Use of Monte Carlo simulations for propagation of light in biomedical tissues

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1. Introduction
There is a great deal of interest currently in studies relating to light propagation in biomedical tissues (see, for example, [1,2] and references therein). The reason for this interest lies in the fact that measurement of reflected, transmitted, and scattered light contains information about tissue properties and, hence, has the potential to be used for noninvasive characterization of biomedical tissues, which could lead to the development of techniques for the early detection of cancer (see, for example, [3–9]). To achieve this, as a first step, it is necessary to understand the theory describing the propagation of light in the tissue. Thus, many approaches have been developed to predict results of light propagation in tissues [1,2]. In one of the often used approaches, the tissue is modeled as a turbid medium, and the Monte Carlo (MC) simulation is used to compute quantities such as diffuse reflectance, diffuse transmittance, and fluence [10,11], which, in turn, may be used to infer tissue characteristics.

The scatterers in the tissue may be assumed to be randomly distributed particles in an otherwise homogeneous medium (see, for example, [1,2]). Tissue models have been constructed with monodisperse as well as polydisperse particles. A model that has proved to be reasonably successful in simulating tissue optical properties assumes constituents to be homogeneous spherical scatterers following a fractal size distribution law [8,12–15]. Details of the model will be discussed later in the paper.

A widely used computer program to carry out simulation of propagation of unpolarized light in tissues is that of Jacques and Wang [10]. In the literature, this program has been referred to as MCML. The input quantities required in this program are the scattering coefficient, absorption coefficient, and phase function of the tissue. In most utilizations of this program for discrete particle models, average values of these quantities over the size distribution are computed and employed. Effectively, the tissue is taken to be a collection of identical scatterers, with each scatterer representing the effect of an average of tenuous collection of size distribution of particles within which multiple scattering is absent. The phase function of these identical equivalent scatterers, termed the phase function of the tissue and the propagation of light between these scattering centers, is taken care of by MC simulations. The
original MCML program employs an approximate phase function known as the Henyey–Greenstein phase function (HGPF) \([10,16]\), in lieu of the average of exact phase functions for particle sizes. This is simply because of the convenience that the HGPF offers in the computation of the scattered direction of a photon after the scattering event. The program was modified to be used with average Mie (exact) phase function by Sharma and Banerjee \([11]\). Hereafter, when we refer to MCML, it is tacitly assumed that the phase function employed is the average Mie phase function (MPF), unless and until stated otherwise.

Several MC simulation programs have also been developed that take into account the polarization of incident light \([17–23]\). One such program is from Ramella-Roman et al., \([17,18]\). Their first paper \([17]\) addresses a monodispersion of particles. In the second paper in this series, they present computations for a polydisperse system. In the computer program utilized in their second paper, scattering and absorption coefficients \(\mu_s\) and \(\mu_a\) are taken as the average quantities over the size distribution, as in the use of MCML, but instead of using an average phase function to represent scatterings inside the tissue, the particle size parameter and, hence, the phase function are changed at every scattering event according to a predefined size distribution.

A natural question that arises is: do the simulation of light propagation in a biomedical tissue with an average phase function approach (hereafter referred to as MC1) and the simulation with an individual phase function approach (hereafter referred to as MC2) yield identical results? This question is relevant to polarized as well as unpolarized incident light. For unpolarized light, Berrocal et al. \([24]\) have inquired into this question in connection with spray diagnostics. They compared the light intensity distribution on the front and the back surface of the scattering medium and found that the two approaches need not yield the same result. However, the particle size range and particle size distribution considered by them were very different from those of interest in tissue optics. Hence, a separate investigation is required in the context of tissue optics.

The main purpose of the present work is to compare and contrast the yields from MC1 and MC2 for a fractal tissue model. It will be demonstrated in this paper that a large disagreement is found between predictions of MC1 and MC2 for the fractal tissue model. This result is very important for better understanding and appropriate use of MC simulations in a tissue and is crucial for unambiguous interpretation of measured quantities.

This paper is organized as follows. In Section 2, we begin by describing the tissue model employed in the present work. The basic physical model employed here is same as was used by Wang \([12]\), Gelebart et al. \([13]\), Schmitt and Kumar \([14]\) and by Sharma and Banerjee \([9]\). Descriptions of MC1 and MC2 are provided in Section 3. Section 4 is devoted to the comparison of various observable quantities computed using MC1 and MC2. It is shown that, in general, MC1 and MC2 simulations do not yield identical results, and the source of this disagreement is traced in this section. Finally, conclusions and implications of this work for computations of light propagation in biomedical tissues are discussed in Section 5.

2. Tissue Model

The model tissue consists of an infinitely wide single layer of fluid of refractive index \(n_f\) and thickness \(t\), and the scatterers of refractive index \(n_s\) are embedded in it. \(n_o\) is taken to be 1.35, corresponding approximately to the refractive index of cytoplasm, and \(n_s = 1.50 + i0.0001\) is taken to correspond to the refractive index of a nucleus. The refractive index of the surrounding medium \(n_1\) is taken to be equal to \(n_2\) in this paper for the reason specified in Section 4. A small imaginary part has been introduced in \(n_3\) to provide absorption in the model tissue.

In the fractal model, the number of particles with diameter \(d_i\) in a spherical volume of diameter \(d_0\) is given by the relation

\[
N(d_i) = (d_0/d_i)^a,
\]

where \(a\) is the fractal volume dimension that determines the size distribution. For \(a > 1\), which is the case for biomedical tissues, \(N(d_i)\) decreases as \(d_i\) increases. Further, it may also be noted that a larger value of \(a\) indicates a relatively smaller number of large particles. If scatterers are treated as homogeneous spheres, the volume fraction of the \(i\)th diameter sphere within a volume of diameter \(d_0\) can be written as \([12]\)

\[
\eta(d_i) = (\pi d_i^3/6) N(d_i)/\pi d_0^3/6 = \eta_0 d_i^{3-a},
\]

where \(\eta_0 = d_0^{3-a}\) is a scale-dependent constant. For a tissue containing a distribution of particle sizes, the particle concentration in the tissue, \(T_v\), is

\[
T_v = \eta_0 \sum_{i=1}^{m} d_i^{3-a},
\]

where \(m\) is the number of particle sizes in the distribution. The average scattering coefficient, absorption coefficient, phase function, and asymmetry parameter for the tissue are determined by the following relations:

\[
\mu_s = (6\eta_0/\pi) \sum_{i=1}^{m} d_i^{-a} \sigma_s(d_i),
\]

\[
\mu_a = (6\eta_0/\pi) \sum_{i=1}^{m} d_i^{-a} \sigma_a(d_i),
\]
\[ p(\theta) = \sum_{i=1}^{m} d_i^{-a} \sigma_s(d_i)p(\theta, d_i)/\sum_{i=1}^{m} d_i^{-a} \sigma_s(d_i), \quad (6) \]

\[ g = \sum_{i=1}^{m} d_i^{-a} \sigma_s(d_i)g(d_i)/\sum_{i=1}^{m} d_i^{-a} \sigma_s(d_i), \quad (7) \]

respectively, with \( \sigma_s(d_i) \) and \( \sigma_a(d_i) \) being the scattering and absorption cross sections of a particle of size \( d_i \).

The Wang model [12] assumes scatterers to be in the size range from 5 nm to 30 \( \mu \)m in steps of 5 nm. Schmitt and Kumar [14] considered particle sizes in the range 5 nm \( \leq d \leq 25.6 \mu \)m. They used 10 mean sphere diameters in this range in powers of 2 (0.05, 0.10, 0.2, 0.4, 0.8, 1.6, 3.2, 6.4, 12.8, and 25.6 \( \mu \)m) to represent the particles in the model tissue. Four, six, and eight size models were investigated by Gelebart et al. [13]. Computations showed that \( \mu_s \) and \( \mu_a \) can be reproduced reasonably well by appropriately adjusting the fractal dimension. The computed phase functions are also in good qualitative agreement with experimentally observed phase functions, except for a small difference at backward angles. The disagreement at backward angles can be reduced by introducing some inhomogeneity in the homogeneous scatterer model [25]. For the present study, this is not important and this paper considers only the homogeneous spherical scatterers. In this work the scatterer size range is taken to be 5 nm \( \leq d \leq 25.6 \mu \)m in steps of 5 nm as in our earlier investigations [9,11].

3. Description of MC1 and MC2 Simulations

A well-known and extensively used computer code for simulation of unpolarized light propagation in a biomedical tissue is from Jacques and Wang [10]. In this code, each photon packet enters the medium that contains the scattering particles and is tracked as it travels through the medium. The code requires values of \( \mu_s \), \( \mu_a \), and \( g \) as input. In practice, for the discrete particle model, the average values given by Eqs. (4), (5), and (7), respectively, may be used as input. Here, \( g \) is needed as input because the original MCML employs the HGPF, which is determined completely by the \( g \) value:

\[ p(\theta)_{\text{hgpf}} = \frac{(1-g^2)}{2(1+g^2-2g \cos \theta)^{3/2}}, \quad (8) \]

where

\[ \int_{-1}^{1} p(\mu) d\mu = 1, \quad (9) \]

where \( \mu = \cos \theta \) and \( \theta \) is the scattering angle. The subscript hgpf stands for the Henyey–Greenstein phase function. The condition (9) allows one to interpret the phase function as a probability density function that defines the distribution of \( \theta \) over the interval \( 0^\circ - 180^\circ \). The quantity

\[ \xi(\mu) = \int_{-1}^{\mu} p(\mu') d\mu', \quad (10) \]

then gives the probability that the scattering angle lies between \( \cos^{-1} \mu \) and \( \pi \). The use of the HGPF simplifies the problem of selection of the scattered direction because Eq. (10) can be solved analytically for \( p(\theta)_{\text{hgpf}} \) to yield the scattering direction as

\[ \cos \theta = \frac{1}{2g} \left[ 1 + g^2 - \left( \frac{1-g^2}{1-g+2g\xi} \right)^2 \right], \quad (11) \]

where \( \xi \) is an equally spaced random number between 0 and 1.

Sharma and Banerjee replaced the HGPF with the average MPF in the original MCML of Jacques and Wang [10] and employed it for calculating quantities such as diffuse reflectance, fluence, and transmittance in a fractal tissue model. Because MPF cannot be cast in a closed analytic form, the scattered photon direction needs to be determined numerically. To this end, following Toublanc [26], a table of \( p(\theta) \) versus scattering angle \( \theta \) is created. The phase function satisfies the normalization condition \( \sum_{j=1}^{n} P_j = 1 \), where \( n \) is the number of \( \theta \) values for which \( p(\theta) \) has been tabulated. A random number \( \xi \) is then generated with a uniform distribution between 0 and 1 and compared with the probability distribution to obtain the angle \( \theta \). Computationally, this may be done by implementing the following condition:

\[ \sum_{j=1}^{v-1} p_j < \xi \leq \sum_{j=1}^{v} p_j, \quad (12) \]

where the left sum is zero when \( v = 1 \). That this modification is reliable was verified by employing a given phase function in analytic and tabular forms in the MCML program and comparing the results so obtained [11].

In MC2, this table is generated once and for all by averaging phase functions over a given size distribution via Eq. (6). At each scattering event, the same phase function and, hence, the same table is used to determine the direction of the scattered photon. In MC2 however, the particle size changes at every scattering event in accordance with a predetermined size distribution (fractal size distribution). The probability \( P(d_i) \) of a particle of diameter \( d_i \) being countered by a photon packet is given by [24]

\[ P(d_i) = d_i^{-a} \sigma_{\text{ext}}(d_i)/\sum_{d=d_{\text{min}}}^{d_{\text{max}}} d^{-a} \sigma_{\text{ext}}(d), \quad (13) \]

where the effective area of a scatterer, as seen by the photon, is the extinction cross section [27,28]. A random number \( \xi \) may then be generated with a uniform distribution between 0 and 1, and the diameter may be determined from the relation
\[ \sum_{i=1}^{n-1} P(d_i) < \xi \leq \sum_{i=1}^{n} P(d_i), \]  

where the left sum is zero when \( n = 1 \). Once the size is chosen, the scattering angle is determined by using Eq. (12). The rest of the simulation remains unaltered.

A program for polydisperse particles has been used by Ramella-Roman et al. [18] but is not available on the Internet. In this paper, the computer program by Ramella-Roman et al. for monodispersions [17] has been adapted and modified suitably, as described above, to be applicable to polydispersions. This program is referred to as POLMC in this paper. The method of implementation has already been indicated in Eqs. (13) and (14). Three different ways to build a MC program for light propagation with polarization have been described in [17]. We have adapted the one referred to as the Euler MC method. The scattering step is chosen based on the rejection method, as in [17].

The adapted POLMC program has been validated in the following ways: (i) it is confirmed that it reproduces the results given in [17] for monodispersions and (ii) MCML and POLMC have been shown to yield almost identical results for diffuse reflectance as well as fluence. This has been shown for diffuse reflectance and fluence, respectively, in Figs. 1(a) and 1(b) for MC1 for two volume concentrations. In these figures, the radial distance \( r \) is the source–detector separation and \( z \) is the depth in the tissue. The diffuse reflectance, \( R_d(r) \), is defined as the probability of a photon escaping per unit area at \( r \) and fluence, \( \phi(z) \), is defined as the probability of photon flow per unit area at a depth \( z \). The agreement in Fig. 1 can be seen to be excellent. In all these comparisons, incident light is taken to be unpolarized. The values of the scattering coefficient \( \mu_s \), absorption coefficient \( \mu_a \), and the average anisotropy \( g \), as defined in Eq. (7), are given in the respective figure captions.

A vector light field can be described by the well-known Stokes vector \( S = [I \, \nu \, V \, U] \) (see, for example, [28]), where \( I \) is the intensity, \( \sqrt{Q^2 + U^2 + V^2} / I \) is the degree of polarization, \( V / I \) is the degree of circular polarization, and \( U \) is related to the azimuth and ellipticity of the vibration ellipse. The Stokes parameters of interest in this paper are \([1 0 0 0], [1 1 0 0], \) and \([1 0 0 1] \) for unpolarized, linearly polarized, and right-handed circularly polarized light. For every launched Stokes vector, the POLMC program generates four data files corresponding to the four elements of the Stokes vector \( IQUV \). In this paper, we restrict our interest only to the \( I \) component of the final Stokes vector element.

4. Numerical Comparisons of MC1 and MC2

In diffuse reflectance measurements, a narrow beam of light is directed on the tissue and diffusely reflected light is measured at the surface of the tissue at a source–detector separation \( r \). Computations presented here are for the matched boundary case, and, therefore, diffuse reflectance is the same as total reflectance. The matched boundary case has been chosen here because this is the case considered in [17,18]. However, we have confirmed that the main conclusions of this work are valid for the unmatched boundary case \((n_1 \neq n_2)\), too. Values of \( \alpha \) for soft tissues have been found to be in the range \( 4.0 \leq \alpha \leq 5.0 \) by Wang [12]. In this paper, typical results have been presented only for \( \alpha = 5 \). But, results remain valid also for \( \alpha = 4.0 \). The wavelength of the incident light in all computations is 632.8 nm.

Figure 2 shows the variation of diffuse reflectance \( R_d(r) \) as a function of \( r \) for MC1 as well as for MC2. The incident Stokes vector in this case is \([1 0 0 0] \). It may be noted that results from MC1 and MC2 do not concur. Clearly, the average phase function approach and the individual phase function approach do not yield the same results. The volume concentration of particles in this graph is \( T_v = 0.2 \) and
The variation of fluence with depth is shown in Fig. 3. In this simulation, \( a = 5.0, T_v = 0.20 \), and the incident Stokes vector is the same as in Fig. 2. As expected, the disagreement noted between MC1 and MC2 for \( R_d(r) \) versus \( r \) in Fig. 2 is present for fluence as well.

The variations of \( R_d(r) \) with \( r \) and of \( \phi(z) \) with \( z \) are shown in Figs. 4(a) and 4(b), respectively, for plane polarized as well as circularly polarized incident light. MC1 and MC2 can be seen to disagree for these incident polarizations, too. The incident Stokes vector for plane polarized and circularly polarized light are [1 1 0 0] and [1 0 0 1], respectively. It is noted that the variation is the same for both incident polarizations of light. Indeed, a look at Fig. 2 for diffuse reflectance and Fig. 3 for fluence shows that the graph for variation of unpolarized light is also identical. This is as it should be and is in line with the observations of Ramella-Roman et al. [18], where the total reflectance has been noted to be identical for all incident polarizations.

Table 1 displays numerical values of the computations of total reflectance obtained by employing MC1 and MC2 methods for unpolarized light, linearly polarized light, and circularly polarized light. These correspond to the Stokes vectors [1 0 0 0], [1 1 0 0], and [1 0 0 1], respectively. It is clear from the entries in the table that the \( R_d \) predicted by MC1 and MC2 yield widely different results. The POLMC program has been used in these computations.

For further confirmation of our results regarding disagreement between MC1 and MC2, we have also compared results of MC1 and MC2 computations for the eight-particle model of Gelebart et al. [13] in the context of white brain matter. The particle sizes in this model are 0.1, 0.15, 0.4, 0.06, 0.8, 1.0, 3.0, and

\[
T_v = 0.0278.
\]

The only difference in the graphs for two \( T_v \) is that, while the curves for MC1 and MC2 cross each other at some point for higher \( T_v \), they do not cross each other for lower \( T_v \). They would perhaps cross each other at a higher value of \( r \). The important point being reinforced is the conclusion that MC1 and MC2 need not yield the same result. The result in Fig. 2 also rules out that the volume concentration could be a source of disagreement between MC1 and MC2.

Fig. 2. Comparison of \( R_d(r) \) versus \( r \) for MC1 and MC2 for \( T_v = 0.2 \) [corresponding to \( \mu_s/(cm^{-1}) = 266.165, \mu_a/(cm^{-1}) = 3.995 \)] and \( T_v = 0.20 \) [corresponding to \( \mu_s/(cm^{-1}) = 36.305, \mu_a/(cm^{-1}) = 0.545 \)]. The incident light is unpolarized, and the average \( g \) value is 0.74.

Fig. 3. Comparison of \( \phi(z) \) versus \( z \) for MC1 and MC2. The incident light is unpolarized and \( T_v = 0.2 \) [corresponding to \( \mu_s/(cm^{-1}) = 266.165, \mu_a/(cm^{-1}) = 3.995 \)]. The average \( g \) value is 0.74.

Fig. 4. (a) Comparison \( R_d(r) \) versus \( r \) from MC1 and MC2 for incident light polarized linearly [1 1 0 0] and circularly [1 0 0 1]. Volume fraction \( T_v = 0.2 \) [corresponding to \( \mu_s/(cm^{-1}) = 266.165, \mu_a/(cm^{-1}) = 3.995 \)] and \( a = 5.0 \): lines, linearly polarized light; points, circularly polarized light. The average \( g \) value is 0.74. (b) Comparison of \( \phi(z) \) versus \( z \) from MC1 and MC2 for incident light polarized linearly [1 1 0 0] and circularly [1 0 0 1]. Volume fraction \( T_v = 0.2 \) [corresponding to \( \mu_s/(cm^{-1}) = 266.165, \mu_a/(cm^{-1}) = 3.995 \)] and \( a = 5.0 \): lines, linearly polarized light; points, circularly polarized light. The average \( g \) value is 0.74.
10.0 µm, \( T_s = 0.2 \), \( x = 5.0 \), and incident polarization was taken to be [1100]. The results of comparison between MC1 and MC2 for this model are depicted in Figs. 5(a) and 5(b), respectively, for diffuse reflectance and fluence. Once again, a large disagreement between MC1 and MC2 may be noted.

Having established that the utilization of procedures MC1 and MC2 need not always yield an identical result in the simulation of light propagation in tissue, we now attempt to trace the source of this disagreement and try to answer the question of under what conditions MC1 and MC2 could give equivalent results. Toward this end, we consider a truncated size range, \( 1.0 \mu m \leq d \leq 25.6 \mu m \), of the same distribution. Figures 6(a) and 6(b), respectively, depict a comparison of the variation of \( R_d(r) \) with \( r \) and a variation of \( \phi(z) \) with \( z \) computed using the MC1 and MC2 methods for this truncated size range. The incident Stokes vector is [1100], \( T_s = 0.2 \), \( x = 5.0 \) in these figures. It is clear from these figures that the divergence between the results of MC1 and MC2 has almost completely disappeared. This observation has been ratified with another example of truncated distribution. This is an even more narrow range: \( 2.0 \mu m \leq d \leq 4.0 \mu m \). This range has been used by Ramella-Roman et al. [15] for a modified gamma distribution. As can be seen from Figs. 7(a) and 7(b), the agreement between MC1 and MC2 predictions is very good for this range, too. It may also be recalled [Figs. 1(a) and 1(b)] that MC1 and MC2 agree completely for monodispersion of scatterers. This observation regarding size range and agreement between MC1 and MC2 is qualitatively similar to the size range dependence noted by Berrocal et al. [24] in the context of spray diagnostics. Table 2 shows the numerical values of total reflectance obtained using

### Table 1. Comparison of Total Reflectance in MC1 and MC2 for Three Polarizations

<table>
<thead>
<tr>
<th>Stokes Vectors</th>
<th>[1 0 0 0]</th>
<th>[1 1 0 0]</th>
<th>[1 0 0 1]</th>
</tr>
</thead>
<tbody>
<tr>
<td>MC1</td>
<td>0.1888</td>
<td>0.1889</td>
<td>0.1885</td>
</tr>
<tr>
<td></td>
<td>0.5235</td>
<td>0.5221</td>
<td>0.5222</td>
</tr>
</tbody>
</table>

*Here \( T_s = 0.2 \) and \( x = 5.0 \). Particle size range in the distribution is \( 0.05 \mu m \leq d \leq 26.5 \mu m \).*
MC1 and MC2 for various polarizations for the truncated ranges. In contrast to the results for the full size range in Table 1, Table 2 shows extremely good agreement between predictions of MC1 and MC2 for truncated size ranges. Although the \( \mu_s \) and \( \mu_a \) values in these examples do not correspond to biomedical tissue values, these have been used here for illustrative purpose.

It was noted by us [11] some time back that the exact shape of the tissue phase function is far less important in MC calculations, as long as the asymmetry parameter \( g \) of the phase functions is same. The investigation was done for \( g = 0.9 \). It may be recalled that the asymmetry parameter \( g \) is a measure of the asymmetry of the phase function around 90° scattering angle. Figure 8 shows the variation of asymmetry parameter with particle size. It may be noted that at first, \( g \) rises rapidly as \( d \) increases. However, once \( d \geq 1 \) or the size parameter = \( nd/\lambda \leq 5 \), the \( g \) value is nearly constant. There are small oscillations superimposed on it. This suggests that the variation between the average phase function and the range of individual phase functions of particles in distribution will diminish for scatterers of large size or when the range of particle sizes in the distribution is small. This is indeed what has been observed in computations. It is found that the average \( g \) value for the full size range is \( g = 0.74 \) and the two extremes in the range are \( g_{\text{min}} = 0.019 \) at \( x = 0.05 \) and \( g_{\text{max}} = 0.972 \) at \( x = 2.45 \). For the truncated range, \( 1.0 \leq d \leq 25.6 \), average \( g = 0.959, g_{\text{min}} = 0.921 \) at \( x = 9.30 \) and \( g_{\text{max}} = 0.972 \) at \( x = 2.45 \). Because the extreme values differ very little from the average values, MC1 and MC2 agree for the truncated case. In the event of a monodispersion, the \( g_{\text{max}}, g_{\text{min}} \) as well as average \( g \) all have the same value.

This discrepancy between MC1 and MC2 may also be understood in terms of a reduced scattering coefficient. As has been noted by Wang and Jacques [29], the results obtained using anisotropic \( (g = 0.9) \) and isotropic \( (g = 0) \) scattering phase functions were almost identical for samples having the same reduced scattering coefficient \( \mu_s' = \mu_s(1-g) \). For narrow size distributions, where dispersion in \( g \) values is small, the reduced scattering coefficient in MC2 could be imagined to be close to that in MC1, while for a wide distribution of \( g \) values, this may not be the case.

5. Conclusions

This paper compares and contrasts the results from two approaches in MC simulations of diffuse reflectance and fluence for light propagation in a fractal modeled biomedical tissue. The first approach employs an average phase function and average scattering coefficient at each scattering center and has been referred to as MC1. This is the approach that has been used extensively till recently. The second approach selects a particle of a different size at each scattering event, in accordance with a predetermined size distribution. The scattering coefficient is taken

Table 2. Comparison of Total Reflectance in MC1 and MC2 for Three Polarizations for Truncated Size Distributions

<table>
<thead>
<tr>
<th>Stokes Vectors</th>
<th>[10 000]</th>
<th>[1 10 0]</th>
<th>[10 0 1]</th>
</tr>
</thead>
<tbody>
<tr>
<td>MC1 ( \mu_s ) ( \mu_a ) &amp; 0.5717 &amp; 0.5655 &amp; 0.5728</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MC2 ( \mu_s ) ( \mu_a ) &amp; 0.5637 &amp; 0.5921 &amp; 0.5645</td>
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<tr>
<td>MC1 ( \mu_s ) ( \mu_a ) &amp; 0.5426 &amp; 0.5365 &amp; 0.5435</td>
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<td></td>
<td></td>
</tr>
<tr>
<td>MC2 ( \mu_s ) ( \mu_a ) &amp; 0.5399 &amp; 0.5422 &amp; 0.5374</td>
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</table>

\*Here \( T_v = 0.2 \) and \( \alpha = 5 \). Particle size range of the distribution for the first row is \( 1.0 \mu m \leq d \leq 26.5 \mu m \) and for the second row is \( 2.0 \mu m \leq d \leq 4.0 \mu m \).
to be the same as in MC1. This simulation has been referred to as MC2. The results of comparisons of MC1 and MC2 predictions exhibit that the two approaches do not always agree.

The reason for the disagreement in results from MC1 and MC2 has been investigated and has been traced to the large size range of the distribution and the associated large range of the \( g \) values. As the phase function influences the MC simulations via its \( g \) value, the two approaches converge if the variation of individual \( g \) values from average \( g \) value is small. This happens as the lower limit in the size range is increased. Most \( g \) values are then close to the average \( g \) value. This is perhaps the reason why the MC2 results in [18] agree with the MC1 results.

Similar studies, as have been done in this paper, have been carried out by Berrocal et al. [24] for a log-normal distribution of drop sizes in the range from 2 to 200 \( \mu m \). It has been noted that the two approaches agree very well in the size range \( 10 \mu m \leq d \leq 200 \mu m \). It is shown that for particles smaller than \( 10 \mu m \), discrepancies in the two methods begin to appear. As the number of scatterers below \( 10 \mu m \) increases, the disagreement increases. The study of Berrocal, therefore, supports the conclusions arrived at in the present work within the context of light propagation in a tissue.

References