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Subject-specific human body (sub-)models developed by morphing

L. Hynčík

New Technologies – Research Centre, University of West Bohemia, Univerzitní 8, 301 00 Plzeň, Czech Republic

Virtual biomechanical human body models contribute to designing safe and user-friendly products through virtual prototyping. Contemporary trends focus on personalized approach to implement safety systems, protective equipment and personalized health care for a specific person. Here a virtual prototyping plays an irreplaceable role. For designing personal protective equipment or personal tool and approaches in health care by virtual prototyping, subject-specific human body models seem to be a promising tool for personalized approach. As the person-specific model development is a complex task, the virtual human model of a generic body is used and adopted to the particular person. There are two basic approaches for developing a person-specific human body model, particularly scaling and personalization. Whilst scaling changes only the global dimensions (anthropometry, mass and stiffness) based on the general anthropometric parameters [3], personalization updates the local geometrical and biomechanical details of the particular human body segments [2]. Additional mesh morphing refines particular details of the segment discretized by a finite element mesh [4].

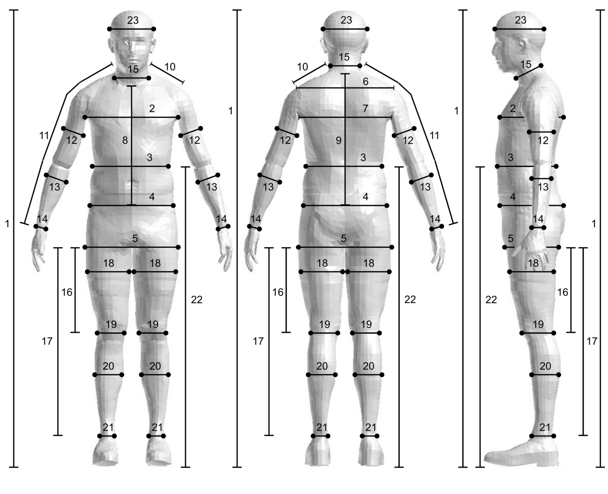

Fig. 1. Clothing industry dimensions

The personalization method upgrades the local dimensions by addressing the measured dimensions and so it develops a subject-specific virtual human body model. The presented algorithm benefits from the implementation of the clothing industry dimensions, see Fig. 1. The external body shape is personalized using polynomial functions to secure the continuous and smooth body surface, which is desired mainly for applications where the human body comes into contact with other subjects or external objects. We use polynomials of degree n_i^s in the form

$$p_i^s(i) = \sum_{k=0}^{n_i^s} c_{ik}^s i^k \tag{1}$$

to interpolate the body shape along each spatial axis $i \in \{x, y, z\}$ where vector $\mathbf{c}_i^s = [c_{i0}^s, \ldots, c_{in}^s]$ contains the polynomial coefficients in spatial direction $i \in \{x, y, z\}$ for each body segment $s \in \{0, \ldots, 15\}$, when dividing the human body for 15 basic segments as shown in Table 1.

Table 1. Basic human body segments for personalization

Segment	Head	Neck	Thorax	Abdomen	Arm	Forearm	Palm	Thigh	Calf	Foot
Left	3	2	1	0	4	5	6	10	11	12
Right					7	8	9	13	14	15

The polynomial interpolation might suffer from inaccuracy and unrealistic overshoots in the polynomial shape if we interpolate incomparable values, which is why the scaling [3] is carried out in the first step before the personalization. Fig. 2 shows an example of the personalized human body model of a 45 years-old male with the height 176 cm and the weight 85 kg.

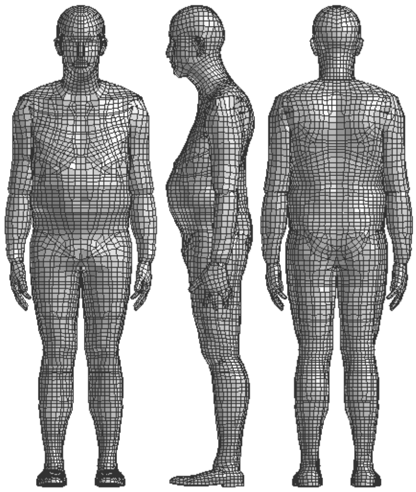

Fig. 2. Subject-specific human body model

Mesh morphing as one of the morphing approaches accommodates radial basis functions to interpolate function $f(\mathbf{X})$ at the point $\mathbf{X}$ having m corresponding landmarks on both the original (baseline) $\mathbf{X}_{Lj}$ and the target (morphed) $\mathbf{X}_{Tj}$ models, $j \in \{1, \ldots, m\}$ as [1]

$$f(\mathbf{X}) = p(\mathbf{X}) + \sum_{j=1}^{m} \lambda_j \varphi \left(\|\mathbf{X} - \mathbf{X}_j\|\right) + \alpha, \tag{2}$$

where $p(\mathbf{X})$ is a low order polynomial, λ_j, $j \in \{1, \ldots, m\}$, are the weighting coefficients, φ is the basis function and α is a constant, which we choose zero. A first order polynomial

$$p(\mathbf{X}) = [1, x, y, z] \, [c_0, c_1, c_2, c_3]^{\mathrm{T}} = \mathbf{X}\mathbf{c} \tag{3}$$

and the thin plate spline basis function $\varphi = r^2 \log r$ results in a smooth function $f(\mathbf{X})$ in Eq. (2) [2, 5]. Considering function $f(\mathbf{X}) = [x_{Ti}, y_{Ti}, z_{Ti}] = \mathbf{X}_{Ti}$ represents the target mesh with n nodes, $i \in \{1, \dots, n\}$, Eq. (2) can be written as

$$\mathbf{X}_{Ti} = \sum_{j=1}^{m} \lambda_j \varphi \left(\|\mathbf{X}_{Li} - \mathbf{X}_{Tj}\| \right) + \mathbf{X}_{Li}\mathbf{c}, \quad j \in \{1, \dots, m\} \tag{4}$$

or in the matrix form as

$$\begin{bmatrix} \mathbf{A} & \mathbf{B} \\ \mathbf{B}^{\mathrm{T}} & \mathbf{0} \end{bmatrix} \begin{bmatrix} \boldsymbol{\lambda} \\ \mathbf{c} \end{bmatrix} = \begin{bmatrix} \mathbf{T} \\ \mathbf{0} \end{bmatrix}, \tag{5}$$

where

$$\mathbf{A} = A_{ij} = \varphi\left(r_{ij}\right) = r_{ij}^2 \log r_{ij} \tag{6}$$

is a $m \times n$ matrix containing the distances between the pairs of the baseline and the target landmarks $r_{ij} = \|\mathbf{X}_{Li} - \mathbf{X}_{Tj}\|$, $\forall i, j \in \{1, \dots, m\}$,

$$\mathbf{B} = \begin{bmatrix} 1 & x_{L1} & y_{L1} & z_{L1} \\ \vdots & \vdots & \vdots & \vdots \\ 1 & x_{Lm} & y_{Lm} & z_{Lm} \end{bmatrix} \tag{7}$$

is a $m \times 4$ matrix containing the coordinates of the baseline model landmarks,

$$\mathbf{T} = \begin{bmatrix} x_{T1} & y_{T1} & z_{T1} \\ \vdots & \vdots & \vdots \\ x_{Tm} & y_{Tm} & z_{Tm} \end{bmatrix} \tag{8}$$

is a $m \times 3$ matrix containing the coordinates of the target model landmarks and $\mathbf{c}$ is a constant matrix. Solving Eq. (5) brings the matrix $\boldsymbol{\lambda}$ of size $m \times 3$ and the matrix $\mathbf{c}$ of size 4×3. Once they are determined, by assuming that the number of nodes in the baseline model is n, the coordinates of the nodes in target model $\bar{\mathbf{T}}$ (a matrix of size $n \times 3$) can be calculated as

$$\begin{bmatrix} \bar{\mathbf{T}} \\ \mathbf{0} \end{bmatrix} = \begin{bmatrix} \bar{\mathbf{A}} & \bar{\mathbf{B}} \\ \mathbf{B}^{\mathrm{T}} & \mathbf{0} \end{bmatrix} \begin{bmatrix} \boldsymbol{\lambda} \\ \mathbf{c} \end{bmatrix}, \tag{9}$$

where

$$\bar{\mathbf{T}} = \begin{bmatrix} \bar{x}_1 & \bar{y}_1 & \bar{z}_1 \\ \vdots & \vdots & \vdots \\ \bar{x}_n & \bar{y}_n & \bar{z}_n \end{bmatrix} \tag{10}$$

is a $n \times 3$ matrix containing the coordinates of the nodes in the target model,

$$\bar{\mathbf{A}} = \bar{A}_{ij} = \varphi\left(r_{ij}\right) = r_{ij}^2 \log r_{ij} \tag{11}$$

is a $n \times m$ matrix, where $i \in \{1, \dots, n\}$ are the nodes in the baseline model, $j \in \{1, \dots, m\}$ are the baseline model landmarks and

$$\bar{\mathbf{B}} = \begin{bmatrix} 1 & x_1 & y_1 & z_1 \\ \vdots & \vdots & \vdots & \vdots \\ 1 & x_n & y_n & z_n \end{bmatrix} \tag{12}$$

is a $n \times 4$ matrix containing the coordinates of all nodes in the baseline model. As the thin plate spline function is chosen, the coincident baseline and target landmarks ($\log r_{ij} \to -\infty$) contribute to the particular position in the matrix $\mathbf{A}$ by zero.

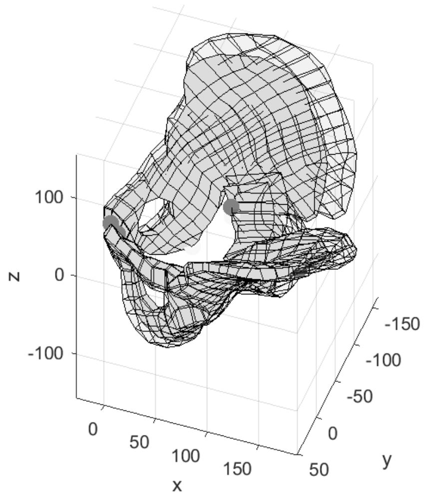

Fig. 3. Example of a morphed simple pelvic bone finite element model

Scaling is a convenient tool for creating generic human body models representing a population group for virtual prototyping, safety systems in mobility or designing personal protective equipment. Personalization is a sufficient tool for developing subject-specific human body models. For local segment refinement, the mesh morphing algorithm is an efficient tool to update the finite element mesh based on a set of chosen landmarks. Modern technologies enable personalized products to be designed, so if we want to address a subject-specific approach for protective equipment or personal tool and approaches in health care, personalization and morphing is a good solution for the subject-specific anthropometry.

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