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# Extension of Anatomical Models of the Human Body: Three-Dimensional Interpolation of Muscle Fiber Orientation Based on Restrictions

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A three-dimensional anatomical model of the human body is extended with information on the orientation of muscle fibres. The orientation is interpolated using two sets with restrictions of different types. These sets consist of points, for which either the orientation or a normal of the orientation is known from detection by manual or automatic methods. The interpolation works iteratively and is based on averaging orientations in the 6-neighbourhood. The average of orientations is calculated by determination of their principal axis.

*Keywords:* Anatomical model, tissue orientation, eigenvector transform, principal component transform, discrete Karhunen-Loeve transform, Hotelling transform

## Introduction

Anatomical models of the human body are of great interest for education purposes as well as to support answering medical and technical questions [Höhne et al., 1994] [Malmivuo and Plonsey, 1995] [Gandhi and Chen, 1992] [Gandhi et al., 1996]. These models mainly consist of information about tissue distribution in the body. Generally the models are created from medical imaging modalities using advanced strategies of digital image processing [Gonzalez and Woods, 1992].

A further anatomical information of interest is the orientation of tissue fibres.

This property is of great importance for accurate modelling of anisotropic physical behaviour of tissue. For example, muscle structures show an anisotropic behavior of electric conductivities and elastomechanic parameters.

The topic of this paper is the extension of a detailed anatomical model [Sachse et al., 1996a] [Sachse et al., 1996b] with the three-dimensional orientation of skeletal muscle fibres (Figure 1).

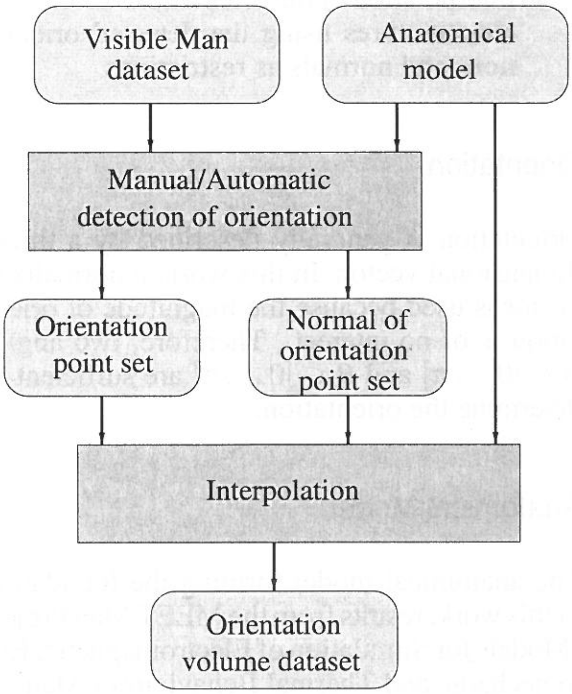


*Fig. 1.* Block diagram for determination of muscle fibre orientation.

The orientation is interpolated based on two sets with restrictions of different types. The first set consists of points for which the orientation is known. The second set consists of points with an assigned normal of orientation. These sets are created by detection with manual or automatic methods using techniques of digital image processing.

The interpolation works iteratively employing the averaging orientations in the 6-neighbourhood. The average of neighbouring orientations is calculated by determination of their principal axis.

## Methods

Extension of a three-dimensional anatomical model with the orientation of muscle fibres is accomplished by an additional orientation dataset, which consists of volume elements containing information on orientation. Creation of the dataset is divided into two steps:

- Detection of orientations and normals of orientations by texture analysis and methods of filtering in medical images
- Interpolation of the orientations in all muscle structures using the detected orientations and normals as restrictions

## Orientation

Orientation is generally described by a three-dimensional vector. In this work, a normalized vector is used because the magnitude of orientation is of no interest. Therefore, two angles $\phi \in [0 \ldots \pi]$ and $\theta \in [0 \ldots \pi]$ are sufficient to determine the orientation.

## Anatomical Model

The anatomical model forming the foundation of this work, results from the MEET Man Project (Models for Simulation of Electromagnetic, Elastomechanic and Thermal Behaviour of Man).

This is a project of the Institute of Biomedical Engineering at the University of Karlsruhe (Germany). The purpose of the project is creation of models for simulating the physical behaviour of man [Sachse et al., 1995].

The anatomical model originates from computertomographic scans and thin-section photos of the Visible Man dataset [Ackerman, 1991], which are provided by the National Library of Medicine, Bethesda, Maryland (USA). Creation of the model involved the use of advanced strategies of digital image processing [Sachse et al., 1996b] [Sachse et al., 1996a].

The model is stored in a three-dimensional dataset, which consists of approximately 400 million cubic voxels. Each voxel has a size of 1 mm x 1 mm x 1 mm and is assigned to one out of thirty different tissue classes, for example bone, cartilage and muscle (Figure 2).

## Determination of Principal Axes

Determination of principal axes is the main step of the principal component transform, which is in literature also known as discrete Karhunen-Loeve, eigenvector and Hotelling transform [Gonzalez and Woods, 1992].

The transform is built on the fundamentals of statistics. It works based on a population $x$ of $K$ random vectors of the following notation:

$$x = (\vec{x}_0, \vec{x}_1, \ldots, \vec{x}_{K-1})^T \tag{1}$$

The vectors $\vec{x}_i$ with $i \in \{1, \ldots, n\}$ are $M$-dimensional and can be described in the following notation:

$$\vec{x}_i = (x_{i\,0}, x_{i\,1}, \ldots, x_{i\,M})^T \tag{2}$$

The mean vector $\vec{m}_x$ of a population $x$ is defined as $\vec{m}_x = \vec{E}(x)$, where $\vec{E}(x)$ is the expected value. The mean vector can be approximated from N vector samples of the population:

$$\vec{m}_x \approx \frac{1}{N} \sum_{i=1}^{N} \vec{x}_i \tag{3}$$

The covariance matrix $C_x$ of a population $x$ is defined as:

$$C_x = E((\vec{x} - \vec{m}_x)(\vec{x} - \vec{m}_x)^T) \tag{4}$$

The covariance matrix can be approximated from N vector samples of the population:

$$C_x \approx \frac{1}{N} \sum_{i=1}^{N} \vec{x}_i \vec{x}_i^T - \vec{m}_x \vec{m}_x^T \tag{5}$$

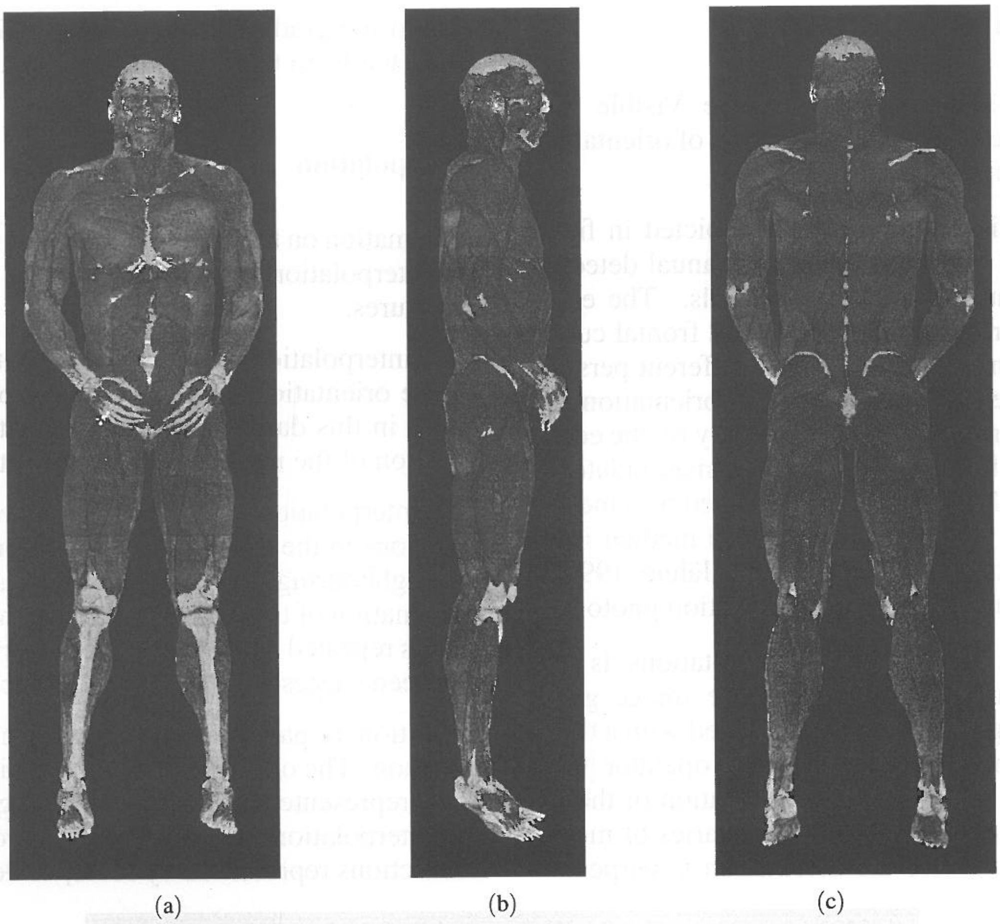

(a) (b) (c)

*Fig. 2.* Muscles, bones and cartilage of the anatomical model.
The model is shown from (a) ventral, (b) lateral, and (c) dorsal view.

One way to determine the principal axes is the diagonalization of the covariance matrix. A diagonal matrix $D$ and a rotation matrix $R$ have to be found, which fulfill the following condition:

$$D = RC_xR^T \tag{6}$$

This can be achieved by calculation of eigenvalues $\lambda_i$ and eigenvectors $\vec{e}_i$, which are determined by:

$$C_x\vec{e}_i = \lambda_i\vec{e}_i \tag{7}$$

The eigenvalues are real, because the covariance matrix is symmetric [Bronštejn and Semendjaev, 1991]. They can be notated in descending order:

$$\lambda_1 \geq \lambda_2 \geq \ldots \geq \lambda_M \tag{8}$$

The diagonal matrix $D$ has the following form:

$$D=\begin{pmatrix} \lambda_1 & 0 & \ldots & \ldots & \ldots & 0 \\ 0 & \lambda_2 & 0 & \ldots & \ldots & 0 \\ \ldots & \ldots & \ldots & \ldots & \ldots & \ldots \\ 0 & \ldots & \ldots & 0 & \lambda_{M-1} & 0 \\ 0 & \ldots & \ldots & \ldots & 0 & \lambda_M \end{pmatrix} \tag{9}$$

The rotation matrix $R$ consists of the eigenvectors:

$$R = (\vec{e}_1, \ldots, \vec{e}_M) \tag{10}$$

The first eigenvector $\vec{e}_1$ is referred to the first principal axis, the i-th eigenvector $\vec{e}_i$ is called the i-th principal axis.

## Restrictions

The orientation of muscle fibres is interpolated based on two sets of restrictions:

- a set $R_O$, which consists of points and their associated orientation
- a set $R_T$, which consists of points and their associated normal of orientation

These sets are detected by automatic and manual methods inside and on the surface of muscle structures.

## Detection

The thin-section photos of the Visible Man dataset are used for the detection of orientations and their normals.

A three-dimensional editor, depicted in figure 3, is used for the interactive, manual detection of orientations and their normals. The editor displays transversal, sagittal and frontal cuts in medical image datasets from different perspectives. Default values for the orientation and normals are created automatically by the editor. The user has the possibility to manipulate the default values. They are calculated by a method of texture analysis. The applied method is the determination of principal axes [Jähne, 1993] in spherical regions of the thin-section photos.

Detection of normals of orientations is performed automatically using the image gradient. This gradient is approximated with a three-dimensional variant of the Sobel operator [Gonzalez and Woods, 1992]. Utilization of the Sobel operator is limited to boundaries of muscle structures, where the orientation is perpendicular to the gradient. These boundaries can be extracted from the anatomical model.

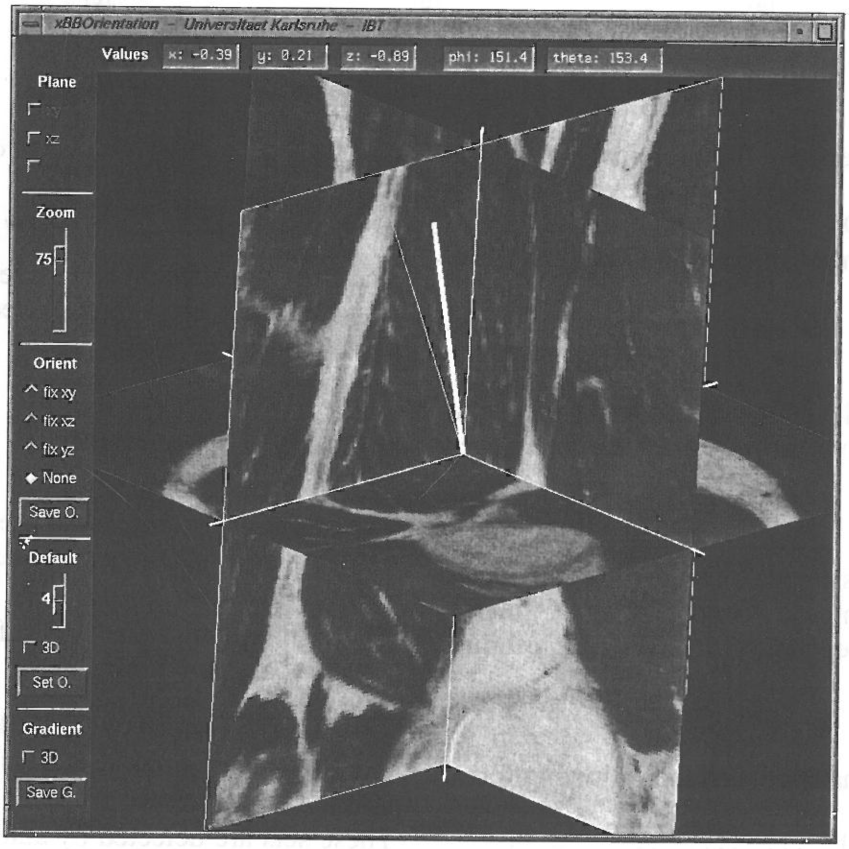
## Interpolation

Information on the anatomical model is used for the interpolation. It is limited to areas of muscle structures.

The interpolation starts with an initialization of the orientation dataset. Orientation of each voxel in this dataset is initialized with the orientation of the nearest point in the set $R_O$.

The interpolation continues with averaging orientations in the 6-neighbourhood. The average of neighbouring orientations is calculated by determination of their principal axis. The calculation is repeated until the changes of orientations between successive steps are negligible.

Attention is payed to the restrictions in each iteration. The orientation of voxels with restrictions represented by set $R_O$ is unchanged during the interpolation. The orientation of voxels with restrictions represented by set $R_T$ is determined



Values x: -0.39 y: 0.21 z: -0.89 phi: 151.4 theta: 153.4

*Fig. 3.* Interactive three-dimensional editor for the manual detection of orientations and their normals. Displayed are transversal, sagittal and frontal cuts in the thin-section photos of the Visible Man dataset from different perspectives.

*Fig. 4.* Two examples of one-dimensional interpolation of orientations. (a) The interpolation is determined based on the given orientations O1 and O2. (b) The interpolation is calculated using the given orientation O3 and normal of orientation N1. The number of iterations amounts to 10.

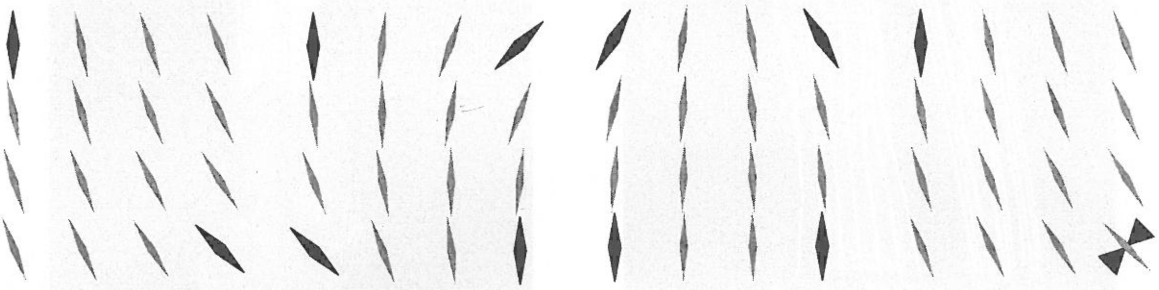


*Fig. 5.* Some examples of two-dimensional interpolation of orientations. The interpolation is calculated using as restrictions (a) two orientations and (b)(c) four orientations. (d) The interpolation is determined using an orientation and a normal of orientation. The number of iterations is 20.

by calculating the average orientation in the 6-neighbourhood. The result is projected into the plane perpendicular to the given normal of the orientation.

Results of the interpolation with different sets of test data are shown in figures 4, 5, and 6. For each interpolation the number of iterations, orientations and normals of orientations are given.

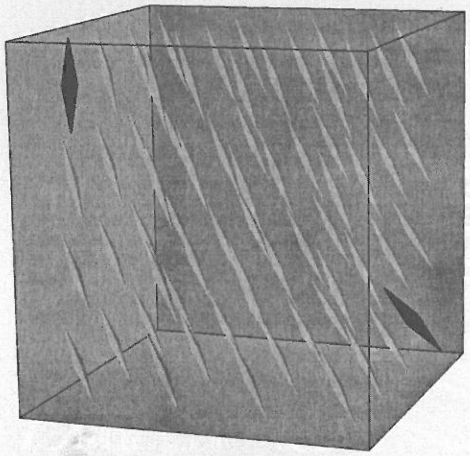


*Fig. 6.* An example of three-dimensional interpolation of orientations. The interpolation is determined from two given orientations. The number of iterations amounts to 20.

## Results and Conclusions

Results of the extension of the anatomical model with muscle fibre orientation are presented in figures 7 and 8 including the number of iterations, orientations and normals of orientations used to interpolate the regions.

Limitation of the presented approach can be assigned to the manual detection of orientations. This step requires fundamental knowledge of muscle anatomy. The knowledge is needed to judge the correctness of default values and to change these values to achieve a correct orientation.

Another limitation can be put down to the fact that the voxel size of 1 mm x 1 mm x 1 mm does not allow detection of minor muscle structures. These are not of importance for many applications. Also, the limitation can be overcome by usage of datasets with higher resolution, eg the Visible Female Dataset, which is provided by the National Library of Medicine, Bethesda, Maryland (USA).

The muscle fibre orientation dataset was revised by human experts with the help of anatomical atlases. Therefore the visualization techniques presented in figure 7 and 8 are employed.

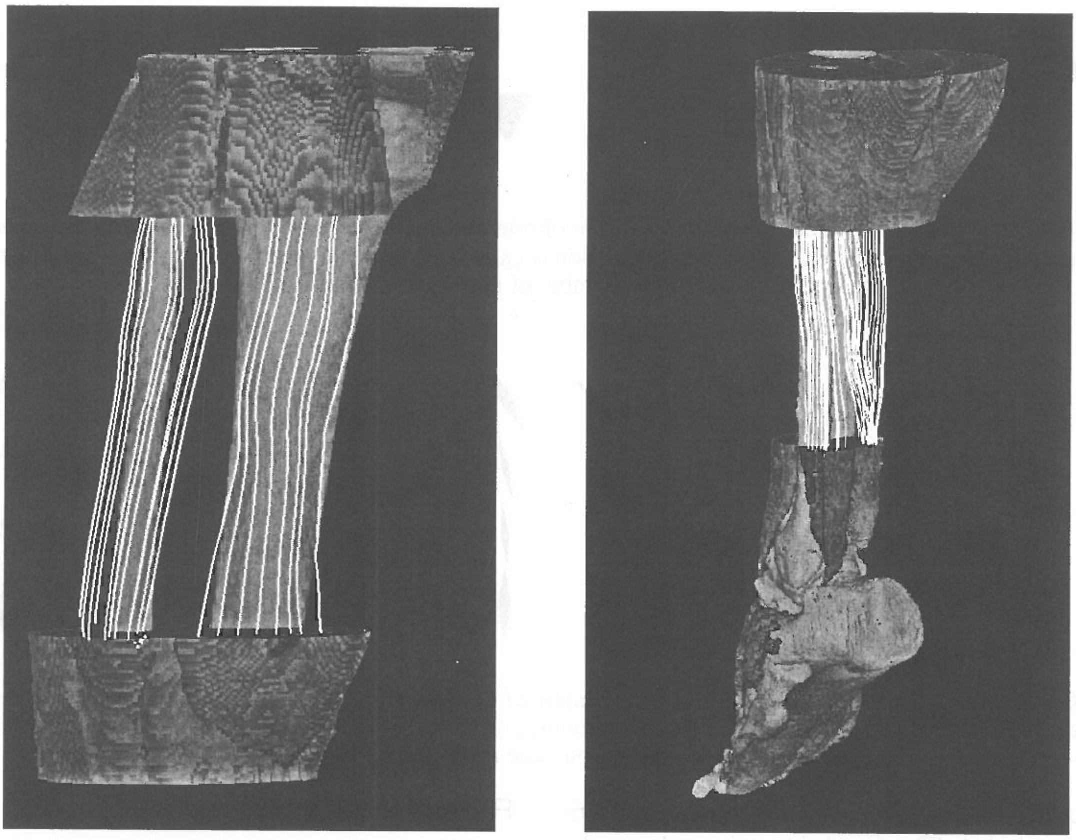


*Fig. 7.*(a)(b) Muscle fibre orientations in the lower leg. The interpolation is calculated using 200 orientations determined with the three-dimensional editor and 7 000 normals of gradients calculated with automatic methods. The number of iterations is 60. The white lines indicate fibre orientation. They are constructed by following the orientation starting from user defined points.

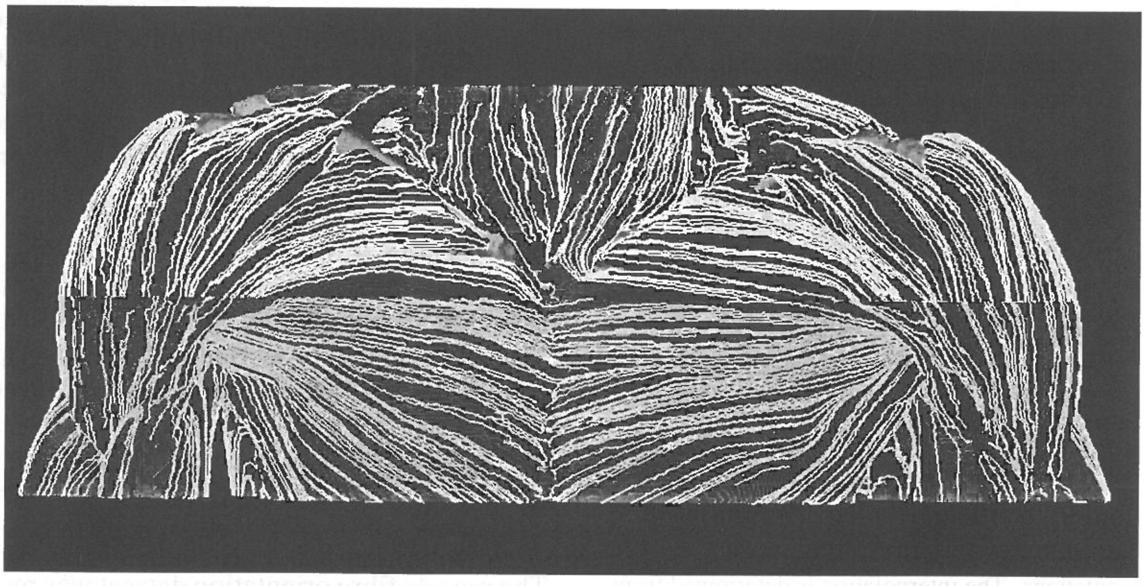


*Fig. 8.* Fibre orientations projected onto the surface of the thoracic muscle structures. The interpolation is determined outgoing from 400 manually detected orientations and 30 000 automatically detected normals of gradients. The number of iterations amounts to 60. The white lines are constructed by following the fibre orientation on the surface, starting from chosen points.

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