i)}}{\sum_{i=1}^{M} \frac{\pi(\alpha_i, \beta_i | x)}{g(\alpha_i, \beta_i)}}$$

- ▶ The same samples can be used for every posterior expectation
- ► R code

Importance Sampling Probit Analysis

Example: Probit posterior importance sampling approximation

 \triangleright y are binary variables, and we have covariates $x \in \mathbb{R}^p$ such that

$$\Pr(y=1|x) = 1 - \Pr(y=0|x) = \Phi(x^{\mathrm{T}}\beta), \quad \beta \in \mathbb{R}^p.$$

- ▶ We return to the dataset Pima.tr, x=BMI
- ightharpoonup A GLM estimation of the model is (using centered x)

```
>glm(formula = y ~ x, family = binomial(link = "probit"))
```

Coefficients:

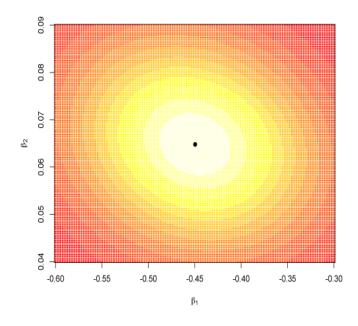
Signif. codes: 0 *** 0.001 ** 0.01 * 0.05 . 0.1

So BMI has a significant impact on the possible presence of diabetes.

Importance Sampling Bayesian Probit Analysis

- ▶ From a Bayesian perspective, we use a vague prior $\triangleright \beta = (\beta_1, \beta_2)$, each having a $\mathcal{N}(0, 100)$ distribution
- \blacktriangleright With Φ the normal cdf, the posterior is proportional to

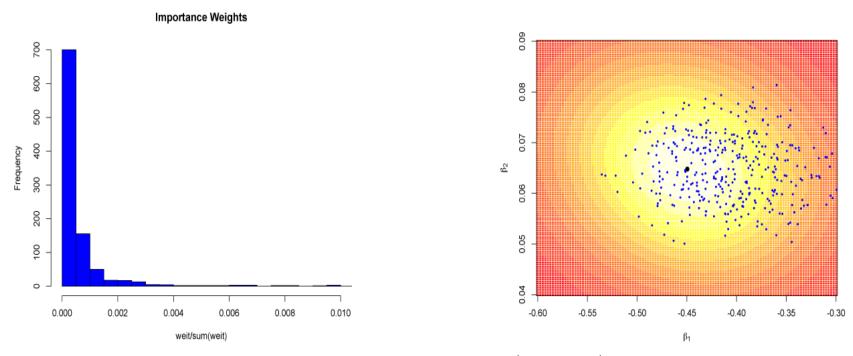
$$\prod_{i=1}^{n} \left[\Phi(\beta_1 + (x_i - \bar{x})\beta_2)^{y_i} \left[\Phi(-\beta_1 - (x_i - \bar{x})\beta_2)^{1-y_i} \times e^{-\frac{\beta_1^2 + \beta_2^2}{2 \times 100}} \right] \right]$$



- ► Level curves of posterior
- ► MLE in the center
- ► R code

Importance Sampling Probit Analysis Importance Weights

- ▶ Normal candidate centered at the MLE no finite variance guarantee
- ▶ The importance weights are rather uneven, if not degenerate



- ► Right side = reweighted candidate sample (R code)
- Somewhat of a failure

Chapter 5: Monte Carlo Optimization

"He invented a game that allowed players to predict the outcome?"

Susanna Gregory

To Kill or Cure

This Chapter

- ► Two uses of computer-generated random variables to solve optimization problems.
- ► The first use is to produce stochastic search techniques
 - ▷ To reach the maximum (or minimum) of a function
 - ▷ Avoid being trapped in local maxima (or minima)
 - > Are sufficiently attracted by the global maximum (or minimum).
- ▶ The second use of simulation is to approximate the function to be optimized.