

Computer system for definition of the quantitative geometry of musculature from CT images

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The computer system for quantitative determination of musculoskeletal geometry from computer tomography (CT) images has been developed. The computer system processes series of CT images to obtain three-dimensional (3D) model of bony structures where the effective muscle fibres can be interactively defined. Presented computer system has flexible modular structure and is suitable also for educational purposes.

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Keywords: Muscle model; Image processing; Quantitative anatomy; Computer tomography

1. Introduction

One of the main problems in the biomechanics of the musculoskeletal system is to determine forces acting in various anatomical structures [1]. Assessing the forces applied to the joint and estimating how these forces are distributed to the muscles, ligaments and articular surfaces is fundamental for understanding the joint function, injury and disease [2–5]. In mathematical modelling, the human body is usually modelled as a system of absolutely stiff segments connected by joints while motion of the segments is performed by the muscles spanning the joints [1,6].

The definition of the multibody mechanical system of muscles and bones is a complex and time consuming process [7]. Therefore, in previous studies, musculoskeletal models are usually taken from previous experimental measurements performed on a limited number of patients [7,8]. To adjust the muscle model for an individual patient, generic models are usually linearly scaled to fit the patient bone geometry [9,10]. Scaled muscular geometry may not fit the geometry of an individual patient which leads to the inaccuracy in determination of musculoskeletal load.

The aim of this study is to introduce an original computer system that can improve assessment of the quantitative muscle model geometry for an individual patient. The muscle model will be determined according to the patient bone geometry obtained directly from computer tomography (CT).

2. Methods

In development of the system, combination and adaptation of previously developed computer programs was chosen instead of development of an unique new computer system. Hence, the presented computer program has modular structure in which several subprograms are utilised. Assessment of the three-dimensional (3D) musculoskeletal model was divided into three steps (figure 1):

- (i) processing of CT images
- (ii) visualisation of 3D bone geometry
- (iii) definition of the muscle model

2.1 Processing of CT images

Processing of CT images consists of filtering, histogram equalisation, reducing the noise, etc. The methods of enhancing the image are defined as mathematical operations on the two-dimensional matrix of the image pixels [11].

We have assumed that CT scan of the region of interest consists of series of images in ordinary medical image format DICOM [12]. Dicom2, a free command-line driven program [13], converts the DICOM files into device-independent bitmap format (bmp).

The bmp is imported into computational environment for numerical calculation—GNU Octave [14]. GNU Octave provides a convenient command line interface

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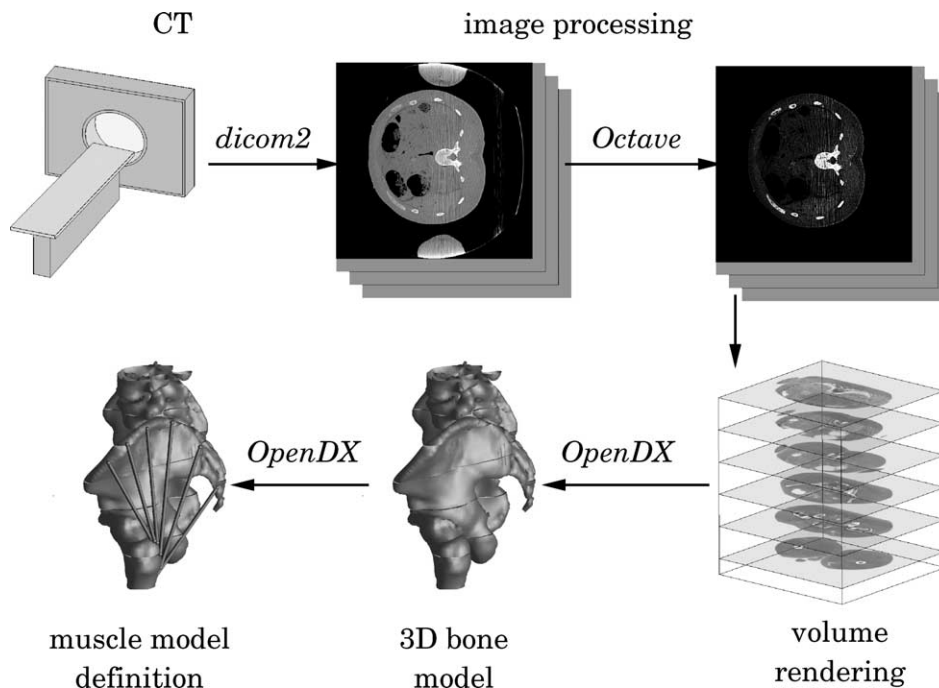


Figure 1. Flow diagram of the method for determination of the quantitative muscular anatomy from CT images.

for image processing, by using predefined methods like image display, image analysis, contrast enhancement methods, geometric transformation, filtering, Fourier transformation, etc. Using the script language which is mostly compatible with Matlab, new filters and special transformation function on the image can be defined and series of images can be processed (figure 2).

The whole series of the images is processed and the output is written into the file, where 3D pixel positions and values are defined (figure 1).

2.2 Generation of 3D bone geometry

The system for 3D interactive visualisation was programmed in the scientific visualisation environment OpenDX—also known as Data Explorer (DX). OpenDX is a programming environment for data visualisation and analysis that employs a data-flow driven client-server execution model [15]. In our work, a graphical user interface, visual programming and a high-level scripting language was used to build final application. The application performs data import, volume

rendering and 3D isosurface calculation (figure 1). As the bone structures are well-separated on the CT images, the isosurface extracts 3D bone image well (figures 1,3). Alternatively, skeletal structures can be visualised as polygonal models [16].

2.3 Definition of muscle geometry

In biomechanical analysis, whole muscles are usually represented as elastic fibres with a certain line of action [9,10]. The line of action of a muscle may be considered to go directly from the origin to the insertion site [6]. Therefore in our work, the geometry of a single muscle was defined by the position of the proximal and the distal attachment points. We have programmed special visualisation module in the OpenDX, that gets input from user (through mouse) and displays 3D position at the specified points on the bone isosurface. When the proximal and the distal attachment points are defined, a tube representing the line of muscle is shown (figures 1,4).

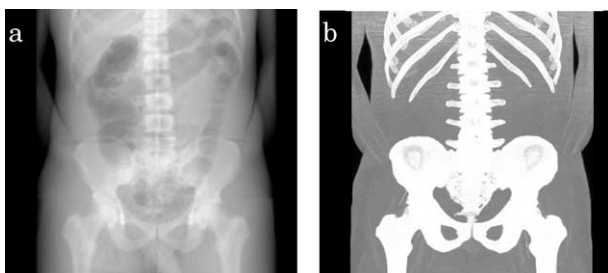


Figure 2. Reconstruction of the “radiographic” image from CT images using original (a) and filtered CT images (b).

3. Results

The possibilities of the visualisation system are demonstrated on the CT image dataset obtained from the Human Visible Project [17]. The CT images of the abdominal and pelvic region were selected and processed.

In the processing of CT images the low-pass Fourier filter was used to reduce the noise. To present the possibilities of application of program for numerical calculations (GNU Octave) in image processing, special filters were developed and the X-ray image was simulated from the series of CT

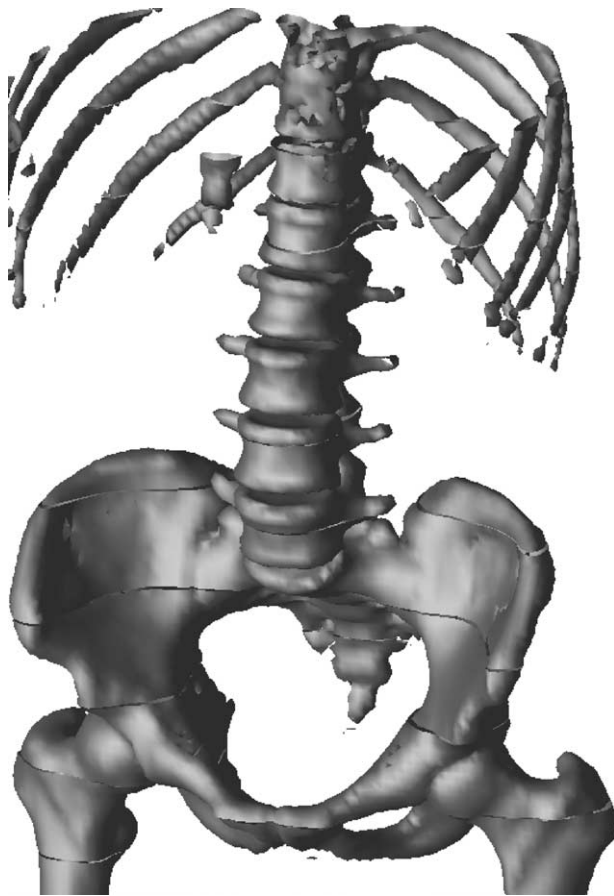


Figure 3. Isosurface of bony structures.

images. This filter performs a simple projection of the CT data to the frontal plane of the body (figure 2a). To depict bony structures, the threshold filter was used on the CT images and the resultant projection is shown in figure 2b.

After importing the data into OpenDX and isosurface calculation, the 3D interactive model of the bony surface was

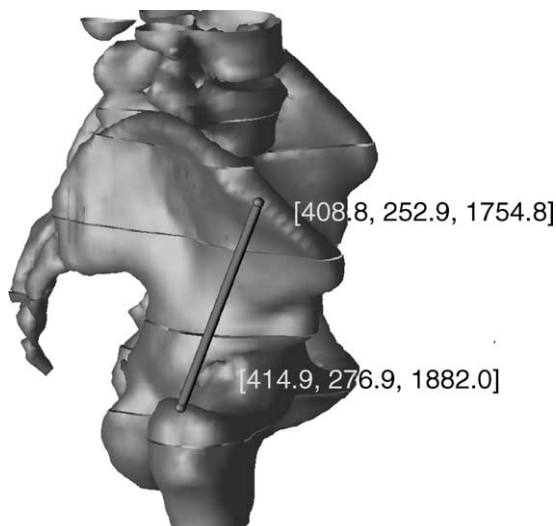


Figure 4. Determination of line of action of single muscle fibre, screenshot of the program. Positional vectors of attachment's points are shown.

obtained (figure 3). To decrease the computational requirements the mesh representing the volumetric data was reduced twice using a build-in module of the OpenDX [15].

Figure 4 shows application of module for assessment of the 3D position of proximal and distal attachment point of the muscle. This method requires a knowledge of the position of the muscle insertion points with respect to the bone structures. Using the anatomical landmarks, the quantitative anatomy of the skeletal musculature can be determined for any part of the body.

The presented program can visualise musculoskeletal anatomy defined by other methods as well. Fig. 5 shows visualisation of the musculoskeletal model of lower extremity published by Delp *et al.* [16]. Skeletal structures are visualised as polygonal models while the 27 effective muscular units of the hip are shown as tubes (figure 5).

4. Discussion

The developed computer system has is modular, flexible and freely available. Modularity of the system means, the parts of the system which works independently and can be replaced by other programs if necessary. For example, the bony isosurface can be visualised as polygonal model (figure 5) or more sophisticated methods for image analysis can be used

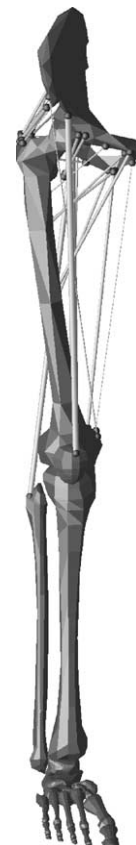


Figure 5. The 3D model of lower leg. Polygonal models of the bones and attachment points of the hip muscles were taken from Delp *et al.* [16].

[18]. The first property of the computer system (modularity) implies its second property (flexibility).

The system is flexible in such manner as it may be easily adjusted for special requirements. For example, special modules can be defined within the visualisation system that imports the data from finite element method stress analysis and displays the stress distribution parallel with the muscle forces. The presented system can be used also for quantitative analysis of the skeletal system [19].

The computer system is based on the freely distributable software published under GNU Public Licence [20]. Therefore, the whole system can be freely distributed and modified. Hence, it nominates itself to be a suitable didactical tool for teachers and students of medical visualisation (e.g. students of biomedical engineering and physics). The students can follow the whole process of visualisation interactively, i.e. they are allowed to modify it. By manipulating the model, students can quickly explore the effects of changing visualisation process. Moreover, the computer system can be run on ordinary PC and does not require any special hardware.

The defined geometry of the musculoskeletal system obtained from the presented system can be used as an input into commercial programs like Software for Interactive Musculoskeletal Modeling (SIMM) [21] or AnyBody [22] that computes the load of the musculoskeletal system during various human activities.

There are certain points at which the system can be upgraded further. The computer system models a muscle as a fibre from the origin to the insertion point and does not include the way muscle wraps around bony structures. However, the position of wrapping points of the muscles can be assessed as an additional attachment points.

In addition to the position of the attachment points, the physiological cross-sectional area of the muscle should be known to construct a biomechanical muscular model [23]. Therefore, it would be useful to determine the physiological cross-sectional area of the muscle within the program.

5. Conclusion

The presented computer system is useful for quantification of the musculoskeletal geometry needed for calculation of the muscle and joint forces by using the method of inverse or forward dynamical analysis. Its modular structure makes it useful also in the medical visualisation classrooms.

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