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ABSTRACT

The current manuscript reports on the development status of a software framework to scale (personalize) and position Human Body Models used in safety applications, i.e. the PIPER framework. The framework is both model and code agnostic and it was successfully used with Thums, GHBMC and the new PIPER scalable child model. Various transformation methods to scale or positioning were implemented in an interactive application. The software was released under the Open Source General Public License (GPL) version 2. More details can be found at http://piper-project.org

INTRODUCTION

Human Body Models based on the Finite Element methods (HBM) are now widely available. For adult, they include in particular the Thums (Toyota RD, Japan) and the GHBMC (GHBMC, Plymouth, MI) families. These models are now stable and their responses can approach most known responses based on PMHS testing. However, HBM are typically only available in sizes matching the dummy dimension, and in one posture only (their development posture) which can make them difficult to use to simulate a diverse population in diverse environments (vehicle, PMHS testing, Out of position, precrash, etc.).

While methods have been developed to scale HBM, they are typically based on custom workflows developed to be used with a specific HBM and finite element solver, and they were mostly used in research settings. Recent examples include Vavalle et al. (2014), Jolivet et al. (2015), Hwang et al (2016) and Beillas and Berthet (2017) for the GHBMC or Thums models. All are using scripting languages such as Matlab or Scilab. The scripts are used to read the nodes of the model, access the transformation target (geometry which is typically owned or developed by the authors of the study) and finally to perform the transformation using interpolation algorithms. As such, they seem specific to the model, workflow and context.

For positioning, as HBM typically do not include robotic joints which would be easy to modify with geometrical transformations (as for dummy positioning), positioning is typically based on simulation in the FE solver by pulling and pushing (mechanically) on segments of the model. Hence, the end position results from a combination of user input (constraints) and mechanical behavior of the HBM. Running a full FE model simulation, which can be costly, is therefore required not only for the transformation of the model but also to preview the final position (and know if the constraints are sufficient). More fundamentally, the properties of HBMs are typically selected such that their responses are reasonable under impact conditions. They are not necessarily appropriate for physiological levels, both in terms of stiffness and deformation mode (e.g. the volume conservation at the element level may not be appropriate to simulate the transformation of a muscle during postural change). Furthermore, they do not account for physiological relationships (e.g. coordination of vertebrae) or postural preferences. A few attempts have been made using geometrical methods (e.g. MARATHE et al. 2011) but their implementations are typically limited to a body region and are tightly related to a HBM (model specificity).

Overall, current scaling (or personalizing) and positioning approaches can present significant challenges in terms of performance, applicability for different HBM, and usability (complexity) for non-research users. Their limited availability (Intellectual Property, IP) can also make positioning and scaling challenging especially considering the future needs for specifications and reproducibility. The objectives of the EC Funded PIPER project (2013-2017, 10 partners) were defined based on these observations. The project aims to work on technical/scientific gaps related to scaling/positioning (and child modeling) and organizational/IP gaps by making all results available under an Open Source license.

The main objectives of the current manuscript are to report on the development of a software framework to scale and position HBM.

METHODS

The specifications of the software framework were designed based on previous studies, preliminary comparisons of existing techniques and feedback from possible users gathered through an online poll. Key specifications / design targets and assumptions are summarized below:

- HBM and code agnosticity: the methods implemented in the software should be applicable to any major HBM and code such that the development efforts can be shared and results compared
- Modularity: the framework should be modular such that different numerical methods or approaches can be implemented by different developers and compared. The software does not assume that a method should be the standard as such selection should result from objective comparisons (which will be facilitated by the availability of the software). It should cover both scaling and positioning needs, and be able to integrate both numerical transformations approaches and *a priori* knowledge that can be used to drive the transformation

- Open Source: the choice of an Open Source approach is believed to be meaningful for reproducibility, effort sharing and re-use, and as an alternative to the relative lack of business models associate with HBM
- Interactivity: the tool should be interactive as many decisions about the plausibility of the scaling or positioning seem driven by the user expertise.

Based on these specifications, a software framework with different modules was developed and tested with leading adult HBM (e.g. GHBMC M50 detailed occupant model, Thums V3 and V4 occupant model) as well as a new scalable child model (PIPER Child model) developed during the project.

The result section will provide an overview of the framework structure with examples of workflows involving different modules.

RESULTS

Software framework

Design and GUI. The software was designed as a modular framework. In practice, this means that the input and output (i.e. interpretation of the HBM and export) are shared by all functions. In between import and export, modules can modify/update the data that were imported and that is stored in a simplified model (PIPER model). Modules can for example change node coordinates or model parameters.

For user interactions, the software provides a GUI with a model display and menus that allow defining or refining the transformation target (e.g. dimension or position constraint), selecting the module to be used and its parameters. A non-interactive batch mode covering parts of the features is also provided.

As it is Open Source, numerous libraries could be re-used to provide both performance and advanced functionalities. The software is largely written in C++ and uses extensively VTK, QT, the Sofa framework, Eigen, Mesquite, CMake among others. Scripting interfaces include Python (tightly integrated) and Octave (loose integration). The software runs both under Microsoft Windows and Linux.

An illustration of the PIPER child model in the application is provided in Figure 1 below.
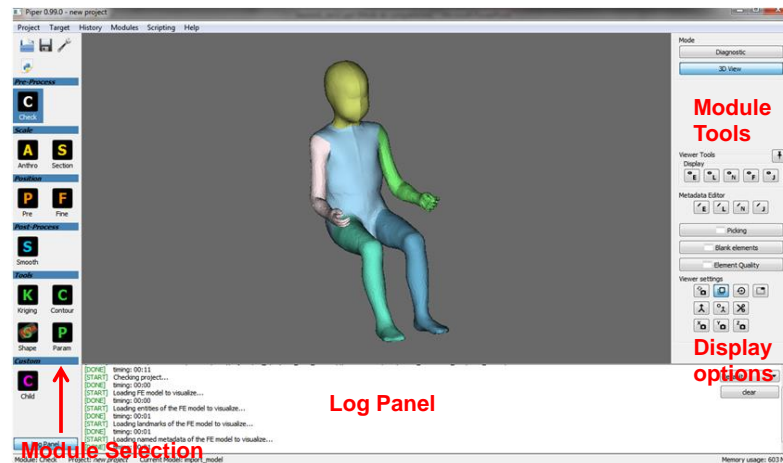

Figure 1: PIPER application with the Child model loaded

Input and Output: metadata. A metadata and parsing rule system was designed to allow importing various HBM in different codes without having to recompile the software. The basic idea is that, rather than implementing a complex templating system for each of the codes used in the field, simple rules could be used to indicate to the software:

- where the entities that need to be updated by the scaling or positioning are located (often: mainly nodes). Most options in the FE model (e.g. hourglass) do not need to be read.

- Which parts of the model correspond to specific anatomical entities. This is required for both scaling (e.g. knowing where the head location is important to update its circumference) and positioning (e.g. bones are not expected to deform during positioning and should be labelled as such).

In practice, the user:
- defines FE groups using standard pre-processing software to describe anatomical entities, landmarks, contacts. These groups are saved in the FE Format.
- associates groups and anatomical entities, joints, contacts. These associations are stored in XML files. To normalize the vocabulary, anatomical names are defined in a database containing body regions, landmarks, joints etc. released with the software (AnatomyDB, released under the more liberal LGPLv2 such that it can be reused in other software).
- Selects rules to parse the FE input format. These rules indicate how to read nodes, elements, etc. The user can edit them, add new rules such that new FE features can be imported in PIPER, or implement them for a new code without recompiling.

Basic rules for Ls-dyna and Pamcrash are provided with the software.

Workflow example 1: scaling based on anthropometric predictors

Target body dimensions: anthropometry prediction module. When aiming to scale a model by anthropometry, the user does not typically know the full set of targeted anthropometric dimensions but only a few population characteristics (e.g. 50th percentile stature, BMI 25, …) and would like to predict the most likely dimensions matching these characteristics.

The anthropometric module allow to compute dynamically a likely set of anthropometric dimensions based on an arbitrary set of predictors (e.g. gender, statures, dimensions) and anthropometric databases. It is based on the methodology described in Parkinson and Reed (2010) and uses virtual populations to compensate for limited data. Three databases are provided with the software (two at the time of the workshop):
- The public ANSUR database for adults
- The public Snyder database for children
- The CCANTHRO databased for elderly PMHS (released by CEESAR)

The module options allow to select predictors dynamically and then to sample both input and output to predict either a mean set of dimensions or a distribution. The results are saved using the PIPER target format (XML based) which can be re-used by other modules.

A simple interface to the GEBOD regressions is also provided.

Associate dimensions to the HBM: scaling constraint module. The next step is then to associate anthropometric dimensions to the HBM. Anthropometric dimensions are typically lengths or circumferences measured on the skin or estimated by palpation of bony landmarks. Some can be posture dependent, and they may need to be adjusted depending on the HBM specific anatomy and posture. This can be a tedious and complex task in the absence of visual feedback.

The scaling constraint module provides an interactive interface allowing to associate lengths or circumferences to the HBM, and to adjust them. The association is made through a simplified scalable model (structured stick man) which is positioned with respect to the skeleton using bony landmarks. Dimensions and circumferences are then computed on the HBM model by intersection on the skin. The complete process can be performed interactively. At the end of the adjustment, control points can be generated. These will be used by the transformation module using Kriging.

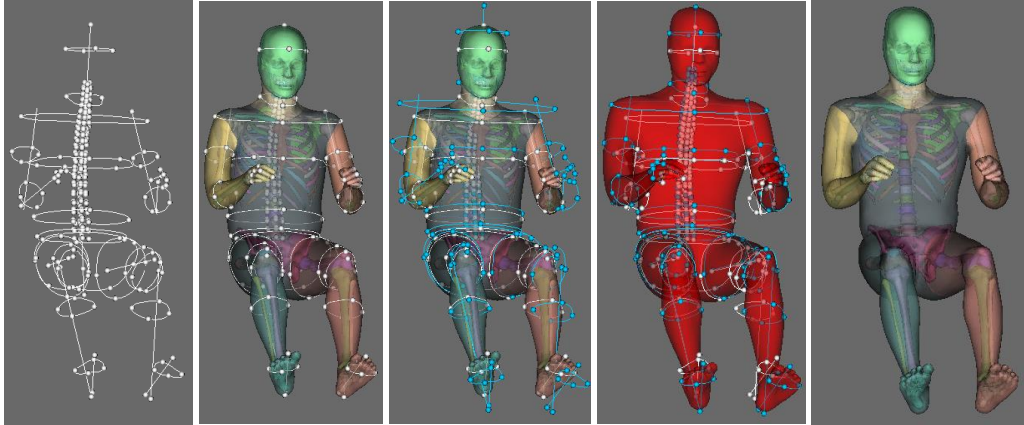An illustration is provided in Figure 2 below.

Figure 2: from left to right: an anthropometric model based on the dimensions from the ANSUR database associated to the GHBMC M50 model, anthropometric model scaled to the target dimensions (predicted by the anthropometric prediction module), preview of the skin transformation and model full transformation (see next subsection). The process (from definition to transformation is fully interactive)

Transform the model: kriging module. The next step is then to transform the model based on the output of the scaling constraint module. An interpolation method known as Kriging (described in details in Jolivet et al., 2015) is used to transform the full HBM. Various options are provided with the module to handle arbitrary number of control points, smoothness parameters, etc.

Optional final steps and export. The model shown in transformations such as the one of Figure 2 can typically be exported and run in the FE code. However, transformations can also lead to poor quality issues when the constraints are not defined appropriately. Several features can provide help with degraded element quality:

- Element quality: the element quality can be displayed (using either Mesquite or VTK definition). The variation of element quality between the source and the transformed model can also be displayed to better understand the effect of the transformation (separated from the quality of the original model).
- Element smoothing can be performed in 3D using the Mesquite library, or in 2D using a simple Taubin algorithm
- Transformation smoothing: the transformation (not the mesh) between the source and target can also be smoothed while respecting the skin and/or bone envelope. This typically allows improving the element quality inside the mesh without creating issues with contacts or penetrations.

These post-processing options can be applied to any workflow (including based on simulation outside PIPER). Once the element quality is deemed acceptable, the model can be exported. The export process corresponds to an update of the sections read using the rules. The exported file can be run in the FE solver.

Workflow example 2: positioning

Target definition: pre-positioning module. Using the HBM and metadata describing the body structure, the pre-positioning module can automatically create a lightweight physics model (i.e. with a limited number of degrees or freedom) that can be simulated in real time and that the user can interact with. The model and simulation are based on the Sofa Framework (https://www.sofa-framework.org/) developed for computer graphics applications. While simplified, this model allows taking into account:

- Functional constraints such as bone collisions (to respect the bone interactions), sliding contacts (preventing opening), joints…
- User constraints, typically derived from the knowledge of the environment or target: these include fixed bone, joint angle, landmark position controllers…

- *A priori* knowledge constraints, based on biomechanics or ergonomics to increase the realism of the transformation. Currently, a spinal curvature predictor is implemented to help drive the HBM spine towards physiologically plausible postures.

These constraints can interact in real time and different weights can be provided to them. Combined, they help provide a plausible posture and skeletal position for the HBM. Illustrations are provided in the Figure 3 below.
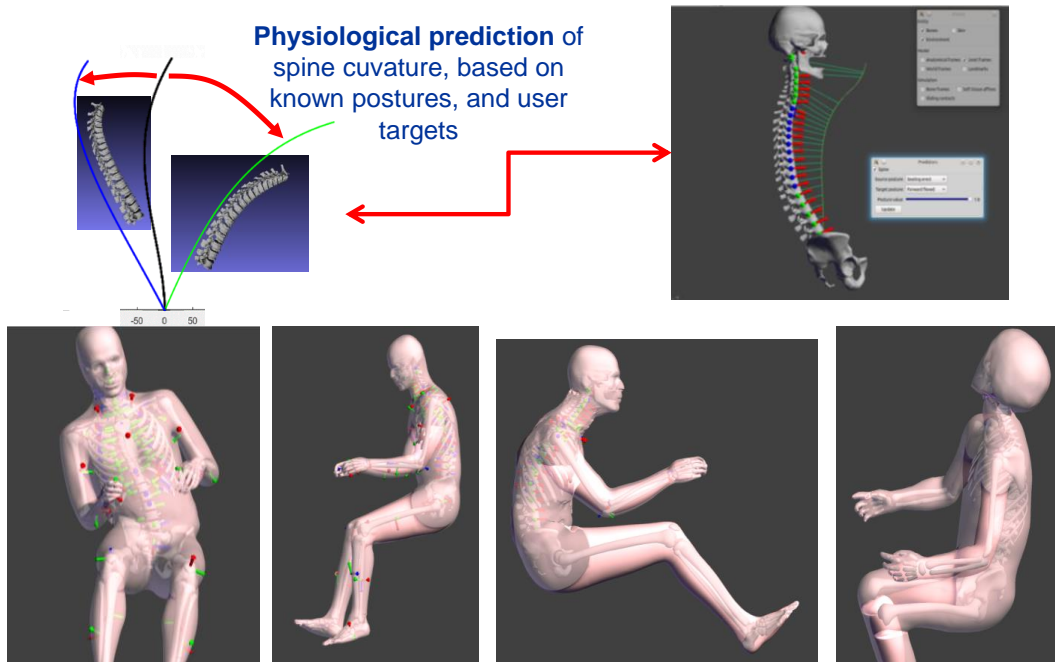

Figure 3: Pre-positioning module. Top: principles of the spine curvature prediction capability to integrate a priori knowledge in the transformation. Bottom: examples of simulations and transformations. The process is fully interactive

Positioning options. Because the pre-positioning module is very simplified for the soft tissues in particular, significant artefacts can appear around the joints during pre-positioning and the model may not be runnable if exported after pre-positioning due to insufficient element quality (negative volumes). Once the target position is defined, several options are available in the PIPER software. All can be followed by skin and transformation smoothing (which can result in very significant improvement of the element quality):

1. For small range of motions: updating the model directly in the pre-positioning module and smoothing the skin and the transformation (see previous section) may be sufficient to obtain a model that is runnable without error in the FE solver
2. Use the target position as input of a refined physics based simulation (Fine positioning module, similar to prepositioning but with more details) to transform the model. While more costly (time), this second simulation allows obtaining a more plausible skin surface for larger ranges of motion.
3. Use the target position to transform the model using the Contour transformation module. This module uses a series of contours defined around the HBM to drive the interpolation around the bones.
4. Use the target position to generate the input of a full FE simulation towards that position. This approach is now fully automated using Python scripts provided with the application (and that can be customized). The model can be re-imported after the simulation to be smoothed.

CONCLUSIONS

Scaling capability: status

Several HBM scaling workflows were implemented within the PIPER software. The main approach is based on anthropometry scaling. The modules provide the capability to predict an anthropometry (based on provided databases), associate it with a HBM, adjust it, and transform the HBM. The methodology was tested and appears functional. The main limitation is that with this approach, dimensions are only provided on the external surface of the body and may result in inappropriate skeletal geometry (in particular for large changes of BMI).

Scaling taking into account internal constraints would seem desirable. The PIPER software already has the capability to transform independently the bones and the skin (separate interpolation and combination) but the data needed to drive the transformation at the full body level is partially missing. Constraint using sets of bony landmarks (at the full body level) derived from PMHS full body CT scans are currently being implemented. This should be provided in the near future with the software. An effort was also started to define statistical shape models at the full body level but while software tools were developed, segmentation issues prevented the completion of the task. It is hoped that this can be restarted after the end of the project. In the meantime, changes of BMI may already be possible by fixing the skeleton and transforming the skin surface using the scaling constraint module.

Local scaling of bone cortical thickness when modeled with hexa elements was not implemented and would likely require a specific module. Parameters scaling (e.g. shell cortical thickness, material scaling) is already possible using a parameter module. Material scaling was implemented as an experimental feature in a module (not described here) dedicated to the PIPER Child scalable model (Beillas et al., 2016).

Positioning capability: status

Several positioning workflows are also implemented within the PIPER software. Positioning appeared more challenging (in order to get runnable models) than scaling. The pre-positioning module provides what is believed to be a novel approach to try to combine constraints from *a priori* knowledge, user, and model specificity (e.g. bone collision) in a (near) real time approach. The result from this module (a plausible posture?) can be the starting point for several other approaches (fine positioning, contour, full FE) which, after possible transformation smoothing, can all result in runnable and plausible models. More testing is required to better understand the strengths and limits of each of the approaches put in place.

It must be remembered however that for large range of motion, the element quality may be degraded independently of the deformation method that is used. It was also observed during the development that the current HBM design may limit their positioning ability in some cases (e.g. continuous mesh with lack of sliding around a joint).

Summary and perspectives

A novel modular software framework was developed and successfully applied to scale or position (i.e. up to generating plausible and runnable models) several major HBM. The framework allows for interactions between the user intention (target definition), *a priori* knowledge (about the dimension or position) and advanced numerical methods to transform the model (e.g. interpolation and smoothing, lightweight physics simulation). Beyond the specific features implemented, it is hoped that it will help formalize the concepts needed to specify scaling and positioning transformation (definition of targets…) and provide a workbench for others to implement new modules and data. Future modules will be able to benefit from the common infrastructure (import and export capability, display, etc) and from other modules. Besides new features and options, future activities should include testing and evaluation to better understand the limits of the methods implemented and the biomechanical performance of the models after scaling or positioning.

A first version of the software was released under the GPLv2 or later Open Source license on April 25, 2017 at the project final workshop and will be updated soon online. More details about the software and open source project can be found at http://piper-project.org and http://piper-project.eu.

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