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Design of a Multiple Component Geometric Breast Phantom

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ABSTRACT

The quality and realism of simulated images is currently limited by the quality of the digital phantoms used for the simulations. The transition from simple raster based phantoms to more detailed geometric (mesh) based phantoms has the potential to increase the usefulness of the simulated data. A preliminary breast phantom which contains 12 distinct tissue classes along with the tissue properties necessary for the simulation of dynamic positron emission tomography scans was created (activity and attenuation). The phantom contains multiple components which can be separately manipulated, utilizing geometric transformations, to represent populations or a single individual being imaged in multiple positions. A new relational descriptive language is presented which conveys the relationships between individual mesh components. This language, which defines how the individual mesh components are composed into the phantom, aids in phantom development by enabling the addition and removal of components without modification of the other components, and simplifying the definition of complex interfaces. Results obtained when testing the phantom using the SimSET PET/SPECT simulator are very encouraging.

Keywords: synthetic images, geometric phantoms, digital simulators, breast, SimSET, positron emission tomography

INTRODUCTION

Obtaining “ground-truth” data in medical imaging is an almost impossible quest when pathology reports are not available. One way to circumvent this limitation is by creating digital synthetic phantoms with the appropriate physical properties and characteristics that can be imaged using digital simulators.

Digital simulators can be used to study system design, acquisition protocols, reconstruction techniques, and evaluate image processing algorithms. In addition to providing a precise ground truth, they can be used to save significant time and money compared to recruiting volunteers, scheduling and paying for scanner time. The simulator selected for this work is SimSET for PET/SPECT.

The University of Washington has developed a PET/SPECT simulator based on Monte Carlo techniques that models the physical processes and instrumentation used in emission imaging. SimSET^{1,2,3,4,5}, which can be used to model both single photon emission computed tomography (SPECT) and positron emission tomography (PET), models the important physical phenomena including photoelectric absorption, Compton’s scattering, coherent scattering, photon non-collinearity, and positron range. It supports a variety of collimator and detector designs, and already includes the attenuation properties for many common materials. If the attenuation and activity properties are known for each voxel the gamma signal can be generated. SimSET and its source code can be downloaded from ⁶. The code is written in a modular format as shown in Figure 1.

Even at this preliminary stage in our research it was realized that the computational complexity of the simulator may be a limitation for its utility due to the extremely long time required to run realistic simulations. To overcome this difficulty, we have proposed and accomplished a parallel implementation based on the Condor distributed computing environment^{7,8,9}.

The utility of simulators such as SimSET is currently determined by the availability of digital phantoms with appropriate physical properties for use during simulation. The current generation of raster (voxel) based phantoms are limited in

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utility because it is difficult to manipulate them in order to represent different individuals or positions. Furthermore, it is difficult for medical illustrators to create realistic 3D raster phantoms because it is challenging to create a 3D object one slice at a time.

Figure 1¹ Block diagram of SimSET modules.

METHODS

The quality and realism of the simulated images is currently limited by the quality of the digital phantoms used for the simulations. The transition from simple raster (voxel) based phantoms to more detailed geometric (mesh) based phantoms has the potential to increase the usefulness of simulated data. By defining each tissue component separately and utilizing geometric transformations (ie. scaling, rotation, translation, skewing), a single phantom can be used to model a population of individuals or a single individual being imaged in different positions. Individual tissues can be manipulated independently or even added and removed. Since the phantoms are defined in a continuous space, with a proper interpolation function, they can be used to perform simulations at any resolution. Performing these tasks on raster phantoms is challenging, often requiring redesign of the phantom from the ground up.

The phantoms can be either designed to the desired level of realism by medical illustrators, or created by segmenting previously acquired medical data sets. A time dimension can provide the dynamic properties of the tissue and can be utilized in the simulation of dynamic studies. The geometric phantoms used here are defined as a set of enclosed surfaces in 3D space. The surfaces define the boundary of a tissue and anything within the area is identified as containing that tissue. The surfaces are defined as a series of adjacent triangle elements as shown in Figure 2.

Figure 2. Example surface of a geometric phantom.

Each component of the phantom is defined as a separate surface that can be individually manipulated using geometric transformations or more complex displacement fields. The nature of the phantoms makes them robust and easy to modify.

Phantom Design

A breast phantom was designed and created using MilkShape 3D¹¹, a graphics model creation package by chUmbaLum sOft. The phantom is designed to support current and future projects on breast imaging. The phantom, when combined

¹ Adapted from ¹⁰.

with appropriate physical properties, can be used with SimSET, or another simulator. The phantom contains ten different tissues including adipose, areola, blood, bone (rib), ductal tissue, Cooper's ligament, lobule, muscle (pectoral), skin, and stroma connective tissue. Many of these components such as the blood and lobules are comprised of many discrete parts that can be further divided as desired.

Each component is defined by a series of connected triangles that define an orientable manifold (closed surface with a defined interior and exterior). The ordering of the triangle vertices is used to specify the front or back face of the triangle. This can be done using standard culling techniques. If the normal of the triangle is pointed towards an observer they are looking at the front face of the triangle, and if the normal points away from the observer they are looking at the back of the triangle. The normal of the triangle can be found using Equation 1, where P_0 , P_1 , and P_2 are three element vectors representing the location of the vertices of the triangle labeled in a counter-clockwise order. The vector cross product operator is represented by $\times$.

$$N = (P_1 - P_0) \times (P_2 - P_0) \quad (1)$$

Figure 3 shows the interface of MilkShape 3D used for creating the phantom. The model for one of the lobes is displayed. This model consists of 1,442 triangles. Similar models were created for the other tissue components providing an 83,278 triangle model.

Figure 3. Screen shot of MilkShape 3D. A lobe shown as three orthogonal projections and a 3D rendering (bottom right).

The interior of the breast model is shown in Figure 4. Five tissues are visible in the image including: skin, areola, lobule, ductal, blood. Additional information on the design can be obtained by displaying the phantom as a wire frame (Figure 5). The wire frame shows the vertices and edges used to define the model.

Figure 4. Interior of breast phantom shown using surface rendering techniques. Tissues present include skin, areola, lobule, ductal, and blood.

Figure 5. Portions of phantom shown in Figure 4 displayed as a wire frame.

The exterior of the phantom is shown as a wire frame in Figure 6. The phantom is bounded by a layer of skin at the front, and by pectoral muscle at the back. As can be seen from Figure 7 the skin consists of two mesh layers that meet and form a closed surface at the base of the breast. The areola tissue overlaps the skin and occupies a region at the apex of the phantom. The pectoral muscle is a layer covering the back of the breast along with the ribs.

Figure 6. Exterior of breast phantom shown as a wire frame. Tissues present include skin, areola, and ribs.

The interior consists of a layer of adipose tissue which is similar to, but thicker than, the layer of skin. The center of the phantom is filled with connective tissue. The Cooper's ligaments run from the skin through the adipose tissue to the connective tissue. Ductal tissue branches out of the areola with lobule tissue located along it. Veins and arteries enter and spread out from the posterior, narrowing and tapering off as they head toward the apex.

The phantom, while robust for simulation, is still a simplification of the actual breast. For example, human tissue has a more complex vascular structure than the phantom. Some simplifications were made because they have potential benefits. One example is the limited extent of the blood vessels. In the phantom they only extend approximately two-thirds of the way throughout the breast (a geometric transform of the vascular component could make them extend throughout the entire breast). This leaves a portion of the simulated images unaffected by the activity from the blood, and will provide a simpler area to test segmentation or classification algorithms.

Relationships Between Components

A relational descriptive language which indicates the relationship between the component meshes was developed. For example, if a point in space is contained in both the blood component mesh and the adipose tissue component mesh then the point should be considered blood. Using a descriptive language will allow for special behavior for different combinations of tissues, as well as simplifying mesh design since the mesh author will not be required to have all of the component meshes fit together perfectly like a puzzle. In our previous example, the potential user was not required to modify the adipose tissue mesh to have openings for the veins. This simplifies mesh design, permitting modification of tissue components or allowing additional ones to be added later, without requiring modification of the other components. This will allow for more complex phantoms and faster phantom development.

The tissue located at a point is determined by comparing the signature at the point to a series of mask pairs. The first mask pair matched determines the tissue properties for that point. The signature is the binary string representing the components the point is contained within. For the breast phantom this string is [adipose, areola, blood, bone, Cooper's, ductal, lobule, pectoral, skin, connective]. If a point is located within the Cooper's ligament component and the adipose component it will have the signature [1000100000].

The first mask in each mask pair determines the components the mask is interested in, it is referred to as the interest mask. The second identifies the requirements for those components, and is called the relation mask. For example, to require a point to be located in the adipose component but not the blood component we would use the mask pairs ([1010000000], [1000000000]). Here the first mask identifies the components we are interested in (the first and third), and the second mask determines the values required in the signature for those components (contained within the first component but not the third). The values located in the other bits of the second mask are ignored.

Simple binary operators are used to determine if a signature matches a mask pair. Equation 2 shows this operation. Here $\oplus$ is the binary exclusive or operation, $\vee$ is the binary inclusive or operation, and $\neg$ is the binary negation operation. If Match_Value evaluates to the binary string composed entirely of ones then the signature matched the mask pair.

$$\begin{array}{r} \text{Signature} \\ \oplus \neg \text{Relation_Mask} \\ \vee \neg \text{Interest_Mask} \\ \hline \text{Match_Value} \end{array} \quad (2)$$

As an example we will consider the mask given above for a point contained within the adipose and Cooper's ligament components. Comparison of this mask to the previously given mask pair for a point located in the adipose, but not the blood component, is given by Equation 3. As expected, since the signature represents a point located within the adipose, but not the blood component, the result of the comparison is a binary string of ones indicating the signature matched the mask pair.

$$\begin{aligned} \text{Match_Value} &= (\text{Signature} \oplus \neg \text{Relation_Mask}) \vee \neg \text{Interest_Mask} \\ &= ([1000100000] \oplus \neg [1000000000]) \vee \neg [1010000000] \\ &= ([1000100000] \oplus [0111111111]) \vee [0101111111] \\ &= [1111011111] \vee [0101111111] \\ &= [1111111111] \end{aligned} \quad (3)$$

The signature is compared to each mask pair in a predetermined order. The first mask pair matched determines the physical properties that are assigned to that location. Table I lists the masks that are used for the breast phantom in the order that they are applied.

This signature-and-mask pairs format was selected due to its simplicity. Implementation of the operations is trivial and can easily be included in any application that works with digital phantoms. Conversion of a set of mask pairs into an if-

then-else format is easily performed at run-time. The language is extremely robust permitting a large number of relational situations.

Table 1. Masks for tissue assignment of breast phantom.

Interest Mask	Relation Mask	Assigned Tissue
0010000000	0010000000	Blood
0001000000	0001000000	Bone
1100000000	0100000000	Areola
1000100001	1000100000	Cooper's Ligament
0000000110	0000000010	Skin
0000000100	0000000100	Pectoral
0000001000	0000001000	Lobule
0000010000	0000010000	Ductal
0000000001	0000000001	Connective
1000000000	1000000000	Adipose
0000000000	0000000000	Air

Phantom Sampling

The majority of medical image simulators, including SimSET, require raster phantoms. Until simulator software evolves, mesh based phantoms will need to be converted into raster data for use with the simulators. To address this shortcoming a software package that samples (finds phantom values at evenly spaced locations) was designed to convert mesh phantoms into raster phantoms. The algorithm used by the software will be the focus of this section.

The application was written in C++ leveraging the computational advantages of threading. It provides a generic mesh class for compatibility with a large number of mesh types, such as those provided by Autodesk's 3ds Max (3D Studio MAX)¹², Autodesk's AutoCAD¹³, Microsoft's Direct X¹⁴, and NewTek's Lightwave 3D¹⁵. Input parameters provide the necessary inputs such as mesh files, relational masks, dimensions, and sampling resolution.

The sampling uses a standard intersection of a ray and a triangle algorithm, similar to the one provided by Lengyel¹⁶, and the "odd parity" rule introduced by Sutherland and Hodgman^{17,18} in order to perform point location. The "odd parity" rule states that to determine the location of a point with respect to a polygon, a ray from the point can be drawn in any direction to infinity. If the ray intersects the polygon an odd number of times the point is located within the polygon, else it is located outside of the polygon.

For each sampling point a ray is traced in an arbitrary direction. The number of times the ray intersects each component is counted in order to determine the location of the point with regards to each component. The intersection of the ray with each component is determined by counting the number of triangles defining the component that the ray intersects.

The normal of each triangle is first found using Equation 1. The plane containing the triangle is defined by the normal and a signed distance of the plane from the origin calculated using Equation 4, where $\bullet$ is the dot product.

$$D = -N \bullet P_0 \quad (4)$$

Note that the signed distance is negative and scaled by the length of N . The plane containing the triangle can then be defined as Equation 5, where P is any point on the plane.

$$N \bullet P + D = 0 \quad (5)$$

Letting P_s be the point that is being sampled and V be the ray direction, the ray extending from point P_s to infinity is defined by Equation 6.

$$R(t) = P_s + tV \quad (6)$$

The intersection of the ray with the plane of the triangle is first confirmed. If the dot product of N and V do not equal zero (Equation 7), then the ray and plane are not parallel and must meet at some point.

$$N \bullet V \neq 0 \quad (7)$$

The intersection of the plane and ray can then be found by substituting Equation 6 into Equation 5 and solving for t (Equation 8).

$$\begin{aligned} N \bullet R(t) + D &= 0 \\ N \bullet (P_s + tV) + D &= 0 \\ t &= \frac{-(N \bullet P_s) - D}{N \bullet V} \end{aligned} \quad (8)$$

The point of intersection is then given by Equation 9.

$$R(t) = P_s + \left(\frac{-(N \bullet P_s) - D}{N \bullet V} \right) V \quad (9)$$

Area coordinates (sometimes referred to as natural or homogeneous barycentric coordinates) can then be used to determine if the point of intersection lies within the bounds of the triangle. Area coordinates define the location of a point with respect to a triangle. As shown by Figure 7, given a point and a triangle, three new triangles can be formed. If the sum of the areas of these new triangles equals the area of the original triangle then the point is located within the triangle.

Figure 7. Area coordinates of a triangle. The location of the red point is defined by providing the area of the three triangles formed by the red point and the vertices of the triangle.

After the location of each sampling point is found with regards to each of the components, the relational descriptive language and the masks are used to determine the value at that point within the raster phantom.

IMPLEMENTATION

Prior to generating simulated images of the phantom appropriate imaging properties need to be assigned for each tissue type. Specifically, radiotracer concentration and attenuation coefficients need to be provided.

Activity

Radiotracer concentrations were assigned based on manual selection of regions of interest corresponding to specific tissues from a dynamic pet series acquired using a GE Advance NXi².

Figure 8 and Figure 9 indicate the regions selected. The clearly visible vertebra was selected to provide the activity values for bone which were assigned to the ribs. The higher activity region in the center of the breast consisting of connective and glandular tissue was selected to represent the connective tissue (Cooper's ligament and stroma). The glandular tissue (ductal and lobule) which is also located throughout this region and is generally more active, was assigned activity values one standard deviation higher than that of connective tissue. The areola was assigned the same value, due to the large concentration of ducts and increased blood flow. The activity for pectoral muscle was assigned from the area of higher activity along the chest wall. The adipose tissue was assigned values from the lower activity region between the surface of the breast and connective tissue because of the relatively thick layer of fatty tissue that backs the skin. Blood which in general influences the entire image was measured in the left ventricle of the heart¹⁹ which is easily identified due to the distinctive shape of the myocardium. Skin which is generally not visible in PET images was assigned a very low level of activity.

² Courtesy of SUNY Upstate Medical Radiology Department, Syracuse, NY.

Figure 8. Regions selected to provide radiotracer concentrations for breast phantom.

Figure 9 Regions selected to provide radiotracer concentrations for breast phantom.

The concentrations were recorded for each of the six volumes of the dynamic series providing concentrations at 9.3, 20.4, 30.8, 41.7, 52.3, and 69.7 minutes after administration of the radiopharmaceutical. The measured values are shown in Table 2. These values should be considered approximate and relative. They do not take into account effects like spill over (e.g., between myocardium and left ventricle) due to the low resolution of PET.

Table 2. Radiotracer Concentrations (Bq/ml).

Time (minutes)	9.3	20.4	30.8	41.7	52.3	69.7
Adipose	3206	2504	2391	2261	1998	580
Air	0	0	0	0	0	0
Bone	1840	2246	2607	2504	1829	1779
Connective (Cooper's Ligament, Stroma)	8065	9689	9390	9047	6446	6014
Glandular (Ductal, Lobule, Areola)	9050	10408	10424	9807	7214	6616
Left Ventricular (Blood)	19231	13522	12745	11568	10472	8631
Muscle (Pectoral)	7011	8324	6388	5407	4958	3895
Skin	360	400	360	320	280	280

As shown in Figure 10 the time activity curves follow expected uptake and washout trends.

Figure 10. Relative time activity curves for breast phantom.

Attenuation

The attenuation in SimSET is based upon the linear attenuation coefficient and probability of photoelectric absorption, Compton, and coherent scattering. Known elemental compositions and densities of selected tissues have been used to calculate these values for photons from 5 to 1000 keV from a database of photon interaction behaviors for elements with atomic numbers from 1 to 100⁵.

Attenuation properties were assigned to the phantom by matching them with the tissues already supported in SimSET as shown in Table 3. Refer to the SimSET attenuation files for details on the attenuation properties for each tissue type⁶.

Table 3. Tissue attenuation properties for breast phantom.

Phantom Tissue Type	SimSET Tissue Type
Adipose	Fat
Air	Air
Bone	Bone
Connective (Cooper's Ligament, Stroma)	Connective Tissue
Glandular (Ductal, Lobule, Areola)	Connective Tissue
Left Ventrical (Blood)	Blood
Muscle (Pectoral)	Muscle
Skin	Fat

RESULTS AND CONCLUSIONS

A standard 3D mode system geometry was selected for the simulations. The system consists of a ring of detectors positioned around the object being imaged. End shields are used to reduce the number of random coincidences. This geometry is shown in Figure 11.

Figure 11. Simulated PET system geometry.

The port diameter was set to 70 cm and the axial field of view (FOV) to 60cm. Modeling of decays and photon tracking within the object and port was modeled using the Photon History Generator. The Collimator Module was used to track the photons from the port to the detector ring. 11 cm end-shields made out of lead were used to limit the field of view. No septa were modeled during the simulation as a fully 3D PET system was being modeled.

The Detector Module was used to track the photons from the detector ring inner diameter until energy deposition or photon escape. The detector was a scintillator array consisting of 2.5 cm thick LSO (lutetium oxyorthosilicate) crystals. The Binning Module was used to record the location of energy deposition. 20 bins were used along the axial dimension and 175 along the transaxial. 256 azimuthal angles spanning 180 degrees were used. This allows reconstruction to an in-plane resolution of 4.29×4.29 mm.

The object to be imaged was placed analogous to a patient positioned prone at the center of the field of view. The phantom was scaled to 14.4 cm^3 , with a distance of approximately 12.3 cm from apex to chest wall and a width of 12.7 cm at the chest wall.

Reconstruction

Prior to image reconstruction the raw data were attenuation corrected. A transmission scan of the phantom was simulated using a rotating gamma ray source. The transmission data was used to scale the recorded signal from each line of response to correct for the attenuation that occurred during image acquisition.

Image reconstruction was performed using STIR (Software for Tomographic Image Reconstruction)^{20,21}. STIR is an open source software package maintained by Kris Thielemans. The 3D reconstruction algorithm 3DRP^{22,23} (Three-Dimensional Reprojection), developed by Kinahan and Rogers, was selected to reconstruct the simulated data. This algorithm was selected due to its wide acceptance. In general, it serves as a gold standard and was the first fully 3D reconstruction algorithm supported by clinical scanners.

The algorithm operates as follows: During the first step standard two-dimensional filtered back projection is performed using the direct projections to provide a first estimate of the object being imaged. Other projections that are nearly orthogonal to the scanner axis may be used to improve this initial estimate using rebinning techniques.

A second step is performed in which projections of the initial estimate are taken in order to obtain values for lines of response which had low efficiency or were truncated due to the limited axial field of view of the scanner. These estimated lines of response are then merged with the measured lines of response in step three. This provides a complete set of projections for all detector ring pairs.

The estimated projections provide no additional data, but prepare the projections for filtering, in particular correcting spatial variance. The complete set of projections is then used to perform three-dimensional filtered back projection.

Simulation Results

The simulation took approximately 82 hours on a SunBlade 1500 (1.503GHz) workstation. The simulation would have taken a fraction of the time using the previously mentioned parallel implementation. 2×10^8 decays and photon histories were recorded providing 1.2×10^8 detected coincidences. Figure 12 shows two reconstructed slices from the simulation.

Figure 12. Result of breast phantom simulation and reconstruction. Sagittal image shown on left and axial on right.

Desired characteristics are present in the simulated images, specifically: 1) an area of higher activity is visible at the rear of the breast marking the chest wall (due to pectoral muscle), 2) area of lower activity surrounding exterior of breast (due to skin and adipose tissue), 3) an area of higher activity within the center of the breast (due to connective and glandular tissue), and 4) variation in intensity of the high activity region of the breast due to different tissues (connective vs. glandular).

This proof-of-concept work has demonstrated that geometric phantoms can be created with appropriate physical properties to be imaged with current PET/SPECT simulators. More realistic phantoms can be created by segmenting actual medical images or by medical illustrators.

There is room for technological advancements such as integration of simulators to provide a single environment for multimodal simulation. In particular, closer integration with other software packages for phantom creation and manipulation or image processing and reconstruction would increase simulator utility. The need for improving simulator efficiency by taking advantage of recent computational advancements such as distributed computing, threading, and short vector architectures exists to ensure the ability to perform realistic simulations.

The importance of developing algorithms, tools and procedures for multimodal imaging can not be overstated. With the growing use of medical imaging and the desire to utilize all collected and available information, more effort will be dedicated to optimizing the use of each individual modality and finding ways to use the complementary information provided from multiple sources.

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