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ABSTRACT

The use of integrated models of the human body in three-dimensional environments enables the study of the anatomic structures with a high degree of interactivity and detail. The geographical information systems approach in building topological models allows overcoming certain limitations found in anatomical atlases. In this study, an integrated (vector-raster) 3D model, which defines the external surface of the human body, is expanded by adding the corresponding anatomical structures. The reconstruction of the anatomical structures begins with their segmentation, performed on transverse RGB images of the body. The expanded model, built with explicit topological features, enhances the functionality of the input model by optimizing the identification function and developing an inclusion analysis in 3D. The features of the expanded model allow exploring more efficiently the human body information and representation.

KEYWORDS


INTRODUCTION

Anatomical atlases have been used to represent, explore, and study the human body. Since representations, such as “De Humani Corporis Fabrica” from year 1543 (Vesalius, 1998), to current atlases (Netter, 2014; Paulsen & Waschke, 2013), there was a great evolution in terms of reliability, quality, quantity and diversity of the presented information.

The emergence of the technologies for acquiring data of the human body and the increasing computer performance, allowed the development of digital atlases in which it is possible to integrate different sources of information and to develop tools that enhance the interactive exploration of 3D models (Argosy Publications, 2008; Biodigital Human, 2013).

Current digital systems based on non-topological models present limitations concerning the spatial analysis capabilities (António Barbeito, Cabral, Painho, & O’Neill, 2014). Thus, the representation of the human anatomy can benefit from the use of 3D topological models (4D, when modelling temporal phenomena is necessary). Advantages of topological models in representing anatomical structures have been already demonstrated in some studies (Martone et al., 2008; Zaslavsky, Baldock, & Boline, 2015; Zaslavsky, He, Tran, Martone, & Gupta, 2004).
Since the information regarding the human body is a type of geographical information, the use of geographical information systems (GIS) can be considered to build anatomical atlases. For this purpose, it is essential that GIS improve some features of the existing applications, such as:

- The ability to integrate data from different sources, e.g., raster and vector data;
- The possibility of using spatial analytic functions associated with topological models. For instances, current digital anatomical atlases allow querying databases but, contrary to GIS, they have difficulty in performing analysis based on spatial relationships, e.g., neighborhood and inclusion analysis;
- The high level of interaction with the geometric components of the model;
- The ability to develop applications within a single working environment to solve specific problems.

Assuming the interest of this approach, the main objective of this paper is to improve an initial model of the human body by using GIS capabilities, i.e., providing a GIS topological model of the human body embedded in a graphical user interface (GUI) with the appropriate functionalities. The final system should provide the type of information found in the anatomical atlases and overcome some of its limitations. This goal is subdivided in 4 sub-objectives: (i) to develop a semi-automatic segmentation method that takes advantage of the specificity of the input data; (ii) to update the GIS model with the segmented structures; (iii) to integrate the model in a graphical interface provided with navigation, identification and visualization tools; (iv) the development of a spatial analysis tool based on the containment information of the updated model.

In the next section, we detail the related work about digital atlases found in the literature. Subsequent sections are dedicated to describe data, present conceptual models and procedures, present and discuss results, and draw conclusions about this study.

RELATED WORK

Since the appearance of the Visible Human projects (Visible Human Project (VHP) (Spitzer et al., 2004), Chinese Visible Human Project (CVH) (Zhang, Heng, & Liu, 2006), and Visible Korean Human (VKH) (Park, Chung, Hwang, Shin, & Park, 2006)) different approaches have been used in the segmentation of anatomical structures on axial images. Leaving aside purely manual operations, the segmentation methods can be classified as semi-automatic or automatic. As semi-automatic methods (Imelińska, Downes, & Yuan, 2000), (Beveridge, Minhua, Rea, Bale, & Anderson, 2013) require the intervention of an operator, the high volume and complexity of data justify the research works that propose automatic segmentation methods (Li et al., 2014; Xue, Antani, Long, Demner-Fushman, & Thoma, 2014). However, errors are inherent to segmentation procedures. For example, the algorithm presented by (Xue et al., 2014), leads to an overall accuracy of 98.8% for computed tomography (CT) imaging and 99% for cryosection images. According to (Wu et al., 2012), after the primary segmentation, the main errors that are produced include the segmentation error and the segmentation missing. Intra-observer variation between experts is also referred. Thus the complexity and the inevitability of errors in segmentation procedures is clear. The existence of errors, even if they are small, shows that the supervision and human intervention are not negligible. In many cases, the tolerance to segmentation errors can be related to the further use of the obtained results. For example, if the results are used to reconstruct three-dimensional models, a single wrong pixel outside the segmented structure, can lead to a highly deformed anatomical structure. In this particular case, it is absolutely necessary to eliminate such errors. The necessity to optimize the segmentation methods by minimizing the execution times and controlling the final quality, explains the use of semi-automatic procedures involving several types of data such as, cryosection images, CT, and Magnetic resonance imaging (MRI).
The reconstruction of 3D models after segmentation is implemented in several works (Höhne & MAN, 2009; V Spitzer et al., 2004; Yanamadala et al., 2014). In general, these models emphasize the accuracy and realism of anatomical representations. They provide the structure identification functionalities, organize the information in separate layers, and provide interactive tools for simulating medical procedures (TolTech, 2014). The anatomical atlases are widely used in the study of the human body and also provide representations of the human body associated to descriptive information. In general, they contain wide information but the user has only access to descriptive texts or images. However, the interaction with a human body model, the ability to perform spatial analysis and generate information beyond the provided data, and the possibility of creating user defined visualizations, constitute the most significant limitations of these systems.

Given that the representations of the human body deal with alphanumeric data and spatial data (Burchianti, Barros, & Curcio, 2015; Dixon, Bowden, Ellis, & Logan, 2015) and the previously mentioned limitations of the existing models call for the need of a platform to operate more efficiently with this type of data. For example, there are currently well-developed systems to store and manage alphanumeric data, e.g., database management systems (DBMS), and spatial data, e.g., computer-aided design systems (CAD). Both systems manipulate efficiently the type of data for which they were conceived but have limitations regarding other types of data such as the limitations of databases for storing 3D geometric objects (Bonham-Carter, 2014), and the difficulty of CAD in manipulating non-spatial attributes and raster data (Shojaei, Rajabifard, Kalantari Soltanieh, Bishop, & Aien, 2012). This is the context in which the GIS can be effectively introduced in this area. GIS are systems specifically designed to operate with alphanumeric and spatial data. Another key feature of GIS is the implementation of topology on their models, i.e., the relationship between spatial objects including adjacency, connectivity, and containment. These relations, although well explored in two-dimensional systems, remains a current topic of research in three-dimensional systems (Löwner, 2013). The explicit definition of topology facilitates the development of powerful spatial analysis functions that, in turn, allow to explore the model more efficiently.

The containment topology, which is present in the initial and final models of this work, is used to develop an analysis inclusion function. These analyses are widely used in 2D GIS, being solved by point-in-polygon algorithms (Rigaux, Scholl, & Voisard, 2001). The limitations of 2D GIS in modelling three-dimensional objects (Zlatanova, Rahman, & Shi, 2004) led to the development of 2.5D and 3D systems. 3D GIS solve the inclusion analyses with point-in-polyhedron algorithms (Liu, Chen, Maisog, & Luta, 2010), which have a higher degree of complexity. This type of analysis can be simplified if the model has a raster component. This is the case of integrated models, which combine vector and raster components. These models bring together some of the advantageous characteristics of the vector models (e.g., topology) and of raster models (e.g., the ability to adequately represent continuous structures). In the case of inclusion analysis, the raster component partitions the entire space, describing the containment topology. By using this information, the inclusion analyses can be solved by reading the values contained in the voxels, which simplifies the point-in-polyhedron algorithms used in the vector models (A Barbeito, Cabral, & Painho, 2011).

Although there are human body models built with explicit topological features (Beylot et al., 1996), the topological relationships, as implemented in GIS, are inexistente to our knowledge. The comparison of models used in the representations of the human body can be found in (Antonio Barbeito et al., 2014). These authors describe, in particular, the vector, raster, and integrated topological models, concluding that the topological integrated models enable a comprehensive representation of the human body and are specifically suited for the development of features that allow the study of the human body.
DATA AND METHODS

In this section the input data components (images of the interior of a human body and a 3D integrated model of the same body) are described as well as the procedures that lead to the final model and the functions developed to explore the model.

Data

The VHP provides MRI, CT and cryosection anatomical images with red, green and blue bands (RGB), referring to axial sections of the human body. The RGB images of the VHP and an integrated model of the human body (Antonio Barbeito et al., 2014) constitute the input data used in this work.

Cryosection anatomical RGB data from the VHP consist of axial images of a male with 24-bit color depth, spaced 1 mm along the vertical axis, and a pixel of 0.33 mm on the horizontal plane.

The input model integrates two geometric components: raster (for the representation of internal structures) and vector (for the representation of the body surface). The raster component has two distinct structures: (1) the voxels with RGB values, which contain true color information of the internal structures and (2) the matrix obtained from the segmentation of the body, the Layer Matrix (LM), which allows to distinguish the inside and outside of the human body through the values 1 and 0, respectively. The surface vector component is constituted by a triangle mesh that surrounds the region identified with the value of 1 in the LM. This component was generated by a Screened-Poisson algorithm (Kazhdan & Hoppe, 2013) from the point cloud formed by the border voxels of the LM. The LM and the surface vector model were built from the RGB images of the VHP. Figure 1 depicts the flow chart of the input model.
The input model is integrated in a graphical interface with several features that allow the user to interact with it. In addition to the navigation features available in the GUI through tools that include zooming, panning, rotating and scaling, two supplementary functions were developed to explore more efficiently the information contained in the model: (i) a visualization feature that shows the internal anatomical structures through the definition of cutting planes; and (ii) identification functions that return the name of the pointed out structures that may be connected to an external document. The identification tasks use clusters of voxels. The clustering procedure groups voxels that belong to the same anatomical structure. This procedure, performed manually in some areas, is not an exhaustive segmentation of anatomical structures. This means that there is a gap in the information needed to feed the identification functions. With the segmentation of anatomical structures, a systematic procedure for overcoming this gap is set.

Segmentation

The input images, which represent horizontal sections of the human body, are separated by a distance of 1mm and, therefore, exhibit many similarities. The segmentation method uses this information through the image segmentation made in the previous images. Techniques involving the determination of statistical parameters such as, manual intervention, and image matching are used. The similarities between images are used in two ways: (i) by applying to each new image the statistical parameters and the sequence of operations performed in the previous images, and (ii) by using and adjusting a previous segmentation polygon through image matching. This is a semi-automatic method that allows a continuous control of the segmented anatomical structures since the manual and automatic components are available at each step of the procedure. In these circumstances, there is a high degree of dependence between the final quality of the segmentation of each structure and the knowledge of its morphology by the operator. As mentioned above, this knowledge is essential because the subsequent three-dimensional reconstruction of structures cannot depend on wrong delimitations. With the segmentations, the LM is expanded with the morphology of the anatomical structures, which allows to generate three-dimensional representations of the anatomic structures.

The segmentation of a given structure begins with the manual definition of a Region Of Interest (ROI) in which the training data (Canty, 2014) is selected. An optional second step consists in defining a bounding polygon that encloses the area to be segmented. This polygon can be useful, for example, to isolate this area from other regions with similar RGB properties. In the next step, an RGB ellipsoid is built from the parameters calculated in the ROI; the center and the axes of the ellipsoid correspond to the average and the standard deviation of the three RGB colors, respectively. The segmentation region results from the adjustment of the standard deviations through the interactive application of a scale factor. Once obtained the initial segmented area, several operations can be applied depending on the characteristics of the image, including: filling holes, morphological dilation or erosion, eliminating noise outside de segmented area, and smoothing borders. Finally, the segmentation polygon may be manually adjusted by creating, deleting, or moving vertices.

After validating a segmented area, the algorithm reaches the next image. The parameters and the operations applied to the previous image can be reproduced and the segmentation polygon can be adjusted through image matching. In the case of adjustment an image matching technique was used.

For each point of the segmentation polygon a template image around the point is built. The image matching technique consists of positioning the template image in the subsequent image. To perform this operation, the convolution between the new image and the template image rotated 180 degrees was calculated. The resulting matrix is the cross-correlation, since the convolution performed in this way corresponds to the correlation operation (Smith, 1997). The maximum value in the cross-correlation matrix corresponds to the position of best fit between each template image and the new image. From this position it is possible to extract the coordinates of the segmentation polygon in the new image which may be, however, manually adjusted.
The convolution between the two images was done through the Fast Fourier Transform implementation (Frigo & Johnson, 2014) of the Discrete Fourier Transform. By applying the convolution theorem (Bracewell, 2000), the convolution of the two images is converted into a multiplication operation of the respective Fourier transforms. The Inverse Discrete Fourier Transform is then applied to obtain the desired result. Expression (1) refers to the convolution between images $x$ and $y$:

$$x \ast y = DFT^{-1} \left[DFT \{x\}.DFT \{y\}\right]$$

(1)

To reduce the possibility to produce false positives in the cross-correlation matrix, the complete image is reproduced only in the neighborhood of the starting point, being represented by zeros in the remaining points.

Once covered all images, the voxels corresponding to the segmented structure are encoded with a unique identifier (ID) in the LM. Table 1 shows automatic and manual features that are included in the segmentation method.

The degree of automation of the method may vary from manual to automatic after setting the ROI. The quality of the segmentation depends on the quality of the input data and the capabilities of the operator with regard to the correct identification of the anatomical structures.

Before applying the segmentation method, and noting that the similarity between consecutive images is a premise for the segmentation method, a quantitative parameter is calculated to evaluate the level of similarity between the consecutive and the non-consecutive images. The quantitative parameter, $D_{f_{abs}}$, measures the percentage of absolute difference of the RGB values per pixel in the two images through the expression (2):

$$D_{f_{abs}} = 100 \times \frac{\sum_{i=1}^{n} \left|R_1 - R_2\right| + \left|G_1 - G_2\right| + \left|B_1 - B_2\right|}{3n}$$

(2)

where $R_1$, $G_1$, $B_1$, $R_2$, $G_2$, $B_2$, values correspond, respectively, to the values of $R$, $G$, and $B$ in the image $k$; $n$ is the number of pixels used in the calculation process. The differences are calculated only in the pixels in which there is information in both images, i.e., nonzero pixels.

Table 1. Automatic and manual features of the segmentation method

<table>
<thead>
<tr>
<th>Manual functionalities</th>
<th>Automatic functionalities</th>
</tr>
</thead>
<tbody>
<tr>
<td>• ROI drawing</td>
<td>• Creation of the segmented region by applying the statistical parameters of the RGB ellipsoid</td>
</tr>
<tr>
<td>• Boundary polygon drawing</td>
<td>• Segmentation polygon drawing</td>
</tr>
<tr>
<td>• Segmentation polygon manipulation: creation, deletion and displacement of vertices</td>
<td>• Recording of segmented structures</td>
</tr>
<tr>
<td>• Choice of scale factors to be applied to standard deviation values of the RGB ellipsoid</td>
<td>• Segmentation polygon adjustment by image matching</td>
</tr>
<tr>
<td>• Parameter Setting: size of the moving average, multiple of sigma, neighborhood 4/8, size of error spots, size of dilation and erosion</td>
<td>• Morphological operations: Dilation, erosion</td>
</tr>
<tr>
<td></td>
<td>• Fill Holes</td>
</tr>
<tr>
<td></td>
<td>• Delete islands</td>
</tr>
<tr>
<td></td>
<td>• Edge smoothing with moving average filter</td>
</tr>
<tr>
<td></td>
<td>• Navigation tools: zoom and pan</td>
</tr>
</tbody>
</table>
Vector-Raster Integration

The visualization of anatomical structures is based on the definition of cutting planes. The application of a cutting plane to an anatomical structure requires cutting the surface vector component of the model and resampling the RGB values of the raster component on the cutting plane. Thus, the cutting procedure uses the two integrated components of the model. Although the integration of model components occurs at the level of their structure, the same cannot be said in terms of visualization, if the two components are directly depicted in the GUI. To eliminate the visual gaps between the raster and vector components, a triangulation was built on the cutting plane. To perform this triangulation two sets of points are generated: (i) a regular grid on the plane and (ii) a reconstruction of border points so that its distance is of the order of the pixel resolution. It is important to ensure that the distance between the points does not exceed a predetermined value to apply the alpha-shape method of triangulation (Ganapathy, Ramu, & Muthuganapathy, 2015), which allows to create a triangulation on a non-convex polygonal region. To perform the triangulation, the method is calibrated with a radius parameter greater than the pixel resolution, which ensures the inexistence of non-connected border points. Once built the triangle mesh on the cutting plane, the color information contained in the raster component is then resampled at the centroids of the triangles. The developed system enables resample the color through 3 alternative interpolation methods: (i) Nearest neighbor, (ii) linear and (iii) cubic.

With this procedure, the cut of an anatomical structure consists of show in the GUI two integrated vector components: the surface component of the model and the new component built on the cutting plane.

Inclusion Analysis

The GIS environment consists of a user interface that contains the segmented model and several tools, namely navigation, visualization, identification, and inclusion analysis. The inclusion function, based on the containment information provided by the raster component, simulates the insertion of a needle in a given point of the body surface. Five parameters are used in the implementation of this function (Figure 2): (1) the insertion position on the surface of the body \( P \); (2) the length of the needle, \( L \); (3) the depth of needle insertion, \( D \), and (4) the horizontal and vertical angles that define the orientation of the needle \( \vec{V} \). Based on these parameters, the extreme points of the needle, \( P_i \) and \( P_f \), are determined. Then, the needle body is materialized by a set of points spaced 0.33 mm by default. The analysis is achieved by reading LM and is displayed by coding the needle with different colors according to the crossed structures, whose identification is described in a map legend.

Figure 2. Insertion parameters of a needle into the human body
RESULTS AND DISCUSSION

The results presented in this section and the respective discussion are focused on the procedures applied in obtaining the final model and in the new functions that enhance the capabilities of the system.

Segmentation

The image matching technique implemented in the segmentation method depends on the similarity between the input images. To evaluate the level of similarity, three different comparisons were carried out (figure 3): (i) between images whose RGB values are randomly generated; (ii) between consecutive RGB images; and (iii) between non-consecutive RGB images. In each case, the absolute differences were calculated. In the case of similarity between the input images, it is expected that the difference obtained in the first case should be considerably greater than in the other two cases. Furthermore, the difference in the second case should also be lower than in the third case. If so, the similarity between the input images can be used by the image matching technique.

The absolute differences were calculated for 600 pairs of images. The average values for random, consecutive and non-consecutive images are shown in Table 2. These results show that the consecutive images have a high degree of similarity and superior to non-consecutive images. Nevertheless, it should be noted that the segmentation does not necessarily depend on the image matching algorithm. In fact, this technique proposes the segmented area in each new image but the final segmentation is validated by the user. Thus, the proposed segmented areas can be accepted or not, and corrections can be made if they are found necessary.

The segmentation method was applied on the cryosection anatomical images in which 211 structures were segmented totaling 39660 segmentations: the bones and the muscles of the lower limb and various organs of the abdominal and thoracic regions (heart, lungs, liver, stomach, small intestine, large intestine and skin). Figure 4 shows some of the techniques included in the segmentation module such as: (i) using the RGB ellipsoid after setting the ROI; (ii) correcting errors (filling holes inside and eliminating spots outside); (iii) smoothing the border of the segmentation area; (iii) using the bounding polygon; and (iv) using the image matching technique to update the segmentation polygon.

Figure 3. Evaluating the similarity between the cryosection anatomical images: (a) random image; (b) overlapping random images; (c) overlapping consecutive RGB images; (d) overlapping non-consecutive RGB images
Table 2. Absolute differences per pixel between two images (percentage averages)

<table>
<thead>
<tr>
<th>Relative position of the images</th>
<th>Absolute difference per pixel (percentage average)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Consecutive images</td>
<td>1.8</td>
</tr>
<tr>
<td>Non-consecutive images</td>
<td>2.5</td>
</tr>
<tr>
<td>Random images</td>
<td>19.8</td>
</tr>
</tbody>
</table>

Figure 4. Segmentation of anatomical structures: (a) ROI definition and segmentation of the femur without the bounding polygon; (b) ROI and bounding polygon definition and segmentation of the left rectus abdominis muscle; (c) and (d) evolution of the tibial segmentation from image 2611 to image 2616 with the image matching technique
The main difficulties with the method relate to the situations where similar structures present common borders. In these cases, manual intervention is required, which implies a greater expenditure of time. Solutions to mitigate such problems can be found through the use of additional data such as CT images (Beylot et al., 1996). This approach can be used in the current semi-automatic method by updating the application in order to store, segment and integrate with CT data.

After the segmentation stage, the segmented structures are coded in the LM carrying out the desired model expansion. The LM updating enhances the containment information of the model. In fact, with this new information the identification and the analysis functions provide a more detailed and correct response to requests made by the users.

The final results of segmentations are voxel clusters in a three-dimensional space. These voxels allow to generate three-dimensional views of the segmented structures (Figure 5). By inspecting the three-dimensional structures, it is possible to evaluate the quality of the segmentation. From the user point of view, the reconstructed 3D structures allow to have a more realistic idea of its morphology, which is not so evident from the direct inspection of the input data.

**Vector-Raster Integration**

When cutting an anatomical structure, direct visualization of the raster and vector components creates gaps at the periphery of cutting plane. As shown in Figure 6, this problem is solved by converting the raster component in a triangle mesh designed to be integrated with the surface component. This vector-raster integration allows to load the GUI only with vector components.

Figure 5. Visualization of the segmented structures from the information contained in the LM: (a) three-dimensional reconstruction of voxels representative of the left femur with segmentation color (one color for each structure) and with the color assigned to all the skeletal system; (b) RGB image overlaid with the corresponding LM plane
It should be noted that the resampling of the raster component causes some degradation compared to the original data. However, this resampling is required to create the proper color information on the cutting plane, either using the raster component directly either with the visual integration of the proposed method.

**Functions**

The functions that act on the model allow to extract information on the surface and within the anatomical structures. The process of obtaining the RGB images caused some smaller structures to collapse, so they do not appear in the original dataset. It is therefore not possible to obtain adequate information from these structures. One possibility to overcome this problem is to fill the gaps with simulated information.

The identification function that was already present in the initial model allows to obtain, at the level of the voxel, the name of each selected structure. After updating the model, the identification of the structures can be showed with the RGB data or the LM data. In any case, an identification label is generated on the required structures (Figure 7). This function is available on any cutting plane defined by the user.

Like the identification function, the inclusion analysis uses the information contained in the LM. This analysis function is designed to simulate the insertion of a needle into the human body. Once identified the five parameters of the insertion, the position of the needle is calculated and a code color is applied according the surrounding anatomical structures. The coding process is completed by...
generating the corresponding legend. Figure 8 depicts results of the inclusion analysis function and compares the discrimination capability of the initial and final models. In the final model the inclusion analysis has the ability to identify all of the structures classified and it creates the unclassified item in the legend to represent non-classified areas.

**Procedures, Models, and Functions**

The current system presents a specific model to represent the human body and functions that allow exploring the model. The model and the functions are developed through procedures based in techniques described in current studies and partially developed and adapted to the specific features of the present work. Table 3 relates these issues as they are treated in this study and in the current literature.

**CONCLUSION**

This paper presents a system to model the human body in a GIS environment. The system consists of three major components: a topological model, a graphical interface, and functions to operate with the model. The GIS approach intends to overcome certain limitations found in the anatomical atlases, which are essentially operations defined by the user, namely, the creation of required views, the extraction of information from these views, and the execution of analysis operations, in particular spatial analysis.

In the model building process several anatomic structures were segmented. For that, an application was built taking advantage of the specific characteristics of the input data. The proposed solution is a semi-automatic method that uses the similarity between the input images in the automatic component, while the manual component intended to correct errors and to monitor the quality of the segmentations. The segmentation procedure carried out on various structures allowed to validate the method and to simultaneously expose their main limitations, which are mainly related to the nature of the input images.
The developed system allows the user interacting with a model of the human body, by performing dissections through the definition of cutting planes. This function depicts real data from the human body on a region defined by the user. It differs from the usual approaches that present the images and the 3D model separately, in which the raster component is depicted through pre-defined transverse, sagittal, and coronal planes. However, this system does not simulate exactly a real dissection, since
these procedures involve cutting anatomical structures through “free surfaces” and not as the result of applying a rigid plane.

Another limitation of the current model concerns its own structure. At this stage, the raster component is segmented by anatomical structures. However, there are no corresponding 3D surface vector components, which means that the model has a monolayer structure. It is, therefore, not possible to isolate the anatomical structures in the 3D interface to manipulate them, but only the whole body.

Considering the current state of the segmentation method and the main system, some aspects must be taken into account regarding future work. On the one hand, the segmentation method update should include the capacity to operate with CT data along with the RGB images. On the other, the deepening of GIS features present in the system should be considered, namely, (i) the development of a multilayer layer system, which can be facilitated through the reconstruction of vector surfaces for the segmented anatomical structures; (ii) the expansion of the containment topological features in order to include the structures of the model; (iii) the definition of new types of topology including neighborhood and connectivity; (iv) the present system creates visual integration with raster and vector components when the user defines interactively cutting planes. The current system is built with a specific model of the human body and does not allow the integration with other sets of images. The

Table 3. Comparison of procedures, models, and functions in this study and in the current literature

<table>
<thead>
<tr>
<th>Procedures</th>
<th>State of the Art</th>
<th>In this study</th>
</tr>
</thead>
<tbody>
<tr>
<td>Segmentation</td>
<td>Semi-automated methods are usual with this type of data. Despite the use of sophisticated techniques in segmenting target regions, the use of previous information in segmenting subsequent images is unusual (Imelińska, Downes, &amp; Yuan, 2000; Beveridge, Minhua, Rea, Bale, &amp; Anderson, 2013).</td>
<td>Semi-automated method. Takes advantage of the sequential data by using the information of previous images to perform segmentations on subsequent images through image matching.</td>
</tr>
<tr>
<td>3D reconstruction</td>
<td>Among the reconstruction methods found in the literature, the screened Poisson is a state of the art technique (Kazhdan &amp; Hoppe, 2013).</td>
<td>Screened Poisson surface reconstruction.</td>
</tr>
<tr>
<td>Visual integration / Dissections through cutting planes</td>
<td>The presentation of the raster and vector components in the same 3D interface after applying cutting planes is unusual in the anatomical atlases (Höhne &amp; MAN, 2009; V Spitzer et al., 2004; Yanamadala et al., 2014).</td>
<td>The raster and vector components are presented in the same 3D interface after applying a cutting plane. The components are visually integrated through 3D interpolation an alpha-shape triangulation.</td>
</tr>
</tbody>
</table>

Model

| 3D GIS topological integrated models are not usual in the representation of the human body. There are models that integrate raster and vector components and provide topological information. The containment topology and the correlated functions in 3D are unusual (Höhne & MAN, 2009; V Spitzer et al., 2004; Yanamadala et al., 2014). | Contains a vector surface component that connects to the raster interior representation. The partition of the interior space provides containment topological information. |

Functions

| Identification functions on raster data are usual (TolTech, 2014). | All the structures segmented are coded in the raster component which allows applying the identification function. |
| Inclusion analysis in 3D models of the human body are unusual (Anatronica, 2010; Argosy Publications, 2008; Biodigital Human, 2013; CG Studio, 2014; Database Center for Life Science, 2009; TolTech, 2014). | Inclusion analysis is implemented in the 3D model through a function that simulates the insertion of a needle. |
development of georeferencing tools may provide the integration of new images in the system that can be depicted alternatively in the visual interface based on the user action, and (v) the development of new features based on the previous items.

CONFLICT OF INTEREST

The authors declare that there are no conflicts of interest.

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