



NOVÉ TECHNOLOGIE
VÝZKUMNÉ CENTRUM
ZÁPADOČESKÉ
UNIVERZITY
V PLZNI

*ODBOR MODELOVÁNÍ HETEROGENNÍCH MATERIÁLŮ A BIOMECHANICKÝCH
SYSTÉMŮ*

AUTORIZOVANÝ SOFTWARE

SCAPY

***SOFTWARE FOR SCALING OF RIGID BODY BASED
HUMAN MODELS***

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Číslo projektu: *CG911-044-150*

Číslo výsledku: *NTC-SW-01-09*

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Documentation of ScaPy software (version 2009)

1 INTRODUCTION

Human is not uniform, everyone is an original being from both the anthropometrical point of view and concerning mechanical characteristics. However, the development of a particular human body model for each of us is not the effective way of modeling. The idea is to have a couple of standard models as a basic set which can be modified to create additional models. This is the motivation to create a scaling tool that enables automatic generation of human body models depending on age, sex and body stature expressed by anthropometric percentiles.

For scaling a large set of statistical data based on around 13.000 specimens previously measured by assoc. Prof. Pavel Bláha from the Faculty of Science, Charles University in Prague is used. The data concerns major anthropometric dimensions for male, female and children within the population of the Czech Republic between 3 and 75 years.

The basic family of human articulated rigid body models developed on the PAM computational platform [9] is used as a reference test set. The family is created using the public anthropometric databases [5] and includes a model of a 50% male, a 5% female and a six years old child. All the models consist of rigid bodies separated into segments connected by biomechanical joints [7]. The models also contain all main skeletal muscles implemented.

The original scaling software written in C programming language [8] stands behind this new updated and extended version. The current program for scaling rigid body based models ScaPy (Scaling in Python) is implemented as a modulus of the Python programming language. Why just Python is chosen? Python is free, fast and available for all major operating systems. It disposes of complete and user friendly documentation and extensive standard libraries offering a wide range of facilities.

2 METHOD

2.1 Scaling factors

In [1] the authors discuss a scaling method which they developed and applied to crash-dummy models. In their study, different scaling factors are specified for x (depth), y (width), and z (length) body dimensions. Furthermore different scaling factors are applied for different body parts. Thus the model geometry can be adapted freely to desired anthropometry parameters. The scaling input is a set of target anthropometry parameters which are summarized in Table 1. The anthropometric body points used for determination of the anthropometric parameters are marked in Fig. 1.

Segment	Depth	Width	High (Length)
Head–Neck	Head maximal circumference		Difference between vertex and suprasternale
Thorax	Chest sagittal diameter	Chest transversal diameter	Difference between suprasternale and iliocristale
Abdomen	Bicristal width, i.e. left and right iliocristale distance		Difference between iliocristale and iliospinale
Pelvis	Thigh gluteal circumference	Bispinal width, i.e. left and right iliospinale distance	Difference between iliospinale and symphision
Arm	Distal humeral epiphysis		Difference between akromiale and radiale
Forearm	Wrist width		Difference between radiale and stylium
Hand	Hand width		Difference between stylium and dactylium
Thigh	Distal femoral epiphysis		Difference between symphision and tibiale
Leg	Ankle width		High of tibiale
Foot	Difference between pterion and acropodium	Difference between metatarsale tibiale and metatarsale fibulare	High of tibiale

Table 1: Anthropometric measures used to scale segments in three major dimensions

Happee et al. note in [1] that scaling is performed assuming that all material properties are invariant with subject size. Biomechanically this seems to be an acceptable approach for adult subjects. For scaling towards children, or to simulate elderly persons the variation of material properties should be included. Hence, the scaling of joint characteristics using the main idea published in [1] is included. The assumption of equal density leads to analytical scaling rules for mass, centre of gravity and rotational inertia. For the scaling of stiffness and damping the assumption of identical material parameters leads to simple scaling rules. For instance when scaling the force deflection behavior of an ellipsoid, deflection scales with the representative length and force scales with surface and thereby with length to the second power.

The above-mentioned anthropometric parameters are also evaluated for the reference models which are to be scaled. Database of real anthropometric parameters is based on the Bláha's measurements. Initial scaling factors are simply derived as the ratio of target parameters (measured subject) divided by reference model parameters. The resulting scaling factors are then applied to the reference model. Using the above-mentioned segmentation, all major dimensions of particular segments are scaled as a function of gender, age and percentile. For a chosen age, we provide average anthropometric dimensions based on the measured data.

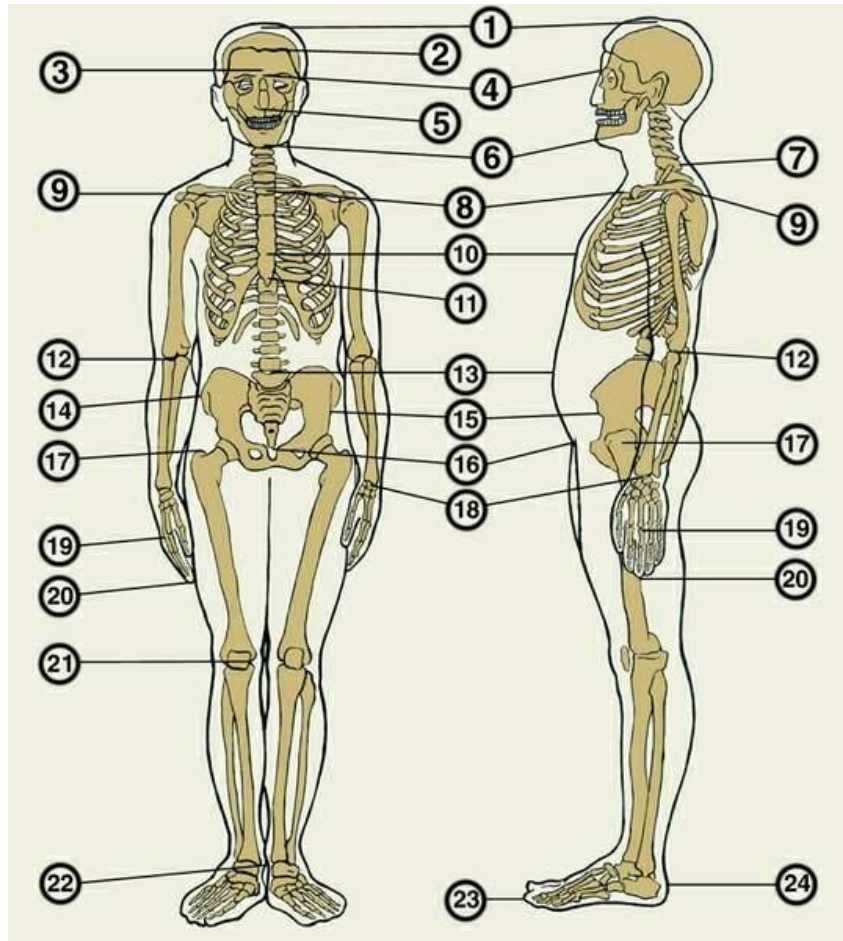


Figure 1: Anthropometric measures: 1 vertex, 2 trichion, 3 metopion, 4 nasion, 5 subnasale, 6 gnation, 7 cervicale, 8 suprasternale, 9 acromion, 10 mesosternale, 11 xiphion, 12 radiale, 13 omphalion, 14 iliocristale, 15 iliospinale anteius, 16 symphision, 17 trochanterion, 18 stylium, 19 phalangion, 20 dactylion, 21 tibiale, 22 sphyrion, 23 acropodion, 24 pterion; adapted from [5].

2.2 Scaling algorithm

The reference model is composed of rigid bodies connected by joints. Each rigid body is defined via geometrical surface, e.g. nodes defining the position. Each joint connecting two rigid bodies is defined via two nodes, each belonging to one rigid body. These two nodes create a joint element. Simply saying, the scaling algorithm is nothing else than scaling the nodes and re-position all scaled rigid bodies in order to be connected in the same way as before scaling. For the rigid body based model, the algorithm scales the dynamical characteristics (masses and inertias) for the rigid bodies as well.

In the reference model, there are more rigid bodies than major anthropometric segments and hence some rigid bodies form a single segment for scaling while some are coupled to one segment as displayed in Figure 2.

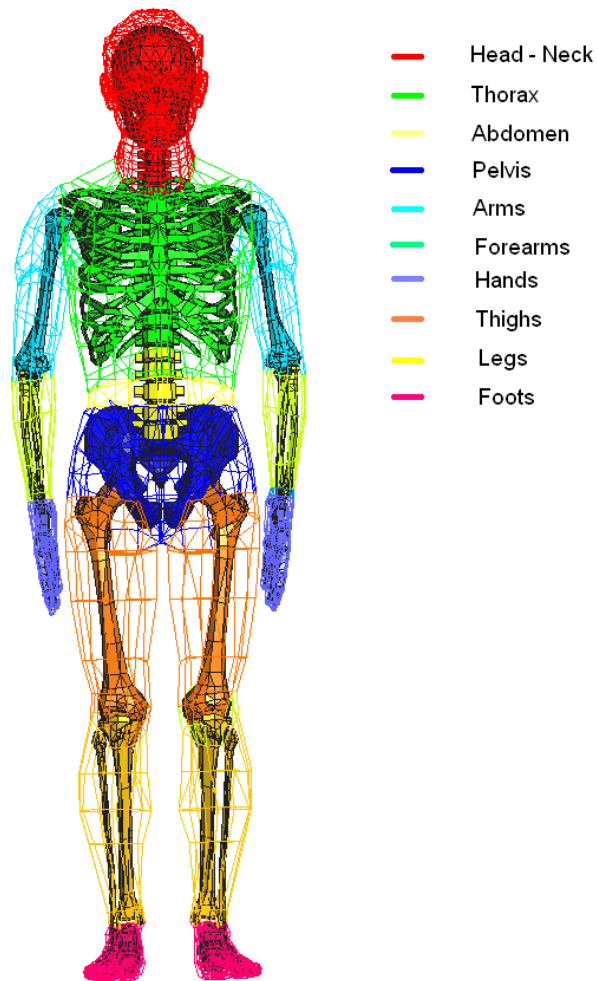


Figure 2: Anthropometric segmentation of the tested reference model [4].

The scaling algorithm can be divided into following steps:

1. **Scaling of all segments.** For particular segment, each node is scaled in all three directions.
2. **Update of inertia matrix.** The dynamical characteristics of each rigid body (mass and moments of inertia) are re-computed based on the scaling procedure changing the shape.
3. **Update of joint structure.** Using the tree definition of the segments, all segments are reconnected back in order the joints defined have the same initial offset as before scaling (two nodes of a kinematic joint should have the same distance in all three global directions as before scaling).
4. **Reposition of the H-point.** The whole structure is moved in order the H-point's coordinates are the same as before scaling. H-point is in the middle between the hip joints and the reference model, and simultaneously it is the origin of the global coordinate system.
5. **Update of muscles.** New muscle elements lengths are computed and the muscles forces are scaled.
6. **Update of joint characteristics.** The joint characteristics describing the range of movement are updated based on the experiments [1].

Scaling of geometry (ad 1, 3 and 4)

The anthropometric dimensions of particular segments are used to scale the segments of the reference human body models in a global coordinate system. Each structural node is defined by the vector

$$\mathbf{x} = \begin{bmatrix} x \\ y \\ z \end{bmatrix}$$

where x , y and z are coordinates in the global 3D coordinate system. The scaled coordinates are proceed as

$$\mathbf{x}_{scaled} = \begin{bmatrix} k_1 & 0 & 0 \\ 0 & k_2 & 0 \\ 0 & 0 & k_3 \end{bmatrix} \mathbf{x}$$

where k_i , $i = 1, 2, 3$ are the scaling factors. Each segment has defined its own scaling matrix with different scaling factors. After scaling all segments, it is necessary to re-connect them in order the joints are in the original position. The basic location of the whole model in space is settled by the H-point. So firstly, the segment accommodating the age point is moved in order the H-point to be in the original position. Then, by the definition of the open tree structure, we move following segments from the segment accommodating H-point in order to have the original joint geometry kept. Here the necessity of an open tree is shown. However, if we want to scale a model having closed tree inside, we can open it by releasing the joint closing a tree and modify the geometry after scaling manually.

Scaling of rigid bodies (ad 2)

Based on [1], it is supposed that density of human body parts remains constant during scaling and the segment mass can be expressed as

$$m = \int_V \rho dV = \rho \int_V dV = \rho \int_V dx dy dz.$$

The new segment mass is then naturally computed as

$$m_{scaled} = k_1 k_2 k_3 m.$$

Having the scaling factors k_1 , k_2 and k_3 and the inertia matrix of the particular rigid body in the form

$$\mathbf{D} = \rho \int_V \begin{bmatrix} y^2 + z^2 & -xy & -xz \\ -xy & x^2 + z^2 & -yz \\ -xz & -yz & x^2 + y^2 \end{bmatrix} dV,$$

new inertial characteristics (denoted for clarity by left upper index s) are given by the expressions

$${}^s I_x = k_1 k_2^3 k_3 N_y + k_1 k_2 k_3^3 N_z,$$

$${}^s I_y = k_1^3 k_2 k_3 N_x + k_1 k_2 k_3^3 N_z,$$

$${}^s I_z = k_1^3 k_2 k_3 N_x + k_1 k_2^3 k_3 N_y,$$

$${}^s D_{xy} = k_1^2 k_2^2 k_3 D_{xy},$$

$${}^s D_{xz} = k_1^2 k_2 k_3^2 D_{xz},$$

$${}^s D_{yz} = k_1 k_2 k_3^2 D_{yz},$$

where

$$N_x = \frac{1}{2} (I_x + I_y + I_z), \quad N_y = \frac{1}{2} (-I_x + I_y + I_z), \quad N_z = \frac{1}{2} (I_x + I_y - I_z)$$

The derivation is based on the following substitution

$$I_x = N_y + N_z, \quad I_y = N_x + N_z, \quad I_z = N_x + N_y.$$

However, it can not be forget that for original as well as scaled inertias still holds $I_k + I_l > I_m$ for $k, l, m = x, y, z$.

Scaling of muscles (ad 5)

The new rest length of all muscle segments (bar elements) is computed. It is known that the muscle force is proportional to the muscle physiological cross-sectional area

$$F_{max} = k \cdot PCSA$$

Hence, it is supposed that the muscle cross-sectional area changes in the same rate as the transverse section of the particular segment. And the new muscle force is multiplied by the depth and width scale coefficients as

$${}^{scaled} F_{max} = k_1 k_2 F_{max}.$$

Scaling of joint characteristics (ad 6)

The method of joint characteristics scaling is based on the flexitest [1]. Flexitest consists of measuring and evaluating of the maximum passive range of motion of 20 body joint movements (36 if considered bilaterally), including the ankles, knees, hips, trunk, wrist, elbows and shoulders. Each movement of a concrete person is evaluated by the number from zero to four. Such analysis is performed for each movement and joint, and the results are summed to obtain a global index of flexibility or joint mobility called flexindex. The entire mobility spectrum ranges between 0 and 80.

It is assumed that joint characteristics change for all joints in the same manner so that for the particular range of motion holds

$$\alpha_{scaled} = \alpha \frac{FI}{FI_{max}}$$

where α is the joint angle and FI denotes the flexindex.

3 IMPLEMENTATION

3.1 Installation and run

The source code is implemented in the Python scripting language. The code consists of the main file *ScaPy_main.py* and the executive file *ScaPy_fun.py* which contains all important functions. To run the ScaPy, the user should install the Python language (for example Python 2.6.2, accessible at [7]). The installation is free and available for any kind of platform. Further it is necessary to download the directory *Data* containing all anthropometric measures.

The ScaPy can be started up through Python application (e.g. Pylab) or using the standard command line. It expects three input parameters that are the sex, age and percentile of the output model:

```
>> ScaPy_main.py -s m -a 30 -p 50
```

For the help use following command

```
>> ScaPy_main.py -h
```

Available parameter inputs are summarized in Table 2. According to given age appropriate reference model is chosen.

Model	Sex	Age	Percentile
Man	m	22-75	1, 5, 25, 50, 75, 95, 99
Woman	f	22-75	1, 5, 25, 50, 75, 95, 99
Child	m, f	3-7	3, 50, 97

Table 2: Summary of ScaPy input parameters.

It is necessary to keep the original organization of all input files.

3.2 Structure of input files

The structure of human models regarding rigid bodies, segments and muscles is defined in specific files which are imported to the ScaPy. The files except mapping vectors are automatically generated from the reference model source file, and they have given formats. All of them are listed below.

Man50p_N_vector.txt (*Woman05p_N_vector.txt*, *Child6YO_N_vector.txt*): mapping vector of nodes.

node number	segment number
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Man50p_N_matrix.txt (*Woman05p_N_matrix.txt*, *Child6YO_N_matrix.txt*): nodal coordinates in the global coordinate system. The position of each node corresponds to its position in the mapping vector.

x coordinate	y coordinate	z coordinate
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Man50p_J_matrix.txt (*Woman05p_J_matrix.txt*, *Child6YO_J_matrix.txt*): joint nodal numbers and particular segment numbers. Each joint can connect rigid bodies in the frame of one segment, or can connect two segments.

first joint node number	second joint node number	first joint node segment number	second joint node segment number
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Man50p_R_vector.txt (*Woman05p_R_vector.txt*, *Child6YO_R_vector.txt*): mapping vector of rigid bodies.

rigid body number	segment number
-------------------	----------------

Man50p_R_matrix.txt (*Woman05p_R_matrix.txt*, *Child6YO_R_matrix.txt*): rigid body characteristics. The position of each rigid body corresponds to its position in the mapping vector.

m	I_x	I_y	I_z
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Man50p_M_vector.txt (*Woman05p_M_vector.txt*): mapping vector of muscles.

muscle number	segment number
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Man50p_M_force.txt (*Woman05p_M_force.txt*): Column of maximum isometric muscle forces. The position of particular muscle force determines its muscle number through the mapping vector.

Man50p_M_name.txt (*Woman05p_M_name.txt*): Column of skeletal muscle names. The position of particular muscle name determines its muscle number through the mapping vector.

Man50p_M_nodes.txt (*Woman05p_M_nodes.txt*): Numbers of skeletal muscles bars. Each muscle is created by one or more bar elements. This file contains numbers of all particular muscle bars formatted by rows so that each row corresponds to one muscle. The position of muscle determines its muscle number through the mapping vector.

Man50p_J_flex.txt (*Woman05p_J_flex.txt*, *Child6YO_J_flex.txt*): Number of joint functions that are to be scaled (angle-moment dependencies of spherical joints).

Also the file containing the anthropometric data depending on the percentile is imported. Each file contains all anthropometric parameters listed in Table 1 depending on age. The age ranges from 22 to 75 years in case of adult male and female, and from 3 to 7 years in case of children. The files containing flexindexes useful for joint scaling are also included. Anthropometric measures of basic model are not naturally age dependent.

Reference model anthropometric input files:

anthropometry_Man50p.txt

anthropometry_Woman05p.txt

anthropometry_Child6YO.txt

Male anthropometric input files:

anthropometry_male_01_Blaha_2009.txt

anthropometry_male_05_Blaha_2009.txt

anthropometry_male_25_Blaha_2009.txt

anthropometry_male_50_Blaha_2009.txt

anthropometry_male_75_Blaha_2009.txt

anthropometry_male_95_Blaha_2009.txt

anthropometry_male_99_Blaha_2009.txt

flex_index_male_age22-75.txt

Female anthropometric input files:

anthropometry_female_01_Blaha_2009.txt

anthropometry_female_05_Blaha_2009.txt

anthropometry_female_25_Blaha_2009.txt

anthropometry_female_50_Blaha_2009.txt

anthropometry_female_75_Blaha_2009.txt
anthropometry_female_95_Blaha_2009.txt
anthropometry_female_99_Blaha_2009.txt
flex_index_female_age22-75.txt

Child anthropometric input files:

anthropometry_child_male_3-7_03p_CS_1987.txt
anthropometry_child_male_3-7_50p_CS_1987.txt
anthropometry_child_male_3-7_97p_CS_1987.txt
flex_index_male_age5-7.txt

3.3 List of declared functions

input_files: reads of all necessary input files containing the model structure.

input_files_muscle: reads of all necessary input files containing the muscle data.

scale_maty: computes the matrix of scaling coefficients.

scale_node: moves structural nodes. The coordinates of each node are multiplied by particular scaling coefficients.

save_node: prints scaled nodal coordinates into specific file. The file is structured in the format for PAM environment.

scale_rbody: scales rigid bodies. The mass and inertias of each rigid body are updated, and inertia correctness is checked.

save_rbody: prints updated rigid body properties into file format for PAM environment.

scale_save_joint: scales joint characteristics depending on the age, sex and percentile. Each function describing the joint range is multiplied by particular scaling coefficient.

scale_muscle_len: computes new muscle rest lengths.

scale_muscle_force: updates muscle forces. Each muscle force is multiplied by particular scaling coefficients.

save_muscle: prints updated muscle cards, file format for PAM environment

move_joint: translates joint nodes to the end of segment to obtain to the original movement characteristics

move_model: translates the whole new model to be in the reference position. It means that the H-point placed between the hip joints is in the origin of the global coordinate system.

save_rbody_support: support function used in printing new rigid bodies into output file.

save_ctrl: prints updated main model file in the PAM file format.

3.4 Output

The scaled models are saved in the output ASCII files with the specific format required by the PAM environment. Current model age and percentile are contained in the new file names. These files are linked in the main model file (**_ctrl.pc*) together with the unchanged files and the new model is prepared to next processing.

Man_perc_age_ctrl.pc (Woman_perc_age_ctrl.pc, Child_perc_age_ctrl.pc)
Man_perc_age_nodes.inc (Woman_perc_age_nodes.inc, Child_perc_age_nodes.inc)
Man_perc_age_KJRB.inc (Woman_perc_age_KJRB.inc, Child_perc_age_KJRB.inc)
Man_perc_age_muscles.inc (Woman_perc_age_muscles.inc)

4 CONCLUSION

The ScaPy software for scaling rigid body human models was created. ScaPy is implemented as a program unit of Python programming language. It is based on real anthropometric data measured on the Czech population.

Against the original version written in C language, ScaPy comprises scaling of muscle elements and joint characteristics, the input anthropometric database is updated and the scaling of the child model is enabled.

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