

OSCCAR: FUTURE OCCUPANT SAFETY FOR CRASHES IN CARS



Demonstrator for continuous integrated virtual assessment of complex crash simulation tasks including HBMs

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ABBREVIATIONS AND DEFINITIONS

Abbreviations	Term	Definition
	Posture	Describes the relative position of body parts to each other. E.g. "sitting posture" defines how the body parts of a HM are positioned relative to each other, but not in relation to a certain seat.
	Position	The coordinates of one or more landmarks. Allows the description of an HM in relation to its environment, e.g. the seat.
	Target position	The position of an HM which should be reached by the model. Could be reached by simulation or pre-processing.
	Original position	The position of an HM at its delivery state. Means all coordinates of its nodes
	Initial position	The posture and position of an HM at the beginning of a simulation or pre-processing to reach the settled position.
	Settled position	The posture and position of an HM is the final state of a pre-processing simulation. In the settled position, the HM fulfils certain boundaries with the environment (e.g. contact force, energies,..). The settled position is the starting point for load case simulations (Pre- or In-crash simulations)
	Test data	Coordinates, trajectories, from a PMHS or volunteer test
	T ₀	Initial point for the In-Crash phase
AHM	Active Human Model	Simcenter™ Active Human Model
ASIS	Anterior superior iliac spine	
C1-7	Vertebrae of the cervical spine	
COG	Center of Gravity	
DYNASAUR		Postprocessing Software which enable a time-efficient harmonised data extraction and calculation of criteria for the postprocessing of simulation results
Euro NCAP	European New Car Assessment Program	
FE	Finite Element	
HBM	Human Body Model (HBM)	Finite Element Human Body Model (e.g. THUMS, ViVA, GHBM)
HM	Human Model (HM)	Human Model (FE and MB)
H-Point	Hip Point	

Abbreviations	Term	Definition
ISO MME		ISO specification for the multimedia data exchange in impact tests
L1-5	Vertebrae of the lumbar spine	
LAB (seat)	Lab Ceesar (seat)	
LS-Dyna		FE-Solver
MB	Multibody	
MUTANT		Visualization tools which allows the user to understand simulation
PIPER		Open source software to scale an position HBMs
PSIS	Posterior superior iliac spine	
RAMSIS	“Rechnergestütztes Anthropometrisch-Mathematisches System zur Insassen-Simulation”	Daimler anthropometric model for occupant simulation
SUFEHM	Strasbourg University FE Head Model	FE head model
T1-12	Vertebrae of the thoracic spine	
THUMS	Total Human Model of Safety	Commercial HBM – developed by Toyota
TUC	THUMS User Community	
UVa	University of Virginia	
VPS / VCP	Virtual Crash Pam by ESI	FE Solver
ViVA	Virtual Vehicle Assessment	Open source HBM provided by Chalmers
WP	Workpackage	

1 EXECUTIVE SUMMARY

In order to objectively and continuously compare results when employing different solvers, simulation techniques and occupant models in complex crash simulation tasks, OSCCAR partners developed a set of methods and tools. This report describes and demonstrates the three relevant areas of continuous occupant model assessment. These are the positioning of the occupant, the seamless occupant model transition from pre- to in-crash and a comparable kinematic and injury assessment of the occupant. Further, a corresponding tool for each step is demonstrated (see chapter 3.2.4, 3.3.3 and 3.4.2). The correct function of the tools and methods are shown in application examples in each chapter. The application of the tools and methods by several partners in the OSCCAR homologation test case is foreseen to be reported in Deliverable 4.3 and 4.4.

Positioning

The description of an occupant's position and posture is usually done with anatomical landmarks that can be determined at real human occupants as well as on state-of-the-art human models (HM). To compare the landmark positions of the different occupant models in use within OSCCAR a list of common landmarks was defined that can be identified on all models, regardless of modelling technique (Multibody (MB) and Finite Element (FE) models) and solver type (Siemens - Madymo, ESI - Virtual Performance (VPS) and LSTC/ Ansys LS-Dyna). For the positioning of MB models, the Madymo pre-processor XMADgic is used, whereas for the FE models, a tool was specially developed. This tool, based on the open-source software Piper¹ reads landmark coordinates of e.g., PMHS or volunteer study, creates target landmark coordinates according to the specific HBM's anthropometry and calculates landmark trajectories the HBM from its origin position to the target position. Further FE positioning simulation files, which contain the calculated trajectories and the necessary FE elements are created for either VPS or LS-Dyna which allow to conduct the positioning simulation.

Transition

As the occupant models for pre- and in-crash simulation are not necessarily the same, a tool is presented, which initializes an in-crash simulation starting from the final kinematic state of a pre-crash simulation. That is done by prescribing the observed motion of the pre-crash only model again to the in-crash only model. The method can adapt minor anthropometric differences which allows to exchange the models with a similar anthropometric percentile. This tool can work with either MB or FE models for the transition input, by handing over the kinematic information between these two technologies.

Assessment

For the OSCCAR common occupant assessment the open-source software Dynasaur² is used and improved, further capability was developed to process output files of Madymo, VPS solvers, and LS-Dyna). The possibility of processing SUFEHM³ data within Dynasaur was added. Processing of stability related output data like added mass, timestep and energies was integrated for all FE solvers.

Keywords: HBM positioning, FE/MB kinematic transition, HBM assessment

2 OBJECTIVES

To meet the overall OSCCAR goal of developing a fully integrated assessment method for future occupant safety, three steps for a harmonized occupant simulation approach are presented in this report.

The aim of this report is to introduce the tools, methods and definitions, which have been developed to achieve a continuous integrated virtual assessment of complex crash simulation tasks for different types of Human Models (HM) including the multibody Active Human Model (AHM) and Finite Element Human Body Models (HBM). Differences between AHM and HBM are explained in the abbreviations and definitions section.

The report therefore covers reproducible methods for positioning of the model, definitions of target postures, methods for transferring kinematic information from one model to another model, as well as harmonized evaluation procedures to interpret the generated simulation results.

Defining the mentioned target postures requires a harmonized list of anatomical landmarks for the used human models. That is further used to conduct harmonized occupant simulations in Task 4.3 and moreover contributes to the overall goal for harmonization.

For executing the mentioned steps, tools were developed, and already existing tools were enhanced. Two of them are based on the EU funded software Piper (for model positioning and transition) and one on the open-source software Dynasaur (for harmonized assessment).

The tools enable continuous integrated simulation and assessment with all kind of HMs and furthermore in different FE and MB software packages (LS-DYNA, VPS, Simcenter Madymo). For certain steps like belting, the involved partners have their own in-house routines and tools, which are also mentioned in this deliverable. Nevertheless, a simple OSCCAR routine is presented to provide a functional and continuous tool/method chain.

The deliverable focuses on the methods and tools only and therefore does only include exemplary application for demonstration purposes. To avoid misinterpretation abbreviations and definitions are listed at the end of this report.

3 DESCRIPTION OF WORK

3.1 Partner contribution

Eight partners were involved in Task 4.2. Several web-meetings were held and two WP4 workshops in combination with WP5 were held additionally to physical OSCCAR general assembly meetings (November 2018 and May 2019). One WP4/5 workshop was executed virtually in June 2020 and one WP4 workshop in November 2020.

BOSCH took part in several web-meetings and shared their experience and ideas concerning belting and transition approaches.

LMU took part in the definition of the harmonized landmark list and as a link to WP 5.

MERCEDES took part in web-meetings and share their experience and ideas.

VIF was leading this task and was involved in defining the harmonized landmark list, programming the positioning and the transition scripts.

SIEMENS took part in the definition of the harmonized landmark list, the positioning and transitions approaches as the point of contact for multibody models

TME took part in web-meetings and share their experience and ideas concerning belting and transition approaches.

TUG contributed to the definition of the harmonized landmark list and enhanced the Assessment Software DYNASAUR

UNISTRA contributed and supported the adaption of the Dynasaur tool to assess the results of the SUFEHM.

VW took part in the web-meetings and contributed in the development of the positioning/transition script by checking and reporting issues for the application of the tool using the VPS code, as well as sharing their ideas and experience with a gravity-based sitting procedure.

3.2 Positioning

The basis to obtain comparable and consistent occupant simulation results with FE or MB human body models (HBMs) lies in a determined initial position. As the handling between FE and MB models differs fundamentally, different strategies were pursued (3.2.2.1 and 3.2.2.2). The link between the posture descriptions in both kind of models are certain anatomical points (landmark names) and their corresponding coordinates. (see paragraph 3.2.1).

The state of the art concerning positioning methods was investigated by the presentation of established methods from the active involved partners. For OSCCAR a method was developed which is available open source and without the need for an additional commercial software and is capable of processing various HBMs.

3.2.1 Human posture description with landmarks

A set of landmarks was identified as a result of multiple discussions, which is identifiable among the different HBMs used in OSCCAR. For a better understanding of the following definitions Figure 3-1 shows the terms for anatomical orientation and directions.

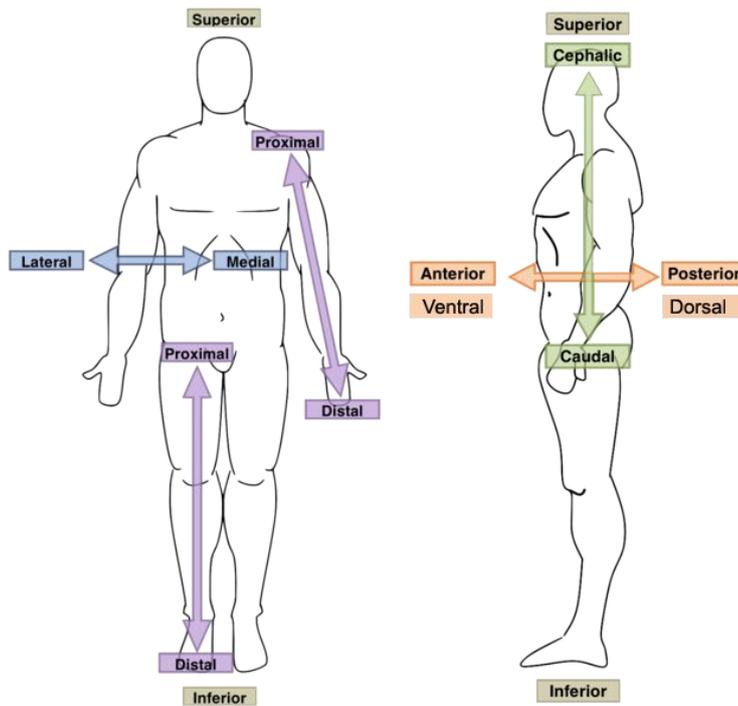


Figure 3-1: Anatomical orientation and directions⁴

We started with 227 landmarks, which were based on the ISB recommendations from Wu et al., 2002⁵ and Wu et al., 2005⁶. In the end, the following consolidated list remained. Discussions with WP5 on the harmonized naming and related ISO MME codes are still ongoing and will be disseminated as WP5 activity toward the end of OSCCAR. The landmarks in the HBMs were identified based on the recommendations by the THUMS user community. As no recommendations for the spine were available from TUC, guidelines from the Euro NCAP TB024 v2.0⁷ were used for this area.

In the FE models the nodes should be linked to the surrounding structures as defined in Euro NCAP TB024 and shown in Table 1. For the AHM these landmarks are visualized with special defined landmark ellipsoids of which the center of the ellipsoid represents the landmark coordinate.

Table 1: Slave node interpolation constraints⁸

Code	Keyword	Recommended Parameters
LS-DYNA	*CONSTRAINED_INTERPOLATE	DDOF=123456, CIDD=0, ITYP=1, IDOF=123, TWGHTi=RWHGTi=0
VPS	OTMCO_ /	DOFCOD=111000, IMETH=0, IELM=1, ITYP=0, RADIUS=0, WTFAC=1

3.2.1.1 Head

The following landmarks⁹ were selected for the head:

- Head center of gravity: The centre of gravity (mass center) of all parts of the head (including brain, skin, face) up to the brain stem and the foramen magnum. The node

should be linked to the skull using an interpolation constraint in HBMs. In the AHM the COG is marked with the “Head_COG_ell” ellipsoid.

- To measure the head angle, the Frankfurt plane is used. Therefore, a plane between the lower margin of the orbits and the uppermost point of the external auditory canal should be used. In the AHM also the “Head angle” from “head bod” can be used directly as it has a fixed offset with respect to the Frankfurt plane. At zero head angle, the Frankfurt plane is tilted forward 0.1 rad (~5.73 deg).

3.2.1.2 Thorax

To define the spine posture, the following points are used, where the name of the corresponding AHM location is shown in brackets:

- center of vertebral body of C1 (AHM: C1_ell)
- center of vertebral body of C7 (AHM: C7_ell)
- center of vertebral body of T8 (AHM: T8_ell)
- center of vertebral body of T12 (AHM:T12_ell)

The geometric centre (averaged coordinates of all nodes) of the vertebral body (without spinal process), as defined in TB024 is used for C7, T8 and T12. For C1 the whole vertebra is used.

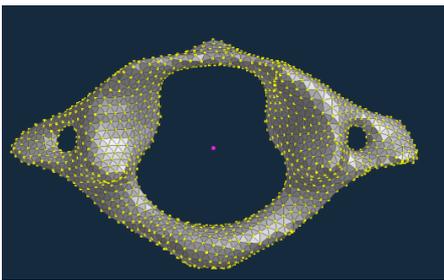


Figure 3-2: Center of vertebral body of C1¹⁰

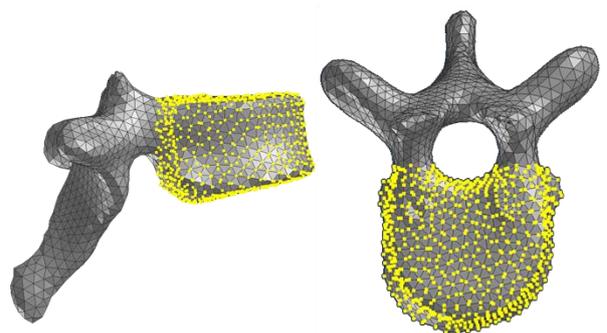


Figure 3-3: Definition of vertebral body for C7-T12¹¹

To compare the chest/ribcage orientation, the following landmarks are used for the HBMs:

- incisura jugularis: uppermost (superior) point of the sternum at the sagittal plane.
- xiphoid process: lowermost (inferior) point of the sternum in the sagittal plane.

For the AHM, due to the lack of detailed rib geometry, the “SuprasternalNotch_ell” landmark and the “Thorax2FTHorax3F_poi” point object on a thorax flexible body can be used.

For the documentation of the belt routing, the following landmarks are (additionally) needed:

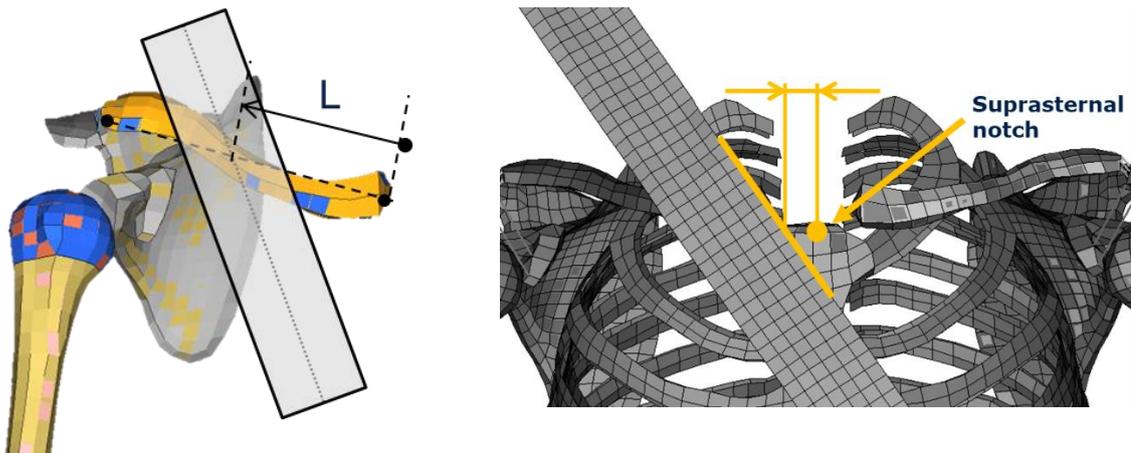


Table 2: Belt position parameters

- The clavicle length from the ventral point of the sternoclavicular joint to the dorsal point of the acromioclavicular joint to the center line of the belt.
- The lateral distance between the center line of the belt to the uppermost point of the sternum (incisura jugularis / suprasternal notch).

3.2.1.3 Upper extremities

To describe the orientation of the upper extremities, the following points are used:

- **Glenohumeral rotation center:** The definition from the THUMS User Community is applied for this point: The MatLabScript `Center Calculation` is applied to find the point where the variance of the distance to all points of the outer surface of the humeral head is minimal. For AHM, the Glenohumeral[L/R]_jnt location is used with landmark ellipsoid "ShoulderJC_[L/R]_ell".
- The **midpoint of lateral and medial epicondyle on Humerus** is used to define the elbow joint. The most caudal point of the medial and lateral epicondyle (EL and EM as defined in Wu et al., 2005¹²) is averaged as described in TB024, which is also in line with the TUC recommendations. For the AHM, the epicondyle landmarks are defined and Elbow[L/R]_jnt is used for the elbow joint location.
- The **ulnar styloid** (US as defined in Wu et al., 2005) is used for HMs for the definition of the lower arm orientation. It is defined as the most caudal–medial point on the ulnar styloid.
- The **radius styloid** (RS as defined in Wu et al., 2005) is used for HMs for the definition of the wrist orientation (orientation of the radioulnar joint). It is defined as the most caudal–lateral point on the radial styloid.
- For the AHM, the ulnar and radius styloid landmarks and Wrist[L/R]_jnt are used to define the overall lower arm and wrist posture.

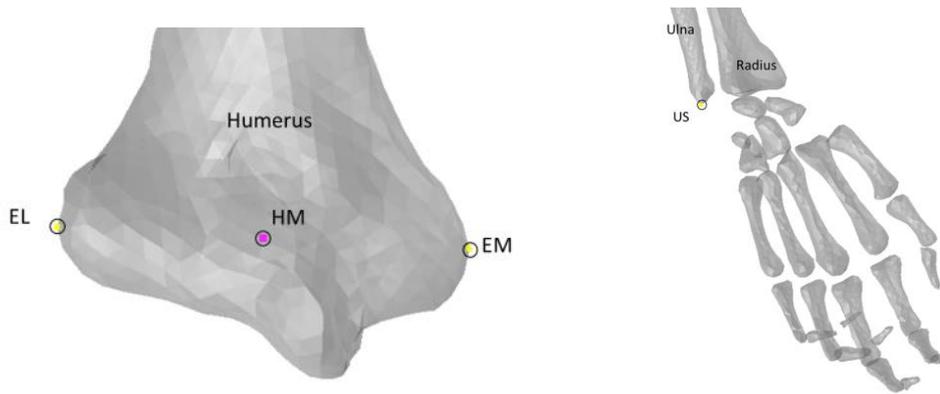


Figure 3-4: Anatomic landmarks of the elbow joint and wrist ¹³

3.2.1.4 Lower extremities

For the definition of the pelvis orientation the following points, as defined in Wu et al., 2002, are used for the HBMs and the AHM:

- posterior superior iliac spine (PSIS), which is called PSIS[L/R]_ell in AHM
- anterior superior iliac spine (ASIS), which is called ASIS[L/R]_ell in AHM

To compare the seat contact points with e.g. seat pressure mats, the most caudal point of the **ischial tuberosity** are furthermore used.

The **center of acetabuli** is used as reference point for the hip. The TUC definition is used, where the MatLabScript `Center Calculation` is applied to find the point where the variance of the distance to all points of the outer surface of the acetabulum is minimal for the right and left acetabulum. The midpoint of the left and right center of acetabuli is then used as the reference point. For the AHM the hip joint centers are marked by the “HipJC_[L/R]_ell” ellipsoids. “HipJC_C_ell” is used to visualize the midpoint of the hip joint centers and the starting point of the human MB chain model (“Human_jnt”).

To define the knee joint location, the **midpoint of lateral and medial femoral epicondyle is used for the HBM** based on the TUC definition. MatLabScript `Center Calculation` is applied to find the point where the variance of the distance to all points of the outer surface of the circular surface of the posterior lateral femur condyle is minimal. For AHM, the epicondyles are defined as well as their midpoint landmarks “Knee[L/R]_centre_EL_EM_ell”. These landmarks are based on bone geometry and differ slightly from the MB chain defined knee joint location “KneeJC_[L/R]_ell”.

As a reference point for the ankle the **inter-malleolar point (IM)**, located midway between the tip of the medial malleolus (MM) and tip of the lateral malleolus (LM), is used according to Wu et al., 2002, which is in line with TB024 and the TUC recommendations. For AHM, the ankle joint location is used to define the IM landmark (“AnkleJC_[L/R]_ell”) and not the MM (“Ankle[L/R]_MM_ell”) and LM (“Ankle[L/R]_LM_ell”) landmarks.

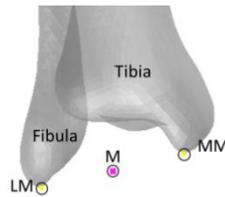


Figure 3-5: The right inter-malleolar point (MR) located midway between MM and LM¹⁴

3.2.2 Positioning approach (tool and method)

Positioning HBMs is done separately for FE and MB models. As for the Madymo AHM a pre-processor for positioning is available, no further enhancement concerning a positioning tool was done in OSCCAR. For the different FE HBMs it was decided to provide an independent tool in OSCCAR.

HBMs are delivered in a certain posture and further need to be positioned in a seat and vehicle interior model. As the seat geometry, the vehicle interior and the HBM delivery posture most likely don't match exactly, a positioning procedure for HBMs is needed. Obtaining comparable and therefore reliable results from an HBM occupant simulation requires a reproducible sitting method and a well-defined initial simulation position.

The method / tool needs to fulfill following requirements:

- Reproducible method
- Same results when the tool is repeated several times with the same data. That assumes an automated process or a very detailed protocol.
- HBM independent
- The method or tool needs to work HBM independent and be capable of dealing with minor anthropometric differences between the HBM and the individual target position data. Of course, the HBM to be positioned should represent roughly the same anthropometric percentile as the target position data.
- Predictable, continuous kinematic
The kinematics, which transfer the HBM from the delivery position to the target position must follow a steady trajectory. That is necessary, to increase the chance of a stable positioning process. For the AHM this means that the described positioning and settling procedure should be followed to obtain a stable settled position.
- Avoidance of unphysical re-meshing
The tool creates the necessary kinematics to transfer the HBM to the target position, but the positioning process must be computed by a FE solver to avoid unphysical mesh changes. For the AHM two models are available, one for standing postures and one for seated postures, within those pre-defined postures remeshing of the (FE) skin is not required.

Since the handling of FE and MB models is quite different the approaches for AHM positioning differ too. The positioning process for the FE models is therefore covered in a positioning tool. Whereas for the MB models a similar positioning result is achieved with the Madymo-own positioning procedure. Chapter 3.2.2.1 to 3.2.2.3 demonstrate three positioning approaches.

3.2.2.1 FE

A tool was developed which can work as a script, executable in Piper¹⁵. It uses some Piper offered features and converts landmark coordinates to continuous trajectories. The output of the script are

FE solver input files, which allow to conduct an occupant positioning simulation. The advantage of an FE solver over a remeshing algorithm is, that the FE solver calculation is based on physical laws considering e.g. material properties.

Figure 3-6 shows the necessary steps of the positioning process. As mentioned, the positioning of FE HBMs is done by FE simulation. The HBMs are pulled from their delivery posture to the target posture by prescribing a kinematic towards certain Landmarks. The initial posture which can be gained from e.g. volunteer tests is scaled to the HBMs anthropometry. Further the necessary trajectories are calculated. To finalize the positioning procedure and get a model with a realistic contact situation two options are available. Either the contact force is checked, and the landmark coordinates are updated or the position simulation is done with a “gravity sitting” option. The two options are described in the next paragraph.

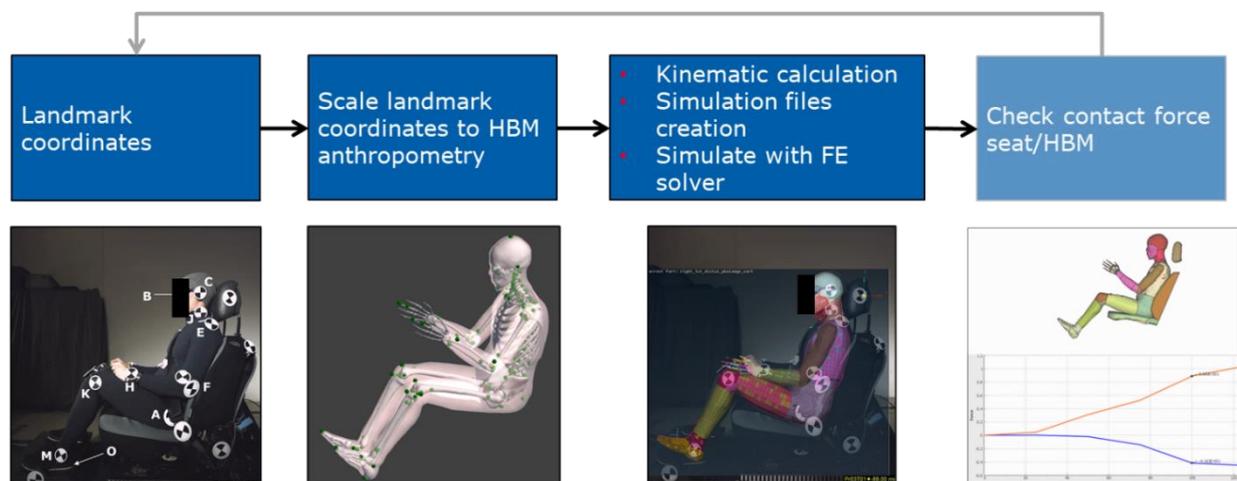


Figure 3-6: Method for HBM positioning

3.2.2.1.1 Workflow Positioning FE models

Scale landmarks coordinates to HBM anthropometry

As the anthropometry of the target data is most likely not coincident with the HBMs anthropometry, the coordinates for the Landmarks, which describe the target posture, need to be adapted. Therefore, the anthropometry of the models is described with a kinematic linkage model.

The kinematic linkage model is a vector based description of the anthropometry based on the landmarks suggested e.g. in Wu et al¹⁶¹⁷, TUC or TB024. This model is needed for two reasons:

- Landmark coordinate scaling

As the HBM anthropometry most likely is not coincident with the individual anthropometry of the input data, the landmark coordinates of the input data are scaled to the HBMs anthropometry. Therefore, this vector-based description of the HBM is used.

- Kinematic calculation

The kinematic which transfers the HBM to the target position is determined with the vector description model.

The vector-based structure (Figure 3-7) is specified in an adaptable definition file. The vector-based description requires at least one basepoint, to which the vectors are related. The default setting defines the basepoint midway between the left and the right acetabular centre.

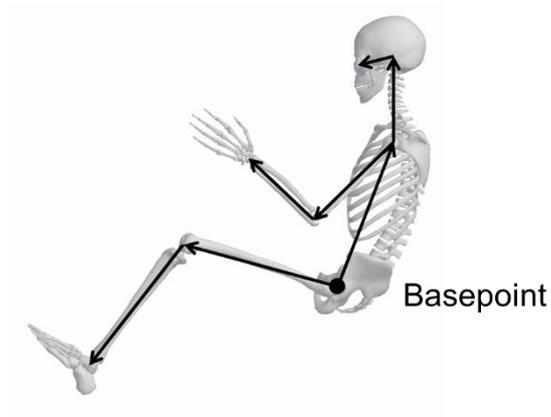


Figure 3-7: Example for a vector based HBM posture description

For the anthropometric scaling, the assumption is made, that the HBM is positioned to the equal angles as the target data source. The anthropometric scaling is explained in detail in Appendix A. The output of the anthropometric scaling are the coordinates of the target data which are adapted to the anthropometry of the HBM. The next step is to calculate the trajectories to pull the model to the target position.

Kinematic calculation

The HBM is pulled from its delivery position to its target position by prescribing trajectories. These trajectories are calculated on basis of the vector-based structure shown in Figure 3-7. All trajectories for a positioning simulation are discretized by the same amount of interpolation points. Hence the determination of the trajectories can be basically described with a “multi-pendulum” approach. A detailed description of the trajectory calculation is given in Appendix B.

Obtaining realistic contact forces

When positioning the HBM, foam materials of the seat and soft tissue materials of the HBM have contact and are deformed. Two methods were developed to simulate the positioning process and to reach a realistic contact situation. Either the HBM is moved against the seat, or a gravity sitting method is applied. In both cases the contact forces are checked after the positioning process.

Check contact forces

To obtain proper deformed elements in the contact area it is necessary, to start the sitting simulation in a position, where no contact between the HBM in the seat occurs. This procedure is divided into two phases. First the HBM is transferred to the seat to establish a realistic contact situation. In this phase, the same motion vector is applied to all used landmarks. That includes also the base point of the vector structure (Figure 3-8).

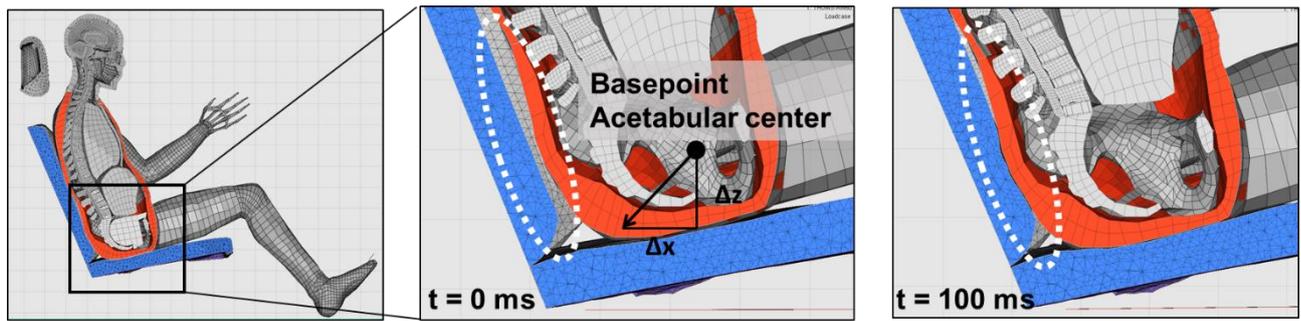


Figure 3-8: HBM positioning considering seat deformation

In the second phase, upper and lower limbs, and spine are moved towards their target positions. Finally, the contact forces between the seat and the HBM are checked to avoid an unrealistic contact at the target position. As a rough estimation the contact force should be slightly below the weight of the HBM, since the feet have contact with other structure. In case of an unrealistic contact force, the complete set of target coordinates is modified by the same distance.

Gravity sitting method

The positioning of the HBM to the target position takes place with z-offset to the seat. After the hold-time (to compensate the positioning) the gravity starts to ramp from zero to full gravity. At the same time, the displacement of all positioning points of the HBM in x and y direction are locked and selected body parts (respectively the skeleton) are switched rigidly. This ensures that the approached landmark position is maintained during the sitting process.

3.2.2.1.2 Positioning tool

To conduct the calculation and data processing automatically, a tool was developed. The tool is a script which is executable in the software Piper. An HBM (and its necessary Piper files) needs to be imported to Piper before the positioning tool can be executed.

As mentioned in paragraph 3.2.2.1.1 the method requires a kinematic linkage model. This model is described in a separate file and can be easily adapted by the user. Different kind of elements can be used to define the linkage model.

```

bone_lms = {
  "Hip_bone" : {
    "base_point" : "Acetabular_center",
    "moving_points" : (
      "LPSIS",
      "RPSIS",
      "Anterior_point_of_the_sacral_plate",
    ),
    "rotation_points" : (
      "Anterior_point_of_the_sacral_plate",
    ),
  },
  "left_femur" : {
    "base_point" : "left_acetabular_center",
    "moving_points" : (
      "lateral_epicondyle_of_left_femur",
      "medial_epicondyle_left_femur"
    ),
  },
  "left_fibula" : {
    "moving_points" : (
      "tip_lateral_malleolus_of_left_fibula",
      "tip_medial_malleolus_of_left_fibula"
    ),
    "parent" : "left_femur"
  },
}

```

Elements which are connected to the basepoint

The model needs one basepoint, which stays static during the positioning process (e.g. the acetabular center). Additional points which are mandatory in the element description are moving points, for which the motion is prescribed in the positioning process

Figure 3-9: Element in the kinematic linkage model with a connection to the basepoint

Elements which are connected to other elements

Those elements again need motion points for the prescribing of the motion. No basepoint is defined in this case, but a parent element needs to be defined. The rotation center for the child element is either between the first and second moving point of the parent element, or an alternative rotation point is defined in the parent element. Every child element can be a parent element as well.

```
bone_lms = {
  "Hip_bone" : {
    "base_point" : "Acetabular_center",
    "moving_points" : (
      "LPSIS",
      "RPSIS",
      "Anterior_point_of_the_sacral_plate",
    ),
    "rotation_points" : (
      "Anterior_point_of_the_sacral_plate",
    ),
  },
  "left_femur" : {
    "base_point" : "left_acetabular_center",
    "moving_points" : (
      "lateral_epicondyle_of_left_femur",
      "medial_epicondyle_left_femur"
    ),
  },
  "left_fibula" : {
    "moving_points" : (
      "tip_lateral_malleolus_of_left_fibula",
      "tip_medial_malleolus_of_left_fibula"
    ),
    "parent" : "left_femur"
  },
},
```

Figure 3-10: Element in the kinematic linkage model which is connected to another element

```
bone_lms = {
  "Hip_bone" : {
    "base_point" : "Acetabular_center",
    "moving_points" : (
      "LPSIS",
      "RPSIS",
      "Anterior_point_of_the_sacral_plate",
    ),
    "rotation_points" : (
      "Anterior_point_of_the_sacral_plate",
    ),
  },
  "left_femur" : {
    "base_point" : "left_acetabular_center",
    "moving_points" : (
      "lateral_epicondyle_of_left_femur",
      "medial_epicondyle_left_femur"
    ),
  },
  "left_fibula" : {
    "moving_points" : (
      "tip_lateral_malleolus_of_left_fibula",
      "tip_medial_malleolus_of_left_fibula"
    ),
    "parent" : "left_femur"
  },
},
```

Figure 3-11: Element in the kinematic linkage model with connection to the basepoint and an alternative rotation center

The tool consists of three modules (Figure 3-12), which basically represent the steps of the workflow in paragraph 3.2.2.1.1:

- Add virtual test landmarks: Additional landmarks are added to the set of testdata by projecting the HBMs anthropometry to the testdata
- Testdata to target: Scales the testdata to the HBMs anthropometry and creates a Piper target file (.ptt, xml Structure)
- Positioning: Calculates trajectories for positioning and creates the FE input files for selected code (VPS or LS-Dyna)

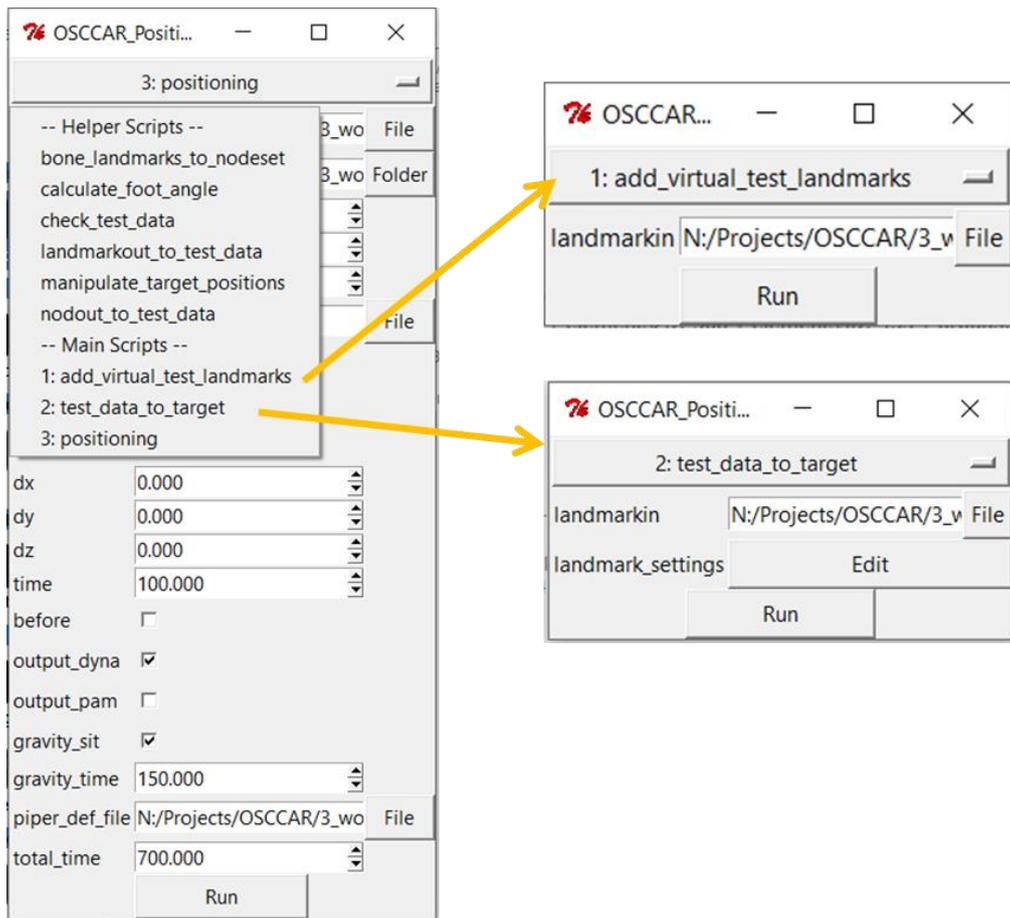


Figure 3-12: Modules of the positioning tool

Add virtual test landmarks

For the kinematic linkage model (see Figure 3-7) it is mandatory, to define landmarks for certain joints (e.g. the humerus). As these landmarks are not necessarily documented in every data source, a method which determines “virtual test landmarks” is necessary. The required landmark position is calculated by projecting the anthropometrical relations of a set of landmarks from the HBM to the test data (Figure 3-13).

```

landmarks = {
  "Head_center_of_left_humerus":
    ("Lateral_epicondyle_of_left_humerus", "Acromioclavicular_joint_L"),
  "Head_center_of_right_humerus":
    ("Lateral_epicondyle_of_right_humerus", "Acromioclavicular_joint_R")
}

```

Figure 3-13: Definition of a virtual test landmark

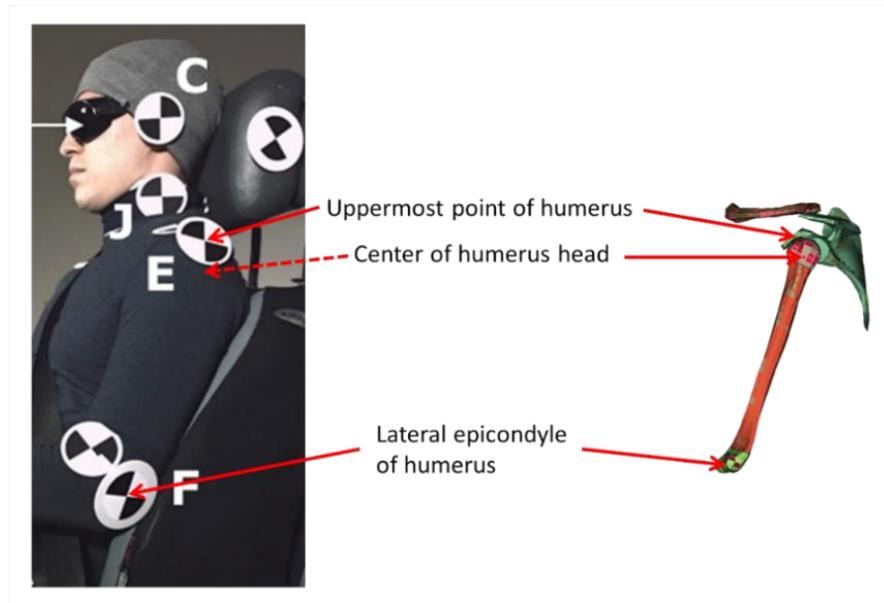


Figure 3-14: Projecting the HBM anthropometry to the test data set allows the determination of virtual test landmarks

Figure 3-14 shows an example, where the centre of the humerus head is determined in the test data. The uppermost point of the humerus and the lateral epicondyle of the humerus are known both in the test data and in the HBM. The Center of the humerus head is known in the HBM only. The developed method calculates the coordinates of the humerus head for the test data and adds them to the test data set. A more detailed description is given in Appendix C.

Testdata to target

This module converts the input data from an .csv file format which contains the coordinates of e.g. a volunteer study to target coordinates for certain landmarks which fits to the anthropometry of the HBM. As mentioned, the assumption is made, that the “same” position is interpreted as reaching the same angles of the body parts. Further information concerning the calculation is given in Appendix B. The output of the module is a Piper target file, which can be further processed within the positioning tool, or separately loaded into Piper. This .ptt file basically has a .xml file structure (see Figure 3-15).

```
<?xml version="1.0" ?>
<piper-target version="0.9.0">
  <targetList>
    <target type="Landmark">
      <name>Tip_lateral_malleolus_of_right_fibula</name>
      <value dof="x">-656.307375551</value>
      <value dof="y">133.50076</value>
      <value dof="z">-223.272350688</value>
      <unit length="mm"/>
      <kriginParameter>
        <use_bone>0.5</use_bone>
        <use_skin>0.5</use_skin>
      </kriginParameter>
      <landmark>Tip_lateral_malleolus_of_right_fibula</landmark>
    </target>
  </targetList>
</piper-target>
```

Figure 3-15: Structure of the piper target file

Positioning

The positioning module finally determines the necessary trajectories, pulling the module to its target position.

The module requires following inputs:

LandmarkIn: Input file

Sim_dir: Output Folder

Num_steps: Number of interpolation points

Motion time: Amount of time for the motion part of the simulation

Hold_time: time in which the model is kept in its target position and soft tissue parts can reduce vibrations which occur due to inertia

Calc_info: "log file" for the calculation

Test: Provides detailed information about the calculation process in the command line of Piper

Soft sit: Allows the positioning into a seat to get realistic element deformations in the contact area

dx, dy, dz: motion which is applied for the sitting process

dt: Time of the sitting process

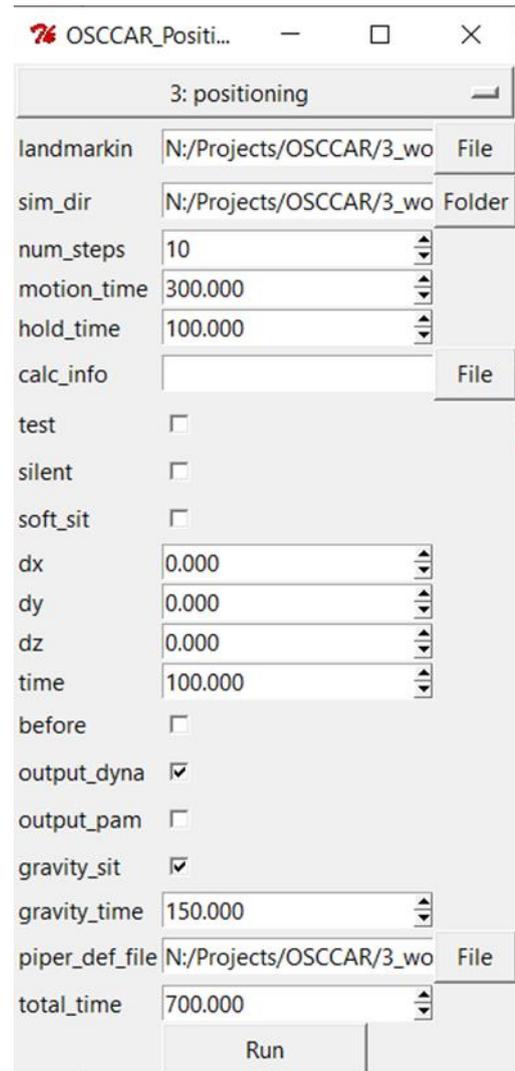
Output Dyna/Output pam: Output files are available either for LS-Dyna or VPS

Gravity_sit: Optional gravity based sitting method

Gravity time: Duration of gravity ramping

Piper_def_file: Piper definition file (solver related)

Total_time: Complete simulation time



3.2.2.2 MB

The Simcenter Madymo Active Human Model (AHM) comes in two flavours when released; A standing AHM for applications that require an upright AHM and a sitting AHM for use in seated applications. The original posture of the AHM, as provided with the Simcenter Madymo software release, is most likely not the exact posture desired for use in a seat and environment model. This section treats the positioning procedure for the AHM in Madymo. The procedural steps for positioning are based on work performed for simulating the Autoliv UVa homologation load case in Madymo, making use of the generic OSCCAR application models.

Environment and test data preparation

A prerequisite for performing the positioning is the environment setup modelled in Madymo. Seat, foot support, and restraining system(s) should all be modelled.

For the positioning of the AHM one can make use of a known target position (joint angles), possible positioning target landmarks, and/or other relevant information from the test data.

When target landmark data for positioning is available, this data can be processed for use within the simulation environment. Most major landmarks are available for the AHM and can be visually compared to the location of target landmarks during the positioning process. In a separate system model, the target landmark coordinates can be identified via small ellipsoids. This allows for easy incorporation when positioning the model and easy removal when positioning is done. An example target landmark include file and the AHM with its available landmarks can be seen in Figure 3-16.



Figure 3-16: Target and AHM landmarks; a) Example target landmark include file. b) Standing AHM with available landmarks visible as small ellipsoids

H-Point determination

The positioning procedure for the Simcenter Madymo AHM is similar to the positioning of an ATD in a simulation environment. When positioning an ATD (in a physical test or simulation), the H-point of the dummy should be placed within a certain tolerance of the H-point of the seat in order to comply with test seating procedures. The AHM also has an H-point which is defined mid between the hip joint centers and marks the beginning of the MB chain of the AHM and which is used as the initial positioning point of the AHM. It is assumed that a seat (model) has a dedicated (design) H-point, its location is ideally provided by the manufacturer of the seat. However, when the location of the seat H-point is unknown it should be determined before the positioning procedure can start using the H-point manikin (either on the physical seat or on the simulation model).

There are two options for determining the seat H-point (Figure 3-17):

(1) Derive the seat H-point location from test data. - When the H-point of the seat is not known but test data contains sufficient information on the volunteer pelvis position relative to the seat, test data

could be used to define a target H-point relative to which the AHM H-point will be set in the positioning procedure. In the seat model it is a recommended modelling practice to define a dedicated H-point body (connected to the seat) at the found target H-point location derived from the test data. In the generic Madymo interior model as developed for OSCCAR WP 2 this would mean an adjustment of the position of the “*Oscar_H_point_bod*” body, see also Section 4.4.1 in¹⁸.

(2) Check with the Madymo H-point Manikin (d_hpmanfc v1.5) model if the seat H-point matches with the Manikin model (it is assumed that the seat model is validated with the physical seat).

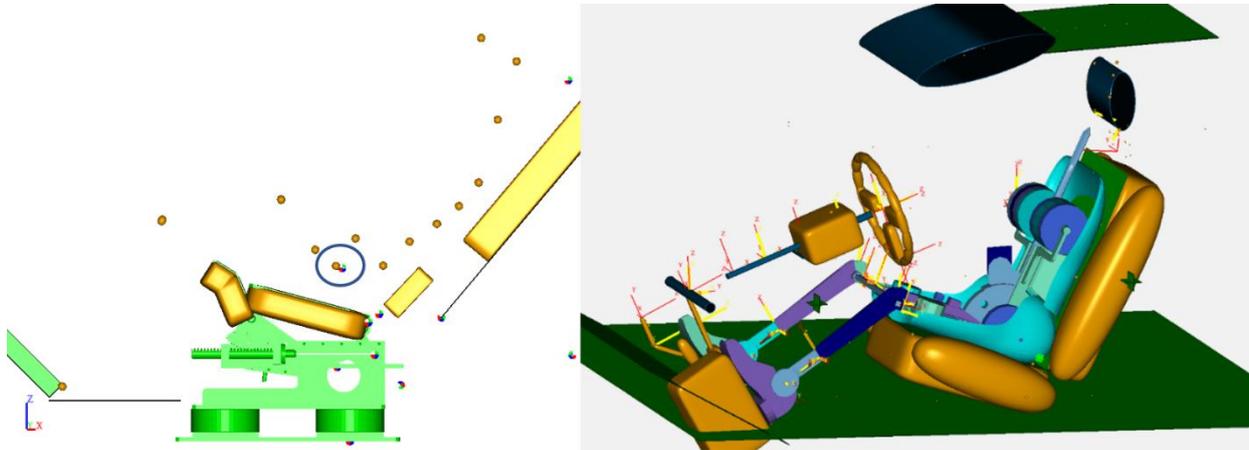


Figure 3-17: Two options for determining the seat/target H-point

The AHM shows two options for determining the seat/target H-point. On the left side the H-point setting is based on landmarks from test data. On the right side the Madymo H-point Manikin Model (d_hpmanfc v1.5) is positioned in a generic seat.

AHM DEFINE based positioning

The AHM makes use of a DEFINE based positioning method. This positioning method makes use of parameters (DEFINES) that manipulate initial joint positions of the AHM. Positioning defines are present for the most relevant joints in the AHM. The DEFINE based positioning method was developed to enable users to quickly achieve a certain spine posture. Instead of setting each spine vertebra angle manually, two DEFINES can be used to set the spine posture. Thorax slouch sets the curvature of the thoracic spine whereas the Lumbar slouch parameter sets the lumbar spine curvature. A slouch value of zero and one respectively represent a default standing and sitting spine posture. A visualization of different spine slouch settings, applied to a seated AHM, can be seen in Figure 3-18. The lumbar slouch values both set to 0 (blue), 1 (green), and 2 (yellow).



Figure 3-18: Example of seated AHM with three different spine slouch parameter settings.

Positioning of the AHM

As described in section 4.4.1 of¹⁹ AHM settling models are available with the same set-up as the load case models. To perform the positioning steps and the subsequent settling run as described below, use of the dedicated **_settling.xml* model file for optimal use of the DEFINE based positioning method is recommended. The settling models have the same vehicle setup as the load case models but belt and airbag systems are disabled and hysteresis is ignored. For the AHM only the neck and spine are set active (1) for settling. The extremities are inactive (0) to maintain their flexibility during settling. *DelayEnable_def* is set to zero to minimize the time to reach an equilibrium state.

1. The H-point of the AHM, located mid between the hip joint centers, marks the beginning of the MB chain that make up the AHM. Start with its location relative to the H-point of the seat and position it such that the AHM is positioned slightly above the seat (probably slightly above a target H-point). Setting the H-point offset will most likely require 1 or 2 settling iterations as mentioned in step 5.
2. With the AHM H-point positioned, the pelvis pitch angle should be set to get the desired pelvis orientation. In the generic Madymo model, pelvis pitch is set to 35.74 degrees for a seated AHM with a default seatback angle of 25 degrees.
3. To position the spine, the desired T1 location is used as a target position. By modifying the Lumbar and Thoracic Slouch defines the spine can be manipulated, where 1 is for the nominal seated spine posture and 0 for nominal standing spine posture.
4. Roughly position legs and arms in a similar position as the target position. Be careful with possible contact with the environment or self-contact and make sure there is no to very little contact (high initial contact penetrations may cause problems when settling the model later).
5. With the first four positioning steps performed, the location of the H-point can be validated by running a settling simulation. If necessary, the H-point (x, y and z) offsets can be modified to bring the AHM more in line with the initially defined position targets. The settling run will find

the equilibrium between the AHM and the environment and can potentially provide a better H-point that brings the AHM H-point closer to the target H-point. One or two iterations should be enough.

NOTE: Do not import joint positions at this stage as doing this will remove the define based positioning functionality. Manually check the settled H-point and modify the define values to get the new H-point closer to the found settled H-point.

6. When the newfound H-point location is satisfactory, check that the pelvis and spine are still in the right place. Focus on pelvis angle, location of T1, and the general shape of the spine.
7. With the pelvis and torso of the AHM in place, use hip, knee, and ankle angle defines to position the legs to their target position.
8. Do the same for the arms using shoulder, elbow, and wrist angle defines.
9. Perform a settling run to get to the equilibrium state of a positioned and settled AHM. Resulting joint positions and control values are used for initializing the load case simulation.
10. In this step the load case simulation can be prepared, since the positioning and settling of the AHM in the environment is completed. Switch to the load case simulation file (**.xml*), and no longer use **_settling.xml*). Import the end state joint positions (*.jps*) and activation control parameters (*.control*) from the settling simulation (9.) into the load case simulation model. This can be done manually but the preferred route is using the “*Active Human Initialiser*” tool in XMG - Simcenter Madymo Workspace.

3.2.2.3 Mercedes Benz In-house positioning approach

The use of Human Body Models (HBM) is becoming more and more prevalent due to the developments happening for autonomous vehicles. The new interior concepts which are being developed for these vehicles, requires occupant models used in the assessment of restraint systems, to achieve more comfortable seating postures. This requirement is posing, as a major hurdle for the ATDs’ to suffice and paving the way for use of HBMs’. Mercedes Benz has developed an in-house posture calculation approach for positioning the occupants for any desired complex seating posture using ergonomics data. The mentioned approach makes use of RAMSIS tool for the same.

RAMSIS can predict, with minimal user interference, how a person with given anthropometric features will most likely perform typical driver or passenger tasks in the car that is being designed. RAMSIS manikins can be made to represent occupants with a large variety of body dimensions and be based on a number of anthropometry databases from around the world (Seidl, 2007). The postures are generated by using the Mercedes Benz customized User defined Posture Method (UPM) and Mercedes Benz templates. The simulated RAMSIS postures are validated regularly at Mercedes Benz with tests. The steps below explain the posture generation and positioning procedure.

Step #1: Model Preparation - “Equivalent RAMSIS THUMS Manikin” is created based on THUMS (FE) model anthropometry data & fulfilling default posture as illustrated in Figure 3-19 below (Hemanth Kumar G, 2020).

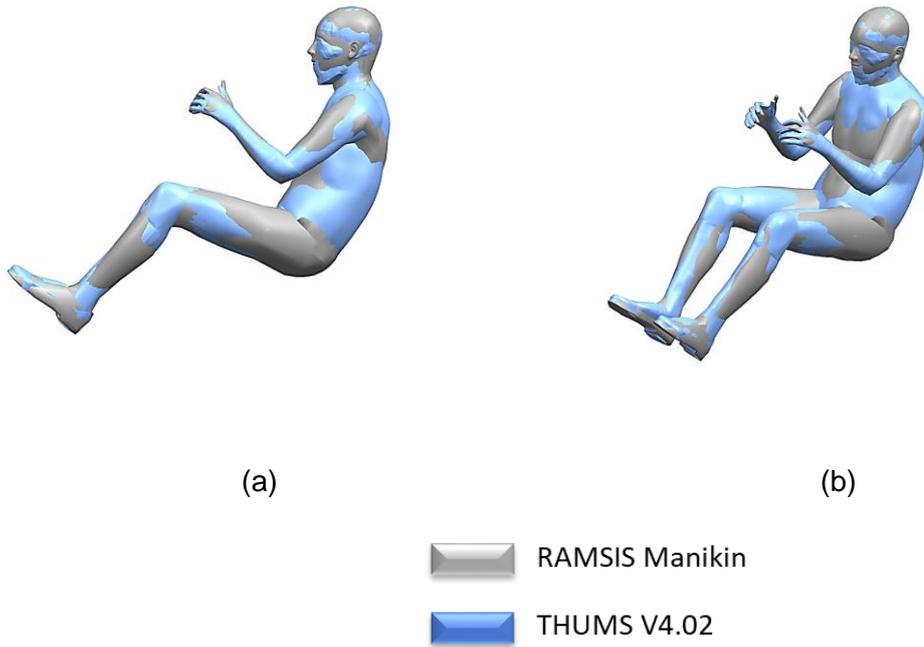


Figure 3-19: RAMSIS Manikin development for THUMSv4 anthropometry

Step #2: Model Preparation - “Equivalent RAMSIS THUMS Manikin” is then compared to THUMSv4.02 (FE) model based on landmark (source) points as illustrated in Figure 3-20 below

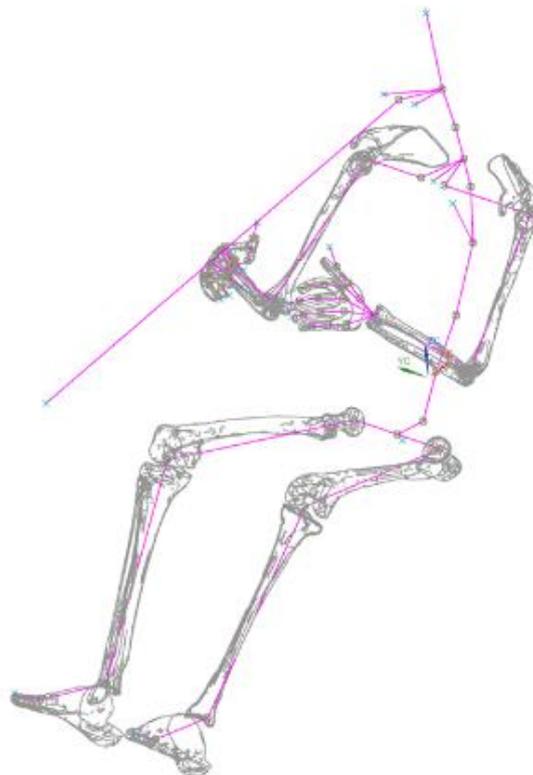


Figure 3-20: Superimposed THUMSv4.02-RAMSIS manikin in default posture using landmarks

Step #3 : “Equivalent RAMSIS THUMS Manikin” is then used in RAMSIS vehicle environment to achieve the target posture as in Figure 3-21.

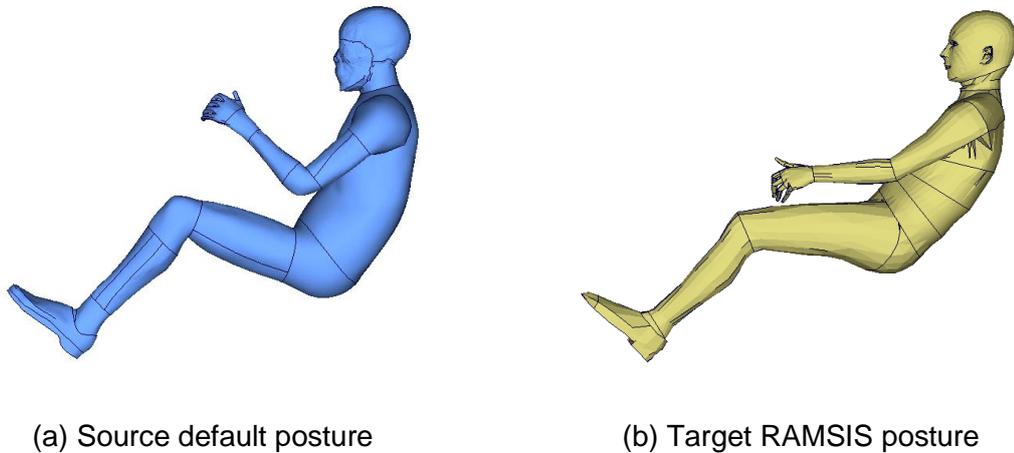


Figure 3-21: THUMSv4.02 RAMSIS manikin in default posture and target RAMSIS posture

Step #4: Target points as shown in Figure 3-22 below from RAMSIS are then exported in csv format for posture generation of the THUMSv4.02 FE model.

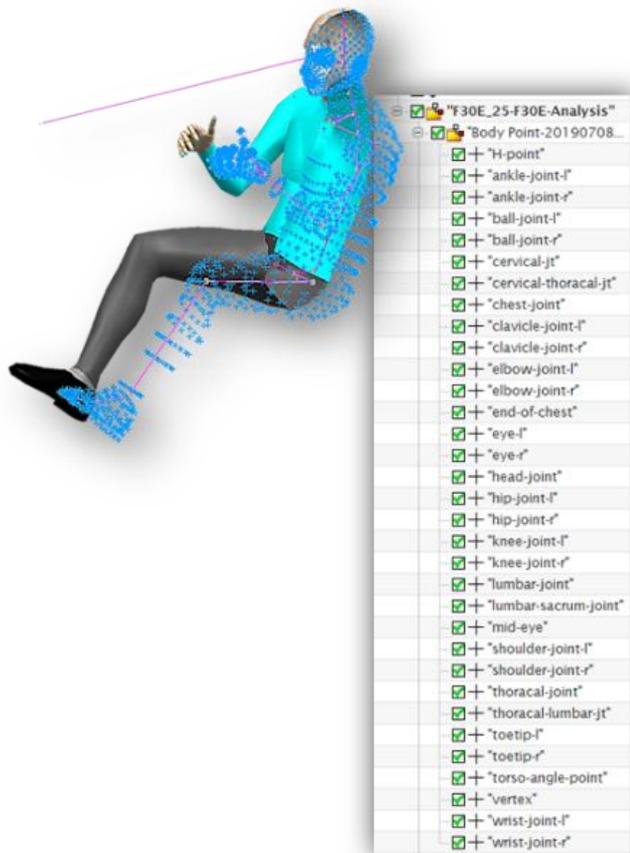


Figure 3-22: Landmark (target) points in RAMSIS

Step #5: ADAPT tool version 3.0 (Developed by Dynamore and sponsored by Mercedes Benz AG) is used to map source and target points (Figure 3-23 below) to achieve the desired posture for the THUMSv4.02 FE model.

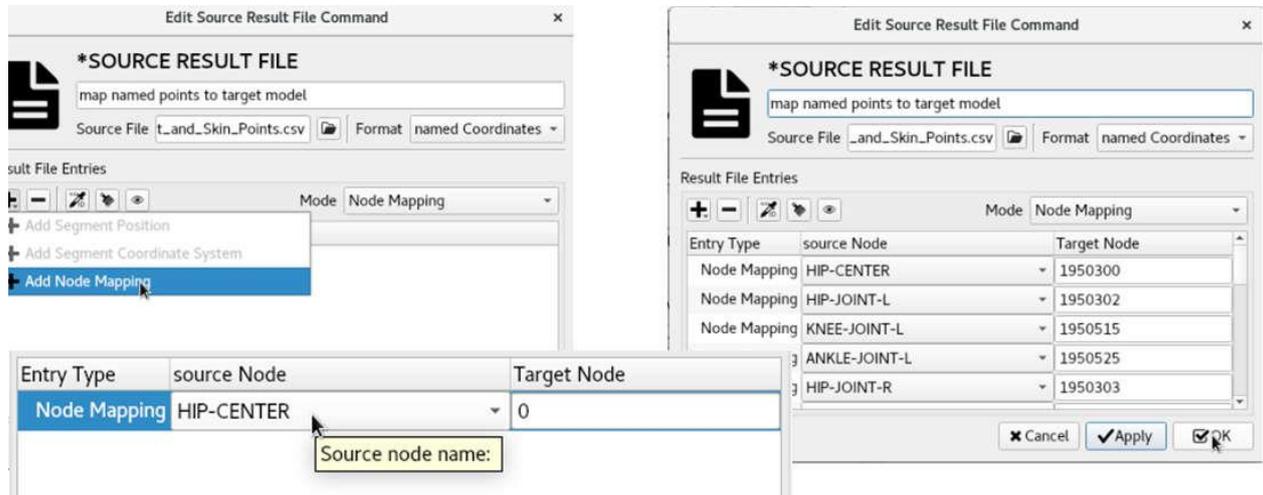


Figure 3-23 Landmark (target) points in RAMSIS

Step #6: Adapt Tool Version 3.0 has scripts developed for moving the THUMSv4.02 FE model based on ghosting approach. Figure 3-24 illustrates the final desired procedure achieved using the above-mentioned technique.

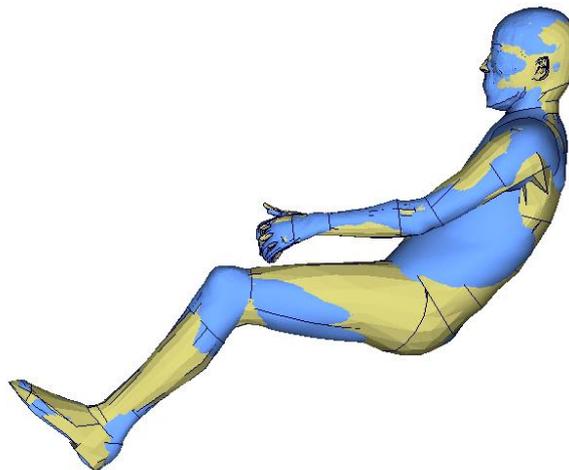


Figure 3-24 Final desired posture of the THUMSv4.02 FE model

3.2.3 Belting approach

As most partners have their own advanced in-house methods for belt positioning, it was decided to give an overview of available methods and develop a simple belting approach which does not require a certain commercial software.

3.2.3.1 SOTA approaches OSCCAR partners

Bosch method

Bosch applies the state of the art belting approach which is enclosed in the standard Simcenter Madymo software package and well described in 3.1.3.3. The BeltFitter tool delivers acceptable

results for HMs as well as Dummy models. It experienced several revisions over the years since Bosch started to use it, so that it delivers good results prior to start the pre- as well as in-crash simulations.

Mercedes Benz method

Mercedes Benz uses Oasys PRIMER software feature for belt path definition and belt fitting to the occupant. The belt route path follows internal guidelines or are as per the requirements of the test.

The belt routing procedure used by Mercedes Benz, is explained below for the OSCCAR Homologation Case environment. The environment model comprised of seat model, belt system & THUMSv4.02 Human Body Model. The buckle and D-Ring position existing in the model formed the basis for deriving the belt path in the current evaluation.

The first step was to position the THUMSv4 HBM in the reclined seating position based on the procedure defined by VIF in previous section. Figure 3-25 below illustrates the final reclined posture of the occupant in the seat.

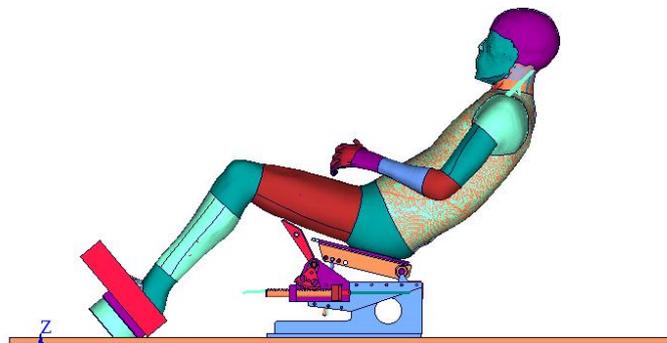


Figure 3-25: Posture of the occupant (THUMSv4.02 HBM) after the positioning

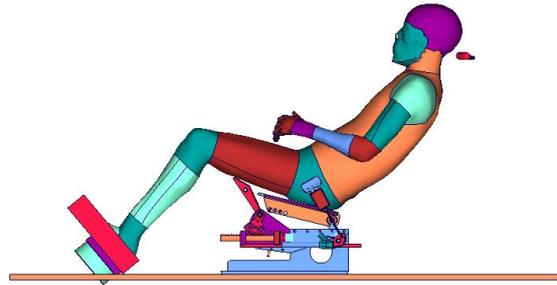
The following steps were then undertaken to complete the belt routing process.

1. Extract the surface model from the final posture and store it as a separate LS-Dyna file as shown in the adjacent image.



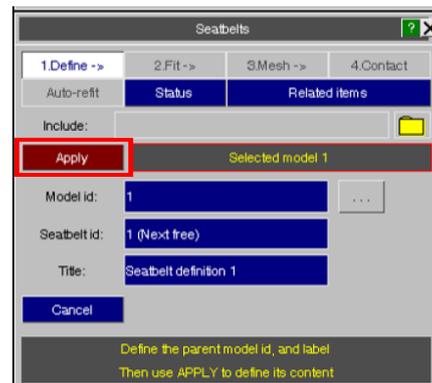
Surface model of the final posture

- The surface model along with the seat and belt environment (D-Ring & buckle) excluding the seatbelt 2D shell elements is imported in PRIMER as illustrated in adjacent image.

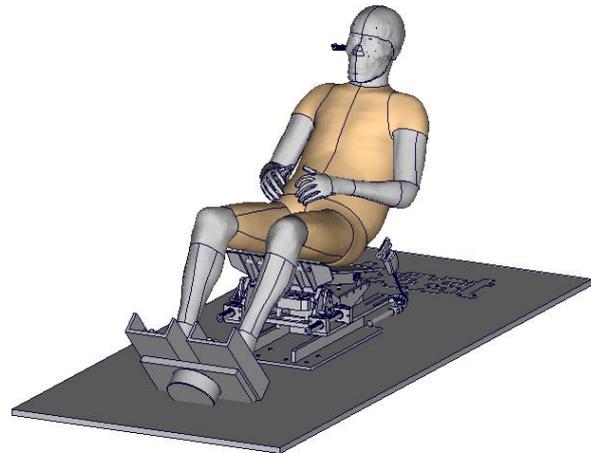


THUMSv4 surface & seat environment

- Create the seatbelt definitions in PRIMER and assign to the new belt a seatbelt definition ID using the option in the adjacent image.

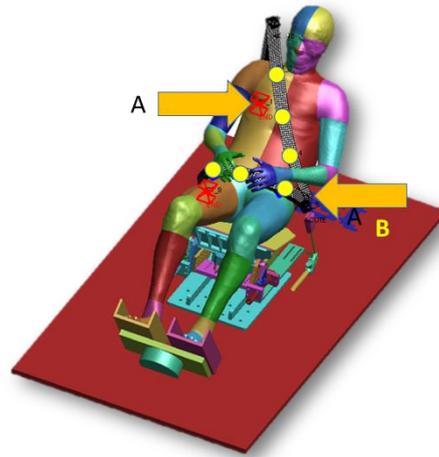


- Body regions are then selected on THUMSv4 (shown in adjacent image in burlywood color) occupant HBM about which the seatbelt was routed.



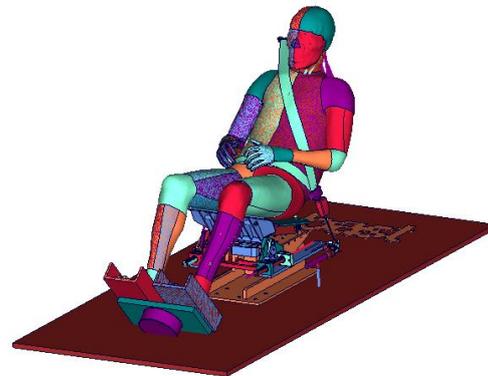
Body regions selected in PRIMER for belt routing

5. Path across which the belt is then defined (in YELLOW) using nodes on the finite element model as per the internal guidelines/test data. Additionally points were defined for representing retractor and slings (points A & B) so that they don't move during the belt fitting process.



Routing path for belt fitting

6. Define the dimensions to belt as per the internal guidelines/component data and later the fitting process are activated in Seatbelt tool in PRIMER. The fitting procedure in PRIMER is an iterative process and 2D belt elements are created after a satisfactory belt routing is achieved. The final belted occupant is shown in adjacent image.



Final routed belt

Table 3: Mercedes positioning method

TME method

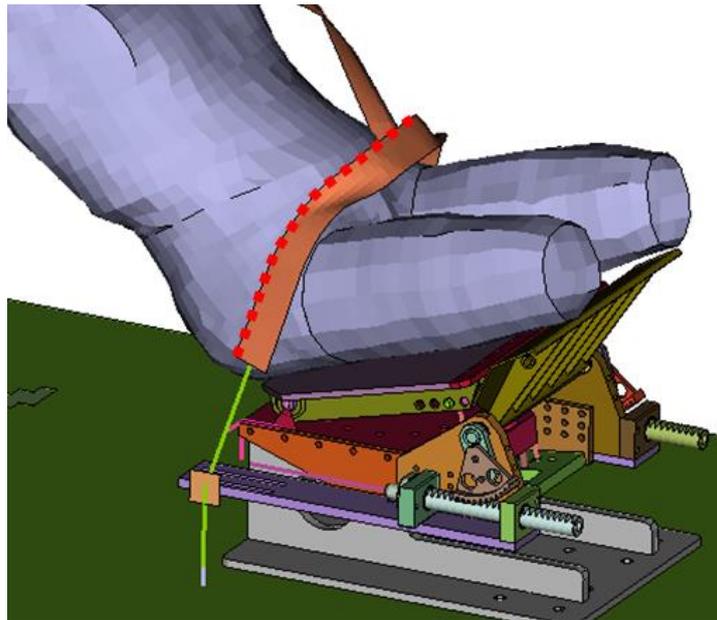
Toyota uses Oasys PRIMER software feature for belt path definition and belt fitting to the occupant. The belt path is defined according to internal guidelines or to reproduce test belt routes.

Volkswagen method

Volkswagen has its own internal belting tool for belting dummies or HBMs. However, in OSCCAR where a base belt system was yet given by the Homologation Test Case setup with the THOR dummy, the re-routing of the belt for the HBM was achieved using the "Belt Tool" provided in VCP (Visual-Crash Pam by ESI).

3.2.3.2 OSCCAR belting approach

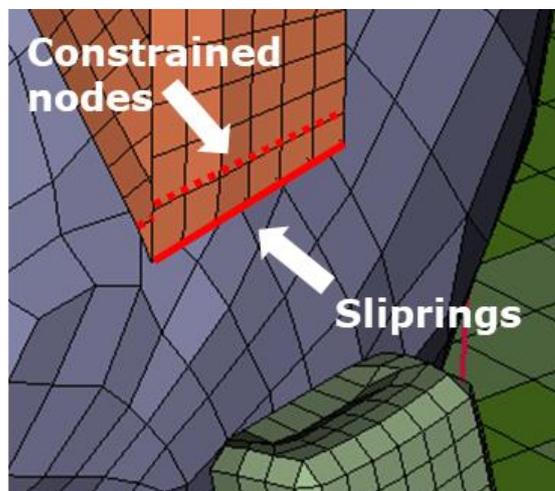
The environment model which is used in the OSCCAR project contains a belt, which was already routed for a THOR dummy. That belt routing must be determined for an HBM. To reach an appropriate belt route and to avoid folds and problems when restarting the geometry, some boundaries were set:

Constrained nodes (upper node line in the 2D lap belt elements)**Figure 3-26: Boundaries for the 2D lap belt**

In order to avoid folds of the belt during the first contacts with the rigid torso, the upper line of nodes for the lap belt are fixed in space with a boundary single point constraint (see Figure 3-26). A release time for this boundary is also added, which releases the nodes right before the torso contacts the belt.

Constrained nodes to buckle (no slip through during belting process)

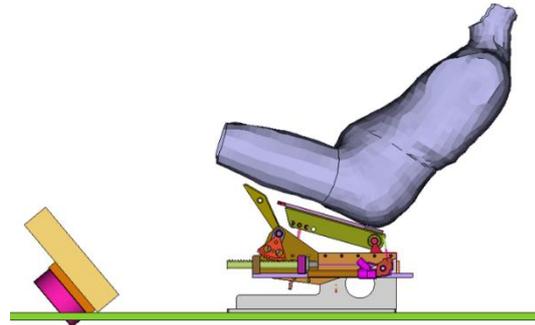
For the initialization of the 2D seatbelt the IDs of the shell elements which directly contact the slirping on both sides need to be specified. That applies also for restarting the belt with a new geometry (after the belting process). 2D elements slip through the slirping in the belting process and the geometrical situation in the last time step does not necessarily allow to determine the 2D elements which directly contact the slirping line.. Therefore, the closest two lines of nodes to the slirpings are constrained to the buckle (see Figure 3-27). That prevents the 2D belt elements from slipping through the buckle during the belting process.

**Figure 3-27: Constrained nodes in the close range of the slirpings**

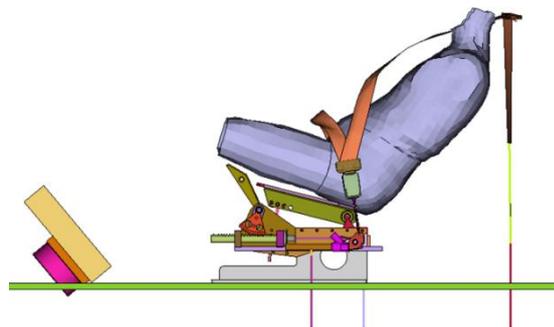
Workflow for belting

The belting approach which is applied at VIF is done in 4 steps.

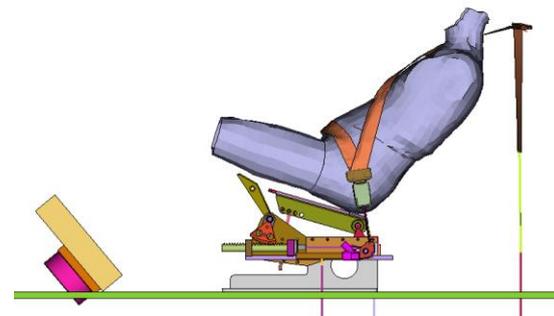
1. The outer surface of the positioned HBM is transformed into a rigid shell (for the torso parts)



2. To avoid initial penetrations by the belt, this rigid torso is positioned with a gap to its actual position.



3. The gap is closed by prescribing a motion to the rigid torso, which moves it back to the actual position. During this motion, the belt gets in contact with the torso. When reaching the actual position, the rigid torso remains in the position.



4. When the torso reaches its actual position, the belt is pulled. Finally, the nodes for the 2D belt elements are saved in this position. That allows to reposition the belt model for the simulation with a positioned HBM. Note that this step is conducted to only determine the node coordinates of the 2D belt. The contact between the buttock and the seat is not activated for this step. A deformation of the torso due to belt forces is also neglected, since the belt geometry should represent a belt which just overlays the torso.

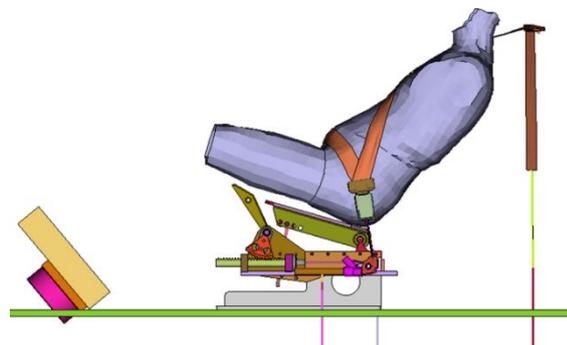


Table 4: OSCCAR belting approach

3.2.3.3 Workflow belting approach Madymo

Having an appropriate belt model available from the generic Madymo interior model, a belt fit on the AHM can be performed. Use the belt-fitter tool in Simcenter Madymo XMADgic and information about the belt and its position in the test data to create a similar belt routing in the simulation model.

With the belt anchor points positioned correctly in the model, the belt-fitter tool was started. With the belt system model readily available, the belt to be fitted on the AHM is selected. AHM surfaces are selected on which to place the belt [Figure 3-28]. Here it is convenient to make use of the predefined FE surface groups, the BodyNoArms_gfe FE surface group being the default option. This group contains the outer surfaces of the entire AHM with the exception of the upper extremities.

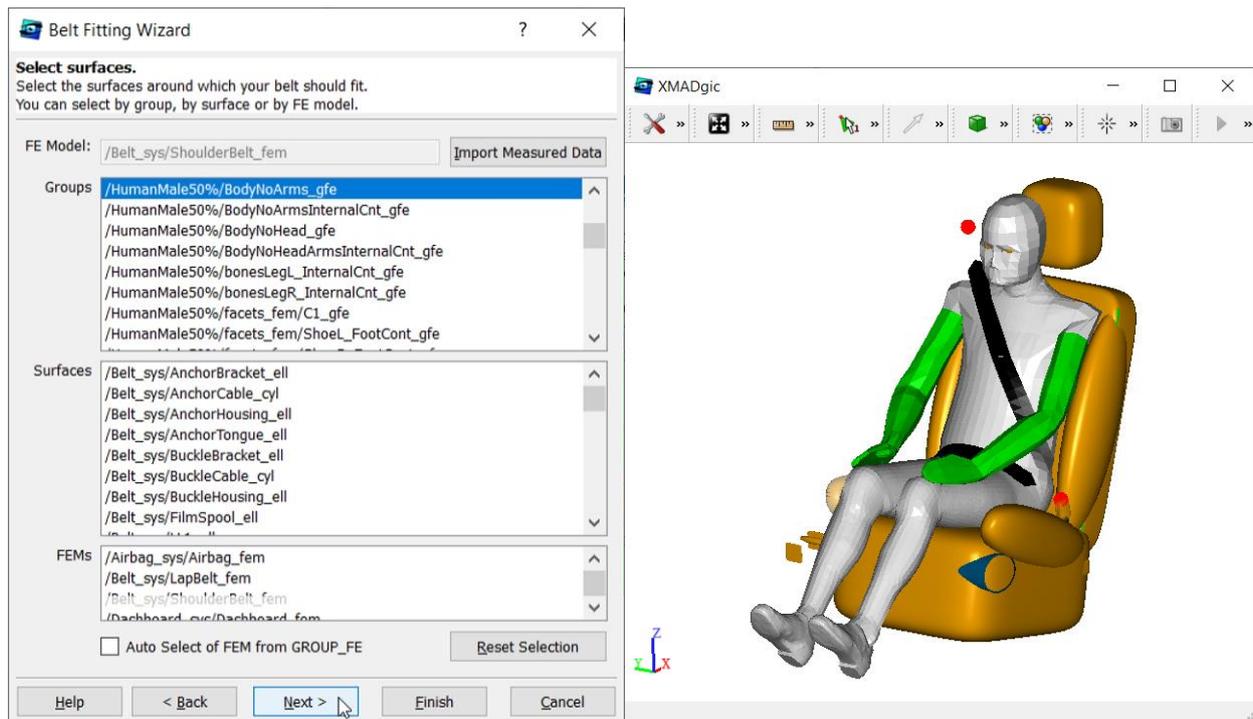


Figure 3-28: Belt Fitting Wizard surface selection menu and geometry viewer showing the selected surfaces in grey

The next step in the belt fitting wizard in XMADgic was used to position the belt. The position of a belt is defined by the position of the attachment (anchor) points and a third point, called the Midpoint. The midpoint is shown in the Geometry Viewer as a green dot with a dragger to enable positioning and a grey cutting plane is shown to indicate the center line of the belt when fitted using this midpoint position [Figure 3-29]. By changing the position of the Midpoint, the belt routing can be altered, visualized by the grey plane that moves along. Besides changing the routing of the belt, also the length of the MB parts of the belt at the start and end of the belt can be modified.

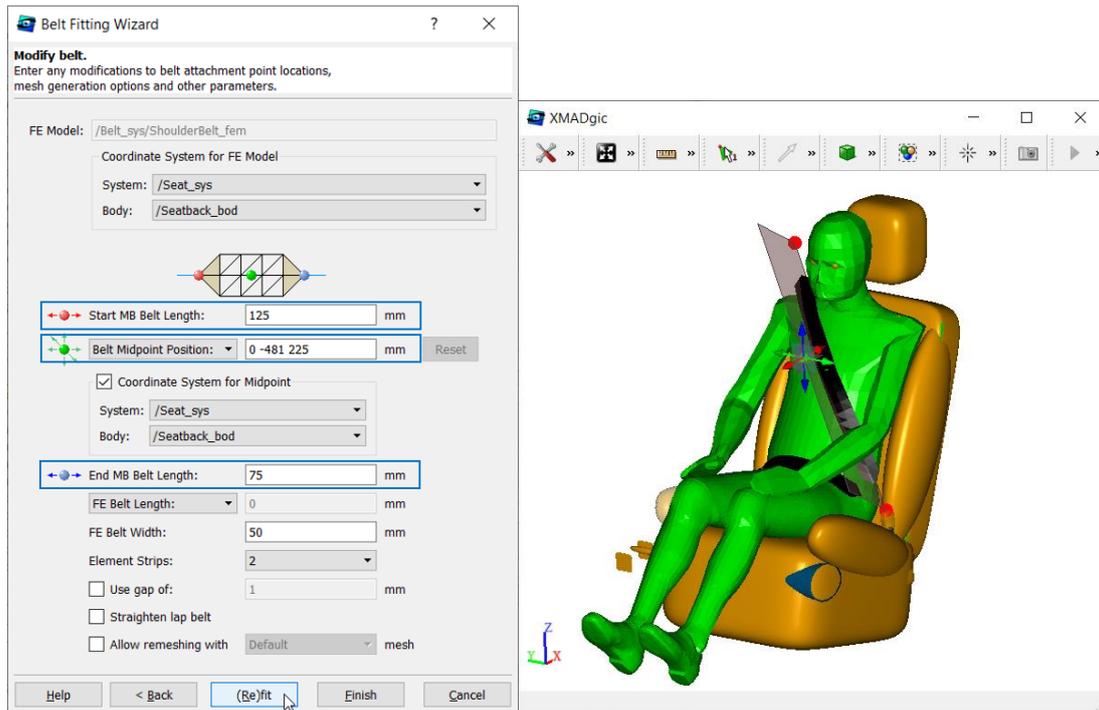


Figure 3-29: Belt fitting wizard menu

By clicking on the “(Re)fit” button, the belt was fitted on the AHM and the result can be seen in the viewer. Satisfied with the beltfit, the tool was closed by clicking “Finish” in the belt fitting wizard. Belt include files were saved to keep the changes that were made by the belt fitter.

3.2.4 Application example

To demonstrate the developed positioning method, a positioning simulation for a 23 deg reclined posture is executed with an AHM and a THUMS v3 in LS-Dyna. It is applied in an environment model (LAB seat) which is available within the OSCCAR project. Since no complete test data (volunteer or PMHS) which covers pelvis, thorax, head, spine and upper/lower limbs in a lab seat is available, the test data are created on the basis of several data sources. The sources for the body regions are:

- H-Point in the LAB seat: LAB PMHS data²⁰
- Sacrum/L5 + spine: UMTRI posture prediction ²¹
- Knee and ankle: UVa/Autoliv PMHS study²²

3.2.4.1 Positioning of AHM in 23 degree reclined posture

Environment and target data preparation

The environment is already available in the generic OSCCAR Madymo model. Seat and belt system selection DEFINEs were adjusted to place the LabCeasar and Autoliv belt in the environment model.

Target landmark coordinates, provided in a .csv file, were added in a Madymo include file where the landmarks are represented with small ellipsoids (Figure 3-30). The target landmark include file was added to the model to be able to view the target landmarks together with the environment and the AHM with its own landmarks. The body to which the target landmark ellipsoids are attached was positioned in the environment using information about the target landmarks origin in relation to the seat geometry.

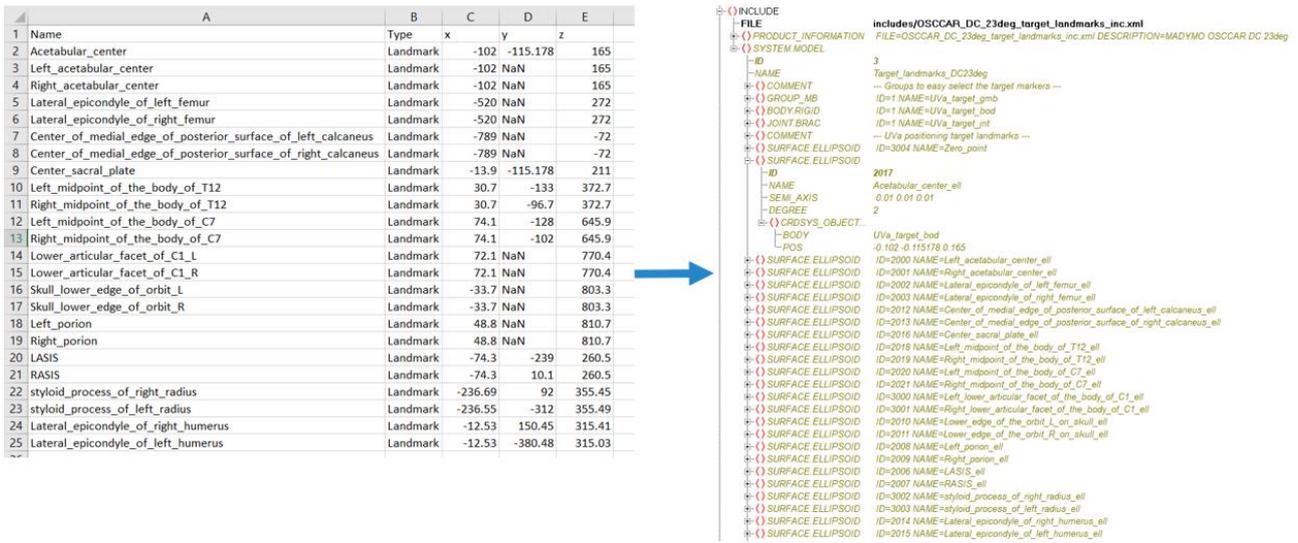


Figure 3-30: Target landmarks in .csv format (left) and for Madymo include (right)

Figure 3-30 shows the target landmarks in .csv format (left) to target landmarks Madymo include file (right). The H-point of the LabCeesar seat is unknown but the point mid between the hip joint centres of the volunteer is available from the target landmarks data. Hence, the “Oscar_H_point_bod” position in the seat model was adjusted to match this target H-point as shown in Figure 3-31: Alignment of seat H-point (Oscar_H_point_bod) to target H-point.

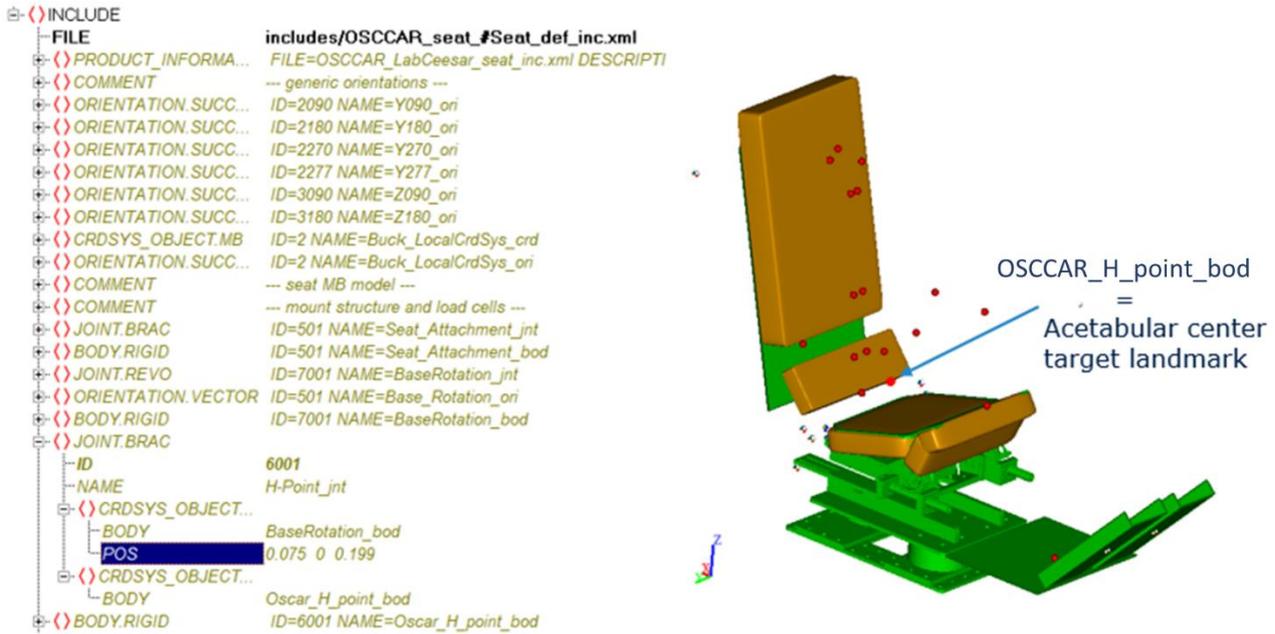


Figure 3-31: Alignment of seat H-point (Oscar_H_point_bod) to target H-point

Positioning AHM

The positioning and the settling run are performed using the dedicated *_settling.xml file.

1. The H-point was initially set to (0 0 10) offset from the target H-point.
2. Next, the pelvis pitch angle was set to get the desired pelvis orientation. In the generic OSCCAR Madymo model, pelvis pitch is set to 35.74 degrees for a seated AHM with a default seatback angle of 25 degrees. Since the example is for a 23-degree reclined seated AHM, pelvis pitch was adjusted to 33.74 degrees.
3. The spine position was kept as a nominal seated spine posture with both slouch parameters at 1. This gave a good approximation for the location of T1. At this stage also the seatback angle of the alternative backrest, used with the LabCeesar seat in this Madymo example, was adjusted from its default value to -14 degrees to better follow the back of the AHM.
4. Legs were positioned such that there was minimal to no initial contact with the seat and the foot supports. Hip-, knee-, and ankle pitch angles were set to respectively 72, 58, and 10 degrees. Arm posture was modified by decreasing the shoulder pitch (20 deg.) and increasing upper arm outward rotation (5 deg.) and elbow pitch (85 deg.) to better match the arm target landmarks.
5. With the first four positioning steps performed, the location of the H-point can be validated. As expected, the settling brought the AHM H-point closer to the target H-point. However, it was not far off and therefore the H-point offset was not modified. It did become clear that the arm positions needed some more adjustments (Figure 3-32).
6. In settled position the spine posture is still satisfactory with good agreement for the pelvis and its estimated orientation based on ASIS and Sacral target marker (latter not available in AHM and therefore L5 was used to get an indication).
7. Leg position did not need further adjustments based on settling outcome.
8. Based on settling outcome, shoulder- and elbow pitch angles were slightly adjusted to better match the target landmarks. Shoulder- and elbow pitch angles were set to 15 and 80 degrees respectively. As hand position was not known, wrist angles were set to a posture that was considered appropriate for the given arm posture.
9. A final settling run was performed to get to the state of a positioned and settled AHM (Figure 3-32). Resulting joint positions and control values are used for initializing the load case simulation.

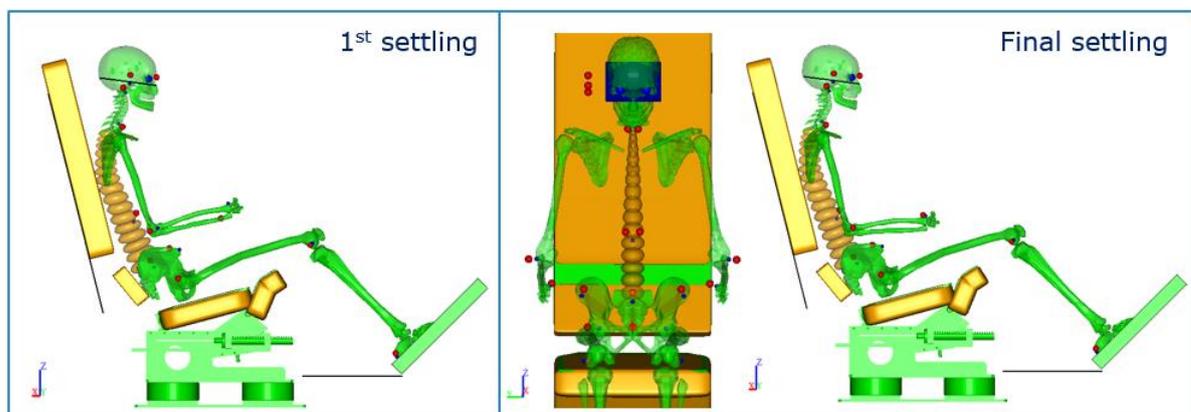


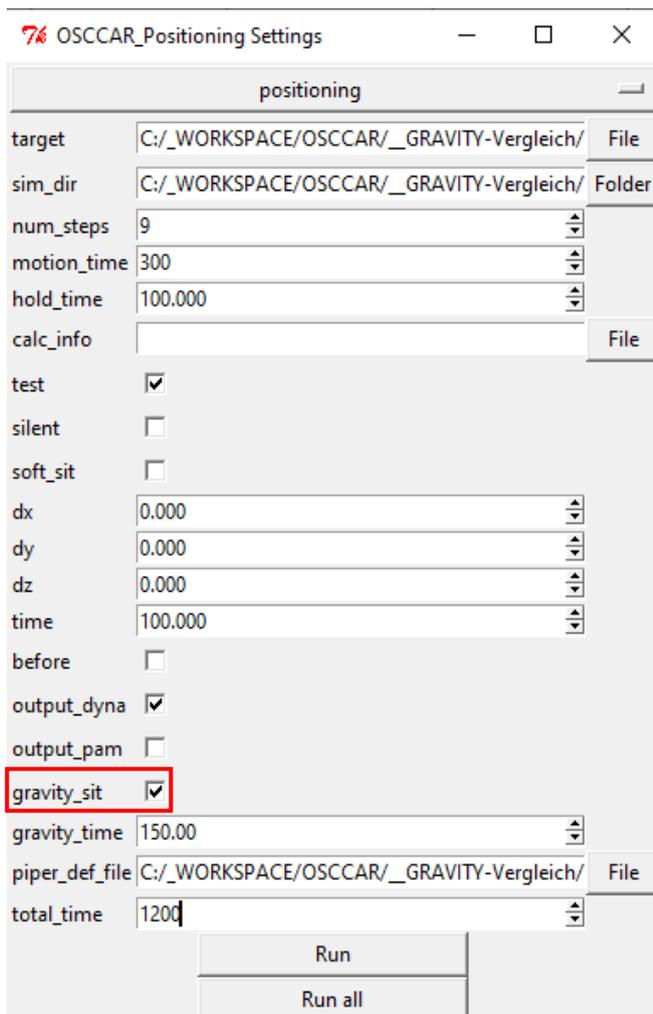
Figure 3-32: Result of settling simulations. Left the first from step 5 and right the result from step 9

Switched to the load case model file, the H-point offset define values were updated to align with the settling model used in step 9. Next, the “*Active Human Initialiser*” tool in XMadGic was used to import the joint positions (.jps) and muscle and actuator control values (.control) from the final settling simulation output.

3.2.4.2 Positioning of THUMS v3 in 23 degree reclined posture

For the demonstrator case it was chosen to use the gravity based sitting method. Following steps document how the sitting was done.

Gravity sitting



- Execute the Positioning Tool as usual and create "targetdata.ptt".
 - Under Positioning create the FE input files for the simulation with gravity seating (see left)
 - Check the Gravity function
 - Select the time period for which the gravity should be ramped (recommended ~100ms)
 - Select the Piper Definition File. The tool extracts necessary body parts which are rigidly switched during gravity.
 - Select the total duration of the simulation (=motion_time+hold_time+gravity_time+ buffer). After the Gravity is fully ramped, a time is needed (~500ms) until the HM is completely in the seat and swung out.
 - Create a z-offset between HBM and seat (recommended ~30mm) in the simulation environment.
 - e.g. in LS-Dyna with: *INCLUDE_TRANSFORM card

Figure 3-33: Gravity sitting in OSCCAR positioning tool

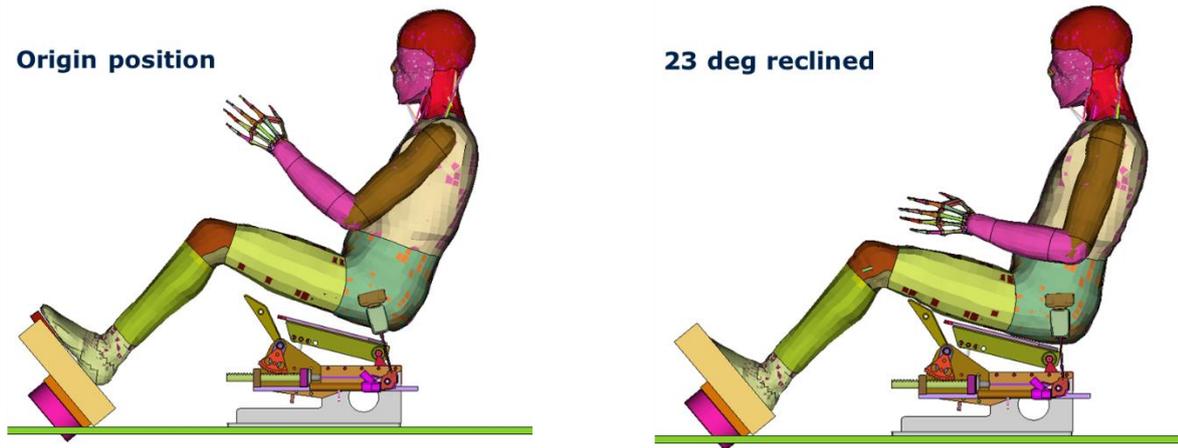


Figure 3-34: Positioning a THUMS v3 to a 23 deg reclined posture

3.2.4.3 Results

Following diagram shows the target coordinates for the landmarks according to the test data, the calculated target coordinates and finally the coordinates of the positioned FE HBM (THUMS v3) and the MB AHM. The base point for all models is the acetabular centre. The models were positioned to meet exactly the same coordinates in the heel (Center of medial edge of posterior surface of left calcaneus) and the same x-coordinates at the ear (Porion). Further the Madymo AHM was positioned to meet the exact coordinates in the hand (Styloid process of the radius). The remaining landmarks were positioned to finally achieve the same posture by keeping the angles of the vector structure.

Minor differences are visible at certain landmarks or distances between landmarks. These are caused by the different anthropometries of the models and the data source (volunteer, PMHS).

The positions are inspected visually if their static coordinates are identical. It is not investigated, if a certain selection of identical landmark would lead to more identical kinematic in a pre- or in-crash phase. The reason is that for different pulses different selections of landmarks might be necessary. Hence a general criterion is not developed for this deliverable.

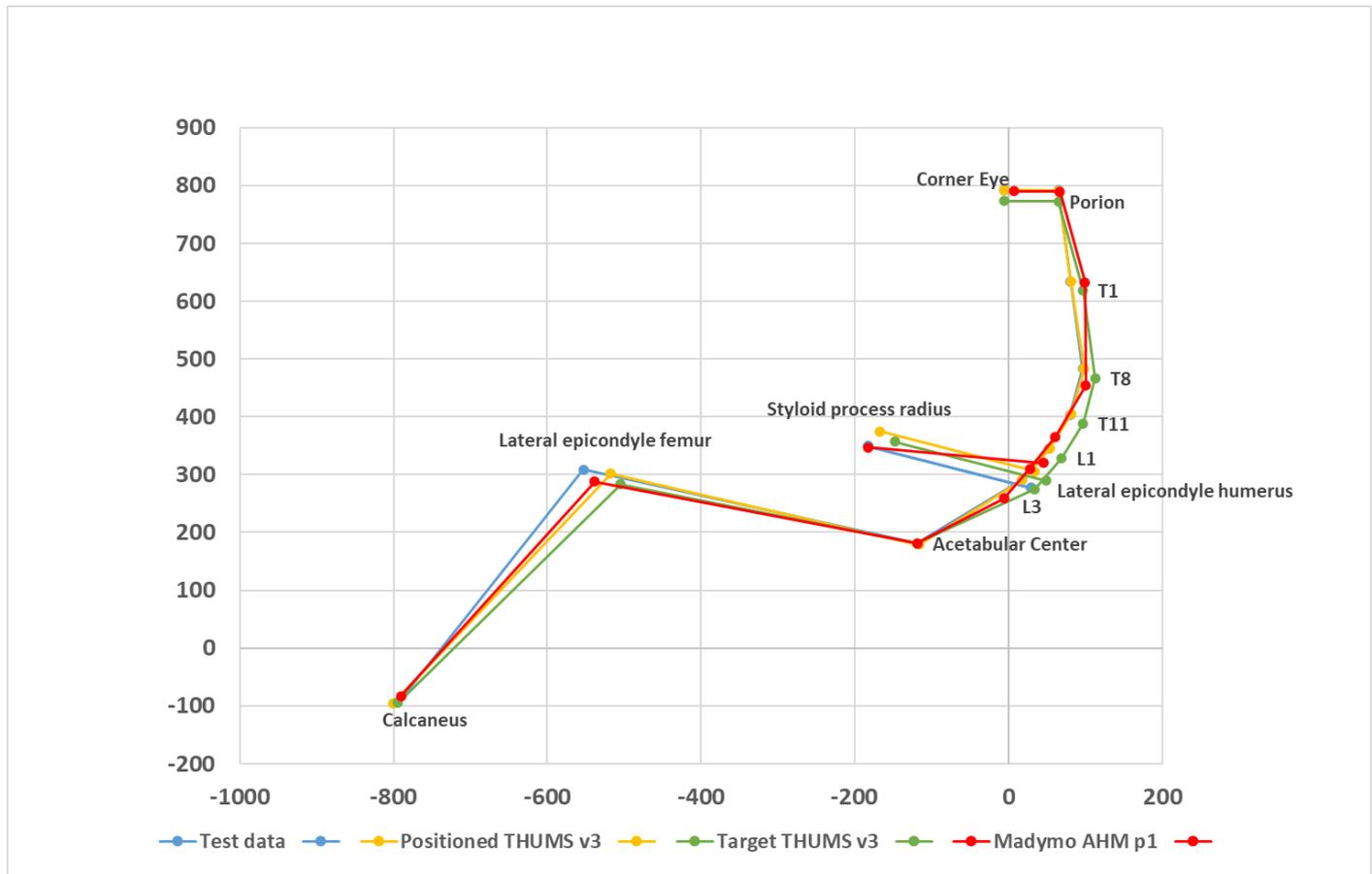


Figure 3-35: x-z coordinates of 23 deg reclined posture

3.3 Transition methods

In absence of adequate tool-independent procedures, some partners use their own in-house methods. Their state of the art was presented in web-meetings and an OSCCAR internal tool/method was developed which allows the transition of kinematics for various HMs. In order to demonstrate the effectiveness of the new advanced protections system developed in WP2 along with the updated HMs from WP3 and their impact on occupant safety within the demonstration example (homologation scenario) a general method and tool is needed. Additional ingredient is the tool-independent quality check tool reported in D4.1. Thus, an integrated assessment tool chain for all three involved codes LS-Dyna, VPS and Simcenter Madymo using the same general input and assessment method was developed.

3.3.1 SOTA approaches at OSCCAR partners

Bosch

Bosch applies the standard Simcenter Madymo seamless approach, by using the same HM in the pre-crash as well as crash phase. In this case the HM is represented by the same parameter in both phases. There is no transition in form of a defined stop at the end of the pre-crash phase, transfer of parameter and kinematic setting to a crash phase and re-start / continuation of the simulation in the crash phase. As example a combined pre-crash / crash simulation from WP2 T2.3 protection Principle 1 “rotating seat” is shown.

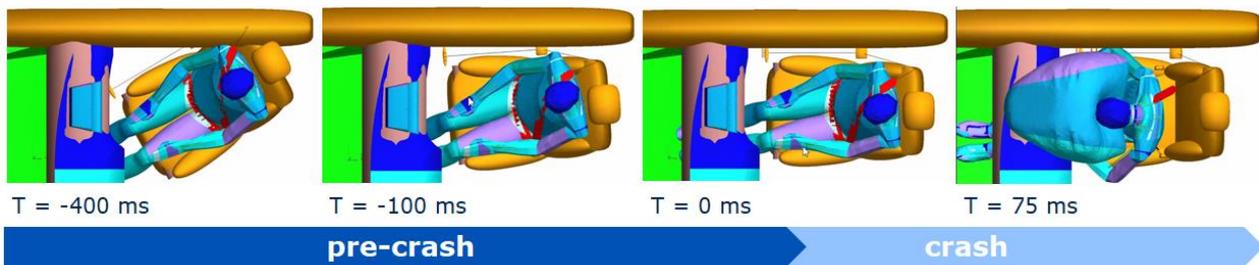


Figure 3-36 Example of standard Madymo transition method using the example of WP2 T2.3 Protection Principle 1 “rotating seat” simulation

The positioning of the model is done taking into account the Madymo positioning guidelines. As occupant model the Simcenter Madymo AHM is used. Bosch is not doing any “own” HM development, but uses commercially available Simcenter AHM model, which is available for pre- and in-crash. Basis of this model is a validation report. The validation basis for pre- and in-crash is chosen according to Simcenter Madymo guidelines and description. No own validation with the model was done. A limited cross-check study with OM4IS (2009 – 2012) data was done.

In the assessment part of our s-o-t-a procedure typically only kinematic and selected deformation and kinematic measures (e.g. distance of ribs to rear) are measured and analyzed. No defined injury criteria are analyzed. The challenge in this procedure may be to determine injury criteria and do an injury assessment with this model, which is the plan within WP3.

With the described procedure and set up of a seamless tool chain covering all relevant phases, the “normal” driving, pre-crash and in-crash phase can be assessed. Within WP4 Homologation case activities together with other partners a Simcenter Madymo showcase is created. The impact demonstration and assessment of the integrated safety systems is foreseen to be presented in detail in D4.3 “Homologation scenario demonstration using advanced harmonized HBMs”.

TME

In order to perform pre-crash and in-crash simulations, Toyota uses a transition method which is based on two main simulations, one for the pre-crash phase using THUMS Version 5 and one for the in-crash phase using THUMS Version 4.

THUMS Version 5 is an active human model which simulates the muscular response of an occupant during an emergency braking in order to predict the occupant posture change under such event. THUMS Version 4 is a detailed human model that can predict the kinematics and the injuries of an occupant during a crash. Pre-crash and in-crash simulation phases are combined using the method shown in Figure 3-37.

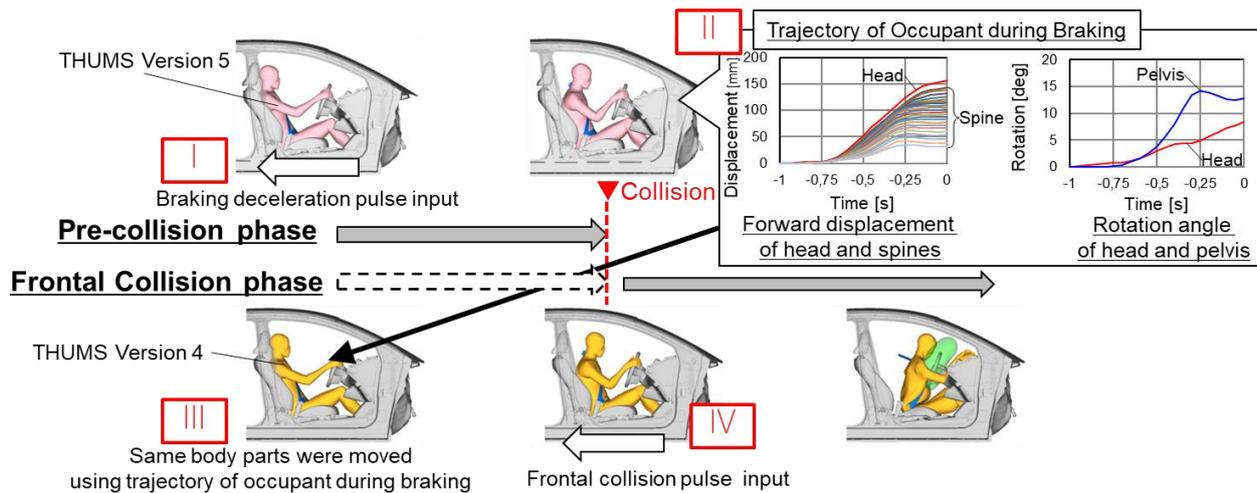


Figure 3-37: Toyota transition method (Yamada K., Gotoh M., Kitagawa Y. and Yasuki T., 2016)

At first the THUMS Version 5 is set in the vehicle seat at the defined H-point and the gravity is applied until the model is stable (takes around 450 ms). Secondly, the pre-crash pulse is applied to the vehicle and displacement/rotation history curves of THUMS Version 5 nodes of main body parts (head, shoulders, hands, 1st thoracic vertebra, 12th thoracic vertebra, pelvis, knees, feet) are set as output. The seatbelt forces and seat reaction forces are extracted from the pre-crash phase and are reproduced at the start of the crash-phase. Thirdly, the THUMS Version 5 displacements and rotations are applied to the THUMS Version 4 within 100 ms. Finally, the crash pulse is applied to the vehicle.

The step-by-step method is detailed below:

1. Initial positioning in seat using THUMS V5
 - a. Move THUMS to the target H-point
 - i. *BOUNDARY_PRESCRIBED_MOTION in 50ms
 - b. Release model and apply gravity during 450ms
 - c. Keep the seat cushion deformation for future pre-crash simulations
 - i. *INITIAL_FOAM_REFERENCE_GEOMETRY
2. Transition pre-crash to in-crash phase: from THUMS V5 to THUMS V4
 - a. Re-simulate pre-crash phase with THUMS V4 using node outputs of THUMS V5
 - i. Identify corresponding target nodes in THUMS V4
 - ii. Create Rigid Bodies (RB) from skeleton parts (incl. target nodes)
 1. *DEFORMABLE_TO_RIGID
 2. In total 10 RBs created (Head, Shoulders, Hands, T1, T12, Pelvis, Knees)
 3. BIRTH and DEATH are specified to create and release the RBs
 - iii. Prescribe the motion of the RBs in XYZ using THUMS V5 node outputs
 1. *BOUNDARY_PRESCRIBED_MOTION_RIGID applied to Shell elements of the Master RB
 2. Applied within 100 ms
 - iv. Remove RBs at DEATH time
 - v. Apply zero velocity to all nodes of THUMS V4
 1. *BOUNDARY_PRESCRIBED_MOTION with BIRTH and DEATH times
3. In-crash simulation
 - a. Apply crash pulse to the vehicle model
 - b. Seat and Restraint system

- i. Their behaviour are simulated from the pre-crash to the in-crash phase using THUMS V4

Volkswagen

Volkswagen applies its THUMS TUC-VW AHBM within the pre- and in-crash phase in a seamless process without any transition. The method was already successfully applied to the protection principle analyses in WP2 (reported in Deliverable 2.4 accordingly) and to the Homologation Scenario for the simulations in which the pre-crash is included (foreseen to be reported in OSCCAR Deliverable 4.3). When the in-crash phase starts the muscle activation in the AHBM is deactivated – set to zero - which represents the only change to the HBM settings between pre- and in-crash phase. Nonetheless, the influence of the pre-activation of the muscles in the in-crash has been analysed numerically using different activation approaches (foreseen to be reported in OSCCAR Deliverable 3.2), leading to different injury indicator levels depending on the level and approach used for the activation²³.

3.3.2 OSCCAR approach + method/tool

In this task a method for different human models (FE and MB) was developed to realize a continuous simulation chain for the occupant kinematics consisting of pre-crash and in-crash phase. As the occupant's position and velocity at the end of the pre-crash phase (caused by emergency braking as presented in OSCCAR deliverable 2.4) influences the kinematics during the in-crash phase, the in-crash model needs to be initialized at the correct position and velocity.

Basically, the pre-crash kinematics of the pre-crash occupant model (HM A) is prescribed to the in-crash model (HM B). This requires an appropriate pre-crash simulation with HM A. The trajectories of the individual landmarks must be recorded and stored (LS-DYNA provides nodout file, Madymo provides .lps file). Using this information in combination with the algorithm for anthropometric scaling (explained in detail in Appendix A), the identical motion can be impressed on HM B. The developed tool is able to read MB and FE pre-crash simulation result files and adapt the trajectories to the anthropometry of the in-crash model (FE only).

That guarantees, that the in-crash model starts at the proper initial position for the in-crash phase. The in-crash vehicle model does not have to perform the descriptive maneuvers, the occupant movement is achieved solely through prescribing the defined trajectories.

Workflow

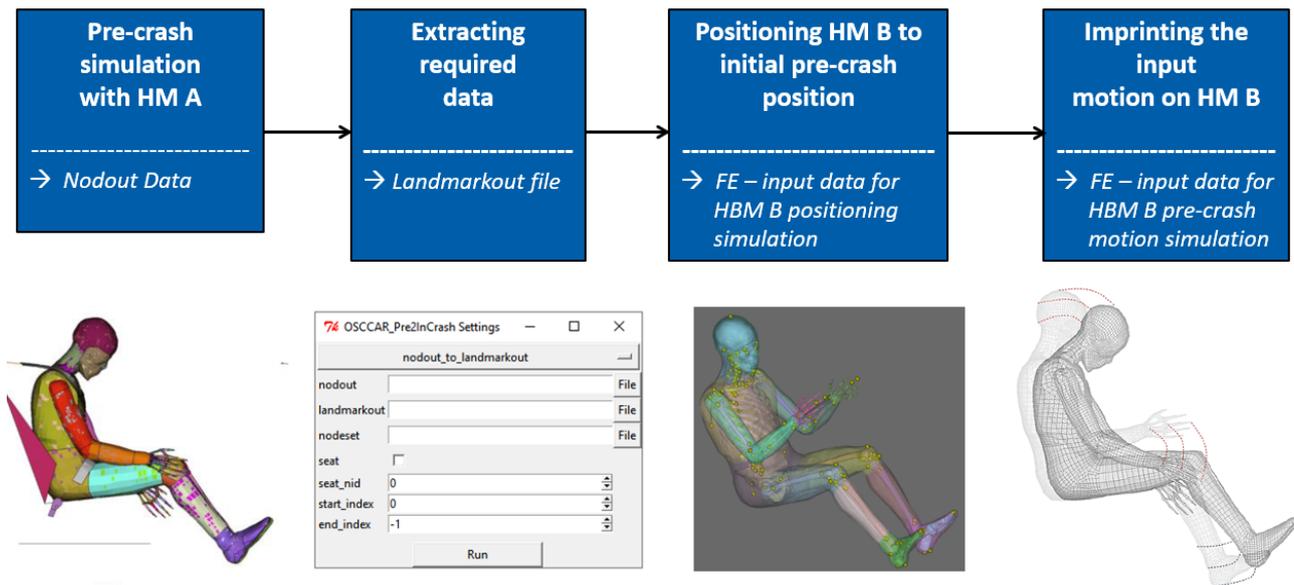


Figure 3-38: Method for transition of motion

Figure 3-38 shows the necessary steps of the transition process. As already mentioned, the input data is the file containing the node trajectories of the HM A pre-crash simulation. The first step is to open PIPER and load the corresponding model (except Madymo), then run the OSCCAR tool "Pre2InCrash". Using the scripts "nodout_to_landmarkout" or "madyomo_to_landmarkout" the trajectories of the necessary landmarks are extracted and saved. The selection of the landmarks used for the extraction of the input data as well as for the imprinting of the movement is also declared via the kinematic linkage model (see paragraph 4.1.2.1.1). Before the recorded movement from HBM A can be impressed on HBM B, it must be positioned in the initial position (position of HM A at the beginning of the pre-crash simulation). For this purpose, the landmarkout file can be used to create a positioning simulation with the OSCCAR tool "Positioning" to the desired timestep (e.g. $t=0$). The positioned HBM B can then be loaded with PIPER and the FE input data for the imprinted pre-crash simulation can be generated with the tool.

In the next section the individual steps are shown in more detail and the handling of the OSCCAR tool "Pre2InCrash" is explained.

1. Create „Landmarkout“ File:

This script reads in a nodout from LS-Dyna and converts the node ID's into landmark names. The result will be written to a file called landmarkout. This file contains a python dictionary with all landmarks and corresponding coordinates of every time step and a list containing the times.

Additionally, a LS-Dyna keyword file containing a nodeset can be provided. This nodeset is used to filter the correct nodes from the nodout. A seat node can be specified to calculate the total motion relative to the seat motion. With the start and end index the recorded data can be reduced to the desired time range.

This script needs to be executed on the model of the simulation.

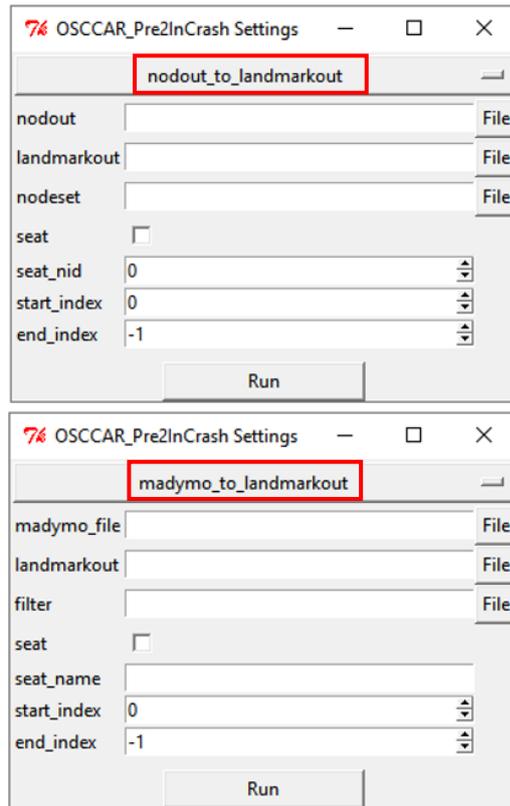


Figure 3-39 shows the keys for the script to create a landmarkout file for LS-Dyna input

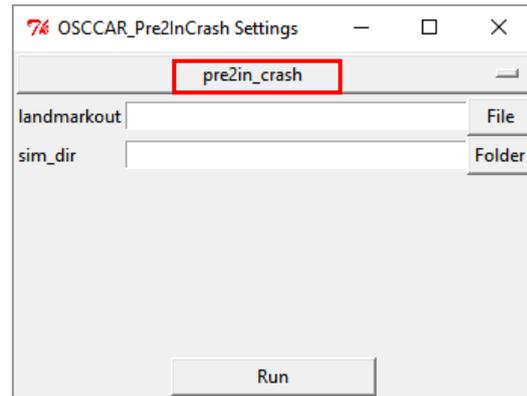
Name	Type	value	optional
nodout	string	path/to/nodout	
landmarkout	string	path/to/output/file	
nodeset	string	path/to/dyna/file/containing/nodeset	X
seat	bool	Wether to enable the seat node	X
seat_nid	int	The node id of the seat	X
start_index	int	The first index of the time frame that should be extracted	X
end_index	int	The last index of the time frame that should be extracted	X

Figure 3-39: Keys for the script nodout_to_landmarkout

In case the input data is provided by Madyemo, the corresponding script "madyemo_to_landmarkout" must be executed. The handling of the tool is done in a similar way.

2. Create FE – Simulation Input Data

This script applies the generated motion on the desired HM. A landmarkout needs to be provided as well as a folder for all the generated LS-Dyna FE simulation input files. The anthropometry can differ between the landmarkout and the HM in Piper. The script takes care of that (see appendix A). To achieve that a bone_landmarks file is used to describe the connection between the bones. This file can be found at packs_p2ic/bone_landmarks.py



3.3.3 Application example

The developed method is demonstrated in this chapter by applying it on a FE-to-FE transition and on a MB-to-FE transition:

1. Default pre-crash movement of THUMS V3 AM50 is transferred to VIVA Open HBM
2. Default pre-crash movement of MADYMO (calculated by Siemens) is transferred to THUMS V3 AM50

The following demonstration includes the positioning process to the initial position and a restart simulation to imprint the pre-crash motion. The restraint system is deactivated for the following calculations.

The pulse shown below (see D 2.4, Chapter 3.2.3.1 “Boundary conditions and simulation model”) is applied to the established 23° HM posture to generate the default pre-crash kinematics with a duration of 500ms. Since the pulse is applied on two different model types (THUMS V3 AM50 (passive) and MADYMO AHM (active)) to derive a pre-crash movement the kinematic between these two models will differ.

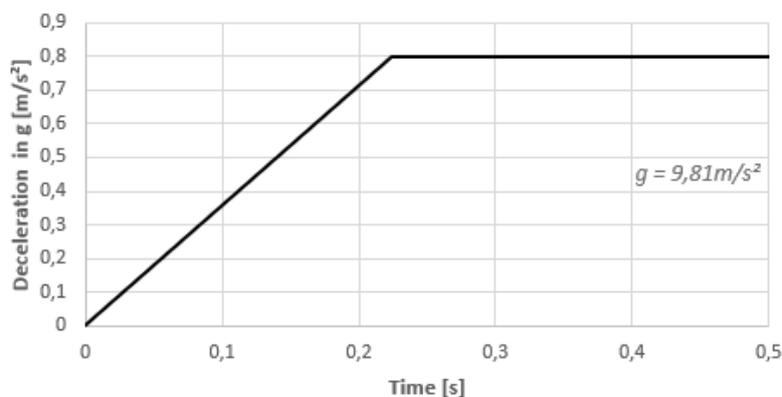


Figure 3-40: Pre-crash pulse for application example

3.3.3.1 Demonstration for THUSM v3 AM50 and VIVA OpenHBM

The figure below shows the pre-crash motion of the THUMS at the beginning, middle and end state.

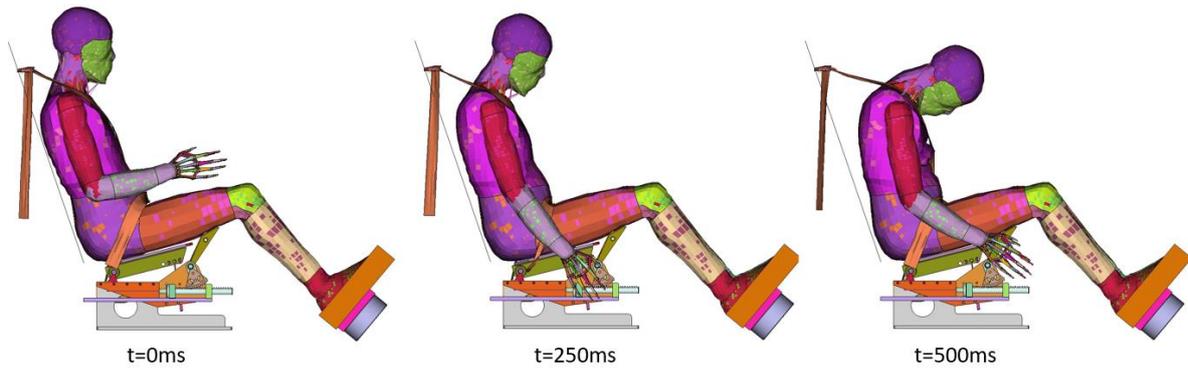


Figure 3-41: Pre-crash simulation THUMS

For the following evaluation of the results, the skeletal structure of the two HM's is compared to each other to provide better information.

- **Positioning of VIVA from original position to initial position (THUMS at t=0ms):**

Using the OSCCAR Positioning Tool and the generated landmarkout file of the THUMS simulation, the VIVA model was first positioned from the delivery state to the initial position.

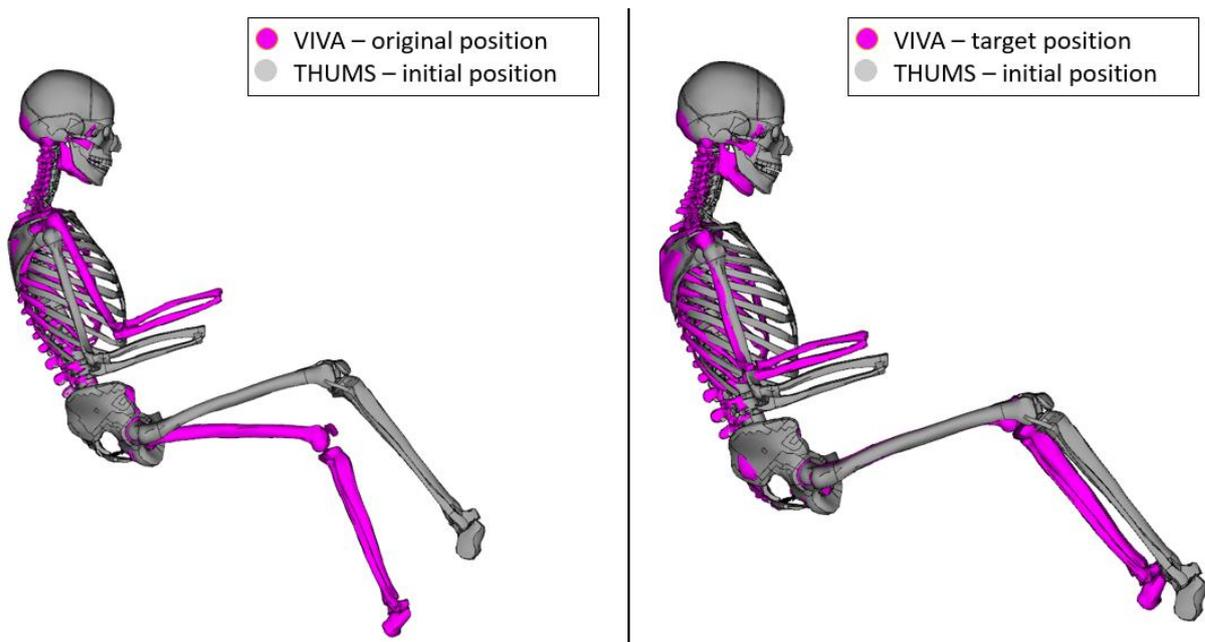


Figure 3-42: VIVA original (left) positioned to THUMS initial position t=0ms (right)

The resulting new geometry of the VIVA model is then used to generate and calculate the impressed motion using the OSCCAR Transition-Tool. Deviations can be seen in the shoulder region as well as in the cervical spine and in the head position. The reason for this is in the first case the shoulder anthropometry of the THUMS model compared to the VIVA model and in the second case the different modeling in the cervical spine.

To achieve exact landmark positions (e.g. for the hand position on the steering wheel), the OSCCAR Positioning Tool is also able to calculate exact positions. This example is extended to show this function of the tool (see figure below).

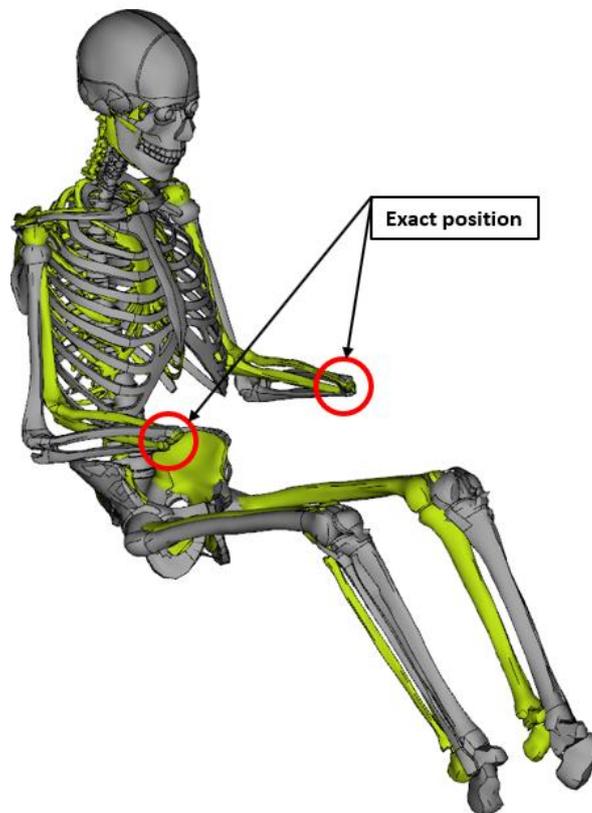


Figure 3-43: OSCCAR Positioning-Tool - Exact hand position for the steering wheel

For the imprinting of the THUMS pre-crash motion, the obtained VIVA geometry of the correctly scaled anthropometry approach is used.

- **Imprinting of the extracted motion on positioned VIVA:**

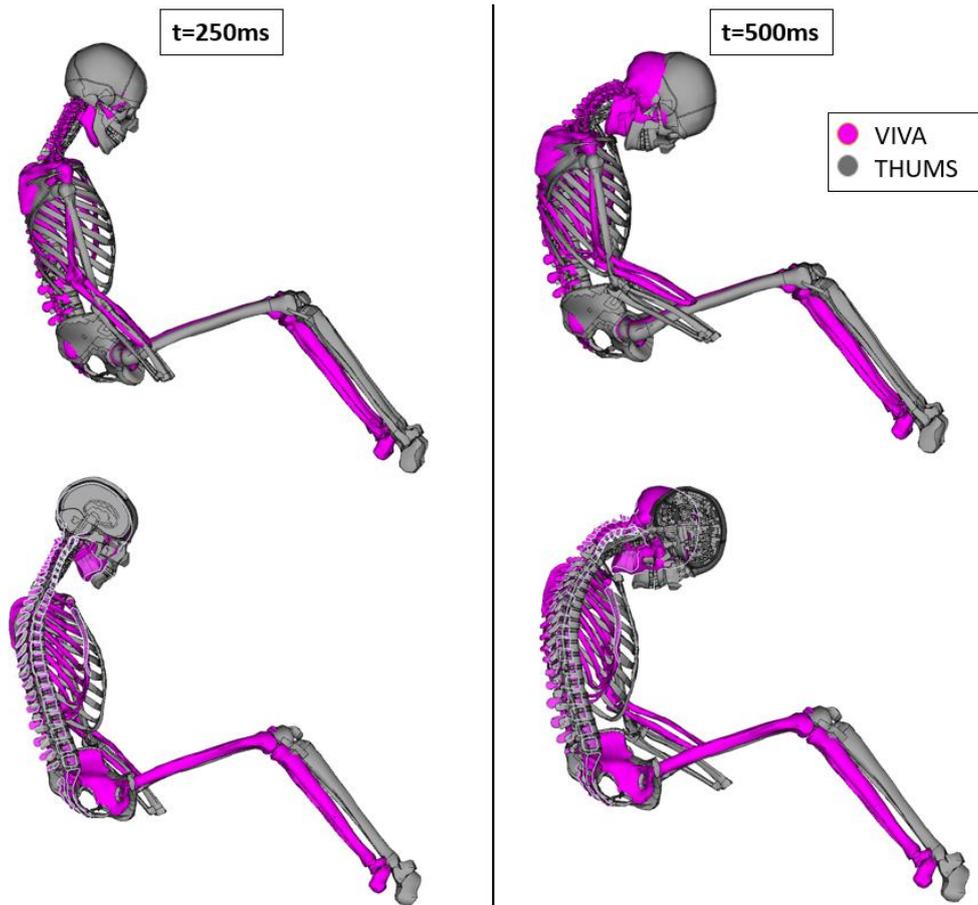


Figure 3-44: Skeleton comparison VIVA and THUMS at 250ms and 500ms (full display on top; sectional display at bottom)

The motion is properly scaled and imprinted on the anthropometry of the VIVA. The following figure shows very good agreement with the default pre-crash motion (see Figure 3-39).

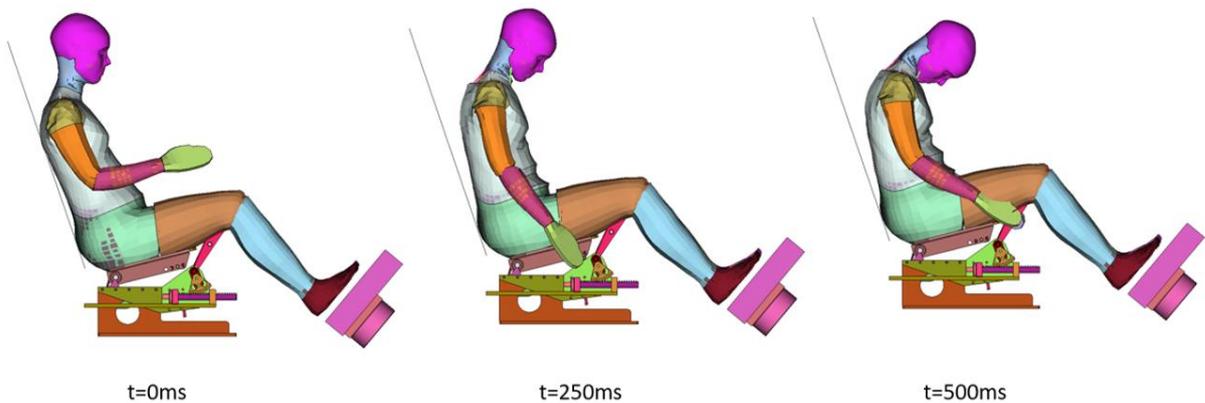


Figure 3-45: Impressed pre-crash motion on VIVA

3.3.3.2 Demonstration for AHM (Madymo) and THUMS V3 AM50

The figure below shows the pre-crash motion of the MADYMO at the beginning, middle and end state.

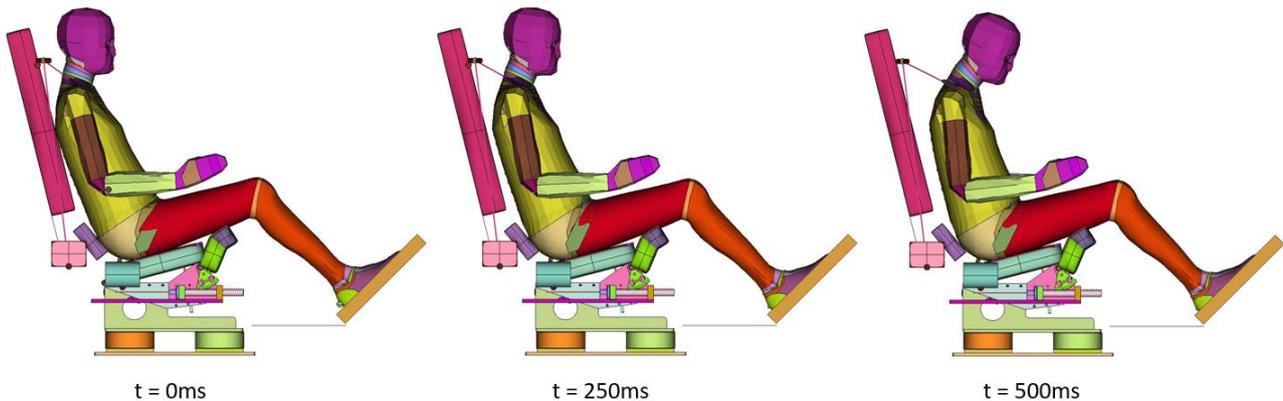


Figure 3-46: Pre-crash simulation MADYMO (Siemens)

For the following evaluation of the results, the skeletal structure of the two HM's is compared to each other to provide better information.

- **Positioning of THUMS from original position to initial position (MADYMO at t=0ms):**

Using the OSCCAR Positioning Tool and the generated landmarkout file of the MADYMO simulation, the THUMS model was first positioned from the delivery state to the initial position.

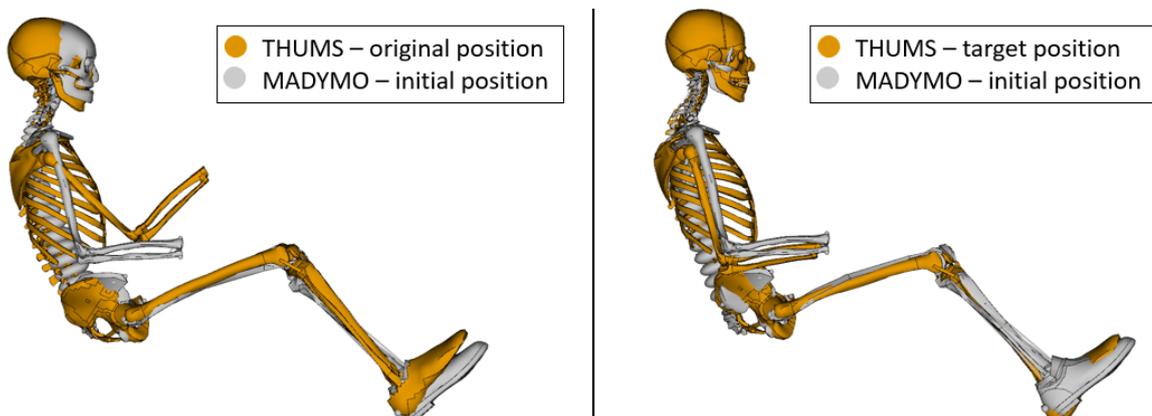


Figure 3-47: THUMS original (left) positioned to MADYMO initial position (right)

The resulting new geometry of the THUMS model is then used to generate and calculate the impressed motion using the OSCCAR Transition-Tool.

- **Imprinting of the extracted motion on the positioned THUMS:**

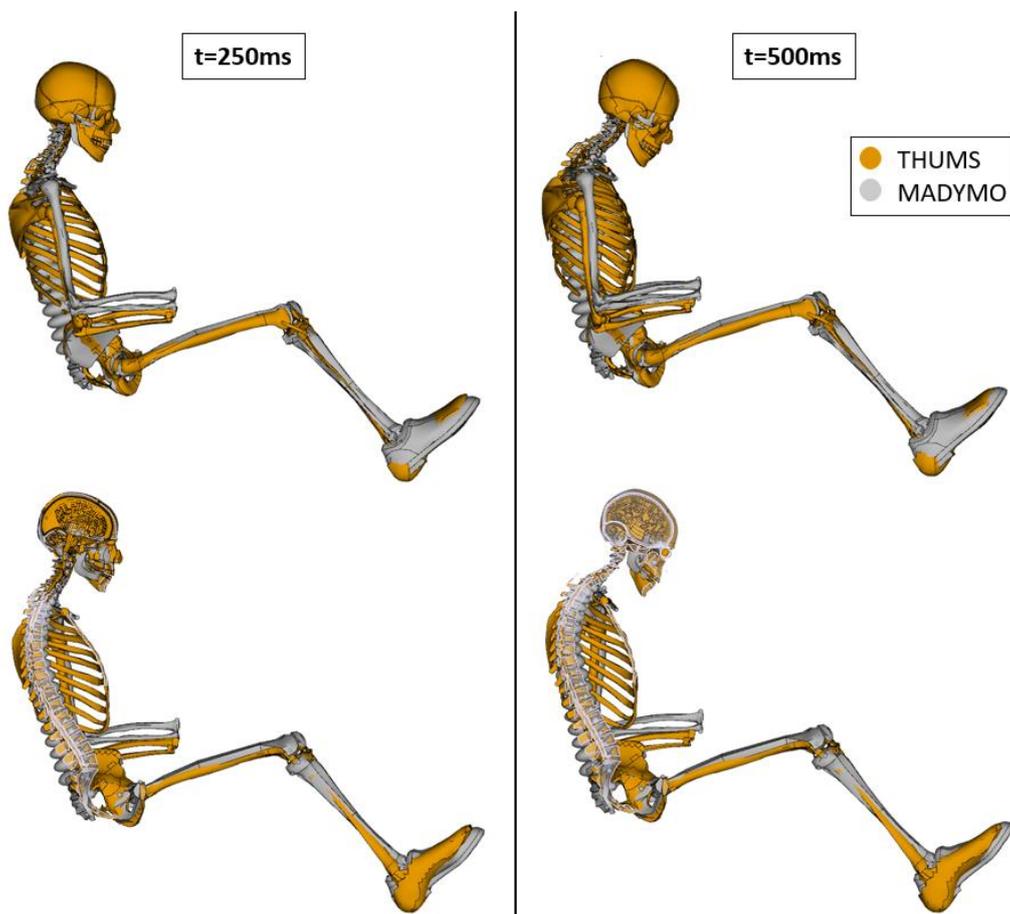
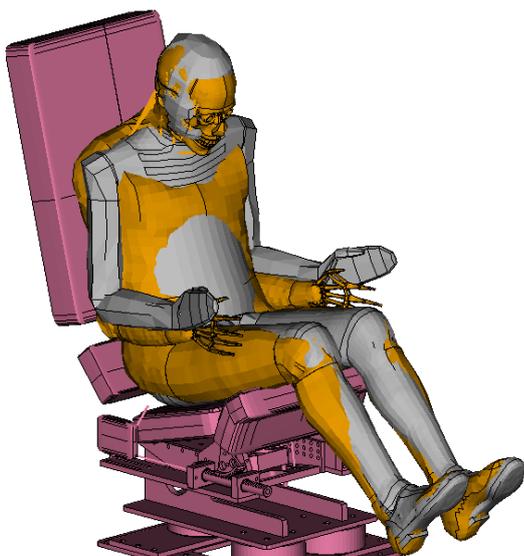


Figure 3-48: Skeleton comparison THUMS and MADYMO at 250ms and 500ms (full display on top; sectional display at bottom)

The motion is properly scaled and imprinted on the anthropometry of the THUMS.



At the technically interesting time range at the end of the motion ($t=500\text{ms}$) the THUMS model correctly fulfills the predefined position.

Deviations in the shoulder area are due to the anthropometry of the THUMS V3 AM50.

Figure 3-49: THUMS overlaid on MADYMO simulation at the end of the pre-crash phase

3.4 Assessment

3.4.1 DYNASAUR

DYNASAUR (Dynamic simulation analysis of numerical results) is an open source postprocessing tool for data analysis of simulation results which was launched by the Vehicle Safety Institute of TU Graz. It has been published prior to OSCCAR, but further enhanced within the project. It is a python3 library (<https://pypi.org/project/DYNASAUR/>), it can be directly installed with the Package management system pip and the source code is hosted on gitlab.com (<https://gitlab.com/VSI-TUGraz/DYNASAUR>)

The library was designed to extract major quantities from FE simulation results in an easy manner and its basic structure is shown in Figure 3-50:

The basic structure of DYNASAUR:

- DYNASAUR reads the output from the binary simulation files.
- The two classes *CriteriaController* and *DataVisualizationController* build the main interface for the assessment. For the first one, the final result is a single value while the output of the second one is a two-dimensional data matrix (e.g. time series).
- Calculation procedures using standard-functions are defined in a specific definition file (*calculation_procedures.def*) to evaluate simulation results. As these files can be shared among partners and are independent of the code and model, they push forward harmonization of postprocessing procedures.
- The HBM specific definition file *object.def* is needed to translate IDs from the simulation model to DYNASAUR objects and definitions (e.g. part IDs 990000-990000 represent the object “brain” which is used in the *calculation_procedures.def* to define which elements should be considered for a CSDM calculation).
- The output of DYNASAUR are .csv files which contain criteria and data channels.
- For further visualizations, the tool “MUTANT”²⁴ can be used. Mutant allows to easily filter simulation results based on input settings or outputs. Furthermore, different criteria can be combined to group assessments^{25,26}.

Further information on both tools and user manuals and tutorials are available on gitlab²⁷ and are regularly updated.

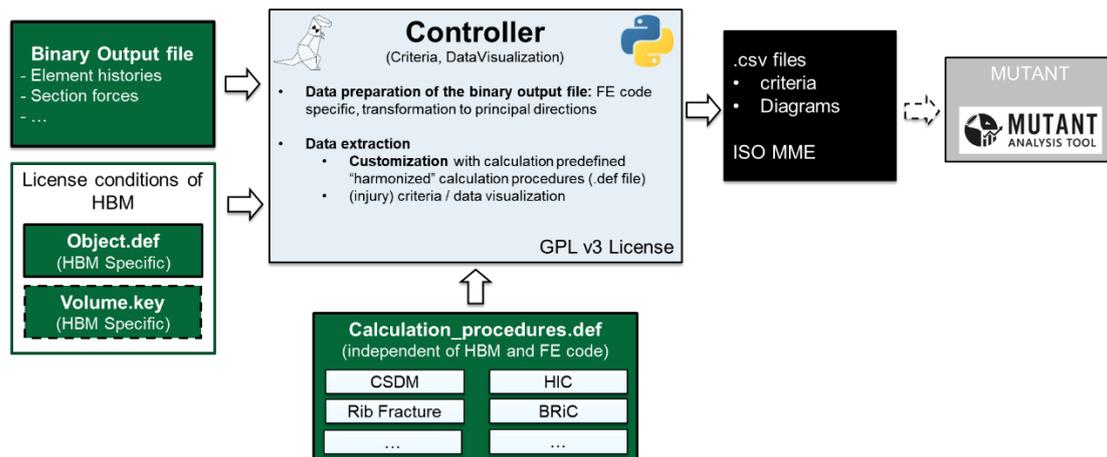


Figure 3-50: DYNASAUR structure

The developments listed in chapter 3.4.1.1, 3.4.1.2 and 3.4.1.3 have been performed within OSCCAR.

3.4.1.1 Input Routines

DYNASAUR was originally developed as postprocessing tool for LS-DYNA with specific focus on Human Body Models. To allow users to use DYNASAUR also as postprocessor for MADYMO and VPS simulations, new input routines were developed within OSCCAR.

The input routines prepare the datasets from the different codes in a harmonized format, so that the same assessment controllers can be applied independent of the original output format.

3.4.1.2 Scripting and structure of definition files

DYNASAUR was modified such that the postprocessing procedures can be run automatically without requiring the use of the GUI within OSCCAR. This enables a more time-efficient, repeatable, reproducible and harmonized evaluation for the users.

In order to configure what should be extracted, the user has the possibility to create *definition files* (.def). Definition files contain information about parts and their assignment to corresponding objects as well as calculation procedures. Definition files are structured as JSON files. JSON is commonly used as readable data exchange format (similar to XML) and its syntactical correctness can be checked easily.

The structure of the DYNASAUR input files was adjusted, such that the calculation procedures can be shared among the partners within the restrictions of the license agreements of the specific models. Therefore, **object definition** and **calculation procedures** are defined in two separated files, which enhances reusability and standardization.

Furthermore, easy-to-use standard functions were implemented in OSCCAR and additional types of outputs were added. Quality criteria defined in the Euro NCAP TB024 v2.0 were implemented into DYNASAUR to allow the users to perform a harmonized automatic quality check of the simulation results e.g. check of mass scaling, energy balance, contact forces, ...).

3.4.1.2.1 Object Definition

The object definition file contains information about the simulated models and defines identifiers which are further used within the calculation routines. Such as "objects". An object can be used to group parts. Associated parts can be defined with their ID from the LS-DYNA model. The "OBJECTS" entry is a list of JSON objects which are defined by "type", "name" and "id". Examples for types are node, object, contact, element, discrete, cross_section, seat_belt, energy_part, energy_global) and are independent of the code. However, not all types are available in all codes. The current status can be found here: <https://gitlab.com/VSI-TUGraz/DYNASAUR/-/wikis/Types> The name of an DYNASAUR Object ("name") can be freely chosen by the user and are further used as identifier for the input of the calculation procedures. The "id" entry contains a list of ids, which are associated with the object.

In the following listing, the file structure is outlined exemplary, where a node ID, which represents the head CoG, a part ID which represents the skull and a contact ID which represents the contact between the head and the airbag is defined.

```
{
  "OBJECTS" : [
    {
      "type" : "NODE",
      "name" : "head CoG",
      "id" : [1200011]
    },
    {
      "type" : "OBJECT",
      "name" : "skull",
      "id" : [1200012]
    },
    {
      "type" : "CONTACT",
      "name" : "contact between head and airbag",
      "id" : ["1111114s", "1111114m"]
    }
  ]
}
```

3.4.1.2.2 Calculation Procedure Definition File

The postprocessing procedures (i.e. what should be extracted and which calculations are performed for the respective DYNASAUR objects) itself are defined within the calculation procedure definition files. Therefore three definition sections can be used:

- UNIT: The "UNIT" entry defines which units have been used within the simulation
- CRITERIA: The "CRITERIA" entry contains the declaration of different quantities, i.e. single values that are calculated for the whole simulation, such as injury criteria. Each declaration is defined by a "name" and further entries, which define meta information about the quantity as well as the actual calculation procedure and is structured in 5 parts:
 - First of all, a name for the criterion has to be defined (e.g. "name": "MaxShearForce").
 - Then the type of the criterion has to be defined (e.g. "type_of_criteria" : "kinematic"). Five different types are currently available: "injury" , "kinematic" , "load", "metadata", "energy"

- The "part_of" entry indicates a (body) part to which the quantity is assigned. "part_of" + "name" build a unique which can be used to calculate the particular quantity with the use of the Assessment Controller identifier (e.g. "part_of": "HEAD").
- The "limits" entry is optional and can be used for the assessment with Mutant (e.g. "limits" : [1,2,3]). It contains a list of three entries which indicate threshold of the quantity for best, marginal and poor performance.
- The "function" entry indicates the definition of the calculation procedure. The following listing outlines an example, in which the maximum acceleration in x direction of a node element is calculated.

```
"function": {
  "name": "max",
  "param": {
    "data_vector": {"type": "NODE", "ID": "Neck_node", "array":
["(0, x_acceleration)"]},
  }
}
```

- The "name" entry of the "function" object, points to an underlying python implementation.
 - The entries of the "param" object depends on the used function for the calculation. In general, arbitrary functions can be used and plugged together.
 - In the definition of the data vector, "type" refers to the data type (e.g. "ELEMENT", "NODE", etc.).
 - The ID is an internal identifier that refers to the *object definition file*.
 - The array contains components that have to be extracted from the specified ID (e.g. acceleration from the node history)
- DATA VISUALIZATION is used to define two dimensional matrices (e.g. acceleration as a function of time). Declarations work similar as for the CRITERIA section. A "part_of" entry as well as "x" and "y" entries have to be defined. "x" and "y" entries determine the data channels, which can be defined through functions. A basic structure is outlined below:

```
{
  "DATA VISUALIZATION": [{
    "name": "NIC_time",
    "part_of": "NECK",
    "y" : {"function": {...}},
    "x" : { "type": "NODE", "ID": "Head", "array": ["(0, time)"]}
  }]
}
```

3.4.1.2.3 Standards Functions

Several standard-functions which are widely used in the area of vehicle safety were included in DYNASUR and can be now used in the definition file to evaluate simulation results. An overview of the implemented functions is given in Table 5. The calculation procedures will be further refined until the end of the OSCCAR project.

Table 5: DYNASAUR standard functions

Basic calculations	DYNASAUR Function name	(Dummy) Injury criteria	DYNASAUR Function name
CFC filters	CFC	Head Injury Criterion	HIC15, HIC36
Resultant	res	Brain Injury Criterion	BrIC, uBRIC
Absolute	Abs (can be also used with other functions as prefix [abs])	Cumulated acceleration	a3ms
Offset	transform2origin	Neck Injury Criteria	NIJ, NIC
Maximum	[abs]max	Viscous Criterion	VC
Minimum (min)	min	Tibia Index	TIBIA_INDEX
Multiplication (mult)	mult		
Subtract	[abs]sub		
Addition	[abs]add		
Differentiate	central_differences		

3.4.1.2.4 Plugins for HBM Injury Assessment

The current version of DYNASAUR includes three different plugins, which have been specifically developed for the analysis of tissue-based injury criteria in Human Body Models.

- Rib fracture assessment based on Forman et al., 2012²⁸: `forman_rib_criteria`
- Age-dependent probabilistic assessment of specific number of risk fractures
- Stress or Strain analysis of DYNASAUR “objects”²⁹: `object_data`
 - Calculation of values in principal direction
 - Calculation of specific percentiles
 - Calculation of tension and compression separately
 - Calculation of number of elements that exceeds a specific limit
 - Calculation of equivalent von Mises stresses
- Cumulative Strain Damage Measure (CSDM) Analysis
 - Calculation of volume of elements that exceeds a specific threshold
 - Volume.key file needed for these type of analyses

As validation example, one simulation of the Strasbourg University FE Head Model (SUFEHM), was postprocessed once using DYNASAUR and once using the IRA tool (Injury Risk Assessment) of Uni Strasbourg. The IRA tool is dedicated exclusively to extract the brain injury risk from SUFEHM

(Strasbourg University Finite Elements Head Model) developed by Deck et al 2008³⁰ and Sahoo et al. 2013³¹.

The SUFEHM, shown in Figure 3-51 is a numerical model of the human head including realistic brain and skull material laws and permits the computation of the mechanical brain response to an impact. Validation of this head model was proposed by Deck and Willinger (2008, 2009)³² against local brain motion data from Hardy et al. (2001, 2007)^{33,34} as well as intracranial pressure data from Nahum et al. (1977)³⁵ and Trosseille et al. (1992)³⁶. In addition to the model validation, 109 real-world head trauma cases were simulated with this head model to derive brain injury criterion in terms of intracerebral Von Mises stress to predict moderate neurological injuries or short coma. Based on an in-depth statistical analysis of different intra-cerebral parameters, it was shown that brain Von Mises stress was the most appropriate metric to predict short loss of consciousness also called moderate diffuse axonal injuries (mDAI). The proposed brain injury tolerance limit for a 50% risk of mDAI, which corresponds to a loss of consciousness known to be reversible brain injury, has been established at 37 kPa (Deck et al, 2009³⁷, Deck et al. 2019³⁸).

The same strain values and injury risk curves were derived from the simulation with both tools, which is shown in Figure 3-52 and Figure 3-53.

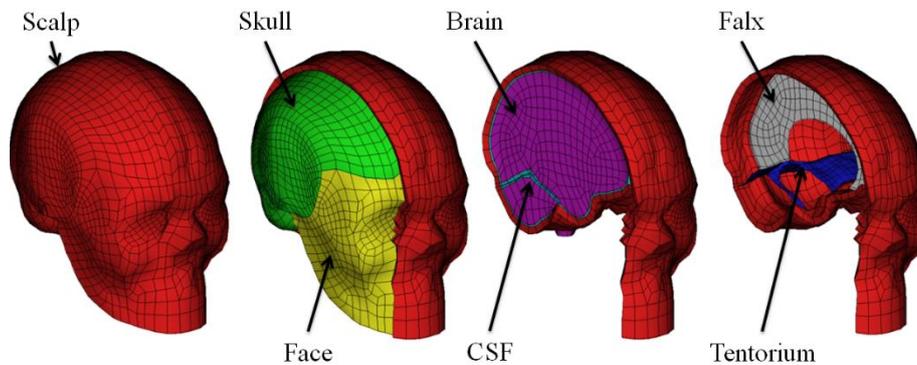


Figure 3-51: The Strasbourg University finite element head model (SUFEHM)

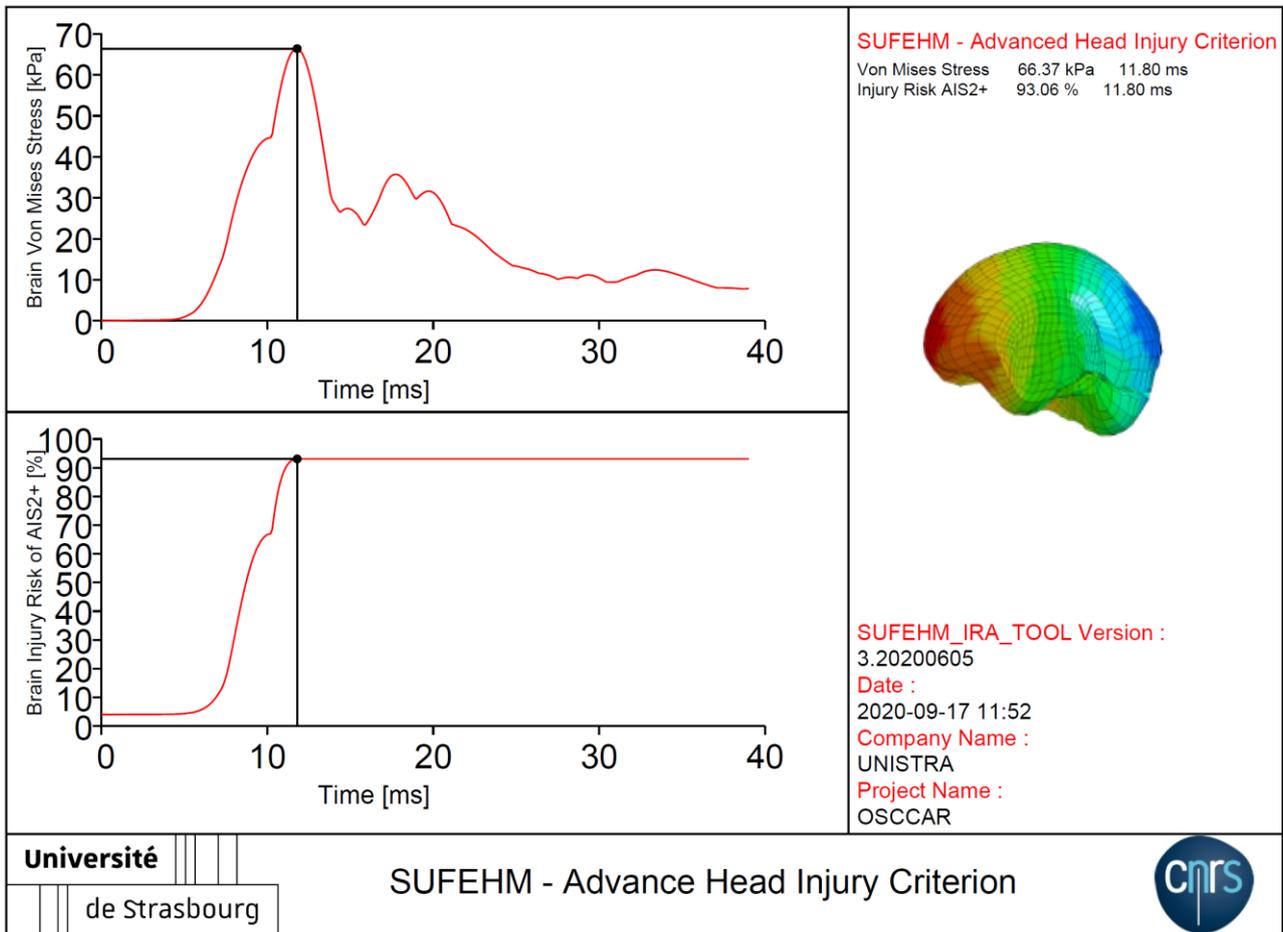


Figure 3-52: SUFEHM result using IRA tool

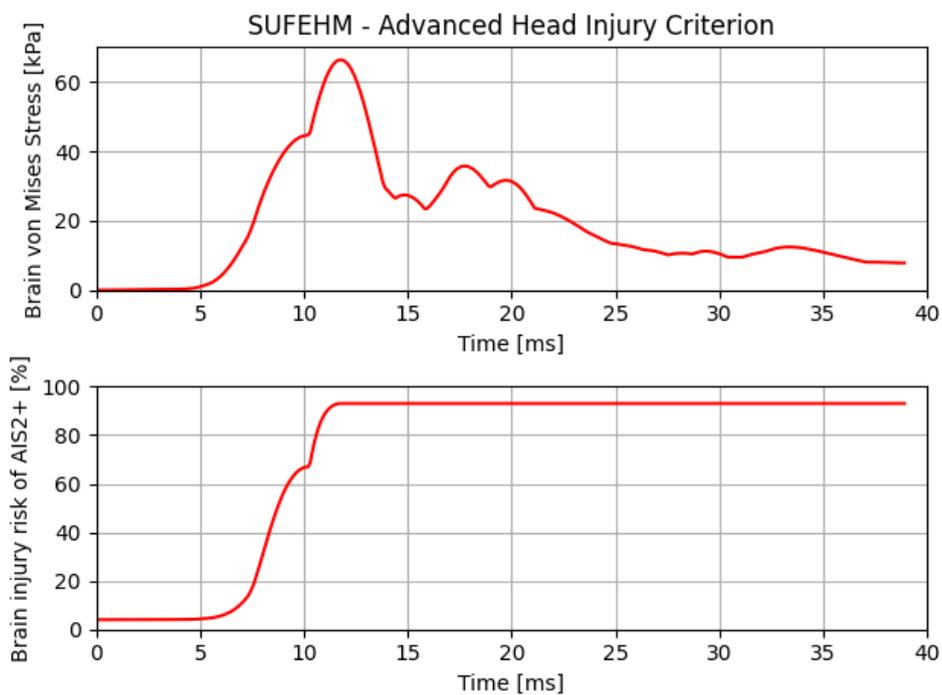


Figure 3-53 SUFEHM result using DYNASAUR (max. v.M. stress=66.37 kPa → 93.06% AIS 2+ risk)

3.4.1.2.5 Simulation quality criteria

Additionally to injury criteria or kinematic outputs, also quality criteria for the evaluation of the overall plausibility of the simulation can be assessed (also see Deliverable 4.1)

The following outputs have been prepared in the OSCCAR postprocessing routines so far:

- Data visualisation (time history)
 - Total Energy
 - Internal Energy
 - Hourglass Energy
 - Added Mass
 - Timestep
- Criteria:
 - Hourglass Energy / Internal Energy
 - Max (Total Energy) / Min (Total Energy)
 - Max (Hourglass Energy)
 - Max (Added Mass)
 - Max (Added Mass in Percent of total mass)

Additional criteria can be easily added to the shared calculation_procedure.def file.

3.4.1.2.6 Script file

Within the script file, the CriteriaController and the VisualizationController as well as the initialisation of the corresponding input is executed.

When initializing the controller object, the location of the binary data (data_file) as well as the definition file locations (calculation_procedure_def_file, object_def_file) have to be provided. A volume_def_file is optional but needs to be present if the CSDM value is calculated. Further, additional functions, other than standard implementations, can be defined and passed as an object to the controller. Further information can be found here.

The following section is an example of how the CriteriaController can be used:

```
from DYNASAUR.plugins.criteria_controller import CriteriaController as CC

crit_ctrl = CC(calculation_procedure_def_file="\calc_proc.def",
               object_def_file="\object.def",
               data_source="\binout",
               code_type="LS-DYNA",
               user_function_object=None,
               volume_def_file=None)
```

After the initialization, the calculation procedures which should be applied on the specific dataset are defined. E.g.:

```
crit_ctrl.calculate({'criteria': 'HEAD_HIC15', 't_start':0.2,
                    't_end': 200.0})
```

The optional parameters 't_start' and 't_end', can be used to crop the data in certain time ranges. Values for 't_start' and 't_end' should be set according to the unit definition.

The CriteriaController object has a member, defined as data. It contains the values which were calculated before.

```
crit_ctrl.data
```

A further option is to use the method write_csv(self, directory, filename) which generates a CSV file of the calculated values. The filename is optional. If undefined, the file is written out as "CRITERIA_YYYY-MM-DD-hh:mm:ss.csv"

```
directory = "/path/to/directory"
filename = "criteria.csv"
crit_ctrl.write_CSV(directory, filename)
```

3.4.1.3 Outputs

The type of output is defined in the script file as explained above.

Additionally to the csv output, a direct output into ISO MME files was enabled. Therefore, once outputs are fixed and harmonized within OSCCAR, output files can be created, which can be easily exchanged and understood by other partners due to a harmonized output format.

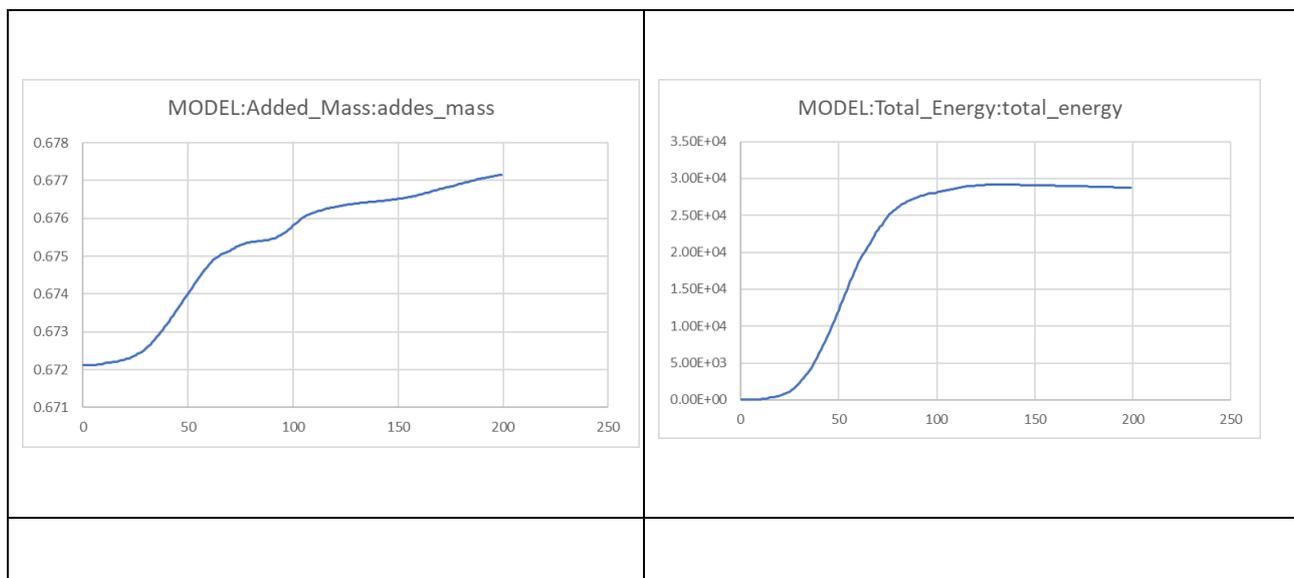
The exported csv files can be used for further processing and plotting (e.g. with MUTANT).

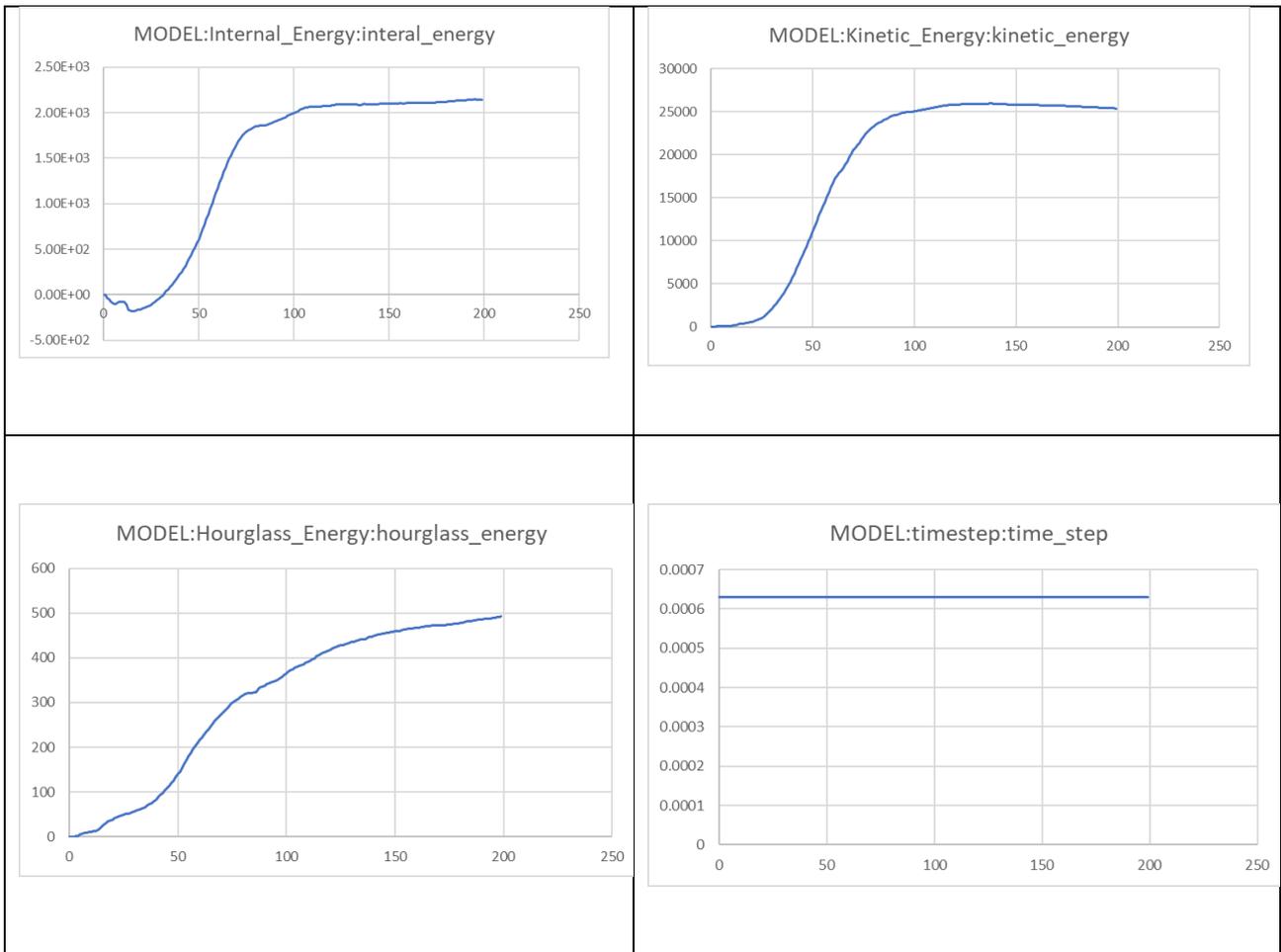
3.4.2 Application example

Besides the coordinates of defined landmarks and the calculation of defined injury risk indicators, Dynasaur also exports simulation criteria to indicate quality problems within a simulation (see Paragraph 3.4.1.2.5). These criteria are time series of total energy, internal energy, hourglass energy, kinetic energy, added mass and timestep.

Additionally, single criteria values are exported of the maximum increase of the total energy, the maximum added mass and the maximum hourglass energy.

Following diagrams show exemplarily these criteria for a 48° reclined simulation.





4 DISSEMINATION, EXPLOITATION AND STANDARDISATION

The developed tools for HM positioning and kinematic transition will be released open source under a GPL v3 license. The link will be available on the OSCCAR homepage³⁹. Further it is planned to publish the developed positioning and transition method at conferences or journal publications.

Standardization topics like a harmonized landmark list, which were developed in close cooperation with Work package 5 in OSCCAR are still part of an ongoing discussion and will be disseminated in WP5 context and respective public deliverables.

All updates of DYNASAUR that are described in the current report are publicly available on gitlab, acknowledging funding from OSCCAR: <https://gitlab.com/VSI-TUGraz/DYNASAUR>

The developed tools will be used by the involved partners to execute the homologation test case which is foreseen to be shown in Deliverable 4.3.

5 CONCLUSIONS, ISSUES AND NEXT STEPS

Conclusion

This report demonstrates the developed tools (see chapter 3.2.4, 3.3.3 and 3.4.2), methods, and definitions to establish an integrated virtual assessment framework for advanced protections systems for future sitting positions. Figure 5-1 shows how the tools and methods are directly linked within the toolchain with inputs from other tasks.

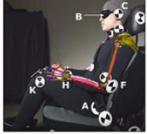
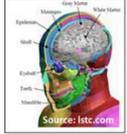
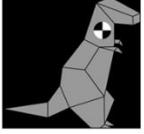
	Quality check	Positioning	Pre-Crash Phase	Transition	In-Crash Phase	Assessment
						
OSSCAR activity	Check list / tool Task 4.1	Positioning tool & method Task 4.2.1	Active models Task 3.3	Transition tool Task 4.2.2	Enhanced HBMs Task 3.2	Harmonized assessment based on DynaSaur tool Task 4.2.3

Figure 5-1: Task 4.2 activities and inputs from other tasks

In detail, following tools and methods were developed.

- **Definition of a common landmark list**

To enable the common positioning of (FE) HBMs and (MB) AHM a list of landmarks was defined, which can be found in both kind of models and which describes the posture of the HBMs. A standardized naming for the landmarks will be published by WP 5 in OSCCAR.

- **Development of a model and tool independent FE HBM positioning tool which is applicable for LS-Dyna and VPS**

A script which allows a reproducible settling simulation, by using the FE solver was developed. The script is executable in Piper⁴⁰ and provides a GUI for simple usability. Piper is a free HBM pre-processor, which was developed in another EU funded project. The positioning script computes the trajectories, which are necessary to pull the HBM from its original position to its target position and creates the necessary FE input file for LS-Dyna or VPS.

- **Development of a positioning method towards standardization of AHM positioning procedures**

A 10-step procedure was developed that guides the user in positioning the AHM. The method makes use of define based positioning allowing for quick and intuitive posture modifications. Parameterized spine positioning with two user slouch parameters is embedded to obtain well-distributed spine postures without the need for setting each vertebra angle individually.

Landmarks defined for use in positioning were implemented for the AHM and can be added to the model when needed for performing a positioning procedure where target landmarks are available.

- **Development of a model and tool independent FE HBM kinematic transition tool applicable for LS-Dyna and VPS**

The developed tool enables the transfer of a movement from one HM to another HM (with similar anthropometry). More precisely, the movement is recorded using landmarks and imprinted on the desired HM. For each time step of the motion sequence the principle of anthropometric scaling (explained in detail in Appendix A) is applied. This ensures that the movement is geometrically possible and that the corresponding position and velocity of all body parts are identical at the end of the movement.

The tool runs as a script in PIPER and has a GUI for ease of use. The output of the script consists of FE input files either in LS-Dyna or in VPS code.

- **Enhancement of the open source Software DYNASAUR**

DYNASAUR was enhanced so that it can be applied on results from multiple codes, postprocessing scripts can be shared among different users and therefore harmonisation is improved. Furthermore, several standard functions were included, and it was implemented as python library, so that the installation and application is much more user-friendly than before. As a next step, user acceptance and experience will be evaluated within the homologation loadcase. Furthermore, the harmonised injury criteria developed in WP3 and 5 will be implemented in the upcoming months of the project and the tool will be further enhanced based on user feedbacks until the end of the project.

Issues

All main goals were reached in Task 4.2. At present some minor issues stays open until the end of the project or for further research.

- **Common landmark names**

The mentioned list of anatomical landmarks is not named harmonized yet. That open point will be done by WP 5.

- **Anthropometric adaption of coordinates**

HMs were positioned to the (anthropometric) adapted coordinates of PMHS. The adaption of the coordinates assumes, that the model and the PMHS anthropometry does not differ too much. The method worked for the existing data and models, but the limits for that method (concerning anthropometric difference) were not investigated.

- **Basic principle for positioning and kinematic transition**

As demonstrated in this deliverable it was decided to position certain HM parts either to the equal angles or equal positions as the target data (PMHS in this case). These two options can be realized in the developed tool. It was not investigated, if any other “best fit” criteria would lead to better results.

Next steps

This deliverable presents the developed method and tools and includes an application example to demonstrate the correct function. The application of the developments of T 4.2 and the further steps are listed in the following paragraphs.

- **Application in Task 4.3.1 “Demonstration of a homologation scenario”**

The developed tools and methods from T 4.2 will be applied to execute a homologation scenario. Therefore, all participated partners will use the same environment model and execute occupant simulations under the same boundary conditions for a pre- and in-crash

scenario with their human models. To ensure similar initial conditions (sitting positions), a harmonized kinematic hand over from pre- to in-crash and a harmonized assessment the developed methods will be applied by the partners.

- **Application in Task 4.3.2 “Overall impact demonstration”**

To demonstrate the overall impact, the complete toolchain which was developed in OSCCAR needs to be applied for new sitting position scenarios. That includes the outcome of all OSCCAR work packages and demonstrates the benefit of HBMs and shows the overall impact of new sitting positions. The contribution from WP4 to this demonstration is the toolchain covering harmonized sitting positions, a method for kinematic transition and a harmonized assessment.

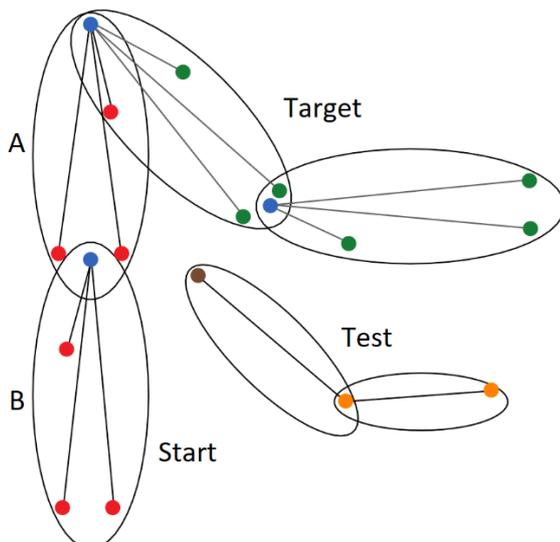
A. ANTHROPOMETRY SCALING

To apply the same trajectories onto different HMs the trajectories must be adapted according to the target HMs anthropometry. This is achieved using the `test_data_to_target` python script of the Positioning repository. It takes a file containing test data (e.g. from a volunteer test) as an input and outputs a Piper target file containing the appropriate target positions that only fit the HM that has been loaded inside Piper.

TERMS AND DEFINITIONS

There are a few core classes that make up all the data structures of the script.

- **Vector**
This is a representation of a 3D Vector. There are some utility methods as well as some overloaded operators to ease the use in the script. Important here is that all the methods are call by value since the script often copies Vectors.
- **Point**
This is a representation of a landmark. It consists of three Vectors:
 - **Start**
The position at beginning of the simulation. This is also the current position of the landmark of the HM.
 - **Target**
The position at the end of the simulation
 - **Test**
The position from the test data file
- **Bone**
The biggest class of this script is the Bone class. As the name suggests it represents a bone. Not a real bone of the HM but a virtual one. The most important parts of this class are these lists of Points. All Points need to refer to a certain Landmark in the HM:



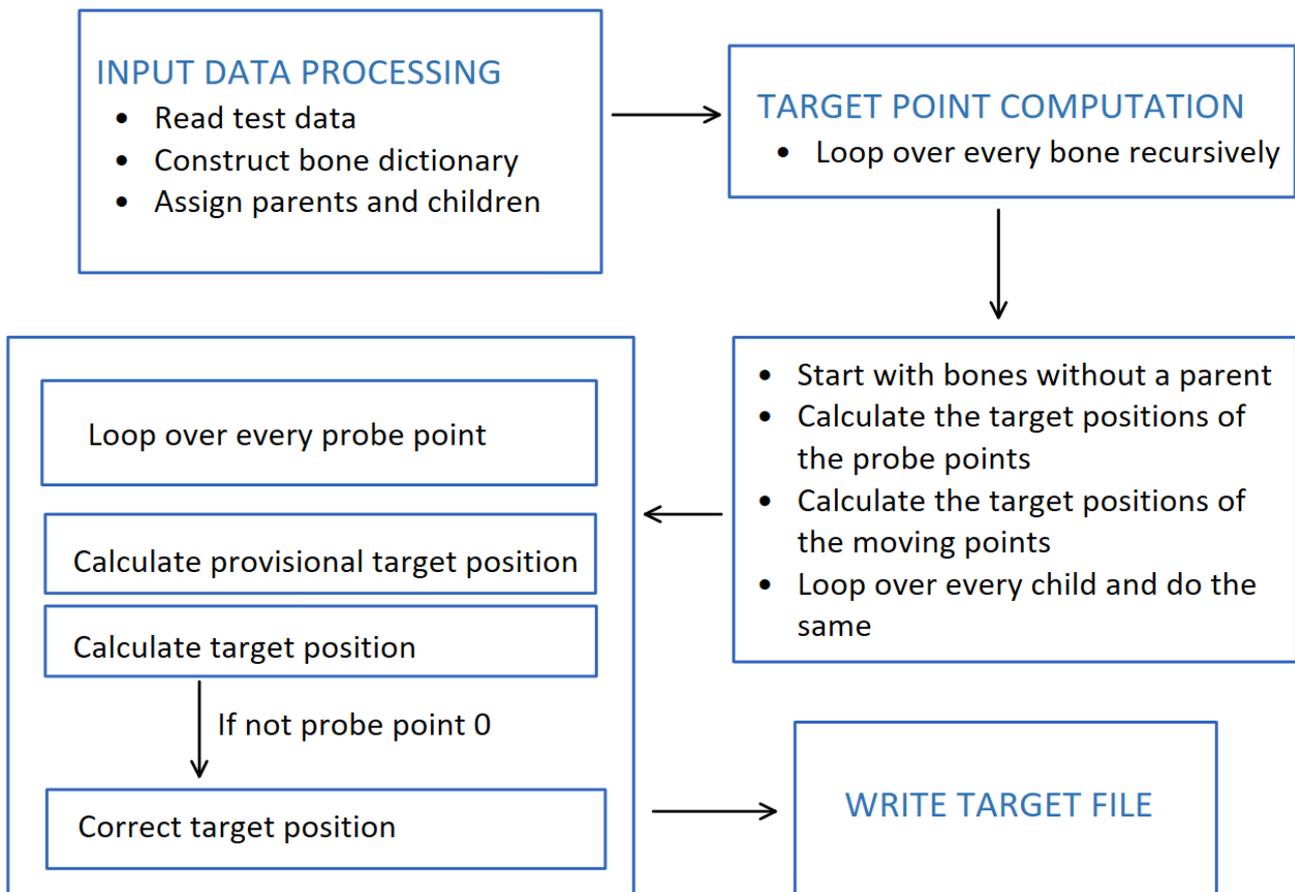
- **Probe points (start, target, test)**
These are the moving points that are found inside the provided test data file.
- **Base points (start, target, test)**
These are the points that make up the rotation center of the bone
- **Calculation base points**
This list is the same as the base point list, so it also contains the rotation center of the bone. But its elements are only taken from the probe points list of the parent.
- **Moving points (start, target)**
In this list are all moving points of the bone. The probe points are included as well. They are called like that since these are the points which will move in the simulation by rotating them around the base point.

In this figure two bones (A and B) are shown. B is a child of A and their target positions will be calculated based the provided test data.

The colors of the figures are consistent throughout this section.

- Start and target position of the base points
- Start positions of the moving points
- Target positions of the moving points
- Test position of the base points
- Test position of the probe points

OVERVIEW



INPUT DATA PROCESSING

At the start of the script the test data will be read and a dictionary containing bones and their respective names as keys will be created. Bones can have a parent and multiple children.

When a bone is a parent of another bone it means that this bone is connected to the other one. More specifically it means that the moving points of the parent will be used as base points for the child. If more than one moving point is available, the mean of the first two moving points will be used.

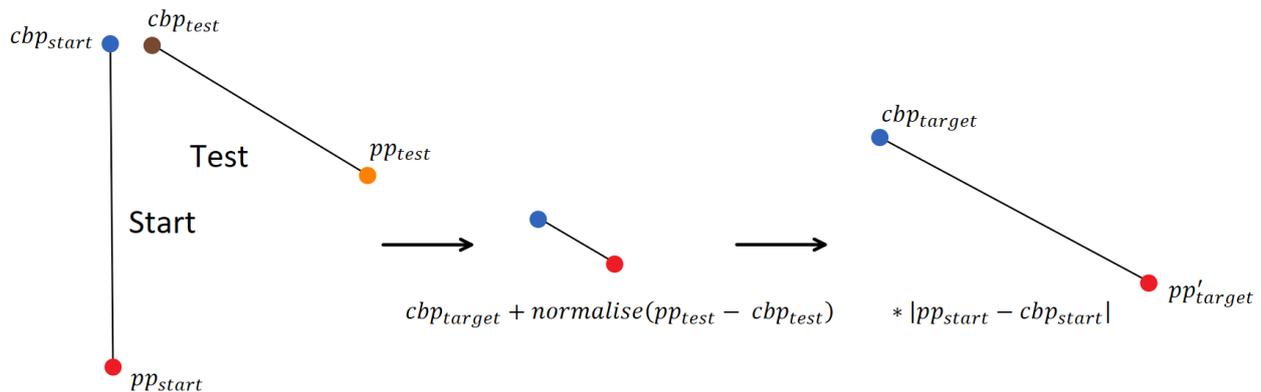
After the construction of the dictionary the target points are calculated. The method is called for every bone without a parent and it is called recursively for every child. In this method the scaling of the anthropometry happens.

TARGET POINT COMPUTATION

CALCULATE PROVISIONAL TARGET POSITION

$$pp'_{target} = cbp_{target} + normalise(pp_{test} - cbp_{test}) * |pp_{start} - cbp_{start}|$$

- pp'_{target} Provisional target position of the probe point that is currently being calculated
- cbp_{target} The target position of the calculation base point
- pp_{test} The test data position of the probe point that is currently being calculated
- cbp_{test} The test data position of the calculation base point
- pp_{start} The start position of the probe point that is currently being calculated
- cbp_{start} The start position of the calculation base point
- $normalise$ This is the unit vector $\frac{v}{|v|}$



This is the core formula that does the scaling of the anthropometry. The unit relative vector from the test position of the calculation base point to the test position of the probe point is scaled by the length of the relative vector between the start position of the calculation base point and the start position of the probe point. This scaled vector is then added to the target position of the calculation base point. The target point of a base point is equal to the start position if the bone does not have a parent since it does not move.

CALCULATE TARGET POSITION

$$pp_{target} = bp_{target} + normalise(pp'_{target} - bp_{target}) * |pp_{start} - bp_{start}|$$

- bp_{target} The target position of the base point
- bp_{start} The start position of the base point

This formula is only relevant if the calculation base point is not equal to the base point. This is only the case when there are less landmarks inside the test data file than there are moving points defined inside the kinematic linkage definition of a bone. The target position of the probe point gets corrected so that the distance between it and the base point is the same between start and target.

The order of the probe points is important. The first two points define the rotation of the bone. All other probe points will be ignored and calculated based on the distance to the first two probe points and the base point.

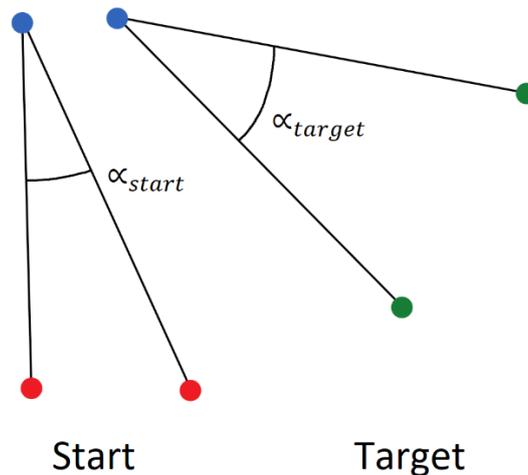
CORRECT TARGET POSITION 1

If there is a second probe point, the target position of the first one and the second one will be corrected. Otherwise the distance between them would be too long or too short. To do this the following algorithm is executed.

$$\alpha_{start} = \text{angle}(pp_{start} - bp_{start}, pp_{0_{start}} - bp_{start})$$

$$\alpha_{target} = \text{angle}(pp_{target} - bp_{target}, pp_{0_{target}} - bp_{target})$$

- α_{start} The angle between the relative vector from the base point to the probe point and the relative vector from the base point to the first probe point at the start of the simulation
- α_{target} The angle between the relative vector from the base point to the probe point and the relative vector from the base point to the first probe point at the end of the simulation
- $pp_{0_{start}}$ The start position of the first probe point
- $pp_{0_{target}}$ The target position of the first probe point



The angle gets calculated as follows.

$$\alpha = \cos^{-1} \frac{v_1 \cdot v_2}{|v_1| |v_2|}$$

Then a rotation matrix gets calculated based on the difference between α_{start} and α_{target} .

$$axis = \text{normalise} \left(\text{cross} \left(\text{normalise}(pp_{target} - bp_{target}), \text{normalise}(pp_{0_{target}} - bp_{target}) \right) \right)$$

$$matrix_0 = \text{rotation_matrix} \left(axis, -\frac{\alpha_{target} - \alpha_{start}}{2} \right)$$

$$matrix = \text{rotation_matrix} \left(axis, \frac{\alpha_{target} - \alpha_{start}}{2} \right)$$

- $axis$ The unit vector perpendicular to the plane of $pp_{target} - bp_{target}$ and $pp_{0_{target}} - bp_{target}$
- $matrix_0$ A rotation matrix that rotates $pp_{0_{target}} - bp_{target}$ towards $pp_{target} - bp_{target}$ by $\frac{\alpha_{target} - \alpha_{start}}{2}$
- $matrix$ A rotation matrix that rotates $pp_{target} - bp_{target}$ towards $pp_{0_{target}} - bp_{target}$ by $\frac{\alpha_{target} - \alpha_{start}}{2}$

The rotation matrix is calculated as follows.

$$a = \cos\left(\frac{\alpha}{2}\right)$$

$$b = -\left(a_x * \sin\frac{\alpha}{2}\right)$$

$$c = -\left(a_y * \sin\frac{\alpha}{2}\right)$$

$$d = -\left(a_z * \sin\frac{\alpha}{2}\right)$$

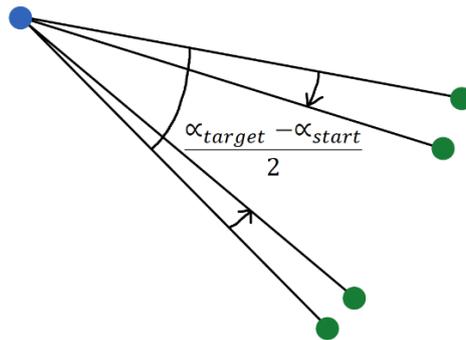
$$matrix = \begin{matrix} a^2 + b^2 - c^2 - d^2 & 2 * (b * c + a * d) & 2 * (b * d - a * c) \\ 2 * (b * c - a * d) & a^2 + c^2 - b^2 - d^2 & 2 * (c * d + a * b) \\ 2 * (b * d + a * c) & 2 * (c * d - a * b) & a^2 + d^2 - b^2 - c^2 \end{matrix}$$

- a_x The x value of *axis*
- a_y The y value of *axis*
- a_z The z value of *axis*
- α The angle of the rotation

The rotation matrices are applied as follows.

$$pp_{0target} = bp_{target} + matrix_0 * (pp_{0target} - bp_{target})$$

$$pp_{target} = bp_{target} + matrix * (pp_{target} - bp_{target})$$



Target

Now distances between the first two probe points and the distances between the first two probe points and the base point stays the same.

CORRECT TARGET POSITION 2

If there are more probe points, its target positions will be calculated using a trilateration algorithm. The positions are determined according to the distance between each one and the first and second probe point and the base point at the beginning of the simulation. The following algorithm is also used to calculate the target positions of the moving points.

$$r_1 = |pp_{start} - bp_{start}|$$

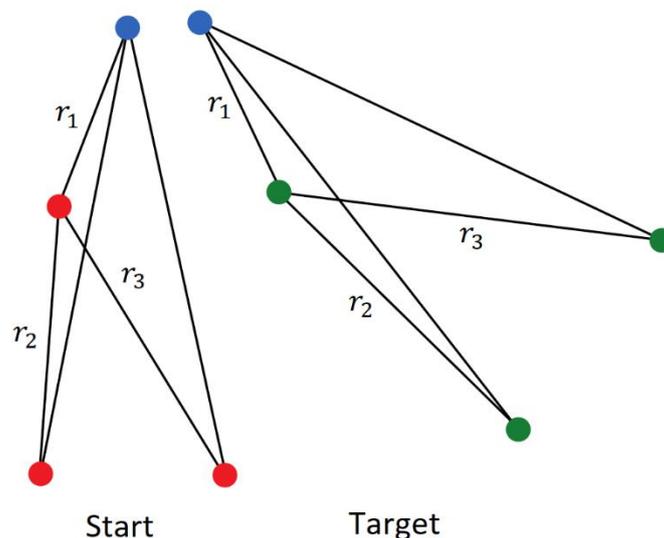
$$r_2 = |pp_{start} - pp_{0_{start}}|$$

$$r_3 = |pp_{start} - pp_{1_{start}}|$$

- $pp_{1_{start}}$ The position of the second probe point at the start of the simulation
- r_1 The distance between the probe point and the base point at the beginning of the simulation
- r_2 The distance between the probe point and the first probe point at the beginning of the simulation
- r_3 The distance between the probe point and the second probe point at the beginning of the simulation

$$pp_{target_{12}} = trilaterate (bp_{target}, pp_{0_{target}}, pp_{1_{target}}, r_1, r_2, r_3)$$

- $pp_{1_{target}}$ The target position of the second probe point
- $pp_{target_{12}}$ Two possible target positions of the probe point



The trilateration algorithm works as follows.

$$\begin{aligned}
 e_x &= \text{normalise} \left(pp_{0_{target}} - bp_{target} \right) \\
 i &= e_x \cdot \left(pp_{1_{target}} - pp_{0_{target}} \right) \\
 e_y &= \text{normalise} \left(\left(pp_{1_{target}} - bp_{target} \right) - e_x * i \right) \\
 e_z &= \text{cross}(e_x, e_y) \\
 d &= \left| pp_{0_{target}} - bp_{target} \right| \\
 j &= e_y \cdot \left(pp_{1_{target}} - bp_{target} \right) \\
 x &= \frac{r_1^2 - r_2^2 + d^2}{2 * d} \\
 y &= \frac{r_1^2 - r_3^2 + i^2 + j^2}{2 * j - \frac{i}{j} * x} \\
 z &= \sqrt{r_1^2 - x^2 - y^2} \\
 pp_{target_1} &= bp_{target} + e_x * x + e_y * y + e_z * z \\
 pp_{target_2} &= bp_{target} + e_x * x + e_y * y - e_z * z
 \end{aligned}$$

- The \cdot is a dot product.

Now that there are two solutions the right one must be chosen. The decision is based on the distance between the target position that it would have had if it had been rotated as usual and the two solutions. The one that is closer to this position will be chosen.

$$\begin{aligned}
 \alpha_0 &= \text{angle} \left(pp_{0_{start}} - bp_{start}, pp_{0_{target}} - bp_{target} \right) \\
 axis_0 &= \text{normalise} \left(\text{cross} \left(\text{normalise} \left(pp_{0_{start}} - bp_{start} \right), \text{normalise} \left(pp_{0_{target}} - bp_{target} \right) \right) \right) \\
 matrix_0 &= \text{rotation_matrix}(axis_0, \alpha_0)
 \end{aligned}$$

- α_0 The angle between the relative vector $pp_{0_{start}} - bp_{start}$ and $pp_{0_{target}} - bp_{target}$
- $axis_0$ The unit vector perpendicular to the plane of $pp_{0_{start}} - bp_{start}$ and $pp_{0_{target}} - bp_{target}$
- $matrix_0$ The matrix that represents the rotation from $pp_{0_{start}} - bp_{start}$ to $pp_{0_{target}} - bp_{target}$

The matrix is applied as follows.

$$pp'_{target} = bp_{target} + matrix_0 * (pp_{start} - bp_{start})$$

- pp'_{target} The target position of the probe point if it would have been rotated as usual

Then this vector will be used to determine the final target position of the probe point.

$$pp_{target} = \begin{cases} pp_{target_1} & \text{if } |pp'_{target} - pp_{target_1}| < |pp'_{target} - pp_{target_2}| \\ pp_{target_2} & \text{if } |pp'_{target} - pp_{target_2}| < |pp'_{target} - pp_{target_1}| \end{cases}$$

CALCULATE THE TARGET POSITIONS OF THE MOVING POINTS

When the calculation of the target positions of the probe points is done, the target positions of the moving points will be calculated. The algorithm used for this is the same as in [CORRECT TARGET POSITION 2](#).

B. TRAJECTORY CALCULATION

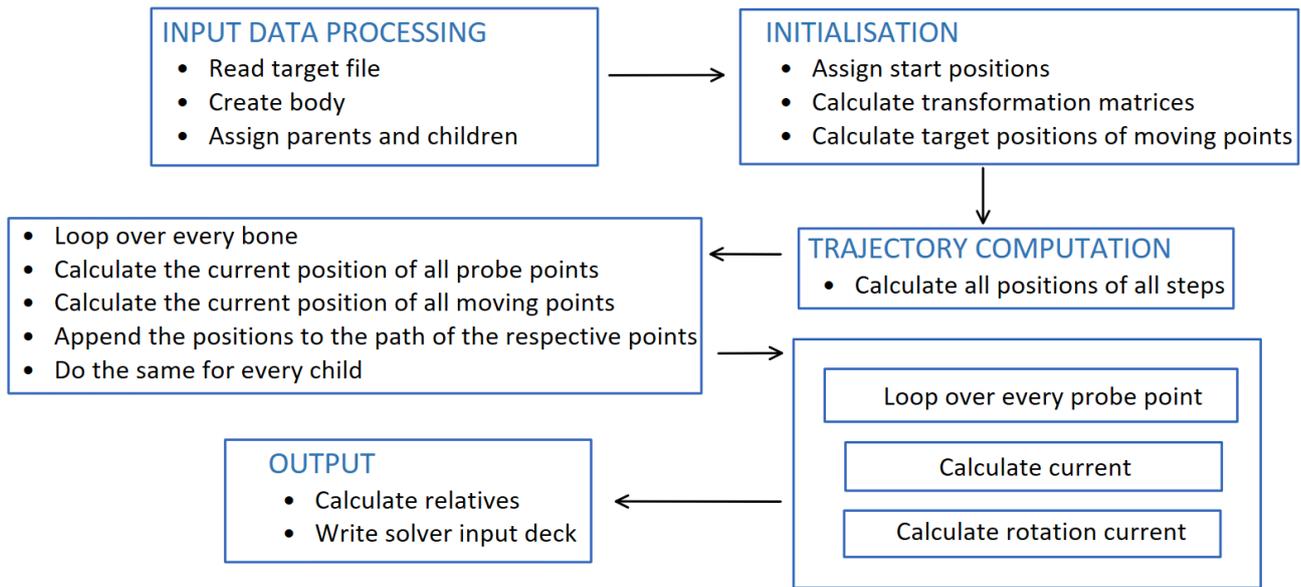
To position a HM smoothly, trajectories of multiple landmarks are calculated. The script that does this is the **positioning** script of the Positioning repository. The structure is similar to the Anthropometry Scaling. The main difference is that the moving points will be rotated towards the target positions step wise.

TERMS AND DEFINITIONS

The terms used in this section are the same as in the Anthropometry Scaling Section. There are just a few new terms.

- **Body**
This class holds a dictionary of bones and handles everything that should be applied to all bones.
- **Current**
This term refers to the position of a point in the current step.
- **Rotation** **current**
A rotation current is also a position of a point in the current step, but this one is used to calculate the current. In every step a point is rotated using a transformation matrix and then corrected to assure that the distances between the points stay the same. The rotation current is the current but without this correction. We need to store this because we need the rotation current of the last step to correct the current.
- **Last**
The position of the point in the last step
- **Path**
This is a list that stores all positions of all steps

OVERVIEW



INPUT DATA PROCESSING

First all positions of the target file are read and a body containing all bones gets constructed. Then the parents get their children assigned and the body is read for the computation.

INITIALISATION

Before the computation can start the initial positions need to be set first. Then the transformation matrices get calculated

CALCULATE TRANSFORMATION MATRICES

$$\alpha = \text{angle}(pp_{start} - bp_{start}, pp_{target} - bp_{target})$$

$$a = \text{normalise}\left(\text{cross}\left(\text{normalise}(pp_{start} - bp_{start}), \text{normalise}(pp_{target} - bp_{target})\right)\right)$$

$$T = \text{rotation_matrix}\left(a, \frac{\alpha}{n}\right)$$

- α The angle between $pp_{start} - bp_{start}$ and $pp_{target} - bp_{target}$
- a The unit vector perpendicular to the plane of $pp_{start} - bp_{start}$ and $pp_{target} - bp_{target}$
- n The number of steps
- T The rotation matrix that rotates $pp_{start} - bp_{start}$ to $pp_{target} - bp_{target}$ after n steps

This matrix gets calculated for every probe point and is then used to calculate the rotation current of every step. The moving points use the transformation matrix of the probe point 0.

CALCULATE TARGET POSITIONS OF MOVING POINTS

The calculation of the target position of a moving point is the same as **CORRECT TARGET POSITION 2** of the Anthropometry Scaling.

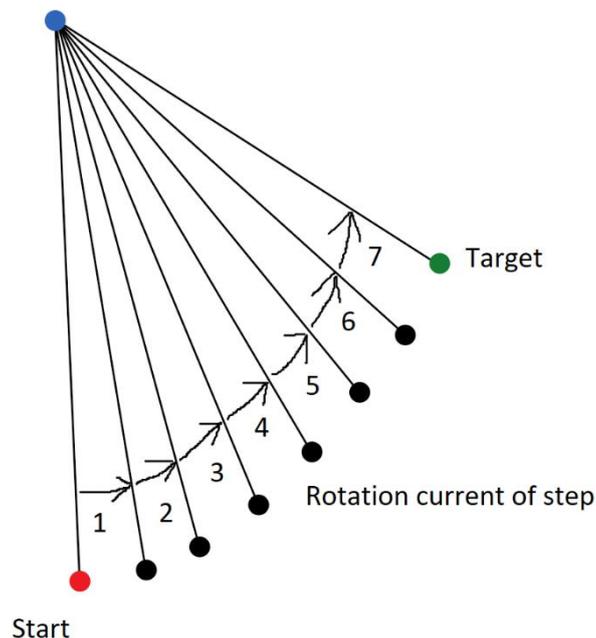
TARGET COMPUTATION

For probe points the rotation current gets calculated before the current and for moving points the rotation current gets calculated after the current. This means that the rotation current during the calculation of a current of a moving point is actually the rotation current of the last step.

CALCULATE ROTATION CURRENT

$$mp_{rotationcurrent} = bp_{current} + T * (mp_{rotationcurrent-1} - bp_{last})$$

- $mp_{rotationcurrent}$ The rotation current of the moving point that is getting calculated
- $bp_{current}$ The current of the base point
- T The transformation matrix
- $mp_{rotationcurrent-1}$ The rotation current of the last step
- bp_{last} The position of the base point in the last step



This formula rotates the moving point one step closer to the target. The position is then corrected so that the distances between the points stays the same.

CALCULATE CURRENT

PROBE POINTS

At first the current of probe point 0 is set to be equal to the rotation current. Then the current of probe point 0 and probe point 1 gets corrected using the algorithm of **CORRECT TARGET POSITION 1** of the Anthropometry Scaling. But instead of the target position the current should be used. Since there is no current for probe point 1 yet, rotation current should be used instead.

MOVING POINTS

When the current of the probe points has been calculated the current of the moving points gets calculated. This will be achieved using the algorithm of **CORRECT TARGET POSITION 2** of the Anthropometry Scaling. But instead of start last should be used and instead of target current should be used. Since there is no current of the moving point yet, rotation current should be used.

OUTPUT

CALCULATE RELATIVES

FE Solvers work with relative positions. So every path of every moving point has to be converted. The result is a list of points starting with a zero vector representing the start position.

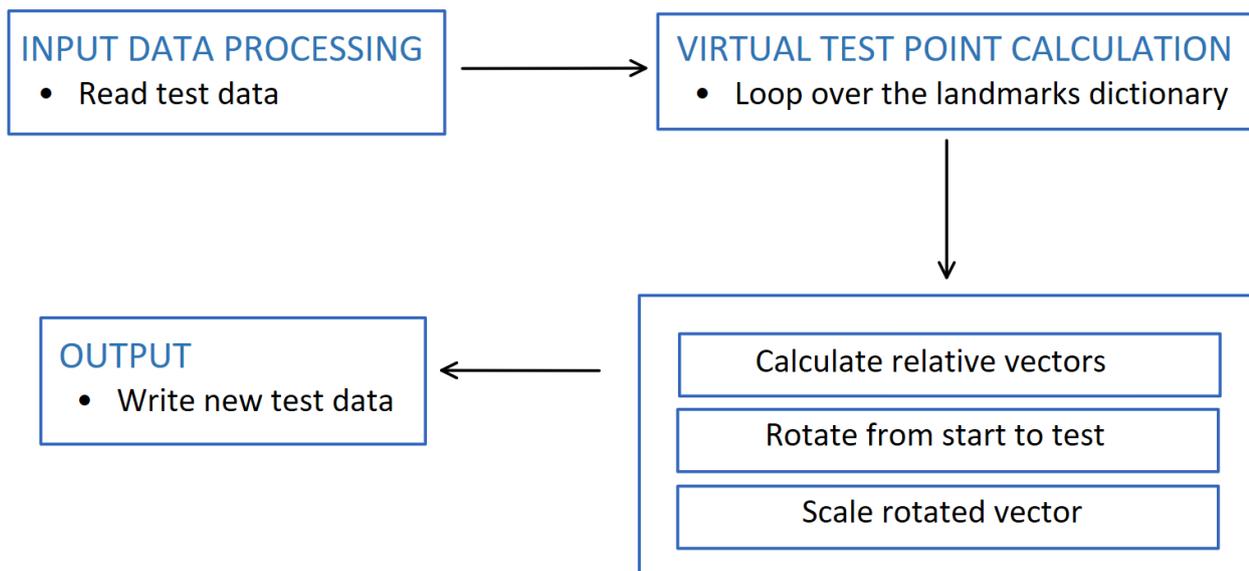
C. VIRTUAL TESTPOINTS

This section describes the process that calculates a test position of a landmark using two other landmarks of the same bone. The script that does this is the **add_virtual_test_landmarks** script of the Positioning repository.

TERMS AND DEFINITIONS

- **P1**
One of the points provided for the calculation. Namely the first one specified in the landmarks tuple.
- **P2**
One of the points provided for the calculation. Namely the second one specified in the landmarks tuple.
- **P3**
The point for which a test position should be calculated.

OVERVIEW



VIRTUAL TEST POINT CALCULATION

CALCULATE RELATIVE VECTORS

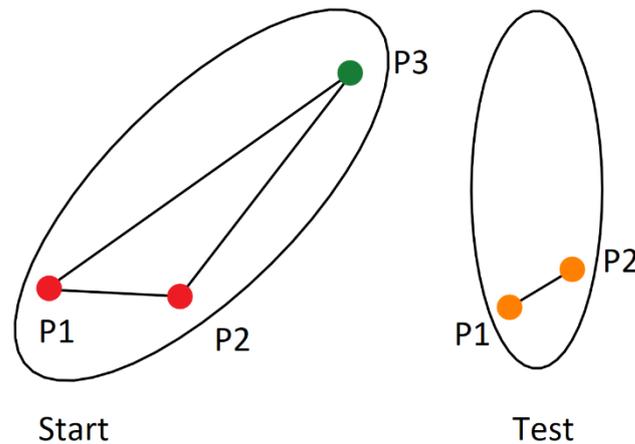
All mathematical operations are performed on relative vectors between the three Points. At first these relative vectors get calculated.

$$P_1P_{2_{test}} = P_{2_{test}} - P_{1_{test}}$$

$$P_1P_{2_{start}} = P_{2_{start}} - P_{1_{start}}$$

$$P_1P_{3_{start}} = P_{3_{start}} - P_{1_{start}}$$

- $P_{1_{test}}$ The test position of P1
- $P_{2_{test}}$ The test position of P2
- $P_{1_{start}}$ The start position of P1
- $P_{2_{start}}$ The start position of P2
- $P_{3_{start}}$ The start position of P3
- $P_1P_{2_{test}}$ The relative vector from the test position of P1 to the test position of P2
- $P_1P_{2_{start}}$ The relative vector from the start position of P1 to the start position of P2
- $P_1P_{3_{start}}$ The relative vector from the start position of P1 to the start position of P3



ROTATE FROM START TO TEST

Now the relative vectors will be rotated to fit the angles of the test data.

$$\alpha = \text{angle}(P_1P_{2_{start}}, P_1P_{2_{test}})$$

$$a = \text{normalise} \left(\text{cross} \left(\text{normalise}(P_1P_{2_{start}}), \text{normalise}(P_1P_{2_{test}}) \right) \right)$$

$$T = \text{rotation_matrix}(a, \alpha)$$

- α The angle between $P_1P_{2_{start}}$ and $P_1P_{2_{test}}$
- a The unit vector perpendicular to the plane of $P_1P_{2_{start}}$ and $P_1P_{2_{test}}$
- T The rotation matrix that rotates $P_1P_{2_{start}}$ to $P_1P_{2_{test}}$

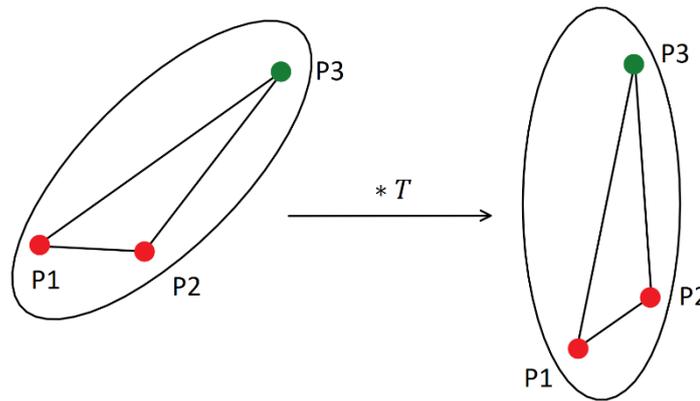
This rotation matrix is applied as follows.

$$P_1P_{2_{start_r}} = T * P_1P_{2_{start}}$$

$$P_1P_{3_{start_r}} = T * P_1P_{3_{start}}$$

$$P_2P_{3_{start_r}} = P_1P_{3_{start_r}} - P_1P_{2_{start_r}}$$

- $P_1P_{2_{start_r}}$ The relative vector $P_1P_{2_{start}}$ rotated to match the orientation of the test data
- $P_1P_{3_{start_r}}$ The relative vector $P_1P_{3_{start}}$ rotated to match the orientation of the test data
- $P_2P_{3_{start_r}}$ The relative vector from P2 to P3 in the orientation of the test data



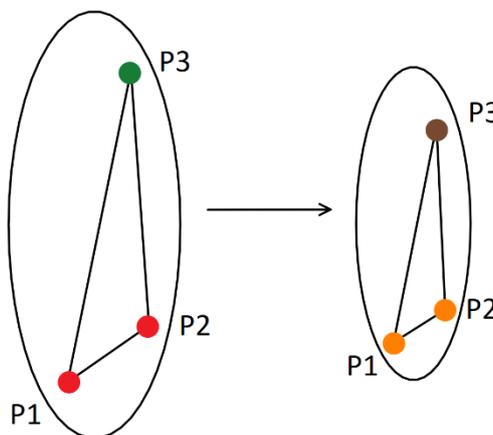
SCALE ROTATED VECTOR

Now the vectors are orientated correctly. The only thing that is left is the correct scaling of the vectors so that the test position can be determined.

$$L_1 = \frac{|P_1P_{2_{test}}|}{|P_1P_{2_{start_r}}|} * |P_2P_{3_{start_r}}|$$

$$P_{3_{test}} = P_{2_{test}} + \text{normalise}(P_2P_{3_{start_r}}) * L_1$$

- L_1 The approximate distance between $P_{2_{test}}$ and $P_{3_{test}}$
- $P_{3_{test}}$ The test position of P3



An assumption is made to scale the relative vector P_2P_{3start} . It is assumed that the relation between the lengths of the relative vectors of the start positions and those of the test positions stays the same

$$\frac{|P_1P_{2test}|}{|P_1P_{2start}|} = \frac{|P_2P_{3test}|}{|P_2P_{3start}|}$$

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