Accuracy of the Born approximation in calculating the scattering coefficient of biological continuous random media

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A rigorous error analysis is presented for the scattering coefficient of biological random continuous media in the Born (or single-scattering) approximation. The analysis is done in two dimensions (2-D) for simplicity of numerical computation. Scattering coefficients of various tissue-like random media are numerically calculated via statistical finite-difference-time-domain analysis. The results are then checked against analytical formulas for the scattering coefficient in the Born approximation. The validity ranges for the correlation length and the refractive index fluctuation strength of the medium are clearly identified. These 2-D results show promise for future 3-D investigations. © 2009 Optical Society of America

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The *scattering coefficient* (μ_s) of a random medium is defined as the total scattered power per unit volume of the medium under unit incident parallel-beam light intensity. It is a commonly used theoretical and experimental parameter in many scattering problems in physics and engineering. It is well known that μ_s plays an important role in the multiple-scattering theory for discrete random media [1,2]. For continuous random media, the theoretical tools are relatively less developed. Nevertheless, for weakly scattering media such as biological tissue, a perturbation (or Born) expansion of the scattered wave proves to be valuable. Retaining only the first term in this expansion is usually termed the Born (or single-scattering) approximation [3]. In this approximation, the scattering coefficient μ_s as defined above becomes an essential element in the multiple-scattering theory of a continuous random medium [4,5]. It is important to keep in mind, however, that this approximation is valid only for weak refractive-index fluctuations. For stronger fluctuations, the very definition of μ_s (scattered power per unit volume) gradually loses its meaning, as other wave effects such as localization take effect [4]. In this Letter, we investigate the accuracy of the Born approximation in calculating μ_s in continuous random media with refractive index (RI) properties resembling biological tissue. Although we consider 2-D random media for ease of numerical computation, our results should be valuable for inferring approximate criteria for the full 3-D case, for which a theoretical model was presented in [6].

For the assessment of theoretical approximations, one needs a rigorous numerical solution to the light-scattering problem. One of these numerical techniques is the finite-difference time-domain (FDTD) method [7]. This method relies on the numerical solution of full-vector Maxwell's equations directly in the time domain, thereby providing a broadband response in a single simulation. The tremendous efficiency offered by FDTD in simulating very complex media with arbitrary refractive index distributions is an attractive feature for studying biological tissues. Recently, it has become possible to obtain more detailed and accurate data on the RI distributions of biological tissue [8–10]. The information thus gathered can be used to construct a random model for the biological medium and fed as an input to such electromagnetic modeling tools as FDTD.

In the following, we first derive analytical equations for the scattering coefficient μ_s in the Born approximation. We then numerically calculate the scattering coefficient μ_s of various 2-D continuous random media using statistical FDTD analysis and compare the results with theoretical values. We define a meaningful measure of the "error" in the scattering coefficient and plot this error for a range of random medium parameters.

The *normalized RI fluctuation* of a medium is defined by $\Delta n(\bar{\rho}) = (n(\bar{\rho}) - n_0)/n_0$, where n_0 is the average RI of the medium. In this Letter, we consider a specific random (or stochastic) model for the normalized RI fluctuation and discuss the implications of this model in detail. In this model, the normalized RI fluctuation is represented by a 2-D statistically homogeneous Gaussian random field with correlation

$$B_n(\Delta\rho) = \sigma_n^2 \frac{\Delta\rho}{l_c} K_1\left(\frac{\Delta\rho}{l_c}\right), \tag{1}$$

in which $\Delta\rho$ is the distance between two points, σ_n is the *fluctuation strength*, l_c is the *correlation length*, and $K_1(\cdot)$ is the modified Bessel function of second kind and order 1. The specific choice for the correlation function is of comparatively little concern, because the accuracy of the Born approximation is more influenced by l_c and σ_n than by the exact shape of the correlation function.

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The random sample with correlation (1) is illuminated by a plane wave from direction $\hat{k}_i$, and the radiated scattered field is observed at direction $\hat{k}_o$. If the electric-field polarization vector $\hat{e}_i$ of the plane wave lies along the axis of invariance, the excitation is TM, or scalar. Otherwise, the excitation is TE, or vector. In 3-D space, scattering parameters such as the total or differential scattering cross section are defined *per unit volume* [1]. Since we are concerned with a 2-D geometry, the same parameters are defined *per unit area*. The *differential scattering cross section per unit area* $\sigma(\hat{k}_o,\hat{k}_i)$ is defined as [1]

$$\sigma(\hat{k}_o,\hat{k}_i) = \langle |f(\hat{k}_o,\hat{k}_i)|^2 \rangle / S, \tag{2}$$

in which $f(\hat{k}_o,\hat{k}_i)$ is the scattered wave amplitude at direction $\hat{k}_o$, S is the differential surface area, and the mean $\langle\cdot\rangle$ is taken over the ensemble of differential areas with correlation (1). Using methods similar to those in [1], a closed-form expression for $\sigma(\hat{k}_o,\hat{k}_i)$ can be obtained in the Born approximation. For TM (scalar) excitation,

$$\sigma_{\mathrm{TM}}(\hat{k}_o,\hat{k}_i) = \frac{2\sigma_n^2 k^3 l_c^2}{(1+4k^2 l_c^2 \sin^2(\theta/2))^2}, \tag{3}$$

in which $k=(\omega/c)n_0$ is the wavenumber corresponding to the average RI of the medium and θ is the angle between $\hat{k}_i$ and $\hat{k}_o$. The corresponding result for TE excitation is simply Eq. (3) multiplied by a dipole factor $\cos^2\theta$. Finally, the scattering coefficient μ_s is found by integrating the differential scattering cross section per unit area $\sigma(\hat{k}_o,\hat{k}_i)$ over $0<\theta<2\pi$,

$$\mu_{s_{\mathrm{TM}}} = \frac{4\sigma_n^2 k^3 l_c^2 (1+2k^2 l_c^2)\pi}{(1+4k^2 l_c^2)^{3/2}}, \tag{4}$$

$$\mu_{s_{\mathrm{TE}}} = \sigma_n^2[-1-4k^4 l_c^4 + 8k^6 l_c^6 + \sqrt{1+4k^2 l_c^2} + 2k^2 l_c^2(-3 + 2\sqrt{1+4k^2 l_c^2})]\pi/k l_c^2 (1+4k^2 l_c^2)^{3/2}. \tag{5}$$

In the following, we test the accuracy of Eqs. (4) and (5) in tissuelike 2-D media by comparison with rigorous numerical results obtained using statistical FDTD analysis.

For the statistical FDTD analysis of scattering from a random medium, averaging is needed over many samples with the correlation specified in Eq. (1). The random samples are generated using an inverse-Fourier-transform approach, in which the 2-D spatial Fourier transform of the random medium is generated first and inverse transformed to spatial domain for the final result. The method is based on a straightforward generalization of the principle that the Fourier transform of a stationary random process is nonstationary white noise with variance equal to the power-spectral density of the random process. Grayscale images of some random samples generated using this method can be found in [11].

The RI distribution of biological media has been the focus of many experimental investigations. Values ranging between 1.35 and 1.38 are encountered in the literature for the average RI (or the cytoplasm RI), n_0, of biological cells [8,10]. Fluctuation strengths (σ_n) ranging from 0.007 to 0.022 are also reported in the mentioned studies. In the following examples, we use the common value of $n_0=1.38$ for the average RI. We consider different values of σ_n and l_c, and calculate the error in the scattering coefficient predicted by Eqs. (4) and (5).

The FDTD model applied in this Letter uses the same techniques as described in [7]. This yields a computed differential scattering cross section for canonical scatterers within ±1 dB of the exact solution for all scattering angles over a dynamic range exceeding 50 dB. Specifically, the FDTD simulations are carried out as follows. A differential area of dimensions $L\times L$ is placed in the center of a 2-D FDTD grid with grid spacing $\Delta=13.3$ nm and time step $\Delta t = 0.98(\Delta/c)/\sqrt{2}$. The grid is terminated by a convolution perfectly matched layer [7] of thickness 266 nm. A plane wave with TE polarization is sourced into the FDTD grid using the total-field/scattered-field approach [7]. The results for TM incidence are almost identical and are omitted for brevity. The electric field of the plane wave is a Gaussian-modulated sinusoidal pulse in time, the spectral amplitude of which is above −20 dB of its maximum between 400 nm and 700 nm in vacuum, which corresponds to the visible range of the electromagnetic spectrum. The radiated far field obtained via the near-field-to-far-field transformer [7] is normalized by the spectrum of the plane wave, numerically integrated over all angles, divided by the differential area, and finally averaged over 200 realizations of the random medium to obtain the scattering coefficient $\mu_{s_{\mathrm{TE}}}$.

In Fig. 1, the normalized scattering coefficient μ_s/k is given for two different kl_c values and a range of normalized differential-area dimensions, kL. In Figs. 1(a) and 1(b), the correlation lengths are $l_c=0.3\lambda$, and $l_c=3.45\lambda$, respectively, which correspond to cellular-scale fluctuations in the visible-light spectrum. The value of σ_n is 0.02 for both figures. The solid horizontal line denotes the μ_s value predicted by the Born approximation [Eqs. (4) and (5)], and the dashed line denotes the Rayleigh limit [12], where the scattering coefficient is proportional to the sample area: $\mu_s = \sigma_n^2 k^3 L^2/2$. It is seen that the Born approximation is inaccurate at the two extremes of kL: For small kL, there is not enough spatial averaging for the correlation (1) to take effect. For large kL, multiple scattering effects become dominant. This latter case is signified by decreased *mean-free path* l_s, which is customarily defined in transport theory as $l_s=1/\mu_s$. When l_s becomes comparable with the sample dimension L, the Born approximation becomes less accurate, as seen in the large-kL regions of Figs. 1(a) and 1(b). In summary, the Born approximation is valid for sample sizes that are larger than l_c (for adequate spatial averaging) and smaller than l_s (for single scattering.) If no such range for L exists [as in Fig. 1(b)], the Born approximation ceases to be valid. The sample size can thus be eliminated from the validity

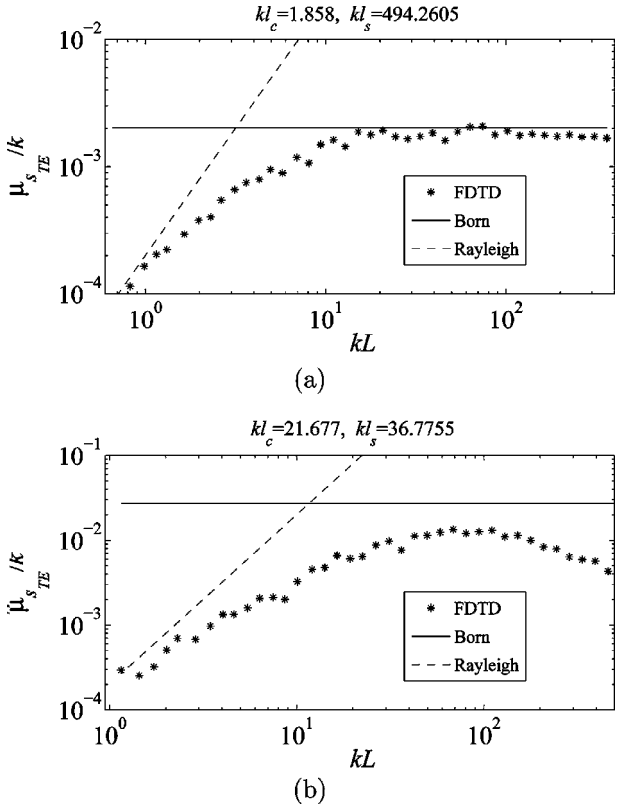

Fig. 1. Normalized TE scattering coefficient $\mu_{s_{\mathrm{TE}}}/k$ as a function of the normalized sample dimension kL: (a) small-error case, (b) large-error case.

criterion by writing $l_c \ll l_s = 1/\mu_s$. Using Eqs. (4) and (5), this can be rewritten as

$$\begin{aligned} \sigma_n^2 (kl_c)^3 &\ll 1 \quad \text{for } kl_c \ll 1 \\ \sigma_n^2 (kl_c)^2 &\ll 1 \quad \text{for } kl_c \gg 1 \end{aligned}. \tag{6}$$

As a heuristic measure of the error in the Born approximation, we consider the minimum percentage difference between the FDTD result and the Born approximation in Fig. 1. A third-order polynomial is fitted to the FDTD plot to reduce the error caused by spurious minima. In reference to expression (6), and considering the fact that $kl_c > 1$ is frequently satisfied in biological tissue, the error is plotted with respect to $\sigma_n kl_c$ in Fig. 2. The curves are seen to coincide for different values of σ_n and kl_c, which lends more support to the criterion

$$\sigma_n^2 (kl_c)^2 \ll 1. \tag{7}$$

An immediate consequence of Fig. 2 is that a maximum 20% error can be attained for the scattering coefficient in the Born approximation if $\sigma_n kl_c < 0.1$.

Extrapolating the above method to 3-D, it follows from [6] that the corresponding criterion for 3-D is $\sigma_n^2 (kl_c)^2 \ll 1$, which is the same as expression (7) for 2-D.

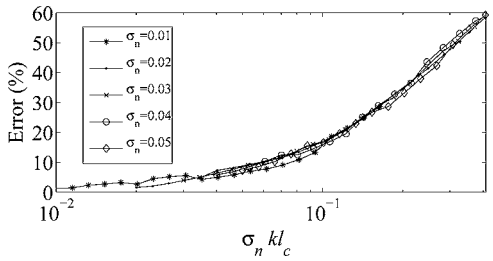

Fig. 2. Percentage error caused by the Born approximation in calculating the TE scattering coefficient $\mu_{s_{\mathrm{TE}}}$.

In this Letter, we have presented a rigorous assessment of the Born approximation in calculating the scattering coefficient of biological random media using the FDTD method, which is a full-vector electromagnetic simulation tool widely used in the scattering analysis of complex media. A validity condition $\sigma_n^2 (kl_c)^2 \ll 1$ was derived and numerically justified for the specific correlation function (1). Although the results are for 2-D random media, they provide valuable information regarding the range of validity of the Born approximation in a general 3-D setting, which remains to be investigated in a future study.

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