Journal of Computational Physics **160,** 612–622 (2000)
doi:10.1006/jcph.2000.6477, available online at http://www.idealibrary.com on IDEAL®

An Extension of Alias Sampling Method for Parametrized Probability Distributions

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Received May 3, 1999; revised November 30, 1999

An extension of the alias sampling technique for distribution functions depending on a number of parameters was developed. It takes advantage of modern computer architectures with large amounts of cheap memory, by using discrete representations of probability distribution functions. The sampling is done by fast interpolation techniques involving only elementary logical and arithmetical operations, allowing one to keep a higher degree of accuracy as the grids spacing is controlled by the user. By this method it is possible to obtain the value of interest by direct interpolation between the sampled values obtained with the same set of random numbers for the grid values of the parameters adjacent to the values of interest. Sampling tests carried for the case of Molière electron multi-scatter angle distribution show that this method can be successfully used in Monte Carlo codes for sampling complex probability distributions.

Key Words: Monte Carlo; random variable; sampling; probability; Molière; multi-scatter.

1. INTRODUCTION

In a Monte Carlo code for simulating physical processes, as a particle transport simulation system, a significant part of the running time is spent generating random variables according to different probability density functions (PDFs). Therefore, in developing such codes it is necessary to have methods that provide fast algorithms for generating random variables according to the various PDFs given by the laws describing the physical processes involved. As the shape of probability distributions and also the form of presentation (mathematical formula, tabulated data, or algorithmic description) can be very different from case to case, for rapid development of simulation codes it is very useful to have a general method for sampling random variables which can treat all these cases in a uniform manner.

0021-9991/00 $35.00

2. SAMPLING A RANDOM VARIABLE

Theoretically any random variable $x \in (a, b)$ with probability density $p(x)$, satisfying $1 = \int_a^b p(x)\,dx$ and cumulative probability distribution

$$F(x) = \int_a^x p(x')\,dx' \tag{1}$$

can be sampled using the inverse function method or the direct method, which gives

$$\hat{x} = F^{-1}(\zeta), \tag{2}$$

where ζ is a random number uniformly distributed in the interval (0, 1). But to apply this method it is necessary to have an analytical formula for the inverse function F^{-1}: $(0, 1) \to (a, b)$, which is possible only in a few particular cases. This disadvantage can be overcome by taking a discretization in N points of F^{-1} over an equally spaced division of the interval (0, 1), resulting in a division of the random variable domain (a, b) into equally probable intervals delimited by the points $\{x_i\}_{i=\overline{0,N}}$, where $x_i = F^{-1}(\frac{i}{N})$. For sampling, the interval i is selected first as the integer part of $[\zeta N]$, where ζ is a random number uniformly distributed in (0, 1); then a value $\hat{x}$ in the selected interval $(x_i,\ x_{i+1})$ is sampled. As a first approximation a uniformly distributed number

$$\hat{x} = (1 - t)x_i + tx_{i+1}, \tag{3}$$

where t is the fractional part of $\{\zeta N\}$, can be used. A higher degree of accuracy is achieved if the linear interpolation formula of probability distribution over the selected interval is used,

$$f_i(x) = (1 - u)p_i + up_{i+1}, \tag{4}$$

where $u = (x - x_i)/(x_{i+1} - x_i)$, and $p_i = p(x_i)$. An elegant method using only elementary operations is described in [1]. First the uniformly distributed value $\hat{x}$ is selected:

$$\hat{x} = tx_i + (1 - t)x_{i+1}. \tag{5}$$

Then a second random number ζ uniformly distributed in the interval $(0,\ p_i + p_{i+1})$ is selected. If $f_i(\hat{x}) > \zeta$ the value $\hat{x}$ is accepted; otherwise the following value is chosen:

$$\hat{x} = (1 - t)x_i + tx_{i+1}. \tag{6}$$

In fact this is a modified rejection method exploiting the symmetry properties of linear distributions.

This method of equally probable intervals spacing is fast, as only a few elementary operations are involved, but in the case of intervals where the events are less probable the spacing is larger and the accuracy decreases; moreover, in the case of distributions given as tabulated data the transformations of the original grid to a grid with equally probable intervals may lead to an avoidable loss of precision. If the point spacing does not correspond to equally probable intervals then the selection of the interval requires the search a table of cumulative probabilities, which is a very time-consuming operation.

2.1. *Alias Sampling Method*

An alternative to the search operation is the use of the alias sampling method proposed by Walker [2, 3]. Suppose we have an arbitrary division $\{x_i\}_{i=\overline{0,N}}$ of random variable domain (a, b) and consider as elementary events the selection of one of the intervals $(x_i,\ x_{i+1})$. In the alias sampling method the above elementary events are grouped in pairs of two in order to obtain a table of equally probable compound events. The selection is done in two steps: first, as in the method of equally probable intervals such a compound event is sampled, and second, from the pair of elementary events one of them is selected, according to their relative probabilities. For a PDF given in tabulated form $\{x_i,\ p_i\}_{i=\overline{0,N}}$ where p_i is the density probability in the point x_i, such a discretization divides the whole domain into N intervals (x_i, x_{i+1}), $i = \overline{0,\ N-1}$, each with the probability of selection

$$P_i = \frac{p_i + p_{i+1}}{2}(x_{i+1} - x_i), \qquad \text{satisfying: } 1 = \sum_{i=0}^{N-1} P_i. \tag{7}$$

The compound events are stored in a special data arrangement $\{j_i,\ r_i\}_{i=\overline{0,N-1}}$, into which to each interval i is associated a second interval j_i and a real number r_i. For selecting the interval, first a compound event i is selected with equal probabilities, then a second random number $\zeta \in (0, 1)$ is used to decide whether the associated interval j_i (if $\zeta > r_i$) or the interval i (if $\zeta \le r_i$) is selected. An elegant method for making such arrangement of data is the Walker algorithm [2]. Successively the array $\{P_k\}_{k=\overline{0,N-1}}$ is searched for the intervals with the minimum (P_i) and respectively maximum (P_j) probabilities; in fact, it is sufficient to search for pairs of intervals where $P_i < P_{\text{ave}} = 1/N$ and $P_j > P_{\text{ave}}$. The compound event i is formed from the interval with the same index i and probability P_i to which the interval $j_i = j$ with the probability $1/N - P_i$ is added. In this way each compound event has the probability $1/N$ and $r_i = P_i N$. The probability of the interval j, P_j is updated by subtracting the quantity added to the compound event $P_j \leftarrow P_j - (1/N - P_i)$. A new search is performed, but excluding the interval i, just prepared, from the search array $\{P_k\}$, and so on, until it becomes empty. By mathematical induction it can be proved that this arrangement is always possible.

3. THE CASE OF PARAMETRIZED PDFs

3.1. *Direct Interpolation*

Let us consider first the case of a random variable x with the PDF depending on a single parameter $p(x,\ \alpha)$, where α is a real number taking values in the interval $[\alpha_{\min},\ \alpha_{\max}]$. In this case a grid with a convenient spacing, linear or logarithmic, is created $\{\alpha_k\}_{k=\overline{0,N_\alpha}}$. For techniques such as the inverse function method, or equally probable intervals spacing method, a sample at a given point $\alpha \in [\alpha_i,\ \alpha_{i+1})$ can be determined by interpolating samples taken from distributions in the points α_i and α_{i+1} using the same random numbers.

Briefly, the method is as follows: using the same random numbers, the values, $\hat{x}_1$, according to distribution $p(x,\ \alpha_k)$ and $\hat{x}_2$, according to distribution $p(x,\ \alpha_{k+1})$, are selected. The sampled value for the distribution $p(x,\ \alpha)$ is finally given by

$$\hat{x} = (1-u)\hat{x}_1 + u\hat{x}_2, \qquad \text{where } u = \frac{\alpha - \alpha_k}{\alpha_{k+1} - \alpha_k}, \quad u' = 1 - u. \tag{8}$$

By this procedure the random variable is obtained by interpolation between the inverse of the cumulative distribution functions

$$\tilde{F}^{-1}(y, \alpha) = u' F^{-1}(y, \alpha_k) + u F^{-1}(y, \alpha_{k+1}). \tag{9}$$

And if for α_k the random variable takes values inside the interval (a_k, b_k), and for α_{k+1} it takes values inside the interval $(a_{k+1},\ b_{k+1})$, then the interpolated random variable will take values inside the interval $(u'a_k + ua_{k+1}, u'b_k + ub_{k+1})$, an adjustment of the domain in which the interpolated variable lies, also being obtained.

This kind of interpolation fails if it is applied directly with the alias sampling method. Therefore it was considered that the major difficulty with the alias sampling technique is that conventional interpolation between tabulated distribution is not possible [1] since the specially formatted distribution no longer allows direct manipulation of the probabilities.

3.2. *Statistical Interpolation*

An interpolation technique that can be used in conjunction with the alias sampling method is statistical interpolation. It gives a way of approximating an interpolated distribution by sampling from one of the two neighboring distributions. Given two known distributions at α_k and α_{k+1} and a point $\alpha \in [\alpha_k,\ \alpha_{k+1})$, choosing a random number $\zeta \in (0,\ 1)$, statistical interpolation calls for sampling from the α_k distribution if

$$\zeta \leq \frac{\alpha_{k+1} - \alpha}{\alpha_{k+1} - \alpha_k}; \tag{10}$$

otherwise the α_{k+1} distribution is used. In fact, the statistical interpolation overlaps, with different weights, the PDFs at the extreme points of the interval. The PDF of the random variable by this procedure is

$$\tilde{p}(x, \alpha) = u' p(x, \alpha_k) + u p(x, \alpha_{k+1}), \tag{11}$$

where u and u' have the same meaning as in (8). The values domain of the interpolated random variable is then $(a_k,\ b_k) \cup (a_{k+1},\ b_{k+1})$.

Due to its simplicity, statistical interpolation with alias sampling is very convenient for use with PDFs given in tabulated form. According to [1, 4] statistical interpolation yields satisfactory results for various PDFs used for Monte Carlo simulation of particle transport, but in certain cases the simple weighted superposition is not recommended. In such cases additional rescalings or application of variable transformations must be considered in order to improve the results (see Fig. 1).

3.3. *Extension of Alias Sampling Technique to Direct Interpolation*

The impossibility of applying the alias sampling technique with conventional (direct) interpolation is due to the attempt to use independently the arrangements for interval selection at each parameter value α_k and α_{k+1}. This inconvenience can be avoided if for both values α_k and α_{k+1} an unique arrangement for sampling the intervals is used, with only the values at the extreme points of the intervals being different.

More precisely, if at the start for each value α_k of the parameter we have a division of the random variable domain into the points $\{x_i^{(k,1)}\}$, $i = \overline{0, N}$ with corresponding probability

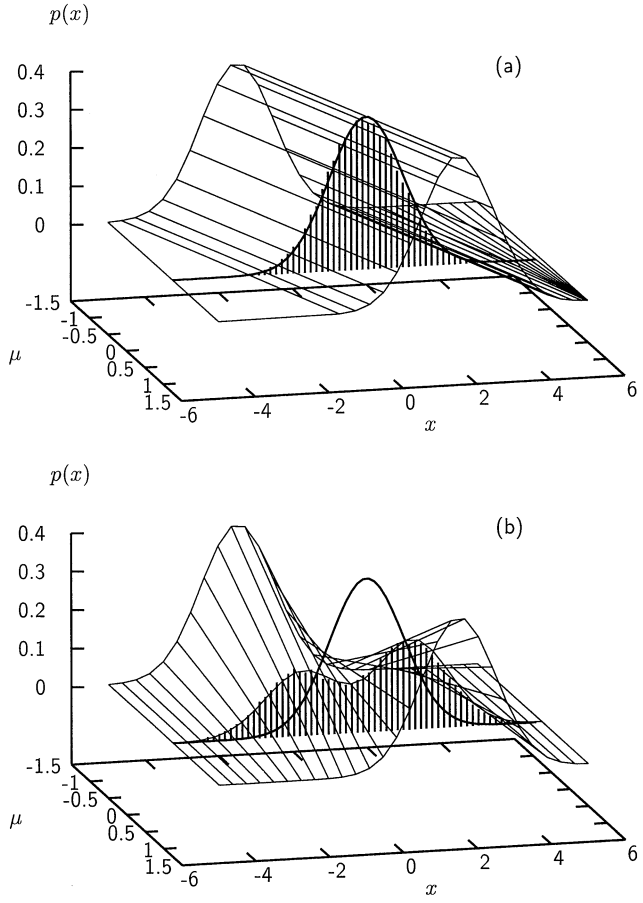

FIG. 1. Comparisons between direct interpolation (a) and statistical interpolation (b) for a PDF having a peak with position depending on a parameter. This example shows the case of a Gaussian $p(x, \mu, \sigma) = (1/\sigma\sqrt{2\pi})\exp[-(x-\mu)^2/2\sigma^2]$, in which μ was taken as a parameter and $\sigma = 1$. The plotted surfaces represent the interpolated PDF by the two methods $\tilde{p}(x, \mu)$ between distributions $p(x, -1.5)$, respectively $p(x, 1.5)$. Vertical bars represent the sampled distributions obtained for the point $\mu = 0.25$, while the thick line represents the theoretical distribution in the same point.

densities $\{p_i^{(k,1)}\}$, and with the alias sampling arrangement $\{j_i^{(k)}, r_i^{(k)}\}_{i=\overline{0,N-1}}$, then for each next value of the parameter α_{k+1} an additional division $\{x_i^{(k,2)}\}$ is created with the condition that the probabilities for corresponding intervals to be the same as for the grid $\{x_i^{(k,1)}\}$ at the parameter value α_k.

If for α_k the values of the cumulative distribution function are

$$Q_i = F\left(x_i^{(k,1)}, \alpha_k\right), \qquad i = \overline{0, N}, \tag{12}$$

then for α_{k+1} the points $x_i^{(k,2)}$ are given by

$$x_i^{(k,2)} = F^{-1}(Q_i,\ \alpha_{k+1}), \qquad i = \overline{0, N}. \tag{13}$$

Finally the values $p_i^{(k,2)} = p(x_i^{(k,2)}, \alpha_{k+1})$ are computed.

By this procedure the alias sampling arrangement obtained with the Walker algorithm for the division $\{x_i^{(k,1)}\}$ for α_k, is identical with the corresponding arrangement obtained

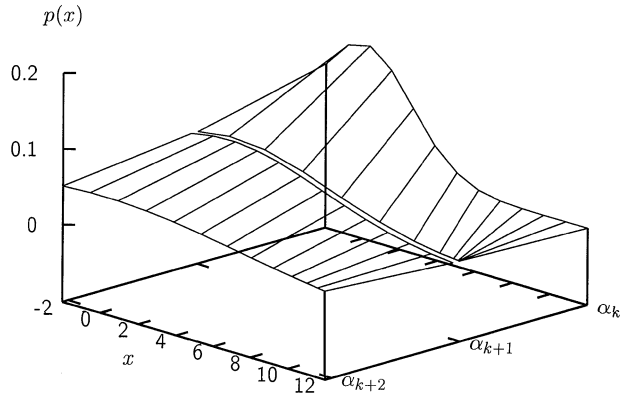

FIG. 2. Graphical representation of sampling arrangements for a parametrized distribution. The plotted surfaces represent the probability density function $p(x, \alpha)$ as given by the sampling arrangements divisions points for two consecutive grid intervals. For the first interval $[\alpha_k, \alpha_{k+1})$ the plotted surface is given by the points $\{x_i^{(k,1)}, p_i^{(k,1)}\}$ for α_k parameter value and $\{x_i^{(k,2)}, p_i^{(k,2)}\}$ for α_{k+1}. For the second interval $[\alpha_{k+1}, \alpha_{k+2})$ the plotted surface is given by the points $\{x_i^{(k+1,1)}, p_i^{(k+1,1)}\}$ for α_{k+1} and $\{x_i^{(k+1,2)}, p_i^{(k+1,2)}\}$ for α_{k+2}.

for the division $\{x_i^{(k,2)}\}$ for α_{k+1}. A graphical representation of this kind of arrangement is given in Fig. 2.

For a parameter point $\alpha \in [\alpha_k, \alpha_{k+1})$ the sampling is done as follows:

- Using a first random number an interval i according to alias sampling arrangement $\{j_i^{(k)}, r_i^{(k)}\}$ prepared for α_k is selected.
- Then using a second sequence of random numbers the following values are sampled: $\hat{x}_1$ for α_k, according to the interpolated PDF between points $(x_i^{(k,1)}, p_i^{(k,1)})$ and $(x_{i+1}^{(k,1)}, p_{i+1}^{(k,1)})$, and $\hat{x}_2$, for α_{k+1}, according to the interpolated PDF between points $(x_i^{(k,2)}, p_i^{(k,2)})$ and $(x_{i+1}^{(k,2)}, p_{i+1}^{(k,2)})$.
- Finally the value of $\hat{x}$ is obtained by interpolation between points $(\hat{x}_1, \alpha_k)$ and $(\hat{x}_2, \alpha_{k+1})$ using Eq. (8).

In the case when the random variable PDF depends on two parameters $p(x, \alpha, \beta)$, it is necessary to interpolate between the points of a two-dimensional grid $\{\alpha_k, \beta_l\}, k = \overline{0, N_\alpha}, l = \overline{0, N_\beta}$. In this case if for each grid point (α_k, β_l) with $k < N_\alpha, l < N_\beta$ is given a division of random variable domain $\{x_i^{(1)}\}_{i=\overline{0,N}}$ with PDF values $\{p_i^{(1)}\}_{i=\overline{0,N}}$, and with alias sampling arrangement $\{j_i, r_i\}_{i=\overline{0,N-1}}$ using analogue relations with (12), (13) three additional divisions are constructed $\{x_i^{(2)}\}$, $\{p_i^{(2)}\}$ for parameter points (α_{k+1}, β_l), $\{x_i^{(3)}\}$, $\{p_i^{(3)}\}$ for (α_k, β_{l+1}) and $\{x_i^{(4)}\}$, $\{p_i^{(4)}\}$ for $(\alpha_{k+1}, \beta_{l+1})$ in order to obtain intervals with probabilities identically with those given by the division $\{x_i^{(1)}\}$ at the parameter point (α_k, β_l). Here for a more fluent reading the k, l superscripts were skipped.

The selection method for the parameters pair $\alpha \in [\alpha_k, \alpha_{k+1})$ and $\beta \in [\beta_l, \beta_{l+1})$ is done by following steps:

- A first random number is used for sampling the interval i according to alias sampling arrangement $\{j_i, r_i\}$ obtained for the grid $\{x_i^{(1)}\}$ at the parameter point (α_k, β_l).
- Then using the same sequence of random numbers the following values are sampled: $\hat{x}_1$ according to the interpolated PDF between points $(x_i^{(1)}, p_i^{(1)})$ and $(x_{i+1}^{(1)}, p_{i+1}^{(1)})$, $\hat{x}_2$ according to the interpolated PDF between points $(x_i^{(2)}, p_i^{(2)})$ and $(x_{i+1}^{(2)}, p_{i+1}^{(2)})$, $\hat{x}_3$ according

to the interpolated PDF between points $(x_i^{(3)}, p_i^{(3)})$ and $(x_{i+1}^{(3)}, p_{i+1}^{(3)})$, and finally $\hat{x}_4$ according to the interpolated PDF between points $(x_i^{(4)}, p_i^{(4)})$ and $(x_{i+1}^{(4)}, p_{i+1}^{(4)})$.

- Finally $\hat{x}$ is obtained by interpolating between the grid points $(\hat{x}_1, \alpha_k, \beta_l)$, $(\hat{x}_2, \alpha_{k+1}, \beta_l)$, $(\hat{x}_3, \alpha_k, \beta_{l+1})$, and $(\hat{x}_4, \alpha_{k+1}, \beta_{l+1})$ using the equation

$$\hat{x} = u'v'\hat{x}_1 + uv'\hat{x}_2 + u'v\hat{x}_3 + uv\hat{x}_4, \tag{14}$$

where

$$u = \frac{\alpha - \alpha_k}{\alpha_{k+1} - \alpha_k}, \qquad u' = 1 - u,$$
$$v = \frac{\beta - \beta_l}{\beta_{l+1} - \beta_l}, \qquad v' = 1 - v.$$

These algorithms based on the extension of the alias sampling method for random sampling of parametrized probability distributions were coded using the C++ object-oriented programming language. Two class hierarchies were defined; the first is introduced to provide an uniform interface to the various probability distributions given in different forms (mathematical formula, tabulated data, or algorithmic description) and the second class hierarchy is used for alias sampling arrangements preparation and runtime sampling for zero, one, or two parametric PDFs.

4. APPLICATION FOR SAMPLING THE MOLIÈRE ELECTRON MULTIPLE SCATTERING DISTRIBUTION

The multi-scatter angular distribution for swift charged particles passing through matter usually is written in a two parametric form $p(\theta, T, s)\,\mathrm{d}\Omega$, where θ is the angular deflection, our random variable, and the parameters are T, the average kinetic energy during the step, and s, the step length. For distributions using the small angle approximation, such as the Molière theory, this is equivalent with the form $f(\theta, T, s)\theta\,\mathrm{d}\theta$.

In the Molière [5–7] theory, by a change of variable, the above two parametric form is reduced to a single parameter one

$$f(\theta, T, s)\theta\,\mathrm{d}\theta = f_M(\vartheta, B)\vartheta\,\mathrm{d}\vartheta, \tag{15}$$

where

$$\vartheta = \frac{\theta}{\chi_c\sqrt{B}} \tag{16}$$

is called the reduced angle, and B and χ_c are defined by the equations

$$B - \ln B = \ln\,\Omega_0 \tag{17}$$

$$\chi_c = \chi_{cc}\frac{\sqrt{s}}{\beta^2 E}, \tag{18}$$

where b_c and χ_{cc} are constants which depend only on the medium in which the transport takes place. Ω_0 can be interpreted as the number of atomic collisions that contribute to the

scattering and is related to the step length by the equation

$$\Omega_0 = \frac{b_c s}{\beta^2}, \tag{19}$$

for elements

$$b_c = 6702.33 \frac{\rho Z^{1/3}(Z+\xi)}{A} \cdot \frac{1}{1+0.000178 \cdot Z^2} \,[\mathrm{cm}^{-1}] \tag{20}$$

$$\chi_{cc} = 0.39612 \sqrt{\frac{\rho Z(Z+\xi)}{A}} \,[\mathrm{MeV} \cdot \mathrm{cm}^{-1/2}], \tag{21}$$

where ρ is the density in $\mathrm{g/cm}^3$, s is the step length in cm, Z is the atomic number of the element, and A is the atomic mass in atomic mass units. E is the electron total energy in MeV, and ξ is a correction term introduced to take into account the inelastic scatterings with atomic electrons and it is usually taken equal to unity; an additional correction to χ_{cc} is given by Fano [8].

The Molière function is given as a series expansion,

$$f_M(\vartheta, B) = f^{(0)}(\vartheta) + \frac{1}{B} f^{(1)}(\vartheta) + \frac{1}{B^2} f^{(2)}(\vartheta) + \cdots, \tag{22}$$

where

$$f^{(n)}(\vartheta) = \frac{1}{n!} \int_0^\infty J_0(\eta\vartheta) e^{-\eta^2/4} \left(\frac{\eta^2}{4} \ln \frac{\eta^2}{4} \right)^n \eta \cdot d\eta; \tag{23}$$

J_0 is the zeroth order Bessel function. In Eq. (23) for $n = 0$ we have a Gaussian curve

$$f^{(0)}(\vartheta) = 2e^{-\vartheta^2}, \tag{24}$$

but for $n \geq 1$ the Molière functions must be computed using numerical methods. Terms until of order two proved to be sufficiently accurate.

Molière considered his theory valid for $\Omega_0 > 20$. Originally derived as a small-angle theory, Molière's multiple-scattering theory has been modified by Bethe to predict accurately large-angle scattering by multiplying the right side of Eq. (15) with a correction term $\sqrt{\theta/\sin\theta}$. The minimum step size $s_{\min}$ required to ensure sufficient number of scatterings is given by

$$s_{\min} = \frac{\Omega_0 \beta^2}{b_c} \,[\mathrm{cm}], \tag{25}$$

with $\Omega_0 = 20$, while the maximum step size derived by Bethe is

$$s_{\max} = \frac{E^2 \beta^4}{\chi_{cc} \ln(b_c E^2 \beta^2 / \chi_{cc})} \,[\mathrm{cm}]. \tag{26}$$

For testing the extension of the alias sampling method, both cases of Molière distributions, the two parametric form $f(\theta, T, s)$ and the single parameter form $f_M(\vartheta, B)$, were considered.

In the case of the single parameter form, due to the requirement of preparing only material independent sampling arrangements for a unidimensional grid, the memory usage is kept

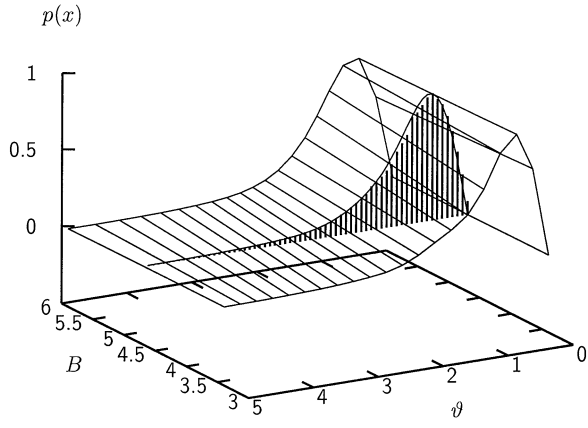

FIG. 3. Comparison between Molière function sampled distribution (vertical bars) and theoretical distribution (continuous curve) for the same $B = 4.7$ parameter value. The drawn surface represents the $f_M(\vartheta, B)$ distribution as it is given by the sampling arrangements grid points with $B = 3.4$, respectively $B = 5.9$.

low, but the sampling speed suffers because additional calculations of the deflection angle as a function of the reduced angle are required and, also, a rejection loop for the Bethe correction factor $\sqrt{\theta/\sin\theta}$ must be considered. A graphical comparison between a sampled distribution and the corresponding theoretical curve $f_M(\vartheta, B)$ is shown in Fig. 3.

The use of the two parametric form has the advantage of direct sampling of angular deflection, but with a large amount of memory usage because, for each material considered in the simulation, sampling arrangements for a two-dimensional grid must be prepared. An example of using this form for sampling of Molière multi-scatter angle distribution is given in Fig. 4.

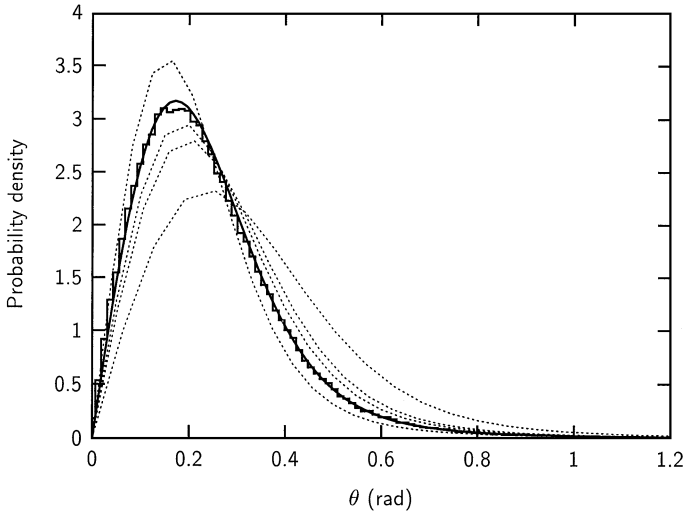

FIG. 4. Comparison between the sampled values (histogram) of the two parametric form of Molière multiple-scattering distribution, $f(\theta, T, s)$ and the theoretical distribution (continuous curve) for 2.8 MeV electrons traversing 3.0×10^{-2} cm of germanium. Dotted lines represent the distributions at the four parametric points between which the interpolations were made; these are the corners of the square with left-bottom corner (2.42 MeV, 2.74×10^{-2} cm) and right-top corner (3.00 MeV, 4.22×10^{-2} cm).

TABLE I

Comparison of Running Speed Obtained with Different Versions of Alias Sampling Technique and with the Classical Approach Used in EGS, for the Molière Electron Multiple-Scattering Distribution

	Running speed (generated values per second)		
Method	386DX 40 MHz	Pentium 133 MHz	Digital Alpha 233 MHz
C-EGS	4.12×10^3	4.91×10^4	8.05×10^4
AS1	3.32×10^3	4.34×10^4	7.20×10^4
AS1s	4.40×10^3	5.04×10^4	8.43×10^4
AS2	3.54×10^3	5.96×10^4	8.68×10^4
AS2s	6.39×10^3	7.99×10^4	14.35×10^4

Note. In all cases the same random number generator was used.

A test program was written and run on UNIX systems (Linux on Intel platforms and Digital UNIX on a Digital Alpha workstation). Several cases were tested. The first cases were the single parameter form of the Molière distribution (AS1) and the two parameter form (AS2), in which for the PDF interpolation inside the selected intervals the method given by Eqs. (5) and (6) was used. Second, two simplified versions (AS1s, AS2s), which use Eq. (3) for the PDF interpolation, were considered; in this case it is no longer necessary to store the probability density values ($p_i^{(k,1)}$, $p_i^{(k,2)}$, etc.), and the loss of precision can be compensated by taking more refined grids. Finally, a classical approach (C-EGS) based on the method used in the EGS system, as described in [9], was considered.

A comparison of the running speed results is presented in Table I. As was mentioned before, in the case of the single parameter form (AS1, AS1s) the sampling speed suffers due to the additional calculations made. An important factor for improving the scores is the speed of retrieving data from memory. This fact is emphasized by comparing the scores obtained on the 386 system with those obtained on the enhanced systems based on Pentium or Digital Alpha. During the generation of a random variable, repeated readings of data spread on a relatively large amount of computer memory are made. Therefore special care must be taken during implementation, in order to use efficiently the CPU internal or external memory cache. The use of structured types of data and dynamical memory allocation to group together data needed for sampling of a certain random variable value (alias sampling arrangements and grids with interpolation points) can lead to a significant increase in speed, up to doubling it, according to our experience. Additional optimizations, which were not considered here, such as direct sampling of memory addresses, rather than operating with indices for intervals sampling, can also speed up the algorithm.

5. CONCLUSION

A method of direct interpolation for sampling of random variables with parametrized probability distributions that allows the use of the alias sampling technique is presented. It takes advantage of modern computer architectures with large amounts of cheap and fast memories by using discrete representations of probability distribution functions. The sampling is done by fast interpolation techniques involving only elementary logical and

arithmetical operations, allowing for a higher degree of accuracy, as the grid spacing is controlled by the user.

This method can be successfully used as an alternative to the sampling arrangements commonly used in Monte Carlo codes where, for complex probability distributions, from case to case, after a careful study of function properties, combinations of sampling techniques (e.g., superposition, rejection and inverse function methods) are used. The method proposed here allows one to develop flexible Monte Carlo simulation codes, while the application of specific sampling techniques like those mentioned above makes the resultant code strongly dependent on the theories used.

ACKNOWLEDGMENT

The author expresses his gratitude to Professor O. Sima from the Physics Department of Bucharest University for his support and critical reading of this paper.

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