Phase function estimation from a diffuse optical image via deep learning

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Abstract

Objective. The phase function is a key element of a light propagation model for Monte Carlo (MC) simulation, which is usually fitted with an analytic function with associated parameters. In recent years, machine learning methods were reported to estimate the parameters of the phase function of a particular form such as the Henyey-Greenstein phase function but, to our knowledge, no studies have been performed to determine the form of the phase function. Approach. Here we design a convolutional neural network (CNN) to estimate the phase function from a diffuse optical image without any explicit assumption on the form of the phase function. Specifically, we use a Gaussian mixture model (GMM) as an example to represent the phase function generally and learn the model parameters accurately. The GMM is selected because it provides the analytic expression of phase function to facilitate deflection angle sampling in MC simulation, and does not significantly increase the number of free parameters. Main Results. Our proposed method is validated on MC-simulated reflectance images of typical biological tissues using the Henyey-Greenstein phase function with different anisotropy factors. The mean squared error of the phase function is 0.01 and the relative error of the anisotropy factor is 3.28%. Significance. We propose the first data-driven CNN-based inverse MC model to estimate the form of scattering phase function. The effects of field of view and spatial resolution are analyzed and the findings provide guidelines for optimizing the experimental protocol in practical applications.

1. Introduction

Optical properties of biological tissues are important in developing optical technologies for diagnostic and therapeutic applications. The commonly used optical properties include the absorption coefficient (\(\mu_a\)), reduced scattering coefficient (\(\mu_s'\)), scattering coefficient (\(\mu_s\)), scattering phase function \(p(\theta, \psi)\) where \(\theta\) and \(\psi\) are the deflection and azimuthal angles respectively, scattering anisotropy (\(g\)), and tissue refractive index (\(n\)) (Jacques 2013). Since optical parameters are directly related to structural and biochemical properties of tissues, they provide contextual information and reflect physiological and pathological states (Calabro and Bigio 2014, Stier et al 2021).

Generally speaking, techniques for measuring tissue optical properties can be divided into direct and indirect methods with relative advantages and limitations. The direct method measures a particular microscopic coefficient in the way that is independent of any model of light propagation in tissue (Wilson 1995). However, the direct method is limited to optically thin samples that typically require complicate preparation procedures. The indirect methods estimate the optical parameters by solving the inverse problem of a light propagation model. Since it is not limited to thin samples, indirect methods suit well nondestructive applications; for example, evaluation of kidney transplant viability (Rowland et al 2019) and tissue damage (Hokr and
The indirect measurement methods involve either analytic approximations of the radiative transfer model (Ishimaru 1978) (such as diffusion approximation equation (Wang and Wu 2007), simplified spherical harmonics equations (Klose and Larsen 2006), and hybrid models (Chen et al 2016)) or Monte Carlo (MC) simulation (Wang et al 1995). Despite the huge computational burden, MC simulation is very successful in many applications (Yaroslavsky et al 1999), and has become the gold standard for studying the light propagation in biological tissues (Periyasamy and Pramanik 2017).

When performing the MC simulation, a prerequisite is the knowledge of the phase function, which describes the probability distribution for light to be deflected into different scattering angles at each scattering location (Bodenschutz et al 2015). Since direct measurement of the phase function using a goniophotometer is limited to thin samples and is particularly difficult for media with high anisotropy factor (Yaroslavsky et al 1999), the analytically approximated phase functions are appealing in biomedical studies. Many such phase functions were formulated in the literature, such as the Henyey–Greenstein (Henyey 1941), modified Henyey–Greenstein (Bevilacqua and Depeursinge 1999) and Gegenbauer kernel (Yaroslavsky et al 1999). Among them, the heuristic Henyey–Greenstein function, although proposed 80 years ago, is the most commonly used in the MC software (Wang et al 1995, Fang and Boas 2009, Ren et al 2013). However, the validity and accuracy of the phase function model depend not only on the characteristics of the media (Canpolat and Mourant 2000, Gkioulekas et al 2013) but also the experimental setup. For example, the Henyey–Greenstein function performs well in the diffuse domain but fails in the subdiffusive domain where the source-detector distance is short (Canpolat and Mourant 2000, Calabro and Bigio 2014) or in the spatial frequency domain imaging mode at sufficiently high spatial frequencies (Nagič et al 2019). Due to the optically heterogeneous nature of biological tissues, the selection of the phase function and the estimation of its parameters remains a rather challenging task, especially when the tissue geometry is complex.

In the past few years, the rapid advancement in artificial intelligence, especially deep learning, has revolutionized many areas of research such as computer vision and natural language processing (Bengio et al 2021), tomographic imaging (Wang et al 2020), and photonics (Goda et al 2020). Specifically, for tissue optical parameter estimation, a neural network was proposed to estimate $\mu_a$ and $\mu'_s$ and two subdiffusive parameters ($\gamma$ and $\delta$) from subdiffusively resolved reflectance Ivančić et al (2018), where the simulated observations were directly fed into a regression network consisting of three fully connected (FC) layers. Similarly, FC networks were also employed in Zhao et al (2018) and Sun et al (2021) but with more layers to estimate $\mu_a$ and $\mu'_s$ using simulated data in the spatial frequency domain. In a similar spirit, a four-layer FC network was designed by Hokr and Bixler (2021) to estimate $\mu_a$, $\mu'_s$ and $n$ simultaneously in terms of the moments of the profiles of spatial-temporal diffuse reflectance. In Chen et al (2020), advanced deep learning techniques including convolutional and generative adversarial networks were employed to learn a content-aware transformation from single illumination images to optical property ($\mu_a$ and $\mu'_s$) maps.

Although the aforementioned studies indeed leveraged deep learning methods, none of them have explored the feasibility of estimating the functional form of the phase function. As the Henyey–Greenstein model is insufficient to describe the scattering phase function in the subdiffusive regime, previous studies show that extending the inverse model by additional quantifiers improves the estimation of optical parameters (Nagič et al 2016, Bodenschutz et al 2016). Nevertheless, the phase function models expressed analytically with a number of associated parameters are usually specialized scenario-wises. They perform well when the media characteristics and experimental setup satisfy their assumptions, but they may fail when the assumptions are violated, which is quite the case in complicated practical applications (such as optical molecular tomography of small animals as human disease models (Hielscher 2005)). The successes of deep learning methods inspired us to think about their potential to estimate the functional form of the phase function directly from surface reflectance data, which is a new approach in the context. For this purpose, we design a dedicated convolutional neural network (CNN), and conduct extensive simulations on 11 typical biological tissues using a modified graphics processing units (GPU)-accelerated MC software package CUDEMCMCML (Alerstam et al 2008), which is based on the pioneering work on the steady-state MC simulation of multi-layered turbid media, which is widely known as MCML (Wang et al 1995). Whereas the experiments were performed in the diffuse domain and continuous wave (CW) mode, the proposed method could in principle be extended to other scenarios, such as the subdiffusive domain and the spatial-temporal or spatial-frequency imaging modes. We plan to investigate along this direction.

Our main contributions can be summarized as follows. First, we propose the first data-driven CNN-based inverse MC model to estimate the scattering phase function from diffuse reflectance data. The functional form of the phase function is assumed to be in the space of the Gaussian mixture model (GMM), which is quite general and computationally efficient (the analytic expression of the phase function facilitates deflection angle sampling and does not significantly increase the number of free parameters). Also, we investigate the effects of field of view (FOV) and spatial resolution on the accuracy of the phase function estimation and optimize the estimation accuracy, which promises a wide array of applications in the field of biomedical optics.
2. Materials and methods

2.1. Biological tissues

This study focuses on the estimation of the functional form of the phase function in the MC simulations with 11 typical biological tissues of known \( \mu_s \) and \( \mu'_s \) and varying g values. This choice is made based on the fact that existing techniques are more robust for measurement of \( \mu_s \) and \( \mu'_s \) but not so for \( \mu_a \) and g due to the diffusive nature of biological tissues (Jacques 2013). The \( \mu_s \) and \( \mu'_s \) values of the selected tissues are calculated based on the empirical functions with the parameters provided in Alexandrakis et al (2005). The photon wavelength is 670 nm, at which the absorption and reduced scattering coefficients are listed in Table 1. Based on the classification criteria and empirical thresholds summarized in Chen et al (2016), the tissues are classified into high scattering and low scattering categories. Among the 11 tissues, liver, spleen, muscle, and whole blood are low scattering tissues, while the others are high scattering tissues.

| Tissue          | \( \mu_s \) (cm\(^{-1}\)) | \( \mu'_s \) (cm\(^{-1}\)) | Scattering category |
|-----------------|----------------------------|-----------------------------|---------------------|
| Adipose         | 0.038                      | 12.077                      | high               |
| Bone            | 0.603                      | 24.953                      | high               |
| Bowel           | 0.117                      | 11.490                      | high               |
| Heart wall      | 0.583                      | 9.639                       | high               |
| Kidneys         | 0.654                      | 22.530                      | high               |
| Liver and spleen| 3.490                      | 6.781                       | low                |
| Lung            | 1.948                      | 21.739                      | high               |
| Muscle          | 0.863                      | 4.291                       | low                |
| Skin            | 0.699                      | 22.190                      | high               |
| Stomach wall    | 0.113                      | 14.369                      | high               |
| Whole blood     | 11.621                     | 18.140                      | low                |

There are several MC software packages available, including MCML (Wang et al 1995), MCX (Fang and Boas 2009) and MOSE (Ren et al 2013) for optical transport simulation. The absorption coefficient \( \mu_a \), scattering coefficient \( \mu_s \), and anisotropy factor g are essential for MC simulation. The reduced scattering coefficient incorporates the scattering coefficient \( \mu_s \) and the anisotropy g: \( \mu'_s = \mu_s (1 - g) \). The g value is selected in section 2.5. The use of g implies that the phase function is the Henyey–Greenstein function, which is the only type of the phase function supported by CUDAMCML and most other existing MC software packages. However, this is not a problem for validating our proposed neural network for phase function estimation.

2.2. MC simulation

Diffuse reflectance images of tissues are simulated using CUDAMCML (Alerstam et al 2008), a GPU-accelerated implementation of MCML (Wang et al 1995). Since MCML uses a Cartesian coordinate system to trace photon packets and a cylindrical coordinate system to record diffuse reflectance signals, we modified CUDAMCML to record the Cartesian coordinates of photon packets as they hit the tissue surface to generate reflectance images in the \( xy \)-plane. The spatial resolution \( \Delta r \) in the radial direction defines the resolution in the \( xy \)-plane. The size of the reflectance image \( W \times H \) (in pixels) is determined by the total number of grid elements \( N_r \) in the radial direction, i.e. \( W = H = 2N_r + 1 \). For simplicity, the FOV of the reflectance image is reported as \( 2N_r \Delta r \times 2N_r \Delta r \). The modified CUDAMCML is build with CUDA 11.1 under Xubuntu 18.04.

2.3. Phase function representation

Estimating the phase function is basically a regression problem, which can be implemented using a neural network as follows:

\[
p(\theta, \psi) = f(I_R(\mu_{al}, \mu_s, g)),
\]

where \( I_R \) is a reflectance image generated in the MC simulation and f is the nonlinear feedforward mapping of the neural network. In thicker tissues where multiple scattering occurs, such as the semi-infinite tissues used in this study, it is valid to express the scattering phase function \( p(\theta, \psi) \) as a function of the polar angle \( \theta \) while omitting the dependence on the azimuthal angle \( \psi \) (Jacques 2013, Bodenschatz et al 2016).

The popular Henyey–Greenstein function is well known as

\[
p(\theta) = \frac{1}{4\pi} \frac{1 - g^2}{(1 + g^2 - 2g \cos(\theta))^{3/2}},
\]
where the anisotropy factor $g$ is defined as the average cosine of the scattering angle, i.e. $g = \langle \cos(\theta) \rangle$. Since the integral of $\bar{p}(\theta) = 2\pi p(\theta) \sin(\theta)$ over $\pi$ is unity, the normalized Henyey–Greenstein function $\bar{p}(\theta)$ is used in the following. Without confusion, it is still denoted as $p(\theta)$. In MC implementations, equation (2) is often written as a function of $\mu = \cos(\theta)$:

$$p(\mu) = \frac{1}{2} \frac{1 - g^2}{(1 + g^2 - 2\mu g)^{3/2}},$$

(3)

which facilitates the sampling of the deflection angle at each scattering location based on the analytic inverse CDF of $p(\mu)$ (Wang et al 1995).

Unlike the other methods that estimate the unknown parameters of a known function form of the phase function, the goal of our study is to use a neural network to estimate both the form and parameters of the phase function based on reflectance signals. An intuitive approach is to use $p(\theta)$ or $p(\mu)$ as the target for the neural network to learn. However, this leads to two problems. The first is how to discretize $\theta$ or $\mu$, which determines the number of neurons in the output layer of the neural network. Too few grids would lead to too large fitting errors but too many grids would take too much computational resources. The other problem is that when the discretized phase function representation is used in the MC simulation, numerical sampling methods, such as the lookup table-based methods (Naglić et al 2017), are required but these methods are rather memory intensive.

Considering the above two issues, we propose to employ an analytic representation, the widely used GMM, to specify the functional form of the underlying phase function. A GMM is defined as the superposition of some basic Gaussian densities in the following form

$$p_{\text{GMM}}(x) = \sum_{k=1}^{K} \pi_k \mathcal{N}(x|m_k, \sigma_k),$$

(4)

where $\pi_k$, $m_k$ and $\sigma_k$ are the mixing coefficient, mean and variance of the $k^{th}$ Gaussian density $\mathcal{N}(x|m_k, \sigma_k)$, respectively, and $K$ is the number of Gaussian components (NoG). The mixing coefficients must satisfy the requirements of $0 \leq \pi_k \leq 1$ and $\sum_{k=1}^{K} \pi_k = 1$. With a sufficient number of Gaussian components and suitable mixing coefficients, GMM can approximate almost any continuous density up to an arbitrary accuracy (Bishop 2006).

In the phase function estimation, there are two choices for the formal parameter $x$ in equation (4): $\theta$ or $\mu = \cos(\theta)$. Figure 1 plots $p(\theta)$ and $p(\mu)$ for representative $g$ values. Due to the symmetry of the Gaussian density, the asymmetric form of $p(\mu)$ makes it difficult to be approximated by GMM. Hence, we choose the normalized Henyey–Greenstein function $p(\theta)$ as the target for the neural network to learn. It can be seen in figure 1(a) that the larger the anisotropy factor $g$, the narrower and steeper the Henyey–Greenstein function. Therefore, for large $g$ values, it is more difficult to fit the Henyey–Greenstein function using GMM, which is also confirmed in the simulation experiments below.

2.4. Neural network model

To design a neural network model for our purpose, several factors should be considered as follows:
augmentation. At the testing stage, the size was 220 for all datasets. The commonly used horizontal and vertical scheduler was used with an initial learning rate of 0.005, step size of 10 epochs, and drop rate of 0.1. The batch optimizer for 30 epochs with a momentum of 0.9 and a weight decay of 0.005. A step-wise learning rate decay

Graphics card. At the LOGO cross-validation and training stages, the models were trained with momentum SGD.

3. Implementation details

2.5. Experimental setup

The spatial resolution $\Delta r$ and the total number of grid elements $N_r$ in the radial direction are two key parameters in the MC simulation, which defines the spatial resolution and FOV of the simulated reflectance field. In the preliminary experiments, we found that the estimation accuracy of the phase function was not better with larger FOV or higher spatial resolution while keeping other parameters the same. This is in contradiction to our common sense of imaging systems, since we usually obtain better measurements using larger FOV and higher spatial resolution. To provide insight into this situation, we investigated the impacts of FOV and resolution on the phase function estimation in comparative experiments.

Five reflectance image datasets were simulated using CUDAMCML to investigate the effects of FOV and spatial resolution on the estimation accuracy of the phase function. The details of the datasets are presented in table 2. All 11 tissue types were covered by each of the five datasets. Each dataset has its own training and test subsets. The diffuse reflectance images of the tissues were simulated separately using CUDAMCML in a semi-infinite slab geometry and an infinitely narrow incident beam with 10 million photons. The tissue thickness was set to 100 cm to ensure the validity of the semi-infinite assumption.

In typical biological tissues, the anisotropy factor $g$ ranges between 0.75 and 0.99 (Cheong et al 1990, Calabro and Bigio 2014). In our experiments, the lower bound of $g$ was set to 0.6. For each tissue, $g$ varied from 0.65 to 0.95 with a step size of 0.1 to generate training data, and varied from 0.6 to 0.9 with a step size of 0.1 for the test data. The intention is to make the phase functions of the training and test data have different shapes as shown in figure 1, so as to verify the generalization ability of the proposed model. For each set of parameters ($\mu_\alpha$, $\mu_\mu$, and $g$), 200 samples were generated for training, and 40 samples for testing. The total numbers of images for training and testing in each dataset are 8800 and 1760 respectively.

3. Experimental results

3.1. Implementation details

The proposed PhaseNet model was implemented with Pytorch 1.8.2 on a single NVIDIA GeForce RTX 3090 graphics card. At the LOGO cross-validation and training stages, the models were trained with momentum SGD optimizer for 30 epochs with a momentum of 0.9 and a weight decay of 0.005. A step-wise learning rate decay scheduler was used with an initial learning rate of 0.005, step size of 10 epochs, and drop rate of 0.1. The batch size was 220 for all datasets. The commonly used horizontal and vertical flipping were utilized for data augmentation. At the testing stage, the five PhaseNet models for each dataset were respectively tested on the
corresponding test data to produce the estimation errors (MSE) on average. The code of PhaseNet is publicly available at https://github.com/liangyuxuan1/phasefunction2.

### 3.2. Model selection

Since the backbone of PhaseNet is fixed as ResNet-18, the NoG (K in equation 4) becomes the key parameter to determine the PhaseNet architecture. The optimal NoG for a given training dataset can be determined via cross-validation or with an analytic criterion such as the Akaike information criterion (AIC) or Bayesian information criterion (BIC) (Bishop 2006). In our experiments, it is found that AIC and BIC tend to favor overly simple models. This is because AIC and BIC use a term penalizing the number of model parameters. In PhaseNet, the number of free parameters in the FC layer is $512 \times 2$ as the reference, the performance gain was computed for the other datasets. Reducing the NoG from 2 to 12. After obtaining the optimal NoG, the PhaseNet models were trained on each dataset separately.

### 3.3. Representative results

Table 3 summarizes our key experimental results. For simplicity, the units of FOV (mm²) and spatial resolution (mm) are omitted, and an FOV is denoted together with the spatial resolution when necessary, e.g. $4 \times 4@0.02$. The MSE is presented as the average over all tissues and anisotropy factors for each dataset. The performance gain is defined as the relative error with respect to the MSE of the reference dataset $D_{S_2}$. The minus sign represents performance degradation. The relative error of $g$ is defined as $(|g - \hat{g}| / g) \times 100\%$.

| Dataset (FOV) | MSE   | Gain (%) | Relative error of $g$ (%) |
|---------------|-------|----------|---------------------------|
| $D_{S_1}(2 \times 2@0.02)$ | $0.012 \pm 0.016$ | $-16.7$ | $3.421 \pm 4.426$ |
| $D_{S_1}(4 \times 4@0.02)$ | $0.010 \pm 0.013$ | $-1.2$ | $3.280 \pm 3.047$ |
| $D_{S_1}(6 \times 6@0.02)$ | $0.017 \pm 0.013$ | $-41.2$ | $3.910 \pm 3.450$ |
| $D_{S_1}(4 \times 4@0.01)$ | $0.029 \pm 0.022$ | $-65.5$ | $5.232 \pm 5.302$ |
| $D_{S_1}(4 \times 4@0.04)$ | $0.011 \pm 0.016$ | $-9.1$ | $3.151 \pm 3.263$ |

As shown in table 3, the best estimation accuracy was achieved on $D_{S_2}$ (FOV = $4 \times 4@0.02$). Using the performance on $D_{S_1}$ as the reference, the performance gain was computed for the other datasets. Reducing the FOV to $2 \times 2$ ($D_{S_2}$) or expanding it to $6 \times 6$ ($D_{S_3}$) at the same resolution of 0.02 resulted in 16.7% and 41.2% drop in accuracy respectively. When keeping the FOV unchanged but increasing the resolution to 0.01 ($D_{S_4}$) or decreasing it to 0.04 ($D_{S_5}$), the estimation error was increased by 65.5% and 9.1% respectively. The relative errors of $g$ shared the trends of the MSE data.

The MSE values do not provide sufficient information on how close the estimated phase functions is to the ground truth. However, the nonlinear nature of the phase function estimation (regression) prevents us from using the R-squared statistic to evaluate the fitness of PhaseNet. Therefore, we visually inspect the experimental results. Figure 2 show two examples with the smallest and largest estimation errors on $D_{S_2}$. In both examples, the reflectance images look very similar despite the different tissue parameters of $\mu_s$ and $g$. PhaseNet did capture the
basic form of the Henyey–Greenstein phase function but apparently it was challenged near the boundary of $\theta = 0$ and for large $g$ value such as 0.9, for which the phase function is much steeper and narrower.

3.4. Effect of FOV on estimation accuracy

The MSE of the phase functions estimated by PhaseNet on $DS_1$, $DS_2$ and $DS_3$ are shown in figure 3. These datasets have different FOVs but have the same spatial resolution of 0.02. At the first glance, the larger the FOV, the larger the estimation error. In order to quantify the statistical difference, the Wilcoxon rank sum test was used to test the differences in MSE measures across FOVs at each $g$ value separately because the errors are not normally distributed ($p < 0.05$, Shapiro–Wilk test). The results indicate that the MSEs are significantly different ($p < 0.05$) at all $g$ values except for that with FOV $2 \times 2$ (blue dot) versus $6 \times 6$ (purple dot) at $g = 0.9$. The error plots for FOV $2 \times 2$ and $4 \times 4$ cross each other, but the average error of FOV $4 \times 4$ is smaller. The estimation error of FOV $6 \times 6$ is significantly larger than that with the other two FOVs. Figure 4 shows the estimation errors of individual tissues averaged across the FOVs. When $g = 0.9$, the errors of all tissues are significantly larger compared to that at smaller $g$ values. At $g = 0.6$, the errors of muscle and liver are significantly larger than that of other tissues. According to table 1, these two tissues are low scattering tissues.
3.5. Effect of spatial resolution on estimation accuracy

Figure 5 shows the phase function estimation accuracy on $DS_2$, $DS_4$ and $DS_5$, where the FOV was fixed at $4 \times 4$ while the spatial resolution varied from 0.02 ($DS_2$) to 0.01 ($DS_4$) or 0.04 ($DS_5$). Relative to the reference resolution of 0.02 (red dots), the estimation error was increased by 65.5% (table 3) when the resolution was increased to 0.01 (orange dots). When the resolution was reduced to 0.04 (green dots), the estimation error was increased by 9.1%. The increment of the error is mainly due to the large error with $g = 0.9$. At the other $g$ values, the estimation errors at resolution 0.04 were smaller than those at resolution 0.02. Figure 6 shows the estimation errors for individual tissues, averaged across the different resolutions. Similar to the results in figure 4, the errors are significantly larger at $g = 0.9$ compared to that at smaller $g$ values. At the other $g$ values, the three low scattering tissues, muscle, liver, and blood, were subject to significantly higher errors than the high scattering tissues.
4. Discussions

Some of the above-described experimental results might appear somewhat unreasonable at the first glance. For example, increasing the FOV and improving the spatial resolution are unhelpful and even harmful in some cases to the estimation accuracy. In general, we always want an imaging system to have as high resolution as possible with a sufficiently large FOV to guarantee the measurement accuracy. To justify the results, we investigate the distribution of the reflectance signals and the similarity of the reflectance images for different tissues and anisotropy factors.

4.1. Why expanding FOV unfavorable

Considering the radial symmetry of the reflectance images, the horizontal profiles through the incident points of the test images in DS$_2$ and DS$_4$ are shown in figure 7. The profiles are extracted from the images with $g = 0.6$ because the stronger scattering makes it easier to extract information on different tissues.

Since our experimental setup employs an infinitely narrow incident beam and does not consider the camera model, the simulated reflectance images are actually the ideal impulse response of different tissues sampled at different FOVs and spatial resolutions. Figure 7(a) shows the profiles at the FOV of $4 \times 4$ and the resolution of 0.02. It can be seen that the reflectance signals are mainly concentrated in the range of [-1, 1] mm, corresponding to a FOV of $2 \times 2$ mm$^2$. The estimation errors are comparable for the FOVs of $2 \times 2$ and $4 \times 4$ (figure 3), with the errors for FOV $4 \times 4$ a little better on average (table 3). This indicates that the region between FOV $2 \times 2$ and $4 \times 4$ contains some discriminative information despite the difference is small between the reflectance signals. However, further increasing the FOV to $6 \times 6$ would increase the estimation error significantly, as shown in figure 3 and table 3. We believe that as the FOV expands, the reflectance signals become less distinguishable in terms of amplitude and distribution.

As pointed out in Bodenschatz et al (2016), the further away photons are detected from the incident beam, the deeper they have penetrated into the tissues. The reflectance intensities far away from the incident point are

![Figure 6. Phase function estimation errors for individual tissues, averaged across the resolutions in figure 5.](image1)

![Figure 7. Profiles through test images. (a) DS$_2$, FOV = $4 \times 4@0.02$, and (b) DS$_4$, FOV = $4 \times 4@0.01$. The anisotropy factor $g = 0.6$ in both cases.](image2)
mostly contributed by the diffusive background, while the proximal intensities are composed of both the subdiffusive scattering and diffusive background. Since the diffusive background is weakly influenced by the scattering phase function, a more elaborate network design and more training samples may be required to take full advantage of it for phase function estimation.

4.2. Why refining resolution unfavorable
Figure 7(b) shows the profiles for the FOV of 4 × 4 and the resolution of 0.01. Compared with 7(a), the profiles have narrower lobes, larger amplitudes, and more clearly delineated fluctuations. This result is easily explained since the higher spatial resolution used to sample the diffuse reflectance field, the less blurring in the sampled image, and the more structural details captured in the image. However, the distances between these tissue profiles have become smaller and even intersected, thus greatly increasing the difficulty for PhaseNet to discriminate different phase functions, compromising the estimation accuracy.

The increased fine details in the reflectance images with high spatial resolution suggest that the learning task becomes more difficult. Without changing the network structure, a simple solution is to increase the number of training samples. To test this idea, the number of training samples per parametric setting in DS1 was increased from 200 to 400, thus doubling the total number of training data. Five PhaseNet models were trained with the same hyperparameters as before and tested on the original test dataset DS1. The resulting MSE is 0.016 ± 0.017 and the relative error of g is 4.201 ± 3.805%. That is, the MSE has been decreased by 44.8% with the doubled size of training data.

4.3. Why large g troublesome
The results in section 3 show that at $g = 0.9$ (the largest value we assumed at testing), the estimation errors are significantly higher than that for other g values, regardless FOV, resolution or tissue type. When the anisotropy factor is large, the propagation of light is dominated by forward-scattering. As a result, the reflectance image becomes much closer to a two-dimensional impulse function than that for a smaller g. This will require a higher spatial resolution to delineate the reflectance distribution. In other words, the reflection image at a large g value is more likely to be spatially undersampled.

4.4. Why low scattering tissues troublesome
Figures 4 and 6 show that in most cases the estimation errors are larger for muscle, liver and blood than for the other tissue types. All the three types of tissues are low scattering, as classified in table 1. Low scattering means that more photons are forward scattered or absorbed. This results in a lower intensity and smaller spot size in reflectance images. As shown in figure 7, the lowest amplitude and the smallest width of the profiles are found for muscle and liver. Similar to the case of large g values, the small main lobe width in the reflectance image explains why the estimation error becomes larger in the case of low scattering tissues.

The representational similarity analysis (RSA) (Kriegeskorte et al 2008) can be employed to analyze this issue in more depth. RSA is widely used in neuroscience to compare representations across domains using the representational dissimilarity matrices (RDMs). RDMs are square symmetric matrices with zero diagonal that encode the (dis)similarity between all pairs of data samples or conditions in a dataset. We compute the RDMs using Euclidean distance for two representations of the reflectance image, namely the profiles of the original image and the image features extracted by PhaseNet. The output of the global pooling layer in PhaseNet is used as the image feature. The resulting RDMs of $DS_2$ are shown in figure 8. Since there are 1760 images (11 tissues, 4 g values, 40 samples per g value) in the test set, the size of RDMs is $1760 \times 1760$ pixels. The images are sorted by tissue type first and then by g value.

The RDMs in figure 8 seem composed of small cells. The size of the cells is $40 \times 40$ pixels, demonstrating that the variation between images generated with same parameters ($\mu_o, \mu_s, \text{and } g$) is small. A square of $4 \times 4$ cells indicates the degree to which each pair of tissues is distinguished, or the differentiability of the same tissue with different g values when the square is on the diagonal. It can be seen that there are four large dark squares of size $8 \times 8$ cells in the top-left quarter of figure 8(a), indicating that adipose, blood, bowel and heart are closer to each other. The closer relationship between bone, kidneys, lung and skin can also be observed. It is worth noting that the four dark squares correspond to liver and muscle. They show not only that liver and muscle have similar reflectance characteristics but also that it is difficult to distinguish between livers or muscles with different g values due to the homogeneity in the squares. Therefore, it is easy to understand why the estimation errors for liver and muscle are larger than that for other tissues. As for blood, it has the largest absorption coefficient among the tissues. Since a large amount of light is absorbed, the estimation error is large for high absorption tissues. Our results are consistent with the optical parameter estimation data in Hokr and Bixler (2021). In the RDM of the image features (figure 8(b)), the dark square effect is significantly weakened and the heterogeneity of
each square is remarkably increased. This shows a better discriminability among involved tissue types and $g$ values in the feature space.

4.5. Limitations

There are several limitations that should be acknowledged when interpreting the results of this study. First, the experimental configuration does not consider the incident light beam form, imaging system model, and noise distribution. The reflectance images are the ideal impulse response of tissues. Therefore, the FOV and resolution values in the experimental results are not applicable to a real imaging system. Second, the optimal number of Gaussian components for $DS_2$ is assumed for all other datasets because we hope to keep the experimental factors consistent except for FOV and resolution. This may degrade the performance on these datasets. Third, since FOV, resolution and image size are interrelated, the image size of the datasets should be adjusted as well after varying the FOV and resolution. Comparing the PhaseNet models with different input image sizes is not totally fair, but our results should be reasonable to show the feasibility, since we do not want to introduce interpolation errors by normalizing the image sizes.

Another point to note is that in our current model design, the PhaseNet outputs a set of parameters representing one phase function. As a result it cannot be directly applied to heterogeneous tissue samples. If the network is changed to a semantic segmentation-based architecture, such as the U-Net used in Chen et al (2020), it could be possible to estimate the spatial variance of $g$ and other parameters of heterogeneous tissues.

As a proof-of-concept study, our approach currently employs a supervised learning strategy. The proposed PhaseNet model was trained and tested on Henyey–Greenstein phase functions. Its generalizability has been verified on $g$ values that are quite different from the training values. Nevertheless, the PhaseNet performance may degrade if it is trained on the Henyey–Greenstein function but tested on other types of phase functions. Inadequate generalization across datasets is a common problem of deep learning. To improve our study, combination of data-driven machine learning approaches and analytic light propagation models would be a promising direction of future research.

5. Conclusion

In conclusion, we have proposed a novel deep learning approach to estimate the functional form and parameters of the phase function directly from diffuse reflectance data. The GMM has been used to specify the phase function using a modified ResNet-18 regression model. The proposed network has been validated on MC simulated reflectance images of 11 biological tissues and the Henyey–Greenstein phase function with typical anisotropy factors. In our experiments, the mean-squared-error and the relative error of the anisotropy factor are 0.01 and 3.28% respectively, demonstrating the feasibility and accuracy of using a convolutional neural network for phase function estimation. A comparative study has been performed to analyze the effects of FOV and spatial resolution on the estimation accuracy. The results suggested that larger FOV and higher spatial resolution do provide more information about the diffusive reflectance for deep learning but to fully utilize this information for estimation of the underlying phase function, a more elaborate network design and/or more training data are required. Our study has demonstrated the feasibility of using machine learning for phase
function estimation and lays the foundation for extended research into the subdiffusive domain and for in vivo measurements.

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Appendix. Architecture of PhaseNet

The detailed architecture of the proposed PhaseNet is shown in figure A1.

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