A hybrid voxel sampling method for constructing Rad-HUMAN phantom (postprint)

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Abstract

An accurate and fast sampling method was developed for modeling a voxel phantom called Rad-HUMAN for radiation protection in MC-based radiation transport and simulation. The segmented organ voxels, which were assigned three-dimensional (3D) coordinates, were simplified using a two-step hybrid sampling algorithm. First, certain voxels were sampled into a coordinate matrix using nearest neighbor sampling. Second, the coordinate matrix was updated using weighted sampling. For visualization and comparison with the sampling, the resulting matrix was used to extract the contours of organs/tissues to construct a polygon-surface phantom. The feasibility and effectiveness of the sampling method were verified through modeling of large organs (e.g., skeleton system) and application of transformations to MC computational geometries.

Full Text

Preamble

A Hybrid Voxel Sampling Method for Constructing Rad-HUMAN Phantom

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An accurate and fast sampling method was developed for modeling a voxel phantom called Rad-HUMAN for radiation protection in Monte Carlo-based radiation transport and simulation. The segmented organ voxels, which were assigned three-dimensional (3D) coordinates, were simplified through a two-step hybrid sampling algorithm. First, certain voxels were sampled into a coordinate matrix using nearest neighbor sampling. Second, the coordinate matrix was renewed using weighted sampling. To enable visualization comparison with the sampling, the resultant matrix was used to extract organ/tissue contours for constructing a polygon-surface phantom. The feasibility and effectiveness of the sampling method were verified through modeling large organs (e.g., skeleton system) and applying transformation to Monte Carlo computational geometries.

Keywords: Sampling, Monte Carlo, Voxel, 3D, Rad-HUMAN
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Introduction

Computational phantoms have been used extensively in radiation protection for Monte Carlo-based radiation transport and simulation [1]. The accuracy of the phantom plays a critical role in dose calculation [2, 3], and computational phantoms based on color photographic images containing detailed human body information have been developed in many countries [4, 6]. However, dealing with massive voxels accurately poses a significant challenge [5]. Many refinement methods were developed that did not focus directly on the original voxels, and sometimes voxels were sampled with interpolation. This may generate ambiguity that can cause serious problems in whole-body phantom construction. Due to limitations in computer performance, large organs (e.g., skeleton system) from image slices cannot be constructed as a whole accurately.

Based on high-resolution sectioned images from a Chinese Visible Human (CVH) dataset, a voxel phantom called Rad-HUMAN (Accurate whole-body computational phantom of Chinese adult female) was established by the FDS Team (www.fds.org.cn). This CVH dataset contains 3641 slices with 3286 × 1586 pixel resolution, obtained from a Chinese female cadaver. Each voxel in the dataset measures 0.15 mm × 0.15 mm × 0.25 mm for the head and neck, and 0.15 mm × 0.15 mm × 0.5 mm for the rest of the body. The total number of voxels is approximately 16.8 billion. Segmentation [6] (Fig. 1 [Figure 1: see original paper]) was processed manually and calibrated by MCAM (Multi-Physics Coupling Analysis Modeling Program) developed by the FDS Team [7–9]. In addition to the fact that the voxel phantom was difficult for Monte Carlo dose calculation, demonstrating its geometry was also laborious [6].

In this work, a flexible sampling method was investigated for modeling the Rad-HUMAN voxel phantom. Based on this method, visualization was compared and computational geometries for Monte Carlo dose calculation were discussed.

Voxel Sampling Method

A. Nearest Neighbor Sampling

After segmentation, organs were distinguished by different RGB colors. In this paper, the dataset of voxels assigned with 3D coordinates can be written as:

$$(d_{i,j,k})_{w\times l\times h} = (0,0,h-1) \quad (w-1,0,h-1) \quad (0,l-1,h-1) \quad ... \quad (w-1,l-1,h-1), \quad i,j \in [0,w{-}1/l{-}1];$$

where w, l, and h are the width, length, and height of the CVH dataset, respectively; and i, j, and k are the position subscripts of the voxels.

It is unnecessary to obtain all voxels of a certain organ to arduously construct its model. In nearest neighbor sampling, the segmented voxels are appropriately enlarged and sampled from their nearest neighbors. When changing the voxel array from $w \times l \times n$ to $w' \times l' \times n'$, the sampling enlargement factor can be expressed as:

$$\text{Enlargement factor} = \left(\frac{w'}{w}, \frac{l'}{l}, \frac{n'}{n}\right) = (S_x, S_y, S_z).$$

Step 1: Obtain coordinate matrix α of an organ as referenced in Eq. (3).

Step 2: Map the matrix α to a sampling matrix β. Supposing $(x_\alpha, y_\alpha, z_\alpha)$ is an element of α, the element of β becomes $(S_x, S_y, S_z) = \left(\frac{w'}{w}, \frac{l'}{l}, \frac{n'}{n}\right)$.

To be consistent with subsequent sampling, the voxel coordinates of an organ can be described as a sparse matrix α:

$$\alpha = (\alpha_{i,j,k})_{w\times l\times h}, \quad \alpha_{i,j,k} = \begin{cases} d_{i,j,k}, & \exists F(d_{i,j,k}) \\ 0, & \nexists F(d_{i,j,k}) \end{cases}$$

where $\exists F(d_{i,j,k})$ (or $\nexists F(d_{i,j,k})$) means that $d_{i,j,k}$ is (or is not) a coordinate of the original organ.

In nearest neighbor sampling, the sampled organ $f(x,y,z)$ is acquired from an original organ $F(X,Y,Z)$ described as:

$$f(x,y,z) = F([S_x \times x],[S_y \times y],[S_z \times z]),$$

where the symbol "[ ]" stands for rounding off the number for the result. Thus, the resultant coordinate matrix of the sampled organ can be described as:

$$\gamma = (\gamma_{i,j,k})_{w'\times l'\times h'}, \quad \gamma_{i,j,k} = \begin{cases} d_{i,j,k}, & \exists F(d_{[i\times S_x],[j\times S_y],[k\times Sz]}) \\ 0, & \nexists F(d_{[i\times S_x],[j\times S_y],[k\times Sz]}) \end{cases}.$$

To decrease the demand for computer memory, in the present study, the nonzero coordinates ($\gamma_{i,j,k}$) were stored on disk in file format corresponding to exclusive addresses for compressed storage.

B. Weighted Sampling

As accuracy loss is significant with nearest sampling, a weighted sampling method was proposed in this study. With the same enlargement factor defined in Eq. (2), a sampling unit can be enclosed by a lattice with size $S_x \times S_y \times S_z$. Obviously, the voxels in the lattice cannot always belong to one organ; hence a weighted factor is needed to judge whether the voxels of the sampling unit can be regarded as a voxel after sampling.

After sampling, the relative position of the voxel changes corresponding to the sampled voxel array ($w' \times l' \times n'$). That is, the coordinates must be scaled by a factor of $(1/S_x) \times (1/S_y) \times (1/S_z)$ for consistency. In addition, described as coordinates with exclusive addresses, the original voxels of the lattice can be projected to a new address of the sampled storage. This enables effective counting of the number of voxels belonging to one organ being projected. Therefore, according to a defined weight of the voxels in the lattice, the voxels of a certain organ can be sampled quickly. The detailed steps for weighted sampling are as follows.

Step 1: Obtain coordinate matrix α of an organ as referenced in Eq. (3).

Step 2: Map the matrix α to a sampling matrix β, where the mapped address in β can be described as θ with the element obtained from:

$$\theta = (x_\alpha, y_\alpha, z_\alpha) \cdot \tau$$

$$S_x \times S_y \times \left(\frac{1}{S_x \times S_y \times S_z} \right)$$

where ω and τ in Eq. (7) are factors that multiply every element of α.

Step 3: Record the weights of certain coordinates which are mapped into the same locations. Let (x, y, z) be a coordinate after sampling, which is mapped from σ (a region of sampling lattice):

$$\sigma \in \{([x \times S_x], [y \times S_y], [z \times Sz]), ([(x+1) \times S_x], [(y+1) \times Sy], [(z+1) \times Sz])\}.$$

In this step, the coordinates in σ are stored at the same location with $\delta(x, y, z)$ recording their amounts.

Step 4: Filter the coordinates from β, with weights no less than a weight factor. Supposing the weights are defined as the proportional amounts of the sampling

unit which is 0.5, the filtered coordinate matrix γ can be selected from β with the condition:

$$\delta(x, y, z) > 0.5 \times S_x \times S_y \times S_z.$$

The resultant coordinate matrix γ can also be stored on disk in file format in sequential order.

C. Hybrid Voxel Sampling

Nearest sampling is a fast way to reduce data size. However, it is not recommended for smaller data due to serious accuracy losses. In this paper, we combine it with weighted sampling as a two-step hybrid sampling algorithm. In hybrid sampling, the sampling unit is divided into smaller lattices for nearest sampling, and then the smaller lattice can be assigned weights for weighted sampling.

To this end, the enlargement factor (S_x, S_y, S_z) was divided into (N_x, N_y, N_z) and (P_x, P_y, P_z) for nearest sampling and proportional sampling, respectively:

$$(P_x, P_y, P_z) = \left(\frac{S_x}{N_x}, \frac{S_y}{N_y}, \frac{S_z}{N_z}\right).$$

Using an enlargement factor of (N_x, N_y, N_z) for nearest sampling, the original coordinate matrix can be obtained according to Eq. (5) where:

$$\alpha_{i,j,k} = \begin{cases} d_{i,j,k}, & \exists F(d_{[i\times N_x],[j\times N_y],[k\times N_z]}) \\ 0, & \nexists F(d_{[i\times N_x],[j\times N_y],[k\times N_z]}) \end{cases}.$$

In order to combine nearest sampling with weighted sampling for hybrid sampling, the factors in Eqs. (6) and (7) for mapping and locating become:

$$\omega = \left(\frac{1}{P_x}, \frac{w}{P_y \times S_x}, \frac{w \times l}{P_z \times S_x \times S_y}\right)$$

and

$$\tau = \left(\frac{1}{P_x}, \frac{w}{P_y \times S_x}, \frac{w \times l}{P_z \times S_x \times S_y}\right),$$

respectively. The detailed steps to implement the hybrid sampling algorithm are shown in Fig. 2 [Figure 2: see original paper].

Results and Discussion

A. Application in Construction of Polygon-Surface Phantom

Organs or tissues of interest (e.g., lungs, liver, skin, etc.) from the original tomographic photography were identified by assigning each pixel an identification number. All these numbers can be stored sequentially as a pixel matrix that can be used to extract an equivalent matrix, from which the polygon-surface model can be constructed using Marching Cubes [10]. The equivalent matrix can be acquired by the last step of the sampling method. For example, in weighted sampling, for the purpose of generating matrix γ, coordinates satisfying the condition $\delta(x, y, z) > 0.5 \times S_x \times S_y \times S_z$ are set as one identification number, while coordinates not satisfying that condition are set as another identification number. The transformed matrix γ can then be used as the equivalent matrix with the VTK toolkit to generate the polygon-surface model.

Preliminarily, these sampling methods were processed with a single CPU of a 3.10 GHz Intel Core™ 2 Quad Processor i5-2400 64-bit operating system. To compare two special cases of hybrid sampling, the construction of a heart organ containing 265 slices was used as an example. Defining proportional amounts as weights, Table 1 presents relevant sampling parameters between nearest and weighted sampling methods, which are compared visually in Figs. 3(a) and 3(b).

When voxels were increased by a factor of 2.0 in x, y, and z directions, the time expenditure for nearest sampling was approximately 7.09% of that for proportional sampling. The number of holes and model size produced by weighted sampling were 84% and 95% of those produced by nearest sampling, respectively. With weighted sampling, incorrect models resulting from segmentation can be repaired (Fig. 3 Figure 3: see original paper). Parameters between the two methods (Table 1) mainly depend on computer performance and dataset resolution, among other factors. For precision adjustment, the proportional weight factor can be utilized.

B. Improvement on Sampling and Analysis

The nearest and weighted sampling methods in this paper are treated as two special cases of hybrid sampling. To discuss their combined criteria, an additional experiment was conducted with a large organ (e.g., skeleton system, including marrow, pelvis, cartilage, etc.). With the same enlargement size of $4.0 \times 4.0 \times 4.0$ and a proportional weight of 0.5 for both proportional and hybrid methods, modeling parameters for the three sampling approaches are given in Table 2 , and visualization comparisons are illustrated in Fig. 4 [Figure 4: see original paper].

In hybrid sampling, the enlargement size of $4.0 \times 4.0 \times 4.0$ was divided into $2.0 \times 2.0 \times 2.0$ for both nearest and weighted sampling. The time expenditure for hybrid sampling was approximately 18.15% of that for proportional sampling. Additionally, the number of holes in the model produced by hybrid sampling

was about 16.43% of that produced by nearest sampling. This is advantageous for creating accurate models quickly for visualization [11, 12]. The visualization of models constructed by the three sampling methods is shown in Fig. 4.

Nearest sampling may cause severe distortion (Fig. 4(a)) when the sampling enlargement factor becomes larger. Hybrid sampling, therefore, is an appropriate method to compensate for such deficiencies and enhance the process. It is a flexible sampling method that can evolve from one approach to another with a distributed enlargement factor. The combined criterion depends on sampling ratio, dataset size, computer performance, etc. Generally, considering visual impact, the enlargement size allocated for nearest sampling should not exceed $2.0 \times 2.0 \times 2.0$. This can largely reduce data size for fast processing with current personal computer configurations. For applications demanding higher model accuracy (Figs. 4(b) and 4(c)), the enlargement factor allocated for weighted sampling should be larger. Because the whole phantom contains many organs, hybrid sampling can provide acceptable visualization and geometry checking times.

From Table 2, the percentage of holes to faces for nearest, weighted, and hybrid sampling is 1.26%, 0.17%, and 0.20%, respectively. Based on the visualization in Fig. 4, a hole-to-face percentage of about 0.20% can serve as a reference acceptance criterion for better visualization.

Using hybrid sampling with voxels enlarged by a factor of $4.0 \times 4.0 \times 4.0$, the entire skeleton system can be shown in Fig. 5 [Figure 5: see original paper].

C. Application in Monte Carlo Computational Geometries

For dose calculation in lattice geometry, the methods presented in this paper can be applied [13]. In this case for Monte Carlo simulation, the pixel matrix of the whole phantom should be generated. The weight definition can be designed based on material, density, or other biological properties. Next, accumulate the weights from the resultant coordinate matrix (e.g., γ), locate voxels in the pixel matrix satisfying the weighted factor, and assign them identification numbers. Finally, the pixel matrices of the body can be transferred to lattice representation geometry in MCNP codes [14, 15].

However, in addition to lattice geometry [16, 17], the polygon-surface model constructed by Marching Cubes [18] can hardly avoid surface intersections and holes. For dose calculations with deformable phantoms [19, 20], repair/improvement (e.g., filling, relaxation) is needed to eliminate imperfections or interference, and to transfer the model into formats accepted by MC codes (e.g., MCNP, Geant4, etc.).

Conclusion

In this paper, a hybrid voxel sampling algorithm that merges nearest sampling and weighted sampling was proposed. Through discussions of model construc-

tion, the three sampling methods are capable of handling massive voxel datasets. For accurate sampling, weighted and hybrid sampling are effective. As a flexible sampling approach, hybrid sampling demonstrates high performance, especially in constructing large organs. It is a valid sampling method for visualizing the Monte Carlo geometries of human voxel phantoms.

Furthermore, based on these methods, geometries for Monte Carlo dose calculation were analyzed. The phantom of polygon-surface geometry or lattice representation geometry can be transferred to MC codes for dose calculations. Finally, through the proposed sampling, more accurate CAD (Computer Aided Design) models (STEP, etc.) can be constructed for medical diagnosis and other scientific research fields.

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Note: Figure translations are in progress. See original paper for figures.