Version plan

* Version 0.1: Running with AMS 6.0.4 implying that overall structure is fixed
  + AMS 6.0.4
    1. ~~Fix reference bug (MEL bugreport) (MD/JDT)~~
    2. fix no-files handling (MD)
       - Error meassages are still confusing. Fx
* ERROR(OBJ.FILE1) : E:/U..s/MEL/G..b/a..p/M..l/JointsAndDriversOptimized.any(10) : FileReader.FileName : Problem with file : E:\Users\MEL\GitHub\hammelmodel\Tmp\S060T00D-euler-trunk.txt : The data file does not exist.
* ERROR(OBJ.FILE1) : E:/U..s/MEL/G..b/a..p/M..l/JointsAndDriversOptimized.any(10) : FileReader.FileName : Problem with file : E:\Users\MEL\GitHub\hammelmodel\Tmp\S060T00D-euler-trunk.txt : Reloading data from file found different number of elements on data lines. Data in file is ignored.
  + 1. Class Templates parser issues (JDT)
       - Dots in default argument values
       - Minus in (front off)template argument values
    2. SetView ClassOperation (JDT)
    3. OptStudy: (MD)
       - No DesVar handling
       - Better DesVar linkage (pointer, PickDown)
       - DesVar reference does not save/load properly (MEL bugreport)
       - Save as anyset
       - DesVar (marker) visualization (e.g. via DesVar::Active or DesStudyPtrArr set by studies)
    4. SetValue saving ( only save changed value)
    5. C3Dreader (MD)
       - Bug: Filters do not work when no analog data
       - Disable filters (+ warning) when single/too few samples (BUG)
  + AnyMoCap
    1. ~~Restructured model for readability and easy access~~
    2. ~~Separation of Trial/subject/lab specific data (MEL)~~
    3. ExtraDrivers included properly (depends on reference bug) (MEL)
    4. 2-step analysis with file-based data transfer
       - Remove muscles for faster kinematics (using double-load procedure) (MEL)
    5. StandingReference -> multiple linked trials (MEL)
       - Multiple marker protocols
       - Saving design vars when ParameterOpt exists
       - ~~Loading Design from previous trial ????~~
    6. Exclude markers in specific trials (weight, MechObjectExclude, ..) (MEL/MD)
* Version 0.2: (more ready to users without special introduction)
  + Documentation
    1. General document/slides
       - Parameter descriptions (systematic way)
    2. DocComments in code
  + Example
  + Test
    1. LTHT
    2. ETH
    3. Hammel
    4. TLEMsafe
    5. Vicon plugin
* Version 0.3: AMS 6.1 features
  + Make it unnecessary to consider ApproxVelAccPertubation in tStart and tEnd
    1. Make ApproxVelAccPertubation perturb only inside the interval
    2. Make Interpol functions work outside interval
* Version 1.0 (in AMMR 1.7, AMS 6.1):
  + Template model
* Version 2.0
  + GRF update
    1. GRF prediction
    2. Force plates from C3D reader
    3. Simple coupling between feet and already defined force plates (if needed, i.e. when not using GRF prediction)
  + Single model load and single study functionality

# List from meeting

~~Strike-through~~: When MEL has considered the item in the grouped lists below

Double strike through: When consider in version list above

* Exclude marker
* ~~Initial position of model (calculated using markers)~~
* ~~Initial segment scaling (calculated using markers)~~
* ~~Range of motion for joints (to assist kinematics)~~
* ~~GRF prediction~~
* ~~Model independent of windows folder structure~~
* ~~Model independent of AnyScript folder structure (position of HumanModel and EnvironmentModel, C3DFileData etc)~~
* ~~tStart/tEnd perturbation to allow calc of Vel and Acc in the inverse dynamic model~~
* Parameters of #define ?????
* Marker drop-out handling?????
* ~~Marker renaming vs. standard protocols~~
* ~~Single Model-load-step~~
* Separation of Trial/subject/lab specific data.
* ~~Fusion of AnyGait/Mocap~~
* Optimization of bodypart without marker ?????? (ST)
* Multiple calibration trials ( standing, dynamic reference)
* ~~Study to just visualize the C3D data~~
* Comparing trials ??????
* ~~Ea~~sy to read and understand model ( hiding vs. showing the complexity of model)
* ~~Residual reduction algorithm to segment parameters (mass/inertia)~~
* ~~More environment directly created from the c3d files.~~

# ======================================================== Structured in groups

**New model features (in anyscript)**

* GRF prediction
* Study to visualize markers
* Range of motion for joints to assist kinematic analysis
* Initial segment scaling / position from markers
* Residual reduction algorithm for segment parameters.
* Use default arguments in ClassTemplates
* Overwrite lowpass filter for individual markers
  + Could be added to existing CreateMarkerClassTemplates and with default argument to not be used.
* Create environments from C3D files

**New Featrures in AnyBody**

* Make it unnecessary to consider ApproxVelAccPerturb when setting tStart/tEnd
* Delay reading joint angles from files until it should be used.
* New way of transferring kinematics from the kinematics model to the inverse dynamic model
  + I have tried the OperationSetValue but it can’t point to output folders.
* Fix bug in ClassTemplate that prevents default values to contain ‘.’ (dots)
* Fix bug that prevent template arguments to start with minus ‘-‘

**Mocap model customization to specific usecases**

* Marker definition for many marker protocols.
* Fusion with AnyGait (and future concepts)
* Multiple calibrations trials (standing and dynamic reference)

**General structure/appearance of the model**

* Make it easier to understand the model ( especially for beginners)
* Model independent of windows folder structure
* Model independent of HumanModel/Environment model
* Separate Trial/subject/ lab specific data
* Fusion with AnyGait (and future concepts)

# Mocap model issues:

## Transferring joint angles:

Files: JointAngleOutputs.any, JointsAndDriversOptimized.any

Problems:

* Model does not load unless the files exist. This is a real problem with the combined model where both kinematics and inverse dynamics are in one model.
* Model has to be reloaded after joint angles are save to the file
* Adding new body parts or other things to the model is a pain.

## Model should work without specifying a special AnyMan.any file in the model model config

ERROR(SCR.PRS9) : C:/U..s/M..n/D..s/G..b/a..p/E..s/LTHT/LabSpecificData\_LTHT.any(24) : Defined at : C:/U..s/M..n/D..s/G..b/a..p/M..l/OptimizeAnthropometricsOnOffNew.any(21) : 'AnthroSegmentLengths' : Unresolved object

## Model fails when using the BM\_MANNEQUIN\_DRIVER\_DEFAULT ON

Might be because the muscles are include

Unexpected error in computational kernel

Constraint no. #0 in 'Main.HumanModel.BodyModel.Right.ShoulderArm.Mus.ArtificialRake.LinCom2Drv' above error tolerance 0.001000, error = 0.100000.

Constraint no. #0 in 'Main.HumanModel.BodyModel.Left.ShoulderArm.Mus.ArtificialRake.LinCom2Drv' above error tolerance 0.001000, error = 0.100000.

ERROR(OBJ.MCH.KIN3) : C:/Users/M..n/D..s/G..b/a..p/M..l/BaseModel.any(34) : KinematicStudy.InitialConditions : Kinematic analysis failed in time step 0

## BodyModel\_no\_muscles\_hack.any should not be used. It should be possible to exclude the muscles in a different way.

## Making class templates independent of hard-coded model structure.

Files: CreateMarkerDriverClassNew.any, OptimizeAnthropometricsOnOff.any

It should be possilble to write the following in

#class\_template Cr…iver (MarkerName,

MarkerPlacement,

WeightX=1, WeightY=1, WeightZ=1,

OptX="Off", OptY = "Off",OptZ="Off",

sRelOptScalingOnOff = "On",

PARAMETER\_OPT\_STUDY = ParameterIdentification,

C3D\_OBJECT = Main.AlternativeC3DFile,

BODY\_MODEL\_FOLDER = BodyModel

){

Dot “.” In default values are not allowed

## Filter specification should work when no analog data is included in the model

Model should load even if no markers are included and no segments are optimized.  
ERROR(OBJ3) : C:/U..s/M..n/D..s/G..b/a..p/B..l/BaseModel\_Both.any(23) : ParameterIdentification : Member expectations are not satisfied :

Members of class AnyDesVar or derived are expected in AnyOptKinStudy : 0 found, 1..Inf expected.