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Quantitative comparison of freeware software for bone mesh from DICOM files

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ABSTRACT

Musculo-skeletal modelling, 3D printing of bone models and also custom design of relevant prostheses starts from accurate STL files. These are obtained from medical imaging after careful segmentation and 3D reconstruction using specialized software, but most of these are very expensive. The aim of the present study is to assess and compare alternative software available for free. Three freeware software were selected from the most popular, and one standard platform was made available at the institute of the authors. Using each of these four software and starting from available DICOM files obtained previously by a CT scanner, three different bone models were reconstructed from each of five different human anatomical areas for a total of 60 bone model reconstructions. A young radiographer performed the bone reconstruction without specific technical training. 3D spatial matching of corresponding anatomical models was also performed to determine distance-maps for the assessment of final surface quality. In all four software many valuable features were available, with minimum differences, and bone models of good quality were obtained. Large differences in file sizes (mean range over the five anatomical models 66-338) and in the number of triangles (870-1350 thousands) were found, with triangles for MByte ratio ranging from about 4 to 20 thousands. The distance-map analysis revealed that root mean square deviation averaged over the five anatomical models ranged from 0.13 to 2.21 mm for the six spatial matches between the four software. These software are suitable for 3D bone model reconstruction, and do not require special training, and as such these can open up opportunities for biomechanical modelling and medical education.

1. Introduction

Three-dimensional (3D) reconstruction of bone shape is the first step in biomechanics for any personalized musculo-skeletal modelling, and is also necessary for statistical shape modelling (Nolte et al., 2016; Zhang and Besier, 2017). 3D models of bones are essential in orthopaedics for custom design of internal prostheses or scaffolds. Another recent area of growth in this respect is 3D printing, because additive manufacturing can allow for quick and cheap production of high-precision replicas of complex bony anatomical structures (Auricchio and Marconi, 2017). These physical models show huge potential, not only for the comprehension of real physiological and pathological conditions of the subject, but also for relevant pre-operative planning and simulation. This would have a particular impact in medical education and physician-patient communication (Coakley et al., 2014; Cloonan et al., 2014; Malik et al., 2015; Martelli et al., 2016). Despite the relatively recent exploitation of custom-made surgical interventions, there are a number of applications already in clinical trials (Liang et al., 2017).

The process starts from medical images, typically Dicom files from standard computed tomography (CT) or magnetic resonance imaging instruments (Buecking et al., 2017). The large number of images collected must be segmented, i.e. traced to identify the separate anatomical structures, which implies a long process of manual or semi-automatic identification of the bony structures. Dedicated software supports this, and eventually creates a corresponding 3D object, by implementing interpolation algorithms to all the segmented images. For a better model representation, relevant uniform meshes are then generated. These are also of use for design and planning of orthopaedic implants. Eventually these computer models of the bones are exported, typically in STL format, for additional musculo-skeletal modelling or for 3D printing. This extensive work, frequently performed by radiologist,

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technicians and bioengineers all together, means that only a few critical clinical cases are addressed with 3D model reconstruction. In addition, there has been an increasing demand for physicians to contribute more actively in the surgical planning process, and also for patients to communicate more clearly with physicians. Current professional software products feature many highly technical tools, but are very expensive, and require robust hardware and demanding training. Therefore there is a great demand for cheap and user-friendly software tools (Sander et al., 2017), which still provide accurate image segmentation and model reconstruction. The use of these would no longer need high technical competence and experience or large investments.

Nowadays, a number of these software tools can be obtained for free. These are in addition to those offered by the local medical imaging services in the hospitals. There are concerns however on the real performance and the final results attained from these software (Huotilainen et al., 2014; Soodmand et al., 2018). The aim of the present study is to compare the features and the outputs of a number of these software. Using these, STL bone models were obtained from DICOM files of five different anatomical areas, to remove the possible bias introduced by a single joint of the human body. To limit the sources of difference associated to final parameters of the mesh, the comparison is based only on the 2D image segmentation and 3D model reconstruction phases.

2. Materials and methods

Medical images were acquired by a CT scanner (Brilliance 16, Philips Medical Systems; Best, The Netherlands), with size of the matrix 512x512 and thickness of the layer 0.5 mm. Standard scans were taken from the ankle, knee, shoulder, elbow, and wrist, from three different subjects for each joint, for a total of 15 anatomical models to be reconstructed in 3D. Due to the relevant different volumes and bone density, it was not possible to apply the same CT scan parameters to all cases (Table 1). The datasets were saved in DICOM format.

Each of these joints were analyzed with four software (Table 2): three freeware selected from the web by their relevance in terms of citations in biomedical publications, and one made available at the institute of the authors. The general operation principle was very similar, including importing the DICOM files in the three anatomical projections, image segmentation using various tools and threshold values, and manual correction with the selected mask. The latter allowed the user to draw or remove isolated depictions of selected areas. Next, using the built-in mask, the program created a 3D model of the object, which was exported in the STL format.

Table 1
Parameters from the 15 CT scans.

	kV	ms	mA	mAs
ANKLE	140	1090	126	137
	120	1792	112	201
	140	1090	135	147
KNEE	120	1712	117	200
	120	1712	117	200
	140	1090	136	148
SHOULDER	140	1090	121	132
	140	1090	115	125
	140	1090	127	138
ELBOW	140	923	32	30
	140	1090	132	144
	120	1332	99	132
WRIST	120	1332	113	151
	120	1792	67	120
	140	1090	130	142

The following software and tools were used in the presented order. A young radiographer performed the analyses and reconstructions with no experience in these software, trained only using tutorials from the web.

3DSlicer (Fedorov et al., 2012) (version 4.9.1; Brigham and Women's Hospital, Inc., Boston MA, USA)**.** Data was imported using the Add Data tool. The Segment Editor tool was used to create the mask in which the Threshold function allowed selection of a most appropriate threshold for image intensity. Draw and Erase effects were then applied to image correction. A 3D model in STL format was created and saved.

InVesalius (version 3.1.1; Renato Archer Information Technology Center, Brazil)**.** Data was imported using the Import DICOM tool. In the Create-new-mask section, the threshold value for the anatomical structure "Bone" is always initially set to 226. Draw and Erase tool, in the Manual Edition section, was used to manually adjust the image. Then, on the corrected mask, a 3D surface was created and exported in STL format.

Itk-SNAP (version 3.6.0; Penn Image Computing and Science Laboratory – PICSL -, and Scientific Computing and Imaging Institute - SCI, USA)**.** Data was imported using the Open Main Image tool. Using the Active Contour Segmentation Mode tool, the Pre-segmentation phase was performed, where the mask was created using the threshold function, and then filled with Bubbles and continued with the Evolution process. With the help of this mask, a 3D model was created and exported in STL format.

VuePACS3D (version 12.1.5.0440; Carestream, USA). Images in the DICOM format were imported into the VuePACS3D, and an automatic generation of the models was obtained and exported in STL format; from these only the noisy objects were removed.

All four software allowed editing after the automated segmentations. However, since the aim of our work was to objectively compare the 3D digital model obtained before possible subjective refinements, no additional tools, such as shaping and meshing, were used. The meshes created by the segmentation were not separated for the individual bones.

To determine the agreement of the mesh surfaces obtained from these software, a 3D spatial matching of corresponding anatomical models was performed for each joint (MeshLab-2016.12 version, ISTI-CNR, Pisa, Italy), which provided a distance-map for each couple of models.

3. Results

All the analyses were performed over a one month period. The different features observed with these software during the analyses, in terms of their capabilities, tools availability, and procedure complexity are reported in Table 2, along with hardware requirements, programs functionality and 3D modelling properties. Available to all software were the following: No limit in the number of slices; Multiplanar visualization/representation; Correspondence between the axial, sagittal and coronal orientations; Enlarging image area & Crop; Brightness and contrast; Separation of the different regions of interest; Linear, angular, and volumetric measures; Simultaneous views of images and surfaces; Data export, of surfaces and images; STL file format export.

The distance-map analysis (exemplary matching results in Fig. 1) showed a good superimposition between the models obtained. The best results, in terms of maximum and root-mean-square (RMS) distances averaged over the five anatomical models, were found for the combination between 3DSlicer and Itk-SNAP (2.84 and 0.13 mm respectively; see Table 3), while the worst results were found between Itk-SNAP and InVesalius (13.14 and

Table 2
Main features of the software analyzed. The results are means over the five anatomical models and the three subjects analyzed. The move, rotation, zoom, and transparency features apply to the 2D images itself and the segmented contours/masks, but also to the 3D point clouds, meshes, and final models.

Parameters	3DSlicer	InVesalius	Itk-SNAP	VuePACS3D
Technical requirements				
Processor	64-bits processor	64-bits processor Intel Core 2 Duo 2.5 GHz or equivalent	64-bits processor	64-bits processor SingleCore 2.0 GHz or superior
Minimum RAM [GB]	4	4	4	4
Hard disk space [MB]	690	353	60	80
Operating system	Windows, GNU/Linux, MAC OS	Windows, GNU/Linux, MAC OS	Windows, GNU/Linux, MAC OS	Windows XP
Computational time				
Processor	AMD Dual Core 1.65 GHz, 8 GB RAM			Intel Xeon CPU 2 GHz, 64 bit, 8 GB RAM
Time to import [min]	10–15	1–2	1–2	<1
Time to create the model [min]	15–20	10–15	35–50	1–2
Operability and Results				
Move	Y	Y	Y	Y
Rotation	Y	Y	N	Y
Zoom	Y	Y	Y	Y
Transparency	Y	Y	N	Y
Segmentation: Threshold	Y	Y	Y	N
Manual	Y	Y	Y	N
Hounsfield Units preservation	Y	Y	Y	–
Data management: Mask	Y	Y	Y	N
Surface 3D	Y	Y	Y	N
Format of STL code	Binary	Binary	ASCII	ASCII
Mean number of triangles	1,356,464	866,541	1,038,054	1,314,377
(st.dev. over 15 models)	(795,324)	(491,707)	(631,617)	(781,675)
Mean file size [MByte]	66	42	184	338
(st.dev. over 15 models)	(39)	(24)	(114)	(201)
Triangles for MByte (percentage difference over the 15 anatomical models)	20,481 (±0.28%)	20,477 (±0.61%)	5704 (±5.79%)	3893 (±0.01%)
Steps to get the final model	9	6	7	8

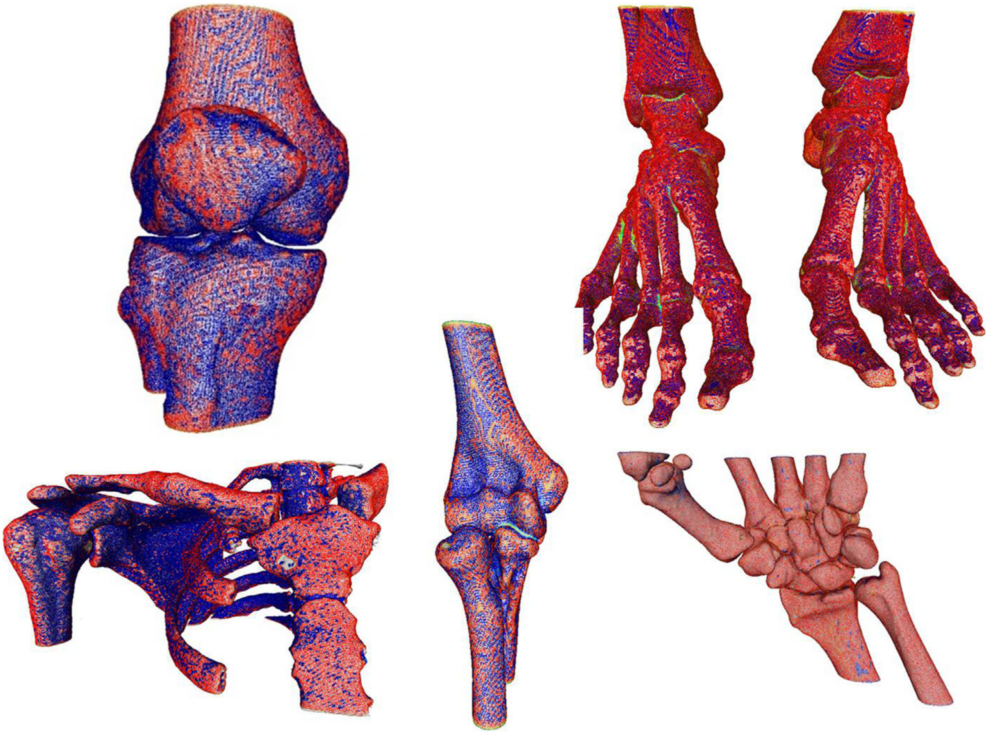

Fig. 1. Exemplary results for the distance map calculation of the 3D matching for the five anatomical models analysed (ankle, knee, shoulder, elbow and wrist), taken from the comparison between 3DSlicer to Itk-SNAP, which showed to be the best among the six possible matches between software-to-software; the RMS distance was respectively 0.200, 0.184, 0.120, 0.148, and 0.001 mm. The colour scale changes from model to model, and ranges to represent maximal penetration (deep blue) and separation (deep red), best shape fitting being in green. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.) (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

Table 3
Results from the distance-map analysis between bone models from the four software: 3DSlicer (3DSl), InVesalius (InVe), Itk-SNAP (ItkS), and VuePACS3D (VPAC). For each joint and each possible model comparison the absolute maximum, the mean and the RMS distances are reported. Average values over the five different anatomical models are also reported. Measurements are in mm.

		3DSl - ItkS	3DSl - InVe	ItkS - InVe	3DSl - VPAC	InVe - VPAC	ItkS - VPAC
ANKLE	max	2.29	13.71	16.64	12.07	5.24	14.82
	mean	0.13	1.34	1.92	0.76	0.85	1.07
	RMS	0.20	2.17	3.04	1.28	0.98	2.07
KNEE	max	2.58	14.46	18.31	13.37	7.27	17.51
	mean	0.11	0.80	1.99	0.54	0.66	1.07
	RMS	0.18	1.42	3.15	0.82	0.83	2.16
SHOULDER	max	6.23	11.63	16.46	11.26	4.91	21.02
	mean	0.00	0.63	1.25	0.68	0.67	1.11
	RMS	0.00	0.97	2.02	0.92	0.80	1.81
ELBOW	max	1.10	5.74	7.10	3.84	2.88	6.79
	mean	0.07	0.46	0.76	0.30	0.54	0.41
	RMS	0.12	0.68	1.35	0.39	0.64	0.83
WRIST	max	2.01	3.78	7.19	3.76	2.79	7.20
	mean	0.09	0.26	0.91	0.48	0.55	0.50
	RMS	0.15	0.37	1.47	0.59	0.65	0.63
Average	max	2.84	9.86	13.14	8.86	4.62	13.46
	mean	0.08	0.70	1.37	0.55	0.65	0.83
	RMS	0.13	1.12	2.21	0.80	0.78	1.50

2.21 mm respectively). Overall, the models in 3DSlicer showed the best values.

4. Discussion

In the present work, the objective advantages and disadvantages of freeware software (3DSlicer, InVesalius, and Itk-SNAP) for the creation of STL bone models are investigated, by limiting as much as possible any manual intervention by the operator. In addition to these three software, the more advanced VuePACS3D was also assessed, accessible free of charge in our radiological unit. In our mind this is a typical condition that would represent what a standard operator can access to with no expenses. Similar comparison work has been reported for cardiovascular image analysis (Heiberg et al., 2010) and for dental and cranial modelling (Poleti et al., 2016), but very little has been published for the human diarthrodial joints, which are frequently investigated for major orthopaedic surgery. In the literature, in fact, little work has been dedicated to freeware software, which are relatively frequently used in a number of medical and research centres. To the knowledge of the authors, these three freeware software are the most popular for use. Other options may be available, but in general these are very basic and lack the file export tool. The present work does not deal with issues associated to automatic segmentation and reconstruction, but seeks to track and assess only the major features and the gross results obtained using these software.

The radiographer operator had no experience with these analyses, but despite this the anatomical models were obtained in a short time and without problems using all four software. Only the optimal threshold value for a best mask visualisation was set by the operator, on each individual DICOM file, particularly according to relevant density of the bone under analysis. This is enabled differently by three of the present software, not in VuePACS3D. Both the triangle size and density compared well among the software. The segmentation algorithms of these software are not known, and thus comparison on this respect is not possible. As for the STL file formats, the ASCII requires more space to store the same amount of data as the Binary (Table 2), but has the advantage of text readable data, a valuable feature for debugging and coding.

In assessing more general features of these software, a good level of automation has been experienced. In all these freeware software, apart VuePACS3D, the obtained 3D bone models can also be edited manually. The segmentation algorithms use voxel and pixel based classification, though spline fitting can be used. In addition, most of these software create an interlinked mesh; only InVesalius can generate separate meshes of the individual bones, with the automatic function “Split all disconnected surfaces”. Finally, mesh parameters, such as number and density of the triangles in the mesh, can be only qualitatively specified; the exact numbers are realised only after the final file is generated. Of course, the individual physical size of the triangles depends on the size and on the geometrical regularity of the bone segmented.

The present results combine well with recent findings from the literature. A recent experimental analysis on the accuracy of the calculated bone kinematics from Dicom (Tan et al., 2017) showed that this is not significantly influenced by variations in CT scan resolution, segmentation threshold and reconstruction algorithm.

Despite the present abilities of freeware software, these cannot currently be used in clinical practice because of the lack of necessary certification. The main result of this work is the finding that these software are definitely suitable for 3D bone model reconstruction, easy to use, and do not require special training. Therefore, these software open up opportunities for a more general use of bone models, with obvious advantages for biomechanical research, prosthesis design, clinical practice, and medical education. An expanded investigation on all current commercial software could establish quantitatively the differences with the freeware analysed here.

Conflict of interest statement

I confirm that there are no conflicts of interested for the matters discussed in this study.

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